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errata

Reconciling the spectrum of Sagittarius A* with a two-temperature plasma model

Rohan Mahadevan

Nature 394, 651-653 (1998)

A misleading typographical error was introduced into the second sentence of the bold introductory paragraph of this Letter: the word "infrared" should be "inferred".

Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome sequence

S. T. Cole, R. Brosch, J. Parkhill, T. Garnier, C. Churcher, D. Harris, S. V. Gordon, K. Eiglmeier, S. Gas, C. E. Barry III, F. Tekaia, K. Badcock, D. Basham, D. Brown, T. Chillingworth, R. Connor, R. Davies, K. Devlin, T. Feltwell, S. Gentles, N. Hamlin, S. Holroyd, T. Hornsby, K. Jagels, A. Krogh, J. McLean, S. Moule, L. Murphy, K. Oliver, J. Osborne, M. A. Quail, M.-A. Rajandream, J. Rogers, S. Rutter, K. Seeger, J. Skelton, R. Squares, S. Squares, J. E. Sulston, K. Taylor, S. Whitehead & B. G. Barrell

Nature 393, 537-544 (1998)

As a result of an error during film output, Table 1 was published with some symbols missing. The correct version can be found at http://www.sanger.ac.uk and is reproduced again here (following pages).

Also, in Fig. 2, we incorrectly labelled Rv0649 as *fadD37* instead of *fabD2*. Two of the genes for mycolyl transferases were inverted: Rv0129c encodes antigen 85C and not 85C' as stated, whereas Rv3803c codes for the secreted protein MPT51 and not antigen 85C (*Infect. Immun.* **59,** 372–382; 1991); Rv3803c is now designated *fbpD*. We thank Morten Harboe and Harald Wiker for drawing this to our attention.

The sequence of Rv0746 from *M. bovis* BCG-Pasteur presented in Fig. 5b was incorrect and should have shown a 16-codon deletion instead of 29, as indicated here:

H37Rv	GSGAPGGAGGAGLWGTGGAGGAGGSSAGGGGAGGA	AGGAGGWLLGDGGAGGIGGAST
		:::::::::::::::::::::::::::::::::::::::
BCG	GSGAPGGAGGAAGLWGTGGA	-GGAGGWLLGDGGAGGIGGAST

Table 1. Functional classification of M	lvcobacterium tuberculosis	protein-coding genes

		netabolism	D 0004		superfamily	Rv3543c	fadE29	acyl-CoA dehydrogenase
A. Degrad		da.	Rv2831	echA16		Rv3560c	fadE30	acyl-CoA dehydrogenase
Rv0186	compound bglS	as β-αlucosidase	Rv3039c	echA17	superfamily enoyl-CoA hydratase/isomerase	Rv3562 Rv3563	fadE31 fadE32	acyl-CoA dehydrogenase acyl-CoA dehydrogenase
Rv2202c	cbhK	carbohydrate kinase	HV30390	echa ii	superfamily	Rv3564	fadE33	acyl-CoA dehydrogenase
Rv0727c	fucA	L-fuculose phosphate aldolase	Rv3373	echA18		Rv3573c	fadE34	acyl-CoA dehydrogenase
Rv1731	gabD1	succinate-semialdehyde dehydro-			superfamily, N-term	Rv3797	fadE35	acyl-CoA dehydrogenase
		genase	Rv3374	echA18'		Rv3761c	fadE36	acyl-CoA dehydrogenase
Rv0234c	gabD2	succinate-semialdehyde dehydro-			superfamily, C-term	Rv1175c	fadH	2,4-Dienoyl-CoA Reductase
Direct	galE1	genase	Rv3516	echA 19		Rv0855	far	fatty acyl-CoA racemase
Rv0501 Rv0536	galE1 galE2	UDP-glucose 4-epimerase UDP-glucose 4-epimerase	Rv3550	echA20	superfamily enoyl-CoA hydratase/isomerase	Rv1143 Rv1492	mcr mutA	α-methyl acyl-CoA racemase methylmalonyl-CoA mutase, β
Rv0620	galK	galactokinase	1100000	CUIAZU	superfamily	1101432	muuA	subunit
Rv0619	galT	galactose-1-phosphate uridylyl-	Rv3774	echA21	enoyl-CoA hydratase/isomerase	Rv1493	mutB	methylmalonyl-CoA mutase, α
		transferase C-term			superfamily			subunit
Rv0618	galT'	galactose-1-phosphate uridylyl-	Rv0859	fadA	β oxidation complex, β subunit	Rv2504c	scoA	3-oxo acid:CoA transferase, α sub-
Rv0993		transferase N-term	Rv0243	6100	(acetyl-CoA C-acetyltransferase)	Duoroo-	0	unit
HV0993	galU	UTP-glucose-1-phosphate uridylyl- transferase	Rv1074c	fadA2 fadA3	acetyl-CoA C-acetyltransferase acetyl-CoA C-acetyltransferase	Rv2503c	scoB	3-oxo acid:CoA transferase, β sub- unit
Rv3696c	glpK	ATP:glycerol 3-phosphotrans-	Rv1323	fadA4	acetyl-CoA C-acetyltransferase	Rv1136		probable carnitine racemase
	07	ferase			(aka thiL)	Rv1683		possible acyl-CoA synthase
Rv3255c	manA	mannose-6-phosphate isomerase	Rv3546	fadA5	acetyl-CoA C-acetyltransferase			
Rv3441c	mrsA	phosphoglucomutase or phospho-	Rv3556c	fadA6	acetyl-CoA C-acetyltransferase	4. Phosph		
Rv0118c	ova4	mannomutase	Rv0860	fadB	β oxidation complex, α subunit	Rv2368c	phoH	ATP-binding <i>pho</i> regulon
Rv3068c	oxcA pgmA	oxalyl-CoA decarboxylase phosphoglucomutase	Rv0468	fadB2	(multiple activities) 3-hydroxyacyl-CoA dehydroge-	Rv1095	phoH2	component PhoH-like protein
Rv3257c	pmmA	phosphomannomutase			nase	Rv3628	рра	probable inorganic pyrophos-
Rv3308	pmmB	phosphomannomutase	Rv1715	fadB3	3-hydroxyacyl-CoA dehydroge-			phatase
Rv2702	ppgK	polyphosphate glucokinase			nase	Rv2984	ppk	polyphosphate kinase
Rv0408	pta	phosphate acetyltransferase	Rv3141	fadB4	3-hydroxyacyl-CoA dehydroge-	5.5		
Rv0729 Rv1096	xylB -	xylulose kinase carbohydrate degrading enzyme	Rv1912c	fadB5	nase 3-hydroxyacyl-CoA dehydroge-	B. Energy 1. Glycoly:		em
1101030	-	carbonydrate degrading enzyme	11013120	IAUDS	nase	Rv1023	eno	enolase
2. Amino a	acids and	amines	Rv1750c	fadD1	acyl-CoA synthase	Rv0363c	fba	fructose bisphosphate aldolase
Rv1905c	aao	D-amino acid oxidase	Rv0270	fadD2	acyl-CoA synthase	Rv1436	gap	glyceraldehyde 3-phosphate dehy-
Rv2531c	adi	ornithine/arginine decarboxylase	Rv3561	fadD3	acyl-CoA synthase			drogenase
Rv2780	ald	L-alanine dehydrogenase	Rv0214 Rv0166	fadD4	acyl-CoA synthase	Rv0489	gpm mf/sA	phosphoglycerate mutase I
Rv1538c Rv1001	ansA arcA	L-asparaginase arginine deiminase	Rv1206	fadD5 fadD6	acyl-CoA synthase acyl-CoA synthase	Rv3010c Rv2029c	pfkA pfkB	phosphofructokinase I phosphofructokinase II
Rv0753c	mmsA	methylmalmonate semialdehyde	Rv0119	fadD7	acyl-CoA synthase	Rv0946c	pgi pgi	glucose-6-phosphate isomerase
		dehydrogenase	Rv0551c	fadD8	acyl-CoA synthase	Rv1437	pgk	phosphoglycerate kinase
Rv0751c	mmsB	methylmalmonate semialdehyde	Rv2590	fadD9	acyl-CoA synthase	Rv1617	pykA	pyruvate kinase
		oxidoreductase	Rv0099	fadD10	acyl-CoA synthase	Rv1438	tpi	triosephosphate isomerase
Rv1187	rocA	pyrroline-5-carboxylate dehydro-	Rv1550	fadD11	acyl-CoA synthase, N-term	Rv2419c	-	putative phosphoglycerate mutase
Rv2322c	rocD1	genase ornithine aminotransferase	Rv1549 Rv1427c	fadD11' fadD12	acyl-CoA synthase, C-term acyl-CoA synthase	Rv3837c	-	putative phosphoglycerate mutase
Rv2321c	rocD1	ornithine aminotransferase	Rv3089	fadD12	acyl-CoA synthase	2. Pyruvat	e dehvdro	genase
Rv1848	ureA	urease γ subunit	Rv1058	fadD14	acyl-CoA synthase	Rv2241	aceE	pyruvate dehydrogenase E1 com-
Rv1849	ureB	urease β subunit	Rv2187	fadD15	acyl-CoA synthase			ponent
Rv1850	ureC	urease α subunit	Rv0852	fadD16	acyl-CoA synthase	Rv3303c	lpdA	dihydrolipoamide dehydrogenase
Rv1853	ureD ureF	urease accessory protein	Rv3506	fadD17 fadD18	acyl-CoA synthase	Rv2497c	pdhA	pyruvate dehydrogenase E1 com-
Rv1851 Rv1852	ureG	urease accessory protein urease accessory protein	Rv3513c Rv3515c	fadD19	acyl-CoA synthase acyl-CoA synthase	Rv2496c	pdhB	ponent α subunit pyruvate dehydrogenase E1 com-
Rv2913c	-	probable D-amino acid	Rv1185c	fadD10	acyl-CoA synthase	11024000	punb	ponent β subunit
		aminohydrolase	Rv2948c	fadD22	acyl-CoA synthase	Rv2495c	pdhC	dihydrolipoamide acetyltransferase
Rv3551	-	possible glutaconate CoA-	Rv3826	fadD23	acyl-CoA synthase	Rv0462	-	probable dihydrolipoamide dehy-
		transferase	Rv1529	fadD24	acyl-CoA synthase			drogenase
3. Fatty ac	nide		Rv1521 Rv2930	fadD25 fadD26	acyl-CoA synthase acyl-CoA synthase	3. TCA cy	مام	
Rv2501c	accA1	acetyl/propionyl-CoA carboxylase,	Rv0275c	fadD27	acyl-CoA synthase	Rv1475c	acn	aconitate hydratase
200.0	400, 17	α subunit	Rv2941	fadD28	acyl-CoA synthase	Rv0889c	citA	citrate synthase 2
Rv0973c	accA2	acetyl/propionyl-CoA carboxylase,	Rv2950c	fadD29	acyl-CoA synthase	Rv2498c	citE	citrate lyase β chain
		α subunit	Rv0404	fadD30	acyl-CoA synthase	Rv1098c	fum	fumarase
Rv2502c	accD1	acetyl/propionyl-CoA carboxylase,	Rv1925	fadD31	acyl-CoA synthase	Rv1131	gltA1 gltA2	citrate synthase 3
Rv0974c	accD2	β subunit acetyl/propionyl-CoA carboxylase,	Rv3801c Rv1345	fadD32 fadD33	acyl-CoA synthase acyl-CoA synthase	Rv0896 Rv3339c	icd1	citrate synthase 1 isocitrate dehydrogenase
11000740	accor	β subunit	Rv0035	fadD34	acyl-CoA synthase	Rv0066c	icd2	isocitrate dehydrogenase
Rv3667	acs	acetyl-CoA synthase	Rv2505c	fadD35	acyl-CoA synthase	Rv0794c	lpdB	dihydrolipoamide dehydrogenase
Rv3409c	choD	cholesterol oxidase	Rv1193	fadD36	acyl-CoA synthase	Rv1240	mdh	malate dehydrogenase
Rv0222	echA1	enoyl-CoA hydratase/isomerase	Rv0131c	fadE1	acyl-CoA dehydrogenase	Rv2967c	pca	pyruvate carboxylase
Rv0456c	echA2	superfamily enoyl-CoA hydratase/isomerase	Rv0154c Rv0215c	fadE2 fadE3	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv3318 Rv3319	sdhA sdhB	succinate dehydrogenase A succinate dehydrogenase B
11704000	COMAZ	superfamily	Rv0231	fadE4	acyl-CoA denydrogenase acyl-CoA dehydrogenase	Rv3316	sanb sdhC	succinate denydrogenase B succinate dehydrogenase C sub-
Rv0632c	echA3	enoyl-CoA hydratase/isomerase	Rv0244c	fadE5	acyl-CoA dehydrogenase			unit
		superfamily	Rv0271c	fadE6	acyl-CoA dehydrogenase	Rv3317	sdhD	succinate dehydrogenase D sub-
Rv0673	echA4	enoyl-CoA hydratase/isomerase	Rv0400c	fadE7	acyl-CoA dehydrogenase	Durant		unit
Duceze	20h A.C	superfamily	Rv0672	fadE8	acyl-CoA dehydrogenase	Rv1248c	sucA	2-oxoglutarate dehydrogenase
Rv0675	echA5	enoyl-CoA hydratase/isomerase superfamily	Rv0752c	fadE9	(aka <i>aidB</i>) acyl-CoA dehydrogenase	Rv2215	sucB	dihydrolipoamide succinyltrans- ferase
Rv0905	echA6	enovl-CoA hydratase/isomerase	Rv0873	fadE10	acyl-CoA dehydrogenase	Rv0951	sucC	succinyl-CoA synthase β chain
		superfamily (aka eccH)	Rv0972c	fadE12	acyl-CoA dehydrogenase	Rv0952	sucD	succinyl-CoA synthase α chain
Rv0971c	echA7	enoyl-CoA hydratase/isomerase	Rv0975c	fadE13	acyl-CoA dehydrogenase			
D. 40==		superfamily	Rv1346	fadE14	acyl-CoA dehydrogenase	4. Glyoxyl		
Rv1070c	echA8	enoyl-CoA hydratase/isomerase	Rv1467c	fadE15	acyl-CoA dehydrogenase	Rv0467	aceA	isocitrate lyase
Rv1071c	echA9	superfamily enoyl-CoA hydratase/isomerase	Rv1679 Rv1934c	fadE16 fadE17	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv1915 Rv1916	aceAa aceAb	isocitrate lyase, α module isocitrate lyase, β module
11010710	COIINO	superfamily	Rv1933c	fadE18	acyl-CoA dehydrogenase	Rv1837c	glcB	malate synthase
Rv1142c	echA10		Rv2500c	fadE 19	acyl-CoA dehydrogenase	Rv3323c	gphA	phosphoglycolate phosphatase
		superfamily			(aka <i>mmgC</i>)			
Rv1141c	echA11	enoyl-CoA hydratase/isomerase	Rv2724c	fadE20	acyl-CoA dehydrogenase			te pathway
Dv4.470	och A +C	superfamily	Rv2789c	fadE21	acyl-CoA dehydrogenase	Rv1445c	devB	glucose-6-phosphate 1-dehydro-
Rv1472	echA12	enoyl-CoA hydratase/isomerase superfamily	Rv3061c Rv3140	fadE22 fadE23	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv1844c	gnd	genase 6-phosphogluconate dehydroge-
Rv1935c	echA13	enoyl-CoA hydratase/isomerase	Rv3140	fadE24	acyl-CoA denydrogenase	11010440	grid	nase (Gram –)
		superfamily	Rv3274c	fadE25	acyl-CoA dehydrogenase	Rv1122	gnd2	6-phosphogluconate dehydroge-
Rv2486	echA14	enoyl-CoA hydratase/isomerase	Rv3504	fadE26	acyl-CoA dehydrogenase		-	nase (Gram +)
Duggzo	och A + F	superfamily	Rv3505	fadE27	acyl-CoA dehydrogenase	Rv1446c	opcA	unknown function, may aid
Rv2679	echA15	enoyl-CoA hydratase/isomerase	Rv3544c	fadE28	acyl-CoA dehydrogenase			G6PDH

Rv2436 Rv1408 Rv2465c	rbsK rpe rpi	ribokinase ribulose-phosphate 3-epimerase phosphopentose isomerase	Rv3250c	rubB	rubredoxin B idoreductases and oxygenases 171	Rv1878 Rv2860c Rv2918c	glnA3 glnA4 glnD	probable glutamine synthase proable glutamine synthase uridylyltransferase
Rv1448c		transaldolase	7. MISCEIR	aneous ox	idoreduciases and oxygenases 171	Rv2221c	gInE	glutamate-ammonia-ligase
Rv1449c		transketolase	8. ATP-pro	oton motiv	e force	11022210	yııı_	adenyltransferase
Rv1121	zwf	glucose-6-phosphate 1-dehydro-	Rv1308	atpA	ATP synthase α chain	Rv3859c	gltB	ferredoxin-dependent glutamate
Rv1447c	zwf2	genase glucose-6-phosphate 1-dehydro-	Rv1304 Rv1311	atpB atpC	ATP synthase a chain ATP synthase ε chain	Rv3858c	gltD	synthase small subunit of NADH-dependent
11014470	24/12	genase	Rv1310	atpD	ATP synthase β chain		-	glutamate synthase
			Rv1305	atpE	ATP synthase c chain	Rv3704c	gshA	possible γ-glutamylcysteine syn-
6. Respira			Rv1306	atpF	ATP synthase b chain	Du0407a	nro1	thase
a. aerobio Rv0527	ccsA	cytochrome c-type biogenesis	Rv1309 Rv1307	atpG atpH	ATP synthase γ chain ATP synthase δ chain	Rv2427c Rv2439c	proA proB	γ-glutamyl phosphate reductase glutamate 5-kinase
TIVOOLI	003/1	protein	1101007	uipi i	741 Synthase o onam	Rv0500	proC	pyrroline-5-carboxylate reductase
Rv0529	ccsB	cytochrome c-type biogenesis	C. Central	l intermedi	iary metabolism		,	
	_	protein	1. Genera			Asparta		
Rv1451	ctaB	cytochrome c oxidase assembly	Rv2589	gabT	4-aminobutyrate aminotransferase	Rv3708c	asd	aspartate semialdehyde dehydro-
Rv2200c	ctaC	factor cytochrome <i>c</i> oxidase chain II	Rv3432c Rv1832	gadB gcvB	glutamate decarboxylase glycine decarboxylase	Rv3709c	ask	genase aspartokinase
Rv3043c		cytochrome c oxidase chairi ii	Rv1826	gcvB gcvH	glycine decarboxylase glycine cleavage system H protein	Rv2201	asn asnB	asparagine synthase B
		peptide I	Rv2211c	gcvT	T protein of glycine cleavage	Rv3565	aspB	aspartate aminotransferase
Rv2193	ctaE	cytochrome c oxidase poly-			system	Rv0337c	aspC	aspartate aminotransferase
D 1510		peptide III	Rv1213	glgC	glucose-1-phosphate adenylyl-	Rv2753c	dapA	dihydrodipicolinate synthase
Rv1542c Rv2470	glbN glbO	hemoglobin-like, oxygen carrier hemoglobin-like, oxygen carrier	Rv3842c	alnO1	transferase glycerophosphoryl diester phos-	Rv2773c Rv1202	dapB dapE	dihydrodipicolinate reductase
Rv2249c		glycerol-3-phosphate dehydroge-	NV36420	glpQ1	phodiesterase	HV1202	uaμ⊑	succinyl-diaminopimelate desuc- cinylase
	3.5-1	nase	Rv0317c	glpQ2	glycerophosphoryl diester phos-	Rv2141c	dapE2	ArgE/DapE/Acy1/Cpg2/yscS
Rv3302c	glpD2	glycerol-3-phosphate dehydroge-			phodiesterase			family
		nase	Rv3566c	nhoA	N-hydroxyarylamine o-acetyltrans-	Rv2726c	dapF	diaminopimelate epimerase
Rv0694	IIdD1	L-lactate dehydrogenase	Dunter	nnt A A	ferase	Rv1293	lysA mat4	diaminopimelate decarboxylase
Rv1872c	IIdD2	(cytochrome) L-lactate dehydrogenase	Rv0155	pntAA	pyridine transhydrogenase sub- unit α1	Rv3341 Rv1079	metA metB	homoserine <i>o</i> -acetyltransferase cystathionine γ-synthase
Rv1854c		probable NADH dehydrogenase	Rv0156	pntAB	pyridine transhydrogenase sub-	Rv3340	metC	cystathionine β-lyase
Rv3145	nuoA	NADH dehydrogenase chain A			unit a2	Rv1133c	metE	5-methyltetrahydropteroyltrigluta-
Rv3146	nuoB	NADH dehydrogenase chain B	Rv0157	pntB	pyridine transhydrogenase			mate-homocysteine methyltrans-
Rv3147	nuoC	NADH dehydrogenase chain C	Design	····	subunit β	District	ma -41 1	ferase
Rv3148 Rv3149	nuoD nuoE	NADH dehydrogenase chain D NADH dehydrogenase chain E	Rv1127c	ppdK	similar to pyruvate, phosphate dikinase	Rv2124c	metH	5-methyltetrahydrofolate-homo- cysteine methyltransferase
Rv3149	nuoE	NADH denydrogenase chain F			dikillase	Rv1392	metK	S-adenosylmethionine synthase
Rv3151	nuoG	NADH dehydrogenase chain G	2. Glucone	eogenesis		Rv0391	metZ	o-succinylhomoserine sulfhy-
Rv3152	nuoH	NADH dehydrogenase chain H	Rv0211	pckA	phosphoenolpyruvate carboxy-			drylase
Rv3153	nuol	NADH dehydrogenase chain I			kinase	Rv1294	thrA	homoserine dehydrogenase
Rv3154	nuoJ	NADH dehydrogenase chain J	Rv0069c	sdaA	L-serine dehydratase 1	Rv1296 Rv1295	thrB thrC	homoserine kinase
Rv3155 Rv3156	nuoK nuoL	NADH dehydrogenase chain K NADH dehydrogenase chain L	3. Sugar r	nucleotides		UA15	inic	homoserine synthase
Rv3157	nuoL	NADH denydrogenase chain M	Rv1512	epiA	nucleotide sugar epimerase	3. Serine f	amilv	
Rv3158	nuoN	NADH dehydrogenase chain N	Rv3784	epiB	probable UDP-galactose 4-	Rv0815c	cysA2	thiosulfate sulfurtransferase
Rv2195	qcrA	Rieske iron-sulphur component of			epimerase	Rv3117	cysA3	thiosulfate sulfurtransferase
Diratos	e arD	ubiQ-cytB reductase	Rv1511	gmdA	GDP-mannose 4,6 dehydratase	Rv2335	cysE	serine acetyltransferase
Rv2196	qcrB	cytochrome β component of <i>ubiQ-cytB</i> reductase	Rv0334	rmlA	glucose-1-phosphate thymidyl- transferase	Rv0511	cysG	uroporphyrin-III c-methyltrans- ferase
Rv2194	qcrC	cytochrome b/c component of	Rv3264c	rmlA2	glucose-1-phosphate thymidyl-	Rv2847c	cysG2	multifunctional enzyme, siroheme
	•	ubiQ-cytB reductase			transferase		,	synthase
,			Rv3464	rmlB	dTDP-glucose 4,6-dehydratase	Rv2334	cysK	cysteine synthase A
b. anaero. Rv2392		3'-phosphoadenylylsulfate (PAPS)	Rv3634c Rv3468c	rmlB2 rmlB3	dTDP-glucose 4,6-dehydratase	Rv1336 Rv1077	cysM cysM2	cysteine synthase B cystathionine β-synthase
1102092	cysH	reductase	Rv3465	rmIC	dTDP-glucose 4,6-dehydratase dTDP-4-dehydrorhamnose	Rv0848	cysM3	putative cysteine synthase
Rv2899c	fdhD	affects formate dehydrogenase-N			3,5-epimerase	Rv1093	glyA	serine hydroxymethyltransferase
Rv2900c	fdhF	molybdopterin-containing oxidore-	Rv3266c	rmlD	dTDP-4-dehydrorhamnose	Rv0070c	glyA2	serine hydroxymethyltransferase
D		ductase		, .	reductase	Rv2996c	serA	D-3-phosphoglycerate dehydro-
Rv1552	frdA	fumarate reductase flavoprotein subunit	Rv0322	udgA	UDP-glucose dehydrogenase/GDP-mannose 6-	Rv0505c	serB	genase probable phosphoserine phos-
Rv1553	frdB	fumarate reductase iron sulphur			dehydrogenase	11000000	3610	phatase
		protein	Rv3265c	wbbL	dTDP-rhamnosyl transferase	Rv3042c	serB2	C-term similar to phosphoserine
Rv1554	frdC	fumarate reductase 15kD anchor	Rv1525	wbbL2	dTDP-rhamnosyl transferase	_	_	phosphatase
Distree	feed D	protein	Rv3400	-	probable β-phosphoglucomutase	Rv0884c	serC	phosphoserine aminotransferase
Rv1555	frdD	fumarate reductase 13kD anchor protein	4. Amino	sugars		4. Aromati	c amino s	acid family
Rv1161	narG	nitrate reductase α subunit	Rv3436c		glucosamine-fructose-6-	4. Aloman Rv3227	aroA	3-phosphoshikimate
Rv1162	narH	nitrate reductase β chain		J	phosphate aminotransferase			1-carboxyvinyl transferase
Rv1164	narl	nitrate reductase γ chain	F 0 · ·			Rv2538c	aroB	3-dehydroquinate synthase
Rv1163 Rv1736c	narJ narX	nitrate reductase δ chain	5. Sulphui			Rv2537c	aroD aroE	3-dehydroquinate dehydratase
Rv2391	narX nirA	fused nitrate reductase probable nitrite reductase/sulphite	Rv0711 Rv3299c	atsA atsB	arylsulfatase proable arylsulfatase	Rv2552c Rv2540c	aroE aroF	shikimate 5-dehydrogenase chorismate synthase
. 142001		reductase	Rv0663	atsD	proable aryisulfatase	Rv2178c	aroG	DAHP synthase
Rv0252	nirB	nitrite reductase flavoprotein	Rv3077	atsF	proable arylsulfatase	Rv2539c	aroK	shikimate kinase I
Rv0253	nirD	probable nitrite reductase small	Rv0296c	atsG	proable arylsulfatase	Rv3838c	pheA	prephenate dehydratase
		subunit	Rv3796 Rv1285	atsH	proable arylsulfatase ATP:sulphurylase subunit 2	Rv1613 Rv1612	trpA trpB	tryptophan synthase α chain tryptophan synthase β chain
c. Flectro	n transport	•	Rv1285	cysD cysN	ATP:sulphurylase subunit 2 ATP:sulphurylase subunit 1	Rv1612	trpB trpC	indole-3-glycerol phosphate
Rv0409	ackA	acetate kinase	Rv2131c	cysQ	homologue of M.leprae cysQ			synthase
Rv1623c		cytochrome bd-ll oxidase	Rv3248c	sahH	adenosylhomocysteinase	Rv2192c	trpD	anthranilate phosphoribosyltrans-
F		subunit I	Rv3283	sseA	thiosulfate sulfurtransferase	B		ferase
Rv1622c	cydB	cytochrome d ubiquinol oxidase	Rv2291	sseB	thiosulfate sulfurtransferase	Rv1609	trpE	anthranilate synthase
Rv1620c	cydC	subunit II ABC transporter	Rv3118 Rv0814c	sseC sseC2	thiosulfate sulfurtransferase thiosulfate sulfurtransferase	Rv2386c	trpE2	component l anthranilate synthase
Rv1621c		ABC transporter	Rv3762c	-	probable alkyl sulfatase		"PLL	component I
Rv2007c	fdxA	ferredoxin			,	Rv3754	tyrA	prephenate dehydrogenase
Rv3554	fdxB	ferredoxin	D. Amino		rnthesis			
Rv1177	fdxC	ferredoxin 4Fe-4S	1. Glutam			5. Histidin		a la constitución de la constitu
Rv3503c Rv3029c		probable ferredoxin electron transfer flavoprotein	Rv1654 Rv1652	argB argC	acetylglutamate kinase N-acetyl-γ-glutamyl-phosphate	Rv1603	hisA	phosphoribosylformimino-5- aminoimidazole carboxamide
1100230	IMA	β subunit	1101002	aryo	reductase			ribonucleotide isomerase
Rv3028c	fixB	electron transfer flavoprotein α	Rv1655	argD	acetylornithine aminotransferase	Rv1601	hisB	imidazole glycerol-phosphate
		subunit	Rv1656	argF	ornithine carbamoyltransferase			dehydratase
Rv3106	fprA	adrenodoxin and NADPH ferre-	Rv1658	argG	arginosuccinate synthase	Rv1600	hisC	histidinol-phosphate aminotrans-
Rv0886	fprB	doxin reductase ferredoxin, ferredoxin-NADP	Rv1659 Rv1653	argH argJ	arginosuccinate lyase glutamate N-acetyltransferase	Rv3772	hisC2	ferase histidinol-phosphate aminotrans-
		reductase	Rv2220	glnA1	glutamine synthase class I		OL	ferase
Rv3251c	rubA	rubredoxin A	Rv2222c	glnA2	glutamine synthase class II	Rv1599	hisD	histidinol dehydrogenase
								-

Rv2122c hisl phosphoribosyl-AMP cyclohydro-lase Rv3052c nrd Nrdl/Yas	nt of NrdEF system o//rmaA family	rin biosynthesis rin biosynthesis e kinase exobutanoate hyltransferase alanine ligase decarboxylase te 5'-phosphate
Iase Probable phosphoribosyl-AMP 1,6 Provable phosphoribosyl-AMP 1,6 Provable phosphoribosyl-AMP 1,6 Provable thy probable phosphoribosyl-AMP 1,6 Provable phosphoribosyl-AMP	D/YmaA family te kinase te synthase otide reductase, class II synthase otide reductase, class II e synthase I e synthase ot the synthase I e synthas	rin biosynthesis rin biosynthesis rin biosynthesis rin biosynthesis rin biosynthesis rity to <i>E. coli</i> MoaA rity to <i>E. coli</i> MoeB rolved in rin biosynthesis rin biosynthesis rin biosynthesis e kinase exxobutanoate hyltransferase alanine ligase decarboxylase ue 5'-phosphate synthase oxidase ucleotide pyrophos- nthesis, pyrimidine thylpyrimidine kinase nthesis, thiazole
RV0114 - similar to HisB RV0764 thyA thymidyli Rv07570 nrdZ ribonucie RV3752c - probable amina acid family Rv1599 /i/A threonine dearminase acetolactate synthase large subunit Rv0313c add probable Rv33030 i/νB acetolactate synthase large subunit Rv0313c add probable Rv33000 i/νB acetolactate synthase large subunit Rv0378c i/νB acetolactate synthase large subunit Rv0313c add probable Rv33000 i/νB acetolactate synthase large subunit Rv0313c add probable Rv33000 i/νB acetolactate synthase large subunit Rv0378 deoC probable Rv3307 deoD probable Rv0189c i/νD dihydroxy-acid dehydratase Rv2310c i/νE branched-chain-amino-acid transaminase phosphosphosphosphosphosphosphosphosphos	te synthase to thick reductase, class II synthase to the synthase to the reductase, class II synthase to the reductase, control to the reductase to the reduct	rin biosynthesis rin biosynthesis rin biosynthesis rin biosynthesis rin biosynthesis rin biosynthesis polyed in rin biosynthesis e kinase excobutanoate pyttransferase alanine ligase edecarboxylase e 5'-phosphate e 5'-phosphate e synthase exidase ucleotide pyrophosphatesis, pyrimidine thylpyrimidine kinase enthesis, thiazole
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8. Pyruvate family Rv3423c alr alanine racemase 7. Branched amino acid family Rv1559 i/vA threonine deaminase 8. Rv3003c ilvB acetolactate synthase I large subunit Rv3470c ilvB2 acetolactate synthase large subunit Rv3001c ilvC ketol-acid reductoisomerase Rv0180c ilvD dilvd branched-chain-amino-acid transaminase Rv210c ilvC branched-chain-amino-acid transaminase Rv210c ilvV acetolactate synthase II small subunit Rv3710 leuA cisopropylmalate dehydrogenase Rv298c leuC 3-isopropylmalate dehydratase Rv298c leuC 3-isopropylmalate deh	e exidine/deoxycytidylate e RV3338c moeW RV1681 moeX RV1385c moeY RV3355c moeZ RV3206c moeZ molybdopter partoate-9-aspartate 1-busylater-9-aspartate 1-busylater-9	rin biosynthesis rin biosynthesis rin biosynthesis rin biosynthesis rin biosynthesis rin biosynthesis e kinase exobutanoate hyptransferase alanine ligase decarboxylase bi-phosphate e 5'-phosphate e 5'-
R. Pyruvate family RN34230 alr alanine racemase 7. Branched amino acid family RN3599 i/vA threonine deaminase RN30030 iivB acetolactate synthase I large subunit RN3470c iivB2 acetolactate synthase large subunit RN3011c iivC ketol-acid reductoisomerase RN3001c iivC iivE acetolactate synthase large subunit RN3001c iivC iivE branched-chain-amino-acid transaminase RN2210c iivE branched-chain-amino-acid transaminase RN2210c iivV acetolactate synthase II small subunit RN3002c iivN acetolactate synthase I small subunit RN3710 ieuA acisopropylmalate dehydrogenase RN2995c ieuB 3-isopropylmalate dehydratase RN2998c ieuC 3-isopropylmalate dehydratase RN2998c ieuB 3-isopropylmalate dehydratase RN2988c ieuB 3-isoprop	RV1681 moeX weak similar moeX hucleotides adenosine deaminase phosphoribosyltrans-phorphate aldolase purine nucleoside phosphoribosyltransferase incosine-uridine nucleoside hydrolase phosphoribosyltransferase incosine-uridine nucleoside hydrolase plase from Pnp/MtaP phoribosyltransferase incosine-uridine nucleoside reactions adenylate kinase pleoxyguanosine ate hydrolase ing protein LepA lesopentenylpyrophosisferase elighosphate kinase eloiholding protein synthase I posthetic groups and settle from phosphored thiamine synthase I probable this phate kinase osthetic groups and settle from Pnp/MtaP phoribosyltransferase incosine-uridine phoribosyltransferase phoribosyltransferase ing protein LepA lesopentenylpyrophosisferase elighosphate kinase osthetic groups and settle from Pnp/MtaP phoribosyltransferase phoribosyltransferase phoribosyltransferase phoribosyltransferase phoribosyltransferase phoribosyltransferase phoribosyltransferase phoribosyltransferase protein settle phoribosyltransferase ph	rity to E. coli MoaA rity to E. coli MoaA rity to E. coli MoaB rolved in rin biosynthesis rin biosynthesis e kinase excobutanoate hyltransferase alanine ligase decarboxylase e 5'-phosphate e 5'-phosphate e synthase exidase ucleotide pyrophosnthesis, pyrimidine thylpyrimidine kinase nthesis, thiazole
RV3423c alr alanine racemase 7. Branched amino acid family RV1559 ilvA threonine deaminase RV3003c ilvB acetolactate synthase large subunit RV3010c ilvB2 acetolactate synthase large subunit RV3011c ilvC ketol-acid reductoisomerase RV2110c ilvE branched-chain-amino-acid transaminase RV2210c ilvV acetolactate synthase large subunit RV3509c ilvX probable acetohydratase large subunit RV3509c ilvX probable acetohydroxyacid synthase large subunit RV2997c leuB 3-isopropylmalate dehydratase large subunit RV2987c leuD 3-isopropylmalate dehydratase large subunit RV298	Rv1355c moe Y moez probably inv molybdopter pantoate-β-c myridoxamin oxidase molydase finade molybdopter pantoate-β-c myridoxamin oxidase finade molybdopter pantoate-β-c myridoxamin oxidase finade molybdopter pantoate-β-c molybdopter pantoate-β-c myridoxamin oxidase finade molybdopter pantoate-β-c myridoxamin oxidase finade molybdopter pantoate-β-c molybdopter pantoate-β-c myridoxamin oxidase finade molybdopter pantoate-β-c molybdopter pantoate-β-c molybdopter pantoate-β-c myridoxamin oxidase finade molybdopter pantoate-β-c molybdopter pantoate-β-c molybdopter pantoate-β-c myridoxamin oxidase finade molybdopter pantoate-β-c myridoxamin oxidase finade molybdopter pantoate-β-c myridoxamin oxidase finade mucleotide finade f	rity to <i>E. coli</i> MoeB olved in rin biosynthesis rin biosynthesis e kinase excobutanoate hyptransferase alanine ligase decarboxylase e 5'-phosphate e 5'-phosphate e synthase oxidase ucleotide pyrophosinthesis, pyrimidine thylpyrimidine kinase nthesis, thiazole
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unit ketol-acid reductoisomerase dihydroxy-acid dehydratase Rv2210c ilvC branched-chain-amino-acid transaminase Rv3307 deoD probable phosphor phor probable phosphor phosphor phosphor identification phosphor phosphor indicates phosphor probable phosphor probable phosphor probable phosphor probable phosphor probable phosphor probable phosphor indicates phosphor	se-phosphate aldolase ourine nucleoside phosphosyltransferase inosine-uridine nucleoside hydrolase ylase from Pnp/MtaP cleotide reactions adenylate kinase deoxyguanosine ate hydrolase ing protein LepA -isopentenylpyrophosisferase e diphosphate kinase e eliphosphate kinase isosthetic groups and evaluate for thick in the probable this synthase I sosthetic groups and expressions in the purity of the probable this phate kinase out the pour interest out the part of the part	oxobutanoate nyltransferase alanine ligase decarboxylase ue 5'-phosphate synthase oxidase ucleotide pyrophos- nthesis, pyrimidine thylpyrimidine kinase nthesis, thiazole
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Rv2210c ilvE branched-chain-amino-acid transaminase Rv3624c hpt probable phospho phospho phospho phospho phospho probable acetolactate synthase II Rv3393 iunH probable phospho phospho probable phosphoribosylaminase Rv3509c ilvX probable acetohydroxyacid synthase I large subunit Rv3390 ilvX probable acetohydroxyacid synthase I large subunit Rv3390c upp uracil phosphoribosyltranse family 2 Rv2995c leuB 3-isopropylmalate dehydrogenase large subunit Sisopropylmalate dehydrogenase large subunit 5. Miscellaneous nucleoside/n Rv0733 adk probable preferrin. Rv2987c leuB 3-isopropylmalate dehydratase small subunit 5. Miscellaneous nucleoside/n Rv0733 adk probable probable proferrin. Rv2987c leuD 3-isopropylmalate dehydratase small subunit Rv2364c bex GTP-bim family Rv2987c leuD 3-isopropylmalate dehydratase small subunit Rv244dc bex GTP-bim family F. Polyamine synthesis Rv24601 spE spermidine synthase Rv2440c lepA GTP-bim family F. Purines, pyrimidines, nucleosides and nucleotides 1. Purine ribonucleotide biosynthesis <	nypoxanthine-guanine bosyltransferase inosine-uridine nucleoside hydrolase ylase from Pnp/MtaP phoribosyltransferase cleotide reactions adenylate kinase ing protein LepA risopentenylpyrophosusferase e diphosphate kinase e diphosphate kinase isopentenylpyrophosusferase e diphosphate kinase isopentenylpyrophosphate kinase isopentenylpyropho	decarboxylase synthase oxidase ucleotide pyrophos- nthesis, pyrimidine thylpyrimidine kinase nthesis, thiazole
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RV3002c i/W acetolactate synthase small subunit RV3509c i/wX probable acetohydroxyacid synthase large subunit RV3710 leuA α-isopropyl malate synthase RV2995c leuB 3-isopropylmalate dehydrogenase RV2988c leuC 3-isopropylmalate dehydratase large subunit RV2987c leuD 3-isopropylmalate dehydratase small subunit RV2601 speE spermidine synthase RV2404c lepA GTP-bim family RV277c miaA tRNA 8(2 phate tra hy2727c miaA tr	nucleoside hydrolase plase from Pnp/MtaP phoribosyltransferase cleotide reactions adenylate kinase ping protein of Era/ThdF kinase deoxyguanosine ate hydrolase ging protein LepA risopentenylpyrophos- isopentenylpyrophos- isferase e diphosphate kinase botheric groups and RV2607 pdxH pyridoxamin oxidase 7. Pyridine nucleotide RV1595 nadB L-aspartate adioxidate-niphatase RV0423c thiC hiamine syr moiety thiamine syr moiety synthase I RV2977c thiL probable thia phate kinase osthetic groups and	synthase oxidase uoleotide pyrophos- nthesis, pyrimidine thylpyrimidine kinase nthesis, thiazole
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large subunit RV2987c leuD 3-isopropylmalate dehydratase small subunit Sisopropylmalate dehydratase small subunit RV2987c leuD 3-isopropylmalate dehydratase small subunit Sisopropylmalate dehydratase small subunit RV2344c dgt probable triphosph RV23610 speE spermidine synthase RV2404c lepA GTP-bim RV2727c miaA tRNA 8(2 phate tra miaA tRNA 8(2 phate tra miaA) translated biosynthesis RV1389 gmk putative guanylate kinase RV2440c obg Obg GTI RV3396c guaA GMP synthase RV3430c guaB1 inosine-5'-monophosphate dehydrogenase reversible sinosine-5'-monophosphate dehydroge	ing protein of Era/ThdF kinase kinase deoxyguanosine ate hydrolase ing protein LepA lisopentenylpyrophos- isferase e biphosphate kinase binding protein synthase I sosthetic groups and Rv0423c thiC 8. Thiamine how thiamine how thiamine how this this how thi	nthesis, pyrimidine thylpyrimidine kinase nthesis, thiazole
Rav2987c leuD 3-isopropylmalate dehydratase small subunit Rv1712 cmk probable triphospherically a comboxylase Rv2001 speE spermidine synthase Rv2404c lepA GTP-bin mica RtNA 8(combox) Rv2797c mica RtNA 8(combox) Rv2440c lepA GTP-bin mica Rv2440c lepA GTP-bin m	kinase Rv0423c thiC thiamine syr moiety sleoxyguanosine ate hydrolase 8. Thiamine spring protein LepA Rv0422c thiD phosphomet sisperase 9 cliphosphate kinase 9 cliphosphate kinase 1 Rv2977c thiL probable this phate kinase 0 sosthetic groups and 1 Rv041vi	thylpyrimidine kinase nthesis, thiazole
small subunit E. Polyamine synthesis RV2601 speE spermidine synthase RV2601 speE spermidine synthase RV277c miaA RV2440c dpp RV2440c obg RV2440c obg RV2440c obg RV2440c obg RV2583c relA (p)ppGpl RV2583c relA (p)pp	kinase Jeoxyguanosine tate hydrolase ing protein LepA Isopentenylpyrophos- isferase e diphosphate kinase Johnding protein synthase I sosthetic groups and Rivo422c thiD phosphomet thiamine syr moiety synthase I Rv2977c thiL probable this phate kinase	thylpyrimidine kinase nthesis, thiazole
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1. Purine ribonucleotide biosynthesis Rv13899 gmk putative guarylate kinase Rv2440c obg GTR Rv3396c guaA GMP synthase inosine-5'-monophosphate dehydrogenase Rv1568 bioA adenosy oxonona Bv11017c prsA ribose-phosphate pyrophosphokinase Rv0357c purA adenylosuccinate synthase Adenylosuccinate lyase Phosphoribosylaminoimidazole succinocarboxamide synthase Rv0777 purB purD phosphoribosylamine-glycine ligase Pv0772 purD phosphoribosylamine-glycine ligase Pv1442 bisC biotin su possible gene Rv0808 purF amidophosphoribosyltransferase-	e diphosphate kinase Rv0417 thiG thiamine syr binding protein moiety synthase I Rv2977c thiL probable this phate kinase osthetic groups and 9. Riboflavin	nthesis, thiazole
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RV3336c guaA GMP synthase inosine-5'-monophosphate dehydrogenase inosine-5'-monophosphate dehydrogenase inosine-5'-monophosphate dehydrogenase inosine-5'-monophosphate dehydrogenase inosine-5'-monophosphate dehydrogenase inosine-5'-monophosphate dehydrogenase ribose-phosphate pyrophosphokinase ribose-phosphate pyrophosphokinase RV1017c prsA adenylosuccinate synthase Rv0357c purA adenylosuccinate synthase Rv0777 purB adenylosuccinate lyase phosphoribosylaminoimidazole synthase phosphoribosylamine-glycine ligase phosphoribosylamine-glycine ligase phosphoribosylaminoimidazole carboxylase RV0808 purF amidophosphoribosyltransferase-	synthase I Rv2977c <i>thiL</i> probable this phate kinase osthetic groups and 9. Ribotlavin	
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RV1017c prsA ribose-phosphate pyrophosphokinase RV1589 bioB dethiobic dethiobic purA adenylosuccinate synthase Rv0777 purB adenylosuccinate lyase phosphoribosylamino-imidazole-succinocarboxamide synthase phosphoribosylamine-glycine ligase Pv1542 bisC biotin synthase phosphoribosylamine-glycine ligase phosphoribosylamine-glycine ligase phosphoribosylamino-imidazole carboxylase phosphoribosylamino-imidazole gene Rv0088 purF amidophosphoribosyltransferase-		ΓP cyclohydrolase II
nase nase Rv1570 bioD dethiobic s-amino-purB adenylosuccinate synthase Rv0777 purB adenylosuccinate lyase Rv0780 purC phosphoribosylaminoimidazole-succinocarboxamide synthase phosphoribosylamine-glycine ligase phosphoribosylamine-glycine ligase phosphoribosylaminoimidazole carboxylase Rv0808 purF amidophosphoribosyltransferase-		nthase α chain
RV0357c purA adenylosuccinate synthase RV1569 bioF 8-aminosynthase Rv0770 purC phosphoribosylamino-imidazole-succinate lyase Rv0772 purD phosphoribosylamine-glycine ligase phosphoribosylamino-imidazole synthase Rv3275c purE phosphoribosylamine-glycine ligase phosphoribosylamino-imidazole carboxylase Rv088 purF amidophosphoribosyltransferase-		oflavin deaminase
RV0777 purB adenýlosuccinate lýase synthase RV0780 purC phosphoribosylaminoimidazole-succinocarboxamide synthase phosphoribosylamine-glycine ligase RV3275c purE phosphoribosylaminoimidazole sarboxylase phosphoribosylaminoimidazole sarboxylase RV088 purF amidophosphoribosyltransferase-succinate lýase synthase RV0032 bioF2 C-termin BioF RV0072 birA biotin ap RV1442 bisC biotin su RV0089 - possible gene	riboflavin kir ribog riboflavin kir riboflavin kir riboflavin bic	
RV0780 purC phosphoribosylaminoimidazole- succinocarboxamide synthase RV0772 purD phosphoribosylamine-glycine lig- ase phosphoribosylaminoimidazole carboxylase phosphoribosylaminoimidazole succinocarboxamide synthase RV3279c birA biotin ap RV1442 bisC biotin su RV0089 - possible gene RV0808 purF amidophosphoribosyltransferase-		nthase β chain
succinocarboxamide synthase Rv0772 purD phosphoribosylamine-glycine ligase phosphoribosylaminoimidazole phosphoribosylaminoimidazole phosphoribosylaminoimidazole prv088 purF amidophosphoribosyltransferase- SioF bioF biotin ap Rv1442 bisC biotin ap Pv089 - possible gene		aminase, riboflavin
ase Rv3275c purE phosphoribosylaminoimidazole Rv0089 - possible carboxylase Rv0808 purF amidophosphoribosyltransferase-	synthesis	•
Rv3275c purE phosphoribosylaminoimidazole Rv0089 - possible carboxylase gene Rv0808 purF amidophosphoribosyltransferase-	-protein ligase	
carboxylase gene Rv0808 purF amidophosphoribosyltransferase-	oxide reductase 10. Thioredoxin, glutaredoxin and	
Rv0808 purF amidophosphoribosyltransferase-		lutamyl transpeptidas ranspeptidase
	Rv2394 <i>ggtB</i> γ -glutamyltr precursor	i ai i spepiluase
Rv0957 purH phosphoribosylaminoimidazole- 2. Folic acid		reductase homologue
		o <i>M. leprae</i> ThiX
Rv3276c <i>purK</i> phosphoribosylaminoimidazole Rv2447c <i>folC</i> folylpolyg	utamate synthase Rv1470 trxA thioredoxin	,
carboxylase ATPase subunit Rv3356c folD methyler	etetrahydrofolate dehy- Rv1471 trxB thioredoxin r	
Rv0803 purL phosphoribosylformylglycin- drogena:		reductase
	phydrolase I Rv3914 trxC thioredoxin	
	ro-6-hydroxymethylpterin phokinase 11. Menaquinone, PQQ, ubiquino	ne and other
	phokinase 11. Menaquinone, PQQ, ubiquinoneroate synthase terpenoids	ne and other
		ylulose 5-phosphate
	volved in folate biosyn- synthase	2 Normale
amidine synthase I thesis	Rv0562 grcC1 heptaprenyl	diphosphate
	enzoate synthase gluta- synthase II	P 1 - 1 -
		diphosphate
	enzoate synthase synthase II	nul nuronhoonbata
lase Rv0812 pabC aminode	xychorismate lyase Rv3398c <i>idsA</i> geranylgerai synthase	nyl pyrophosphate
Pyrimidine ribonucleotide biosynthesis 3. Lipoate		nyl pyrophosphate
	osynthesis protein A synthase	, . , . ,
subunit Rv2217 lipB lipoate b	psynthesis protein B Rv3383c idsB transfergera	nyl, similar geranyl
Rv1384 carB carbamoyl-phosphate synthase	pyrophospha	ate synthase
subunit 4. Molybdopterin		-2-naphthoate
	um cofactor biosynthe- octaprenyltra n A Rv0548c <i>menB</i> naphthoate:	
		syninase enzoate-CoA synthase
		-hydroxy-2,4-cyclo-
		I-carboxylate synthas
Rv1699 <i>pyrG</i> CTP synthase sis, prote	n A Rv0542c <i>menE o</i> -succinylbe	enzoic acid-CoA ligas
	um cofactor biosynthe- Rv3853 <i>menG S</i> -adenosyln	
		nenaquinone
		QQ synthesis
		menaquinone biosyn-
		menaquinone biosyn- yltransferase
		,
	um cofactor biosynthe- 12. Heme and porphyrin	
reductase B2 (eukaryotic-like) sis, prote		VA reductase
		ilinic acid dehydratase
reductase $lpha$ chain subunit 1 Rv1981c $nrdF$ ribonucleotide reductase small Rv0868c $moaD2$ molybdo	terin converting factor Rv0512 <i>hem</i> B δ-aminolevu	gen deaminase
Rv2139 pyrD dihydroorotate dehydrogenase Rv0869c moaA2 molybde sis, prote sis, prote proteine Rv1385 pyrF CTP synthase Rv0438c moaA3 molybde sis, prote proteine Rv2883c pyrH uridylate kinase Rv3110 moaB molybde sis, prote proteine Rv0382c umpA probable uridine 5'-monophosphate synthase Rv0984 moaB2 molybde sis, prote molybde sis, proteine 3. 2'-deoxyribonuclectide metabolism Rv3111 moaC molybde sis, proteine Rv0321 dcd deoxycytidine triphosphate deaminase Rv0864 moaC2 molybde sis, proteine Rv2697c dut deoxycytidine triphosphatase Rv3324c moaC3 molybde sis, proteine Rv0233 nrdB ribonucleoside-diphosphate reductase B2 (eukaryotic-like) Rv3324c moaC3 molybde sis, proteine	um cofactor biosynthe- n A n M n M offactor biosynthe- n B um cofactor biosynthe- n B um cofactor biosynthe- n B um cofactor biosynthe- n C um cofactor biosynthe- n C Rv0553 Rv0542c Rv3853 Rv3853 Rv3897c Rv0693 PqqE coen prote ubiq ubiq thesi n C menE 2-de coen prote ubiq thesi n C S-ad pqyE coen prote ubiq thesi n C Rv0558 Rv0558 ubiE ubiq thesi n C 12. Heme and porphyrin	ccinylbe ccinyl-6 diene-1 ccinylbe lenosylr methylr cene sy zyme F ein E uinone/ s methy

Rv13 Rv05		hemK hemL	protoporphyrinogen oxidase glutamate-1-semialdehyde amino-	2. A sudbus		transferase	Rv2931 Rv2932	ppsA ppsB	phenolpthiocerol synthesis (pksB) phenolpthiocerol synthesis (pksC)
Rv23	88c	hemN	transferase oxygen-independent copropor-	phospholi	pid synthe		Rv2933 Rv2934	ppsC ppsD	phenolpthiocerol synthesis (pksD) phenolpthiocerol synthesis (pksE)
Rv26	770	hemY'	phyrinogen III oxidase protoporphyrinogen oxidase	Rv2289	cdh	CDP-diacylglycerol phosphatidyl- hydrolase	Rv2935 Rv2928	ppsE tesA	phenolpthiocerol synthesis (pksF) thioesterase
Rv14		hemZ	ferrochelatase	Rv2881c	cdsA	phosphatidate cytidylyltransferase	Rv1544	- -	probable ketoacyl reductase
13 C	obalar	min		Rv3804c Rv1886c	fbpA fbpB	antigen 85A, mycolyltransferase antigen 85B, mycolyltransferase	J. Broad r	equilatory	functions
Rv28		cobA	cob(l)alamin adenosyltransferase	Rv0129c	fbpC	antigen 85C, mycolytransferase	1. Repres		
Rv28		cobB	cobyrinic acid a,c-diamide synthase	Rv3803c	fbpD	antigen MPT51, mycolyltrans-	Rv1657	argR_	arginine repressor
Rv22:		cobC cobD	aminotransferase cobinamide synthase	Rv0564c	gpdA1	ferase glycerol-3-phosphate dehydroge-	Rv1267c	embR	regulator of <i>embAB</i> genes (AfsR/Dndl/RedD family)
Rv20		cobG	percorrin reductase	11000040	gparti	nase	Rv1909c	furA	ferric uptake regulatory protein
Rv20		cobH	precorrin isomerase	Rv2982c	gpdA2	glycerol-3-phosphate dehydroge-	Rv2359	furB	ferric uptake regulatory protein
Rv20 Rv20		cobl cobK	Cobl-CobJ fusion protein precorrin reductase	Rv2612c	pgsA	nase CDP-diacylglycerol-glycerol-3-	Rv2919c Rv2711	glnB ideR	nitrogen regulatory protein iron dependent repressor, IdeR
Rv20		cobL	probable methyltransferase	11120120	pgo, i	phosphate phosphatidyltrans-	Rv2720	lexA	LexA, SOS repressor protein
Rv20		cobM	precorrin-3 methylase	D: 1000		ferase	Rv1479	moxR	transcriptional regulator, MoxR
Rv20 Rv22		cobN cobS	cobalt insertion cobalamin (5'-phosphate) synthase	Rv1822	pgsA2	CDP-diacylglycerol-glycerol-3- phosphate phosphatidyltrans- ferase	Rv3692	moxR2	homologue transcriptional regulator, MoxR homologue
Rv22	:07	cobT	nicotinate-nucleotide-dimethyl- benzimidazole transferase	Rv2746c	pgsA3	CDP-diacylglycerol-glycerol-3- phosphate phosphatidyltrans-	Rv3164c	moxR3	transcriptional regulator, MoxR homologue
Rv02:		cobU cobQ	cobinamide kinase cobyric acid synthase	Rv1551	plsB1	ferase glycerol-3-phosphate acyltrans-	Rv0212c Rv0117	nadR oxyS	similar to <i>E.coli</i> NadR transcriptional regulator (LysR
Rv37	13	cobQ2	possible cobyric acid synthase		•	ferase			family)
Rv03	06	-	similar to BluB cobalamin synthesis protein <i>R. capsulatus</i>	Rv2482c	plsB2	glycerol-3-phosphate acyltrans- ferase	Rv1379	pyrR	regulatory protein pyrimidine biosynthesis
				Rv0437c	psd	putative phosphatidylserine	Rv2788	sirR	iron-dependent transcriptional
14. Iro Rv18	on utili 76	ization <i>bfrA</i>	bacterioferritin	Rv0436c	pssA	decarboxylase CDP-diacylglycerol-serine	Rv3082c	virS	repressor putative virulence regulating
Rv38	41	bfrB entC	bacterioferritin	Rv0045c	-	o-phosphatidyltransferase		whiB1	protein (AraC/XyIS family)
Rv32 Rv32		entC entD	probable isochorismate synthase weak similarity to many phospho-			possible dihydrolipoamide acetyl- transferase	Rv3219		WhiB transcriptional activator homologue
Rv28	950	viuB	glycerate mutases similar to proteins involved in	Rv0914c Rv1543	-	lipid transfer protein probable fatty-acyl CoA reductase	Rv3260c	whiB2	WhiB transcriptional activator homologue
Rv35:		VIUD	vibriobactin uptake similar to ferripyochelin binding	Rv1627c Rv1814	-	lipid carrier protein possible C-5 sterol desaturase	Rv3416	whiB3	WhiB transcriptional activator homologue
11000	200	_	protein	Rv1867	-	similar to acetyl CoA synthase/lipid carriers	Rv3681c	whiB4	WhiB transcriptional activator homologue
H. Lip	oid bio	synthesis	•	Rv2261c		apolipoprotein N-acyltrans-	Rv0023	-	putative transcriptional regulator
			and mycolic acids	Duggege		ferase-a	Rv0043c	-	transcriptional regulator (GntR
Rv32	.00	accA3	acetyl/propionyl CoA carboxylase α subunit	Rv2262c	1.110	apolipoprotein N-acyltrans- ferase-b	Rv0067c	-	family) transcriptional regulator
Rv09	04c	accD3	acetyl/propionyl CoA carboxylase β subunit	Rv3523 Rv3720	-	lipid carrier protein C-term similar to cyclopropane	Rv0078		(TetR/AcrR family) transcriptional regulator
Rv37	99c	accD4	acetyl/propionyl CoA carboxylase	HV3720		fatty acid synthases		-	(TetR/AcrR family)
Rv32	80	accD5	β subunit acetyl/propionyl CoA carboxylase	I. Polyketi	de and no	n-ribosomal peptide synthesis	Rv0081	-	transcriptional regulator (ArsR family)
Б.00			β subunit	Rv2940c	mas	mycocerosic acid synthase	Rv0135c	-	putative transcriptional regulator
Rv22	47	accD6	acetyl/propionyl CoA carboxylase β subunit	Rv2384	mbtA	mycobactin/exochelin synthesis (salicylate-AMP ligase)	Rv0144 Rv0158	-	putative transcriptional regulator transcriptional regulator
Rv22	44	асрМ	acyl carrier protein (meromycolate	Rv2383c	mbtB	mycobactin/exochelin synthesis			(TetR/AcrR family)
Rv25	23c	acpS	extension) CoA:apo-[ACP] pantethienephos-	Rv2382c	mbtC	(serine/threonine ligation) mycobactin/exochelin synthesis	Rv0165c	-	transcriptional regulator (GntR family)
			photransferase	Rv2381c	mbtD	mycobactin/exochelin synthesis	Rv0195	-	transcriptional regulator
Rv22		fabD fabD2	malonyl CoA-[ACP] transacylase malonyl CoA-[ACP] transacylase	Rv2380c	mbtE	(polyketide synthase)	Rv0196		(LuxR/UhpA family) transcriptional regulator
Rv14		fabG1	3-oxoacyl-[ACP] reductase (aka	HV23600	THOLE	mycobactin/exochelin synthesis (lysine ligation)	HV0190	-	(TetR/AcrR family)
			MabA)	Rv2379c	mbtF	mycobactin/exochelin synthesis	Rv0232	-	transcriptional regulator
Rv13: Rv20:		fabG2 fabG3	3-oxoacyl-[ACP] Reductase 3-oxoacyl-[ACP] reductase	Rv2378c	mbtG	(lysine ligation) mycobactin/exochelin synthesis	Rv0238	_	(TetR/AcrR family) transcriptional regulator
Rv02		fabG4	3-oxoacyl-[ACP] reductase	11025766	mola	(lysine hydroxylase)	1100200		(TetR/AcrR family)
Rv27		fabG5	3-oxoacyl-[ACP] reductase	Rv2377c	mbtH	mycobactin/exochelin synthesis	Rv0273c	-	putative transcriptional regulator
Rv05:		fabH fas	β-ketoacyl-ACP synthase III fatty acid synthase	Rv0101	nrp	unknown non-ribosomal peptide synthase	Rv0302	-	transcriptional regulator (TetR/AcrR family)
Rv14		inhA	enoyl-[ACP] reductase	Rv1153c	omt	PKS o-methyltransferase	Rv0324	-	putative transcriptional regulator
Rv22	45	kasA	β-ketoacyl-ACP synthase	Rv3824c	papA1	PKS-associated protein, unknown	Rv0328	-	transcriptional regulator
Rv22	46	kasB	(meromycolate extension) β-ketoacyl-ACP synthase	Rv3820c	papA2	function PKS-associated protein, unknown	Rv0348	_	(TetR/AcrR family) putative transcriptional regulator
			(meromycolate extension)			function	Rv0377	-	transcriptional regulator (LysR
Rv16 Rv26		tesB1 tesB2	thioesterase II thioesterase II	Rv1182	papA3	PKS-associated protein, unknown function	Rv0386	_	family) transcriptional regulator
Rv00:		-	possible acyl carrier protein	Rv1528c	papA4	PKS-associated protein, unknown	1.10000		(LuxR/UhpA family)
Rv134 Rv17	44 22	-	possible acyl carrier protein possible biotin carboxylase	Rv2939	papA5	function PKS-associated protein, unknown	Rv0452 Rv0465c	-	putative transcriptional regulator transcriptional regulator
Rv32: Rv34		-	resembles biotin carboxyl carrier possible acyl carrier protein	Rv2946c	pks1	function	Rv0472c	_	(PbsX/Xre family) transcriptional regulator
nv34	12		possible abyl Carrier protein	Rv3825c	pks1 pks2	polyketide synthase polyketide synthase	11004720	-	(TetR/AcrR family)
			ty and mycolic acids	Rv1180	pks3	polyketide synthase	Rv0474	-	transcriptional regulator
Rv33:		acrA1 cmaA1	fatty acyl-CoA reductase cyclopropane mycolic acid	Rv1181 Rv1527c	pks4 pks5	polyketide synthase polyketide synthase	Rv0485	_	(PbsX/Xre family) transcriptional regulator (ROK
			synthase 1	Rv0405	pks6	polyketide synthase			family)
Rv05	03c	cmaA2	cyclopropane mycolic acid syn- thase 2	Rv1661 Rv1662	pks7 pks8	polyketide synthase	Rv0494	-	transcriptional regulator (GntR family)
Rv08:	24c	desA1	acyl-[ACP] desaturase	Rv1662 Rv1664	pks8 pks9	polyketide synthase polyketide synthase	Rv0552	_	putative transcriptional regulator
Rv10	94	desA2	acyl-[ACP] desaturase	Rv1660	pks 10	polyketide synthase (chalcone	Rv0576	-	putative transcriptional regulator
Rv32:		desA3 mmaA1	acyl-[ACP] desaturase methoxymycolic acid synthase 1	Rv1665	pks11	synthase-like) polyketide synthase (chalcone	Rv0586	-	transcriptional regulator (GntR family)
Rv06		mmaA1 mmaA2	methoxymycolic acid synthase 1 methoxymycolic acid synthase 2	11111000	PNSII	synthase-like)	Rv0650	-	transcriptional regulator (ROK
Rv06	43c	mmaA3	methoxymycolic acid synthase 3	Rv2048c	pks12	polyketide synthase (erythronolide			family)
Rv06		mmaA4 ufaA1	methoxymycolic acid synthase 4 unknown fatty acid methyltrans-	Rv3800c	pks13	synthase-like) polyketide synthase	Rv0653c Rv0681	-	putative transcriptional regulator transcriptional regulator
			ferase	Rv1342c	pks 13 pks 14	polyketide synthase (chalcone		-	(TetR/AcrR family)
Rv35	38	ufaA2	unknown fatty acid methyltrans-	Bu2047-	nko 15	synthase-like)	Rv0691c	-	transcriptional regulator (TetR/AcrR family)
			ferase unknown mycolic acid methyl-	Rv2947c Rv1013	pks 15 pks 16	polyketide synthase polyketide synthase	Rv0737	-	(TetH/AcrH family) putative transcriptional regulator
Rv04	69	umaA1							
Rv04		umaA1 umaA2	transferase unknown mycolic acid methyl-	Rv1663 Rv1372	pks17 pks18	polyketide synthase polyketide synthase	Rv0744c Rv0792c	-	putative transcriptional regulator transcriptional regulator (GntR

Rv0823c	_	family) transcriptional regulator	Rv3160c Rv3167c	-	putative transcriptional regulator putative transcriptional regulator	Rv0018c	ppp	truncated putative phosphoprotein phos-
11000200	-	(NifR3/Smm1 family)	Rv3173c	-	transcriptional regulator	11000100	ρρρ	phatase
Rv0827c	-	transcriptional regulator (ArsR	D-0400		(TetR/AcrR family)	Rv2234	ptpA	low molecular weight protein-tyre
Rv0890c	_	family) transcriptional regulator	Rv3183 Rv3208	-	putative transcriptional regulator transcriptional regulator	Rv0153c	_	sine-phosphatase putative protein-tyrosine-phos-
		(LuxR/UhpA family)			(TetR/AcrR family)			phatase
Rv0891c		putative transcriptional regulator	Rv3249c	-	transcriptional regulator			
Rv0894 Rv1019	-	putative transcriptional regulator transcriptional regulator	Rv3291c	_	(TetR/AcrR family) transcriptional regulator			metabolism nodification of macromolecules
		(TetR/AcrR family)			(Lrp/AsnC family)	 Ribosor 	nal protei	n synthesis and modification
Rv1049	-	transcriptional regulator (MarR	Rv3295	-	transcriptional regulator	Rv3420c	riml	ribosomal protein S18 acetyl
Rv1129c	_	family) transcriptional regulator	Rv3334	_	(TetR/AcrR family) transcriptional regulator (MerR	Rv0995	rimJ	transferase acetylation of 30S S5 subunit
		(PbsX/Xre family)			family)	Rv0641	rplA	50S ribosomal protein L1
Rv1151c Rv1152	-	putative transcriptional regulator	Rv3405c Rv3522	-	putative transcriptional regulator	Rv0704 Rv0701	rpIB rpIC	50S ribosomal protein L2 50S ribosomal protein L3
UA1125	-	transcriptional regulator (GntR family)	Rv3557c	-	putative transcriptional regulator transcriptional regulator	Rv0701	rpIC rpID	50S ribosomal protein L4
Rv1167c	-	putative transcriptional regulator			(TetR/AcrR family)	Rv0716	rpIE	50S ribosomal protein L5
Rv1219c Rv1255c	-	putative transcriptional regulator transcriptional regulator	Rv3574	-	transcriptional regulator (TetR/AcrR family)	Rv0719 Rv0056	rpIF rpII	50S ribosomal protein L6 50S ribosomal protein L9
11012330		(TetR/AcrR family)	Rv3575c	-	transcriptional regulator (Lacl	Rv0651	rpIJ	50S ribosomal protein L10
Rv1332	-	putative transcriptional regulator	D 0500		family)	Rv0640	rplK	50S ribosomal protein L11
Rv1353c	-	transcriptional regulator (TetR/AcrR family)	Rv3583c Rv3676	-	putative transcriptional regulator transcriptional regulator (Crp/Fnr	Rv0652 Rv3443c	rpIL rpIM	50S ribosomal protein L7/L12 50S ribosomal protein L13
Rv1358	-	transcriptional regulator	110070		family)	Rv0714	rpIN	50S ribosomal protein L14
		(LuxR/UhpA family)	Rv3678c	-	transcriptional regulator (LysR	Rv0723	rplO	50S ribosomal protein L15
Rv1359 Rv1395	-	putative transcriptional regulator transcriptional regulator	Rv3736	_	family) transcriptional regulator	Rv0708 Rv3456c	rpIP rpIQ	50S ribosomal protein L16 50S ribosomal protein L17
		(AraC/XyIS family)			(AraC/XyIS family)	Rv0720	rpIR	50S ribosomal protein L18
Rv1404	-	transcriptional regulator (MarR	Rv3744	-	transcriptional regulator (ArsR	Rv2904c	rpIS	50S ribosomal protein L19
Rv1423	_	family) putative transcriptional regulator	Rv3830c	-	family) transcriptional regulator	Rv1643 Rv2442c	rplT rplU	50S ribosomal protein L20 50S ribosomal protein L21
Rv1460	-	putative transcriptional regulator			(TetR/AcrR family)	Rv0706	rpIV	50S ribosomal protein L22
Rv1474c	-	transcriptional regulator	Rv3833	-	transcriptional regulator	Rv0703	rplW	50S ribosomal protein L23
Rv1534	-	(TetR/AcrR family) transcriptional regulator	Rv3840	-	(AraC/XylS family) putative transcriptional regulator	Rv0715 Rv1015c	rplX rplY	50S ribosomal protein L24 50S ribosomal protein L25
		(TetR/AcrR family)	Rv3855	-	putative transcriptional regulator	Rv2441c	rpmA	50S ribosomal protein L27
Rv1556 Rv1674c	-	putative transcriptional regulator	2. Two cor	mnonont o	vetame	Rv0105c Rv2058c	rpmB rpmB2	50S ribosomal protein L28 50S ribosomal protein L28
Rv1675c	-	putative transcriptional regulator putative transcriptional regulator	2. 1wo cor Rv1028c	riponeni s kdpD	sensor histidine kinase	Rv0709	гртвг гртС	50S ribosomal protein L29
Rv1719	-	transcriptional regulator (IcIR	Rv1027c	kdpE	two-component response	Rv0722	rpmD	50S ribosomal protein L30
Rv1773c		family) transcriptional regulator (IcIR	Rv3246c	mtrA	regulator two-component response	Rv1298 Rv2057c	rpmE rpmG	50S ribosomal protein L31 50S ribosomal protein L33
11017750		family)	1102400	IIIIA	regulator	Rv3924c	rpmH	50S ribosomal protein L34
Rv1776c	-	putative transcriptional regulator	Rv3245c	mtrB	sensor histidine kinase	Rv1642	rpml	50S ribosomal protein L35
Rv1816 Rv1846c	-	putative transcriptional regulator putative transcriptional regulator	Rv0844c	narL	two-component response regulator	Rv3461c Rv1630	rpmJ rpsA	50S ribosomal protein L36 30S ribosomal protein S1
Rv1931c	-	transcriptional regulator	Rv0757	phoP	two-component response	Rv2890c	rpsB	30S ribosomal protein S2
5 4050		(AraC/XyIS family)	D 0750		regulator	Rv0707	rpsC	30S ribosomal protein S3
Rv1956 Rv1963c	-	putative transcriptional regulator putative transcriptional regulator	Rv0758 Rv0491	phoR regX3	sensor histidine kinase two-component response	Rv3458c Rv0721	rpsD rpsE	30S ribosomal protein S4 30S ribosomal protein S5
Rv1985c	-	transcriptional regulator (LysR	1110401	regrio	regulator	Rv0053	rpsF	30S ribosomal protein S6
D. 4000-		family)	Rv0490	senX3	sensor histidine kinase	Rv0683	rpsG	30S ribosomal protein S7
Rv1990c Rv1994c	-	putative transcriptional regulator transcriptional regulator (MerR	Rv0602c	tcrA	two-component response regulator	Rv0718 Rv3442c	rpsH rpsl	30S ribosomal protein S8 30S ribosomal protein S9
		family)	Rv0260c	-	two-component response	Rv0700	rpsJ	30S ribosomal protein S10
Rv2017	-	putative transcriptional regulator (PbsX/Xre family)	Rv0600c	_	regulator sensor histidine kinase	Rv3459c Rv0682	rpsK rpsL	30S ribosomal protein S11 30S ribosomal protein S12
Rv2021c	-	putative transcriptional regulator	Rv0601c	-	sensor histidine kinase	Rv3460c	rpsM	30S ribosomal protein S13
Rv2034	- 0	transcriptional regulator (ArsR	Rv0818	-	two-component response	Rv0717	rpsN	30S ribosomal protein S14
Rv2175c		family) putative transcriptional regulator	Rv0845		regulator sensor histidine kinase	Rv2056c Rv2785c	rpsN2 rpsO	30S ribosomal protein S14 30S ribosomal protein S15
Rv2250c		putative transcriptional regulator	Rv0902c	-	sensor histidine kinase	Rv2909c	rpsP	30S ribosomal protein S16
Rv2258c		putative transcriptional regulator	Rv0903c	-	two-component response	Rv0710	rpsQ	30S ribosomal protein S17
Rv2282c	-	transcriptional regulator (LysR family)	Rv0981	_	regulator two-component response	Rv0055 Rv2055c	rpsR rpsR2	30S ribosomal protein S18 30S ribosomal protein S18
Rv2308	-	putative transcriptional regulator	1140001		regulator	Rv0705	rpsS	30S ribosomal protein S19
Rv2324	-	transcriptional regulator	Rv0982	-	sensor histidine kinase	Rv2412	rpsT	30S ribosomal protein S20
Rv2358		(Lrp/AsnC family) transcriptional regulator (ArsR	Rv1032c Rv1033c	-	sensor histidine kinase two-component response	Rv3241c	-	member of S30AE ribosomal protein family
		family)			regulator			•
Rv2488c	-	transcriptional regulator	Rv1626	-	two-component response			cation and maturation
Rv2506	_	(LuxR/UhpA family) transcriptional regulator	Rv2027c	_	regulator sensor histidine kinase	Rv1010 Rv2838c	ksgA rbfA	16S rRNA dimethyltransferase ribosome-binding factor A
		(TetR/AcrR family)	Rv2884	-	two-component response	Rv2907c	rimM	16S rRNA processing protein
Rv2621c	-	putative transcriptional regulator	Dv2120-		regulator	2 Amina-	ovi +DNI A	synthases and their modification
Rv2640c	-	transcriptional regulator (ArsR family)	Rv3132c Rv3133c	-	sensor histidine kinase two-component response	3. Aminoa Rv2555c	cyl tHNA alaS	synthases and their modification alanyl-tRNA synthase
Rv2642	-	transcriptional regulator (ArsR			regulator	Rv1292	argS	arginyl-tRNA synthase
Rv2669	_	family) putative transcriptional regulator	Rv3143	-	putative sensory transduction	Rv2572c	aspS cysS	aspartyl-tRNA synthase cysteinyl-tRNA synthase
Rv2745c	-	putative transcriptional regulator putative transcriptional regulator	Rv3220c	-	protein sensor histidine kinase	Rv3580c Rv2130c	cysS cysS2	cysteinyl-tHNA synthase cysteinyl-tRNA synthase
Rv2779c		transcriptional regulator	Rv3764c	-	sensor histidine kinase	Rv1406	fmt	methionyl-tRNA formyltransferas
Rv2887	_	(Lrp/AsnC family) transcriptional regulator (MarR	Rv3765c	-	two-component response regulator	Rv3011c	gatA	glu-tRNA-gln amidotransferase, subunit B
. 142001		family)			rogalator	Rv3009c	gatB	glu-tRNA-gln amidotransferase,
Rv2912c	-	transcriptional regulator			protein kinases and phosphoprotein		•	subunit A
Rv2989	_	(TetR/AcrR family) transcriptional regulator (IcIR	phosphata Rv0015c	ises pknA	serine-threonine protein kinase	Rv3012c	gatC	glu-tRNA-gln amidotransferase, subunit C
. 142303		family)	Rv00130	pknA pknB	serine-threonine protein kinase serine-threonine protein kinase	Rv2992c	gltS	glutamyl-tRNA synthase
Rv3050c	-	putative transcriptional regulator	Rv0931c	pknD	serine-threonine protein kinase	Rv2357c	glyS	glycyl-tRNA synthase
Rv3055 Rv3058c	-	putative transcriptional regulator putative transcriptional regulator	Rv1743 Rv1746	pknE pknF	serine-threonine protein kinase serine-threonine protein kinase	Rv2580c Rv1536	hisS ileS	histidyl-tRNA synthase isoleucyl-tRNA synthase
Rv3060c	-	transcriptional regulator (GntR	Rv0410c	pknG pknG	serine-threonine protein kinase	Rv0041	leuS	leucyl-tRNA synthase
		family)	Rv1266c	pknH	serine-threonine protein kinase	Rv3598c	lysS	lysyl-tRNA synthase
Rv3066	-	putative transcriptional regulator putative transcriptional regulator	Rv2914c Rv2088	pknl pknJ	serine-threonine protein kinase serine-threonine protein kinase	Rv1640c Rv1007c	lysX metS	C-term lysyl-tRNA synthase methionyl-tRNA synthase
Bv3095								
Rv3095 Rv3124	-	transcriptional regulator	Rv3080c	pknK	serine-threonine protein kinase	Rv1649	pheS	phenylalanyl-tRNA synthase α

Rv16	50 phe	T phenylalar subunit	yl-tRNA synthase β	Rv2090	-	partially similar to DNA poly- merase I	2. DNA Rv0670	end	endonuclease IV (apurinase)
Rv28	45c <i>pro</i>		A synthase	Rv2191	-	similar to both PolC and UvrC	Rv1108c	xseA	exonuclease VII large subunit
Rv38						proteins	Rv1107c	xseB	exonuclease VII small subunit
Rv26			NA synthase	Rv2464c	•	probable DNA glycosylase,			
Rv29	06c trmi		nine-N1)-methyltrans-	Rv3201c		endonuclease VIII probable ATP-dependent DNA	3. Proteins Rv3305c	i, peptides <i>amiA</i>	and glycopeptides probable aminohydrolase
Rv33	36c trp5	ferase tryptophar	yl tRNA synthase	11002010	_	helicase	Rv3306c	amiB	probable aminohydrolase
Rv16			IA synthase	Rv3202c	-	similar to UvrD proteins	Rv3596c	clpC	ATP-dependent Clp protease
Rv24	48c <i>val</i> 3			Rv3263	-	probable DNA methylase	Rv2461c	clpP	ATP-dependent Clp protease pro-
4 81.				Rv3644c	-	similar in N-term to DNA poly-	Du0460a	alaD0	teolytic subunit
4. Nu Rv14	ıcleoprotei 107 <i>fmu</i>		mu protein			merase III	Rv2460c	clpP2	ATP-dependent Clp protease pro- teolytic subunit
Rv38				6. Protein	translation	and modification	Rv2457c	clpX	ATP-dependent Clp protease
Rv29		B DNA-bindi	ng protein II	Rv0429c		polypeptide deformylase		•	ATP-binding subunit ClpX
Rv13	888 <i>ml</i> H	<i>IF</i> integration	host factor	Rv2534c	efp	elongation factor P	Rv2667	clpX'	similar to ClpC from M. leprae but
5 DN	IA roplicat	on ropair room	bination and restric-	Rv2882c Rv0684	frr fusA	ribosome recycling factor elongation factor G	Rv3419c	gcp	shorter glycoprotease
	nodification		ibiliation and restile-	Rv0120c	fusA2	elongation factor G	Rv2725c	hflX	GTP-binding protein
	17c alk/		thyladenine glycosi-	Rv1080c	greA	transcription elongation factor G	Rv1223	htr A	serine protease
		dase II		Rv3462c	infA	initiation factor IF-1	Rv2861c	mapA1	methionine aminopeptidase
Rv28 Rv13			age-inducible protein F TP-dependent helicase	Rv2839c Rv1641	infB infC	initiation factor IF-2 initiation factor IF-3	Rv0734	mapA2	probable methionine aminopepti- dase
Rv30			age-inducible protein	Rv0009	ppiA	peptidyl-prolyl <i>cis-trans</i> isomerase	Rv0319	рср	pyrrolidone-carboxylate peptidase
Rv15			NA-damage-inducible	Rv2582	ppiB	peptidyl-prolyl cis-trans isomerase	Rv0125	pepA	probable serine protease
		protein		Rv1299	prfA	peptide chain release factor 1	Rv2213	pepB	aminopeptidase A/I
Rv00	01 dna		nal replication initiator	Rv3105c Rv2889c	prfB tsf	peptide chain release factor 2 elongation factor EF-Ts	Rv0800 Rv2467	pepC pepD	aminopeptidase I probable aminopeptidase
Rv00	58 dna	protein B DNA helic	ase (contains intein)	Rv0685	tuf	elongation factor EF-Tu	Rv2089c	pepE	cytoplasmic peptidase
Rv15			nerase III, α subunit				Rv2535c	pepQ	cytoplasmic peptidase
Rv33	370c dna	E2 DNA polyr	nerase III α chain			NA modification and DNA	Rv2782c	pepR	protease/peptidase, M16 family
Rv23				transcripti Rv1253	on <i>deaD</i>	ATP-dependent DNA/RNA	Rv2109c	nroA	(insulinase) proteasome α-type subunit 1
Rv00 Rv37			nerase III, β subunit nerase III ε chain	HV1253	ueaD	helicase	Rv2109c Rv2110c	prcA prcB	proteasome α-type subunit 1 proteasome β-type subunit 2
Rv37:			nerase III, γ (dnaZ) and	Rv2783c	gpsl	pppGpp synthase and polyribo-	Rv0782	ptrBa	protease II, α subunit
		τ (dnaX)	, , , ,		•	nucleotide phosphorylase	Rv0781	ptrBb	protease II, β subunit
Rv29	24c fpg		pyrimidine-DNA glyco-	Rv2841c	nusA	transcription termination factor	Rv0724	sppA	protease IV, signal peptide pepti-
Rv00	006 gyr	sylase	e subunit A	Rv2533c Rv0639	nusB nusG	N-utilization substance protein B transcription antitermination	Rv0198c	_	dase probable zinc metalloprotease
Rv00			se subunit B	110000	nasa	protein	Rv0457c	_	probable peptidase
Rv20			elicase, Ski2 subfamily	Rv3907c	pcnA	polynucleotide polymerase	Rv0840c	-	probable proline iminopeptidase
Rv21	01 hel2		elicase, Snf2/Rad54	Rv3232c	pvdS	alternative sigma factor for	Rv0983	-	probable serine protease
Rv27	56c hsd	family	iction/modification sys-	Rv3211	rhIE	siderophore production probable ATP-dependent	Rv1977 Rv3668c	-	probable zinc metallopeptidase probable alkaline serine protease
HV27	56C 11SU	tem DNA ı		1100211	IIIL	RNA helicase	Rv3671c	-	probable serine protease
Rv27	55c hsd		iction/modification sys-	Rv1297	rho	transcription termination	Rv3883c	-	probable secreted protease
		tem specif	icity determinant			factor rho	Rv3886c	-	protease
Rv32			ndent helicase	Rv3457c Rv0667	rpoA	α subunit of RNA polymerase	4 Dahrasa	ا ممامنعمام	linanah rasaaha vidaa and mhaamba
Rv30 Rv30				Rv0668	rpoB rpoC	β subunit of RNA polymerase β' subunit of RNA polymerase	lipids	chandes, i	lipopolysaccharides and phospho-
Rv37				Rv1364c	rsbU	SigB regulation protein	Rv0062	celA	cellulase/endoglucanase
Rv10		transcription	on-repair coupling factor	Rv3287c	rsbW	anti-sigma B factor	Rv3915	cwlM	hydrolase
Rv25			system protein	Rv2703	sigA	RNA polymerase sigma factor	Rv0315	-	probable β-1,3-glucanase
Rv29 Rv11				Rv2710	sigB	(aka MysA, RpoV) RNA polymerase sigma factor	Rv1090	-	probable inactivated cellulase/endoglucanase
Rv04				11027 10	Ugb	(aka MysB)	Rv1327c	-	probable glycosyl hydrolase, α-
Rv35		Y probable [NA glycosylase	Rv2069	sigC	ECF subfamily sigma subunit			amylase family
Rv32			ndonuclease VIII	Rv3414c	sigD	ECF subfamily sigma subunit	Rv1333	-	probable hydrolase
Rv36 Rv13			ndonuclease III I-DNA-protein-cysteine	Rv1221 Rv3286c	sigE sigF	ECF subfamily sigma subunit ECF subfamily sigma subunit	Rv3463 Rv3717	-	probable neuraminidase possible N-acetylmuramoyl-L-ala-
nvis	316c ogt	methyltran		Rv0182c	sigG sigG	sigma-70 factors ECF subfamily	1100717		nine amidase
Rv16	29 pole			Rv3223c	sigH	ECF subfamily sigma subunit			
Rv14	02 priA		imosomal protein n'	Rv1189	sigl _,	ECF family sigma factor	5. Esterase		
D. OF	OF	(replication		Rv3328c Rv0445c	sigJ ciak	similar to Sigl, ECF family ECF-type sigma factor	Rv0220 Rv1923	lipC lipD	probable esterase probable esterase
Rv35	85 rad	logue	NA repair RadA homo-	Rv0735	sigK sigL	sigma-70 factors ECF subfamily	Rv3775	lipD lipE	probable hydrolase
Rv27	37c <i>rece</i>		se (contains intein)	Rv3911	sigM	probable sigma factor, similar to	Rv3487c	lipF	probable esterase
Rv06	30c rect	3 exodeoxyr	bonuclease V	D		SigE	Rv0646c	lipG	probable hydrolase
Rv06			bonuclease V	Rv3366	spoU truA	probable rRNA methylase	Rv1399c Rv1400c	lipH lipl	probable lipase probable lipase
Rv06 Rv00			ibonuclease V ation and SOS induc-	Rv3455c	u uA	probable pseudouridylate syn- thase	Rv1900c	iipi IipJ	probable esterase
. 1000	.55 1661	tion	autori and 000 mado	Rv2793c	truB	tRNA pseudouridine 55 synthase	Rv2385	İipΚ	probable acetyl-hydrolase
Rv29		G ATP-deper	ndent DNA helicase	Rv1644	tsnR	putative 23S rRNA methyltrans-	Rv1497	lipL	esterase
Rv16			tion and DNA repair	Du0040		ferase	Rv2284	lipM linN	probable esterase
Rv37	15c recl	RecBC-Ind DNA repai	lependent process of	Rv3649	-	ATP-dependent DNA/RNA heli- case	Rv2970c Rv1426c	lipN lipO	probable lipase/esterase probable esterase
Rv27	'36c <i>rec)</i>		r protein for RecA			550	Rv2463	lipP	probable esterase
Rv25		A Holliday ju	nction binding protein,			cytoplasmic)	Rv2485c	lipQ	probable carboxlyesterase
		DNA helic	ase	Rv1326c	glgB	1,4-α-glucan branching enzyme	Rv3084	lipR	probable acetyl-hydrolase
Rv25			nction binding protein	Rv1328	glgP	probable glycogen phosphory-	Rv3176c Rv2045c	lipS lipT	probable esterase/lipase probable carboxylesterase
Rv25	94c <i>ruv</i> (C Holliday ju deoxyribor	nction resolvase, endo-	Rv1564c	glgX	lase probable glycogen debranching	HV20450 Rv1076	lip I IipU	probable carboxylesterase probable esterase
Rv00	54 ssb		nd binding protein		J.J	enzyme	Rv3203	lipV	probable lipase
Rv12		1 DNA-3-me	thyladenine glycosi-	Rv1563c	glgY	putative α-amylase	Rv0217c	lipW	probable esterase
D	160	dase I	nomara a a	Rv1562c	glgZ	maltooligosyltrehalose trehalohy- drolase	Rv2351c Rv2350c	plcA plcB	phospholipase C precursor
			somerase . glycosylase	Rv0126	_	probable glycosyl hydrolase	Rv23500 Rv2349c	picB plcC	phospholipase C precursor phospholipase C precursor
Rv36			se ABC subunit A	Rv1781c	-	probable 4-α-glucanotransferase	Rv1755c	plcD	partial CDS for phospholipase C
Rv29			se ABC subunit B	Rv2471	-	probable maltase α-glucosidase	Rv1104	-	probable esterase pseudogene
	38 <i>uvri</i>						Rv1105	-	probable esterase pseudogene
Rv29 Rv16 Rv16 Rv14	638 uvri 633 uvrl 120 uvrl	C excinuclea	se ABC subunit C	0.0	takia -	((
Rv29 Rv16 Rv16	638 uvr. 633 uvrl 120 uvr.	excinuclea DNA-depe	se ABC subunit C ndent ATPase I and		lation of ma	acromolecules	6 Aramari	o hudroon	rhone
Rv29 Rv16 Rv16 Rv14 Rv09	338 uvri 333 uvrl 120 uvrl 149 uvrl	excinuclea DNA-depe helicase II	ndent ATPase I and	1. RNA			6. Aromati Rv3469c		
Rv29 Rv16 Rv16 Rv14	338 uvri 333 uvrl 120 uvrl 149 uvrl	2 excinuclea DNA-depe helicase II D2 putative U	ndent ATPase I and			acromolecules peptidyl-tRNA hydrolase RNAse III		c hydrocai <i>mhpE</i>	rbons probable 4-hydroxy-2-oxovalerate aldolase
Rv29 Rv16 Rv16 Rv14 Rv09 Rv31 Rv04 Rv00	338 uvri 333 uvri 120 uvri 149 uvri 1980 uvri 1270 xthi	C excinuclea DNA-depe helicase II D2 putative U exodeoxyr group II in	ndent ATPase I and vrD ibonuclease III ron maturase	1. RNA Rv1014c	pth	peptidyl-tRNA hydrolase RNAse III similar at C-term to ribo-			probable 4-hydroxy-2-oxovalerate aldolase probable muconolactone iso-
Rv29 Rv16 Rv16 Rv14 Rv09 Rv31: Rv04 Rv00 Rv08	638 uvr. 633 uvr. 620 uvr. 649 uvr. 98c uvr. 127c xth. 61c -	C excinuclea D DNA-depe helicase II D2 putative U exodeoxyr group II in probable I	ndent ATPase I and vrD ibonuclease III ron maturase bNA helicase	1. RNA Rv1014c Rv2925c Rv2444c	pth rnc rne	peptidyl-tRNA hydrolase RNAse III similar at C-term to ribo- nuclease E	Rv3469c Rv0316	mhpE	probable 4-hydroxy-2-oxovalerate aldolase probable muconolactone iso- merase
Rv29 Rv16 Rv16 Rv14 Rv09 Rv31 Rv04 Rv00	638 uvr. 633 uvr. 620 uvr. 649 uvr. 98c uvr. 127c xth. 61c -	excinuclea DNA-dependent helicase II D2 putative U A exodeoxyr group II in probable E possible for	ndent ATPase I and vrD ibonuclease III rron maturase NNA helicase rmamidopyrimidine-	1. RNA Rv1014c Rv2925c Rv2444c	pth rnc rne rnhB	peptidyl-tRNA hydrolase RNAse III similar at C-term to ribo- nuclease E ribonuclease HII	Rv3469c	mhpE	probable 4-hydroxy-2-oxovalerate aldolase probable muconolactone iso- merase probable 4-carboxymuconolac-
Rv29 Rv16 Rv16 Rv14 Rv09 Rv31: Rv04 Rv00 Rv08	338	C excinuclea D DNA-depe helicase II putative U exodeoxy group II in probable I possible fc DNA glyco	ndent ATPase I and vrD ibonuclease III rron maturase NNA helicase rmamidopyrimidine-	1. RNA Rv1014c Rv2925c Rv2444c	pth rnc rne	peptidyl-tRNA hydrolase RNAse III similar at C-term to ribo- nuclease E	Rv3469c Rv0316	mhpE	probable 4-hydroxy-2-oxovalerate aldolase probable muconolactone iso- merase

Rv2715		lase 2-hydroxymuconic semialdehyde	Rv1367c Rv1730c	-	probable penicillin binding protein probable penicillin binding protein	Rv1030	kdpB	potassium-transporting ATPase B chain
		hydrolase	Rv1922	-	probable penicillin binding protein	Rv1031	kdpC	potassium-transporting ATPase C
Rv3530c Rv3534c	-	probable <i>cis</i> -diol dehydrogenase 4-hydroxy-2-oxovalerate aldolase	Rv2864c Rv3330	-	probable penicillin binding protein probable penicillin binding protein	Rv3236c	kefB	chain probable glutathione-regulated
Rv3536c	-	aromatic hydrocarbon degrada-	Rv3627c	-	probable penicillin binding protein			potassium-efflux protein
		tion	4. Conser	ved memb	prane proteins	Rv2877c	merT	possible mercury resistance transport system
C. Cell en		A lauch CE	Rv0402c	mmpL1	conserved large membrane	Rv1811	mgtC	probable magnesium transport
i. Lipopro	nems (<i>ippi</i>	A- <i>lpr0</i>) 65	Rv0507	mmpL2	protein conserved large membrane	Rv0362	mgtE	ATPase protein C putative magnesium ion
		harides, lipopolysaccharides, pro-	Dunance.	mmnl 2	protein	Dugge	niaT	transporter
teins and Rv0806c		probable UDP-glucose-4-	Rv0206c	mmpL3	conserved large membrane protein	Rv2856 Rv0924c	nicT nramp	probable nickel transport protein transmembrane protein belonging
Rv3811	non	epimerase	Rv0450c	mmpL4	conserved large membrane protein	Dugen4	trkA	to Nramp family probable potassium uptake pro-
Rv1677	csp dsbF	secreted protein highly similar to C-term Mpt53	Rv0676c	mmpL5	conserved large membrane	Rv2691	ITKA	tein
Rv3794	embA	involved in arabinogalactan syn- thesis	Duteez	mmnl 6	protein conserved large membrane	Rv2692	trkB	probable potassium uptake pro- tein
Rv3795	embB	involved in arabinogalactan syn-	Rv1557	mmpL6	protein	Rv2287	yjcE	probable Na+/H+ exchanger
Rv3793	embC	thesis involved in arabinogalactan syn-	Rv2942	mmpL7	conserved large membrane protein	Rv2723	-	probable membrane protein, tellurium resistance
	embo	thesis	Rv3823c	mmpL8	conserved large membrane	Rv3162c	-	probable membrane protein
Rv3875 Rv0112	esat6 gca	early secretory antigen target probable GDP-mannose dehy-	Rv2339	mmpL9	protein conserved large membrane	Rv3237c	·C	possible potassium channel protein
	•	dratase		,	protein	Rv3743c		probable cation-transporting
Rv0113 Rv2965c	gmhA kdtB	phosphoheptose isomerase lipopolysaccharide core biosyn-	Rv1183	mmpL10	conserved large membrane protein			ATPase
		thesis protein	Rv0202c	mmpL11	conserved large membrane			rganic acids and alcohols
Rv2878c Rv1980c	mpt53 mpt64	secreted protein Mpt53 secreted immunogenic protein	Rv1522c	mmpL 12	protein ? conserved large membrane	Rv2443 Rv3476c	dctA kgtP	C4-dicarboxylate transport protein sugar transport protein
		Mpb64/Mpt64		•	protein	Rv1902c	nanT	probable sialic acid transporter
Rv2875	mpt70	major secreted immunogenic pro- tein Mpt70 precursor	Rv0403c	mmpS1	conserved small membrane protein	Rv1236	sugA	membrane protein probably involved in sugar transport
Rv2873	mpt83	surface lipoprotein Mpt83	Rv0506	mmpS2	conserved small membrane	Rv1237	sugB	sugar transport protein
Rv0899 Rv3810	ompA pirG	member of OmpA family cell surface protein precursor (Erp	Rv2198c	mmpS3	protein conserved small membrane	Rv1238	sugC	ABC transporter component of sugar uptake system
Rv3782	•	protein)			protein	Rv3331	sugl	probable sugar transport protein
Rv1302	rfbE rfe	similar to rhamnosyl transferase undecaprenyl-phosphate α-N-	Rv0451c	mmpS4	conserved small membrane protein	Rv2835c	ugpA	sn-glycerol-3-phosphate permease
Du014Fa	waw21	acetylglucosaminyltransferase	Rv0677c	mmpS5		Rv2833c	ugpB	sn-glycerol-3-phosphate-binding
Rv2145c Rv0431	wag31 -	antigen 84 (aka wag31) tuberculin related peptide (AT103)			protein	Rv2832c	ugpC	periplasmic lipoprotein sn-glycerol-3-phosphate transport
Rv0954 Rv1514c	-	cell envelope antigen involved in polysaccharide syn-	5. Other n	nembrane	proteins 211	Rv2834c	ugpE	ATP-binding protein sn-glycerol-3-phosphate transport
	-	thesis	III. Cell pr				ugpL	system protein
Rv1518	-	involved in exopolysaccharide synthesis	A. Transp 1. Amino		n proteins	Rv2316 Rv2318	uspA uspC	sugar transport protein sugar transport protein
Rv1758	-	partial cutinase	Rv2127	ansP	L-asparagine permease	Rv2317	uspE	sugar transport protein
Rv1910c Rv1919c	-	probable secreted protein weak similarity to pollen antigens	Rv0346c	aroP2	probable aromatic amino acid permease	Rv1200 Rv2038c	-	probable sugar transporter probable ABC sugar transporter
Rv1984c	-	probable secreted protein	Rv0917	betP	glycine betaine transport	Rv2039c	-	probable sugar transporter
Rv1987 Rv2223c	-	probable secreted protein probable exported protease	Rv1704c	cycA	transport of D-alanine, D-serine and glycine	Rv2040c Rv2041c	-	probable sugar transporter probable sugar transporter
Rv2224c	-	probable exported protease	Rv3666c	dppA	probable peptide transport system			probable Sagar transporter
Rv2301 Rv2345	-	probable cutinase precursor of probable membrane	Rv3665c	dppB	permease probable peptide transport system	4. Anions Rv2684	arsA	probable arsenical pump
		protein			permease	Rv2685	arsB	probable arsenical pump
Rv2672 Rv3019c		putative exported protease similar to Esat6	Rv3664c	dppC	probable peptide transport system permease	Rv3578 Rv2643	arsB2 arsC	probable arsenical pump probable arsenical pump
Rv3036c	- 1	probable secreted protein	Rv3663c	dppD	probable ABC-transporter	Rv2397c	cysA	sulphate transport ATP-binding
Rv3449		probable precursor of serine pro- tease	Rv0522	gabP	probable 4-amino butyrate trans- porter	Rv2399c	cysT	protein sulphate transport system perme-
Rv3451 Rv3452	-)	probable cutinase	Rv0411c Rv2564	glnH	putative glutamine binding protein	Rv2398c	cysW	ase protein
Rv3724	-	probable cutinase precursor probable cutinase precursor		glnQ	probable ATP-binding transport protein	NV20900	Cysvv	sulphate transport system perme- ase protein
	sacoulus	and peptidoglycan	Rv1280c	oppA	probable oligopeptide transport protein	Rv1857 Rv1858	modA modB	molybdate binding protein transport system permease,
Rv2911	dacB	penicillin binding protein	Rv1283c	оррВ	oligopeptide transport protein			molybdate uptake
Rv2981c Rv3809c	ddlA glf	D-alanine-D-alanine ligase A UDP-galactopyranose mutase	Rv1282c	oppC	oligopeptide transport system per- mease	Rv1859	modC	molybdate uptake ABC- transporter
Rv1018c	glmU	UDP-N-acetylglucosamine	Rv1281c	oppD	probable peptide transport protein	Rv1860	modD	precursor of Apa (45/47
Rv3382c	lytB1	pyrophosphorylase LytB protein homologue	Rv2320c Rv3253c	rocE -	arginine/ornithine transporter probable cationic amino acid	Rv2329c	narK1	kD secreted protein) probable nitrite extrusion protein
Rv1110	lytB2	very similar to LytB			transport	Rv1737c	narK2	nitrite extrusion protein
Rv1315	murA	UDP-N-acetylglucosamine-1-car- boxyvinyltransferase	Rv3454	-	possible proline permease	Rv0261c Rv0267	narK3 narU	nitrite extrusion protein similar to nitrite extrusion
Rv0482	murB	UDP-N-acetylenolpyruvoylglu-	2. Cations					protein 2
Rv2152c	murC	cosamine reductase UDP-N-acetyl-muramate-alanine	Rv2920c Rv1607	amt chaA	putative ammonium transporter putative calcium/proton antiporter	Rv0934	phoS1	PstS component of phosphate uptake
		ligase	Rv1239c	corA	probable magnesium and cobalt	Rv0928	phoS2	PstS component of phosphate
Rv2155c	murD	UDP-N-acetylmuramoylalanine-D- glutamate ligase	Rv0092	ctpA	transport protein cation-transporting ATPase	Rv0820	phoT	uptake phosphate transport system ABC
Rv2158c	murE	meso-diaminopimelate-adding	Rv0103c	ctpB	cation transport ATPase			transporter
Rv2157c	murF	enzyme D-alanine:D-alanine-adding	Rv3270 Rv1469	ctpC ctpD	cation transport ATPase probable cadmium-transporting	Rv3301c	phoY1	phosphate transport system regulator
		enzyme		•	ATPase	Rv0821c	phoY2	phosphate transport system
Rv2153c	murG	transferase in peptidoglycan syn- thesis	Rv0908 Rv1997	ctpE ctpF	probable cation transport ATPase probable cation transport ATPase	Rv0545c	pitA	regulator low-affinity inorganic phosphate
Rv1338	murl	glutamate racemase	Rv1992c	ctpG	probable cation transport ATPase			transporter
Rv2156c	murX	phospho-N-acetylmuramoyl- petapeptide transferase	Rv0425c	ctpH	C-terminal region putative cation- transporting ATPase	Rv2281 Rv0930	pitB pstA1	phosphate permease PstA component of phosphate
Rv3332	nagA	N-acetylglucosamine-6-P-	Rv0107c	ctpl	probable magnesium transport			uptake
Rv0016c	pbpA	deacetylase penicillin-binding protein	Rv0969	ctpV	ATPase cation transport ATPase	Rv0936	pstA2	PstA component of phosphate uptake
Rv2163c	pbpB	penicillin-binding protein 2	Rv3044	fecB	putative FeIII-dicitrate transporter	Rv0933	pstB	ABC transport component of
Rv0050 Rv3682	ponA1 ponA2	penicillin-bonding protein class A penicillin binding protein	Rv0265c trate	fecB2	iron transport protein FeIII dici- transporter	Rv0935	pstC	phosphate uptake PstC component of phosphate
Rv0017c	rodA	FtsW/RodA/SpovE family	Rv1029	kdpA	potassium-transporting ATPase A			uptake
Rv0907	-	probable penicillin binding protein			chain	Rv0929	pstC2	membrane-bound component of

Rv0932c	pstS	phosphate transport system PstS component of phosphate	Rv1821	secA2	unit SecA, preprotein translocase sub-	Rv3500c - Rv3501c - Rv3896c -	part of <i>moe4</i> operon part of <i>moe4</i> operon putative p60 homologue
Rv2400c		uptake sulphate binding precursor	Rv2587c	secD	unit protein-export membrane protein	Rv3922c -	possible hemolysin
Rv0143c Rv1707	-	probable chloride channel probable sulphate permease	Rv0638 Rv2586c	secE secF	SecE preprotein translocase protein-export membrane protein	B IS elements Re	peated sequences, and Phage
Rv1739c	-	possible sulphate transporter	Rv1440	secG	protein-export membrane protein	1. IS elements	pealed bequeiness, and I mage
Rv3679	-	possible anion transporter	D. 0700		SecG	IS6110	16 copies
Rv3680	-	probable anion transporter	Rv0732	secY	SecY subunit of preprotein translo- case	IS1081 Others	6 copies 34 copies
5. Fatty ac			Rv2462c	tig	chaperone protein, similar to		·
		non-specific lipid transport protein	Discosto		trigger factor	2. REP 13E12 fami	ly 7 copies
Rv3540c	ltp2	non-specific lipid transport protein	Rv2813	-	probable general secretion path- way protein	3. Phage-related fu	unctions
6. Efflux p	roteins				way protein	Rv2894c xerC	integrase/recombinase
Rv2936	drrA	similar daunorubicin resistance			atypical conditions	Rv1701 <i>xerD</i> Rv1054 -	integrase/recombinase
Rv2937	drrB	ABC-transporter similar daunorubicin resistance	Rv1901 Rv3648c	cinA cspA	competence damage protein cold shock protein, transcriptional	Rv1054 - Rv1055 -	integrase-a integrase-b
		transmembrane protein	11100100	00,071	regulator	Rv1573 -	phiRV1 phage related protein
Rv2938	drrC	similar daunorubicin resistance	Rv0871	cspB	probable cold shock protein	Rv1574 -	phiRV1 phage related protein
Rv2846c	efpA	transmembrane protein putative efflux protein	Rv3063	cstA	starvation-induced stress response protein	Rv1575 - Rv1576c -	phiRV1 phage related protein phiRV1 phage related protein
Rv3065	emrE	resistance to ethidium bromide	Rv3490	otsA	probable α,α-trehalose-phosphate	Rv1577c -	phiRV1 possible prohead protease
Rv0783c	-	multidrug resistance protein	D. acces	-4-0	synthase	Rv1578c -	phiRV1 phage related protein
Rv0849 Rv1145	-	possible quinolone efflux pump probable drug transporter	Rv2006	otsB	trehalose-6-phosphate phos- phatase	Rv1579c - Rv1580c -	phiRV1 phage related protein phiRV1 phage related protein
Rv1146	-	probable drug transporter	Rv3372	otsB2	trehalose-6-phosphate phos-	Rv1581c -	phiRV1 phage related protein
Rv1250	-	probable drug efflux protein	D 0750	.,	phatase	Rv1582c -	phiRV1 phage related protein
Rv1258c	-	probable multidrug resistance pump	Rv3758c Rv3757c	proV proW	osmoprotection ABC transporter transport system permease	Rv1583c - Rv1584c -	phiRV1 phage related protein phiRV1 phage related protein
1111100	-	probable drug efflux protein	Rv3759c	proX	similar to osmoprotection proteins	Rv1585c -	phiRV1 phage related protein
Rv1634	-	probable drug efflux protein	Rv3756c	proZ	transport system permease	Rv1586c -	phiRV1 integrase
Rv1819c	-	probable multidrug resistance pump	Rv1026	-	probable pppGpp-5'phosphohydro- lase	Rv2309c - Rv2310 -	integrase excisionase
Rv2136c	-	putative bacitracin resistance pro-				Rv2646 -	phiRV2 integrase
		tein	F. Detoxifi			Rv2647 -	phiRV2 phage related protein
Rv2209 Rv2333c	-	probable drug efflux protein probable tetracenomycin C resis-	Rv2428 Rv2429	ahpC ahpD	alkyl hydroperoxide reductase member of AhpC/TSA family	Rv2650c - Rv2651c -	phiRV2 phage related protein phiRV2 prohead protease
. 1720000		tance protein	Rv2238c	anpD ahpE	member of AhpC/TSA family	Rv2652c -	phiRV2 phoneau protease phiRV2 phage related protein
Rv2994	-	probable fluoroquinolone efflux	Rv2521	bcp	bacterioferritin comigratory protein	Rv2653c -	phiRV2 phage related protein
Rv1877	_	protein probable drug efflux protein	Rv1608c	bcpB	probable bacterioferritin comigra- tory protein	Rv2654c - Rv2655c -	phiRV2 phage related protein phiRV2 phage related protein
Rv2459	-	probable drug efflux protein	Rv3473c	bpoA	probable non-heme bromoperoxi-	Rv2656c -	phiRV2 phage related protein
					dase	Rv2657c -	similar to gp36 of mycobacterio-
B. Chaper Rv0384c	rones/Hea clpB	t shock heat shock protein	Rv1123c	bpoB	probable non-heme bromoperoxi- dase	Rv2658c -	phage L5 phiRV2 phage related protein
Rv0352	dnaJ	acts with GrpE to stimulate DnaK	Rv0554	bpoC	probable non-heme bromoperoxi-	Rv2659c -	phiRV2 integrase
_		ATPase			dase	Rv2830c -	similar to phage P1 <i>phd</i> gene
Rv2373c Rv0350	dnaJ2 dnaK	DnaJ homologue 70 kD heat shock protein, chromo-	Rv3617 Rv1938	ephA ephB	probable epoxide hydrolase probable epoxide hydrolase	Rv3750c - Rv3751 -	excisionase putative integrase
1100000	unan	some replication	Rv1124	ephC	probable epoxide hydrolase	1100/01 -	pulative integrase
Rv3417c	groEL1	60 kD chaperonin 1	Rv2214c	ephD	probable epoxide hydrolase	C. PE and PPE far	nilies
Rv0440 Rv3418c	groEL2 groES	60 kD chaperonin 2 10 kD chaperone	Rv3670 Rv0134	ephE ephF	probable epoxide hydrolase probable epoxide hydrolase	PE family PE subfamily	38 members
Rv0351	grpE	stimulates DnaK ATPase activity	Rv3171c	hpx	probable epoxide riydrolase probable non-heme haloperoxi-	PE_PGRS subfam	
Rv2374c	hrcA	heat-inducible transcription		,	dase	_	
Rv0251c	hsp	repressor possible heat shock protein	Rv1908c Rv3846	katG sodA	catalase-peroxidase superoxide dismutase	2. PPE family	68 members
Rv0353	hspR	heat shock regulator	Rv0432	sodC	superoxide dismutase precursor -	D. Antibiotic produc	ction and resistance
Rv2031c	hspX	14kD antigen, heat shock protein			(Cu-Zn)	Rv2068c blaC	class A β-lactamase
Rv2299c	htpG	Hsp20 family heat shock protein Hsp90 family	Rv1932 Rv0634c	tpx	thiol peroxidase putative glyoxylase II	Rv3290c lat Rv2043c pncA	lysine-∈ aminotransferase pyrazinamide resistance/sensitivity
Rv0563	htpX	probable (transmembrane) heat	Rv2581c	-	putative glyoxylase II	Rv0133 -	possible puromycin N-acetyltrans-
		shock protein	Rv3177	-	probable non-heme haloperoxi-		ferase
Rv2701c	suhB	putative extragenic suppressor			dase	Rv0262c -	aminoglycoside 2'-N-acetyltrans-
Rv3269		protein probable heat shock protein	IV. Other			Rv0802c -	terase acetyltransferase
		·	A. Virulen			Rv1082 -	similar to S. lincolnensis ImbE
C. Cell div	rision fic	naccible call division protein	Rv0169	mce1	cell invasion protein	Rv1170 - Rv1347c -	similar to S. lincolnensis ImbE
Rv3641c Rv3102c	nc ftsE	possible cell division protein membrane protein	Rv0589 Rv1966	mce2 mce3	cell invasion protein cell invasion protein	Rv1347c -	possible aminoglycoside 6'-N- acetyltransferase
Rv3610c	ftsH	inner membrane protein,	Rv3499c	mce4	cell invasion protein	Rv2036 -	similar to lincomycin production
Rv2748c	fte¥	chaperone	Rv3100c	smpB tivA	probable small protein b	By23024	genes similar to <i>S. griseus</i> macrotetrolide
Rv2151c	ftsK ftsQ	chromosome partitioning ingrowth of wall at septum	Rv1694 Rv0024	tlyA -	cytotoxin/hemolysin homologue putative p60 homologue	Rv2303c -	resistance protein
Rv2154c	ftsW	membrane protein (shape determi-	Rv0167	-	part of mce1 operon	Rv3225c -	probable aminoglycoside 3'-phos-
Dv2101a	ftsX	nation)	Rv0168	-	part of mee1 operon	Rv3700c -	photransferases
Rv3101c Rv2921c	πsx ftsY	membrane protein cell division protein FtsY	Rv0170 Rv0171	-	part of <i>mce1</i> operon part of <i>mce1</i> operon	Rv3817 -	probable acetyltransferase probable aminoglycoside 3'-phos-
Rv2150c	ftsZ	circumferential ring, GTPase	Rv0172	-	part of <i>mce1</i> operon	**	photransferase
Rv3919c	gid mas l	glucose inhibited division protein B	Rv0174	-	part of mce1 operon	E Postavia do m	proteins 3
	mesJ parA	probable cell cycle protein chromosome partitioning; DNA -	Rv0587 Rv0588	-	part of <i>mce2</i> operon part of <i>mce2</i> operon	E. Bacteriocin-like	proteins 3
Rv3625c Rv3917c		binding	Rv0590	-	part of mce2 operon	F. Cytochrome P45	50 enzymes 22
Rv3917c	parB	possibly involved in chromosome	Rv0591	-	part of mce2 operon	•	•
		partitioning member of Smc1/Cut3/Cut14	Rv0592 Rv0594	-	part of <i>mce2</i> operon part of <i>mce2</i> operon	G. Coenzyme F42 enzymes	0-dependent 3
Rv3917c Rv3918c	smc.		Rv1085c	-	possible hemolysin	-	
Rv3917c Rv3918c Rv2922c	smc	family		-	putative exported p60 protein	H. Miscellaneous t	ransferases 61
Rv3917c Rv3918c Rv2922c Rv0012	smc -	family possible cell division protein	Rv1477		homologue	I Micaellaneeue ni	
Rv3917c Rv3918c Rv2922c Rv0012 Rv0435c	smc - -	family possible cell division protein ATPase of AAA-family		_	putative exported n60 protein		hosphatases lyases
Rv3917c Rv3918c Rv2922c Rv0012	smc - - -	family possible cell division protein	Hv1477 Rv1478	-	putative exported p60 protein homologue	and hydrolases	hosphatases, lyases, 18
Rv3917c Rv3918c Rv2922c Rv0012 Rv0435c Rv2115c Rv3213c	smc - - -	family possible cell division protein ATPase of AAA-family ATPase of AAA-family possible role in chromosome seg- regation		-	homologue putative exported p60 protein	and hydrolases	18
Rv3917c Rv3918c Rv2922c Rv0012 Rv0435c Rv2115c	smc - - - -	family possible cell division protein ATPase of AAA-family ATPase of AAA-family possible role in chromosome seg- regation possible role in chromosome parti-	Rv1478 Rv1566c	-	homologue putative exported p60 protein homologue		
Rv3917c Rv3918c Rv2922c Rv0012 Rv0435c Rv2115c Rv3213c	smc - - - -	family possible cell division protein ATPase of AAA-family ATPase of AAA-family possible role in chromosome seg- regation	Rv1478	-	homologue putative exported p60 protein homologue part of <i>mce3</i> operon	and hydrolases J. Cyclases	18
Rv3917c Rv3918c Rv2922c Rv0012 Rv0435c Rv2115c Rv3213c Rv1708	- - - - - and pepti	family possible cell division protein ATPase of AAA-family ATPase of AAA-family possible role in chromosome seg- regation possible role in chromosome parti- tioning	Rv1478 Rv1566c Rv1964 Rv1965 Rv1967	-	homologue putative exported p60 protein homologue part of <i>mce3</i> operon part of <i>mce3</i> operon part of <i>mce3</i> operon	and hydrolases J. Cyclases K. Chelatases	18 6 2
Rv3917c Rv3918c Rv2922c Rv0012 Rv0435c Rv2115c Rv3213c Rv1708 D. Protein Rv2916c	- - - - - and pepti	family possible cell division protein ATPase of AAA-family ATPase of AAA-family possible role in chromosome seg- regation possible role in chromosome parti- tioning ide secretion signal recognition particle protein	Rv1478 Rv1566c Rv1964 Rv1965 Rv1967 Rv1968	-	homologue putative exported p60 protein homologue part of mce3 operon part of mce3 operon part of mce3 operon part of mce3 operon	and hydrolases J. Cyclases	18 6 2
Rv3917c Rv3918c Rv2922c Rv0012 Rv0435c Rv2115c Rv3213c Rv1708 D. Protein Rv2916c Rv2903c	- - - - - and pepti ffh lepB	family possible cell division protein ATPase of AAA-family ATPase of AAA-family possible role in chromosome segregation possible role in chromosome partitioning ide secretion signal recognition particle protein signal peptidase I	Rv1478 Rv1566c Rv1964 Rv1965 Rv1967 Rv1968 Rv1969	-	homologue putative exported p60 protein homologue part of mee3 operon	and hydrolases J. Cyclases K. Chelatases V. Conserved hypo	18 6 2 otheticals 912
Rv3917c Rv3918c Rv2922c Rv0012 Rv2113c Rv2113c Rv11708 <i>D. Protein</i> Rv2916c Rv2903c Rv1614	- - - - - and pepti	family possible cell division protein ATPase of AAA-family ATPase of AAA-family possible role in chromosome seg- regation possible role in chromosome parti- tioning ide secretion signal recognition particle protein	Rv1478 Rv1566c Rv1964 Rv1965 Rv1967 Rv1968	-	homologue putative exported p60 protein homologue part of mce3 operon part of mce3 operon part of mce3 operon part of mce3 operon	and hydrolases J. Cyclases K. Chelatases V. Conserved hypo	18 6 2 otheticals 912 606
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Rv3917c Rv3918c Rv2922c Rv0012 Rv2113c Rv2113c Rv11708 <i>D. Protein</i> Rv2916c Rv2903c Rv1614	- - - - and pepti ffh lepB gt	family possible cell division protein ATPase of AAA-family ATPase of AAA-family ATPase of AAA-family possible role in chromosome seg- regation possible role in chromosome parti- tioning ide secretion signal recognition particle protein signal peptidase I prolipoprotein diacylglyceryl trans- ferase	Rv1478 Rv1566c Rv1964 Rv1965 Rv1967 Rv1968 Rv1969 Rv1971 Rv2190c	- - -	homologue putative exported p60 protein homologue part of mce3 operon putative p60 homologue	and hydrolases J. Cyclases K. Chelatases V. Conserved hypo	18 6 2 otheticals 912 606

Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence

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Countless millions of people have died from tuberculosis, a chronic infectious disease caused by the tubercle bacillus. The complete genome sequence of the best-characterized strain of *Mycobacterium tuberculosis*, H37Rv, has been determined and analysed in order to improve our understanding of the biology of this slow-growing pathogen and to help the conception of new prophylactic and therapeutic interventions. The genome comprises 4,411,529 base pairs, contains around 4,000 genes, and has a very high guanine + cytosine content that is reflected in the biased amino-acid content of the proteins. *M. tuberculosis* differs radically from other bacteria in that a very large portion of its coding capacity is devoted to the production of enzymes involved in lipogenesis and lipolysis, and to two new families of glycine-rich proteins with a repetitive structure that may represent a source of antigenic variation.

Despite the availability of effective short-course chemotherapy (DOTS) and the Bacille Calmette-Guérin (BCG) vaccine, the tubercle bacillus continues to claim more lives than any other single infectious agent¹. Recent years have seen increased incidence of tuberculosis in both developing and industrialized countries, the widespread emergence of drug-resistant strains and a deadly synergy with the human immunodeficiency virus (HIV). In 1993, the gravity of the situation led the World Health Organisation (WHO) to declare tuberculosis a global emergency in an attempt to heighten public and political awareness. Radical measures are needed now to prevent the grim predictions of the WHO becoming reality. The combination of genomics and bioinformatics has the potential to generate the information and knowledge that will enable the conception and development of new therapies and interventions needed to treat this airborne disease and to elucidate the unusual biology of its aetiological agent, Mycobacterium tuberculosis.

The characteristic features of the tubercle bacillus include its slow growth, dormancy, complex cell envelope, intracellular pathogenesis and genetic homogeneity². The generation time of *M. tuberculosis*, in synthetic medium or infected animals, is typically ~24 hours. This contributes to the chronic nature of the disease, imposes lengthy treatment regimens and represents a formidable obstacle for researchers. The state of dormancy in which the bacillus remains quiescent within infected tissue may reflect metabolic shutdown resulting from the action of a cell-mediated immune response that can contain but not eradicate the infection. As immunity wanes, through ageing or immune suppression, the dormant bacteria reactivate, causing an outbreak of disease often many decades after the initial infection³. The molecular basis of dormancy and reactivation remains obscure but is expected to be genetically programmed and to involve intracellular signalling pathways.

The cell envelope of M. tuberculosis, a Gram-positive bacterium with a G + C-rich genome, contains an additional layer beyond the peptidoglycan that is exceptionally rich in unusual lipids, glycoli-

pids and polysaccharides^{4,5}. Novel biosynthetic pathways generate cell-wall components such as mycolic acids, mycocerosic acid, phenolthiocerol, lipoarabinomannan and arabinogalactan, and several of these may contribute to mycobacterial longevity, trigger inflammatory host reactions and act in pathogenesis. Little is known about the mechanisms involved in life within the macrophage, or the extent and nature of the virulence factors produced by the bacillus and their contribution to disease.

It is thought that the progenitor of the *M. tuberculosis* complex, comprising *M. tuberculosis*, *M. bovis*, *M. bovis* BCG, *M. africanum* and *M. microti*, arose from a soil bacterium and that the human bacillus may have been derived from the bovine form following the domestication of cattle. The complex lacks interstrain genetic diversity, and nucleotide changes are very rare⁶. This is important in terms of immunity and vaccine development as most of the proteins will be identical in all strains and therefore antigenic drift will be restricted. On the basis of the systematic sequence analysis of 26 loci in a large number of independent isolates⁶, it was concluded that the genome of *M. tuberculosis* is either unusually inert or that the organism is relatively young in evolutionary terms.

Since its isolation in 1905, the H37Rv strain of *M. tuberculosis* has found extensive, worldwide application in biomedical research because it has retained full virulence in animal models of tuberculosis, unlike some clinical isolates; it is also susceptible to drugs and amenable to genetic manipulation. An integrated map of the 4.4 megabase (Mb) circular chromosome of this slow-growing pathogen had been established previously and ordered libraries of cosmids and bacterial artificial chromosomes (BACs) were available^{7,8}.

Organization and sequence of the genome

Sequence analysis. To obtain the contiguous genome sequence, a combined approach was used that involved the systematic sequence analysis of selected large-insert clones (cosmids and BACs) as well as

random small-insert clones from a whole-genome shotgun library. This culminated in a composite sequence of 4,411,529 base pairs (bp) (Figs 1, 2), with a G + C content of 65.6%. This represents the second-largest bacterial genome sequence currently available (after that of *Escherichia coli*). The initiation codon for the *dnaA* gene, a hallmark for the origin of replication, *oriC*, was chosen as the start point for numbering. The genome is rich in repetitive DNA, particularly insertion sequences, and in new multigene families and duplicated housekeeping genes. The G + C content is relatively constant throughout the genome (Fig. 1) indicating that horizontally transferred pathogenicity islands of atypical base composition are probably absent. Several regions showing higher than average G + C content (Fig. 1) were detected; these correspond to sequences belonging to a large gene family that includes the polymorphic G + C-rich sequences (PGRSs).

Genes for stable RNA. Fifty genes coding for functional RNA molecules were found. These molecules were the three species produced by the unique ribosomal RNA operon, the 10Sa RNA involved in degradation of proteins encoded by abnormal messenger RNA, the RNA component of RNase P, and 45 transfer RNAs. No 4.5S RNA could be detected. The *rrn* operon is situated unusually as it occurs about 1,500 kilobases (kb) from the putative *oriC*; most eubacteria have one or more *rrn* operons near to *oriC* to exploit the gene-dosage effect obtained during replication 10. This arrangement may be related to the slow growth of *M. tuberculosis*. The genes encoding tRNAs that recognize 43 of the 61 possible sense codons were distributed throughout the genome and, with one

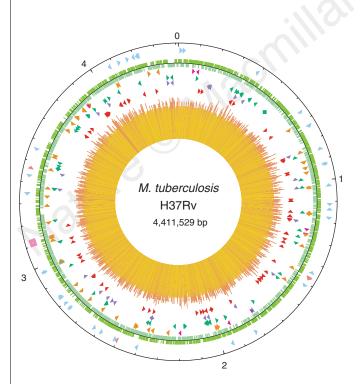


Figure 1 Circular map of the chromosome of M. tuberculosis H37Rv. The outer circle shows the scale in Mb, with 0 representing the origin of replication. The first ring from the exterior denotes the positions of stable RNA genes (tRNAs are blue, others are pink) and the direct repeat region (pink cube); the second ring inwards shows the coding sequence by strand (clockwise, dark green; anticlockwise, light green); the third ring depicts repetitive DNA (insertion sequences, orange; 13E12 REP family, dark pink; prophage, blue); the fourth ring shows the positions of the PPE family members (green); the fifth ring shows the PE family members (purple, excluding PGRS); and the sixth ring shows the positions of the PGRS sequences (dark red). The histogram (centre) represents G + C content, with <65% G + C in yellow, and >65% G + C in red. The figure was generated with software from DNASTAR.

exception, none of these uses A in the first position of the anticodon, indicating that extensive wobble occurs during translation. This is consistent with the high G+C content of the genome and the consequent bias in codon usage. Three genes encoding tRNAs for methionine were found; one of these genes (metV) is situated in a region that may correspond to the terminus of replication (Figs 1, 2). As metV is linked to defective genes for integrase and excisionase, perhaps it was once part of a phage or similar mobile genetic element

Insertion sequences and prophages. Sixteen copies of the promiscuous insertion sequence IS6110 and six copies of the more stable element IS1081 reside within the genome of H37Rv⁸. One copy of IS1081 is truncated. Scrutiny of the genomic sequence led to the identification of a further 32 different insertion sequence elements, most of which have not been described previously, and of the 13E12 family of repetitive sequences which exhibit some of the characteristics of mobile genetic elements (Fig. 1). The newly discovered insertion sequences belong mainly to the IS3 and IS256 families, although six of them define a new group. There is extensive similarity between IS1561 and IS1552 with insertion sequence elements found in *Nocardia* and *Rhodococcus* spp., suggesting that they may be widely disseminated among the actinomycetes.

Most of the insertion sequences in *M. tuberculosis* H37Rv appear to have inserted in intergenic or non-coding regions, often near tRNA genes (Fig. 1). Many are clustered, suggesting the existence of insertional hot-spots that prevent genes from being inactivated, as has been described for *Rhizobium*¹¹. The chromosomal distribution of the insertion sequences is informative as there appears to have been a selection against insertions in the quadrant encompassing *oriC* and an overrepresentation in the direct repeat region that contains the prototype IS6110. This bias was also observed experimentally in a transposon mutagenesis study¹².

At least two prophages have been detected in the genome sequence and their presence may explain why M. tuberculosis shows persistent low-level lysis in culture. Prophages phiRv1 and phiRv2 are both \sim 10 kb in length and are similarly organized, and some of their gene products show marked similarity to those encoded by certain bacteriophages from Streptomyces and saprophytic mycobacteria. The site of insertion of phiRv1 is intriguing as it corresponds to part of a repetitive sequence of the 13E12 family that itself appears to have integrated into the biotin operon. Some strains of *M. tuberculosis* have been described as requiring biotin as a growth supplement, indicating either that phiRv1 has a polar effect on expression of the distal bio genes or that aberrant excision, leading to mutation, may occur. During the serial attenuation of M. bovis that led to the vaccine strain M. bovis BCG, the phiRv1 prophage was lost¹³. In a systematic study of the genomic diversity of prophages and insertion sequences (S.V.G. et al., manuscript in preparation), only IS1532 exhibited significant variability, indicating that most of the prophages and insertion sequences are currently stable. However, from these combined observations, one can conclude that horizontal transfer of genetic material into the free-living ancestor of the M. tuberculosis complex probably occurred in nature before the tubercle bacillus adopted its specialized intracellular niche.

Figure 2 Linear map of the chromosome of *M. tuberculosis* H37Rv showing the position and orientation of known genes and coding sequences (CDS). We used the following functional categories (adapted from ref. 20): lipid metabolism (black); intermediary metabolism and respiration (yellow); information pathways (pink); regulatory proteins (sky blue); conserved hypothetical proteins (orange); proteins of unknown function (light green); insertion sequences and phage-related functions (blue); stable RNAs (purple); cell wall and cell processes (dark green); PE and PPE protein families (magenta); virulence, detoxification and adaptation (white). For additional information about gene functions, refer to http://www.sanger.ac.uk.

Genes encoding proteins. 3,924 open reading frames were identified in the genome (see Methods), accounting for ~91% of the potential coding capacity (Figs 1, 2). A few of these genes appear to have in-frame stop codons or frameshift mutations (irrespective of the source of the DNA sequenced) and may either use frameshifting during translation or correspond to pseudogenes. Consistent with the high G + C content of the genome, GTG initiation codons (35%) are used more frequently than in Bacillus subtilis (9%) and E. coli (14%), although ATG (61%) is the most common translational start. There are a few examples of atypical initiation codons, the most notable being the ATC used by infC, which begins with ATT in both B. subtilis and E. coli^{9,14}. There is a slight bias in the orientation of the genes (Fig. 1) with respect to the direction of replication as ~59% are transcribed with the same polarity as replication, compared with 75% in B. subtilis. In other bacteria, genes transcribed in the same direction as the replication forks are believed to be expressed more efficiently^{9,14}. Again, the more even distribution in gene polarity seen in M. tuberculosis may reflect the slow growth and infrequent replication cycles. Three genes (dnaB, recA and Rv1461) have been invaded by sequences encoding inteins (protein introns) and in all three cases their counterparts in M. leprae also contain inteins, but at different sites¹⁵ (S.T.C. et al., unpublished observations).

Protein function, composition and duplication. By using various database comparisons, we attributed precise functions to ~40% of the predicted proteins and found some information or similarity for another 44%. The remaining 16% resembled no known proteins and may account for specific mycobacterial functions. Examination of the amino-acid composition of the M. tuberculosis proteome by correspondence analysis¹⁶, and comparison with that of other microorganisms whose genome sequences are available, revealed a statistically significant preference for the amino acids Ala, Gly, Pro, Arg and Trp, which are all encoded by G + C-rich codons, and a comparative reduction in the use of amino acids encoded by A + Trich codons such as Asn, Ile, Lys, Phe and Tyr (Fig. 3). This approach also identified two groups of proteins rich in Asn or Gly that belong to new families, PE and PPE (see below). The fraction of the proteome that has arisen through gene duplication is similar to that seen in E. coli or B. subtilis (~51%; refs 9, 14), except that the level of sequence conservation is considerably higher, indicating that there may be extensive redundancy or differential production of the corresponding polypeptides. The apparent lack of divergence following gene duplication is consistent with the hypothesis that M. tuberculosis is of recent descent⁶.

General metabolism, regulation and drug resistance

Metabolic pathways. From the genome sequence, it is clear that the tubercle bacillus has the potential to synthesize all the essential amino acids, vitamins and enzyme co-factors, although some of the pathways involved may differ from those found in other bacteria. M. tuberculosis can metabolize a variety of carbohydrates, hydrocarbons, alcohols, ketones and carboxylic acids^{2,17}. It is apparent from genome inspection that, in addition to many functions involved in lipid metabolism, the enzymes necessary for glycolysis, the pentose phosphate pathway, and the tricarboxylic acid and glyoxylate cycles are all present. A large number (~200) of oxidoreductases, oxygenases and dehydrogenases is predicted, as well as many oxygenases containing cytochrome P450, that are similar to fungal proteins involved in sterol degradation. Under aerobic growth conditions, ATP will be generated by oxidative phosphorylation from electron transport chains involving a ubiquinone cytochrome b reductase complex and cytochrome c oxidase. Components of several anaerobic phosphorylative electron transport chains are also present, including genes for nitrate reductase (narGHJI), fumarate reductase (frdABCD) and possibly nitrite reductase (nirBD), as well as a new reductase (*narX*) that results from a rearrangement of a homologue of the narGHJI operon. Two genes encoding haemoglobin-like

proteins, which may protect against oxidative stress or be involved in oxygen capture, were found. The ability of the bacillus to adapt its metabolism to environmental change is significant as it not only has to compete with the lung for oxygen but must also adapt to the microaerophilic/anaerobic environment at the heart of the burgeoning granuloma.

Regulation and signal transduction. Given the complexity of the environmental and metabolic choices facing M. tuberculosis, an extensive regulatory repertoire was expected. Thirteen putative sigma factors govern gene expression at the level of transcription initiation, and more than 100 regulatory proteins are predicted (Table 1). Unlike B. subtilis and E. coli, in which there are >30 copies of different two-component regulatory systems¹⁴, M. tuberculosis has only 11 complete pairs of sensor histidine kinases and response regulators, and a few isolated kinase and regulatory genes. This relative paucity in environmental signal transduction pathways is probably offset by the presence of a family of eukaryotic-like serine/ threonine protein kinases (STPKs), which function as part of a phosphorelay system¹⁸. The STPKs probably have two domains: the well-conserved kinase domain at the amino terminus is predicted to be connected by a transmembrane segment to the carboxy-terminal region that may respond to specific stimuli. Several of the predicted envelope lipoproteins, such as that encoded by lppR (Rv2403), show extensive similarity to this putative receptor domain of STPKs, suggesting possible interplay. The STPKs probably function in signal transduction pathways and may govern important cellular decisions such as dormancy and cell division, and although their partners are unknown, candidate genes for phosphoprotein phosphatases have been identified.

Drug resistance. *M. tuberculosis* is naturally resistant to many antibiotics, making treatment difficult¹⁹. This resistance is due mainly to the highly hydrophobic cell envelope acting as a permeability barrier⁴, but many potential resistance determinants are also encoded in the genome. These include hydrolytic or drug-modifying enzymes such as β-lactamases and aminoglycoside acetyl transferases, and many potential drug–efflux systems, such as 14 members of the major facilitator family and numerous ABC transporters. Knowledge of these putative resistance mechanisms will promote better use of existing drugs and facilitate the conception of new therapies.

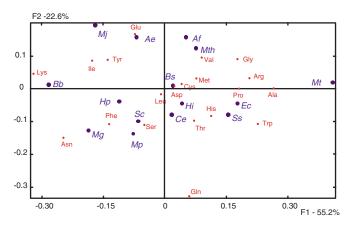


Figure 3 Correspondence analysis of the proteomes from extensively sequenced organisms as a function of amino-acid composition. Note the extreme position of *M. tuberculosis* and the shift in amino-acid preference reflecting increasing G + C content from left to right. Abbreviations used: Ae, Aquifex aeolicus; Af, Archaeoglobus fulgidis; Bb, Borrelia burgdorfei; Bs, B. subtilis; Ce, Caenorhabditis elegans; Ec, E. coli; Hi, Haemophilus influenzae; Hp, Helicobacter pylori; Mg, Mycoplasma genitalium; Mj, Methanococcus jannaschi; Mp, Mycoplasma pneumoniae; Mt, M. tuberculosis; Mth, Methanobacterium thermoautotrophicum; Sc, Saccharomyces cerevisiae; Ss, Synechocystis sp. strain PCC6803. F1 and F2, first and second factorial axes¹⁶.

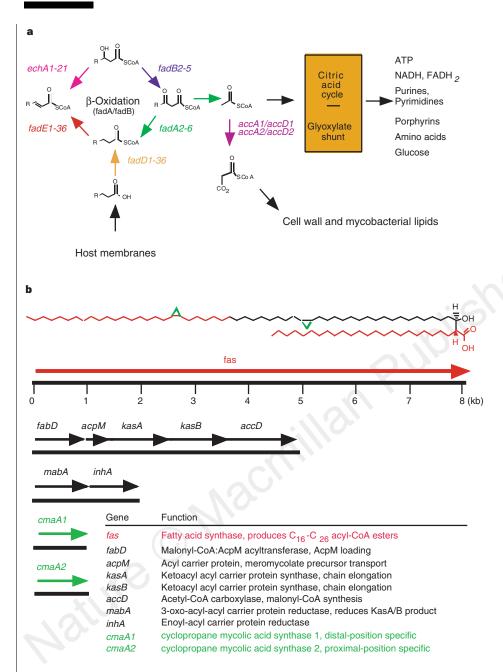
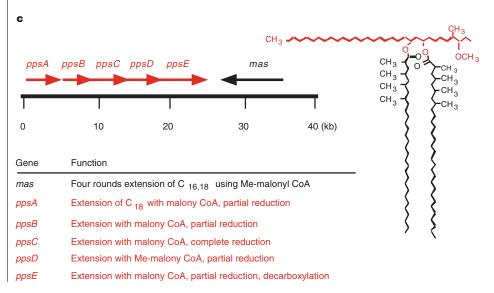


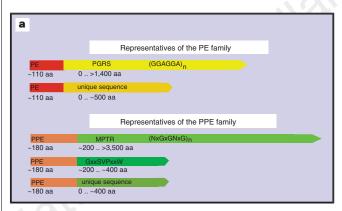
Figure 4 Lipid metabolism. a, Degradation of host-cell lipids is vital in the intracellular life of M. tuberculosis. Host-cell membranes provide precursors for many metabolic processes, as well as potential precursors of mycobacterial cell-wall constituents, through the actions of a broad family of β -oxidative enzymes encoded by multiple copies in the genome. These enzymes produce acetyl CoA, which can be converted into many different metabolites and fuel for the bacteria through the actions of the enzymes of the citric acid cycle and the glyoxylate shunt of this cycle. b, The genes that synthesize mycolic acids, the dominant lipid component of the mycobacterial cell wall, include the type I fatty acid synthase (fas) and a unique type II system which relies on extension of a precursor bound to an acyl carrier protein to form full-length (~80-carbon) mycolic acids. The cma genes are responsible for cyclopropanation. c, The genes that produce phthiocerol dimycocerosate form a large operon and represent type I (mas) and type II (the pps operon) polyketide synthase systems. Functions are colour coordinated.



Lipid metabolism

Very few organisms produce such a diverse array of lipophilic molecules as M. tuberculosis. These molecules range from simple fatty acids such as palmitate and tuberculostearate, through isoprenoids, to very-long-chain, highly complex molecules such as mycolic acids and the phenolphthiocerol alcohols that esterify with mycocerosic acid to form the scaffold for attachment of the mycosides. Mycobacteria contain examples of every known lipid and polyketide biosynthetic system, including enzymes usually found in mammals and plants as well as the common bacterial systems. The biosynthetic capacity is overshadowed by the even more remarkable radiation of degradative, fatty acid oxidation systems and, in total, there are \sim 250 distinct enzymes involved in fatty acid metabolism in M. tuberculosis compared with only 50 in E. $coli^{20}$.

Fatty acid degradation. In vivo-grown mycobacteria have been suggested to be largely lipolytic, rather than lipogenic, because of the variety and quantity of lipids available within mammalian cells and the tubercle² (Fig. 4a). The abundance of genes encoding components of fatty acid oxidation systems found by our genomic approach supports this proposition, as there are 36 acyl-CoA synthases and a family of 36 related enzymes that could catalyse the first step in fatty acid degradation. There are 21 homologous enzymes belonging to the enoyl-CoA hydratase/isomerase superfamily of enzymes, which rehydrate the nascent product of the acyl-CoA dehydrogenase. The four enzymes that convert the 3-hydroxy fatty acid into a 3-keto fatty acid appear less numerous, mainly



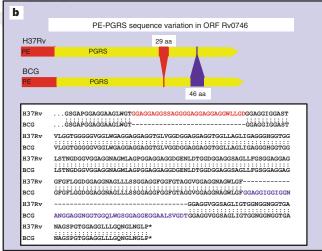


Figure 5 The PE and PPE protein families. **a**, Classification of the PE and PPE protein families. **b**, Sequence variation between *M. tuberculosis* H37Rv and *M. bovis* BCG-Pasteur in the PE-PGRS encoded by open reading frame (ORF) Rv0746.

because they are difficult to distinguish from other members of the short-chain alcohol dehydrogenase family on the basis of primary sequence. The five enzymes that complete the cycle by thiolysis of the β -ketoester, the acetyl-CoA C-acetyltransferases, do indeed appear to be a more limited family. In addition to this extensive set of dissociated degradative enzymes, the genome also encodes the canonical FadA/FadB β -oxidation complex (Rv0859 and Rv0860). Accessory activities are present for the metabolism of odd-chain and multiply unsaturated fatty acids.

Fatty acid biosynthesis. At least two discrete types of enzyme system, fatty acid synthase (FAS) I and FAS II, are involved in fatty acid biosynthesis in mycobacteria (Fig. 4b). FAS I (Rv2524, fas) is a single polypeptide with multiple catalytic activities that generates several shorter CoA esters from acetyl-CoA primers⁵ and probably creates precursors for elongation by all of the other fatty acid and polyketide systems. FAS II consists of dissociable enzyme components which act on a substrate bound to an acyl-carrier protein (ACP). FAS II is incapable of de novo fatty acid synthesis but instead elongates palmitoyl-ACP to fatty acids ranging from 24 to 56 carbons in length^{17,21}. Several different components of FAS II may be targets for the important tuberculosis drug isoniazid, including the enoyl-ACP reductase InhA²², the ketoacyl-ACP synthase KasA and the ACP AcpM²¹. Analysis of the genome shows that there are only three potential ketoacyl synthases: KasA and KasB are highly related, and their genes cluster with acpM, whereas KasC is a more distant homologue of a ketoacyl synthase III system. The number of ketoacyl synthase and ACP genes indicates that there is a single FAS II system. Its genetic organization, with two clustered ketoacyl synthases, resembles that of type II aromatic polyketide biosynthetic gene clusters, such as those for actinorhodin, tetracycline and tetracenomycin in *Streptomyces* species²³. InhA seems to be the sole enoyl-ACP reductase and its gene is co-transcribed with a fabG homologue, which encodes 3-oxoacyl-ACP reductase. Both of these proteins are probably important in the biosynthesis of mycolic acids.

Fatty acids are synthesized from malonyl-CoA and precursors are generated by the enzymatic carboxylation of acetyl (or propionyl)-CoA by a biotin-dependent carboxylase (Fig. 4b). From study of the genome we predict that there are three complete carboxylase systems, each consisting of an α - and a β -subunit, as well as three β -subunits without an α -counterpart. As a group, all of the carboxylases seem to be more related to the mammalian homologues than to the corresponding bacterial enzymes. Two of these carboxylase systems (accA1, accD1 and accA2, accD2) are probably involved in degradation of odd-numbered fatty acids, as they are adjacent to genes for other known degradative enzymes. They may convert propionyl-CoA to succinyl-CoA, which can then be incorporated into the tricarboxylic acid cycle. The synthetic carboxylases (accA3, accD3, accD4, accD5 and accD6) are more difficult to understand. The three extra β-subunits might direct carboxylation to the appropriate precursor or may simply increase the total amount of carboxylated precursor available if this step were ratelimiting.

Synthesis of the paraffinic backbone of fatty and mycolic acids in the cell is followed by extensive postsynthetic modifications and unsaturations, particularly in the case of the mycolic acids^{24,25}. Unsaturation is catalysed either by a FabA-like β-hydroxyacyl-ACP dehydrase, acting with a specific ketoacyl synthase, or by an aerobic terminal mixed function desaturase that uses both molecular oxygen and NADPH. Inspection of the genome revealed no obvious candidates for the FabA-like activity. However, three potential aerobic desaturases (encoded by *desA1*, *desA2* and *desA3*) were evident that show little similarity to related vertebrate or yeast enzymes (which act on CoA esters) but instead resemble plant desaturases (which use ACP esters). Consequently, the genomic data indicate that unsaturation of the meromycolate chain may occur while the acyl group is bound to AcpM.

Much of the subsequent structural diversity in mycolic acids is

generated by a family of S-adenosyl-L-methionine-dependent enzymes, which use the unsaturated meromycolic acid as a substrate to generate cis and trans cyclopropanes and other mycolates. Six members of this family have been identified and characterized²⁵ and two clustered, convergently transcribed new genes are evident in the genome (umaA1 and umaA2). From the functions of the known family members and the structures of mycolic acids in M. tuberculosis, it is tempting to speculate that these new enzymes may introduce the *trans* cyclopropanes into the meromycolate precursor. In addition to these two methyltransferases, there are two other unrelated lipid methyltransferases (Ufa1 and Ufa2) that share homology with cyclopropane fatty acid synthase of E. coli²⁵. Although cyclopropanation seems to be a relatively common modification of mycolic acids, cyclopropanation of plasma-membrane constituents has not been described in mycobacteria. Tuberculostearic acid is produced by methylation of oleic acid, and may be synthesized by one of these two enzymes.

Condensation of the fully functionalized and preformed meromycolate chain with a 26-carbon α-branch generates full-length mycolic acids that must be transported to their final location for attachment to the cell-wall arabinogalactan. The transfer and subsequent transesterification is mediated by three well-known immunogenic proteins of the antigen 85 complex²⁶. The genome encodes a fourth member of this complex, antigen 85C' (fbpC2, Rv0129), which is highly related to antigen 85C. Further studies are needed to show whether the protein possesses mycolytransferase activity and to clarify the reason behind the apparent redundancy. Polyketide synthesis. Mycobacteria synthesize polyketides by several different mechanisms. A modular type I system, similar to that involved in erythromycin biosynthesis²³, is encoded by a very large operon, ppsABCDE, and functions in the production of phenolphthiocerol⁵. The absence of a second type I polyketide synthase suggests that the related lipids phthiocerol A and B, phthiodiolone A and phthiotriol may all be synthesized by the same system, either from alternative primers or by differential postsynthetic modification. It is physiologically significant that the pps gene cluster occurs immediately upstream of mas, which encodes the multifunctional enzyme mycocerosic acid synthase (MAS), as their products phthiocerol and mycocerosic acid esterify to form the very abundant cell-wall-associated molecule phthiocerol dimycocerosate (Fig. 4c).

Members of another large group of polyketide synthase enzymes are similar to MAS, which also generates the multiply methylbranched fatty acid components of mycosides and phthiocerol dimycocerosate, abundant cell-wall-associated molecules⁵. Although some of these polyketide synthases may extend type I FAS CoA primers to produce other long-chain methyl-branched fatty acids such as mycolipenic, mycolipodienic and mycolipanolic acids or the phthioceranic and hydroxyphthioceranic acids, or may even show functional overlap⁵, there are many more of these enzymes than there are known metabolites. Thus there may be new lipid and polyketide metabolites that are expressed only under certain conditions, such as during infection and disease.

A fourth class of polyketide synthases is related to the plant enzyme superfamily that includes chalcone and stilbene synthase²³. These polyketide synthases are phylogenetically divergent from all other polyketide and fatty acid synthases and generate unreduced polyketides that are typically associated with anthocyanin pigments and flavonoids. The function of these systems, which are often linked to apparent type I modules, is unknown. An example is the gene cluster spanning *pks10*, *pks7*, *pks8* and *pks9*, which includes two of the chalcone-synthase-like enzymes and two modules of an apparent type I system. The unknown metabolites produced by these enzymes are interesting because of the potent biological activities of some polyketides such as the immunosuppressor rapamycin.

Siderophores. Peptides that are not ribosomally synthesized are

made by a process that is mechanistically analogous to polyketide synthesis^{23,27}. These peptides include the structurally related iron-scavenging siderophores, the mycobactins and the exochelins^{2,28}, which are derived from salicylate by the addition of serine (or threonine), two lysines and various fatty acids and possible polyketide segments. The *mbt* operon, encoding one apparent salicylate-activating protein, three amino-acid ligases, and a single module of a type I polyketide synthase, may be responsible for the biosynthesis of the mycobacterial siderophores. The presence of only one non-ribosomal peptide-synthesis system indicates that this pathway may generate both siderophores and that subsequent modification of a single ϵ -amino group of one lysine residue may account for the different physical properties and function of the siderophores²⁸.

Immunological aspects and pathogenicity

Given the scale of the global tuberculosis burden, vaccination is not only a priority but remains the only realistic public health intervention that is likely to affect both the incidence and the prevalence of the disease²⁹. Several areas of vaccine development are promising, including DNA vaccination, use of secreted or surface-exposed proteins as immunogens, recombinant forms of BCG and rational attenuation of M. tuberculosis²⁹. All of these avenues of research will benefit from the genome sequence as its availability will stimulate more focused approaches. Genes encoding ~90 lipoproteins were identified, some of which are enzymes or components of transport systems, and a similar number of genes encoding preproteins (with type I signal peptides) that are probably exported by the Secdependent pathway. M. tuberculosis seems to have two copies of secA. The potent T-cell antigen Esat-6 (ref. 30), which is probably secreted in a Sec-independent manner, is encoded by a member of a multigene family. Examination of the genetic context reveals several similarly organized operons that include genes encoding large ATPhydrolysing membrane proteins that might act as transporters. One of the surprises of the genome project was the discovery of two extensive families of novel glycine-rich proteins, which may be of immunological significance as they are predicted to be abundant and potentially polymorphic antigens.

The PE and PPE multigene families. About 10% of the coding capacity of the genome is devoted to two large unrelated families of acidic, glycine-rich proteins, the PE and PPE families, whose genes are clustered (Figs 1, 2) and are often based on multiple copies of the polymorphic repetitive sequences referred to as PGRSs, and major polymorphic tandem repeats (MPTRs), respectively^{31,32}. The names PE and PPE derive from the motifs Pro-Glu (PE) and Pro-Pro-Glu (PPE) found near the N terminus in most cases³³. The 99 members of the PE protein family all have a highly conserved Nterminal domain of ~110 amino-acid residues that is predicted to have a globular structure, followed by a C-terminal segment that varies in size, sequence and repeat copy number (Fig. 5). Phylogenetic analysis separated the PE family into several subfamilies. The largest of these is the highly repetitive PGRS class, which contains 61 members; members of the other subfamilies, share very limited sequence similarity in their C-terminal domains (Fig. 5). The predicted molecular weights of the PE proteins vary considerably as a few members contain only the N-terminal domain, whereas most have C-terminal extensions ranging in size from 100 to 1,400 residues. The PGRS proteins have a high glycine content (up to 50%), which is the result of multiple tandem repetitions of Gly-Gly-Ala or Gly-Gly-Asn motifs, or variations thereof.

The 68 members of the PPE protein family (Fig. 5) also have a conserved N-terminal domain that comprises ~180 amino-acid residues, followed by C-terminal segments that vary markedly in sequence and length. These proteins fall into at least three groups, one of which constitutes the MPTR class characterized by the presence of multiple, tandem copies of the motif Asn–X–Gly–X–Gly–Asn–X–Gly. The second subgroup contains a characteristic, well-conserved motif around position 350, whereas the third contains

proteins that are unrelated except for the presence of the common 180-residue PPE domain.

The subcellular location of the PE and PPE proteins is unknown and in only one case, that of a lipase (Rv3097), has a function been demonstrated. On examination of the protein database from the extensively sequenced *M. leprae*¹⁵, no PGRS- or MPTR-related polypeptides were detected but a few proteins belonging to the non-MPTR subgroup of the PPE family were found. These proteins include one of the major antigens recognized by leprosy patients, the serine-rich antigen³⁴. Although it is too early to attribute biological functions to the PE and PPE families, it is tempting to speculate that they could be of immunological importance. Two interesting possibilities spring to mind. First, they could represent the principal source of antigenic variation in what is otherwise a genetically and antigenically homogeneous bacterium. Second, these glycine-rich proteins might interfere with immune responses by inhibiting antigen processing.

Several observations and results support the possibility of antigenic variation associated with both the PE and the PPE family proteins. The PGRS member Rv1759 is a fibronectin-binding protein of relative molecular mass 55,000 (ref. 35) that elicits a variable antibody response, indicating either that individuals mount different immune responses or that this PGRS protein may vary between strains of M. tuberculosis. The latter possibility is supported by restriction fragment length polymorphisms for various PGRS and MPTR sequences in clinical isolates³³. Direct support for genetic variation within both the PE and the PPE families was obtained by comparative DNA sequence analysis (Fig. 5). The gene for the PE-PGRS protein Rv0746 of BCG differs from that in H37Rv by the deletion of 29 codons and the insertion of 46 codons. Similar variation was seen in the gene for the PPE protein Rv0442 (data not shown). As these differences were all associated with repetitive sequences they could have resulted from intergenic or intragenic recombinational events or, more probably, from strand slippage during replication³². These mechanisms are known to generate antigenic variability in other bacterial pathogens³⁶.

There are several parallels between the PGRS proteins and the Epstein-Barr virus nuclear antigens (EBNAs). Members of both polypeptide families are glycine-rich, contain extensive Gly-Ala repeats, and exhibit variation in the length of the repeat region between different isolates. The Gly-Ala repeat region of EBNA1 functions as a cis-acting inhibitor of the ubiquitin/proteasome antigen-processing pathway that generates peptides presented in the context of major histocompatibility complex (MHC) class I molecules^{37,38}. MHC class I knockout mice are very susceptible to M. tuberculosis, underlining the importance of a cytotoxic T-cell response in protection against disease^{3,39}. Given the many potential effects of the PPE and PE proteins, it is important that further studies are performed to understand their activity. If extensive antigenic variability or reduced antigen presentation were indeed found, this would be significant for vaccine design and for understanding protective immunity in tuberculosis, and might even explain the varied responses seen in different BCG vaccination programmes⁴⁰.

Pathogenicity. Despite intensive research efforts, there is little information about the molecular basis of mycobacterial virulence⁴¹. However, this situation should now change as the genome sequence will accelerate the study of pathogenesis as never before, because other bacterial factors that may contribute to virulence are becoming apparent. Before the completion of the genome sequence, only three virulence factors had been described⁴¹: catalase-peroxidase, which protects against reactive oxygen species produced by the phagocyte; *mce*, which encodes macrophage-colonizing factor⁴²; and a sigma factor gene, *sigA* (aka *rpoV*), mutations in which can lead to attenuation⁴¹. In addition to these single-gene virulence factors, the mycobacterial cell wall⁴ is also important in pathology,

but the complex nature of its biosynthesis makes it difficult to identify critical genes whose inactivation would lead to attenuation.

On inspection of the genome sequence, it was apparent that four copies of mce were present and that these were all situated in operons, comprising eight genes, organized in exactly the same manner. In each case, the genes preceding mce code for integral membrane proteins, whereas mce and the following five genes are all predicted to encode proteins with signal sequences or hydrophobic stretches at the N terminus. These sets of proteins, about which little is known, may well be secreted or surface-exposed; this is consistent with the proposed role of Mce in invasion of host cells⁴². Furthermore, a homologue of smpB, which has been implicated in intracellular survival of Salmonella typhimurium, has also been identified⁴³. Among the other secreted proteins identified from the genome sequence that could act as virulence factors are a series of phospholipases C, lipases and esterases, which might attack cellular or vacuolar membranes, as well as several proteases. One of these phospholipases acts as a contact-dependent haemolysin (N. Stoker, personal communication). The presence of storage proteins in the bacillus, such as the haemoglobin-like oxygen captors described above, points to its ability to stockpile essential growth factors, allowing it to persist in the nutrient-limited environment of the phagosome. In this regard, the ferritin-like proteins, encoded by bfrA and bfrB, may be important in intracellular survival as the capacity to acquire enough iron in the vacuole is very limited.

Methods

Sequence analysis. Initially, ~3.2 Mb of sequence was generated from cosmids⁸ and the remainder was obtained from selected BAC clones⁷ and 45,000 whole-genome shotgun clones. Sheared fragments (1.4-2.0 kb) from cosmids and BACs were cloned into M13 vectors, whereas genomic DNA was cloned in pUC18 to obtain both forward and reverse reads. The PGRS genes were grossly underrepresented in pUC18 but better covered in the BAC and cosmid M13 libraries. We used small-insert libraries⁴⁴ to sequence regions prone to compression or deletion and, in some cases, obtained sequences from products of the polymerase chain reaction or directly from BACs⁷. All shotgun sequencing was performed with standard dye terminators to minimize compression problems, whereas finishing reactions used dRhodamine or BigDye terminators (http://www.sanger.ac.uk). Problem areas were verified by using dye primers. Thirty differences were found between the genomic shotgun sequences and the cosmids; twenty of which were due to sequencing errors and ten to mutations in cosmids (1 error per 320 kb). Less than 0.1% of the sequence was from areas of single-clone coverage, and <0.2% was from one strand with only one sequencing chemistry.

Informatics. Sequence assembly involved PHRAP, GAP4 (ref. 45) and a customized perl script that merges sequences from different libraries and generates segments that can be processed by several finishers simultaneously. Sequence analysis and annotation was managed by DIANA (B.G.B. *et al.*, unpublished). Genes encoding proteins were identified by TB-parse⁴⁶ using a hidden Markov model trained on known *M. tuberculosis* coding and noncoding regions and translation-initiation signals, with corroboration by positional base preference. Interrogation of the EMBL, TREMBL, SwissProt, PROSITE⁴⁷ and in-house databases involved BLASTN, BLASTX⁴⁸, DOTTER (http://www.sanger.ac.uk) and FASTA⁴⁹. tRNA genes were located and identified using tRNAscan and tRNAscan-SE⁵⁰. The complete sequence, a list of annotated cosmids and linking regions can be found on our website (http://www.sanger.ac.uk) and in MycDB (http://www.pasteur.fr/mycdb/).

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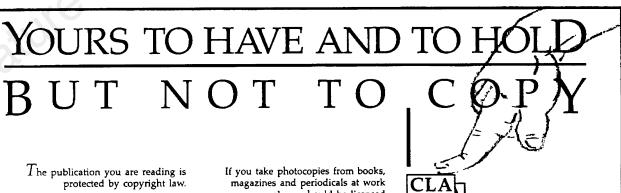
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Table 1. Functional classification of *Mycobacterium tuberculosis* protein-coding genes

		netabolism	_		superfamily	Rv3543c	fadE29	acyl-CoA dehydrogenase
A. Degrad		4-	Rv2831	echA16	enoyl-CoA hydratase/isomerase	Rv3560c	fadE30	acyl-CoA dehydrogenase
Rv0186	n compound bglS	us β-glucosidase	Rv3039c	echA17	superfamily enoyl-CoA hydratase/isomerase	Rv3562 Rv3563	fadE31 fadE32	acyl-CoA dehydrogenase acyl-CoA dehydrogenase
Rv2202c		carbohydrate kinase	1100000	0011111	superfamily	Rv3564	fadE33	acyl-CoA dehydrogenase
Rv0727c		L-fuculose phosphate aldolase	Rv3373	echA18	enoyl-CoA hydratase/isomerase	Rv3573c	fadE34	acyl-CoA dehydrogenase
Rv1731	gabD1	succinate-semialdehyde dehydro-			superfamily, N-term	Rv3797	fadE35	acyl-CoA dehydrogenase
D: 0004-	t- D0	genase	Rv3374	echA18'	enoyl-CoA hydratase/isomerase	Rv3761c	fadE36	acyl-CoA dehydrogenase
Rv0234c	gabD2	succinate-semialdehyde dehydro- genase	Rv3516	echA19	superfamily, C-term enoyl-CoA hydratase/isomerase	Rv1175c Rv0855	fadH far	2,4-Dienoyl-CoA Reductase fatty acyl-CoA racemase
Rv0501	galE1	UDP-glucose 4-epimerase	nvaaio	ecna 19	superfamily	Rv1143	mcr	α-methyl acyl-CoA racemase
Rv0536	galE2	UDP-glucose 4-epimerase	Rv3550	echA20	enoyl-CoA hydratase/isomerase	Rv1492	mutA	methylmalonyl-CoA mutase, β
Rv0620	galK	galactokinase			superfamily			subunit
Rv0619	galT	galactose-1-phosphate uridylyl-	Rv3774	echA21	enoyl-CoA hydratase/isomerase	Rv1493	mutB	methylmalonyl-CoA mutase, α
D: 0040		transferase C-term	D: 0050	C1A	superfamily	D: 0504	4	subunit
Rv0618	galT'	galactose-1-phosphate uridylyl- transferase N-term	Rv0859	fadA	β oxidation complex, β subunit (acetyl-CoA C-acetyltransferase)	Rv2504c	scoA	3-oxo acid:CoA transferase, α sub- unit
Rv0993	galU	UTP-glucose-1-phosphate uridylyl-	Rv0243	fadA2	acetyl-CoA C-acetyltransferase	Rv2503c	scoB	3-oxo acid:CoA transferase, β sub-
	garo	transferase	Rv1074c	fadA3	acetyl-CoA C-acetyltransferase	20000	0002	unit
Rv3696c	glpK	ATP:glycerol 3-phosphotrans-	Rv1323	fadA4	acetyl-CoA C-acetyltransferase	Rv1136	-	probable carnitine racemase
		ferase			(aka thiL)	Rv1683	-	possible acyl-CoA synthase
Rv3255c		mannose-6-phosphate isomerase	Rv3546	fadA5	acetyl-CoA C-acetyltransferase	4. Discourts		Cat
Rv3441c	mrsA	phosphoglucomutase or phospho- mannomutase	Rv3556c Rv0860	fadA6 fadB	acetyl-CoA C-acetyltransferase β oxidation complex, α subunit	4. Phosph Rv2368c	orous com phoH	npounds ATP-binding <i>pho</i> regulon
Rv0118c	oxcA	oxalyl-CoA decarboxylase	HV0000	IauD	(multiple activities)	HV2300C	priori	component
Rv3068c		phosphoglucomutase	Rv0468	fadB2	3-hydroxyacyl-CoA dehydroge-	Rv1095	phoH2	PhoH-like protein
Rv3257c	pmmA	phosphomannomutase			nase	Rv3628	ppa	probable inorganic pyrophos-
Rv3308	pmmB	phosphomannomutase	Rv1715	fadB3	3-hydroxyacyl-CoA dehydroge-			phatase
Rv2702	ppgK	polyphosphate glucokinase	D: 04.44	(ID 4	nase	Rv2984	ppk	polyphosphate kinase
Rv0408 Rv0729	pta xylB	phosphate acetyltransferase	Rv3141	fadB4	3-hydroxyacyl-CoA dehydroge-	B Engrav	motabolic	·m
Rv1096	- XYID	xylulose kinase carbohydrate degrading enzyme	Rv1912c	fadB5	nase 3-hydroxyacyl-CoA dehydroge-	B. Energy 1. Glycoly		III
1111000		carbonyarate degrading enzyme	11010120	iaabo	nase	Rv1023	eno	enolase
2. Amino	acids and	amines	Rv1750c	fadD1	acyl-CoA synthase	Rv0363c	fba	fructose bisphosphate aldolase
Rv1905c		D-amino acid oxidase	Rv0270	fadD2	acyl-CoA synthase	Rv1436	gap	glyceraldehyde 3-phosphate dehy-
Rv2531c		ornithine/arginine decarboxylase	Rv3561	fadD3	acyl-CoA synthase			drogenase
Rv2780	ald	L-alanine dehydrogenase	Rv0214	fadD4	acyl-CoA synthase	Rv0489	gpm	phosphoglycerate mutase I
Rv1538c		L-asparaginase	Rv0166	fadD5	acyl-CoA synthase	Rv3010c	pfkA	phosphofructokinase I
Rv1001 Rv0753c	arcA mmsA	arginine deiminase methylmalmonate semialdehyde	Rv1206 Rv0119	fadD6 fadD7	acyl-CoA synthase acyl-CoA synthase	Rv2029c Rv0946c	pfkB pgi	phosphofructokinase II glucose-6-phosphate isomerase
11007550	IIIIII	dehydrogenase	Rv0551c	fadD8	acyl-CoA synthase	Rv1437	pgi pgk	phosphoglycerate kinase
Rv0751c	mmsB	methylmalmonate semialdehyde	Rv2590	fadD9	acyl-CoA synthase	Rv1617	pykA	pyruvate kinase
		oxidoreductase	Rv0099	fadD10	acyl-CoA synthase	Rv1438	tpi	triosephosphate isomerase
Rv1187	rocA	pyrroline-5-carboxylate dehydro-	Rv1550	fadD11	acyl-CoA synthase, N-term	Rv2419c	-	putative phosphoglycerate mutase
		genase	Rv1549	fadD11'	acyl-CoA synthase, C-term	Rv3837c	-	putative phosphoglycerate mutase
Rv2322c		ornithine aminotransferase	Rv1427c	fadD12	acyl-CoA synthase	0. D		
Rv2321c Rv1848	rocD2 ureA	ornithine aminotransferase	Rv3089 Rv1058	fadD13 fadD14	acyl-CoA synthase	Pyruvat Rv2241	e denyaro <i>aceE</i>	
Rv1849	ureB	urease γ subunit urease β subunit	Rv2187	fadD14	acyl-CoA synthase acyl-CoA synthase	NV2241	acec	pyruvate dehydrogenase E1 com- ponent
Rv1850	ureC	urease α subunit	Rv0852	fadD16	acyl-CoA synthase	Rv3303c	lpdA	dihydrolipoamide dehydrogenase
Rv1853	ureD	urease accessory protein	Rv3506	fadD17	acyl-CoA synthase	Rv2497c	pdhA	pyruvate dehydrogenase E1 com-
Rv1851	ureF	urease accessory protein	Rv3513c	fadD18	acyl-CoA synthase			ponent α subunit
Rv1852	ureG	urease accessory protein	Rv3515c	fadD19	acyl-CoA synthase	Rv2496c	pdhB	pyruvate dehydrogenase E1 com-
Rv2913c	-	probable D-amino acid	Rv1185c	fadD21	acyl-CoA synthase	_		ponent β subunit
D 0==1		aminohydrolase	Rv2948c	fadD22	acyl-CoA synthase	Rv2495c	pdhC	dihydrolipoamide acetyltransferase
Rv3551	-	possible glutaconate CoA-	Rv3826	fadD23	acyl-CoA synthase	Rv0462	-	probable dihydrolipoamide dehy-
		transferase	Rv1529 Rv1521	fadD24 fadD25	acyl-CoA synthase acyl-CoA synthase			drogenase
3. Fatty a	cids		Rv2930	fadD26	acyl-CoA synthase	3. TCA cv	cle	
Rv2501c		acetyl/propionyl-CoA carboxylase,	Rv0275c	fadD27	acyl-CoA synthase	Rv1475c	acn	aconitate hydratase
		α subunit	Rv2941	fadD28	acyl-CoA synthase	Rv0889c	citA	citrate synthase 2
Rv0973c	accA2	acetyl/propionyl-CoA carboxylase,	Rv2950c	fadD29	acyl-CoA synthase	Rv2498c	citE	citrate lyase β chain
		α subunit	Rv0404	fadD30	acyl-CoA synthase	Rv1098c	fum	fumarase
Rv2502c	accD1	acetyl/propionyl-CoA carboxylase,	Rv1925	fadD31	acyl-CoA synthase	Rv1131	gltA1	citrate synthase 3
Rv0974c	accD2	β subunit acetyl/propionyl-CoA carboxylase,	Rv3801c Rv1345	fadD32 fadD33	acyl-CoA synthase acyl-CoA synthase	Rv0896 Rv3339c	gltA2 icd1	citrate synthase 1 isocitrate dehydrogenase
11003740	accoz	β subunit	Rv0035	fadD34	acyl-CoA synthase	Rv0066c	icd2	isocitrate dehydrogenase
Rv3667	acs	acetyl-CoA synthase	Rv2505c	fadD35	acyl-CoA synthase	Rv0794c	lpdB	dihydrolipoamide dehydrogenase
Rv3409c		cholesterol oxidase	Rv1193	fadD36	acyl-CoA synthase	Rv1240	mdh	malate dehydrogenase
Rv0222	echA1	enoyl-CoA hydratase/isomerase	Rv0131c	fadE1	acyl-CoA dehydrogenase	Rv2967c	pca	pyruvate carboxylase
D. 0450	00540	superfamily	Rv0154c	fadE2	acyl-CoA dehydrogenase	Rv3318	sdhA	succinate dehydrogenase A
Rv0456c	echA2	enoyl-CoA hydratase/isomerase superfamily	Rv0215c Rv0231	fadE3 fadE4	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv3319 Rv3316	sdhB sdhC	succinate dehydrogenase B succinate dehydrogenase C sub-
Rv0632c	echA3	enoyl-CoA hydratase/isomerase	Rv0244c	fadE5	acyl-CoA dehydrogenase	1100010	Suite	unit
	2310	superfamily	Rv0271c	fadE6	acyl-CoA dehydrogenase	Rv3317	sdhD	succinate dehydrogenase D sub-
Rv0673	echA4	enoyl-CoA hydratase/isomerase	Rv0400c	fadE7	acyl-CoA dehydrogenase			unit
		superfamily	Rv0672	fadE8	acyl-CoA dehydrogenase	Rv1248c	sucA	2-oxoglutarate dehydrogenase
Rv0675	echA5	enoyl-CoA hydratase/isomerase	D 0==0		(aka <i>aidB</i>)	Rv2215	sucB	dihydrolipoamide succinyltrans-
D.,000E		superfamily	Rv0752c	fadE9	acyl-CoA dehydrogenase	D. 100E1		ferase
Rv0905	echA6	enoyl-CoA hydratase/isomerase superfamily (aka <i>eccH</i>)	Rv0873 Rv0972c	fadE10 fadE12	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv0951 Rv0952	sucC sucD	succinyl-CoA synthase β chain succinyl-CoA synthase α chain
Rv0971c	echA7	enoyl-CoA hydratase/isomerase	Rv0975c	fadE13	acyl-CoA dehydrogenase	1100332	SUCD	Succinyi-Ook Synthase a chain
	00.1/1/	superfamily	Rv1346	fadE14	acyl-CoA dehydrogenase	4. Glyoxyl	ate bypass	5
Rv1070c	echA8	enoyl-CoA hydratase/isomerase	Rv1467c	fadE15	acyl-CoA dehydrogenase	Rv0467	aceA	isocitrate lyase
		superfamily	Rv1679	fadE16	acyl-CoA dehydrogenase	Rv1915	aceAa	isocitrate lyase, α module
Rv1071c	echA9	enoyl-CoA hydratase/isomerase	Rv1934c	fadE17	acyl-CoA dehydrogenase	Rv1916	aceAb	isocitrate lyase, β module
Dud 4 40		superfamily	Rv1933c	fadE18	acyl-CoA dehydrogenase	Rv1837c	glcB	malate synthase
Rv1142c	echA10	enoyl-CoA hydratase/isomerase	Rv2500c	fadE19	acyl-CoA dehydrogenase	Rv3323c	gphA	phosphoglycolate phosphatase
Bv4144-	echA11	superfamily	By27246	fadE20	(aka <i>mmgC</i>)	5 Donton	nhoonho	te nathway
Rv1141c	CUIAII	enoyl-CoA hydratase/isomerase superfamily	Rv2724c Rv2789c	fadE20	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv1445c	devB	te pathway glucose-6-phosphate 1-dehydro-
Rv1472	echA12	enoyl-CoA hydratase/isomerase	Rv3061c	fadE22	acyl-CoA dehydrogenase		2010	genase
		superfamily	Rv3140	fadE23	acyl-CoA dehydrogenase	Rv1844c	gnd	6-phosphogluconate dehydroge-
Rv1935c	echA13	enoyl-CoA hydratase/isomerase	Rv3139	fadE24	acyl-CoA dehydrogenase			nase (Gram -)
D. 6 : 25		superfamily	Rv3274c	fadE25	acyl-CoA dehydrogenase	Rv1122	gnd2	6-phosphogluconate dehydroge-
Rv2486	echA14	enoyl-CoA hydratase/isomerase	Rv3504	fadE26	acyl-CoA dehydrogenase	D.:1440	05-4	nase (Gram +)
Rv2679	echA15	superfamily enoyl-CoA hydratase/isomerase	Rv3505 Rv3544c	fadE27 fadE28	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv1446c	opcA	unknown function, may aid G6PDH
1142013	COLIMIT	5byi Cort nyuratasonsomerase	11700440	IUULZU	as, i sort asriyarogenase			557 DIT

Rv2436	rbsK	ribokinase	Rv3250c	rubB	rubredoxin B	Rv1878	glnA3	probable glutamine synthase
Rv1408	rpe	ribulose-phosphate 3-epimerase				Rv2860c	glnA4	proable glutamine synthase
Rv2465c	rpi	phosphopentose isomerase	Miscella	aneous ox	idoreductases and oxygenases 171	Rv2918c	glnD	uridylyltransferase
Rv1448c	tal	transaldolase			_	Rv2221c	glnE	glutamate-ammonia-ligase
Rv1449c	tkt	transketolase		oton motiv		D 0050	""	adenyltransferase
Rv1121	zwf	glucose-6-phosphate 1-dehydro-	Rv1308	atpA etpB	ATP synthase α chain	Rv3859c	gltB	ferredoxin-dependent glutamate
Rv1447c	zwf2	genase glucose-6-phosphate 1-dehydro-	Rv1304 Rv1311	atpB atpC	ATP synthase α chain ATP synthase ϵ chain	Rv3858c	gltD	synthase small subunit of NADH-dependent
NV 1447C	20012	genase	Rv1310	atpD	ATP synthase β chain	HV3030C	gilD	glutamate synthase
		genace	Rv1305	atpE	ATP synthase c chain	Rv3704c	gshA	possible γ-glutamylcysteine syn-
6. Respira	tion		Rv1306	atpF	ATP synthase b chain		3 -	thase
a. aerobic			Rv1309	atpG	ATP synthase γ chain	Rv2427c	proA	γ-glutamyl phosphate reductase
Rv0527	ccsA	cytochrome c-type biogenesis	Rv1307	atpH	ATP synthase δ chain	Rv2439c	proB	glutamate 5-kinase
_		protein				Rv0500	proC	pyrroline-5-carboxylate reductase
Rv0529	ccsB	cytochrome c-type biogenesis			iary metabolism	0. 4		
Rv1451	ctaB	protein cytochrome <i>c</i> oxidase assembly	1. Genera Rv2589	u gabT	4 aminohuturato aminotraneforaco	Asparta Rv3708c	asd	aspartate semialdehyde dehydro-
NV 145 I	CIAD	factor	Rv3432c	gadB	4-aminobutyrate aminotransferase glutamate decarboxylase	NV3/U00	asu	genase
Rv2200c	ctaC	cytochrome <i>c</i> oxidase chain II	Rv1832	gcvB	glycine decarboxylase	Rv3709c	ask	aspartokinase
Rv3043c	ctaD	cytochrome <i>c</i> oxidase poly-	Rv1826	gcvH	glycine cleavage system H protein	Rv2201	asnB	asparagine synthase B
		peptide I	Rv2211c	gcvT	T protein of glycine cleavage	Rv3565	aspB	aspartate aminotransferase
Rv2193	ctaE	cytochrome c oxidase poly-			system	Rv0337c	aspC	aspartate aminotransferase
		peptide III	Rv1213	glgC	glucose-1-phosphate adenylyl-	Rv2753c	dapA	dihydrodipicolinate synthase
Rv1542c	glbN	hemoglobin-like, oxygen carrier	D. 0040-	-1-04	transferase	Rv2773c	dapB	dihydrodipicolinate reductase
Rv2470	glbO	hemoglobin-like, oxygen carrier	Rv3842c	glpQ1	glycerophosphoryl diester phos-	Rv1202	dapE	succinyl-diaminopimelate desuc-
Rv2249c	glpD1	glycerol-3-phosphate dehydroge-	Rv0317c	alnO2	phodiesterase	Rv2141c	dapE2	cinylase
Rv3302c	glpD2	nase glycerol-3-phosphate dehydroge-	NV03170	glpQ2	glycerophosphoryl diester phos- phodiesterase	NV21410	uapEZ	ArgE/DapE/Acy1/Cpg2/yscS family
11100020	gipbl	nase	Rv3566c	nhoA	N-hydroxyarylamine <i>o</i> -acetyltrans-	Rv2726c	dapF	diaminopimelate epimerase
Rv0694	IIdD1	L-lactate dehydrogenase	50000		ferase	Rv1293	lysA	diaminopimelate decarboxylase
		(cytochrome)	Rv0155	pntAA	pyridine transhydrogenase sub-	Rv3341	metA	homoserine o-acetyltransferase
Rv1872c	IIdD2	L-lactate dehydrogenase			unit α1	Rv1079	metB	cystathionine γ-synthase
Rv1854c	ndh	probable NADH dehydrogenase	Rv0156	pntAB	pyridine transhydrogenase sub-	Rv3340	metC	cystathionine β-lyase
Rv3145	nuoA	NADH dehydrogenase chain A	D 6:		unit α2	Rv1133c	metE	5-methyltetrahydropteroyltrigluta-
Rv3146	nuoB	NADH dehydrogenase chain B	Rv0157	pntB	pyridine transhydrogenase			mate-homocysteine methyltrans-
Rv3147	nuoC	NADH dehydrogenase chain C	D.:1107-	mm all/	subunit β	D::0104a		ferase
Rv3148 Rv3149	nuoD nuoE	NADH dehydrogenase chain D NADH dehydrogenase chain E	Rv1127c	ppdK	similar to pyruvate, phosphate dikinase	Rv2124c	metH	5-methyltetrahydrofolate-homo- cysteine methyltransferase
Rv3150	nuoF	NADH denydrogenase chain F			uikiilase	Rv1392	metK	S-adenosylmethionine synthase
Rv3151	nuoG	NADH dehydrogenase chain G	2. Glucon	eogenesis		Rv0391	metZ	o-succinylhomoserine sulfhy-
Rv3152	nuoH	NADH dehydrogenase chain H	Rv0211	pckA	phosphoenolpyruvate carboxy-			drylase
Rv3153	nuol	NADH dehydrogenase chain I		,	kinase	Rv1294	thrA	homoserine dehydrogenase
Rv3154	nuoJ	NADH dehydrogenase chain J	Rv0069c	sdaA	L-serine dehydratase 1	Rv1296	thrB	homoserine kinase
Rv3155	nuoK	NADH dehydrogenase chain K				Rv1295	thrC	homoserine synthase
Rv3156	nuoL	NADH dehydrogenase chain L		nucleotides				
Rv3157	nuoM	NADH dehydrogenase chain M	Rv1512	epiA	nucleotide sugar epimerase	3. Serine		this as alfata as alformation afaire as
Rv3158 Rv2195	nuoN aarA	NADH dehydrogenase chain N	Rv3784	epiB	probable UDP-galactose 4-	Rv0815c Rv3117	cysA2	thiosulfate sulfurtransferase
NV2195	qcrA	Rieske iron-sulphur component of ubiQ-cytB reductase	Rv1511	gmdA	epimerase GDP-mannose 4,6 dehydratase	Rv2335	cysA3 cysE	thiosulfate sulfurtransferase serine acetyltransferase
Rv2196	qcrB	cytochrome β component of <i>ubiQ</i> -	Rv0334	rmlA	glucose-1-phosphate thymidyl-	Rv0511	cysG	uroporphyrin-III c-methyltrans-
	90.2	cytB reductase			transferase		o, o a	ferase
Rv2194	qcrC	cytochrome b/c component of	Rv3264c	rmIA2	glucose-1-phosphate thymidyl-	Rv2847c	cysG2	multifunctional enzyme, siroheme
		ubiQ-cytB reductase			transferase			synthase
			Rv3464	rmIB	dTDP-glucose 4,6-dehydratase	Rv2334	cysK	cysteine synthase A
b. anaerob		Olasharaharaharah da Mata (PARO)	Rv3634c	rmIB2	dTDP-glucose 4,6-dehydratase	Rv1336	cysM	cysteine synthase B
Rv2392	cysH	3'-phosphoadenylylsulfate (PAPS)	Rv3468c	rmIB3	dTDP-glucose 4,6-dehydratase	Rv1077	cysM2	cystathionine β-synthase
Rv2899c	fdhD	reductase affects formate dehydrogenase-N	Rv3465	rmIC	dTDP-4-dehydrorhamnose 3,5-epimerase	Rv0848 Rv1093	cysM3	putative cysteine synthase
Rv2900c	fdhF	molybdopterin-containing oxidore-	Rv3266c	rmID	dTDP-4-dehydrorhamnose	Rv0070c	<i>glyA</i> glyA2	serine hydroxymethyltransferase serine hydroxymethyltransferase
11120000	iaiii	ductase	11102000	11111112	reductase	Rv2996c	serA	D-3-phosphoglycerate dehydro-
Rv1552	frdA	fumarate reductase flavoprotein	Rv0322	udgA	UDP-glucose			genase
		subunit		Ü	dehydrogenase/GDP-mannose 6-	Rv0505c	serB	probable phosphoserine phos-
Rv1553	frdB	fumarate reductase iron sulphur			dehydrogenase			phatase
		protein	Rv3265c	wbbL	dTDP-rhamnosyl transferase	Rv3042c	serB2	C-term similar to phosphoserine
Rv1554	frdC	fumarate reductase 15kD anchor	Rv1525	wbbl2	dTDP-rhamnosyl transferase		_	phosphatase
Duteer	(mdD	protein	Rv3400	-	probable β-phosphoglucomutase	Rv0884c	serC	phosphoserine aminotransferase
Rv1555	frdD	fumarate reductase 13kD anchor protein	4. Amino	cugare		4. Aromat	io amino a	ooid family
Rv1161	narG	nitrate reductase α subunit	Rv3436c		glucosamine-fructose-6-	Rv3227	aroA	3-phosphoshikimate
Rv1162	narH	nitrate reductase α suburiti nitrate reductase β chain	5-1000	910	phosphate aminotransferase		u. 0/ 1	1-carboxyvinyl transferase
Rv1164	narl	nitrate reductase γ chain				Rv2538c	aroB	3-dehydroquinate synthase
Rv1163	narJ	nitrate reductase $\dot{\delta}$ chain		r metabolis		Rv2537c	aroD	3-dehydroquinate dehydratase
Rv1736c	narX	fused nitrate reductase	Rv0711	atsA	arylsulfatase	Rv2552c	aroE	shikimate 5-dehydrogenase
Rv2391	nirA	probable nitrite reductase/sulphite	Rv3299c	atsB	proable arylsulfatase	Rv2540c	aroF	chorismate synthase
D.:0050	nirD	reductase	Rv0663	atsD	proable arylaulfatase	Rv2178c	aroG	DAHP synthase
Rv0252 Rv0253	nirB nirD	nitrite reductase flavoprotein probable nitrite reductase small	Rv3077 Rv0296c	atsF atsG	proable arylsulfatase proable arylsulfatase	Rv2539c Rv3838c	aroK nhe4	shikimate kinase I prephenate dehydratase
HVU233	טוווט	subunit	Rv3796	atsG atsH	proable arylsulfatase proable arylsulfatase	Rv3838c Rv1613	pheA trpA	tryptophan synthase α chain
			Rv1285	cysD	ATP:sulphurylase subunit 2	Rv1612	trpB	tryptophan synthase β chain
c. Electron	transnor	•	Rv1286	cysN	ATP:sulphurylase subunit 1	Rv1611	trpC	indole-3-glycerol phosphate
Rv0409	ackA	acetate kinase	Rv2131c	cysQ	homologue of <i>M.leprae cysQ</i>			synthase
Rv1623c	appC	cytochrome bd-II oxidase	Rv3248c	sahH	adenosylhomocysteinase	Rv2192c	trpD	anthranilate phosphoribosyltrans-
		subunit I	Rv3283	sseA	thiosulfate sulfurtransferase			ferase
Rv1622c	cydB	cytochrome <i>d</i> ubiquinol oxidase	Rv2291	sseB	thiosulfate sulfurtransferase	Rv1609	trpE	anthranilate synthase
D.:1000-	01/10	subunit II	Rv3118	sseC	thiosulfate sulfurtransferase	D.:0000	tro FO	component I
Rv1620c	cydC cydD	ABC transporter	Rv0814c	sseC2	thiosulfate sulfurtransferase	Rv2386c	trpE2	anthranilate synthase
Rv1621c Rv2007c	cydD fdxA	ABC transporter ferredoxin	Rv3762c	-	probable alkyl sulfatase	Rv3754	tyrA	component I prephenate dehydrogenase
Rv2007c Rv3554	fdxB	ferredoxin	D Amino	acid biosy	nthesis	1170704	LyIA	proprienate deligatogellase
Rv1177	fdxC	ferredoxin 4Fe-4S		acid biosy ate family		5. Histidin	е	
Rv3503c	fdxD	probable ferredoxin	Rv1654	argB	acetylglutamate kinase	Rv1603	hisA	phosphoribosylformimino-5-
Rv3029c	fixA	electron transfer flavoprotein	Rv1652	argC	N-acetyl-γ-glutamyl-phosphate			aminoimidazole carboxamide
		β subunit			reductase			ribonucleotide isomerase
Rv3028c	fixB	electron transfer flavoprotein α	Rv1655	argD	acetylornithine aminotransferase	Rv1601	hisB	imidazole glycerol-phosphate
D. 0111		subunit	Rv1656	argF	ornithine carbamoyltransferase	D. 10		dehydratase
Rv3106	fprA	adrenodoxin and NADPH ferre-	Rv1658	argG	arginosuccinate synthase	Rv1600	hisC	histidinol-phosphate aminotrans-
Rv0886	fprB	doxin reductase ferredoxin, ferredoxin-NADP	Rv1659 Rv1653	argH argJ	arginosuccinate lyase glutamate N-acetyltransferase	Rv3772	hisC2	ferase histidinol-phosphate aminotrans-
1140000	ιριυ	reductase	Rv2220	glnA1	glutamine synthase class I	1100//2	111302	ferase
Rv3251c	rubA	rubredoxin A	Rv2222c	glnA2	glutamine synthase class II	Rv1599	hisD	histidinol dehydrogenase
				-	-			. 0

Rv1605	hisF	imidazole glycerol-phosphate			subunit			subunit 1
D.:0101a	hino	synthase	Rv3048c	nrdG	ribonucleoside-diphosphate small	Rv3119	moaE	molybdopterin-converting factor
Rv2121c Rv1602	nisG hisH	ATP phosphoribosyltransferase amidotransferase	Rv3053c	nrdH	subunit	Rv0866	moaE2	subunit 2
Rv2122c	hish	phosphoribosyl-AMP cyclohydro-	11/30/330	IIIun	glutaredoxin electron transport component of NrdEF system	HV0000	III0aE2	molybdopterin-converting factor subunit 2
11021220	11101	lase	Rv3052c	nrdl	Nrdl/YgaO/YmaA family	Rv3322c	moaE3	molybdopterin-converting factor
Rv1606	hisl2	probable phosphoribosyl-AMP 1,6	Rv3247c	tmk	thymidylate kinase			subunit 2
5		cyclohydrolase	Rv2764c	thyA	thymidylate synthase	Rv0994	moeA	molybdopterin biosynthesis
Rv0114	-	similar to HisB	Rv0570 Rv3752c	nrdZ -	ribonucleotide reductase, class II probable cytidine/deoxycytidylate	Rv3116 Rv2338c	moeB moeW	molybdopterin biosynthesis molybdopterin biosynthesis
6. Pyruvat	e family		11/3/320	-	deaminase	Rv1681	moeX	weak similarity to <i>E. coli</i> MoaA
	alr	alanine racemase				Rv1355c	moeY	weak similarity to <i>E. coli</i> MoeB
					sides and nucleotides	Rv3206c	moeZ	probably involved in
7. Branche			Rv3313c	add	probable adenosine deaminase	D. 0005		molybdopterin biosynthesis
Rv1559 Rv3003c	ilvA ilvB	threonine deaminase acetolactate synthase I large sub-	Rv2584c	apt	adenine phosphoribosyltrans- ferases	Rv0865	mog	molybdopterin biosynthesis
11000000	IIVD	unit	Rv3315c	cdd	probable cytidine deaminase	5. Pantoth	enate	
Rv3470c	ilvB2	acetolactate synthase large sub-	Rv3314c	deoA	thymidine phosphorylase	Rv1092c	coaA	pantothenate kinase
		unit	Rv0478	deoC	deoxyribose-phosphate aldolase	Rv2225	panB	3-methyl-2-oxobutanoate
Rv3001c	ilvC	ketol-acid reductoisomerase	Rv3307	deoD	probable purine nucleoside phos-	D. 0000		hydroxymethyltransferase
Rv0189c Rv2210c	ilvD ilvE	dihydroxy-acid dehydratase branched-chain-amino-acid	Rv3624c	hpt	phorylase probable hypoxanthine-guanine	Rv3602c Rv3601c	panC panD	pantoate-β-alanine ligase aspartate 1-decarboxylase
11022100	L	transaminase	11002-10	npt	phosphoribosyltransferase	1100010	panb	asparlate i desarboxylase
Rv1820	ilvG	acetolactate synthase II	Rv3393	iunH	probable inosine-uridine	Pyridoxi	ine	
Rv3002c	ilvN	acetolactate synthase I small sub-	D 0505		preferring nucleoside hydrolase	Rv2607	pdxH	pyridoxamine 5'-phosphate
Du2E00a	ilvV	unit	Rv0535	pnp	phosphorylase from Pnp/MtaP			oxidase
Rv3509c	ilvX	probable acetohydroxyacid syn- thase I large subunit	Rv3309c	ирр	family 2 uracil phophoribosyltransferase	7. Pyridine	nucleotid	le.
Rv3710	leuA	α-isopropyl malate synthase	1100000	ирр	araon prioprioribodyntariorado	Rv1594	nadA	quinolinate synthase
Rv2995c	leuB	3-isopropylmalate dehydrogenase			cleoside/nucleotide reactions	Rv1595	nadB	L-aspartate oxidase
Rv2988c	leuC	3-isopropylmalate dehydratase	Rv0733	adk	probable adenylate kinase	Rv1596	nadC	nicotinate-nucleotide pyrophos-
D. 0007-	ID	large subunit	Rv2364c	bex	GTP-binding protein of Era/ThdF	D.,0400+	44:0	phatase
Rv2987c	leuD	3-isopropylmalate dehydratase small subunit	Rv1712	cmk	family cytidylate kinase	Rv0423c	thiC	thiamine synthesis, pyrimidine moiety
		oman subumi	Rv2344c	dgt	probable deoxyguanosine			molecty
E. Polyam	nine synthe	esis		3	triphosphate hydrolase	8. Thiamin	е	
Rv2601	speE	spermidine synthase	Rv2404c	lepA_	GTP-binding protein LepA	Rv0422c	thiD	phosphomethylpyrimidine kinase
C Dunings			Rv2727c	miaA	tRNA δ(2)-isopentenylpyrophos-	Rv0414c	thiE	thiamine synthesis, thiazole
		nes, nucleosides and nucleotides tide biosynthesis	Rv2445c	ndkA	phate transferase nucleoside diphosphate kinase	Rv0417	thiG	moiety thiamine synthesis, thiazole
Rv1389	gmk	putative guanylate kinase	Rv2440c	obg	Obg GTP-binding protein	1100417	una	moiety
Rv3396c	guaA	GMP synthase	Rv2583c	relA	(p)ppGpp synthase I	Rv2977c	thiL	probable thiamine-monophos-
Rv1843c	guaB1	inosine-5'-monophosphate dehy-						phate kinase
D.:0411=	DO	drogenase		thesis of c	ofactors, prosthetic groups and	O Dibelle		
Rv3411c	guaB2	inosine-5'-monophosphate dehy- drogenase	carriers 1. Biotin			Riboflav Rv1940	ribA	GTP cyclohydrolase II
Rv3410c	guaB3	inosine-5'-monophosphate dehy-	Rv1568	bioA	adenosylmethionine-8-amino-7-	Rv1415	ribA2	probable GTP cyclohydrolase II
	3	drogenase			oxononanoate aminotransferase	Rv1412	ribC	riboflavin synthase α chain
Rv1017c	prsA	ribose-phosphate pyrophosphoki-	Rv1589	bioB	biotin synthase	Rv2671	ribD	probable riboflavin deaminase
D. 0057-	4	nase	Rv1570	bioD	dethiobiotin synthase	Rv2786c	ribF	riboflavin kinase
Rv0357c Rv0777	purA purB	adenylosuccinate synthase adenylosuccinate lyase	Rv1569	bioF	8-amino-7-oxononanoate synthase	Rv1409 Rv1416	ribG ribH	riboflavin biosynthesis riboflavin synthase β chain
Rv0780	purC	phosphoribosylaminoimidazole-	Rv0032	bioF2	C-terminal similar to <i>B. subtilis</i>	Rv3300c	-	probable deaminase, riboflavin
	<i>p</i>	succinocarboxamide synthase			BioF			synthesis
Rv0772	purD	phosphoribosylamine-glycine lig-	Rv3279c	birA	biotin apo-protein ligase			
D 00==	_	ase	Rv1442	bisC	biotin sulfoxide reductase			taredoxin and mycothiol
Rv3275c	purE	phosphoribosylaminoimidazole carboxylase	Rv0089	-	possible bioC biotin synthesis	Rv0773c Rv2394	ggtA ggtB	putative γ-glutamyl transpeptidase γ-glutamyltranspeptidase
Rv0808	purF	amidophosphoribosyltransferase-			gene	HV2334	ggtB	precursor
Rv0957	purH	phosphoribosylaminoimidazole-	2. Folic ac	id		DUCCE	gorA	glutathione reductase homologue
		priosprioribosylariirioiriidazoie-	Z. I Olic ac			Rv2855	guin	giutati ilone reductase nomologue
Rv3276c		carboxamide formyltransferase	Rv2763c	dfrA	dihydrofolate reductase	Rv0816c	thiX	equivalent to M. leprae ThiX
	purK	carboxamide formyltransferase phosphoribosylaminoimidazole	Rv2763c Rv2447c	dfrA foIC	folylpolyglutamate synthase	Rv0816c Rv1470	thiX trxA	equivalent to <i>M. leprae</i> ThiX thioredoxin
Dv0903		carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit	Rv2763c	dfrA	folylpolyglutamate synthase methylenetetrahydrofolate dehy-	Rv0816c Rv1470 Rv1471	thiX trxA trxB	equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase
Rv0803	purK purL	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycin-	Rv2763c Rv2447c Rv3356c	dfrA foIC foID	folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase	Rv0816c Rv1470 Rv1471 Rv3913	thiX trxA trxB trxB2	equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase
Rv0803 Rv0809	purL	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit	Rv2763c Rv2447c	dfrA foIC	folylpolyglutamate synthase methylenetetrahydrofolate dehy-	Rv0816c Rv1470 Rv1471	thiX trxA trxB	equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase
Rv0809	purL purM	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycin- amidine synthase II 5'-phosphoribosyl-5-aminoimida- zole synthase	Rv2763c Rv2447c Rv3356c Rv3609c Rv3606c	dfrA foIC foID foIE foIK	folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914	thiX trxA trxB trxB2 trxC	equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase
	purL	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide	Rv2763c Rv2447c Rv3356c Rv3609c Rv3606c Rv3608c	dfrA folC folD folE folK folP	folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menacterpenoids	thiX trxA trxB trxB2 trxC	equivalent to M. leprae ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin
Rv0809 Rv0956	purL purM purN	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycin- amidine synthase II 5'-phosphoribosyl-5-aminoimida- zole synthase phosphoribosylglycinamide formyltransferase I	Rv2763c Rv2447c Rv3356c Rv3609c Rv3606c Rv3608c Rv1207	dfrA foIC foID foIE foIK foIP	folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914	thiX trxA trxB trxB2 trxC	equivalent to M. leprae ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate
Rv0809	purL purM	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide	Rv2763c Rv2447c Rv3356c Rv3609c Rv3606c Rv3608c	dfrA folC folD folE folK folP	folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menacterpenoids	thiX trxA trxB trxB2 trxC	equivalent to M. leprae ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin
Rv0809 Rv0956	purL purM purN	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylformylglycinamidine synthase I phosphoribosylformylglycinamidine synthase I phosphoribosylglycinamide	Rv2763c Rv2447c Rv3356c Rv3609c Rv3606c Rv3608c Rv1207	dfrA foIC foID foIE foIK foIP	folylpolyglutamate synthase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosynthesis p-aminobenzoate synthase gluta-	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562	thiX trxA trxB trxB2 trxC quinone, P dxs grcC1	equivalent to M. leprae ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin (QC, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II
Rv0809 Rv0956 Rv0788 Rv0389	purL purM purN purQ purT	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylformylglycinamidine synthase I phosphoribosylglycinamide formyltransferase II phosphoribosylglycinamide formyltransferase II	Rv2763c Rv2447c Rv3356c Rv3609c Rv3606c Rv3608c Rv1207 Rv3607c Rv0013	dfrA foIC foID foIE foIK foIP foIP2 foIX pabA	folylpolyglutamate synthase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosynthesis p-aminobenzoate synthase glutamine amidotransferase	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menacterpenoids Rv2682c	thiX trxA trxB trxB2 trxC quinone, P	equivalent to M. leprae ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate
Rv0809 Rv0956 Rv0788	purL purM purN purQ	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamidine synthase I phosphoribosylglycinamide formyltransferase II phosphoribosylglycinamide formyltransferase II formylterahydrofolate deformy-	Rv2763c Rv2447c Rv3356c Rv3609c Rv3606c Rv3608c Rv1207 Rv3607c Rv0013 Rv1005c	dfrA foIC foID foIE foIK foIP foIP2 foIX pabA pabB	folylpolyglutamate synthase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosynthesis p-aminobenzoate synthase glutamine amidotransferase p-aminobenzoate synthase	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562	thiX trxA trxB trxB2 trxC quinone, P dxs grcC1 grcC2	equivalent to M. leprae ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin (QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase li heptaprenyl diphosphate synthase II
Rv0809 Rv0956 Rv0788 Rv0389	purL purM purN purQ purT	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylformylglycinamidine synthase I phosphoribosylglycinamide formyltransferase II phosphoribosylglycinamide formyltransferase II	Rv2763c Rv2447c Rv3356c Rv3609c Rv3606c Rv3608c Rv1207 Rv3607c Rv0013	dfrA foIC foID foIE foIK foIP foIP2 foIX pabA	folylpolyglutamate synthase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosynthesis p-aminobenzoate synthase glutamine amidotransferase	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562	thiX trxA trxB trxB2 trxC quinone, P dxs grcC1	equivalent to M. leprae ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate
Rv0809 Rv0956 Rv0788 Rv0389 Rv2964	purL purM purN purQ purT purU	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosyldycinamide formyltransferase I phosphoribosylformylglycinamidine synthase I phosphoribosylglycinamide formyltransferase II formyltransferase II formyltransferase II formyltransferase II formyltransferase II formyltetrahydrofolate deformylase	Rv2763c Rv2447c Rv3356c Rv3609c Rv3606c Rv3608c Rv1207 Rv3607c Rv0013 Rv1005c Rv0812	dfrA foIC foID foIE foIK foIP foIP2 foIX pabA pabB	folylpolyglutamate synthase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosynthesis p-aminobenzoate synthase glutamine amidotransferase p-aminobenzoate synthase	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0989c Rv3398c	thiX trxA trxB trxB2 trxC quinone, P dxs grcC1 grcC2 idsA	equivalent to M. leprae ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin (QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase li heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase
Rv0809 Rv0956 Rv0788 Rv0389 Rv2964	purL purM purN purQ purT purU	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamidine synthase I phosphoribosylglycinamide formyltransferase II phosphoribosylglycinamide formyltransferase II formylterahydrofolate deformy-	Rv2763c Rv2447c Rv3356c Rv3609c Rv3606c Rv3608c Rv1207 Rv3607c Rv0013 Rv1005c	dfrA foIC foID foIE foIK foIP foIP2 foIX pabA pabB	folylpolyglutamate synthase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosynthesis p-aminobenzoate synthase glutamine amidotransferase p-aminobenzoate synthase	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562	thiX trxA trxB trxB2 trxC quinone, P dxs grcC1 grcC2	equivalent to M. leprae ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate
Rv0809 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383	purL purN purN purQ purT purU ine ribonucarA	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylformylglycinamidine synthase I phosphoribosylglycinamide formyltransferase II formyltransferase II formyltransferase II formyltetrahydrofolate deformylase cleotide biosynthesis carbamoyl-phosphate synthase subunit	Rv2763c Rv2447c Rv3356c Rv3609c Rv3609c Rv3608c Rv1207 Rv3607c Rv0013 Rv1005c Rv0812 3. Lipoate	dfrA folC folD folE folK folP folP2 folX pabA pabB pabC	folylpolyglutamate synthase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosynthesis p-aminobenzoate synthase glutamine amidotransferase p-aminobenzoate synthase aminodeoxychorismate lyase	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0989c Rv3398c	thiX trxA trxB trxB2 trxC quinone, P dxs grcC1 grcC2 idsA	equivalent to M. leprae ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase ll phosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl
Rv0809 Rv0956 Rv0788 Rv0389 Rv2964	purL purM purN purQ purT purU	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II formyltetrahydrofolate deformylase cleotide biosynthesis carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase	Rv2763c Rv2447c Rv3356c Rv3609c Rv3606c Rv3608c Rv1207 Rv0013 Rv1005c Rv0812 3. Lipoate Rv2218 Rv2217	dfrA folC folD folE folK folP folP2 folX pabA pabB pabC	folylpolyglutamate synthase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosynthesis p-aminobenzoate synthase glutamine amidotransferase p-aminobenzoate synthase aminodeoxychorismate lyase lipoate biosynthesis protein A	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0989c Rv3398c Rv2173 Rv3383c	thiX trxA trxB trxB2 trxC quinone, P dxs grcC1 grcC2 idsA idsA2 idsB	equivalent to M. leprae ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase than the synthase geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase
Rv0809 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384	purL purM purN purQ purT purU ine ribonu carA carB	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II formyltransferase II formylterahydrofolate deformyltase cleotide biosynthesis carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit	Rv2763c Rv2447c Rv3356c Rv3609c Rv3609c Rv3609c Rv1207 Rv3607c Rv0013 Rv1005c Rv0812 3. Lipoate Rv2218 Rv2217	dfrA folC folD folE folK folP folP2 folX pabA pabB pabC	folylpolyglutamate synthase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosynthesis p-aminobenzoate synthase glutamine amidotransferase p-aminobenzoate synthase aminodeoxychorismate lyase lipoate biosynthesis protein A lipoate biosynthesis protein B	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0989c Rv3398c Rv2173	thiX trxA trxB trxB2 trxC luinone, P dxs grcC1 grcC2 idsA idsA2	equivalent to M. leprae ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and ther 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase 4-dihydroxy-2-naphthoate
Rv0809 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384 Rv1380	purL purM purN purQ purT purU iine ribonu carA carB pyrB	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II formyltetrahydrofolate deformyltase clebiosynthesis carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase	Rv2763c Rv2447c Rv3356c Rv3609c Rv3606c Rv3608c Rv1207 Rv0013 Rv1005c Rv0812 3. Lipoate Rv2218 Rv2217	dfrA folC folD folE folK folP folP2 folX pabA pabB pabC	folylpolyglutamate synthase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosynthesis p-aminobenzoate synthase glutamine amidotransferase p-aminobenzoate synthase aminodeoxychorismate lyase lipoate biosynthesis protein A lipoate biosynthesis protein B	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0989c Rv3398c Rv2173 Rv383c Rv0534c	thiX trxA trxB trxB2 trxC luinone, P dxs grcC1 grcC2 idsA idsA2 idsB	equivalent to M. leprae ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase light and the synthase il heptaprenyl diphosphate synthase il geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase
Rv0809 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384	purL purM purN purQ purT purU ine ribonu carA carB	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylformylglycinamidine synthase I phosphoribosylformylglycinamidine synthase I phosphoribosylformylglycinamide formyltransferase II formyltetrahydrofolate deformylase cleotide biosynthesis carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotate dehydrogenase	Rv2763c Rv2447c Rv3356c Rv3609c Rv3609c Rv3609c Rv1207 Rv3607c Rv0013 Rv1005c Rv0812 3. Lipoate Rv2218 Rv2217	dfrA folC folD folE folK folP folP2 folX pabA pabB pabC	folylpolyglutamate synthase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosynthesis p-aminobenzoate synthase glutamine amidotransferase p-aminobenzoate synthase aminodeoxychorismate lyase lipoate biosynthesis protein A lipoate biosynthesis protein B	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0562 Rv398c Rv2173 Rv398c Rv2173 Rv3983c Rv0544c Rv0548c Rv05534c	thiX trxA trxB trxB2 trxC quinone, P dxs grcC1 grcC2 idsA idsA2 idsB	equivalent to M. leprae ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and ther 1-deoxy-D-xylulose 5-phosphate synthase leptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase category of the synthase transfergeranyl pyrophosphate synthase octaprenyltransferase naphthoate synthase o-succinylbenzoate-CoA synthase
Rv0809 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381	purL purM purN purQ purT purU ine ribonu carA carB pyrB pyrC	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II formylterahydrofolate deformyltase Cleotide biosynthesis carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotase dihydroorotase dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxy-	Rv2763c Rv2447c Rv3556c Rv3609c Rv3609c Rv3609c Rv1207 Rv2607c Rv0013 Rv1005c Rv0013 3. Lipoate Rv2217 4. Molybdd Rv3109 Rv0869c	dfrA folC folD folE folK folP folP2 folX pabA pabB pabC	folylpolyglutamate synthase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosynthesis p-aminobenzoate synthase glutamine amidotransferase p-aminobenzoate synthase aminodeoxychorismate lyase lipoate biosynthesis protein A lipoate biosynthesis protein B molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0562 Rv2173 Rv3383c Rv2173 Rv3383c Rv0534c	thiX trxA trxB trxB2 trxC quinone, P dxs grcC1 grcC2 idsA idsA2 idsB menA menB	equivalent to M. leprae ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase light and the synthase II heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase naphthoate synthase o-succinylbenzoate-CoA synthase 2-succinyl-6-hydroxy-2,4-cyclo-
Rv0809 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385	purL purM purN purQ purT purU ine ribonu carA carB pyrB pyrC pyrD pyrF	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylformylglycinamidine synthase I phosphoribosylformylglycinamidine synthase I phosphoribosylformylglycinamidine formyltransferase II phosphoribosylglycinamide formyltransferase II phosphoribosylglycinamide formyltransferase II comyltransferase II comylterahydrofolate deformylase cleotide biosynthesis carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotase dehydrogenase orotidine 5'-phosphate decarboxylase	Rv2763c Rv2447c Rv3356c Rv3609c Rv3606c Rv3608c Rv1207 Rv0013 Rv1005c Rv0812 3. Lipoate Rv2218 Rv2217 4. Molybdi Rv3109	dfrA folC folD folE folK folP folP2 folX pabA pabB pabC	folylpolyglutamate synthase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosyhokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosynthesis p-aminobenzoate synthase glutamine amidotransferase p-aminobenzoate synthase aminodeoxychorismate lyase lipoate biosynthesis protein A lipoate biosynthesis protein B molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis.	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0562 Rv398c Rv2173 Rv3383c Rv0534c Rv0534c Rv0553 Rv0555	thiX trxA trxB trxB2 trxC quinone, P dxs grcC1 grcC2 idsA idsA2 idsB menA menB menC menD	equivalent to M. leprae ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin (QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase II geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase cyanylgeranylera
Rv0809 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699	purL purM purN purQ purT purU iine ribonu carA carB pyrB pyrC pyrD pyrF pyrG	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II formyltetrahydrofolate deformyltase cleotide biosynthesis carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxylase CTP synthase	Rv2763c Rv2447c Rv3356c Rv3609c Rv3609c Rv3609c Rv1207 Rv3607c Rv0013 Rv1005c Rv0812 3. Lipoate Rv2217 4. Molybdr Rv3109 Rv0438c	dfrA folC folD folE folF folP folP2 folX pabA pabB pabC lipA lipB opterin moaA moaA2	folylpolyglutamate synthase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosynthesis p-aminobenzoate synthase glutamine amidotransferase p-aminobenzoate synthase aminodeoxychorismate lyase lipoate biosynthesis protein A lipoate biosynthesis protein B	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0562 Rv398c Rv2173 Rv3383c Rv0534c Rv0553 Rv0555 Rv0555	thiX trxA trxA trxB2 trxB2 trxC uuinone, P dxs grcC1 grcC2 idsA idsA2 idsB menA menB menC menD menE	equivalent to M. leprae ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and ther 1-deoxy-D-xylulose 5-phosphate synthase leptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase -dihydroxy-2-naphthoate octaprenyltransferase naphthoate synthase o-succinylbenzoate-CoA synthase 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase o-succinylbenzoic acid-CoA ligase
Rv0809 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699 Rv2883c	purL purM purN purQ purT purU ine ribonu carA carB pyrB pyrC pyrD pyrF pyrF pyrF pyrF	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II formylterahydrofolate deformyltase Cleotide biosynthesis carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotase dihydroorotase dhydroorotate dehydrogenase orotidine 5'-phosphate decarboxylase UTP synthase uridylate kinase	Rv2763c Rv2447c Rv3556c Rv3609c Rv3609c Rv3609c Rv1207 Rv2607c Rv0013 Rv1005c Rv0013 3. Lipoate Rv2217 4. Molybdd Rv3109 Rv0869c	dfrA folC folD folE folK folP folP2 folX pabA pabB pabC	folyloolyglutamate synthase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosynthesis p-aminobenzoate synthase glutamine amidotransferase p-aminobenzoate synthase aminodeoxychorismate lyase lipoate biosynthesis protein A lipoate biosynthesis protein B molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis.	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0562 Rv398c Rv2173 Rv3383c Rv0534c Rv0534c Rv0553 Rv0555	thiX trxA trxB trxB2 trxC quinone, P dxs grcC1 grcC2 idsA idsA2 idsB menA menB menC menD	equivalent to M. leprae ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and there 1-deoxy-D-xylulose 5-phosphate synthase land the synthase geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase cataprenyltransferase naphthoate synthase o-succinylbenzoate-CoA synthase 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase o-succinylbenzoate acid-CoA ligase S-adenosylmethionine:
Rv0809 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699	purL purM purN purQ purT purU iine ribonu carA carB pyrB pyrC pyrD pyrF pyrG	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylformylglycinamidine synthase I phosphoribosylformylglycinamide formyltransferase II phosphoribosylformylglycinamide formyltransferase II phosphoribosylformylglycinamide formyltetrahydrofolate deformylase cleotide biosynthesis carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxylase CTP synthase uridylate kinase probable uridine 5'-monophos-	Rv2763c Rv2447c Rv3456c Rv3609c Rv3606c Rv3608c Rv1207 Rv3607c Rv0013 Rv1005c Rv0812 3. Lipoate Rv2218 Rv2217 4. Molybdr Rv3109 Rv0869c Rv0438c Rv3110	dfrA folC folD folB folF folP folP2 folX pabA pabB pabC lipA lipB opterin moaA2 moaA3 moaB	folylpolyglutamate synthase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosynthesis p-aminobenzoate synthase glutamine amidotransferase p-aminobenzoate synthase aminodeoxychorismate lyase lipoate biosynthesis protein A lipoate biosynthesis protein B molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein B	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0562 Rv398c Rv2173 Rv3383c Rv0534c Rv0553 Rv0555 Rv0555 Rv0548c Rv0553	thiX trxA trxB trxB2 trxC quinone, P dxs grcC1 grcC2 idsA idsA2 idsB menA menB menC menD menE menG	equivalent to M. leprae ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin (QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase libertaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase II geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase aphthoate synthase o-succinylbenzoate-CoA synthase 2-succinylbenzotae-CoA synthase o-succinylbenzoic acid-CoA ligase S-adenosylmethionine: 2-demethylmenaquinone
Rv0809 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699 Rv2883c Rv0382c	purL purM purN purQ purT purU ine ribonu carA carB pyrB pyrC pyrD pyrF pyrF pyrF pyrH umpA	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II formylterahydrofolate deformyltase Cleotide biosynthesis carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotase dhydrogenase orotidine 5'-phosphate decarboxylase CTP synthase uridylate kinase probable uridine 5'-monophosphate synthase	Rv2763c Rv2447c Rv3656c Rv3609c Rv3609c Rv3609c Rv1207 Rv3607c Rv0013 Rv1005c Rv0812 3. Lipoate Rv2217 4. Molybdd Rv3109 Rv0869c Rv0438c Rv3110 Rv0984	dfrA folC folD folE folK folP folP2 folX pabA pabB pabC lipA lipB opterin moaA2 moaA2 moaA3 moaB2	folyloolyglutamate synthase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosynthesis p-aminobenzoate synthase glutamine amidotransferase p-aminobenzoate synthase aminodeoxychorismate lyase lipoate biosynthesis protein A lipoate biosynthesis protein B molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein B	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0562 Rv398c Rv2173 Rv3383c Rv0534c Rv0553 Rv0555 Rv0555	thiX trxA trxA trxB2 trxB2 trxC uuinone, P dxs grcC1 grcC2 idsA idsA2 idsB menA menB menC menD menE	equivalent to M. leprae ThiX thioredoxin thioredoxin reductase the properties of
Rv0809 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699 Rv2883c Rv0382c 3. 2'-deox;	purL purM purN purQ purT purU ine ribonu carA carB pyrB pyrC pyrD pyrF pyrG pyrH umpA	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylformylglycinamidine synthase I phosphoribosylformylglycinamidine synthase I phosphoribosylformylglycinamide formyltransferase II formyltetrahydrofolate deformyltase cleotide biosynthesis carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotase dehydrogenase orotidine 5'-phosphate decarboxylase CTP synthase uridylate kinase probable uridine 5'-monophosphate synthase otide metabolism	Rv2763c Rv2447c Rv3456c Rv3609c Rv3606c Rv3608c Rv1207 Rv3607c Rv0013 Rv1005c Rv0812 3. Lipoate Rv2218 Rv2217 4. Molybdr Rv3109 Rv0869c Rv0438c Rv3110	dfrA folC folD folB folF folP folP2 folX pabA pabB pabC lipA lipB opterin moaA2 moaA3 moaB	folylpolyglutamate synthase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosynthesis p-aminobenzoate synthase glutamine amidotransferase p-aminobenzoate synthase aminodeoxychorismate lyase lipoate biosynthesis protein A lipoate biosynthesis protein B molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein B	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0562 Rv3398c Rv2173 Rv3383c Rv0534c Rv0553 Rv0555 Rv0542c Rv3853 Rv397c Rv3997c	thiX trxA trxB trxB2 trxC uinone, P dxs grcC1 grcC2 idsA idsA2 idsB menA menB menC menD menE menG phyA pqqE	equivalent to M. leprae ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and ther 1-deoxy-D-xylulose 5-phosphate synthase libertaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase aphthoate synthase 2-succinyl6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase o-succinylbenzoic acid-CoA ligase S-adenosylmethionine: 2-demethylmenaquinone phytoene synthase coenzyme PQQ synthesis protein E
Rv0809 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699 Rv2883c Rv0382c	purL purM purN purQ purT purU ine ribonu carA carB pyrB pyrC pyrD pyrF pyrF pyrF pyrH umpA	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II formylterahydrofolate deformyltransferase II formylterahydrofolate deformylase cleotide biosynthesis carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxylase CTP synthase uridylate kinase probable uridine 5'-monophosphate synthase otide metabolism deoxycytidine triphosphate	Rv2763c Rv2447c Rv3356c Rv3609c Rv3609c Rv3609c Rv1207 Rv3607c Rv0013 Rv1005c Rv0812 3. Lipoatle Rv2217 4. Molybdd Rv3109 Rv0438c Rv3110 Rv0984 Rv3111	dfrA folC folD folE folK folP folP2 folX pabA pabB pabC lipA lipB opterin moaA moaA2 moaA3 moaB moaB2 moaC	folylpolyglutamate synthase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosynthesis p-aminobenzoate synthase glutamine amidotransferase p-aminobenzoate synthase aminodeoxychorismate lyase lipoate biosynthesis protein A lipoate biosynthesis protein B molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein B molybdenum cofactor biosynthesis, protein C	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0562 Rv398c Rv2173 Rv3383c Rv0534c Rv0553 Rv0555 Rv0553 Rv0555 Rv0542c Rv3853 Rv3397c	thiX trxA trxA trxB2 trxB2 trxC uuinone, P dxs grcC1 grcC2 idsA idsA2 idsB menA menB menC menD menE menG phyA	equivalent to M. leprae ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and ther 1-deoxy-D-xylulose 5-phosphate synthase leptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase naphthoate synthase o-succinylbenzoate-CoA synthase 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase o-succinylbenzoic acid-CoA ligase S-adenosylmethionine: 2-demethylmenaquinone phytoene synthase coenzyme PQQ synthesis protein E ubiquinone/menaquinone biosyn-
Rv0809 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699 Rv2883c Rv0382c 3. 2'-deox; Rv0321	purL purM purN purQ purT purU line ribonu carA carB pyrB pyrC pyrD pyrF pyrF pyrF pyrF pyrH umpA	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II formyltetrahydrofolate deformyltase carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotase dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxylase crotidine 5'-phosphate decarboxylase crotidine 5'-phosphate decarboxylase crotidine 5'-monophosphate synthase subunit deoxycytidine 5'-monophosphate synthase crotide metabolism deoxycytidine triphosphate deaminase	Rv2763c Rv2447c Rv3656c Rv3609c Rv3609c Rv3609c Rv1207 Rv3607c Rv0013 Rv1005c Rv0812 3. Lipoate Rv2217 4. Molybdd Rv3109 Rv0869c Rv0438c Rv3110 Rv0984	dfrA folC folD folE folK folP folP2 folX pabA pabB pabC lipA lipB opterin moaA2 moaA2 moaA3 moaB2	folyloolyglutamate synthase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosynthesis p-aminobenzoate synthase glutamine amidotransferase p-aminobenzoate synthase aminodeoxychorismate lyase lipoate biosynthesis protein A lipoate biosynthesis protein B molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein B molybdenum cofactor biosynthesis, protein C molybdenum cofactor biosynthesis.	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0562 Rv3398c Rv2173 Rv3383c Rv0534c Rv0553 Rv0555 Rv0542c Rv3853 Rv397c Rv3997c	thiX trxA trxB trxB2 trxC uinone, P dxs grcC1 grcC2 idsA idsA2 idsB menA menB menC menD menE menG phyA pqqE	equivalent to M. leprae ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and ther 1-deoxy-D-xylulose 5-phosphate synthase libertaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase aphthoate synthase 2-succinyl6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase o-succinylbenzoic acid-CoA ligase S-adenosylmethionine: 2-demethylmenaquinone phytoene synthase coenzyme PQQ synthesis protein E
Rv0809 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699 Rv2883c Rv0382c 3. 2'-deox;	purL purM purN purQ purT purU ine ribonu carA carB pyrB pyrC pyrD pyrF pyrG pyrH umpA	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II formylterahydrofolate deformyltransferase II formylterahydrofolate deformylase cleotide biosynthesis carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxylase CTP synthase uridylate kinase probable uridine 5'-monophosphate synthase otide metabolism deoxycytidine triphosphate	Rv2763c Rv2447c Rv3356c Rv3609c Rv3609c Rv3609c Rv1207 Rv3607c Rv0013 Rv1005c Rv0812 3. Lipoatle Rv2217 4. Molybdd Rv3109 Rv0438c Rv3110 Rv0984 Rv3111	dfrA folC folD folE folK folP folP2 folX pabA pabB pabC lipA lipB opterin moaA moaA2 moaA3 moaB moaB2 moaC	folylpolyglutamate synthase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosynthesis p-aminobenzoate synthase glutamine amidotransferase p-aminobenzoate synthase aminodeoxychorismate lyase lipoate biosynthesis protein A lipoate biosynthesis protein B molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein B molybdenum cofactor biosynthesis, protein C	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0562 Rv3398c Rv2173 Rv3383c Rv0534c Rv0553 Rv0555 Rv0542c Rv3853 Rv397c Rv3997c	thiX trxA trxB trxB2 trxC quinone, P dxs grcC1 grcC2 idsA idsA2 idsB menA menB menC menD menE menG phyA pqqE ubiE	equivalent to M. leprae ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and ther 1-deoxy-D-xylulose 5-phosphate synthase libertaperenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase aphthoate synthase o-succinylbenzoate-CoA synthase 2-succinylbenzoate-CoA synthase o-succinylbenzoic acid-CoA ligase S-adenosylmethionine: 2-demethylmenaquinone phytoene synthase coenzyme PQQ synthesis protein E ubiquinone/menaquinone biosynthesis methyltransferase
Rv0809 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699 Rv2883c Rv0382c 3. 2'-deox; Rv0321 Rv2697c Rv0233	purL purM purN purQ purT purU line ribonucarA carB pyrB pyrC pyrD pyrF pyrF pyrH umpA vyribonucle dcd dut nrdB	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II phosphoribosylglycinamide formyltransferase II formyltetrahydrofolate deformylase cleotide biosynthesis carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxylase cryothase subunit carbamoyl-phosphate decarboxylase children synthase subunit carbamoyl-phosphate decarboxylase cryothase uridylate kinase probable uridine 5'-monophosphate synthase deoxyuridine triphosphate deaminase deoxyuridine triphosphatase ribonucleoside-diphosphate reductase B2 (eukaryotic-like)	Rv2763c Rv2447c Rv3656c Rv3609c Rv3609c Rv3609c Rv1207 Rv3607c Rv0013 Rv1005c Rv0812 3. Lipoate Rv2217 4. Molybdd Rv3109 Rv0869c Rv3110 Rv0984 Rv3111 Rv0984 Rv3111 Rv0864	dfrA folC folD folE folK folP folP2 folX pabA pabB pabC lipA lipB opterin moaA2 moaA2 moaA3 moaB moaB2 moaC moaC2	folyloolyglutamate synthase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosynthesis p-aminobenzoate synthase glutamine amidotransferase p-aminobenzoate synthase aminodeoxychorismate lyase lipoate biosynthesis protein A lipoate biosynthesis protein B molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein B molybdenum cofactor biosynthesis, protein C	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0989c Rv3398c Rv2173 Rv3383c Rv0534c Rv0542c Rv0553 Rv0555 Rv0542c Rv3983 Rv0558	thiX trxA trxB trxB trxB2 trxC luinone, P dxs grcC1 grcC2 idsA idsA2 idsB menA menB menC menD menE menG phyA pqqE ubiE and porph hemA	equivalent to M. leprae ThiX thioredoxin thioredoxin reductase the properties of
Rv0809 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699 Rv2883c Rv0382c 3. 2'-deox; Rv0321 Rv2697c	purL purM purN purQ purT purU ine ribonu carA carB pyrB pyrC pyrD pyrF pyrG pyrH umpA yribonucle dcd dut	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosylf-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase I phosphoribosylformylglycinamidine synthase I phosphoribosylglycinamide formyltransferase II formyltetrahydrofolate deformyltase cleotide biosynthesis carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotase dihydroorotase dihydroorotase crotidine 5'-phosphate decarboxylase crotidine 5'-phosphate decarboxylase crotidine 5'-phosphate decarboxylase crotidine 5'-monophosphate synthase uridylate kinase probable uridine 5'-monophosphate synthase deoxyuridine triphosphate deaminase deoxyuridine triphosphate ribonucleoside-diphosphate	Rv2763c Rv2447c Rv3356c Rv3609c Rv3606c Rv3608c Rv1207 Rv0013 Rv1005c Rv0812 3. Lipoatle Rv2218 Rv2217 4. Molybdr Rv3109 Rv0869c Rv0438c Rv3110 Rv0984 Rv3111 Rv0864	dfrA folC folD folF folK folP folP2 folX pabA pabB pabC lipA lipB opterin moaA2 moaA3 moaB moaB2 moaC2	folyloolyglutamate synthase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosynthesis p-aminobenzoate synthase glutamine amidotransferase p-aminobenzoate synthase aminodeoxychorismate lyase lipoate biosynthesis protein A lipoate biosynthesis protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein B molybdenum cofactor biosynthesis, protein B molybdenum cofactor biosynthesis, protein B molybdenum cofactor biosynthesis, protein C molybdopterin converting factor	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0562 Rv3398c Rv2173 Rv3383c Rv0534c Rv0553 Rv0555 Rv0542c Rv39853 Rv0555 Rv0548c Rv0553 Rv0555 Rv0593 Rv0593 Rv0593 Rv0593 Rv0593 Rv0593 Rv0593 Rv0593 Rv0593	thiX trxA trxB trxB2 trxC uinone, P dxs grcC1 grcC2 idsA idsA2 idsB menA menB menC menD menE menG phyA pqqE ubiE and porph hemA	equivalent to M. leprae ThiX thioredoxin reductase reducta
Rv0809 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699 Rv2883c Rv0382c 3. 2'-deox; Rv0321 Rv2697c Rv0233	purL purM purN purQ purT purU iine ribonu carA carB pyrB pyrC pyrD pyrF pyrG pyrH umpA vyribonucle dcd dut nrdB nrdE	carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II phosphoribosylglycinamide formyltransferase II formyltetrahydrofolate deformylase cleotide biosynthesis carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxylase cryothase subunit carbamoyl-phosphate decarboxylase children synthase subunit carbamoyl-phosphate decarboxylase cryothase uridylate kinase probable uridine 5'-monophosphate synthase deoxyuridine triphosphate deaminase deoxyuridine triphosphatase ribonucleoside-diphosphate reductase B2 (eukaryotic-like)	Rv2763c Rv2447c Rv3656c Rv3609c Rv3609c Rv3609c Rv1207 Rv3607c Rv0013 Rv1005c Rv0812 3. Lipoate Rv2217 4. Molybdd Rv3109 Rv0869c Rv3110 Rv0984 Rv3111 Rv0984 Rv3111 Rv0864	dfrA folC folD folE folK folP folP2 folX pabA pabB pabC lipA lipB opterin moaA2 moaA2 moaA3 moaB moaB2 moaC moaC2	folyloolyglutamate synthase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosynthesis p-aminobenzoate synthase glutamine amidotransferase p-aminobenzoate synthase aminodeoxychorismate lyase lipoate biosynthesis protein A lipoate biosynthesis protein B molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein B molybdenum cofactor biosynthesis, protein C	Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0989c Rv3398c Rv2173 Rv3383c Rv0534c Rv0542c Rv0553 Rv0555 Rv0542c Rv3983 Rv0558	thiX trxA trxB trxB trxB2 trxC luinone, P dxs grcC1 grcC2 idsA idsA2 idsB menA menB menC menD menE menG phyA pqqE ubiE and porph hemA	equivalent to M. leprae ThiX thioredoxin thioredoxin reductase the properties of

Rv1300	hemK	protoporphyrinogen oxidase	Rv0470c	umaA2	unknown mycolic acid methyl-	Rv2931	ppsA	phenolpthiocerol synthesis (pksB)
Rv0524	hemL	glutamate-1-semialdehyde amino-			transferase	Rv2932	ppsB	phenolpthiocerol synthesis (pksC)
		transferase				Rv2933	ppsC	phenolpthiocerol synthesis (pksD)
Rv2388c	hemN	oxygen-independent copropor-			mycoloyltransferases and	Rv2934	ppsD	phenolpthiocerol synthesis (pksE)
D 00==		phyrinogen III oxidase		ipid synthe		Rv2935	ppsE	phenolpthiocerol synthesis (pksF)
Rv2677c	hemY' hemZ	protoporphyrinogen oxidase ferrochelatase	Rv2289	cdh	CDP-diacylglycerol phosphatidyl- hydrolase	Rv2928	tesA -	thioesterase
Rv1485	nemz	ierrocheialase	Rv2881c	cdsA	phosphatidate cytidylyltransferase	Rv1544	-	probable ketoacyl reductase
13. Cobala	amin		Rv3804c		antigen 85A, mycolyltransferase	J. Broad r	equilatory	functions
Rv2849c	cobA	cob(I)alamin adenosyltransferase	Rv1886c		antigen 85B, mycolyltransferase	1. Repres		
Rv2848c	cobB	cobyrinic acid a,c-diamide	Rv3803c		antigen 85C, mycolyltransferase	Rv1657	argR	arginine repressor
		synthase	Rv0129c	fbpC2	antigen 85C', mycolytransferase	Rv1267c	embR	regulator of embAB genes
Rv2231c	cobC	aminotransferase	Rv0564c	gpdA1	glycerol-3-phosphate dehydroge-			(AfsR/DndI/RedD family)
Rv2236c	cobD	cobinamide synthase			nase	Rv1909c	furA	ferric uptake regulatory protein
Rv2064	cobG	percorrin reductase	Rv2982c	gpdA2	glycerol-3-phosphate dehydroge-	Rv2359	furB	ferric uptake regulatory protein
Rv2065	cobH	precorrin isomerase	D.:0010a	1	nase	Rv2919c Rv2711	gInB	nitrogen regulatory protein
Rv2066 Rv2070c	cobl cobK	Cobl-CobJ fusion protein precorrin reductase	Rv2612c	pgsA	CDP-diacylglycerol-glycerol-3- phosphate phosphatidyltrans-	Rv2711	ideR IexA	iron dependent repressor, IdeR LexA, SOS repressor protein
Rv2070c	cobL	probable methyltransferase			ferase	Rv1479	moxR	transcriptional regulator, MoxR
Rv2071c	cobM	precorrin-3 methylase	Rv1822	pgsA2	CDP-diacylglycerol-glycerol-3-	1101473	HUXH	homologue
Rv2062c	cobN	cobalt insertion		pg0/12	phosphate phosphatidyltrans-	Rv3692	moxR2	transcriptional regulator, MoxR
Rv2208	cobS	cobalamin (5'-phosphate)			ferase			homologue
		synthase	Rv2746c	pgsA3	CDP-diacylglycerol-glycerol-3-	Rv3164c	moxR3	transcriptional regulator, MoxR
Rv2207	cobT	nicotinate-nucleotide-dimethyl-			phosphate phosphatidyltrans-			homologue
		benzimidazole transferase			ferase	Rv0212c	nadR	similar to <i>E.coli</i> NadR
Rv0254c	cobU	cobinamide kinase	Rv1551	plsB1	glycerol-3-phosphate acyltrans-	Rv0117	oxyS	transcriptional regulator (LysR
Rv0255c	cobQ	cobyric acid synthase	D. 0400-	1- DO	ferase	D 4070		family)
Rv3713 Rv0306	cobQ2 -	possible cobyric acid synthase similar to BluB cobalamin synthe-	Rv2482c	plsB2	glycerol-3-phosphate acyltrans- ferase	Rv1379	pyrR	regulatory protein pyrimidine biosynthesis
HV0300	-	sis protein <i>R. capsulatus</i>	Rv0437c	psd	putative phosphatidylserine	Rv2788	sirR	iron-dependent transcriptional
		sio protein 71. oapodiatao	1100-070	pou	decarboxylase	1102700	Olliti	repressor
14. Iron ut	ilization		Rv0436c	pssA	CDP-diacylglycerol-serine	Rv3082c	virS	putative virulence regulating
Rv1876	bfrA	bacterioferritin			o-phosphatidyltransferase			protein (AraC/XyIS family)
Rv3841	bfrB	bacterioferritin	Rv0045c	-	possible dihydrolipoamide acetyl-	Rv3219	whiB1	WhiB transcriptional activator
Rv3215	entC	probable isochorismate synthase			transferase			homologue
Rv3214	entD	weak similarity to many phospho-	Rv0914c	-	lipid transfer protein	Rv3260c	whiB2	WhiB transcriptional activator
		glycerate mutases	Rv1543	-	probable fatty-acyl CoA reductase			homologue
Rv2895c	viuB	similar to proteins involved in	Rv1627c		lipid carrier protein	Rv3416	whiB3	WhiB transcriptional activator
Rv3525c	_	vibriobactin uptake similar to ferripyochelin binding	Rv1814 Rv1867	-	possible C-5 sterol desaturase	Rv3681c	whiB4	homologue
NV35250	-	protein	NV1007	-	similar to acetyl CoA synthase/lipid carriers	NV3001C	WIIID4	WhiB transcriptional activator homologue
		protein	Rv2261c	_	apolipoprotein N-acyltrans-	Rv0023	_	putative transcriptional regulator
H. Lipid bi	iosvnthesis		11022010		ferase-a	Rv0043c	-	transcriptional regulator (GntR
		and mycolic acids	Rv2262c		apolipoprotein N-acyltrans-			family)
Rv3285	accA3	acetyl/propionyl CoA carboxylase			ferase-b	Rv0067c	-	transcriptional regulator
		α subunit	Rv3523	-	lipid carrier protein			(TetR/AcrR family)
Rv0904c	accD3	acetyl/propionyl CoA carboxylase	Rv3720	-	C-term similar to cyclopropane	Rv0078	-	transcriptional regulator
Dv27000	D4	β subunit			fatty acid synthases	Dv0001		(TetR/AcrR family)
Rv3799c	accD4	acetyl/propionyl CoA carboxylase β subunit	I Polyko	ido and no	n ribosomal pontido synthosis	Rv0081	-	transcriptional regulator (ArsR
Rv3280	accD5	acetyl/propionyl CoA carboxylase	Rv2940c		n-ribosomal peptide synthesis mycocerosic acid synthase	Rv0135c	_	family) putative transcriptional regulator
1100200	accos	β subunit	Rv2384	mbtA	mycobactin/exochelin synthesis	Rv0144	-	putative transcriptional regulator
Rv2247	accD6	acetyl/propionyl CoA carboxylase	1.1.200		(salicylate-AMP ligase)	Rv0158	-	transcriptional regulator
		β subunit	Rv2383c	mbtB	mycobactin/exochelin synthesis			(TetR/AcrR family)
Rv2244	асрМ	acyl carrier protein (meromycolate			(serine/threonine ligation)	Rv0165c	-	transcriptional regulator (GntR
		extension)	Rv2382c	mbtC	mycobactin/exochelin synthesis			family)
Rv2523c	acpS	CoA:apo-[ACP] pantethienephos-	Rv2381c	mbtD	mycobactin/exochelin synthesis	Rv0195	-	transcriptional regulator
		photransferase	_		(polyketide synthase)	_		(LuxR/UhpA family)
Rv2243	fabD	malonyl CoA-[ACP] transacylase	Rv2380c	mbtE	mycobactin/exochelin synthesis	Rv0196	-	transcriptional regulator
Rv0649	fabD2	malonyl CoA-[ACP] transacylase	D. 0070-		(lysine ligation)	D.,0000		(TetR/AcrR family)
Rv1483	fabG1	3-oxoacyl-[ACP] reductase (aka MabA)	Rv2379c	mbtF	mycobactin/exochelin synthesis (lysine ligation)	Rv0232	-	transcriptional regulator (TetR/AcrR family)
Rv1350	fabG2	3-oxoacyl-[ACP] Reductase	Rv2378c	mhtG	mycobactin/exochelin synthesis	Rv0238	_	transcriptional regulator
Rv2002	fabG3	3-oxoacyl-[ACP] reductase	11020700	moto	(lysine hydroxylase)	1110200		(TetR/AcrR family)
Rv0242c	fabG4	3-oxoacyl-[ACP] reductase	Rv2377c	mbtH	mycobactin/exochelin synthesis	Rv0273c	-	putative transcriptional regulator
Rv2766c	fabG5	3-oxoacyl-[ACP] reductase	Rv0101	nrp	unknown non-ribosomal peptide	Rv0302	-	transcriptional regulator
Rv0533c	fabH	β-ketoacyl-ACP synthase III			synthase			(TetR/AcrR family)
Rv2524c	fas	fatty acid synthase	Rv1153c		PKS o-methyltransferase	Rv0324	-	putative transcriptional regulator
Rv1484	inhA	enoyl-[ACP] reductase	Rv3824c	papA1	PKS-associated protein, unknown	Rv0328	-	transcriptional regulator
Rv2245	kasA	β-ketoacyl-ACP synthase	D. 00000	10	function	D. 0040		(TetR/AcrR family)
Dv0046	kooP	(meromycolate extension) β-ketoacyl-ACP synthase	Rv3820c	papA2	PKS-associated protein, unknown	Rv0348 Rv0377	-	putative transcriptional regulator
Rv2246	kasB	(meromycolate extension)	Rv1182	papA3	function PKS-associated protein, unknown	11000//	-	transcriptional regulator (LysR family)
Rv1618	tesB1	thioesterase II	1141102	ραμπο	function	Rv0386	-	transcriptional regulator
Rv2605c	tesB2	thioesterase II	Rv1528c	papA4	PKS-associated protein, unknown			(LuxR/UhpA family)
Rv0033	-	possible acyl carrier protein			function	Rv0452	-	putative transcriptional regulator
Rv1344	-	possible acyl carrier protein	Rv2939	papA5	PKS-associated protein, unknown	Rv0465c	-	transcriptional regulator
Rv1722	-	possible biotin carboxylase			function			(PbsX/Xre family)
Rv3221c	-	resembles biotin carboxyl carrier	Rv2946c	pks1	polyketide synthase	Rv0472c	-	transcriptional regulator
Rv3472	-	possible acyl carrier protein	Rv1660	pks10	polyketide synthase (chalcone	D. 0474		(TetR/AcrR family)
O Modified	ation of fat	hy and mysolic saids	Dv1665	nko11	synthase-like)	Rv0474	-	transcriptional regulator (PbsX/Xre family)
2. Modifica Rv3391	acrA1	ty and mycolic acids fatty acyl-CoA reductase	Rv1665	pks11	polyketide synthase (chalcone synthase-like)	Rv0485	_	transcriptional regulator (ROK
Rv3392c	cmaA1	cyclopropane mycolic acid	Rv2048c	pks12	polyketide synthase (erythronolide	1100-100		family)
		synthase 1	0-100	F.1012	synthase-like)	Rv0494	-	transcriptional regulator (GntR
Rv0503c	cmaA2	cyclopropane mycolic acid syn-	Rv3800c	pks13	polyketide synthase			family)
		thase 2	Rv1342c	pks14	polyketide synthase (chalcone	Rv0552	-	putative transcriptional regulator
Rv0824c	desA1	acyl-[ACP] desaturase			synthase-like)	Rv0576	-	putative transcriptional regulator
Rv1094	desA2	acyl-[ACP] desaturase	Rv2947c		polyketide synthase	Rv0586	-	transcriptional regulator (GntR
Rv3229c	desA3	acyl-[ACP] desaturase	Rv1013	pks16	polyketide synthase	D. 00		family)
Rv0645c	mmaA1	methoxymycolic acid synthase 1	Rv1663	pks17	polyketide synthase	Rv0650	-	transcriptional regulator (ROK
Rv0644c	mmaA2	methoxymycolic acid synthase 2	Rv1372	pks18	polyketide synthase	D. 2055		family)
Rv0643c	mmaA3	methoxymycolic acid synthase 3	Rv3825c	pks2	polyketide synthase	Rv0653c	-	putative transcriptional regulator
Rv0642c	mmaA4	methoxymycolic acid synthase 4	Rv1180	pks3	polyketide synthase polyketide synthase	Rv0681	-	transcriptional regulator (TetR/AcrR family)
Rv0447c	ufaA1	unknown fatty acid methyltrans- ferase	Rv1181 Rv1527c	pks4 pks5	polyketide synthase polyketide synthase	Rv0691c	_	transcriptional regulator
Rv3538	ufaA2	unknown fatty acid methyltrans-	Rv0405	pks6	polyketide synthase	11400010		(TetR/AcrR family)
5000		ferase	Rv1661	pks7	polyketide synthase	Rv0737	-	putative transcriptional regulator
Rv0469	umaA1	unknown mycolic acid methyl-	Rv1662	pks8	polyketide synthase	Rv0744c	-	putative transcriptional regulator
		transferase	Rv1664	pks9	polyketide synthase	Rv0792c	-	transcriptional regulator (GntR

			D 0400					
Dv00000	-	family) transcriptional regulator		-	putative transcriptional regulator putative transcriptional regulator	Dv00100	nnn	truncated
Rv0823c	-	(NifR3/Smm1 family)	Rv3167c Rv3173c	-	transcriptional regulator	Rv0018c	ppp	putative phosphoprotein phos- phatase
Rv0827c	_	transcriptional regulator (ArsR	11001700		(TetR/AcrR family)	Rv2234	ptpA	low molecular weight protein-tyro-
		family)	Rv3183	-	putative transcriptional regulator		ριρπ	sine-phosphatase
Rv0890c	-	transcriptional regulator	Rv3208	-	transcriptional regulator	Rv0153c	-	putative protein-tyrosine-phos-
		(LuxR/UhpA family)			(TetR/AcrR family)			phatase
Rv0891c	-	putative transcriptional regulator	Rv3249c	-	transcriptional regulator			
Rv0894	-	putative transcriptional regulator	D 0004		(TetR/AcrR family)			metabolism
Rv1019	-	transcriptional regulator	Rv3291c	-	transcriptional regulator			odification of macromolecules
Rv1049	_	(TetR/AcrR family) transcriptional regulator (MarR	Rv3295	_	(Lrp/AsnC family) transcriptional regulator	1. Hibosor Rv3420c	naı proteir <i>riml</i>	n synthesis and modification
11049	-	family)	HV3293	-	(TetR/AcrR family)	NV34200	111111	ribosomal protein S18 acetyl transferase
Rv1129c	_	transcriptional regulator	Rv3334	-	transcriptional regulator (MerR	Rv0995	rimJ	acetylation of 30S S5 subunit
		(PbsX/Xre family)			family)	Rv0641	rplA	50S ribosomal protein L1
Rv1151c	-	putative transcriptional regulator	Rv3405c	-	putative transcriptional regulator	Rv0704	rpIB	50S ribosomal protein L2
Rv1152	-	transcriptional regulator (GntR	Rv3522	-	putative transcriptional regulator	Rv0701	rpIC	50S ribosomal protein L3
D 440=		family)	Rv3557c	-	transcriptional regulator	Rv0702	rpID	50S ribosomal protein L4
Rv1167c		putative transcriptional regulator	D. 0574	_	(TetR/AcrR family)	Rv0716	rpIE	50S ribosomal protein L5
Rv1219c Rv1255c	-	putative transcriptional regulator transcriptional regulator	Rv3574	-	transcriptional regulator (TetR/AcrR family)	Rv0719 Rv0056	rpIF rpII	50S ribosomal protein L6 50S ribosomal protein L9
11012550	_	(TetR/AcrR family)	Rv3575c	-	transcriptional regulator (Lacl	Rv0651	rplJ	50S ribosomal protein L10
Rv1332	-	putative transcriptional regulator			family)	Rv0640	rplK	50S ribosomal protein L11
Rv1353c	-	transcriptional regulator	Rv3583c	-	putative transcriptional regulator	Rv0652	rpIL	50S ribosomal protein L7/L12
		(TetR/AcrR family)	Rv3676	-	transcriptional regulator (Crp/Fnr	Rv3443c	rpIM	50S ribosomal protein L13
Rv1358	-	transcriptional regulator	D 00=0		family)	Rv0714	rpIN	50S ribosomal protein L14
D.:1050	_	(LuxR/UhpA family)	Rv3678c	-	transcriptional regulator (LysR	Rv0723	rpIO	50S ribosomal protein L15
Rv1359 Rv1395	-	putative transcriptional regulator transcriptional regulator	Rv3736	_	family) transcriptional regulator	Rv0708 Rv3456c	rpIP rpIQ	50S ribosomal protein L16 50S ribosomal protein L17
1101000		(AraC/XyIS family)	1110700		(AraC/XyIS family)	Rv0720	rpIR	50S ribosomal protein L18
Rv1404	-	transcriptional regulator (MarR	Rv3744	-	transcriptional regulator (ArsR	Rv2904c	rpIS	50S ribosomal protein L19
		family)			family)	Rv1643	rpIT	50S ribosomal protein L20
Rv1423	-	putative transcriptional regulator	Rv3830c	-	transcriptional regulator	Rv2442c	rpIU	50S ribosomal protein L21
Rv1460	-	putative transcriptional regulator	D.,0000		(TetR/AcrR family)	Rv0706	rpIV	50S ribosomal protein L22
Rv1474c	-	transcriptional regulator	Rv3833	-	transcriptional regulator (AraC/XyIS family)	Rv0703 Rv0715	rpIW rpIX	50S ribosomal protein L23
Rv1534	-	(TetR/AcrR family) transcriptional regulator	Rv3840	_	putative transcriptional regulator	Rv1015c	rpiX rpIY	50S ribosomal protein L24 50S ribosomal protein L25
HV1554	-	(TetR/AcrR family)	Rv3855	-	putative transcriptional regulator	Rv2441c	rpmA	50S ribosomal protein L27
Rv1556	-	putative transcriptional regulator			,	Rv0105c	rpmB	50S ribosomal protein L28
Rv1674c	-	putative transcriptional regulator	2. Two co	mponent s		Rv2058c	rpmB2	50S ribosomal protein L28
Rv1675c		putative transcriptional regulator	Rv1028c	kdpD	sensor histidine kinase	Rv0709	rpmC	50S ribosomal protein L29
Rv1719	-	transcriptional regulator (IcIR	Rv1027c	kdpE	two-component response	Rv0722	rpmD	50S ribosomal protein L30
D. 4770		family)	D: 0040-		regulator	Rv1298	rpmE	50S ribosomal protein L31
Rv1773c	-	transcriptional regulator (IcIR family)	Rv3246c	mtrA	two-component response regulator	Rv2057c Rv3924c	rpmG rpmH	50S ribosomal protein L33 50S ribosomal protein L34
Rv1776c	_	putative transcriptional regulator	Rv3245c	mtrB	sensor histidine kinase	Rv1642	rpml	50S ribosomal protein L35
Rv1816	-	putative transcriptional regulator	Rv0844c	narL	two-component response	Rv3461c	rpmJ	50S ribosomal protein L36
Rv1846c	-	putative transcriptional regulator			regulator	Rv1630	rpsA	30S ribosomal protein S1
Rv1931c	-	transcriptional regulator	Rv0757	phoP	two-component response	Rv2890c	rpsB	30S ribosomal protein S2
D 4050		(AraC/XyIS family)			regulator	Rv0707	rpsC	30S ribosomal protein S3
Rv1956	-	putative transcriptional regulator	Rv0758	phoR	sensor histidine kinase	Rv3458c	rpsD	30S ribosomal protein S4
Rv1963c Rv1985c	-	putative transcriptional regulator	Rv0491	regX3	two-component response	Rv0721	rpsE	30S ribosomal protein S5
UA 1900C	-	transcriptional regulator (LysR family)	Rv0490	senX3	regulator sensor histidine kinase	Rv0053 Rv0683	rpsF rpsG	30S ribosomal protein S6 30S ribosomal protein S7
Rv1990c	_	putative transcriptional regulator	Rv0602c	tcrA	two-component response	Rv0718	rpsH	30S ribosomal protein S8
Rv1994c	-	transcriptional regulator (MerR			regulator	Rv3442c	rpsl	30S ribosomal protein S9
		family)	Rv0260c	-	two-component response	Rv0700	rpsJ	30S ribosomal protein S10
Rv2017	-	putative transcriptional regulator			regulator	Rv3459c	rpsK	30S ribosomal protein S11
D 0004		(PbsX/Xre family)	Rv0600c	-	sensor histidine kinase	Rv0682	rpsL	30S ribosomal protein S12
Rv2021c Rv2034	-	putative transcriptional regulator transcriptional regulator (ArsR	Rv0601c Rv0818	-	sensor histidine kinase	Rv3460c	rpsM	30S ribosomal protein S13
NV2U34	-	family)	NVUOTO	-	two-component response regulator	Rv0717 Rv2056c	rpsN rpsN2	30S ribosomal protein S14 30S ribosomal protein S14
Rv2175c	-	putative transcriptional regulator	Rv0845	-	sensor histidine kinase	Rv2785c	rpsO	30S ribosomal protein S15
Rv2250c	- 1	putative transcriptional regulator	Rv0902c	-	sensor histidine kinase	Rv2909c	rpsP	30S ribosomal protein S16
Rv2258c	- 1	putative transcriptional regulator	Rv0903c	-	two-component response	Rv0710	rpsQ	30S ribosomal protein S17
Rv2282c	-	transcriptional regulator (LysR	D. 225		regulator	Rv0055	rpsR	30S ribosomal protein S18
D. 0000		family)	Rv0981	-	two-component response	Rv2055c	rpsR2	30S ribosomal protein S18
Rv2308 Rv2324		putative transcriptional regulator transcriptional regulator	Rv0982	_	regulator sensor histidine kinase	Rv0705 Rv2412	rpsS rpsT	30S ribosomal protein S19 30S ribosomal protein S20
1172024		(Lrp/AsnC family)	Rv1032c	-	sensor histidine kinase	Rv3241c	-	member of S30AE ribosomal
Rv2358	-	transcriptional regulator (ArsR		-	two-component response			protein family
		family)			regulator			
Rv2488c	-	transcriptional regulator	Rv1626	-	two-component response			cation and maturation
Rv2506	_	(LuxR/UhpA family) transcriptional regulator	Dv0007-		regulator	Rv1010	ksgA rbfA	16S rRNA dimethyltransferase ribosome-binding factor A
NV2506	-	(TetR/AcrR family)	Rv2027c Rv2884	-	sensor histidine kinase	Rv2838c Rv2907c	rbfA rimM	16S rRNA processing protein
Rv2621c	_	putative transcriptional regulator	1112004	-	two-component response regulator	11423076	IIIIIVI	100 IT INA Processing protein
Rv2640c	-	transcriptional regulator (ArsR	Rv3132c	-	sensor histidine kinase	3. Aminoa	cyl tRNA	synthases and their modification
		family)	Rv3133c	-	two-component response	Rv2555c	alaS	alanyl-tRNA synthase
Rv2642	-	transcriptional regulator (ArsR			regulator	Rv1292	argS	arginyl-tRNA synthase
D. 0000		family)	Rv3143	-	putative sensory transduction	Rv2572c	aspS	aspartyl-tRNA synthase
Rv2669 Rv2745c	-	putative transcriptional regulator putative transcriptional regulator	Duggggg		protein	Rv3580c	cysS	cysteinyl-tRNA synthase
Rv27450 Rv2779c	-	transcriptional regulator	Rv3220c Rv3764c	-	sensor histidine kinase sensor histidine kinase	Rv2130c Rv1406	cysS2 fmt	cysteinyl-tRNA synthase methionyl-tRNA formyltransferase
11027730		(Lrp/AsnC family)	Rv3765c	-	two-component response	Rv3011c	gatA	glu-tRNA-gln amidotransferase,
Rv2887	-	transcriptional regulator (MarR	2. 500		regulator		J	subunit B
		family)			-	Rv3009c	gatB	glu-tRNA-gln amidotransferase,
Rv2912c	-	transcriptional regulator			protein kinases and phosphoprotein			subunit A
D. 0000		(TetR/AcrR family)	phosphata		and a discount of the state of	Rv3012c	gatC	glu-tRNA-gln amidotransferase,
Rv2989	-	transcriptional regulator (IcIR	Rv0015c	pknA	serine-threonine protein kinase	D.,0000	-40	subunit C
Rv3050c	_	family) putative transcriptional regulator	Rv0014c Rv0931c	pknB pknD	serine-threonine protein kinase serine-threonine protein kinase	Rv2992c Rv2357c	gltS glyS	glutamyl-tRNA synthase glycyl-tRNA synthase
Rv30500	-	putative transcriptional regulator	Rv1743	pknE	serine-threonine protein kinase serine-threonine protein kinase	Rv2580c	giyS hisS	histidyl-tRNA synthase
Rv3058c	-	putative transcriptional regulator	Rv1746	pknF	serine-threonine protein kinase	Rv1536	ileS	isoleucyl-tRNA synthase
Rv3060c		transcriptional regulator (GntR	Rv0410c	pknG	serine-threonine protein kinase	Rv0041	leuS	leucyl-tRNA synthase
		family)	Rv1266c	pknH	serine-threonine protein kinase	Rv3598c	lysS	lysyl-tRNA synthase
Rv3066	-	putative transcriptional regulator	Rv2914c	pknl	serine-threonine protein kinase	Rv1640c	lysX	C-term lysyl-tRNA synthase
Rv3095	-	putative transcriptional regulator	Rv2088	pknJ	serine-threonine protein kinase	Rv1007c	metS	methionyl-tRNA synthase
Rv3124	-	transcriptional regulator (AfsR/Dndl/RedD family)	Rv3080c Rv2176	pknK pknL	serine-threonine protein kinase serine-threonine protein kinase,	Rv1649	pheS	phenylalanyl-tRNA synthase α subunit
		(7 HOLD HOLD HATTINY)	11421/0	PRIIL	oomie-uneomie protein kinase,			Subulit

Rv1650	pheT	phenylalanyl-tRNA synthase β	Rv2090	-	partially similar to DNA poly-	2. DNA		
Rv2845c	proS	subunit	Rv2191	_	merase I similar to both PoIC and UvrC	Rv0670 Rv1108c	end xseA	endonuclease IV (apurinase) exonuclease VII large subunit
Rv3834c	serS	prolyl-tRNA synthase seryl-tRNA synthase	1102101		proteins	Rv1107c	xseB	exonuclease VII small subunit
Rv2614c	thrS	threonyl-tRNA synthase	Rv2464c	-	probable DNA glycosylase,			
Rv2906c	trmD	tRNA (guanine-N1)-methyltrans-	Dv22010		endonuclease VIII			and glycopeptides probable aminohydrolase
Rv3336c	trpS	ferase tryptophanyl tRNA synthase	Rv3201c	-	probable ATP-dependent DNA helicase	Rv3305c Rv3306c	amiA amiB	probable aminohydrolase
Rv1689	tyrS	tyrosyl-tRNA synthase	Rv3202c	-	similar to UvrD proteins	Rv3596c	clpC	ATP-dependent Clp protease
Rv2448c	valS	valyl-tRNA synthase	Rv3263	-	probable DNA methylase	Rv2461c	clpP	ATP-dependent Clp protease pro-
			Rv3644c	-	similar in N-term to DNA poly-			teolytic subunit
4. Nucleop		de la la Ferra de la Ferra de la			merase III	Rv2460c	clpP2	ATP-dependent Clp protease pro- teolytic subunit
Rv1407 Rv3852	fmu hns	similar to Fmu protein HU-histone protein	6. Protein	translation	and modification	Rv2457c	clpX	ATP-dependent Clp protease
Rv2986c	hupB	DNA-binding protein II	Rv0429c	def	polypeptide deformylase			ATP-binding subunit ClpX
Rv1388	mİHF	integration host factor	Rv2534c	efp	elongation factor P	Rv2667	clpX'	similar to ClpC from M. leprae but
5 DNA		and the second to all the second or all the	Rv2882c Rv0684	frr fusA	ribosome recycling factor elongation factor G	Rv3419c	aan	shorter
tion/modifi		repair, recombination and restric-	Rv0120c	fusA2	elongation factor G	Rv2725c	gcp hflX	glycoprotease GTP-binding protein
Rv1317c		DNA-3-methyladenine glycosi-	Rv1080c	greA	transcription elongation factor G	Rv1223	htrA	serine protease
		dase II	Rv3462c	infA	initiation factor IF-1	Rv2861c	map	methionine aminopeptidase
Rv2836c		DNA-damage-inducible protein F	Rv2839c Rv1641	infB infC	initiation factor IF-2 initiation factor IF-3	Rv0734	map'	probable methionine aminopepti- dase
Rv1329c Rv3056	dinG dinP	probable ATP-dependent helicase DNA-damage-inducible protein	Rv0009	ppiA	peptidyl-prolyl <i>cis-trans</i> isomerase	Rv0319	рср	pyrrolidone-carboxylate peptidase
Rv1537	dinX	probable DNA-damage-inducible	Rv2582	рріВ	peptidyl-prolyl <i>cis-trans</i> isomerase	Rv0125	pepA	probable serine protease
		protein	Rv1299	prfA	peptide chain release factor 1	Rv2213	pepB	aminopeptidase A/I
Rv0001	dnaA	chromosomal replication initiator	Rv3105c Rv2889c	prfB tsf	peptide chain release factor 2	Rv0800	pepC	aminopeptidase I
Rv0058	dnaB	protein DNA helicase (contains intein)	Rv0685	tuf	elongation factor EF-Ts elongation factor EF-Tu	Rv2467 Rv2089c	pepD pepE	probable aminopeptidase cytoplasmic peptidase
Rv1547	dnaE1	DNA polymerase III, α subunit			ololigation table? El Ta	Rv2535c	pepQ	cytoplasmic peptidase
Rv3370c	dnaE2	DNA polymerase III α chain			NA modification and DNA	Rv2782c	pepR	protease/peptidase, M16 family
Rv2343c	dnaG	DNA primase	transcription		ATR dependent DNA/BNA	Dv21000	nro.4	(insulinase)
Rv0002 Rv3711c	dnaN dnaQ	DNA polymerase III, β subunit DNA polymerase III ε chain	Rv1253	deaD	ATP-dependent DNA/RNA helicase	Rv2109c Rv2110c	prcA prcB	proteasome α-type subunit 1 proteasome β-type subunit 2
Rv3711c	dnaZX	DNA polymerase III, γ (dnaZ) and	Rv2783c	gpsl	pppGpp synthase and polyribo-	Rv0782	ptrBa	protease II, α subunit
		τ (dnaX)		•	nucleotide phosphorylase	Rv0781	ptrBb	protease II, β subunit
Rv2924c	fpg	formamidopyrimidine-DNA glyco-	Rv2841c	nusA	transcription termination factor	Rv0724	sppA	protease IV, signal peptide pepti-
Rv0006	gyrA	sylase DNA gyrase subunit A	Rv2533c Rv0639	nusB nusG	N-utilization substance protein B transcription antitermination	Rv0198c	_	dase probable zinc metalloprotease
Rv0005	gyrB	DNA gyrase subunit A DNA gyrase subunit B	110000	naoa	protein	Rv0457c	-	probable peptidase
Rv2092c	helY	probable helicase, Ski2 subfamily	Rv3907c	pcnA	polynucleotide polymerase		-	probable proline iminopeptidase
Rv2101	helZ	probable helicase, Snf2/Rad54	Rv3232c	pvdS	alternative sigma factor for	Rv0983	-	probable serine protease
D0750-	bod 1	family	Rv3211	rhIE	siderophore production probable ATP-dependent	Rv1977 Rv3668c	-	probable zinc metallopeptidase probable alkaline serine protease
Rv2756c	hsdM	type I restriction/modification sys- tem DNA methylase	HVJZTT	IIIL	RNA helicase		-	probable serine protease
Rv2755c	hsdS'	type I restriction/modification sys-	Rv1297	rho	transcription termination		-	probable secreted protease
		tem specificity determinant		\Box	factor rho	Rv3886c	-	protease
Rv3296	lhr '' A	ATP-dependent helicase	Rv3457c Rv0667	rpoA rpoB	α subunit of RNA polymerase β subunit of RNA polymerase	4 Polyego	haridae l	ipopolysaccharides and phospho-
Rv3014c Rv3062	ligA ligB	DNA ligase DNA ligase	Rv0668	rpoC	β' subunit of RNA polymerase	lipids	Jilailaes, i	ipopolysacchandes and phospho-
Rv3731	ligC	probable DNA ligase	Rv1364c	rsbU	SigB regulation protein	Rv0062	celA	cellulase/endoglucanase
Rv1020	mfd	transcription-repair coupling factor	Rv3287c	rsbW	anti-sigma B factor	Rv3915	cwlM	hydrolase
Rv2528c	mrr	restriction system protein	Rv2703	sigA	RNA polymerase sigma factor	Rv0315 Rv1090	-	probable β-1,3-glucanase
Rv2985 Rv1160	mutT1 mutT2	MutT homologue MutT homologue	Rv2710	sigB	(aka MysA, RpoV) RNA polymerase sigma factor	HV1090	-	probable inactivated cellulase/endoglucanase
Rv0413	mutT3	MutT homologue		3-	(aka MysB)	Rv1327c	-	probable glycosyl hydrolase, α-
Rv3589	mutY	probable DNA glycosylase	Rv2069	sigC	ECF subfamily sigma subunit			amylase family
Rv3297	nei	probable endonuclease VIII	Rv3414c	sigD	ECF subfamily sigma subunit		-	probable hydrolase
Rv3674c		and the late of a state of the second		oiaE				probable neuraminidase possible N-acetylmuramoyl-L-ala-
By1316c	nth oat	probable endonuclease III	Rv1221	sigE siaF	ECF subfamily sigma subunit		-	
Rv1316c	ogt	methylated-DNA-protein-cysteine		sigE sigF sigG	ECF subfamily sigma subunit ECF subfamily sigma subunit sigma-70 factors ECF subfamily			nine amidase
Rv1629	ogt polA	methylated-DNA-protein-cysteine methyltransferase DNA polymerase I	Rv1221 Rv3286c Rv0182c Rv3223c	sigF sigG sigH	ECF subfamily sigma subunit sigma-70 factors ECF subfamily ECF subfamily sigma subunit	Rv3717	-	nine amidase
	ogt	methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n'	Rv1221 Rv3286c Rv0182c Rv3223c Rv1189	sigF sigG sigH sigI	ECF subfamily sigma subunit sigma-70 factors ECF subfamily ECF subfamily sigma subunit ECF family sigma factor	Rv3717 5. Esterase	- es and lipa	nine amidase
Rv1629 Rv1402	ogt polA priA	methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y)	Rv1221 Rv3286c Rv0182c Rv3223c Rv1189 Rv3328c	sigF sigG sigH sigI sigJ	ECF subfamily sigma subunit sigma-70 factors ECF subfamily ECF subfamily sigma subunit ECF family sigma factor similar to Sigl, ECF family	Rv3717 5. Esterase Rv0220	- es and lipa	nine amidase ases probable esterase
Rv1629	ogt polA	methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n'	Rv1221 Rv3286c Rv0182c Rv3223c Rv1189	sigF sigG sigH sigI	ECF subfamily sigma subunit sigma-70 factors ECF subfamily ECF subfamily sigma subunit ECF family sigma factor	Rv3717 5. Esterase	- es and lipa	nine amidase
Rv1629 Rv1402 Rv3585 Rv2737c	ogt polA priA radA recA	methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein)	Rv1221 Rv3286c Rv0182c Rv3223c Rv1189 Rv3328c Rv0445c	sigF sigG sigH sigI sigJ sigK	ECF subfamily sigma subunit sigma-70 factors ECF subfamily ECF subfamily sigma subunit ECF family sigma factor similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to	5. Esterase Rv0220 Rv1923 Rv3775 Rv3487c	es and lipa lipC lipD lipE lipF	nine amidase ases probable esterase probable esterase probable hydrolase probable esterase
Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c	ogt polA priA radA recA recB	methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V	Rv1221 Rv3286c Rv0182c Rv3223c Rv1189 Rv3328c Rv0445c Rv0735 Rv3911	sigF sigG sigH sigI sigJ sigK sigL sigM	ECF subfamily sigma subunit sigma-70 factors ECF subfamily ECF subfamily sigma subunit ECF family sigma factor similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE	5. Esterase Rv0220 Rv1923 Rv3775 Rv3487c Rv0646c	- lipC lipD lipE lipF lipG	nine amidase ases probable esterase probable esterase probable hydrolase probable bydrolase probable hydrolase
Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0631c	polA priA radA recA recB recC	methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V	Rv1221 Rv3286c Rv0182c Rv3223c Rv1189 Rv3328c Rv0445c Rv0735 Rv3911	sigF sigG sigH sigI sigJ sigK sigL sigM spoU	ECF subfamily sigma subunit sigma-70 factors ECF subfamily ECF subfamily sigma subunit ECF family sigma factor similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase	5. Esterase Rv0220 Rv1923 Rv3775 Rv3487c Rv0646c Rv1399c	es and lipa lipC lipD lipE lipF lipG lipH	nine amidase ases probable esterase probable esterase probable hydrolase probable esterase probable hydrolase probable hydrolase probable lipase
Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c	ogt polA priA radA recA recB	methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V	Rv1221 Rv3286c Rv0182c Rv3223c Rv1189 Rv3328c Rv0445c Rv0735 Rv3911	sigF sigG sigH sigJ sigK sigL sigM spoU truA	ECF subfamily sigma subunit sigma-70 factors ECF subfamily ECF subfamily ECF subfamily sigma subunit ECF family sigma factor similar to SigI, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate synthase	5. Esterase Rv0220 Rv1923 Rv3775 Rv3487c Rv0646c Rv1400c Rv1900c	- lipC lipD lipB lipF lipG lipH lipI lipJ	nine amidase ases probable esterase probable esterase probable hydrolase probable esterase probable esterase probable lipase probable lipase probable esterase
Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv0003	polA priA radA recA recB recC recD recF	methylated-DNA-protein-cysteine methylatensferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induction	Rv1221 Rv3286c Rv0182c Rv3223c Rv1189 Rv3328c Rv0445c Rv0735 Rv3911 Rv3366 Rv3455c	sigF sigG sigH sigJ sigJ sigK sigL sigM spoU truA	ECF subfamily sigma subunit sigma-70 factors ECF subfamily ECF subfamily sigma subunit ECF family sigma factor similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate synthase tRNA pseudouridine 55 synthase	5. Esterase Rv0220 Rv1923 Rv3775 Rv3487c Rv0646c Rv1399c Rv1400c Rv2385	- lipC lipD lipE lipF lipG lipH lipH lipI lipJ	nine amidase ases probable esterase probable esterase probable hydrolase probable esterase probable hydrolase probable lipase probable lipase probable lipase probable esterase probable esterase
Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv0003	polA priA radA recA recB recC recD recF	methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induction ATP-dependent DNA helicase	Rv1221 Rv3286c Rv0182c Rv3223c Rv1189 Rv3328c Rv0445c Rv0735 Rv3911	sigF sigG sigH sigJ sigK sigL sigM spoU truA	ECF subfamily sigma subunit sigma-70 factors ECF subfamily ECF subfamily sigma subunit ECF family sigma factor similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate synthase tRNA pseudouridine 55 synthase putative 23S rRNA methyltrans-	5. Esterase Rv0220 Rv1923 Rv3775 Rv3487c Rv1399c Rv1400c Rv1900c Rv2900c Rv2900c Rv1497	es and lipa lipC lipE lipF lipF lipG lipH lipJ lipJ lipJ lipL	nine amidase ases probable esterase probable esterase probable hydrolase probable esterase probable hydrolase probable lipase probable lipase probable esterase probable esterase probable acetyl-hydrolase esterase
Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv0003 Rv2973c Rv1696	polA priA radA recA recB recC recD recF	methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induction ATP-dependent DNA helicase recombination and DNA repair	Rv1221 Rv3286c Rv0182c Rv3223c Rv1189 Rv3328c Rv0445c Rv0735 Rv3911 Rv3366 Rv3455c Rv2793c Rv1644	sigF sigG sigH sigJ sigJ sigK sigL sigM spoU truA	ECF subfamily sigma subunit sigma-70 factors ECF subfamily ECF subfamily ECF subfamily sigma subunit ECF family sigma factor similar to SigI, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate synthase tRNA pseudouridine 55 synthase putative 23S rRNA methyltransferase	5. Esterase Rv0220 Rv1923 Rv3775 Rv3487c Rv0646c Rv1399c Rv1400c Rv1900c Rv2385 Rv2385 Rv2284	s and lipa lipC lipD lipE lipF lipG lipH lipJ lipJ lipJ lipJ lipJ lipJ	nine amidase ases probable esterase probable esterase probable hydrolase probable esterase probable lipase probable lipase probable esterase probable ase probable acetyl-hydrolase esterase probable esterase
Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv0003	polA priA radA recA recB recC recD recF	methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induction ATP-dependent DNA helicase	Rv1221 Rv3286c Rv0182c Rv3223c Rv1189 Rv3328c Rv0445c Rv0735 Rv3911 Rv3366 Rv3455c	sigF sigG sigH sigI sigJ sigK sigL sigM spoU truA truB	ECF subfamily sigma subunit sigma-70 factors ECF subfamily ECF subfamily sigma subunit ECF family sigma factor similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate synthase tRNA pseudouridine 55 synthase putative 23S rRNA methyltrans-	5. Esterase Rv0220 Rv1923 Rv3775 Rv3487c Rv1399c Rv1400c Rv1900c Rv2900c Rv2900c Rv1497	es and lipe lipC lipD lipE lipF lipH lipH lipJ lipK lipL lipM lipN lipN	nine amidase ases probable esterase probable hydrolase probable hydrolase probable hydrolase probable lipase probable lipase probable lipase probable acetyl-hydrolase esterase probable esterase probable esterase probable esterase probable esterase
Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv0003 Rv2973c Rv1696 Rv3715c Rv2736c	polA priA radA recA recB recC recD recF recG recN recR	methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induction ATP-dependent DNA helicase recombination and DNA repair RecBC-Independent process of DNA repair regulatory protein for RecA	Rv1221 Rv3286c Rv0182c Rv3223c Rv1189 Rv3328c Rv0445c Rv0735 Rv3911 Rv3366 Rv3455c Rv2793c Rv1644 Rv3649	sigF sigG sigH sigJ sigL sigL sigM spoU truA truB tsnR	ECF subfamily sigma subunit sigma-70 factors ECF subfamily ECF subfamily ECF subfamily ECF subfamily sigma subunit ECF family sigma factor similar to SigI, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate synthase tRNA pseudouridine 55 synthase putative 23S rRNA methyltransferase ATP-dependent DNA/RNA helicase	5. Esterase Rv0220 Rv1923 Rv3775 Rv3487c Rv1399c Rv1400c Rv1900c Rv2385 Rv1497 Rv2284 Rv2970c Rv1426c Rv1426463	as and lipa lipC lipD lipE lipF lipH lipH lipJ lipJ lipJ lipM lipM lipM lipM lipM	nine amidase ases probable esterase probable esterase probable hydrolase probable esterase probable esterase probable lipase probable lipase probable lipase probable esterase
Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv0003 Rv2973c Rv1696 Rv3715c	polA priA radA recA recB recC recF recF	methylated-DNA-protein-cysteine methylatead-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V oxodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V oxodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V oxodeoxyribonuclease V exodeoxyribonuclease V exodeoxyri	Rv1221 Rv3286c Rv0182c Rv3223c Rv1189 Rv3328c Rv0445c Rv0735 Rv3911 Rv3366 Rv3455c Rv2793c Rv1644 Rv3649	sigF sigH sigH sigJ sigV sigL sigM spoU truA truB tsnR	ECF subfamily sigma subunit sigma-70 factors ECF subfamily ECF subfamily ECF subfamily sigma subunit ECF family sigma factor similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate synthase tRNA pseudouridine 55 synthase putative 23S rRNA methyltransferase ATP-dependent DNA/RNA helicase cytoplasmic)	5. Esterase Rv0220 Rv1923 Rv3775 Rv3487c Rv1490c Rv1900c Rv2385 Rv1497 Rv2284 Rv2970c Rv1426c Rv2463 Rv2485c	- lipC lipD lipE lipF lipF lipG lipH lipJ lipJ lipJ lipL lipD lipD lipD lipD lipD lipD lipD lipD	nine amidase ases probable esterase probable esterase probable hydrolase probable sterase probable lipase probable lipase probable lipase probable esterase
Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv0003 Rv2973c Rv1696 Rv3715c Rv2736c Rv2593c	polA priA radA recA recB recC recD recF recR recR recR	methylated-DNA-protein-cysteine methyltansferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induction ATP-dependent DNA helicase recombination and DNA repair ResGC-Independent process of DNA repair regulatory protein for RecA Holliday junction binding protein, DNA helicase	Rv1221 Rv3286c Rv0182c Rv3223c Rv1189 Rv3328c Rv0445c Rv0735 Rv3911 Rv3366 Rv3455c Rv2793c Rv1644 Rv3649	sigF sigH sigH sigJ sigJ sigK sigL sigM spoU truA truB tsnR	ECF subfamily sigma subunit sigma-70 factors ECF subfamily ECF subfamily sigma subunit ECF family sigma factor similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate synthase tRNA pseudouridine 55 synthase putative 23S rRNA methyltransferase ATP-dependent DNA/RNA helicase cytoplasmic) 1,4-c-glucan branching enzyme	5. Esterase Rv0220 Rv1923 Rv3775 Rv3487c Rv1646c Rv1399c Rv1400c Rv1900c Rv2284 Rv2970c Rv1426c Rv2463 Rv2463 Rv2463 Rv2485c Rv3084	s and lips lipC lipC lipE lipF lipF lipH lipI lipJ lipK lipL lipM lipN lipN lipO lipO lipO lipO	nine amidase ases probable esterase probable esterase probable hydrolase probable hydrolase probable lipase probable lipase probable lipase probable acetyl-hydrolase esterase probable catoxivjesterase probable catoxivjesterase probable acetyl-hydrolase
Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv0003 Rv2973c Rv1696 Rv3715c Rv2736c	polA priA radA recA recB recC recD recF recG recN recR	methylated-DNA-protein-cysteine methylatead-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V oxodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V oxodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V oxodeoxyribonuclease V exodeoxyribonuclease V exodeoxyri	Rv1221 Rv3286c Rv0182c Rv3223c Rv1189 Rv3328c Rv0445c Rv0735 Rv3911 Rv3366 Rv3455c Rv2793c Rv1644 Rv3649	sigF sigG sigH sigJ sigV sigK sigL sigM spoU truA truB tsnR - charides (a glgB glgP	ECF subfamily sigma subunit sigma-70 factors ECF subfamily ECF subfamily sigma subunit ECF family sigma factor similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate synthase tRNA pseudouridine 55 synthase putative 23S rRNA methyltransferase ATP-dependent DNA/RNA helicase cytoplasmic) 1,4-a-glucan branching enzyme probable glycogen phosphorylase	5. Esterase Rv0220 Rv1923 Rv3775 Rv3487c Rv1900c Rv1990c Rv2385 Rv1497 Rv2284 Rv2970c Rv1426c Rv2463 Rv2485c Rv3084 Rv3176c Rv2045c	as and lips lipC lipE lipE lipF lipH lipI lipJ lipK lipL lipM lipN lipO lipP lipO lipP lipD lipD	nine amidase ases probable esterase probable esterase probable hydrolase probable hydrolase probable lipase probable lipase probable lipase probable esterase lipase probable esterase/lipase probable carboxylesterase
Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv0003 Rv2973c Rv1696 Rv3715c Rv2736c Rv2593c Rv2593c	polA priA radA recA recB recC recD recF recG recR recR recX ruvA	methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induction ATP-dependent DNA helicase recombination and DNA repair RecBC-Independent process of DNA repair regulatory protein for RecA Holliday junction binding protein, DNA helicase Holliday junction binding protein Holliday junction binding protein Holliday junction resolvase, endodeoxyribonuclease	Rv1221 Rv3286c Rv0182c Rv3223c Rv1189 Rv3328c Rv0445c Rv0735 Rv3911 Rv3366 Rv3455c Rv2793c Rv1644 Rv3649	sigF sigH sigH sigJ sigJ sigK sigL sigM spoU truA truB tsnR	ECF subfamily sigma subunit sigma-70 factors ECF subfamily ECF subfamily sigma subunit ECF family sigma factor similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate synthase tRNA pseudouridine 55 synthase tRNA pseudouridine 55 synthase putative 23S rRNA methyltransferase ATP-dependent DNA/RNA helicase cytoplasmic) 1,4-α-glucan branching enzyme probable glycogen phosphorylase probable glycogen debranching	5. Esterase Rv0220 Rv1923 Rv3775 Rv3487c Rv1646c Rv1399c Rv1400c Rv1900c Rv2284 Rv2970c Rv1426c Rv2463 Rv2463 Rv2463 Rv3176c Rv3176c Rv2045c Rv1076	s and lips lipC lipC lipE lipF lipF lipH lipI lipJ lipK lipL lipM lipN lipN lipO lipP lipO lipP lipD lipD lipD lipD lipD lipD lipD lipD	nine amidase ases probable esterase probable esterase probable hydrolase probable hydrolase probable lipase probable lipase probable lipase probable acetyl-hydrolase esterase probable carbox/lyesterase probable carbox/lyesterase probable esterase/lipase probable carbox/lyesterase probable carbox/lyesterase probable esterase/lipase probable carbox/lesterase probable esterase
Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv0003 Rv2973c Rv1696 Rv3715c Rv2736c Rv2593c Rv2592c Rv2594c Rv0054	polA priA radA recA recB recC recB recF recF recR recR recR recR recR recR	methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induction ATP-dependent DNA helicase recombination and DNA repair RecBC-Independent process of DNA repair regulatory protein for RecA Holliday junction binding protein, DNA helicase Holliday junction binding protein Holliday junction binding protein Holliday junction resolvase, endo-deoxyribonuclease single strand binding protein	Rv1221 Rv3286c Rv0182c Rv3223c Rv1189 Rv3328c Rv0445c Rv0735 Rv3911 Rv3366 Rv3455c Rv2793c Rv1644 Rv3649 8. Polysac Rv1326c Rv1326c Rv1326c	sigF sigG sigH sigJ sigJ sigK sigK sigL sigM spoU truA truB tsnR - charides (i	ECF subfamily sigma subunit sigma-70 factors ECF subfamily ECF subfamily ECF subfamily ECF subfamily sigma subunit ECF family sigma factor similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate synthase tRNA pseudouridylate synthase tRNA pseudouridine 55 synthase putative 23S rRNA methyltransferase ATP-dependent DNA/RNA helicase cytoplasmic) 1,4-α-glucan branching enzyme probable glycogen debranching enzyme probable glycogen debranching enzyme probable glycogen debranching enzyme	5. Esterase Rv0220 Rv1923 Rv3775 Rv3487c Rv1399c Rv1400c Rv2385 Rv1497 Rv2284 Rv2970c Rv1426c Rv2463 Rv2485c Rv3084 Rv3176c Rv2045c Rv1076 Rv2045c Rv1076 Rv3203	es and lipa lipC lipE lipE lipE lipH lipH lipJ lipK lipL lipN lipN lipN lipN lipO lipP lipO lipO lipO lipS lipT lipU	nine amidase ases probable esterase probable esterase probable hydrolase probable hydrolase probable lipase probable lipase probable lipase probable esterase probable carboxlyesterase probable carboxlyesterase probable carboxlyesterase probable carboxlyesterase probable carboxlyesterase probable carboxylesterase probable esterase probable lipase
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Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv1696 Rv3715c Rv2736c Rv2593c Rv2593c Rv2594c Rv0054 Rv1210 Rv3646c Rv2976c Rv1633 Rv1633 Rv1420 Rv0949	polA priA radA recA recB recC recC recCN recR recR recX ruvA ruvB ruvC ssb tagA topA ung uvrA uvrB uvrC uvrD	methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V ob NA replication and SOS induction are provided in the second of	Rv1221 Rv3286c Rv0182c Rv3223c Rv1189 Rv3328c Rv0445c Rv0735 Rv3911 Rv3366 Rv3455c Rv2793c Rv1644 Rv3649 8. Polysac Rv1326c Rv1328 Rv1564c Rv1563c Rv1563c Rv1781c Rv2471 B. Degrad 1. RNA	sigF sigG sigH sigJ sigJ sigK sigK sigK sigL sigM spoU truA truB tsnR - charides (i glgB glgP glgY glgZ - - -	ECF subfamily sigma subunit sigma-70 factors ECF subfamily ECF subfamily ECF subfamily ECF subfamily ECF subfamily sigma subunit ECF family sigma factor similar to SigI, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate synthase tRNA pseudouridylate synthase tRNA pseudouridine 55 synthase putative 23S rRNA methyltransferase ATP-dependent DNA/RNA helicase expropriation of the probable glycogen phosphorylase probable glycogen debranching enzyme probable glycogen debranching enzyme putative α-amylase maltooligosyltrehalose trehalohydrolase probable 4-α-glucanotransferase probable maltase α-glucosidase acromolecules	5. Esterase Rv0220 Rv1923 Rv3775 Rv3487c Rv1990 Rv1490 Rv1490 Rv2385 Rv1497 Rv2284 Rv2970c Rv1426c Rv2463 Rv2485c Rv3084 Rv3176c Rv2045c Rv1076 Rv3203 Rv0217c Rv2351c Rv2349c Rv1755c Rv1104 Rv1105	as and lipa lipC lipE lipE lipH lipH lipH lipJ lipK lipH lipN lipN lipN lipO lipP lipO lipP lipO lipC lipT lipU lipU lipU lipU lipU lipU lipU lipU	nine amidase ases probable esterase probable esterase probable hydrolase probable hydrolase probable lipase probable lipase probable lipase probable esterase probable carboxlyesterase probable carboxlyesterase probable carboxlyesterase probable esteraselipase probable esteraselipase probable esteraselipase probable esterase probable probable lipase probable esterase probable esterase probable esterase probable esterase phospholipase C precursor phospholipase C precursor partial CDS for phospholipase C probable esterase pseudogene probable esterase pseudogene
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		lase	Rv1367c	-	probable penicillin binding protein	Rv1030	kdpB	potassium-transporting ATPase B
Rv2715	-	2-hydroxymuconic semialdehyde		-	probable penicillin binding protein	D.:1001	lada C	chain
Rv3530c	_	hydrolase probable <i>cis</i> -diol dehydrogenase	Rv1922 Rv2864c	-	probable penicillin binding protein probable penicillin binding protein	Rv1031	kdpC	potassium-transporting ATPase C chain
Rv3534c	-	4-hydroxy-2-oxovalerate aldolase	Rv3330	-	probable penicillin binding protein	Rv3236c	kefB	probable glutathione-regulated
Rv3536c	-	aromatic hydrocarbon degrada-	Rv3627c	-	probable penicillin binding protein	Dv00770	morT	potassium-efflux protein
		tion	4. Conserv	ved memb	rane proteins	Rv2877c	merT	possible mercury resistance transport system
C. Cell en			Rv0402c	mmpL1	conserved large membrane	Rv1811	mgtC	probable magnesium transport
1. Lipopro	teins (<i>IppA</i>	I- <i>lpr0</i>) 65	Rv0507	mmpL2	protein conserved large membrane	Rv0362	mgtE	ATPase protein C putative magnesium ion
2. Surface	polysacch	narides, lipopolysaccharides, pro-	HV0307	IIIIIPLZ	protein	110002	myıL	transporter
teins and	antigens		Rv0206c	mmpL3	conserved large membrane	Rv2856	nicT	probable nickel transport protein
Rv0806c	cpsY	probable UDP-glucose-4- epimerase	Rv0450c	mmpL4	protein conserved large membrane	Rv0924c	nramp	transmembrane protein belonging to Nramp family
Rv3811	csp	secreted protein	11004300	ппр	protein	Rv2691	trkA	probable potassium uptake pro-
Rv1677	dsbF	highly similar to C-term Mpt53	Rv0676c	mmpL5	conserved large membrane	D 0000	5	tein
Rv3794	embA	involved in arabinogalactan syn- thesis	Rv1557	mmpL6	protein conserved large membrane	Rv2692	trkB	probable potassium uptake pro- tein
Rv3795	embB	involved in arabinogalactan syn-	1111007	mmpLo	protein	Rv2287	yjcE	probable Na+/H+ exchanger
D. 0700		thesis	Rv2942	mmpL7	conserved large membrane	Rv2723	-	probable membrane protein,
Rv3793	embC	involved in arabinogalactan syn- thesis	Rv3823c	mmpL8	protein conserved large membrane	Rv3162c	_	tellurium resistance probable membrane protein
Rv3875	esat6	early secretory antigen target		·	protein	Rv3237c	-	possible potassium channel
Rv0112	gca	probable GDP-mannose dehy- dratase	Rv2339	mmpL9	conserved large membrane protein	Rv3743c		protein
Rv0113	gmhA	phosphoheptose isomerase	Rv1183	mmpL10	conserved large membrane	11437430		probable cation-transporting ATPase
Rv2965c	kdtB	lipopolysaccharide core biosyn-			protein			
Rv2878c	mpt53	thesis protein secreted protein Mpt53	Rv0202c	mmpL11	conserved large membrane protein	Carbohy Rv2443	/drates, oi <i>dctA</i>	rganic acids and alcohols C4-dicarboxylate transport protein
Rv1980c	mpt64	secreted immunogenic protein	Rv1522c	mmpL12	conserved large membrane	Rv3476c	kgtP	sugar transport protein
D. 0075		Mpb64/Mpt64	D: 0400=	C1	protein	Rv1902c	nanT	probable sialic acid transporter
Rv2875	mpt70	major secreted immunogenic pro- tein Mpt70 precursor	Rv0403c	mmpS1	conserved small membrane protein	Rv1236	sugA	membrane protein probably involved in sugar transport
Rv2873	mpt83	surface lipoprotein Mpt83	Rv0506	mmpS2	conserved small membrane	Rv1237	sugB	sugar transport protein
Rv0899 Rv3810	ompA pirG	member of OmpA family cell surface protein precursor (Erp	Dv21000	mmpS3	protein conserved small membrane	Rv1238	sugC	ABC transporter component of sugar uptake system
NV3010	pira	protein)	Rv2198c	ППРЗЗ	protein	Rv3331	sugl	probable sugar transport protein
Rv3782	rfbE	similar to rhamnosyl transferase	Rv0451c	mmpS4	conserved small membrane	Rv2835c	ugpA	sn-glycerol-3-phosphate
Rv1302	rfe	undecaprenyl-phosphate α-N- acetylglucosaminyltransferase	Rv0677c	mmpS5	protein conserved small membrane	Rv2833c	ugpB	permease sn-glycerol-3-phosphate-binding
Rv2145c	wag31	antigen 84 (aka wag31)	1100770	mmpoo	protein	11120000	идры	periplasmic lipoprotein
Rv0431	-	tuberculin related peptide (AT103)	= O.I.			Rv2832c	ugpC	sn-glycerol-3-phosphate transport
Rv0954 Rv1514c	-	cell envelope antigen involved in polysaccharide syn-	5. Other m	nembrane	proteins 211	Rv2834c	ugpE	ATP-binding protein sn-glycerol-3-phosphate transport
		thesis	III. Cell pr	ocesses			31	system protein
Rv1518	-	involved in exopolysaccharide synthesis	A. Transpo	ort/binding	proteins	Rv2316 Rv2318	uspA uspC	sugar transport protein
Rv1758	-	partial cutinase	Rv2127	ansP	L-asparagine permease	Rv2317	uspE	sugar transport protein sugar transport protein
Rv1910c		probable secreted protein	Rv0346c	aroP2	probable aromatic amino acid	Rv1200	- '	probable sugar transporter
Rv1919c Rv1984c	-	weak similarity to pollen antigens probable secreted protein	Rv0917	betP	permease glycine betaine transport	Rv2038c Rv2039c	-	probable ABC sugar transporter probable sugar transporter
Rv1987	-	probable secreted protein	Rv1704c	cycA	transport of D-alanine, D-serine	Rv2040c	-	probable sugar transporter
Rv2223c Rv2224c	-	probable exported protease	Dygeee	dnn A	and glycine	Rv2041c	-	probable sugar transporter
Rv2301	-	probable exported protease probable cutinase	Rv3666c	dppA	probable peptide transport system permease	4. Anions		
Rv2345	-	precursor of probable membrane	Rv3665c	dppB	probable peptide transport system	Rv2684	arsA	probable arsenical pump
Rv2672	_	protein putative exported protease	Rv3664c	dppC	permease probable peptide transport system	Rv2685 Rv3578	arsB arsB2	probable arsenical pump probable arsenical pump
Rv3019c	-	similar to Esat6	11000040	ирро	permease	Rv2643	arsC	probable arsenical pump
Rv3036c	-	probable secreted protein	Rv3663c	dppD	probable ABC-transporter	Rv2397c	cysA	sulphate transport ATP-binding
Rv3449		probable precursor of serine pro- tease	Rv0522	gabP	probable 4-amino butyrate trans- porter	Rv2399c	cysT	protein sulphate transport system perme-
	- 1	probable cutinase	Rv0411c	glnH	putative glutamine binding protein			ase protein
Rv3452 Rv3724		probable cutinase precursor probable cutinase precursor	Rv2564	glnQ	probable ATP-binding transport	Rv2398c	cysW	sulphate transport system perme- ase protein
1100724		probable cultilase precursor	Rv1280c	oppA	probable oligopeptide transport	Rv1857	modA	molybdate binding protein
		and peptidoglycan	D.:1000-	D	protein	Rv1858	modB	transport system permease,
Rv2911 Rv2981c	dacB ddlA	penicillin binding protein D-alanine-D-alanine ligase A	Rv1283c Rv1282c	oppB oppC	oligopeptide transport protein oligopeptide transport system per-	Rv1859	modC	molybdate uptake molybdate uptake ABC-
Rv3809c	glf	UDP-galactopyranose mutase			mease			transporter
Rv1018c	glmU	UDP-N-acetylglucosamine pyrophosphorylase	Rv1281c Rv2320c	oppD rocE	probable peptide transport protein arginine/ornithine transporter	Rv1860	modD	precursor of Apa (45/47 kD secreted protein)
Rv3382c	lytB	LytB protein homologue	Rv3253c	-	probable cationic amino acid	Rv2329c	narK1	probable nitrite extrusion protein
Rv1110	lytB'	very similar to LytB	D 0454		transport	Rv1737c	narK2	nitrite extrusion protein
Rv1315	murA	UDP-N-acetylglucosamine-1-car- boxyvinyltransferase	Rv3454	-	possible proline permease	Rv0261c Rv0267	narK3 narU	nitrite extrusion protein1 similar to nitrite extrusion
Rv0482	murB	UDP-N-acetylenolpyruvoylglu-	2. Cations					protein 2
D. 0150a		cosamine reductase	Rv2920c	amt	putative ammonium transporter	Rv0934	phoS1	PstS component of phosphate
Rv2152c	murC	UDP-N-acetyl-muramate-alanine ligase	Rv1607 Rv1239c	chaA corA	putative calcium/proton antiporter probable magnesium and cobalt	Rv0928	phoS2	uptake PstS component of phosphate
Rv2155c	murD	UDP-N-acetylmuramoylalanine-D-	D		transport protein	D 0000		uptake
Rv2158c	murE	glutamate ligase meso-diaminopimelate-adding	Rv0092 Rv0103c	ctpA ctpB	cation-transporting ATPase cation transport ATPase	Rv0820	phoT	phosphate transport system ABC transporter
11021000	marz	enzyme	Rv3270	ctpC	cation transport ATPase	Rv3301c	phoY1	phosphate transport system
Rv2157c	murF	D-alanine:D-alanine-adding	Rv1469	ctpD	probable cadmium-transporting	D:-0004 -	nh-Va	regulator
Rv2153c	murG	enzyme transferase in peptidoglycan syn-	Rv0908	ctpE	ATPase probable cation transport ATPase	Rv0821c	phoY2	phosphate transport system regulator
		thesis	Rv1997	ctpF	probable cation transport ATPase	Rv0545c	pitA	low-affinity inorganic phosphate
Rv1338	murl	glutamate racemase	Rv1992c	ctpG ctpЫ	probable cation transport ATPase	Dynnn4		transporter
Rv2156c	murX	phospho-N-acetylmuramoyl- petapeptide transferase	Rv0425c	ctpH	C-terminal region putative cation- transporting ATPase	Rv2281 Rv0930	pitB pstA1	phosphate permease PstA component of phosphate
Rv3332	nagA	N-acetylglucosamine-6-P-	Rv0107c	ctpI	probable magnesium transport			uptake
Rv0016c	pbpA	deacetylase penicillin-binding protein	Rv0969	ctpV	ATPase cation transport ATPase	Rv0936	pstA2	PstA component of phosphate uptake
Rv2163c	pbpA pbpB	penicillin-binding protein 2	Rv3044	tecB	putative FeIII-dicitrate transporter	Rv0933	pstB	ABC transport component of
Rv0050	ponA	penicillin-bonding protein	Rv0265c	fecB2	iron transport protein FeIII dici-			phosphate uptake
Rv3682								
Ry0017c	ponA'	class A penicillin binding protein FtsW/RodA/SpovE family	trate Rv1029	kdpA	transporter potassium-transporting ATPase A	Rv0935	pstC	PstC component of phosphate uptake
Rv0017c Rv0907		class A penicillin binding protein FtsW/RodA/SpovE family probable penicillin binding protein	trate Rv1029	kdpA	transporter potassium-transporting ATPase A chain	Rv0929	pstC2	PstC component of phosphate uptake membrane-bound component of

Rv0932c	pstS	phosphate transport system PstS component of phosphate	Rv1821	secA2	unit SecA, preprotein translocase sub-	Rv3500c - Rv3501c -		part of mce4 oper part of mce4 oper	
11400020	ροιο	uptake	1111021	000/12	unit	Rv3896c		putative p60 home	
Rv2400c		sulphate binding precursor	Rv2587c	secD	protein-export membrane protein	Rv3922c	-	possible hemolysi	n
Rv0143c Rv1707	-	probable chloride channel probable sulphate permease	Rv0638 Rv2586c	secE secF	SecE preprotein translocase protein-export membrane protein	P IC alama	nto Bon	antad anguanan	and Phaga
Rv1739c	-	possible sulphate transporter	Rv1440	secG	protein-export membrane protein	1. IS elemen		eated sequences, a	and Friage
Rv3679	-	possible anion transporter			SecG	IS6110		16 copies	
Rv3680	-	probable anion transporter	Rv0732	secY	SecY subunit of preprotein translo- case	IS 1081 Others		6 copies 37 copies	
5. Fatty ac	id transpo	ort	Rv2462c	tig	chaperone protein, similar to	Others		or copies	
	ltp1	non-specific lipid transport protein			trigger factor	2. REP13E	12 family	7 copies	
Rv3540c	ltp2	non-specific lipid transport protein	Rv2813	-	probable general secretion path-	0 Dhana sa	المعما المعاما		
6. Efflux p	roteins				way protein	3. Phage-re Rv2894c		integrase/recomb	nase
Rv2936	drrA	similar daunorubicin resistance	E. Adapta	tions and	atypical conditions		xerD	integrase/recomb	
D: 0007	-tD	ABC-transporter	Rv1901	cinA	competence damage protein		-	integrase-a	
Rv2937	drrB	similar daunorubicin resistance transmembrane protein	Rv3648c	cspA	cold shock protein, transcriptional regulator	Rv1055 Rv1573		integrase-b phiRV1 phage rel	ated protein
Rv2938	drrC	similar daunorubicin resistance	Rv0871	cspB	probable cold shock protein	Rv1574		phiRV1 phage rel	
		transmembrane protein	Rv3063	cstA	starvation-induced stress	Rv1575	-	phiRV1 phage rel	
Rv2846c Rv3065	efpA emrE	putative efflux protein resistance to ethidium bromide	Rv3490	otsA	response protein probable α, α -trehalose-phosphate	Rv1576c - Rv1577c -		phiRV1 phage reliphiRV1 possible p	
Rv0783c	-	multidrug resistance protein	1100430	Olan	synthase	Rv1578c		phiRV1 phage rel	
Rv0849	-	possible quinolone efflux pump	Rv2006	otsB	trehalose-6-phosphate phos-	Rv1579c		phiRV1 phage rel	
Rv1145 Rv1146	-	probable drug transporter probable drug transporter	Rv3372	otsB2	phatase trehalose-6-phosphate phos-	Rv1580c - Rv1581c -		phiRV1 phage reli phiRV1 phage reli	
Rv1250	-	probable drug efflux protein	HV3372	UISDZ	phatase	Rv1582c		phiRV1 phage rel	
Rv1258c	-	probable multidrug resistance	Rv3758c	proV	osmoprotection ABC transporter	Rv1583c		phiRV1 phage rel	ated protein
Rv1410c	_	pump	Rv3757c Rv3759c	proW proX	transport system permease	Rv1584c Rv1585c		phiRV1 phage rel phiRV1 phage rel	
Rv1634	-	probable drug efflux protein probable drug efflux protein	Rv3756c	proZ	similar to osmoprotection proteins transport system permease	Rv1586c		phiRV1 integrase	ated protein
Rv1819c	-	probable multidrug resistance	Rv1026	-	probable pppGpp-5'phosphohydro-	Rv2309c		integrase	
D.:0100-		pump			lase	Rv2310		excisionase	
Rv2136c	-	putative bacitracin resistance pro- tein	F. Detoxific	ration		Rv2646 Rv2647		phiRV2 integrase phiRV2 phage rel	ated protein
Rv2209	-	probable drug efflux protein	Rv2428	ahpC	alkyl hydroperoxide reductase	Rv2650c	-	phiRV2 phage rel	
Rv2333c	-	probable tetracenomycin C resis-	Rv2429	ahpD	member of AhpC/TSA family	Rv2651c		phiRV2 prohead p	
Rv2994		tance protein probable fluoroquinolone efflux	Rv2238c Rv2521	ahpE bcp	member of AhpC/TSA family bacterioferritin comigratory protein	Rv2652c Rv2653c		phiRV2 phage rel phiRV2 phage rel	
111200-		protein	Rv1608c	bcpB	probable bacterioferritin comigra-	Rv2654c		phiRV2 phage rel	
Rv1877	-	probable drug efflux protein			tory protein	Rv2655c		phiRV2 phage rel	
Rv2459	-	probable drug efflux protein	Rv3473c	bpoA	probable non-heme bromoperoxidase	Rv2656c Rv2657c		phiRV2 phage rel similar to gp36 of	
B. Chaper	ones/Hea	t shock	Rv1123c	bpoB	probable non-heme bromoperoxi-	HV2037C		phage L5	mycobacterio-
Rv0384c	clpB	heat shock protein			dase	Rv2658c		phiRV2 phage rel	ated protein
Rv0352	dnaJ	acts with GrpE to stimulate DnaK ATPase	Rv0554	bpoC	probable non-heme bromoperoxi- dase	Rv2659c Rv2830c		phiRV2 integrase	1 nhd cono
Rv2373c	dnaJ2	DnaJ homologue	Rv3617	ephA	probable epoxide hydrolase	Rv3750c		similar to phage F excisionase	i priu gene
Rv0350	dnaK	70 kD heat shock protein, chromo-	Rv1938	ephB	probable epoxide hydrolase	Rv3751	-	putative integrase	
D. 0417-		some replication	Rv1124	ephC	probable epoxide hydrolase	C DE and I	DDC 40	:::	
Rv3417c Rv0440	groEL1 groEL2	60 kD chaperonin 1 60 kD chaperonin 2	Rv2214c Rv3670	ephD ephE	probable epoxide hydrolase probable epoxide hydrolase	C. PE and F 1. PE family		illes	
Rv3418c	groES	10 kD chaperone	Rv0134	ephF	probable epoxide hydrolase	PE subfamil		38 members	
Rv0351	grpE	stimulates DnaK ATPase activity	Rv3171c	hpx	probable non-heme haloperoxi-	PE_PGRS	subfamily	y 61 members	
Rv2374c	hrcA	heat-inducible transcription repressor	Rv1908c	katG	dase catalase-peroxidase	2. PPE fami	lv	68 members	
Rv0251c	hsp	possible heat shock protein	Rv3846	sodA	superoxide dismutase	2.11 = 10.111	·y	oo membere	
Rv0353	hspR	heat shock regulator	Rv0432	sodC	superoxide dismutase precursor -			tion and resistance	
Rv2031c	hspX	14kD antigen, heat shock protein Hsp20 family	Rv1932	tpx	(Cu-Zn) thiol peroxidase	Rv2068c Rv3290c	biaC lat	class A β-lactama lysine-ε aminotrar	
Rv2299c	htpG	heat shock protein Hsp90 family	Rv0634c	- -	putative glyoxylase II		pncA	pyrazinamide resi	
Rv0563	htpX	probable (transmembrane) heat	Rv2581c	-	putative glyoxylase II	Rv0133	-	possible puromyc	in N-acetyltrans-
Rv2701c	suhB	shock protein putative extragenic suppressor	Rv3177	-	probable non-heme haloperoxidase	Rv0262c		ferase aminoglycoside 2	N acotyltrans
HVZ/UTC	SuliD	protein			uase	HVOZOZC		ferase	-iv-acetyllians-
Rv3269	-	probable heat shock protein	IV. Other			Rv0802c	-	acetyltransferase	
C. Cell div	vicion		A. Viruleno Rv0169		cell invasion protein	Rv1082 Rv1170	-	similar to S. lincol similar to S. lincol	
Rv3641c		possible cell division protein	Rv0589	mce1 mce2	cell invasion protein	Rv1347c	-	possible aminogly	
Rv3102c	ftsE	membrane protein	Rv1966	mce3	cell invasion protein			acetyltransferase	
Rv3610c	ftsH	inner membrane protein,	Rv3499c	mce4	cell invasion protein	Rv2036	-	similar to lincomy	cin production
Rv2748c	ftsK	chaperone chromosome partitioning	Rv3100c Rv1694	smpB tlyA	probable small protein b cytotoxin/hemolysin homologue	Rv2303c	_	genes similar to S. grise	us macrotetrolide
Rv2151c	ftsQ	ingrowth of wall at septum	Rv0024	-	putative p60 homologue			resistance protein	
Rv2154c	ftsW							probable aminogly	coside 3'-phos-
	ILSVV	membrane protein (shape determi-	Rv0167		part of mce1 operon	Rv3225c		nhotraneforesee	
Rv3101c		nation)	Rv0168	-	part of mce1 operon			photransferases probable acetyltra	nsferase
Rv3101c Rv2921c	ftsX ftsY	nation) membrane protein cell division protein FtsY						photransferases probable acetyltra probable aminogly	
Rv2921c Rv2150c	ftsX ftsY ftsZ	nation) membrane protein cell division protein FtsY circumferential ring, GTPase	Rv0168 Rv0170 Rv0171 Rv0172	-	part of <i>mce1</i> operon part of <i>mce1</i> operon part of <i>mce1</i> operon part of <i>mce1</i> operon	Rv3700c		probable acetyltra	
Rv2921c Rv2150c Rv3919c	ftsX ftsY ftsZ gid	nation) membrane protein cell division protein FtsY circumferential ring, GTPase glucose inhibited division protein B	Rv0168 Rv0170 Rv0171 Rv0172 Rv0174	-	part of mce1 operon part of mce1 operon part of mce1 operon part of mce1 operon part of mce1 operon part of mce1 operon	Rv3700c Rv3817	- -	probable acetyltra probable aminogly photransferase	ycoside 3'-phos-
Rv2921c Rv2150c	ftsX ftsY ftsZ	nation) membrane protein cell division protein FtsY circumferential ring, GTPase	Rv0168 Rv0170 Rv0171 Rv0172	-	part of <i>mce1</i> operon part of <i>mce1</i> operon part of <i>mce1</i> operon part of <i>mce1</i> operon	Rv3700c	- -	probable acetyltra probable aminogly photransferase	
Rv2921c Rv2150c Rv3919c Rv3625c Rv3917c	ftsX ftsY ftsZ gid mesJ parA	nation) membrane protein cell division protein FtsY circumferential ring, GTPase glucose inhibited division protein B probable cell cycle protein chromosome partitioning; DNA - binding	Rv0168 Rv0170 Rv0171 Rv0172 Rv0174 Rv0587 Rv0588 Rv0590	-	part of mce1 operon part of mce1 operon part of mce1 operon part of mce1 operon part of mce1 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon	Rv3700c Rv3817	: - cin-like p	probable acetyltra probable aminogly photransferase proteins	ycoside 3'-phos-
Rv2921c Rv2150c Rv3919c Rv3625c	ftsX ftsY ftsZ gid mesJ	nation) membrane protein cell division protein FtsY circumferential ring, GTPase glucose inhibited division protein B probable cell cycle protein chromosome partitioning; DNA - binding possibly involved in chromosome	Rv0168 Rv0170 Rv0171 Rv0172 Rv0174 Rv0587 Rv0588 Rv0590 Rv0591	- - - -	part of mce1 operon part of mce1 operon part of mce1 operon part of mce1 operon part of mce1 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon	Rv3700c Rv3817 E. Bacterioc F. Cytochron	- cin-like p me P450	probable acetyltra probable aminogl photransferase proteins d enzymes	ycoside 3'-phos-
Rv2921c Rv2150c Rv3919c Rv3625c Rv3917c	ftsX ftsY ftsZ gid mesJ parA	nation) membrane protein cell division protein FtsY circumferential ring, GTPase glucose inhibited division protein B probable cell cycle protein chromosome partitioning; DNA - binding	Rv0168 Rv0170 Rv0171 Rv0172 Rv0174 Rv0587 Rv0588 Rv0590	- - - - - -	part of mce1 operon part of mce1 operon part of mce1 operon part of mce1 operon part of mce1 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon	Rv3700c Rv3817	in-like p ne P450	probable acetyltra probable aminogl photransferase proteins d enzymes	ycoside 3'-phos-
Rv2921c Rv2150c Rv3919c Rv3625c Rv3917c Rv3918c Rv2922c	ftsX ftsY ftsZ gid mesJ parA parB	nation) membrane protein cell division protein FtsY circumferential ring, GTPase glucose inhibited division protein B probable cell cycle protein chromosome partitioning; DNA - binding possibly involved in chromosome partitioning member of Smc1/Cut3/Cut14 family	Rv0168 Rv0170 Rv0171 Rv0172 Rv0174 Rv0587 Rv0588 Rv0590 Rv0591 Rv0592 Rv0594 Rv1085c	- - - - - - - -	part of mce1 operon part of mce1 operon part of mce1 operon part of mce1 operon part of mce1 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon possible hemolysin	Rv3700c Rv3817 E. Bacterioo F. Cytochroi G. Coenzyn enzymes	in-like p me P450 ne F420-	probable acetyltra probable aminogli photransferase roteins 0 enzymes -dependent	ycoside 3'-phos- 3 22 3
Rv2921c Rv2150c Rv3919c Rv3625c Rv3917c Rv3918c Rv2922c Rv0012	ftsX ftsY ftsZ gid mesJ parA parB smc	nation) membrane protein cell division protein FtsY circumferential ring, GTPase glucose inhibited division protein B probable cell cycle protein chromosome partitioning; DNA - binding possibly involved in chromosome partitioning member of Smc1/Cut3/Cut14 family possible cell division protein	Rv0168 Rv0170 Rv0171 Rv0172 Rv0174 Rv0587 Rv0588 Rv0590 Rv0591 Rv0592 Rv0594	- - - - - - - - -	part of mce1 operon part of mce1 operon part of mce1 operon part of mce1 operon part of mce1 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon possible hemolysin putative exported p60 protein	Rv3700c Rv3817 E. Bacterioc F. Cytochroi G. Coenzyn	in-like p me P450 ne F420-	probable acetyltra probable aminogli photransferase roteins 0 enzymes -dependent	ycoside 3'-phos- 3 22
Rv2921c Rv2150c Rv3919c Rv3625c Rv3917c Rv3918c Rv2922c	ftsX ftsY ftsZ gid mesJ parA parB	nation) membrane protein cell division protein FtsY circumferential ring, GTPase glucose inhibited division protein B probable cell cycle protein chromosome partitioning; DNA - binding possibly involved in chromosome partitioning member of Smc1/Cut3/Cut14 family	Rv0168 Rv0170 Rv0171 Rv0172 Rv0174 Rv0587 Rv0588 Rv0590 Rv0591 Rv0592 Rv0594 Rv1085c	- - - - - - - - -	part of mce1 operon part of mce1 operon part of mce1 operon part of mce1 operon part of mce1 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon possible hemolysin	Rv3700c Rv3817 E. Bacterioc F. Cytochroi G. Coenzym enzymes H. Miscellar	in-like p me P450 ne F420-	probable acetyltra probable aminogli photransferase roteins 0 enzymes -dependent	ycoside 3'-phos- 3 22 3
Rv2921c Rv2150c Rv3919c Rv3625c Rv3917c Rv3918c Rv2922c Rv0012 Rv0435c Rv2115c	ftsX ftsY ftsZ gid mesJ parA parB smc	nation) membrane protein cell division protein FtsY circumferential ring, GTPase glucose inhibited division protein B probable cell cycle protein chromosome partitioning; DNA - binding possibly involved in chromosome partitioning member of Smc1/Cut3/Cut14 family possible cell division protein ATPase of AAA-family ATPase of AAA-family possible role in chromosome seg-	Rv0168 Rv0170 Rv0171 Rv0172 Rv0174 Rv0587 Rv0588 Rv0590 Rv0591 Rv0592 Rv0594 Rv1085c Rv1477		part of mce1 operon part of mce1 operon part of mce1 operon part of mce1 operon part of mce1 operon part of mce1 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon part of mce2 operon possible hemolysin putative exported p60 protein homologue putative exported p60 protein homologue	Rv3700c Rv3817 E. Bacterioc F. Cytochroi G. Coenzym enzymes H. Miscellar	in-like p me P450 ne F420- neous tra	probable acetyltra probable aminogli photransferase proteins perzymes dependent ansferases	ycoside 3'-phos- 3 22 3
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