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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	vcobacterium tuberculosis	protein-coding genes

I. Small-n	nolecule n	netabolism			superfamily	Rv3543c	fadE29	acyl-CoA dehydrogenase
A. Degrad 1. Carbon		de	Rv2831	echA16	enoyl-CoA hydratase/isomerase superfamily	Rv3560c Rv3562	fadE30 fadE31	acyl-CoA dehydrogenase acyl-CoA dehydrogenase
Rv0186	bglS	us β-glucosidase	Rv3039c	echA17		Rv3563	fadE32	acyl-CoA denydrogenase acyl-CoA dehydrogenase
Rv2202c	cbhK	carbohydrate kinase	D 0070		superfamily	Rv3564	fadE33	acyl-CoA dehydrogenase
Rv0727c Rv1731	fucA gabD1	L-fuculose phosphate aldolase succinate-semialdehyde dehydro-	Rv3373	echA18	enoyl-CoA hydratase/isomerase superfamily, N-term	Rv3573c Rv3797	fadE34 fadE35	acyl-CoA dehydrogenase acyl-CoA dehydrogenase
	•	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	1100010	echa is	superfamily	Rv1143	mer	α-methyl acyl-CoA racemase
Rv0536	galE2	UDP-glucose 4-epimerase	Rv3550	echA20		Rv1492	mutA	methylmalonyl-CoA mutase, β
Rv0620 Rv0619	galK galT	galactokinase galactose-1-phosphate uridylyl-	Rv3774	echA21	superfamily enoyl-CoA hydratase/isomerase	Rv1493	mutB	subunit methylmalonyl-CoA mutase, α
	-	transferase C-term			superfamily			subunit
Rv0618	galTʻ	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-
Rv3696c	er land	transferase	Rv1074c	fadA3	acetyl-CoA C-acetyltransferase	Dud 100		unit
HV30900	glpK	ATP:glycerol 3-phosphotrans- ferase	Rv1323	fadA4	acetyl-CoA C-acetyltransferase (aka thiL)	Rv1136 Rv1683	-	probable carnitine racemase possible acyl-CoA synthase
Rv3255c	manA	mannose-6-phosphate isomerase	Rv3546	fadA5	acetyl-CoA C-acetyltransferase	4. Di		
Rv3441c	mrsA	phosphoglucomutase or phospho- mannomutase	Rv3556c Rv0860	fadA6 fadB	acetyl-CoA C-acetyltransferase β oxidation complex, α subunit	4. Phospr Rv2368c	norous con phoH	npounas ATP-binding <i>pho</i> regulon
Rv0118c	oxcA	oxalyl-CoA decarboxylase			(multiple activities)			component
Rv3068c Rv3257c	pgmA pmmA	phosphoglucomutase phosphomannomutase	Rv0468	fadB2	3-hydroxyacyl-CoA dehydroge- nase	Rv1095 Rv3628	phoH2 ppa	PhoH-like protein probable inorganic pyrophos-
Rv3308	pmmB	phosphomannomutase	Rv1715	fadB3	3-hydroxyacyl-CoA dehydroge-	110020	ρρα	phatase
Rv2702	ppgK	polyphosphate glucokinase	Rv3141	fadB4	nase	Rv2984	ppk	polyphosphate kinase
Rv0408 Rv0729	pta xylB	phosphate acetyltransferase xylulose kinase	NV3141	laub4	3-hydroxyacyl-CoA dehydroge- nase	B. Energy	metabolis	em
Rv1096	-	carbohydrate degrading enzyme	Rv1912c	fadB5	3-hydroxyacyl-CoA dehydroge-	1. Glycoly	rsis	
2. Amino a	ecids and :	amines	Rv1750c	fadD1	nase acyl-CoA synthase	Rv1023 Rv0363c	eno fba	enolase fructose bisphosphate aldolase
Rv1905c	aao	D-amino acid oxidase	Rv0270	fadD2	acyl-CoA synthase	Rv1436	gap	glyceraldehyde 3-phosphate dehy-
Rv2531c Rv2780	adi ald	ornithine/arginine decarboxylase L-alanine dehydrogenase	Rv3561	fadD3 fadD4	acyl-CoA synthase acyl-CoA synthase	Rv0489	~~~	drogenase
Rv1538c	anu ansA	L-asparaginase	Rv0214 Rv0166	fadD4	acyl-CoA synthase	Rv3010c	gpm pfkA	phosphoglycerate mutase I phosphofructokinase I
Rv1001	arcA	arginine deiminase	Rv1206	fadD6	acyl-CoA synthase	Rv2029c	pfkB	phosphofructokinase II
Rv0753c	mmsA	methylmalmonate semialdehyde dehydrogenase	Rv0119 Rv0551c	fadD7 fadD8	acyl-CoA synthase acyl-CoA synthase	Rv0946c Rv1437	pgi pgk	glucose-6-phosphate isomerase phosphoglycerate kinase
Rv0751c	mmsB	methylmalmonate semialdehyde	Rv2590	fadD9	acyl-CoA synthase	Rv1617	pykA	pyruvate kinase
Rv1187	rocA	oxidoreductase pyrroline-5-carboxylate dehydro-	Rv0099 Rv1550	fadD10 fadD11	acyl-CoA synthase acyl-CoA synthase, N-term	Rv1438 Rv2419c	tpi -	triosephosphate isomerase
TV 1 107	IOCA	genase	Rv1549	fadD11	acyl-CoA synthase, N-term	Rv3837c	-	putative phosphoglycerate mutase putative phosphoglycerate mutase
Rv2322c	rocD1	ornithine aminotransferase	Rv1427c	fadD12	acyl-CoA synthase	0 D	ka alahasalaa	
Rv2321c Rv1848	rocD2 ureA	ornithine aminotransferase urease γ subunit	Rv3089 Rv1058	fadD13 fadD14	acyl-CoA synthase acyl-CoA synthase	Rv2241	te dehydro <i>aceE</i>	genase pyruvate dehydrogenase E1 com-
Rv1849	ureB	urease β subunit	Rv2187	fadD15	acyl-CoA synthase			ponent
Rv1850 Rv1853	ureC ureD	urease α subunit urease accessory protein	Rv0852 Rv3506	fadD16 fadD17	acyl-CoA synthase acyl-CoA synthase	Rv3303c Rv2497c	lpdA pdhA	dihydrolipoamide dehydrogenase pyruvate dehydrogenase E1 com-
Rv1851	ureF	urease accessory protein	Rv3513c	fadD18	acyl-CoA synthase	11024370	puna	ponent α subunit
Rv1852	ureG	urease accessory protein	Rv3515c	fadD19	acyl-CoA synthase	Rv2496c	pdhB	pyruvate dehydrogenase E1 com-
Rv2913c	-	probable D-amino acid aminohydrolase	Rv1185c Rv2948c	fadD21 fadD22	acyl-CoA synthase acyl-CoA synthase	Rv2495c	pdhC	ponent β subunit 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 ac			Rv2930	fadD26	acyl-CoA synthase	3. TCA cy		
Rv2501c	accA1	acetyl/propionyl-CoA carboxylase, α subunit	Rv0275c Rv2941	fadD27 fadD28	acyl-CoA synthase acyl-CoA synthase	Rv1475c Rv0889c	acn citA	aconitate hydratase citrate synthase 2
Rv0973c	accA2	acetyl/propionyl-CoA carboxylase,	Rv2950c	fadD29	acyl-CoA synthase	Rv2498c	citE	citrate lyase β chain
Duggoon		α subunit acetyl/propionyl-CoA carboxylase,	Rv0404	fadD30	acyl-CoA synthase	Rv1098c	fum	fumarase
Rv2502c	accD1	β subunit	Rv1925 Rv3801c	fadD31 fadD32	acyl-CoA synthase acyl-CoA synthase	Rv1131 Rv0896	gltA1 gltA2	citrate synthase 3 citrate synthase 1
Rv0974c	accD2	acetyl/propionyl-CoA carboxylase,	Rv1345	fadD33	acyl-CoA synthase	Rv3339c	icd1	isocitrate dehydrogenase
Rv3667	acs	β subunit acetyl-CoA synthase	Rv0035 Rv2505c	fadD34 fadD35	acyl-CoA synthase acyl-CoA synthase	Rv0066c Rv0794c	icd2 lpdB	isocitrate dehydrogenase dihydrolipoamide dehydrogenase
Rv3409c	choD	cholesterol oxidase	Rv1193	fadD36	acyl-CoA synthase	Rv1240	mdh	malate dehydrogenase
Rv0222	echA1	enoyl-CoA hydratase/isomerase superfamily	Rv0131c Rv0154c	fadE1 fadE2	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv2967c Rv3318	pca sdhA	pyruvate carboxylase succinate dehydrogenase A
Rv0456c	echA2	enoyl-CoA hydratase/isomerase	Rv0215c	fadE3	acyl-CoA dehydrogenase	Rv3319	sdhB	succinate dehydrogenase B
Rv0632c	aah 42	superfamily	Rv0231	fadE4 fadE5	acyl-CoA dehydrogenase	Rv3316	sdhC	succinate dehydrogenase C sub-
HV06320	echA3	enoyl-CoA hydratase/isomerase superfamily	Rv0244c Rv0271c	fadE6	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv3317	sdhD	unit succinate dehydrogenase D sub-
Rv0673	echA4	enoyl-CoA hydratase/isomerase	Rv0400c	fadE7	acyl-CoA dehydrogenase			unit
Rv0675	echA5	superfamily enoyl-CoA hydratase/isomerase	Rv0672	fadE8	acyl-CoA dehydrogenase (aka <i>aidB</i>)	Rv1248c Rv2215	sucA sucB	2-oxoglutarate dehydrogenase dihydrolipoamide succinyltrans-
		superfamily	Rv0752c	fadE9	acyl-CoA dehydrogenase			ferase
Rv0905	echA6	enoyl-CoA hydratase/isomerase superfamily (aka eccH)	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	1100002	3400	succinyi-ooA synthase a chain
D. 4070-		superfamily	Rv1346 Rv1467c	fadE14	acyl-CoA dehydrogenase		ate bypass	
Rv1070c	echA8	enoyl-CoA hydratase/isomerase superfamily	Rv1679	fadE15 fadE16	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv0467 Rv1915	aceA aceAa	isocitrate lyase isocitrate lyase, α module
Rv1071c	echA9	enoyl-CoA hydratase/isomerase	Rv1934c	fadE17	acyl-CoA dehydrogenase	Rv1916	aceAb	isocitrate lyase, β module
Rv1142c	echA10	superfamily enoyl-CoA hydratase/isomerase	Rv1933c Rv2500c	fadE18 fadE19	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv1837c Rv3323c	glcB gphA	malate synthase phosphoglycolate phosphatase
		superfamily			(aka mmgC)			
Rv1141c	echA11	enoyl-CoA hydratase/isomerase	Rv2724c	fadE20	acyl-CoA dehydrogenase			te pathway
Rv1472	echA12	superfamily enoyl-CoA hydratase/isomerase	Rv2789c Rv3061c	fadE21 fadE22	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv1445c	devB	glucose-6-phosphate 1-dehydro- genase
		superfamily	Rv3140	fadE23	acyl-CoA dehydrogenase	Rv1844c	gnd	6-phosphogluconate dehydroge-
Rv1935c	echA13	enoyl-CoA hydratase/isomerase superfamily	Rv3139 Rv3274c	fadE24 fadE25	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv1122	gnd2	nase (Gram –) 6-phosphogluconate dehydroge-
Rv2486	echA14	enoyl-CoA hydratase/isomerase	Rv3504	fadE26	acyl-CoA dehydrogenase		-	nase (Gram +)
Rv2679	ech415	superfamily enoyl-CoA hydratase/isomerase	Rv3505 Rv3544c	fadE27 fadE28	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv1446c	opcA	unknown function, may aid G6PDH
0/0	55.,7170		55440					

Rv2436	rbsK	ribokinase	Rv3250c	rubB	rubredoxin B	Rv1878	glnA3	probable glutamine synthase
Rv1408 Rv2465c	rpe rpi	ribulose-phosphate 3-epimerase phosphopentose isomerase			idoreductases and oxygenases 171	Rv2860c Rv2918c	glnA4 glnD	proable glutamine synthase proable glutamine synthase uridylyltransferase
Rv1448c	tal	transaldolase	7. 1011000110	ancodo ox	adoredudiades and oxygenases 171	Rv2221c	gInE	glutamate-ammonia-ligase
Rv1449c		transketolase	8. ATP-pro	oton motiv	e force		J	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
		genase	Rv1310	atpD	ATP synthase β chain	Dv07044	ara la A	glutamate synthase
6. Respira	ation		Rv1305 Rv1306	atpE atpF	ATP synthase c chain ATP synthase b chain	Rv3704c	gshA	possible γ-glutamylcysteine syn- thase
a. aerobio			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 <i>c</i> -type biogenesis			iary metabolism	O. Associates	ta famili	
Rv1451	ctaB	protein cytochrome <i>c</i> oxidase assembly	1. Genera Rv2589	ı gabT	4-aminobutyrate aminotransferase	2. Asparta Rv3708c	te ramily asd	aspartate semialdehyde dehydro-
1111101	Olab	factor	Rv3432c	gadB	glutamate decarboxylase	11107000	404	genase
Rv2200c	ctaC	cytochrome c oxidase chain II	Rv1832	gcvB	glycine decarboxylase	Rv3709c	ask	aspartokinase
Rv3043c	ctaD	cytochrome c oxidase poly-	Rv1826	gcvH	glycine cleavage system H protein	Rv2201	asnB	asparagine synthase B
D 0400	. –	peptide I	Rv2211c	gcvT	T protein of glycine cleavage	Rv3565	aspB	aspartate aminotransferase
Rv2193	ctaE	cytochrome <i>c</i> oxidase poly- peptide III	Rv1213	glgC	system glucose-1-phosphate adenylyl-	Rv0337c Rv2753c	aspC dapA	aspartate aminotransferase dihydrodipicolinate synthase
Rv1542c	glbN	hemoglobin-like, oxygen carrier	1101213	gigo	transferase	Rv2773c	dapA	dihydrodipicolinate synthase
Rv2470	glbO	hemoglobin-like, oxygen carrier	Rv3842c	glpQ1	glycerophosphoryl diester phos-	Rv1202	dapE	succinyl-diaminopimelate desuc-
Rv2249c	glpD1	glycerol-3-phosphate dehydroge-			phodiesterase			cinylase
Duccocc	(00	nase	Rv0317c	glpQ2	glycerophosphoryl diester phos-	Rv2141c	dapE2	ArgE/DapE/Acy1/Cpg2/yscS
Rv3302c	glpD2	glycerol-3-phosphate dehydroge- nase	Rv3566c	nhoA	phodiesterase N-hydroxyarylamine o-acetyltrans-	Rv2726c	dapF	family diaminopimelate epimerase
Rv0694	IIdD1	L-lactate dehydrogenase	11400000	IIIOA	ferase	Rv1293	lvsA	diaminopimelate epimerase diaminopimelate decarboxylase
		(cytochrome)	Rv0155	pntAA	pyridine transhydrogenase sub-	Rv3341	metA	homoserine o-acetyltransferase
Rv1872c	IldD2	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 Rv3146	nuoA nuoB	NADH dehydrogenase chain A NADH dehydrogenase chain B	Rv0157	pntB	unit α2 pyridine transhydrogenase	Rv1133c	metE	5-methyltetrahydropteroyltrigluta- mate-homocysteine methyltrans-
Rv3147	nuoC	NADH denydrogenase chain C	1100137	pmb	subunit β			ferase
Rv3148	nuoD	NADH dehydrogenase chain D	Rv1127c	ppdK	similar to pyruvate, phosphate	Rv2124c	metH	5-methyltetrahydrofolate-homo-
Rv3149	nuoE	NADH dehydrogenase chain E			dikinase			cysteine methyltransferase
Rv3150	nuoF	NADH dehydrogenase chain F	0.01			Rv1392	metK	S-adenosylmethionine synthase
Rv3151 Rv3152	nuoG nuoH	NADH dehydrogenase chain G NADH dehydrogenase chain H	2. Glucone Rv0211	pckA	phosphoenolpyruvate carboxy-	Rv0391	metZ	o-succinylhomoserine sulfhy- drylase
Rv3153	nuol	NADH denydrogenase chain I	1100211	poron	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 nuoM	NADH dehydrogenase chain L	3. Sugar r	nucleotides <i>epiA</i>		2 Carina 4		
Rv3157 Rv3158	nuoN	NADH dehydrogenase chain M NADH dehydrogenase chain N	Rv1512 Rv3784	epiA epiB	nucleotide sugar epimerase probable UDP-galactose 4-	3. Serine f Rv0815c	cvsA2	thiosulfate sulfurtransferase
Rv2195	qcrA	Rieske iron-sulphur component of		90.2	epimerase	Rv3117	cysA3	thiosulfate sulfurtransferase
	•	ubiQ-cytB reductase	Rv1511	gmdA	GDP-mannose 4,6 dehydratase	Rv2335	cysE	serine acetyltransferase
Rv2196	qcrB	cytochrome β component of ubiQ-	Rv0334	rmlA	glucose-1-phosphate thymidyl-	Rv0511	cysG	uroporphyrin-III o-methyltrans-
Rv2194	qcrC	cytB reductase cytochrome b/c component of	Rv3264c	rmlA2	transferase glucose-1-phosphate thymidyl-	Rv2847c	cysG2	ferase multifunctional enzyme, siroheme
NV2194	yorc	ubiQ-cytB reductase	HV32640	IIIIMZ	transferase	NV20470	cysuz	synthase
			Rv3464	rmlB	dTDP-glucose 4,6-dehydratase	Rv2334	cysK	cysteine synthase A
b. anaero			Rv3634c	rmlB2	dTDP-glucose 4,6-dehydratase	Rv1336	cysM	cysteine synthase B
Rv2392	cysH	3'-phosphoadenylylsulfate (PAPS)	Rv3468c	rmlB3	dTDP-glucose 4,6-dehydratase	Rv1077	cysM2	cystathionine β-synthase
Rv2899c	fdhD	reductase affects formate dehydrogenase-N	Rv3465	rmlC	dTDP-4-dehydrorhamnose 3,5-epimerase	Rv0848 Rv1093	cysM3 glyA	putative cysteine synthase serine hydroxymethyltransferase
Rv29900c	fdhF	molybdopterin-containing oxidore-	Rv3266c	rmlD	dTDP-4-dehydrorhamnose	Rv0070c	glyA2	serine hydroxymethyltransferase
		ductase			reductase	Rv2996c	serA	D-3-phosphoglycerate dehydro-
Rv1552	frdA	fumarate reductase flavoprotein	Rv0322	udgA	UDP-glucose			genase
Distre	6-40	subunit			dehydrogenase/GDP-mannose 6-	Rv0505c	serB	probable phosphoserine phos-
Rv1553	frdB	fumarate reductase iron sulphur protein	Rv3265c	wbbL	dehydrogenase dTDP-rhamnosyl transferase	Rv3042c	serB2	phatase C-term similar to phosphoserine
Rv1554	frdC	fumarate reductase 15kD anchor	Rv1525	wbbL2	dTDP-rhamnosyl transferase	11030420	30102	phosphatase
		protein	Rv3400	-	probable β-phosphoglucomutase	Rv0884c	serC	phosphoserine aminotransferase
Rv1555	frdD	fumarate reductase 13kD anchor						
Duddod		protein	4. Amino s		alugas amina funat 0	4. Aromati		
Rv1161 Rv1162	narG narH	nitrate reductase α subunit nitrate reductase β chain	Rv3436c	yirio	glucosamine-fructose-6- phosphate aminotransferase	Rv3227	aroA	3-phosphoshikimate 1-carboxyvinyl transferase
Rv1164	nari	nitrate reductase γ chain			pspilate armitettarioletase	Rv2538c	aroB	3-dehydroquinate synthase
Rv1163	narJ	nitrate reductase δ chain	Sulphur			Rv2537c	aroD	3-dehydroquinate dehydratase
Rv1736c	narX	fused nitrate reductase	Rv0711	atsA	arylsulfatase	Rv2552c	aroE	shikimate 5-dehydrogenase
Rv2391	nirA	probable nitrite reductase/sulphite reductase	Rv3299c Rv0663	atsB atsD	proable arylsulfatase proable arylsulfatase	Rv2540c Rv2178c	aroF aroG	chorismate synthase DAHP synthase
Rv0252	nirB	nitrite reductase flavoprotein	Rv3077	atsD atsF	proable arylsulfatase	Rv2539c	aroG aroK	shikimate kinase I
Rv0253	nirD	probable nitrite reductase small	Rv0296c	atsG	proable arylsulfatase	Rv3838c	pheA	prephenate dehydratase
		subunit	Rv3796	atsH	proable arylsulfatase	Rv1613	trpA	tryptophan synthase α chain
. =-			Rv1285	cysD	ATP:sulphurylase subunit 2	Rv1612	trpB	tryptophan synthase β chain
c. Electroi Rv0409	n transport ackA		Rv1286 Rv2131c	cysN cysQ	ATP:sulphurylase subunit 1	Rv1611	trpC	indole-3-glycerol phosphate synthase
Rv1623c	аска аррС	acetate kinase cytochrome <i>bd-ll</i> oxidase	Rv3248c	cys∪ sahH	homologue of <i>M.leprae cysQ</i> adenosylhomocysteinase	Rv2192c	trpD	anthranilate phosphoribosyltrans-
		subunit I	Rv3283	sseA	thiosulfate sulfurtransferase			ferase
Rv1622c	cydB	cytochrome d ubiquinol oxidase	Rv2291	sseB	thiosulfate sulfurtransferase	Rv1609	trpE	anthranilate synthase
D.:4000	a(C	subunit II	Rv3118	sseC	thiosulfate sulfurtransferase	D:-0000	ten = C	component I
Rv1620c Rv1621c		ABC transporter ABC transporter	Rv0814c Rv3762c	sseC2 -	thiosulfate sulfurtransferase probable alkyl sulfatase	Rv2386c	trpE2	anthranilate synthase component I
Rv2007c		ferredoxin	1100/020	-	probable ainyr sullatase	Rv3754	tyrA	prephenate dehydrogenase
Rv3554	fdxB	ferredoxin	D. Amino	acid biosy	nthesis		.,	,
Rv1177	fdxC	ferredoxin 4Fe-4S	1. Glutama	ate family		5. Histidine		
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 ribonucleotide isomerase
Rv3028c	fixB	β subunit electron transfer flavoprotein $α$	Rv1655	argD	reductase acetylornithine aminotransferase	Rv1601	hisB	imidazole glycerol-phosphate
00200		subunit	Rv1656	argF	ornithine carbamoyltransferase			dehydratase
Rv3106	fprA	adrenodoxin and NADPH ferre-	Rv1658	argG	arginosuccinate synthase	Rv1600	hisC	histidinol-phosphate aminotrans-
D0000	for rP	doxin reductase	Rv1659	argH	arginosuccinate lyase	Du0770	hinon	ferase
Rv0886	fprB	ferredoxin, ferredoxin-NADP reductase	Rv1653 Rv2220	argJ glnA1	glutamate N-acetyltransferase glutamine synthase class I	Rv3772	hisC2	histidinol-phosphate aminotrans- ferase
Rv3251c	rubA	rubredoxin A	Rv2222c	glnA1 glnA2	glutamine synthase class I	Rv1599	hisD	histidinol dehydrogenase
				J	Ç ,		•	, 9

Rv1605	hisF	imidazole glycerol-phosphate synthase	Rv3048c	nrdG	subunit ribonucleoside-diphosphate small	Rv3119	moaE	subunit 1 molybdopterin-converting factor
Rv2121c Rv1602	hisG hisH	ATP phosphoribosyltransferase amidotransferase	Rv3053c	nrdH	subunit glutaredoxin electron transport	Rv0866	moaE2	subunit 2 molybdopterin-converting factor
Rv2122c	hisl	phosphoribosyl-AMP cyclohydro- lase	Rv3052c	nrdl	component of NrdEF system Nrdl/YgaO/YmaA family	Rv3322c	moaE3	subunit 2 molybdopterin-converting factor
Rv1606	hisl2	probable phosphoribosyl-AMP 1,6	Rv3247c	tmk thuA	thymidylate kinase	Dv0004	maa A	subunit 2
Rv0114	_	cyclohydrolase similar to HisB	Rv2764c Rv0570	thyA nrdZ	thymidylate synthase ribonucleotide reductase, class II	Rv0994 Rv3116	moeA moeB	molybdopterin biosynthesis molybdopterin biosynthesis
1100114		Similar to Fried	Rv3752c	-	probable cytidine/deoxycytidylate	Rv2338c	moeW	molybdopterin biosynthesis
Pyruva					deaminase	Rv1681	moeX	weak similarity to E. coli MoaA
Rv3423c	alr	alanine racemase	4 Cobross	a of muolo	asidas and nucleatides	Rv1355c	moeY moeZ	weak similarity to <i>E. coli</i> MoeB
7. Branch	ed amino	acid family	Rv3313c		osides and nucleotides probable adenosine deaminase	Rv3206c	111062	probably involved in molybdopterin biosynthesis
Rv1559	ίΙνΑ	threonine deaminase	Rv2584c	apt	adenine phosphoribosyltrans-	Rv0865	mog	molybdopterin biosynthesis
Rv3003c	ilvB	acetolactate synthase I large sub-			ferases			
Rv3470c	ilvB2	unit acetolactate synthase large sub-	Rv3315c Rv3314c	cdd deoA	probable cytidine deaminase thymidine phosphorylase	5. Pantoth Rv1092c	enate <i>coaA</i>	pantothenate kinase
11004700	IIVDZ	unit	Rv0478	deoC	deoxyribose-phosphate aldolase	Rv2225	panB	3-methyl-2-oxobutanoate
Rv3001c	ilvC	ketol-acid reductoisomerase	Rv3307	deoD	probable purine nucleoside phos-			hydroxymethyltransferase
Rv0189c	ilvD :b:c	dihydroxy-acid dehydratase	D::0004-	6	phorylase	Rv3602c	panC	pantoate-β-alanine ligase
Rv2210c	ilvE	branched-chain-amino-acid transaminase	Rv3624c	hpt	probable hypoxanthine-guanine phosphoribosyltransferase	Rv3601c	panD	aspartate 1-decarboxylase
Rv1820	ilvG	acetolactate synthase II	Rv3393	iunH	probable inosine-uridine	Pyridoxi	ne	
Rv3002c	ilvN	acetolactate synthase I small sub-	D		preferring nucleoside hydrolase	Rv2607	pdxH	pyridoxamine 5'-phosphate
Rv3509c	ilvX	unit probable acetohydroxyacid syn-	Rv0535	pnp	phosphorylase from Pnp/MtaP family 2			oxidase
11000000	11021	thase I large subunit	Rv3309c	upp	uracil phophoribosyltransferase	7. Pyridine	nucleotic	de
Rv3710	leuA	α-isopropyl malate synthase				Rv1594	nadA	quinolinate synthase
Rv2995c	leuB	3-isopropylmalate dehydrogenase			ucleoside/nucleotide reactions	Rv1595	nadB	L-aspartate oxidase
Rv2988c	leuC	3-isopropylmalate dehydratase large subunit	Rv0733 Rv2364c	adk bex	probable adenylate kinase GTP-binding protein of Era/ThdF	Rv1596	nadC	nicotinate-nucleotide pyrophos- phatase
Rv2987c	leuD	3-isopropylmalate dehydratase	,20040	~~~	family	Rv0423c	thiC	thiamine synthesis, pyrimidine
		small subunit	Rv1712	cmk	cytidylate kinase			moiety
F Polyan	nine synthe	esis	Rv2344c	dgt	probable deoxyguanosine triphosphate hydrolase	8. Thiamin	۵	
E. Folyan Rv2601	speE	spermidine synthase	Rv2404c	lepA	GTP-binding protein LepA	Rv0422c	thiD	phosphomethylpyrimidine kinase
		•	Rv2727c	miaA	tRNA δ(2)-isopentenylpyrophos-	Rv0414c	thiE	thiamine synthesis, thiazole
		nes, nucleosides and nucleotides	Du044Ea	nelleA	phate transferase	Du0417	thiC	moiety
Rv1389	gmk	tide biosynthesis putative guanylate kinase	Rv2445c Rv2440c	ndkA obg	nucleoside diphosphate kinase Obg GTP-binding protein	Rv0417	thiG	thiamine synthesis, thiazole moiety
Rv3396c	guaA	GMP synthase	Rv2583c	relA	(p)ppGpp synthase I	Rv2977c	thiL	probable thiamine-monophos-
Rv1843c	guaB1	inosine-5 -monophosphate dehy-	0.01					phate kinase
Rv3411c	guaB2	drogenase inosine-5'-monophosphate dehy-	G. Biosyn carriers	tnesis of d	cofactors, prosthetic groups and	9. Riboflav	in	
11104110	guabe	drogenase	1. Biotin			Rv1940	ribA	GTP cyclohydrolase II
Rv3410c	guaB3	inosine-5'-monophosphate dehy-	Rv1568	bioA	adenosylmethionine-8-amino-7-	Rv1415	ribA2	probable GTP cyclohydrolase II
Rv1017c	prsA	drogenase ribose-phosphate pyrophosphoki-	Rv1589	bioB	oxononanoate aminotransferase biotin synthase	Rv1412 Rv2671	ribC ribD	riboflavin synthase α chain probable riboflavin deaminase
11010170	prom	nase	Rv1570	bioD	dethiobiotin synthase	Rv2786c	ribF	riboflavin kinase
Rv0357c	purA	adenylosuccinate synthase	Rv1569	bioF	8-amino-7-oxononanoate	Rv1409	ribG	riboflavin biosynthesis
Rv0777 Rv0780	purB purC	adenylosuccinate lyase phosphoribosylaminoimidazole-	Rv0032	bioF2	synthase C-terminal similar to <i>B. subtilis</i>	Rv1416 Rv3300c	ribH -	riboflavin synthase β chain probable deaminase, riboflavin
. 100700	pui	succinocarboxamide synthase	1140005	DIOI Z	BioF	1 1400000	-	synthesis
Rv0772	purD	phosphoribosylamine-glycine lig-	Rv3279c	birA	biotin apo-protein ligase	:		·
Rv3275c	purE	ase phosphoribosylaminoimidazole	Rv1442 Rv0089	bisC -	biotin sulfoxide reductase possible <i>bioC</i> biotin synthesis	10. I hiore Rv0773c		taredoxin and mycothiol putative γ-glutamyl transpeptidas
HV32/30	ρuι⊑	carboxylase	HVUUOS	-	gene	Rv2394	ggtA ggtB	γ -glutamyltranspeptidase
Rv0808	purF	amidophosphoribosyltransferase-			9			precursor
Rv0957	purH	phosphoribosylaminoimidazole-	2. Folic ac			Rv2855	gorA	glutathione reductase homologue
Rv3276c	purK	carboxamide formyltransferase phosphoribosylaminoimidazole	Rv2763c Rv2447c		dihydrofolate reductase folylpolyglutamate synthase	Rv0816c Rv1470	thiX trxA	equivalent to <i>M. leprae</i> ThiX thioredoxin
11002700	punt	carboxylase ATPase subunit	Rv3356c		methylenetetrahydrofolate dehy-	Rv1471	trxB	thioredoxin reductase
Rv0803	purL	phosphoribosylformylglycin-			drogenase	Rv3913	trxB2	thioredoxin reductase
Ducces	m. 11.4	amidine synthase II	Rv3609c	folE	GTP cyclohydrolase I	Rv3914	trxC	thioredoxin
Rv0809	purM	5'-phosphoribosyl-5-aminoimida- zole synthase	Rv3606c	folK	7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase	11 Menac	uinone P	QQ, ubiquinone and other
Rv0956	purN	phosphoribosylglycinamide	Rv3608c	folP	dihydropteroate synthase	terpenoids		asignments and other
		formyltransferase I	Rv1207	folP2	dihydropteroate synthase	Rv2682c	dxs	1-deoxy-D-xylulose 5-phosphate
Rv0788	purQ	phosphoribosylformylglycin- amidine synthase I	Rv3607c	folX	may be involved in folate biosyn- thesis	Rv0562	grcC1	synthase heptaprenyl diphosphate
Rv0389	purT	phosphoribosylglycinamide	Rv0013	pabA	p-aminobenzoate synthase gluta-	1100002	givei	synthase II
		formyltransferase II			mine amidotransferase	Rv0989c	grcC2	heptaprenyl diphosphate
Rv2964	purU	formyltetrahydrofolate deformy-	Rv1005c	pabB	p-aminobenzoate synthase	Duggoog	ida A	synthase II
		lase	Rv0812	pabC	aminodeoxychorismate lyase	Rv3398c	idsA	geranylgeranyl pyrophosphate synthase
	line ribonu	cleotide biosynthesis	3. Lipoate			Rv2173	idsA2	geranylgeranyl pyrophosphate
Rv1383	carA	carbamoyl-phosphate synthase	Rv2218	lipA	lipoate biosynthesis protein A	Discoord	ide D	synthase
Rv1384	carB	subunit carbamoyl-phosphate synthase	Rv2217	lipB	lipoate biosynthesis protein B	Rv3383c	idsB	transfergeranyl, similar geranyl pyrophosphate synthase
		subunit	4. Molybd	opterin		Rv0534c	menA	4-dihydroxy-2-naphthoate
Rv1380	pyrB	aspartate carbamoyltransferase	Rv3109	moaA	molybdenum cofactor biosynthe-			octaprenyltransferase
Rv1381 Rv2139	pyrC pyrD	dihydroorotase dihydroorotate dehydrogenase	Rv0869c	moaA2	sis, protein A molybdenum cofactor biosynthe-	Rv0548c Rv0553	menB menC	naphthoate synthase o-succinylbenzoate-CoA synthase
Rv1385	pyrD pyrF	orotidine 5'-phosphate decarboxy-	11400090	1110dAZ	sis, protein A	Rv0555	menC menD	2-succinyl-6-hydroxy-2,4-cyclo-
		lase	Rv0438c	moaA3	molybdenum cofactor biosynthe-			hexadiene-1-carboxylate synthas
Rv1699	pyrG	CTP synthase	Dv2110	maaD	sis, protein A	Rv0542c	menE menG	o-succinylbenzoic acid-CoA ligas
Rv2883c Rv0382c	pyrH umpA	uridylate kinase probable uridine 5'-monophos-	Rv3110	moaB	molybdenum cofactor biosynthe- sis, protein B	Rv3853	menG	S-adenosylmethionine: 2-demethylmenaquinone
	ungura	phate synthase	Rv0984	moaB2		Rv3397c	phyA	phytoene synthase
					sis, protein B	Rv0693	pqqE	coenzyme PQQ synthesis
		otide metabolism	Rv3111	moaC	molybdenum cofactor biosynthe-	BUCKEO	ubi⊑	protein E
Rv0321	dcd	deoxycytidine triphosphate deaminase	Rv0864	moaC2	sis, protein C molybdenum cofactor biosynthe-	Rv0558	ubiE	ubiquinone/menaquinone biosyn- thesis methyltransferase
	dut	deoxyuridine triphosphatase			sis, protein C			•
	(0	ribonucleoside-diphosphate	Rv3324c	moaC3	molybdenum cofactor biosynthe- sis, protein C	12. Heme Rv0509	and porpl hemA	hyrin glutamyl-tRNA reductase
	nrdB	reductace R2 (eukanistia lika)				LIVUDUS	HOIM	unutarriyining reductase
Rv2697c Rv0233 Rv3051c	nraB nrdE	reductase B2 (eukaryotic-like) ribonucleoside diphosphate	Rv3112	moaD	molybdopterin converting factor	Rv0512	hemB	δ-aminolevulinic acid dehydratase
Rv0233			Rv3112 Rv0868c	moaD moaD2	molybdopterin converting factor subunit 1			

Rv1300 Rv0524		protoporphyrinogen oxidase glutamate-1-semialdehyde amino-	O. A mudhumun		transferase	Rv2931 Rv2932	ppsA ppsB	phenolpthiocerol synthesis (pksB) phenolpthiocerol synthesis (pksC)
Rv2388	c <i>hemN</i>	transferase oxygen-independent copropor-	phospholi		mycolyltransferases and esis	Rv2933 Rv2934	ppsC ppsD	phenolpthiocerol synthesis (pksD) phenolpthiocerol synthesis (pksE)
Rv2677	c hemY'	phyrinogen III oxidase protoporphyrinogen oxidase	Rv2289	cdh	CDP-diacylglycerol phosphatidyl- hydrolase	Rv2935 Rv2928	ppsE tesA	phenolpthiocerol synthesis (pksF) thioesterase
Rv1485		ferrochelatase	Rv2881c	cdsA	phosphatidate cytidylyltransferase	Rv1544	-	probable ketoacyl reductase
10 O+h			Rv3804c Rv1886c	fbpA	antigen 85A, mycolyltransferase	1 0		franchism a
13. Cob Rv2849		cob(l)alamin adenosyltransferase	Rv0129c	fbpB fbpC	antigen 85B, mycolyltransferase antigen 85C, mycolytransferase	J. Broad r 1. Repres		
Rv2848	c <i>cobB</i>	cobyrinic acid a,c-diamide synthase	Rv3803c	fbpD	antigen MPT51, mycolyltrans-	Rv1657	argR	arginine repressor
Rv2231 Rv2236		aminotransferase cobinamide synthase	Rv0564c	gpdA1	ferase glycerol-3-phosphate dehydroge-	Rv1267c	embR	regulator of <i>embAB</i> genes (AfsR/Dndl/RedD family)
Rv2064		percorrin reductase	11000040	gpuni	nase	Rv1909c	furA	ferric uptake regulatory protein
Rv2065		precorrin isomerase	Rv2982c	gpdA2	glycerol-3-phosphate dehydroge-	Rv2359	furB	ferric uptake regulatory protein
Rv2066 Rv2070		Cobl-CobJ fusion protein precorrin reductase	Rv2612c	pgsA	nase CDP-diacylglycerol-glycerol-3-	Rv2919c Rv2711	glnB ideR	nitrogen regulatory protein iron dependent repressor, IdeR
Rv2072		probable methyltransferase	11120120	pgori	phosphate phosphatidyltrans-	Rv2720	lexA	LexA, SOS repressor protein
Rv2071		precorrin-3 methylase	D.,1000	10	ferase	Rv1479	moxR	transcriptional regulator, MoxR
Rv2062 Rv2208		cobalt insertion cobalamin (5'-phosphate) synthase	Rv1822	pgsA2	CDP-diacylglycerol-glycerol-3- phosphate phosphatidyltrans- ferase	Rv3692	moxR2	homologue transcriptional regulator, MoxR homologue
Rv2207	cobT	nicotinate-nucleotide-dimethyl- benzimidazole transferase	Rv2746c	pgsA3	CDP-diacylglycerol-glycerol-3- phosphate phosphatidyltrans-	Rv3164c	moxR3	transcriptional regulator, MoxR homologue
Rv0254 Rv0255		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
Rv3713	cobQ2	possible cobyric acid synthase		•	ferase			family)
Rv0306	-	similar to BluB cobalamin synthe- sis protein <i>R. capsulatus</i>	Rv2482c	plsB2	glycerol-3-phosphate acyltrans- ferase	Rv1379	pyrR	regulatory protein pyrimidine biosynthesis
14 Iron	utilization	, ,	Rv0437c	psd	putative phosphatidylserine	Rv2788	sirR	iron-dependent transcriptional
Rv1876		bacterioferritin	Rv0436c	pssA	decarboxylase CDP-diacylglycerol-serine	Rv3082c	virS	repressor putative virulence regulating
Rv3841 Rv3215		bacterioferritin probable isochorismate synthase	Rv0045c	_	o-phosphatidyltransferase possible dihydrolipoamide acetyl-	Rv3219	whiB1	protein (AraC/XyIS family) WhiB transcriptional activator
Rv3214		weak similarity to many phospho-			transferase			homologue
Rv2895	c viuB	glycerate mutases similar to proteins involved in	Rv0914c Rv1543	-	lipid transfer protein probable fatty-acyl CoA reductase	Rv3260c	whiB2	WhiB transcriptional activator homologue
Rv3525	c -	vibriobactin uptake similar to ferripyochelin binding	Rv1627c Rv1814	-	lipid carrier protein possible C-5 sterol desaturase	Rv3416	whiB3	WhiB transcriptional activator homologue
		protein	Rv1867	-	similar to acetyl CoA synthase/lipid carriers	Rv3681c	whiB4	WhiB transcriptional activator homologue
	biosynthesi		Rv2261c	1	apolipoprotein N-acyltrans-	Rv0023	-	putative transcriptional regulator
1. Synth Rv3285		and mycolic acids acetyl/propionyl CoA carboxylase	Rv2262c		ferase-a apolipoprotein N-acyltrans-	Rv0043c	-	transcriptional regulator (GntR family)
		α subunit			ferase-b	Rv0067c	-	transcriptional regulator
Rv0904		acetyl/propionyl CoA carboxylase β subunit	Rv3523 Rv3720	-	lipid carrier protein C-term similar to cyclopropane	Rv0078	-	(TetR/AcrR family) transcriptional regulator
Rv3799		acetyl/propionyl CoA carboxylase β subunit			fatty acid synthases	Rv0081	-	(TetR/AcrR family) transcriptional regulator (ArsR
Rv3280	accD5	acetyl/propionyl CoA carboxylase β subunit	I. Polyketi Rv2940c	de and no mas	on-ribosomal peptide synthesis mycocerosic acid synthase	Rv0135c	_	family) putative transcriptional regulator
Rv2247	accD6	acetyl/propionyl CoA carboxylase	Rv2384	mbtA	mycobactin/exochelin synthesis	Rv0144	-	putative transcriptional regulator
Rv2244	асрМ	β subunit acyl carrier protein (meromycolate	Rv2383c	mbtB	(salicylate-AMP ligase) mycobactin/exochelin synthesis	Rv0158	-	transcriptional regulator (TetR/AcrR family)
	•	extension)			(serine/threonine ligation)	Rv0165c	-	transcriptional regulator (GntR
Rv2523	c acpS	CoA:apo-[ACP] pantethienephos- photransferase	Rv2382c Rv2381c	mbtC mbtD	mycobactin/exochelin synthesis mycobactin/exochelin synthesis	Rv0195	_	family) transcriptional regulator
Rv2243		malonyl CoA-[ACP] transacylase	D 0000		(polyketide synthase)	D 0400		(LuxR/UhpA family)
Rv0649 Rv1483		malonyl CoA-[ACP] transacylase 3-oxoacyl-[ACP] reductase (aka	Rv2380c	mbtE	mycobactin/exochelin synthesis (lysine ligation)	Rv0196	-	transcriptional regulator (TetR/AcrR family)
		MabA)	Rv2379c	mbtF	mycobactin/exochelin synthesis	Rv0232	-	transcriptional regulator
Rv1350		3-oxoacyl-[ACP] Reductase 3-oxoacyl-[ACP] reductase	Du0070*	mala #C	(lysine ligation) mycobactin/exochelin synthesis	Dyonon		(TetR/AcrR family)
Rv2002 Rv0242		3-oxoacyl-[ACP] reductase	Rv2378c	mbtG	(lysine hydroxylase)	Rv0238	-	transcriptional regulator (TetR/AcrR family)
Rv2766		3-oxoacyl-[ACP] reductase	Rv2377c	mbtH	mycobactin/exochelin synthesis	Rv0273c	-	putative transcriptional regulator
Rv0533 Rv2524		β-ketoacyl-ACP synthase III fatty acid synthase	Rv0101	nrp	unknown non-ribosomal peptide synthase	Rv0302	-	transcriptional regulator (TetR/AcrR family)
Rv1484	inhA	enoyl-[ACP] reductase	Rv1153c	omt	PKS o-methyltransferase	Rv0324	-	putative transcriptional regulator
Rv2245	kasA	β-ketoacyl-ACP synthase (meromycolate extension)	Rv3824c	papA1	PKS-associated protein, unknown	Rv0328	-	transcriptional regulator (TetR/AcrR family)
Rv2246	kasB	β-ketoacyl-ACP synthase	Rv3820c	papA2	function PKS-associated protein, unknown	Rv0348	-	putative transcriptional regulator
		(meromycolate extension)	D.:4400		function	Rv0377	-	transcriptional regulator (LysR
Rv1618 Rv2605		thioesterase II thioesterase II	Rv1182	papA3	PKS-associated protein, unknown function	Rv0386	_	family) transcriptional regulator
Rv0033	-	possible acyl carrier protein	Rv1528c	papA4	PKS-associated protein, unknown			(LuxR/UhpA family)
Rv1344 Rv1722	-	possible acyl carrier protein possible biotin carboxylase	Rv2939	papA5	function PKS-associated protein, unknown	Rv0452 Rv0465c	-	putative transcriptional regulator transcriptional regulator
Rv3221 Rv3472		resembles biotin carboxyl carrier possible acyl carrier protein	Rv2946c	pks1	function polyketide synthase	Rv0472c	-	(PbsX/Xre family) transcriptional regulator
			Rv3825c	pks2	polyketide synthase			(TetR/AcrR family)
 Modif Rv3391 	ication of far acrA1	tty and mycolic acids fatty acyl-CoA reductase	Rv1180 Rv1181	pks3 pks4	polyketide synthase polyketide synthase	Rv0474	-	transcriptional regulator (PbsX/Xre family)
Rv3392		cyclopropane mycolic acid	Rv1527c	pks5	polyketide synthase	Rv0485	-	transcriptional regulator (ROK
Rv0503	c cmaA2	synthase 1 cyclopropane mycolic acid syn-	Rv0405 Rv1661	pks6 pks7	polyketide synthase polyketide synthase	Rv0494	_	family) transcriptional regulator (GntR
1100000	UIIIAAZ	thase 2	Rv1662	pks8	polyketide synthase polyketide synthase	1100404		family)
Rv0824		acyl-[ACP] desaturase	Rv1664	pks9	polyketide synthase	Rv0552	-	putative transcriptional regulator
Rv1094 Rv3229		acyl-[ACP] desaturase acyl-[ACP] desaturase	Rv1660	pks10	polyketide synthase (chalcone synthase-like)	Rv0576 Rv0586	-	putative transcriptional regulator transcriptional regulator (GntR
Rv0645	c mmaA1	methoxymycolic acid synthase 1	Rv1665	pks11	polyketide synthase (chalcone			family)
Rv0644	c mmaA2	methoxymycolic acid synthase 2	Du0040		synthase-like)	Rv0650	-	transcriptional regulator (ROK
Rv0643 Rv0642		methoxymycolic acid synthase 3 methoxymycolic acid synthase 4	Rv2048c	pks12	polyketide synthase (erythronolide synthase-like)	Rv0653c	_	family) putative transcriptional regulator
Rv0447		unknown fatty acid methyltrans-	Rv3800c	pks13	polyketide synthase	Rv0681	-	transcriptional regulator
	ufaA2	ferase unknown fatty acid methyltrans-	Rv1342c	pks 14	polyketide synthase (chalcone synthase-like)	Rv0691c	-	(TetR/AcrR family) transcriptional regulator
Hv3538		ferase	Rv2947c	pks 15	polyketide synthase	,		(TetR/AcrR family)
Rv3538	4.4			-1 40	and the state of the state of	D.,0707		Construction and account of the contract of th
Hv3538 Rv0469	umaA1	unknown mycolic acid methyl- transferase	Rv1013 Rv1663	pks16 pks17	polyketide synthase polyketide synthase	Rv0737 Rv0744c	-	putative transcriptional regulator putative transcriptional regulator

Rv0823c	_	family) transcriptional regulator	Rv3160c Rv3167c	-	putative transcriptional regulator putative transcriptional regulator	Rv0018c	ppp	truncated putative phosphoprotein phos-
		(NifR3/Smm1 family)	Rv3173c	-	transcriptional regulator			phatase
Rv0827c	-	transcriptional regulator (ArsR family)	Rv3183	_	(TetR/AcrR family) putative transcriptional regulator	Rv2234	ptpA	low molecular weight protein-tyro sine-phosphatase
Rv0890c	-	transcriptional regulator	Rv3208	-	transcriptional regulator	Rv0153c	-	putative protein-tyrosine-phos-
		(LuxR/UhpA family)	5		(TetR/AcrR family)			phatase
Rv0891c Rv0894	-	putative transcriptional regulator putative transcriptional regulator	Rv3249c	-	transcriptional regulator (TetR/AcrR family)	II Macron	olecule	metabolism
Rv1019	-	transcriptional regulator	Rv3291c	-	transcriptional regulator			nodification of macromolecules
		(TetR/AcrR family)			(Lrp/AsnC family)			n synthesis and modification
Rv1049	-	transcriptional regulator (MarR family)	Rv3295	-	transcriptional regulator (TetR/AcrR family)	Rv3420c	riml	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 Rv0701	rpIB rpIC	50S ribosomal protein L2
Rv1152	-	transcriptional regulator (GntR family)	Rv3522 Rv3557c	-	putative transcriptional regulator transcriptional regulator	Rv0701	rpiC rpID	50S ribosomal protein L3 50S ribosomal protein L4
Rv1167c	-	putative transcriptional regulator			(TetR/AcrR family)	Rv0716	rpIE	50S ribosomal protein L5
Rv1219c		putative transcriptional regulator	Rv3574	-	transcriptional regulator	Rv0719	rpIF	50S ribosomal protein L6
Rv1255c	-	transcriptional regulator (TetR/AcrR family)	Rv3575c	_	(TetR/AcrR family) transcriptional regulator (Lacl	Rv0056 Rv0651	rpll rplJ	50S ribosomal protein L9 50S ribosomal protein L10
Rv1332	-	putative transcriptional regulator			family)	Rv0640	rplK	50S ribosomal protein L11
Rv1353c	-	transcriptional regulator	Rv3583c	-	putative transcriptional regulator	Rv0652	rplL	50S ribosomal protein L7/L12
Rv1358	-	(TetR/AcrR family) transcriptional regulator	Rv3676	-	transcriptional regulator (Crp/Fnr family)	Rv3443c Rv0714	rpIM rpIN	50S ribosomal protein L13 50S ribosomal protein L14
		(LuxR/UhpA family)	Rv3678c	-	transcriptional regulator (LysR	Rv0723	rplO	50S ribosomal protein L15
Rv1359	-	putative transcriptional regulator	D. 0700		family)	Rv0708	rpIP	50S ribosomal protein L16
Rv1395	-	transcriptional regulator (AraC/XyIS family)	Rv3736	-	transcriptional regulator (AraC/XyIS family)	Rv3456c Rv0720	rpIQ rpIR	50S ribosomal protein L17 50S ribosomal protein L18
Rv1404	-	transcriptional regulator (MarR	Rv3744	-	transcriptional regulator (ArsR	Rv2904c	rpIS	50S ribosomal protein L19
D. A. S. S.		family)	D ****		family)	Rv1643	rplT	50S ribosomal protein L20
Rv1423 Rv1460	-	putative transcriptional regulator putative transcriptional regulator	Rv3830c	-	transcriptional regulator (TetR/AcrR family)	Rv2442c Rv0706	rpIU rpIV	50S ribosomal protein L21 50S ribosomal protein L22
Rv1474c		transcriptional regulator	Rv3833	-	transcriptional regulator	Rv0703	rplW	50S ribosomal protein L23
		(TetR/AcrR family)			(AraC/XylS family)	Rv0715	rplX	50S ribosomal protein L24
Rv1534	-	transcriptional regulator (TetR/AcrR family)	Rv3840 Rv3855	-	putative transcriptional regulator putative transcriptional regulator	Rv1015c Rv2441c	rpIY rpmA	50S ribosomal protein L25 50S ribosomal protein L27
Rv1556	-	putative transcriptional regulator	1 140000	-	parative transcriptional regulator	Rv0105c	rpmA rpmB	50S ribosomal protein L27
Rv1674c		putative transcriptional regulator	2. Two cor			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 family)	Rv1027c	kdpE	two-component response regulator	Rv0722 Rv1298	rpmD rpmE	50S ribosomal protein L30 50S ribosomal protein L31
Rv1773c	-	transcriptional regulator (IcIR	Rv3246c	mtrA	two-component response	Rv2057c	rpmG	50S ribosomal protein L33
		family)	D		regulator	Rv3924c	rpmḤ	50S ribosomal protein L34
Rv1776c Rv1816	-	putative transcriptional regulator putative transcriptional regulator	Rv3245c Rv0844c	mtrB narL	sensor histidine kinase two-component response	Rv1642 Rv3461c	rpml rpmJ	50S ribosomal protein L35 50S ribosomal protein L36
Rv1846c		putative transcriptional regulator	11000440	HAIL	regulator	Rv1630	rpsA	30S ribosomal protein S1
Rv1931c	-	transcriptional regulator	Rv0757	phoP	two-component response	Rv2890c	rpsB	30S ribosomal protein S2
Rv1956		(AraC/XyIS family) putative transcriptional regulator	Rv0758	phoR	regulator sensor histidine kinase	Rv0707 Rv3458c	rpsC rpsD	30S ribosomal protein S3 30S ribosomal protein S4
Rv1963c	-	putative transcriptional regulator	Rv0491	regX3	two-component response	Rv0721	rpsE	30S ribosomal protein S5
Rv1985c	-	transcriptional regulator (LysR		-	regulator	Rv0053	rpsF	30S ribosomal protein S6
Rv1990c		family)	Rv0490	senX3	sensor histidine kinase	Rv0683 Rv0718	rpsG	30S ribosomal protein S7
Rv1994c		putative transcriptional regulator transcriptional regulator (MerR	Rv0602c	tcrA	two-component response regulator	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	D. 0000		regulator	Rv3459c	rpsK	30S ribosomal protein S11
Rv2021c	-	(PbsX/Xre family) putative transcriptional regulator	Rv0600c Rv0601c	-	sensor histidine kinase sensor histidine kinase	Rv0682 Rv3460c	rpsL rpsM	30S ribosomal protein S12 30S ribosomal protein S13
Rv2034		transcriptional regulator (ArsR	Rv0818	-	two-component response	Rv0717	rpsN	30S ribosomal protein S14
D 0475		family)	D 0045		regulator	Rv2056c	rpsN2	30S ribosomal protein S14
Rv2175c Rv2250c		putative transcriptional regulator putative transcriptional regulator	Rv0845 Rv0902c	-	sensor histidine kinase sensor histidine kinase	Rv2785c Rv2909c	rpsO rpsP	30S ribosomal protein S15 30S ribosomal protein S16
Rv2258c		putative transcriptional regulator	Rv0903c	-	two-component response	Rv0710	rpsQ	30S ribosomal protein S17
Rv2282c		transcriptional regulator (LysR			regulator	Rv0055	rpsR	30S ribosomal protein S18
Rv2308	_	family) putative transcriptional regulator	Rv0981	-	two-component response regulator	Rv2055c Rv0705	rpsR2 rpsS	30S ribosomal protein S18 30S ribosomal protein S19
Rv2324	-	transcriptional regulator	Rv0982	-	sensor histidine kinase	Rv2412	rpsT	30S ribosomal protein S20
		(Lrp/AsnC family)	Rv1032c	-	sensor histidine kinase	Rv3241c	-	member of S30AE ribosomal
Rv2358	-	transcriptional regulator (ArsR	Rv1033c	-	two-component response			protein family
Rv2488c	-	family) transcriptional regulator	Rv1626	_	regulator two-component response	2. Ribosor	ne modifi	cation and maturation
		(LuxR/UhpA family)			regulator	Rv1010	ksgA	16S rRNA dimethyltransferase
Rv2506	-	transcriptional regulator	Rv2027c	-	sensor histidine kinase	Rv2838c	rbfA rimM	ribosome-binding factor A
Rv2621c	_	(TetR/AcrR family) putative transcriptional regulator	Rv2884	-	two-component response regulator	Rv2907c	rimM	16S rRNA processing protein
Rv2640c		transcriptional regulator (ArsR	Rv3132c		sensor histidine kinase			synthases and their modification
Ducata		family)	Rv3133c	-	two-component response	Rv2555c	alaS	alanyl-tRNA synthase
Rv2642	-	transcriptional regulator (ArsR family)	Rv3143	_	regulator putative sensory transduction	Rv1292 Rv2572c	argS aspS	arginyl-tRNA synthase aspartyl-tRNA synthase
Rv2669	-	putative transcriptional regulator			protein	Rv3580c	cysS	cysteinyl-tRNA synthase
Rv2745c		putative transcriptional regulator	Rv3220c	-	sensor histidine kinase	Rv2130c	cysS2	cysteinyl-tRNA synthase
Rv2779c	-	transcriptional regulator (Lrp/AsnC family)		-	sensor histidine kinase two-component response	Rv1406 Rv3011c	fmt gatA	methionyl-tRNA formyltransferase glu-tRNA-gln amidotransferase,
Rv2887	-	transcriptional regulator (MarR			regulator	1.400110	94171	subunit B
		family)			-	Rv3009c	gatB	glu-tRNA-gln amidotransferase,
Rv2912c	-	transcriptional regulator			protein kinases and phosphoprotein	Bu20124	astC	subunit A
Rv2989	-	(TetR/AcrR family) transcriptional regulator (IcIR	phosphata Rv0015c	ses pknA	serine-threonine protein kinase	Rv3012c	gatC	glu-tRNA-gln amidotransferase, subunit C
		family)	Rv0014c	pknB	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	pknF 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
		parative transcriptional regulator	1 1VZ UOO	PRIN	SOURCE THE CHILD PROTEIN KINGSE	11710076	111010	mennony runna synthase
Rv3095 Rv3124	_	transcriptional regulator	Rv3080c	pknK	serine-threonine protein kinase	Rv1649	pheS	phenylalanyl-tRNA synthase α

Rv1650	pheT	phenylalanyl-tRNA synthase β	Rv2090	-	partially similar to DNA poly-	2. DNA		
		subunit	D::0404		merase I	Rv0670	end	endonuclease IV (apurinase)
Rv28450 Rv38340		prolyl-tRNA synthase seryl-tRNA synthase	Rv2191	-	similar to both PoIC and UvrC proteins	Rv1108c Rv1107c	xseA xseB	exonuclease VII large subunit exonuclease VII small subunit
Rv2614d		threonyl-tRNA synthase	Rv2464c	-	probable DNA glycosylase,		жоод	ononaciones vii cinan cabani
Rv29060	c trmD	tRNA (guanine-N1)-methyltrans-			endonuclease VIII			and glycopeptides
D		ferase	Rv3201c	-	probable ATP-dependent DNA	Rv3305c	amiA amiB	probable aminohydrolase
Rv33360 Rv1689		tryptophanyl tRNA synthase tyrosyl-tRNA synthase	Rv3202c	_	helicase similar to UvrD proteins	Rv3306c Rv3596c	amıb clpC	probable aminohydrolase ATP-dependent Clp protease
Rv24480		valyl-tRNA synthase	Rv3263	-	probable DNA methylase	Rv2461c	clpP	ATP-dependent Clp protease pro-
		,	Rv3644c	-	similar in N-term to DNA poly-		•	teolytic subunit
	oproteins				merase III	Rv2460c	clpP2	ATP-dependent Clp protease pro-
Rv1407 Rv3852	fmu hns	similar to Fmu protein HU-histone protein	6 Protein	translation	and modification	Rv2457c	clpX	teolytic subunit ATP-dependent Clp protease
Rv29860		DNA-binding protein II	Rv0429c	def	polypeptide deformylase	11024070	oipit	ATP-binding subunit ClpX
Rv1388	mIHF	integration host factor	Rv2534c	efp	elongation factor P	Rv2667	clpX'	similar to ClpC from M. leprae but
			Rv2882c	frr	ribosome recycling factor	5		shorter
5. DNA r tion/mod		repair, recombination and restric-	Rv0684 Rv0120c	fusA fusA2	elongation factor G elongation factor G	Rv3419c Rv2725c	gcp hflX	glycoprotease GTP-binding protein
Rv1317d		DNA-3-methyladenine glycosi-	Rv1080c	greA	transcription elongation factor G	Rv1223	htrA	serine protease
		dase II	Rv3462c	infA	initiation factor IF-1	Rv2861c	mapA1	methionine aminopeptidase
Rv28360		DNA-damage-inducible protein F	Rv2839c	infB i=f0	initiation factor IF-2	Rv0734	mapA2	probable methionine aminopepti-
Rv1329d Rv3056		probable ATP-dependent helicase DNA-damage-inducible protein	Rv1641 Rv0009	infC ppiA	initiation factor IF-3 peptidyl-prolyl cis-trans isomerase	Rv0319	рср	dase pyrrolidone-carboxylate peptidase
Rv1537	dinX	probable DNA-damage-inducible	Rv2582	ppiA ppiB	peptidyl-prolyl <i>cis-trans</i> isomerase	Rv0125	pepA	probable serine protease
	4	protein	Rv1299	prfA	peptide chain release factor 1	Rv2213	рерВ	aminopeptidase A/I
Rv0001	dnaA	chromosomal replication initiator	Rv3105c	prfB	peptide chain release factor 2	Rv0800	pepC	aminopeptidase I
D::00E0	·(·· · · D	protein	Rv2889c	tsf	elongation factor EF-Ts	Rv2467	pepD pepE	probable aminopeptidase
Rv0058 Rv1547	dnaB dnaE1	DNA helicase (contains intein) DNA polymerase III, α subunit	Rv0685	tuf	elongation factor EF-Tu	Rv2089c Rv2535c	pepE pepQ	cytoplasmic peptidase cytoplasmic peptidase
Rv3370d		DNA polymerase III α chain	7. RNA sy	nthesis, R	NA modification and DNA	Rv2782c	pepR pepR	protease/peptidase, M16 family
Rv2343d	dnaG	DNA primase	transcripti	on				(insulinase)
Rv0002		DNA polymerase III, β subunit	Rv1253	deaD	ATP-dependent DNA/RNA	Rv2109c	prcA prcB	proteasome α-type subunit 1
Rv37110		DNA polymerase III € chain	Rv2783c	gpsl	helicase pppGpp synthase and polyribo-	Rv2110c Rv0782	ргсв ptrBa	proteasome β-type subunit 2 protease II, α subunit
Rv37210	o dnaZX	DNA polymerase III, γ (dnaZ) and τ (dnaX)		alon,	nucleotide phosphorylase	Rv0782	ptrBb	protease II, β subunit
Rv2924d	o fpg	formamidopyrimidine-DNA glyco-	Rv2841c	nusA	transcription termination factor	Rv0724	sppA	protease IV, signal peptide pepti-
		sylase	Rv2533c	nusB	N-utilization substance protein B	5		dase
Rv0006 Rv0005	gyrA	DNA gyrase subunit A DNA gyrase subunit B	Rv0639	nusG	transcription antitermination protein	Rv0198c Rv0457c	-	probable zinc metalloprotease probable peptidase
Rv2092d	gyrB b 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
		family			siderophore production	Rv1977	-	probable zinc metallopeptidase
Rv27560	c hsdM	type I restriction/modification sys-	Rv3211	rhlE	probable ATP-dependent	Rv3668c	-	probable alkaline serine protease
Rv27550	hsdS'	tem DNA methylase type I restriction/modification sys-	Rv1297	rho	RNA helicase transcription termination	Rv3671c Rv3883c	-	probable serine protease probable secreted protease
11027330	, iisuo	tem specificity determinant	1101207	1110	factor rho	Rv3886c	_	protease
Rv3296	lhr	ATP-dependent helicase	Rv3457c	rpoA	α subunit of RNA polymerase			•
Rv3014d		DNA ligase	Rv0667	rpoB	β subunit of RNA polymerase		charides, I	ipopolysaccharides and phospho-
Rv3062	ligB	DNA ligase	Rv0668 Rv1364c	rpoC rsbU	β' subunit of RNA polymerase SigB regulation protein	lipids Rv0062	celA	cellulase/endoglucanase
Rv3731 Rv1020	ligC mfd	probable DNA ligase transcription-repair coupling factor	Rv3287c	rsbW	anti-sigma B factor	Rv3915	cwiM	hydrolase
Rv25280		restriction system protein	Rv2703	sigA	RNA polymerase sigma factor	Rv0315	-	probable β-1,3-glucanase
Rv2985	mutT1	MutT homologue			(aka MysA, RpoV)	Rv1090	-	probable inactivated
Rv1160	mutT2	MutT homologue	Rv2710	sigB	RNA polymerase sigma factor	D.:1007-		cellulase/endoglucanase
Rv0413	mutT3	MutT homologue	Rv2069	sigC	(aka MysB) ECF subfamily sigma subunit	Rv1327c	-	probable glycosyl hydrolase, α- amylase family
Rv3589 Rv3297	mutY nei	probable DNA glycosylase probable endonuclease VIII	Rv3414c	sigD sigD	ECF subfamily sigma subunit	Rv1333	_	probable hydrolase
Rv3674d		probable endonuclease III	Rv1221	sigE	ECF subfamily sigma subunit	Rv3463	-	probable neuraminidase
Rv13160		methylated-DNA-protein-cysteine	Rv3286c	sigF	ECF subfamily sigma subunit	Rv3717	-	possible N-acetylmuramoyl-L-ala-
D 4000		methyltransferase	Rv0182c	sigG	sigma-70 factors ECF subfamily			nine amidase
Rv1629 Rv1402	polA priA	DNA polymerase I putative primosomal protein n'	Rv3223c Rv1189	sigH sigl	ECF subfamily sigma subunit ECF family sigma factor	5. Esterase	es and lina	3585
1101402	PIIA	(replication factor Y)	Rv3328c	siaJ	similar to Sigl, ECF family	Rv0220	lipC	probable esterase
Rv3585	radA	probable DNA repair RadA homo-	Rv0445c	sigK	ECF-type sigma factor	Rv1923	lipD	probable esterase
		logue	Rv0735	sigL	sigma-70 factors ECF subfamily	Rv3775	lipE	probable hydrolase
Rv2737d		recombinase (contains intein)	Rv3911	sigM	probable sigma factor, similar to	Rv3487c	lipF lipG	probable esterase
Rv0630d Rv0631d		exodeoxyribonuclease V exodeoxyribonuclease V	Rv3366	spoU	SigE probable rRNA methylase	Rv0646c Rv1399c	lipG lipH	probable hydrolase probable lipase
Rv06290		exodeoxyribonuclease V exodeoxyribonuclease V	Rv3455c	truA	probable pseudouridylate syn-	Rv1400c	lipl	probable lipase
Rv0003		DNA replication and SOS induc-			thase	Rv1900c	lipJ	probable esterase
D:-0075		tion	Rv2793c Rv1644	truB ton₽	tRNA pseudouridine 55 synthase	Rv2385	lipK lint	probable acetyl-hydrolase
Rv2973d Rv1696		ATP-dependent DNA helicase recombination and DNA repair	□v 1044	tsnR	putative 23S rRNA methyltrans- ferase	Rv1497 Rv2284	lipL lipM	esterase probable esterase
Rv37150		RecBC-Independent process of	Rv3649	-	ATP-dependent DNA/RNA heli-	Rv2970c	lipN	probable lipase/esterase
		DNA repair			case	Rv1426c	lipΟ	probable esterase
Rv27360		regulatory protein for RecA	0 D-1	ا ادادمام	ar damila amaia)	Rv2463	lipP	probable esterase
Rv25930	c ruvA	Holliday junction binding protein,	8. Polysac Rv1326c	charides (glgB	cytoplasmic) 1,4-α-glucan branching enzyme	Rv2485c Rv3084	lipQ lipR	probable carboxlyesterase probable acetyl-hydrolase
Rv2592d	c ruvB	DNA helicase Holliday junction binding protein	Rv13280	gigP	probable glycogen phosphory-	Rv3176c	lipA IipS	probable esterase/lipase
Rv25940		Holliday junction resolvase, endo-		J J.	lase	Rv2045c	lipT	probable carboxylesterase
		deoxyribonuclease	Rv1564c	glgX	probable glycogen debranching	Rv1076	lipU	probable esterase
Rv0054	ssb	single strand binding protein	Dutenn	aleV	enzyme	Rv3203	lipV lipW	probable lipase
Rv1210	tagA	DNA-3-methyladenine glycosi- dase I	Rv1563c Rv1562c	glgY glgZ	putative α-amylase maltooligosyltrehalose trehalohy-	Rv0217c Rv2351c	lipW plcA	probable esterase phospholipase C precursor
Rv36460	c topA	DNA topoisomerase	1.1010000	3,34	drolase	Rv2350c	picA picB	phospholipase C precursor
Rv29760		uracil-DNA glycosylase	Rv0126	-	probable glycosyl hydrolase	Rv2349c	plcC	phospholipase C precursor
Rv1638	uvrA	excinuclease ABC subunit A	Rv1781c	-	probable 4-α-glucanotransferase	Rv1755c	plcD	partial CDS for phospholipase C
Rv1633	uvrB	excinuclease ABC subunit B	Rv2471	-	probable maltase α-glucosidase	Rv1104	-	probable esterase pseudogene
Rv1420 Rv0949	uvrC uvrD	excinuclease ABC subunit C DNA-dependent ATPase I and	B. Degran	lation of m	acromolecules	Rv1105	-	probable esterase pseudogene
1100349	uviU	helicase II	1. RNA	01 111		6. Aromati	c hydrocar	bons
Rv31980	uvrD2	putative UvrD	Rv1014c		peptidyl-tRNA hydrolase	Rv3469c	mhpE	probable 4-hydroxy-2-oxovalerate
Rv0427d		exodeoxyribonuclease III	Rv2925c	rnc	RNAse III	D. 6010		aldolase
Rv0071	-	group II intron maturase	Rv2444c	rne	similar at C-term to ribo- nuclease E	Rv0316	-	probable muconolactone iso- merase
Rv0861d Rv0944	-	probable DNA helicase possible formamidopyrimidine-	Rv2902c	rnhB	ribonuclease HII	Rv0771	-	probable 4-carboxymuconolac-
		DNA glycosylase	Rv3923c	rnpA	ribonuclease P protein compo-			tone decarboxylase
D 4000	_	probable 3-methylpurine DNA			nent	Rv0939	-	probable dehydrase
Rv1688		glycosylase	Rv1340	rphA	ribonuclease PH	Rv1723		6-aminohexanoate-dimer hydro-

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	orane proteins	Rv2877c	merT	possible mercury resistance transport system
C. Cell en			Rv0402c	mmpL1		Rv1811	mgtC	probable magnesium transport
1. Lipopro	oteins (<i>lpp</i> ,	4- <i>lpr0</i>) 65	Rv0507	mmpL2	protein conserved large membrane	Rv0362	mgtE	ATPase protein C putative magnesium ion
2. Surface	e polysacc	harides, lipopolysaccharides, pro-	1100007	HIHPLE	protein	1100002	mgiL	transporter
teins and		probable UDP-glucose-4-	Rv0206c	mmpL3	conserved large membrane	Rv2856	nicT	probable nickel transport protein
Rv0806c	cps1	epimerase	Rv0450c	mmpL4	protein conserved large membrane	Rv0924c	nramp	transmembrane protein belonging to Nramp family
Rv3811	csp	secreted protein	D 0070		protein	Rv2691	trkA	probable potassium uptake pro-
Rv1677 Rv3794	dsbF embA	highly similar to C-term Mpt53 involved in arabinogalactan syn-	Rv0676c	mmpL5	conserved large membrane protein	Rv2692	trkB	tein probable potassium uptake pro-
		thesis	Rv1557	mmpL6	conserved large membrane			tein
Rv3795	embB	involved in arabinogalactan syn- thesis	Rv2942	mmpL7	protein conserved large membrane	Rv2287 Rv2723	yjcE -	probable Na+/H+ exchanger probable membrane protein,
Rv3793	embC	involved in arabinogalactan syn-			protein			tellurium resistance
Rv3875	esat6	thesis early secretory antigen target	Rv3823c	mmpL8	conserved large membrane protein	Rv3162c Rv3237c		probable membrane protein possible potassium channel
Rv0112	gca	probable GDP-mannose dehy-	Rv2339	mmpL9	conserved large membrane			protein
Rv0113	gmhA	dratase phosphoheptose isomerase	Rv1183	mmpL10	protein conserved large membrane	Rv3743c	-	probable cation-transporting ATPase
Rv2965c	kdtB	lipopolysaccharide core biosyn-			protein			
Rv2878c	mpt53	thesis protein secreted protein Mpt53	Rv0202c	mmpL11	conserved large membrane protein	3. Carbohy Rv2443	/drates, o <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
Rv2875	mpt70	Mpb64/Mpt64 major secreted immunogenic pro-	Rv0403c	mmpS1	protein conserved small membrane	Rv1902c Rv1236	nanT sugA	probable sialic acid transporter membrane protein probably
	·	tein Mpt70 precursor			protein		-	involved in sugar transport
Rv2873 Rv0899	mpt83 ompA	surface lipoprotein Mpt83 member of OmpA family	Rv0506	mmpS2	conserved small membrane protein	Rv1237 Rv1238	sugB sugC	sugar transport protein ABC transporter component of
Rv3810	pirG	cell surface protein precursor (Erp	Rv2198c	mmpS3	conserved small membrane			sugar uptake system
Rv3782	rfbE	protein) similar to rhamnosyl transferase	Rv0451c	mmpS4	protein conserved small membrane	Rv3331 Rv2835c	sugl ugpA	probable sugar transport protein sn-glycerol-3-phosphate
Rv1302	rfe	undecaprenyl-phosphate α-N-	11004310	•	protein	11020000	иурл	permease
Rv2145c	wag31	acetylglucosaminyltransferase antigen 84 (aka wag31)	Rv0677c	mmpS5	conserved small membrane protein	Rv2833c	ugpB	sn-glycerol-3-phosphate-binding periplasmic lipoprotein
Rv0431	-	tuberculin related peptide (AT103)				Rv2832c	ugpC	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	MV20410	-	probable sugar transporter
Rv2301 Rv2345	-	probable cutinase precursor of probable membrane	Duggera	dppB	permease	4. Anions Rv2684	ara4	probable ergenieel nump
1102040	-	protein	Rv3665c	ирры	probable peptide transport system permease	Rv2685	arsA arsB	probable arsenical pump probable arsenical pump
Rv2672 Rv3019c		putative exported protease similar to Esat6	Rv3664c	dppC	probable peptide transport system	Rv3578 Rv2643	arsB2 arsC	probable arsenical pump probable arsenical pump
Rv3036c		probable secreted protein	Rv3663c	dppD	permease probable ABC-transporter	Rv2397c	cysA	sulphate transport ATP-binding
Rv3449	4	probable precursor of serine pro-	Rv0522	gabP	probable 4-amino butyrate trans-	Rv2399c	au a T	protein sulphate transport system perme-
Rv3451	-	tease probable cutinase	Rv0411c	glnH	porter putative glutamine binding protein		cysT	ase protein
Rv3452		probable cutinase precursor	Rv2564	glnQ	probable ATP-binding transport	Rv2398c	cysW	sulphate transport system perme-
Rv3724	-	probable cutinase precursor	Rv1280c	oppA	protein probable oligopeptide transport	Rv1857	modA	ase protein molybdate binding protein
3. Murein Rv2911		and peptidoglycan penicillin binding protein	Dudooo	amm [7]	protein oligopeptide transport protein	Rv1858	modB	transport system permease, molybdate uptake
Rv2981c	dacB ddlA	D-alanine-D-alanine ligase A	Rv1283c Rv1282c	oppB oppC	oligopeptide transport protein oligopeptide transport system per-	Rv1859	modC	molybdate uptake ABC-
Rv3809c	glf	UDP-galactopyranose mutase	Dud 00d -	0	mease	Dutoco		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	lytB1	LytB protein homologue very similar to LytB	Rv3253c	-	probable cationic amino acid transport	Rv2329c	narK1	probable nitrite extrusion protein
Rv1110 Rv1315	lytB2 murA	very similar to Lytb UDP-N-acetylglucosamine-1-car-	Rv3454	-	transport possible proline permease	Rv1737c Rv0261c	narK2 narK3	nitrite extrusion protein nitrite extrusion protein
		boxyvinyltransferase			•	Rv0267	narU	similar to nitrite extrusion
Rv0482	murB	UDP-N-acetylenolpyruvoylglu- cosamine reductase	2. Cations Rv2920c	amt	putative ammonium transporter	Rv0934	phoS1	protein 2 PstS component of phosphate
Rv2152c	murC	UDP-N-acetyl-muramate-alanine	Rv1607	chaA	putative calcium/proton antiporter			uptake
Rv2155c	murD	ligase UDP-N-acetylmuramoylalanine-D-	Rv1239c	corA	probable magnesium and cobalt transport protein	Rv0928	phoS2	PstS component of phosphate uptake
		glutamate ligase	Rv0092	ctpA ctpP	cation-transporting ATPase	Rv0820	phoT	phosphate transport system ABC
Rv2158c	murE	meso-diaminopimelate-adding enzyme	Rv0103c Rv3270	ctpB ctpC	cation transport ATPase cation transport ATPase	Rv3301c	phoY1	transporter phosphate transport system
Rv2157c	murF	D-alanine:D-alanine-adding	Rv1469	ctpD	probable cadmium-transporting			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 Rv2156c	murl murX	glutamate racemase phospho-N-acetylmuramoyl-	Rv1992c Rv0425c	ctpG ctpH	probable cation transport ATPase C-terminal region putative cation-	Rv2281	pitB	transporter phosphate permease
		petapeptide transferase		·	transporting ATPase	Rv0930	pstA1	PstA component of phosphate
Rv3332	nagA	N-acetylglucosamine-6-P- deacetylase	Rv0107c	ctpl	probable magnesium transport ATPase	Rv0936	pstA2	uptake PstA component of phosphate
Rv0016c	pbpA	penicillin-binding protein	Rv0969	ctpV	cation transport ATPase			uptake
Rv2163c Rv0050	pbpB ponA1	penicillin-binding protein 2 penicillin-bonding protein	Rv3044 Rv0265c	fecB fecB2	putative FellI-dicitrate transporter iron transport protein FellI dici-	Rv0933	pstB	ABC transport component of phosphate uptake
Rv3682	ponA2	class A penicillin binding protein	trate		transporter	Rv0935	pstC	PstC component of phosphate
Rv0017c Rv0907	rodA -	FtsW/RodA/SpovE family probable penicillin binding protein	Rv1029	kdpA	potassium-transporting ATPase A chain	Rv0929	pstC2	uptake membrane-bound component of
1100001	-	probable periodini biliding protein			onani	1140020	P3102	membrane-bound component of

Rv0932c	pstS	phosphate transport system PstS component of phosphate uptake	Rv1821	secA2	unit SecA, preprotein translocase sub- unit	Rv3500c - Rv3501c - Rv3896c -	part of <i>mce4</i> operon part of <i>mce4</i> operon putative p60 homologue
Rv2400c		sulphate binding precursor	Rv2587c	secD	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	ooaloa ooqaanooo, ana maga
Rv3679 Rv3680	-	possible anion transporter probable anion transporter	Rv0732	secY	SecG SecY subunit of preprotein translo-	IS6110 IS1081	16 copies 6 copies
		·			case	Others	34 copies
5. Fatty a Rv2790c	acid transpo : /tp1	ort non-specific lipid transport protein	Rv2462c	tig	chaperone protein, similar to trigger factor	2. REP 13E12 famil	y 7 copies
Rv3540c		non-specific lipid transport protein	Rv2813	-	probable general secretion path-		
6. Efflux	proteins				way protein	 Phage-related fu Rv2894c xerC 	nctions integrase/recombinase
Rv2936	drrA	similar daunorubicin resistance			atypical conditions	Rv1701 xerD	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			regulator	Rv1573 -	phiRV1 phage related protein
Rv2938	drrC	similar daunorubicin resistance transmembrane protein	Rv0871 Rv3063	cspB cstA	probable cold shock protein starvation-induced stress	Rv1574 - Rv1575 -	phiRV1 phage related protein phiRV1 phage related protein
Rv2846c		putative efflux protein			response protein	Rv1576c -	phiRV1 phage related protein
Rv3065 Rv0783c	emrE	resistance to ethidium bromide multidrug resistance protein	Rv3490	otsA	probable α,α-trehalose-phosphate synthase	Rv1577c - Rv1578c -	phiRV1 possible prohead protease phiRV1 phage related protein
Rv0849	-	possible quinolone efflux pump	Rv2006	otsB	trehalose-6-phosphate phos-	Rv1579c -	phiRV1 phage related protein
Rv1145 Rv1146	-	probable drug transporter probable drug transporter	Rv3372	otsB2	phatase trehalose-6-phosphate phos-	Rv1580c - Rv1581c -	phiRV1 phage related protein phiRV1 phage related protein
Rv1250	-	probable drug efflux protein			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
Rv1410c	; -	probable drug efflux protein	Rv3759c	proX	similar to osmoprotection proteins	Rv1585c -	phiRV1 phage related protein
Rv1634 Rv1819c	-	probable drug efflux protein probable multidrug resistance	Rv3756c Rv1026	proZ	transport system permease	Rv1586c - Rv2309c -	phiRV1 integrase
		probable multidrug resistance pump	TV 1026	-	probable pppGpp-5'phosphohydro- lase	Rv2309c - Rv2310 -	integrase excisionase
Rv2136c	-	putative bacitracin resistance pro-	E D-1			Rv2646 -	phiRV2 integrase
Rv2209	-	tein probable drug efflux protein	F. Detoxific Rv2428	cation ahpC	alkyl hydroperoxide reductase	Rv2647 - Rv2650c -	phiRV2 phage related protein phiRV2 phage related protein
Rv2333c	; -	probable tetracenomycin C resis-	Rv2429	ahpD	member of AhpC/TSA family	Rv2651c -	phiRV2 prohead protease
Rv2994	_	tance protein probable fluoroguinolone efflux	Rv2238c Rv2521	ahpE bcp	member of AhpC/TSA family bacterioferritin comigratory protein	Rv2652c - Rv2653c -	phiRV2 phage related protein phiRV2 phage related protein
		protein	Rv1608c	bcpB	probable bacterioferritin comigra-	Rv2654c -	phiRV2 phage related protein
Rv1877 Rv2459	-	probable drug efflux protein probable drug efflux protein	Rv3473c	bpoA	tory protein probable non-heme bromoperoxi-	Rv2655c - Rv2656c -	phiRV2 phage related protein phiRV2 phage related protein
					dase	Rv2657c -	similar to gp36 of mycobacterio-
B. Chape Rv0384c	erones/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
Rv2373c	dnaJ2	ATPase DnaJ homologue	Rv3617	ephA	dase probable epoxide hydrolase	Rv2830c - Rv3750c -	similar to phage P1 <i>phd</i> gene excisionase
Rv0350	dnaK	70 kD heat shock protein, chromo-	Rv1938	ephB	probable epoxide hydrolase	Rv3751 -	putative integrase
Rv3417c	groEL1	some replication 60 kD chaperonin 1	Rv1124 Rv2214c	ephC ephD	probable epoxide hydrolase probable epoxide hydrolase	C. PE and PPE fan	niliae
Rv0440	groEL2	60 kD chaperonin 2	Rv3670	<i>ephE</i>	probable epoxide hydrolase	1. PE family	nnes
Rv3418c Rv0351		10 kD chaperone	Rv0134	ephF	probable epoxide hydrolase	PE subfamily	38 members
Rv2374c	grpE : hrcA	stimulates DnaK ATPase activity heat-inducible transcription	Rv3171c	hpx	probable non-heme haloperoxi- dase	PE_PGRS subfami	ly 61 members
Rv0251c	bon	repressor	Rv1908c	katG sodA	catalase-peroxidase	2. PPE family	68 members
Rv0353	: hsp hspR	possible heat shock protein heat shock regulator	Rv3846 Rv0432	sodC	superoxide dismutase superoxide dismutase precursor -	D. Antibiotic produc	etion and resistance
Rv2031c	hspX	14kD antigen, heat shock protein	Durtoco		(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-
Rv2701c	suhB	shock protein putative extragenic suppressor	Rv3177	-	probable non-heme haloperoxi- dase	Rv0262c -	ferase aminoglycoside 2'-N-acetyltrans-
		protein	11/ 01/				ferase
Rv3269	-	probable heat shock protein	IV. Other A. Virulent	ce		Rv0802c - Rv1082 -	acetyltransferase similar to <i>S. lincolnensis ImbE</i>
C. Cell d			Rv0169	mce1	cell invasion protein	Rv1170 -	similar to S. lincolnensis ImbE
Rv3641c Rv3102c		possible cell division protein membrane protein	Rv0589 Rv1966	mce2 mce3	cell invasion protein cell invasion protein	Rv1347c -	possible aminoglycoside 6'-N- acetyltransferase
Rv3610c		inner membrane protein,	Rv3499c	mce4	cell invasion protein	Rv2036 -	similar to lincomycin production
Rv2748c	: ftsK	chaperone chromosome partitioning	Rv3100c Rv1694	smpB tlyA	probable small protein b cytotoxin/hemolysin homologue	Rv2303c -	genes similar to <i>S. griseus</i> macrotetrolide
Rv2151c	ftsQ	ingrowth of wall at septum	Rv0024	-	putative p60 homologue		resistance protein
Rv2154c	: ftsW	membrane protein (shape determi- nation)	Rv0167 Rv0168	-	part of <i>mce1</i> operon part of <i>mce1</i> operon	Rv3225c -	probable aminoglycoside 3'-phos- photransferases
Rv3101c		membrane protein	Rv0170	-	part of <i>mce1</i> operon	Rv3700c -	probable acetyltransferase
Rv2921c Rv2150c		cell division protein FtsY circumferential ring, GTPase	Rv0171 Rv0172	-	part of <i>mce1</i> operon part of <i>mce1</i> operon	Rv3817 -	probable aminoglycoside 3'-phos- photransferase
Rv3919c	gid	glucose inhibited division protein B	Rv0174	-	part of mce1 operon		·
Rv3625c Rv3917c		probable cell cycle protein chromosome partitioning; DNA -	Rv0587 Rv0588	-	part of <i>mce2</i> operon part of <i>mce2</i> operon	E. Bacteriocin-like	oroteins 3
	,	binding	Rv0590	-	part of mce2 operon	F. Cytochrome P45	0 enzymes 22
Rv3918c	parB	possibly involved in chromosome partitioning	Rv0591 Rv0592	-	part of <i>mce2</i> operon part of <i>mce2</i> operon	G. Coenzyme F420	n-denendent
Rv2922c	: smc	member of Smc1/Cut3/Cut14	Rv0594	-	part of mce2 operon	enzymes	aependent 3
	_	family possible cell division protein	Rv1085c Rv1477	-	possible hemolysin putative exported p60 protein	H. Miscellaneous ti	ransferases 61
By0010	-	ATPase of AAA-family		-	homologue		
Rv0012 Rv0435c	; -		Rv1478	-	putative exported p60 protein		osphatases, lyases,
Rv0435c Rv2115c	; -	ATPase of AAA-family			homologue putative exported p60 protein	and hydrolases	18
Rv0435c	; -	ATPase of AAA-family possible role in chromosome seg- regation	Rv1566c	-			
Rv0435c Rv2115c	; -	possible role in chromosome seg- regation possible role in chromosome parti-			homologue	J. Cyclases	6
Rv0435c Rv2115c Rv3213c	; -	possible role in chromosome seg- regation	Rv1566c Rv1964 Rv1965	-		J. Cyclases K. Chelatases	6 2
Rv0435c Rv2115c Rv3213c Rv1708	: - : - - in and pepti	possible role in chromosome seg- regation possible role in chromosome parti- tioning	Rv1964 Rv1965 Rv1967	-	homologue part of <i>mce3</i> operon part of <i>mce3</i> operon part of <i>mce3</i> operon	K. Chelatases	2
Rv0435c Rv2115c Rv3213c Rv1708 <i>D. Protei</i> Rv2916c	: - : - - in and pepti : ffh	possible role in chromosome seg- regation possible role in chromosome parti- tioning ide secretion signal recognition particle protein	Rv1964 Rv1965 Rv1967 Rv1968	- -	nomologue part of <i>mce3</i> operon part of <i>mce3</i> operon part of <i>mce3</i> operon part of <i>mce3</i> operon	*	2
Rv0435c Rv2115c Rv3213c Rv1708	: - : - - in and pepti : ffh	possible role in chromosome seg- regation possible role in chromosome parti- tioning ide secretion signal recognition particle protein signal peptidase I prolipoprotein diacylglyceryl trans-	Rv1964 Rv1965 Rv1967 Rv1968 Rv1969 Rv1971	- - - -	homologue part of mce3 operon	K. Chelatases	2
Rv0435c Rv2115c Rv3213c Rv1708 D. Protei Rv2916c Rv2903c	: - : - - in and pepti : ffh : lepB	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	Rv1964 Rv1965 Rv1967 Rv1968 Rv1969	- - - -	homologue part of mce3 operon	K. Chelatases V. Conserved hypo	2 theticals 912
Rv0435c Rv2115c Rv3213c Rv1708 <i>D. Protei</i> Rv2916c Rv2903c Rv1614	: - - - in and pepti : ffh : lepB gt	possible role in chromosome seg- regation possible role in chromosome parti- tioning ide secretion signal recognition particle protein signal peptidase I prolipoprotein diacylglyceryl trans-	Rv1964 Rv1965 Rv1967 Rv1968 Rv1969 Rv1971 Rv2190c	- - - - -	homologue part of mee3 operon putative p60 homologue	K. Chelatases V. Conserved hypo VI. Unknowns	2 theticals 912 606

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

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The radio source Sagittarius A* is thought to be powered by gas accreting onto a supermassive black hole at the centre of our Galaxy^{1,2}. Using the high infrared accretion rates³, however, standard accretion models4 are unable to explain the observed low luminosity and spectral energy distribution⁵⁻⁸, which has led to the consideration of a new model: advection-dominated accretion flows⁹⁻¹². In an advection-dominated flow, most of the accretion energy is stored as thermal energy in the gas which is then lost as the gas falls into the black hole. This model requires the protons to have a much higher temperature than the electrons, and the gas therefore has a two-temperature structure 10,13,14 Although this model explains the low total luminosity¹⁵⁻¹⁸ and much of the spectral energy distribution (from millimetre wavelengths to hard X-rays), it has been difficult to reconcile with lowfrequency radio observations. Here we show that a neglected emission process associated with the protons naturally explains the radio observations without any 'fine tuning' of the model parameters. This result simultaneously supports the two-temperature model of the gas and suggests that an advection-dominated accretion flow onto a black hole of 2.5×10^6 solar masses provides an accurate description of Sagittarius A*.

Figure 1 shows the most up-to-date observations of the Galactic Centre ¹⁸. The spectrum rises at radio and submillimetre frequencies $\nu \approx 10^9 - 10^{12}$ Hz, where most of the emission occurs, and has a sharp drop in the infrared. The X-ray observations consist of a possible detection at soft X-ray energies, and firm upper limits in the hard X-rays. The X-ray error-box corresponds to uncertainties in the observed photon index which lies between 1.0 and 2.0 (ref. 18). At very high energies, the EGRET satellite has observed γ -ray emission from the Galactic Centre region ⁸. But owing to the low angular resolution of the measurements, $\sim 1^{\circ}$, the observations should perhaps be considered as upper limits.

The spectrum from a two-temperature advection-dominated accretion flow (ADAF) is determined by the cooling properties of the protons and electrons in the flow. The protons are at virial temperatures at all radii (proton temperature $T_{\rm p} \approx 10^{12} \, {\rm K}$ close to the black hole) and cool by creating neutral pions¹⁹, while the electrons have much lower temperatures ($T_{\rm e} \approx 10^{9.5} \, {\rm K}$) and cool by various optically thin processes, such as synchrotron, inverse Compton and bremsstrahlung radiation ^{11,20}.

Figure 1a shows the spectrum from the ADAF model of Sgr A* in ref. 18. This spectrum fits the submillimetre to hard X-ray spectrum quite well, but fails to explain the non-uniform radio spectrum. The radio luminosity, L_{ν} , is well represented by $L_{\nu} \propto \nu^{0.2}$ up to $\nu \approx 43$ GHz, which subsequently rises to $L_{\nu} \propto \nu^{0.8}$ for $\nu \gtrsim 86$ GHz (ref. 21). ADAF models of Sgr A* have always been unable to account for this break, and are substantially underluminous at frequencies below ~ 86 GHz. This poses a serious problem.

The observed excess of radio emission (beyond what the model predicts) has usually been attributed to a weak jet of material that might emerge from the ADAF; jets are known to be strong radio sources. High-resolution radio observations, however, have ruled this out^{22–24}, which severely constrains any outflow models. In this

case, a rather *ad hoc* electron-temperature profile might be needed to account for the excess radio emission¹⁸, which probably does not correspond to physical conditions. More importantly, recent high-resolution measurements constrain the actual size of the emitting region^{5,22}. These observations require large brightness temperatures (in excess of 10¹⁰ K) to explain the observed flux at 43 GHz and 86 GHz. In an ADAF, however, the electron temperature is always well below 10¹⁰ K at all radii¹¹, and therefore cannot account for these high temperatures.

This apparent problem is solved by considering another emission process associated with the protons. In addition to producing neutral pions, energetic proton collisions can also create charged pions, which subsequently decay into positrons and electrons (referred to here as e^{\pm}). This had been neglected in earlier work because these particles do not produce significant amounts of γ -ray

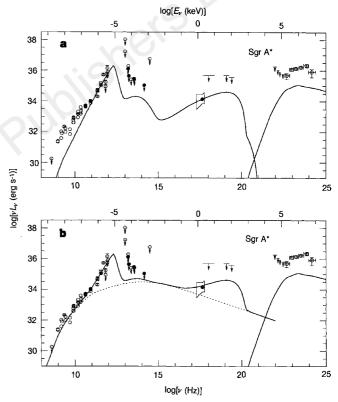


Figure 1 A comparison of the predicted emission from an ADAF model of the Galactic Centre with the observations. **a**, The spectrum of Sgr A*; the horizontal axis is the logarithm of the frequency and the vertical axis is the logarithm of the energy at that frequency. The measured fluxes were converted to luminosities assuming a distance of 8.5 kpc to the Galactic Centre. The data are the most upto-date compilation of observations taken from ref. 18. The arrows represent upper limits, and the 'box' at frequency $\sim 10^{17}$ Hz represents the uncertainty in the observed photon index. The solid line is the spectrum from the baseline ADAF model of Sgr A* used in ref. 18. The ADAF parameters are $\alpha = 0.3$, $\beta = 0.5$, $M=2.5\times10^6\,M_\odot$, and $\dot{M}=7.2\times10^{-6}\,M_\odot\,\mathrm{yr}^{-1}$, where α is the viscosity parameter⁴¹, β determines the strength of the magnetic field, and is defined so that $(1 - \beta)$ is the ratio of magnetic to total pressure, M is the dynamically measured mass of Sgr A* 42,43 , and \dot{M} is the mass accretion rate. For frequencies ≤10²⁰ Hz, the spectrum is determined by the individual optically thin cooling processes of ${\sim}10^{9.5}\,\text{K}$ thermal electrons, while for ${\nu} \gtrsim 10^{20}\,\text{Hz}$ the spectrum is solely due to the decay of neutral pions. The discrepancy between the model and the observations above $\nu \sim 10^{20}$ Hz is not considered serious, as it is unclear at present whether the $\sim 1^{\circ}$ beam of EGRET is detecting a point source or some diffuse emission. These observations should therefore be considered as upper limits rather than detections of a central source. **b**, The solid line represents the total spectrum from the ADAF around Sgr A*, which includes the present results. The parameters used are identical to those in a. The dotted line represents only the synchrotron emission from the positrons and electrons.

emission19

The high-energy e^{\pm} , however, can interact with the magnetic fields in the ADAF to produce synchrotron emission from radio to hard X-ray energies. Because the pions, and therefore the e^{\pm} , are created by proton–proton collisions, the energy spectra of the protons and e^{\pm} are related. This allows a direct investigation of the assumption that the protons have a different average temperature from the electrons, and at the same time determines if the e^{\pm} are created in sufficient number, and with the right energy, to produce the observed radio emission.

Here we assume that the energy spectrum of the protons is represented by a power-law distribution, $N(E_{\rm p}) \propto E_{\rm p}^{-s}$ with index s, where $N(E_{\rm p})$ represents the number of protons with energy $E_{\rm p}$. The index is generally between 2 and 4, and we set it to s=2.75, at the cosmic-ray value, suggesting that a similar acceleration mechanism might be at work in ADAFs¹⁹. The results are insensitive to the exact value of s (ref. 19).

The rate of production and energy spectrum of the e^{\pm} , R(E) is determined by the frequency of proton collisions as well as their energy spectrum. For the assumed power-law proton distribution, the energy distribution of the e^{\pm} is shown in Fig. 2. The spectrum rises at low energies, turns over at $E \approx 35$ MeV, and, as expected, extends as a power-law, E^{-s} , with the same energy dependence as the parent proton distribution²⁵. Because the created charged pion has a mass of ~ 140 MeV and decays into four particles, one of which is an electron or positron, we expect that on average the e^{\pm} should carry away one-quarter of the total energy available (that is, $\sim 140/4 = 35$ MeV)²⁶. This is an expected turnover which is characteristic of e^{\pm} production, and is shown in Fig. 2.

Determining the synchrotron emissivity from the e^{\pm} requires a knowledge of their steady-state energy distribution N(E). At a given energy E, the colliding protons produce R(E) electrons and positrons. However, because the e^{\pm} cool by synchrotron radiation, they lose their energy very efficiently, and the steady-state distribution is therefore determined by the competing effects of the creation

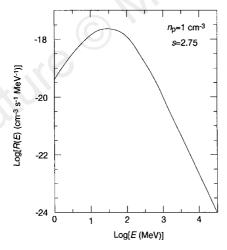


Figure 2 The energy spectrum, R(E), of positrons and electrons that are created by colliding power-law protons with energy index s=2.75. The vertical axis is the logarithm of number of positron and electrons created per unit volume, per second, per energy interval, and the horizontal axis is the logarithm of the energy. The scale on the vertical axis corresponds to a number density of protons equal to unity. For a number density N, the vertical axis must be multiplied by N^2 . The particles that are responsible for most of the emission are determined by the energy at which the function $E^2R(E)$ peaks, which occurs in the range $100\,\mathrm{MeV} < E < 500\,\mathrm{MeV}$. The shape of the spectrum depends only on the physics of particle collisions and decays 25,26 , and at high energies has the spectral shape $R(E) \propto E^{-s}$ (ref. 25). The spectrum therefore contains information about the parent proton distribution, as well as determining the shape of the resulting synchrotron spectrum. It therefore acts as a link between the form of the proton energy distribution and the observed synchrotron spectrum.

and depletion of particles. This requires the net flux of particles between two energies to be equal to their rate of injection, $d[N(E)\dot{E}_S(E)]/dE = R(E)$, where $\dot{E}_S(E)$ is the total synchrotron cooling rate as a function of energy²⁷.

Using the steady-state distribution N(E), the e^{\pm} synchrotron spectrum, from the ADAF around Sgr A*, is shown by the dotted line in Fig. 1b. The spectrum rises at low frequencies, turns over, and extends as a power-law at high frequencies. The spectral break at $\nu \approx 10^{15}\,\mathrm{Hz}$ is a direct consequence of the turn over in the e^{\pm} energy spectrum shown in Fig. 2. At high frequencies, the spectrum is optically thin and has a spectral dependence, $L_{\nu} \propto \nu^{-s/2}$. The spectral slope therefore depends on the proton index s, which is a direct consequence of the e^{\pm} having a steady-state distribution $N(E) \propto E^{-(s+1)}$ (ref. 27). At lower frequencies, the expected optically thin spectral dependence is $L_{\nu} \propto \nu^{-0.5}$ which corresponds to $N(E) \propto E^{-2}$ (ref. 27). However, in an ADAF, the emission at these low frequencies is self-absorbed by the plasma, and the resultant spectrum shown therefore has a different spectral dependence.

The solid curve in Fig. 1b represents the total radiation from the ADAF which includes this spectrum. At high frequencies $\gtrsim 10^{13}$ Hz, the synchrotron emission contributes to, but does not significantly change, the total luminosity. In particular, the agreement with the X-ray flux is not affected, and the additional infrared flux is still well below the stringent upper limits.

At lower energies the result is striking. The emission reproduces the required spectral break at ~86 GHz, is able to account for the 'excess' radio emission below this frequency, and diminishes sufficiently quickly at lower frequencies to agree with the radio upper limit at 400 MHz. As the emission at each radio frequency in Fig. 1a corresponds to a black-body spectrum at a given radius ^{11,20}, the total spectrum shown by the solid line in Fig. 1b indicates that ADAFs produce more emission at a given frequency than the local black-body spectrum. The excess emission is from the high-energy electrons radiating at larger radii. This resolves the problem with the low energy radio emission: no outflow model is needed to account for the observed emission, and the high brightness temperatures inferred^{5,22} are easily accounted for by the non-thermal origin of the emission.

The quite good agreement with the radio observations suggests that the emission observed is most probably from the hot protons in the ADAF. But before drawing any conclusions, we examine the essential ingredients required to explain the radio spectrum. Assuming that the dynamics of the flow are determined, reproducing the radio spectrum requires high-energy electrons (or e^{\pm}) with energies ~100 MeV at all radii. In an ADAF, this requirement is naturally satisfied. Assuming that viscosity primarily heats the protons into a power-law distribution at all radii, the production of high-energy e[±] with the same energy is completely determined by only the nuclear physics of particle collisions and decays^{25,26}. In particular, the shape of the e[±] spectrum (compare Fig. 2) is fixed throughout the flow. We note that the number of e[±] produced is also the right amount; this is a natural consequence of the proton collision time being longer than the accretion time. Whereas shorter collision times would produce excessive amounts of e[±] which would result in too much radio emission, much longer collision times would result in too little radio emission.

The agreement of the theory with the observations depends on two basic assumptions of ADAFs that have always been debated: (1) the existence of a two-temperature plasma, and (2) that viscosity preferentially heats the protons. We have quite good observational evidence that the first assumption is probably true. This is because the radio to hard X-ray spectrum is determined by emission processes associated with both the protons and electrons, at their respective temperatures. If the temperatures of protons and electrons were the same, or were markedly different from their calculated values, the resulting spectrum would be completely different and fail to explain any of the observations.

The second assumption is supported by the present results, and can be discussed in terms of δ , which is the fraction of viscous energy that heats the electrons. The baseline model in ref. 18 set $\delta \approx 0.001$, and showed that for $\delta > 0.01$, too much radiation is produced, and the electron spectrum does not agree with the observations. Here we have a radiation mechanism that accounts for the other fraction $(1-\delta)$ that heats the protons, and have shown that the agreement with the low-energy radio spectrum requires the amount of energy transferred to the electrons to be small. This shows that the average energy of the protons is probably virial.

Although past work has attempted to answer both these questions theoretically^{28–33}, the results here provide indirect observational evidence that these assumptions are probably valid. Further, theoretical models which reach contrary conclusions are probably based on assumptions that are not valid in ADAF^{18,34}. The present results could therefore be used as tools to aid future theoretical work in resolving these complex questions in plasma physics.

The present results have assumed that all the viscous energy is deposited into a power-law proton distribution, which might seem improbable. However, if half the viscous energy were transferred into a power-law distribution, and half into a thermal distribution, the number of e^{\pm} created reduces only by a factor ~ 2 (ref. 19), and the results presented here do not change significantly. Therefore, although the agreement with the radio flux requires a power-law proton distribution, it does not require all of the viscous energy to be deposited into the power-law protons.

It is interesting that the good agreement with observations comes from a model in which both the viscous hydrodynamics and the radiative processes have been included self-consistently. Previous models that have attempted to explain the observed spectrum have been phenomenological^{35–37}, or made simplifying assumptions, such as ignoring the angular momentum of the accreting gas^{3,38,39}, or, as noted previously^{18,40}, have errors in the synchrotron calculation which renders the resulting spectrum suspect^{3,39}. The ADAF models therefore provides us with a unique self-consistent framework which enables accurate prediction of spectra from accreting black holes.

We stress that there is no fine tuning in the present results. Whereas previous work on ADAFs has not included the e^{\pm} synchrotron radiation, the results presented here show that this process is essential to explaining the observed non-uniform radio spectrum. The model used is identical to that presented in ref. 18, and we have simply taken into account an additional physical process and emission mechanism in the two-temperature ADAF. It is remarkably that, using the same parameters as in ref. 18, an emission mechanism associated with the protons is able to naturally reproduce the entire radio spectrum including the observed spectral break at ~ 86 GHz. The agreement of the theory with the observations encourages us to take the natural explanation, and conclude that Sgr A* is in fact a 2×10^6 solar-mass black hole that is accreting by way of a two-temperature ADAF.

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Long-lived giant cells detected at the surface of the Sun

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Giant convective cells have been predicted¹ to exist in the Sun. Such cells should span the entire zone unstable to convective motions—now known to cover the outer 29 per cent of the Sun's radius²—and could be dredging up the magnetic flux that is thought to be the source of solar activity (sunspots). Several studies^{3–5} have failed to detect these giant cells, although there

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

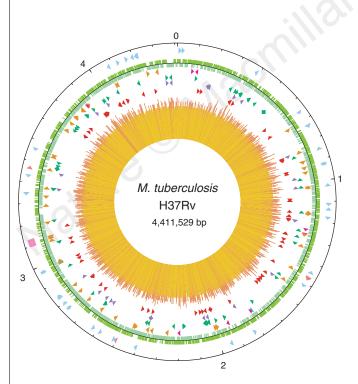


Figure 1 Circular map of the chromosome of M. tuberculosis H37Rv. The outer circle shows the scale in Mb, with 0 representing the origin of replication. The first ring from the exterior denotes the positions of stable RNA genes (tRNAs are blue, others are pink) and the direct repeat region (pink cube); 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 IS*6110*. 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.

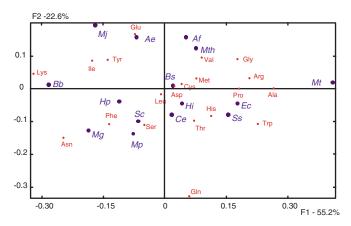


Figure 3 Correspondence analysis of the proteomes from extensively sequenced organisms as a function of amino-acid composition. Note the extreme position of *M. tuberculosis* and the shift in amino-acid preference reflecting increasing G + C content from left to right. Abbreviations used: Ae, Aquifex 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.

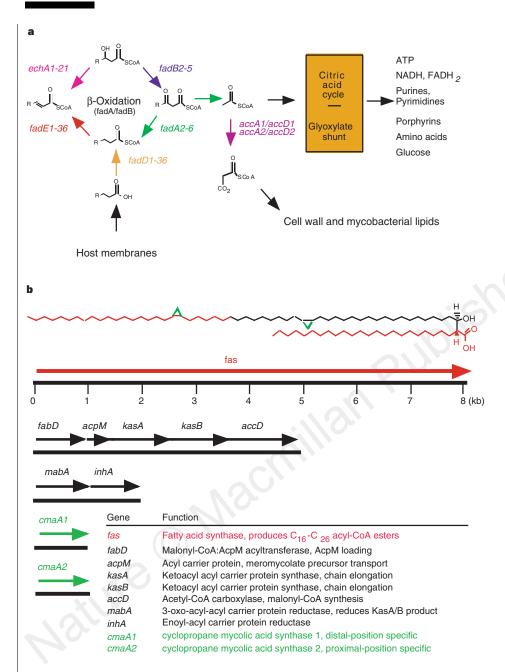
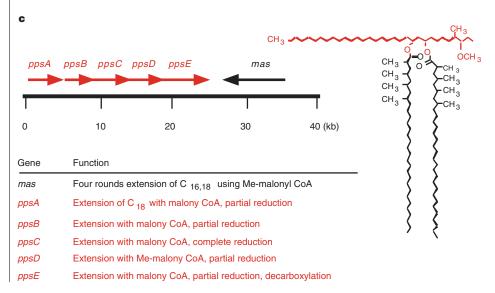


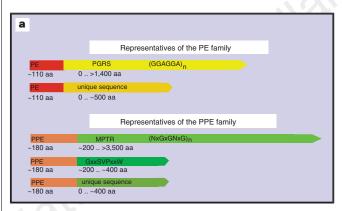
Figure 4 Lipid metabolism. a, Degradation of host-cell lipids is vital in the intracellular life of M. tuberculosis. Host-cell membranes provide precursors for many metabolic processes, as well as potential precursors of mycobacterial cell-wall constituents, through the actions of a broad family of β -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



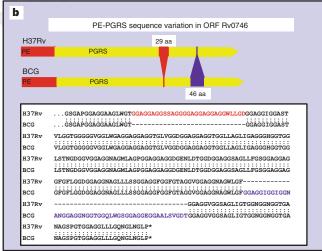


Figure 5 The PE and PPE protein families. **a**, Classification of the PE and PPE protein families. **b**, Sequence variation between *M. tuberculosis* H37Rv and *M. bovis* BCG-Pasteur in the PE-PGRS encoded by open reading frame (ORF) Rv0746.

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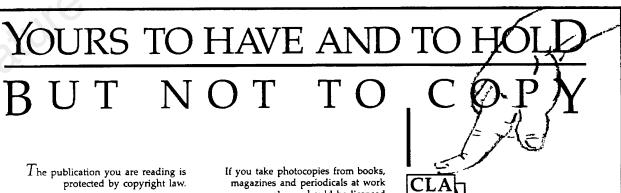
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Table 1. Functional classification of Mycobacterium tuberculosis protein-coding genes

		netabolism	Rv2831		superfamily	Rv3543c	fadE29 fadE30	acyl-CoA dehydrogenase
A. Degrad1. Carbon		de	HV2831	echA16	enoyl-CoA hydratase/isomerase superfamily	Rv3560c Rv3562	fadE30 fadE31	acyl-CoA dehydrogenase acyl-CoA dehydrogenase
Rv0186	bglS	β-glucosidase	Rv3039c	echA17	enoyl-CoA hydratase/isomerase	Rv3563	fadE32	acyl-CoA dehydrogenase
Rv2202c	cbhK	carbohydrate kinase			superfamily	Rv3564	fadE33	acyl-CoA dehydrogenase
Rv0727c	fucA	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. 10004-	600	genase	Rv3374	echA18'		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	1100010	CONTIN	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
D0010	ITI	transferase C-term	D. 0050	for al A	superfamily	D::0504*	1	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	manA	mannose-6-phosphate isomerase	Rv3546	fadA5	acetyl-CoA C-acetyltransferase	4.51		
Rv3441c	mrsA	phosphoglucomutase or phospho-	Rv3556c	fadA6 fadB	acetyl-CoA C-acetyltransferase	4. Phosph		
Rv0118c	oxcA	mannomutase oxalyl-CoA decarboxylase	Rv0860	Iaub	β oxidation complex, α subunit (multiple activities)	Rv2368c	phoH	ATP-binding <i>pho</i> regulon component
Rv3068c	pgmA	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			nase	Rv2984	ppk	polyphosphate kinase
Rv0408	pta	phosphate acetyltransferase	Rv3141	fadB4	3-hydroxyacyl-CoA dehydroge-	D 5		
Rv0729 Rv1096	xylB -	xylulose kinase	Rv1912c	fadB5	nase 3-hydroxyacyl-CoA dehydroge-	B. Energy 1. Glycoly:		m
N 1096	-	carbohydrate degrading enzyme	HV19120	Iaubo	nase	Rv1023	eno	enolase
2. Amino a	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	adi	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	ansA	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
HV07530	IIIIISA	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
D 0000		genase	Rv1549	fadD11'	acyl-CoA synthase, C-term	Rv3837c	-	putative phosphoglycerate mutase
Rv2322c Rv2321c	rocD1 rocD2	ornithine aminotransferase ornithine aminotransferase	Rv1427c Rv3089	fadD12 fadD13	acyl-CoA synthase acyl-CoA synthase	2. Pyruvat	o dobydro	ganasa
Rv1848	ureA	urease γ subunit	Rv1058	fadD13	acyl-CoA synthase	Rv2241	aceE	pyruvate dehydrogenase E1 com-
Rv1849	ureB	urease β subunit	Rv2187	fadD15	acyl-CoA synthase		4002	ponent
Rv1850	ureC	urease α subunit	Rv0852	fadD16	acyl-CoA synthase	Rv3303c	<i>lpdA</i>	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	D: 0400-		ponent α subunit
Rv1852 Rv2913c	ureG -	urease accessory protein probable D-amino acid	Rv3515c Rv1185c	fadD19 fadD21	acyl-CoA synthase acyl-CoA synthase	Rv2496c	pdhB	pyruvate dehydrogenase E1 com- ponent β subunit
NV29130	-	aminohydrolase	Rv2948c	fadD21	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
			Rv1521	fadD25	acyl-CoA synthase			
3. Fatty ac		(Rv2930	fadD26	acyl-CoA synthase	3. TCA cy		
Rv2501c	accA1	acetyl/propionyl-CoA carboxylase,	Rv0275c	fadD27 fadD28	acyl-CoA synthase	Rv1475c	acn citA	aconitate hydratase citrate synthase 2
Rv0973c	accA2	α subunit acetyl/propionyl-CoA carboxylase,	Rv2941 Rv2950c	fadD29	acyl-CoA synthase acyl-CoA synthase	Rv0889c Rv2498c	citE	citrate lyase β chain
1100700	accor iz	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
		β subunit	Rv3801c	fadD32	acyl-CoA synthase	Rv0896	gltA2	citrate synthase 1
Rv0974c	accD2	acetyl/propionyl-CoA carboxylase,	Rv1345	fadD33	acyl-CoA synthase	Rv3339c	icd1	isocitrate dehydrogenase
Rv3667		β subunit	Rv0035 Rv2505c	fadD34	acyl-CoA synthase	Rv0066c	icd2 lpdB	isocitrate dehydrogenase
Rv3409c	acs choD	acetyl-CoA synthase cholesterol oxidase	Rv1193	fadD35 fadD36	acyl-CoA synthase acyl-CoA synthase	Rv0794c Rv1240	приБ mdh	dihydrolipoamide dehydrogenase malate dehydrogenase
Rv0222	echA1	enoyl-CoA hydratase/isomerase	Rv0131c	fadE1	acyl-CoA dehydrogenase	Rv2967c	pca	pyruvate carboxylase
		superfamily	Rv0154c	fadE2	acyl-CoA dehydrogenase	Rv3318	sdhA	succinate dehydrogenase A
Rv0456c	echA2	enoyl-CoA hydratase/isomerase	Rv0215c	fadE3	acyl-CoA dehydrogenase	Rv3319	sdhB	succinate dehydrogenase B
		superfamily	Rv0231	fadE4	acyl-CoA dehydrogenase	Rv3316	sdhC	succinate dehydrogenase C sub-
Rv0632c	echA3	enoyl-CoA hydratase/isomerase	Rv0244c	fadE5 fadE6	acyl-CoA dehydrogenase	Dv2217	sdhD	unit
Rv0673	echA4	superfamily enoyl-CoA hydratase/isomerase	Rv0271c Rv0400c	fadE7	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv3317	SUILD	succinate dehydrogenase D sub- unit
110070	0011114	superfamily	Rv0672	fadE8	acyl-CoA dehydrogenase	Rv1248c	sucA	2-oxoglutarate dehydrogenase
Rv0675	echA5	enoyl-CoA hydratase/isomerase			(aka <i>aidB</i>)	Rv2215	sucB	dihydrolipoamide succinyltrans-
		superfamily	Rv0752c	fadE9	acyl-CoA dehydrogenase			ferase
Rv0905	echA6	enoyl-CoA hydratase/isomerase	Rv0873	fadE10	acyl-CoA dehydrogenase	Rv0951	sucC	succinyl-CoA synthase β chain
D. 0074		superfamily (aka eccH)	Rv0972c	fadE12	acyl-CoA dehydrogenase	Rv0952	sucD	succinyl-CoA synthase α chain
Rv0971c	echA7	enoyl-CoA hydratase/isomerase superfamily	Rv0975c Rv1346	fadE13 fadE14	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	4. Glyoxyla	ate hypaca	
Rv1070c	echA8	enoyl-CoA hydratase/isomerase	Rv1467c	fadE15	acyl-CoA dehydrogenase	Rv0467	aceA	isocitrate lyase
	5511110	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
		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
D.4444	055 6 4 4	superfamily	D. 0704	ford Coo	(aka mmgC)	E Dante	nh	to nothway
Rv1141c	echA11	enoyl-CoA hydratase/isomerase superfamily	Rv2724c Rv2789c	fadE20 fadE21	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	5. Pentose Rv1445c	phosphat devB	e pathway glucose-6-phosphate 1-dehydro-
Rv1472	echA12	enoyl-CoA hydratase/isomerase	Rv3061c	fadE22	acyl-CoA dehydrogenase	11014400	GEVD	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. 04		superfamily	Rv3274c	fadE25	acyl-CoA dehydrogenase	Rv1122	gnd2	6-phosphogluconate dehydroge-
Rv2486	echA14	enoyl-CoA hydratase/isomerase	Rv3504	fadE26	acyl-CoA dehydrogenase	Dv4.440-	ono A	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
1142010	COLLAID	55,. 56/1 Hydratase/isomerase	11100770	144220	ac, contactiyatogettase			SS. 211

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	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
HV1447C	ZVVIZ	genase	Rv1310	atpD	ATP synthase β chain	HV3030C	gilD	glutamate synthase
		genase	Rv1305	atpE	ATP synthase c chain	Rv3704c	gshA	possible γ-glutamylcysteine syn-
Respirat	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			ary 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	gipbe	nase	Rv3566c	nhoA	N-hydroxyarylamine <i>o</i> -acetyltrans-	Rv2726c	dapF	diaminopimelate epimerase
Rv0694	IIdD1	L-lactate dehydrogenase			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	_		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 dehydrogenase 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	rmIA	glucose-1-phosphate thymidyl-	Rv0511	cysG	uroporphyrin-III c-methyltrans-
1112100	q01D	cytB reductase	1110004	,,,,,,,	transferase	110011	oyou	ferase
Rv2194	qcrC	cytochrome <i>b/c</i> 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			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
D.:0000-	44bD	reductase	Rv3465	rmIC	dTDP-4-dehydrorhamnose	Rv0848	cysM3	putative cysteine synthase
Rv2899c Rv2900c	fdhD fdhF	affects formate dehydrogenase-N molybdopterin-containing oxidore-	Rv3266c	rmID	3,5-epimerase dTDP-4-dehydrorhamnose	Rv1093 Rv0070c	<i>glyA</i> glyA2	serine hydroxymethyltransferase serine hydroxymethyltransferase
11023000	IGIII	ductase	11002000	חוווט	reductase	Rv2996c	serA	D-3-phosphoglycerate dehydro-
Rv1552	frdA	fumarate reductase flavoprotein	Rv0322	udgA	UDP-glucose	20000	00171	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
Dutees	6-4D	protein	Rv3400	-	probable β-phosphoglucomutase	Rv0884c	serC	phosphoserine aminotransferase
Rv1555	frdD	fumarate reductase 13kD anchor protein	4. Amino	ellagre		4. Aromat	ic amino s	acid family
Rv1161	narG	nitrate reductase α subunit	Rv3436c		glucosamine-fructose-6-	Rv3227	aroA	3-phosphoshikimate
Rv1162	narH	nitrate reductase β chain		90	phosphate aminotransferase		u. 07 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. 2255	1- 5	reductase	Rv0663	atsD	proable arylsulfatase	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 arylaulfatase	Rv3838c	pheA	prephenate dehydratase
		subunit	Rv3796	atsH	proable arylsulfatase	Rv1613	trpA trpB	tryptophan synthase α chain
o Eloctus	trana	<i>t</i>	Rv1285	cysD cysN	ATP:sulphurylase subunit 2	Rv1612	trpB trpC	tryptophan synthase β chain
c. Electron Rv0409	n transpor ackA	acetate kinase	Rv1286 Rv2131c	cysN cysQ	ATP:sulphurylase subunit 1 homologue of <i>M.leprae cysQ</i>	Rv1611	trpC	indole-3-glycerol phosphate synthase
Rv1623c	аска аррС	cytochrome bd-II oxidase	Rv21310	cysQ 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
		subunit II	Rv3118	sseC	thiosulfate sulfurtransferase			component I
Rv1620c	cydC	ABC transporter	Rv0814c	sseC2	thiosulfate sulfurtransferase	Rv2386c	trpE2	anthranilate synthase
Rv1621c	cydD	ABC transporter	Rv3762c	-	probable alkyl sulfatase	D 0		component I
Rv2007c	fdxA	ferredoxin	D 4	a alal Ists	nth a sin	Rv3754	tyrA	prephenate dehydrogenase
Rv3554	fdxB	ferredoxin		acid biosy	ntnesis	E Distriction		
Rv1177 Rv3503c	fdxC fdxD	ferredoxin 4Fe-4S probable ferredoxin	1. Glutam Rv1654	ate family argB	acetylglutamate kinase	Histidin Rv1603	e <i>hisA</i>	phosphoribosylformimino-5-
Rv3029c	fixA	electron transfer flavoprotein	Rv1652	argС	N-acetyl-γ-glutamyl-phosphate	1101000	III3A	aminoimidazole carboxamide
	1	β subunit		a.90	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-
		doxin reductase	Rv1659	argH	arginosuccinate lyase	5		ferase
Rv0886	fprB	ferredoxin, ferredoxin-NADP	Rv1653	argJ	glutamate N-acetyltransferase	Rv3772	hisC2	histidinol-phosphate aminotrans-
Dv20F4-	ruh A	reductase	Rv2220	glnA1	glutamine synthase class I	Dv4500	hioD	ferase
Rv3251c	TUDA	rubredoxin A	Rv2222c	glnA2	glutamine synthase class II	Rv1599	hisD	histidinol dehydrogenase

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-	HVJUJJU	IIIun	glutaredoxin electron transport component of NrdEF system	HV0000	III0aE2	molybdopterin-converting factor subunit 2
***********	,,,,,,	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
		cyclohydrolase	Rv2764c	thyA	thymidylate synthase	Rv0994	moeA	molybdopterin biosynthesis
Rv0114	-	similar to HisB	Rv0570	nrdZ	ribonucleotide reductase, class II	Rv3116	moeB	molybdopterin biosynthesis
6. Pyruvat	a family		Rv3752c	-	probable cytidine/deoxycytidylate deaminase	Rv2338c Rv1681	moeW moeX	molybdopterin biosynthesis weak similarity to <i>E. coli</i> MoaA
	alr	alanine racemase			deariiriase	Rv1355c	moeY	weak similarity to E. coli MoaA weak similarity to E. coli MoeB
	u.,	ala.iii i rabbiilabb	4. Salvage	of nucleo	sides and nucleotides	Rv3206c	moeZ	probably involved in
Branche			Rv3313c	add	probable adenosine deaminase			molybdopterin biosynthesis
Rv1559	ilvA	threonine deaminase	Rv2584c	apt	adenine phosphoribosyltrans-	Rv0865	mog	molybdopterin biosynthesis
Rv3003c	ilvB	acetolactate synthase I large sub- unit	Rv3315c	cdd	ferases probable cytidine deaminase	5. Pantoth	anata	
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-			hydroxymethyltransferase
Rv0189c	ilvD	dihydroxy-acid dehydratase	D: 0004-	h t	phorylase	Rv3602c	panC	pantoate-β-alanine ligase
Rv2210c	ilvE	branched-chain-amino-acid transaminase	Rv3624c	hpt	probable hypoxanthine-guanine phosphoribosyltransferase	Rv3601c	panD	aspartate 1-decarboxylase
Rv1820	ilvG	acetolactate synthase II	Rv3393	iunH	probable inosine-uridine	6. Pyridoxi	ine	
Rv3002c	ilvN	acetolactate synthase I small sub-			preferring nucleoside hydrolase	Rv2607	pdxH	pyridoxamine 5'-phosphate
		unit	Rv0535	pnp	phosphorylase from Pnp/MtaP			oxidase
Rv3509c	ilvX	probable acetohydroxyacid syn-	D 0000		family 2			
Rv3710	leuA	thase I large subunit	Rv3309c	ирр	uracil phophoribosyltransferase	7. Pyridine Rv1594	nucleotid nadA	
Rv2995c	leuA leuB	α-isopropyl malate synthase 3-isopropylmalate dehydrogenase	5 Miscella	neous nu	cleoside/nucleotide reactions	Rv1594	nadB	quinolinate synthase L-aspartate oxidase
Rv2988c	leuC	3-isopropylmalate dehydratase	Rv0733	adk	probable adenylate kinase	Rv1596	nadC	nicotinate-nucleotide pyrophos-
		large subunit	Rv2364c	bex	GTP-binding protein of Era/ThdF			phatase
Rv2987c	leuD	3-isopropylmalate dehydratase	D. 4740		family	Rv0423c	thiC	thiamine synthesis, pyrimidine
		small subunit	Rv1712	cmk	cytidylate kinase			moiety
E. Polyam	nine synthe	esis	Rv2344c	dgt	probable deoxyguanosine triphosphate hydrolase	8. Thiamin	e	
Rv2601	speE	spermidine synthase	Rv2404c	lepA	GTP-binding protein LepA	Rv0422c	thiD	phosphomethylpyrimidine kinase
	•		Rv2727c	miaA	tRNA δ(2)-isopentenylpyrophos-	Rv0414c	thiE	thiamine synthesis, thiazole
		nes, nucleosides and nucleotides	D: 0445	!! - A	phate transferase	D: 0447	45.10	moiety
Rv1389	ribonucieo <i>gmk</i>	tide biosynthesis putative guanylate kinase	Rv2445c Rv2440c	ndkA obg	nucleoside diphosphate kinase Obg GTP-binding protein	Rv0417	thiG	thiamine synthesis, thiazole moiety
Rv3396c	guaA	GMP synthase	Rv2583c	relA	(p)ppGpp synthase I	Rv2977c	thiL	probable thiamine-monophos-
Rv1843c	guaB1	inosine-5'-monophosphate dehy-		7001	(Þ)ÞÞ ÞÞÞ Þ)		U	phate kinase
		drogenase		thesis of c	ofactors, prosthetic groups and			
Rv3411c	guaB2	inosine-5'-monophosphate dehy-	carriers			9. Riboflav		CTD avalahvidralasa II
Rv3410c	guaB3	drogenase inosine-5'-monophosphate dehy-	1. Biotin Rv1568	bioA	adenosylmethionine-8-amino-7-	Rv1940 Rv1415	ribA ribA2	GTP cyclohydrolase II probable GTP cyclohydrolase II
	gaabo	drogenase		2.07.	oxononanoate aminotransferase	Rv1412	ribC	riboflavin synthase α chain
Rv1017c	prsA	ribose-phosphate pyrophosphoki-	Rv1589	bioB	biotin synthase	Rv2671	ribD	probable riboflavin deaminase
D. 0057-		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
		succinocarboxamide synthase			BioF			synthesis
Rv0772	purD	phosphoribosylamine-glycine lig-	Rv3279c	birA	biotin apo-protein ligase	10 Thiana	مانيمام	to an alongin, and an another al
D 00==		ase	Rv1442	bisC	biotin sulfoxide reductase possible bioC biotin synthesis	Rv0773c		taredoxin and mycothiol putative y-glutamyl transpeptidase
HV32/50	nurF		Rv0089	_				
Rv3275c	purE	phosphoribosylaminoimidazole carboxylase	Rv0089	-	gene	Rv2394	ggtA ggtB	γ -glutamyltranspeptidase
Rv0808	purF	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-				Rv2394	ggtB	γ -glutamyltranspeptidase precursor
		phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase- phosphoribosylaminoimidazole-	2. Folic ac	id	gene	Rv2394 Rv2855	ggtB gorA	γ -glutamyltranspeptidase precursor glutathione reductase homologue
Rv0808 Rv0957	purF purH	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase- phosphoribosylaminoimidazole- carboxamide formyltransferase	2. Folic ac Rv2763c	id <i>dfrA</i>	gene dihydrofolate reductase	Rv2394 Rv2855 Rv0816c	ggtB gorA thiX	γ -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX
Rv0808	purF	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase- phosphoribosylaminoimidazole- carboxamide formyltransferase phosphoribosylaminoimidazole	2. Folic ac Rv2763c Rv2447c	id <i>dfrA</i> folC	dihydrofolate reductase folylpolyglutamate synthase	Rv2394 Rv2855 Rv0816c Rv1470	ggtB gorA thiX trxA	γ -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin
Rv0808 Rv0957	purF purH purK	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit	2. Folic ac Rv2763c	id <i>dfrA</i>	gene dihydrofolate reductase	Rv2394 Rv2855 Rv0816c	ggtB gorA thiX	γ -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX
Rv0808 Rv0957 Rv3276c Rv0803	purF purH	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II	2. Folic ac Rv2763c Rv2447c	id dfrA foIC foID foIE	dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I	Rv2394 Rv2855 Rv0816c Rv1470 Rv1471	ggtB gorA thiX trxA trxB	γ-glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase
Rv0808 Rv0957 Rv3276c	purF purH purK	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5-phosphoribosyl-5-aminoimida-	2. Folic ac Rv2763c Rv2447c Rv3356c	id dfrA foIC foID	gene dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin	Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914	ggtB gorA thiX trxA trxB trxB2 trxC	y -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin
Rv0808 Rv0957 Rv3276c Rv0803 Rv0809	purF purH purK purL purL	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase	2. Folic ac Rv2763c Rv2447c Rv3356c Rv3609c Rv3606c	id dfrA foIC foID foIE foIK	gene dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase	Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914	ggtB gorA thiX trxA trxB trxB2 trxC	γ -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase
Rv0808 Rv0957 Rv3276c Rv0803	purF purH purK purL	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5-phosphoribosyl-5-aminoimida-	2. Folic ac Rv2763c Rv2447c Rv3356c Rv3609c Rv3606c Rv3608c	id dfrA foIC foID foIE	dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase	Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914	ggtB gorA thiX trxA trxB trxB2 trxC	γ-glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin reductase thoredoxin (QQ, ubiquinone and other
Rv0808 Rv0957 Rv3276c Rv0803 Rv0809	purF purH purK purL purL	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide	2. Folic ac Rv2763c Rv2447c Rv3356c Rv3609c Rv3606c	id dfrA foIC foID foIE foIK foIP	gene dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7.8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosyn-	Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c	ggtB gorA thiX trxA trxB trxB2 trxC quinone, P	γ -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin (QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase
Rv0808 Rv0957 Rv3276c Rv0803 Rv0809 Rv0956 Rv0788	purF purH purK purL purM purN	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase-phosphoribosylaminoimidazole-carboxylase ATPase subunit phosphoribosylformylglycin-amidine synthase II 5'-phosphoribosylformylglycin-amidine synthase phosphoribosylglycinamide formyltransferase I phosphoribosylformylglycin-amidine synthase I	2. Folic ac Rv2763c Rv2447c Rv3356c Rv3609c Rv3609c Rv3608c Rv1207 Rv3607c	id dfrA foIC foID foIE foIK foIP foIP2 foIX	gene dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosyn- thesis	Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914	ggtB gorA thiX trxA trxB trxB2 trxC quinone, P	γ-glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin (QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate
Rv0808 Rv0957 Rv3276c Rv0803 Rv0809	purF purH purK purL purM	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycin-amidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylformylglycin-amidine synthase I phosphoribosylglycinamide	2. Folic ac Rv2763c Rv2447c Rv3356c Rv3609c Rv3606c Rv3608c Rv1207	id dfrA foIC foID foIE foIK foIP foIP2	gene dihydrofolate reductase 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-	Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562	ggtB gorA thiX trxA trxB trxB2 trxC quinone, P dxs grcC1	y -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin (QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II
Rv0808 Rv0957 Rv3276c Rv0803 Rv0809 Rv0956 Rv0788 Rv0389	purF purH purK purL purM purN purQ	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylformylglycinamidine synthase I phosphoribosylformylglycinamidine synthase I phosphoribosylglycinamide formyltransferase II	2. Folic ac Rv2763c Rv2447c Rv3356c Rv3609c Rv3606c Rv3608c Rv1207 Rv3607c Rv0013	id dfrA folC folD folE folK folP folP2 folX pabA	gene dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7.8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosyn- thesis p-aminobenzoate synthase gluta- mine amidotransferase	Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c	ggtB gorA thiX trxA trxB trxB2 trxC quinone, P	γ-glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase leptaprenyl diphosphate synthase II heptaprenyl diphosphate
Rv0808 Rv0957 Rv3276c Rv0803 Rv0809 Rv0956 Rv0788	purF purH purK purL purM purN	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycin-amidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylformylglycin-amidine synthase I phosphoribosylglycinamide	2. Folic ac Rv2763c Rv2447c Rv3356c Rv3609c Rv3609c Rv3608c Rv1207 Rv3607c	id dfrA foIC foID foIE foIK foIP foIP2 foIX	gene dihydrofolate reductase 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-	Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562	ggtB gorA thiX trxA trxB trxB2 trxC quinone, P dxs grcC1	y -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin (QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate
Rv0808 Rv0957 Rv3276c Rv0803 Rv0809 Rv0956 Rv0788 Rv0389 Rv2964	purF purH purK purL purM purN purQ purT	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferasephosphoribosylaminoimidazolecarboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycinamidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylformylglycinamidine synthase I phosphoribosylglycinamide formyltransferase II formyltransferase II formyltransferase II formyltetrahydrofolate deformyltase	2. Folic ac Rv2763c Rv2447c Rv3356c Rv3609c Rv3609c Rv3606c Rv1207 Rv3607c Rv0013 Rv1005c Rv0812	id dfrA folC folD folE folK folP folP2 folX pabA pabB	dihydrofolate reductase 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	Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menacterpenoids Rv2682c Rv0562 Rv0989c Rv3398c	ggtB gorA thiX trxA trxB trxB2 trxC quinone, P dxs grcC1 grcC2 idsA	γ-glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase liphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase
Rv0808 Rv0957 Rv3276c Rv0803 Rv0809 Rv0956 Rv0788 Rv0389 Rv2964	purF purH purK purL purM purN purN purQ purT purU	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycin-amidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyttransferase I phosphoribosylglycinamide formyttransferase II phosphoribosylglycinamide formyttransferase II formytterahydrofolate deformylase cleotide biosynthesis	2. Folic ac Rv2763c Rv2447c Rv3356c Rv3609c Rv3609c Rv3608c Rv1207 Rv3607c Rv0013 Rv1005c Rv0812 3. Lipoate	id dfrA folC folD folE folK folP folP2 folX pabA pabB pabC	dihydrofolate reductase 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	Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562	ggtB gorA thiX trxA trxB trxB2 trxC quinone, P dxs grcC1 grcC2	y -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin (QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate geranylgeranyl pyrophosphate
Rv0808 Rv0957 Rv3276c Rv0803 Rv0809 Rv0956 Rv0788 Rv0389 Rv2964	purF purH purK purL purM purN purQ purT	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosyldrormylglycin-amidine synthase II 5'-phosphoribosylglycinamide phosphoribosylglycinamide formyltransferase I phosphoribosylformylglycin-amidine synthase I phosphoribosylformylglycin-amidine synthase I phosphoribosylglycinamide formyltransferase II formyltetrahydrofolate deformylase cleotide biosynthesis carbamoyl-phosphate synthase	2. Folic ac Rv2763c Rv2447c Rv3356c Rv3609c Rv3609c Rv3609c Rv3607c Rv0013 Rv1005c Rv0812 3. Lipoate Rv2218	id dfrA foIC foID foIE foIK foIP2 foIX pabA pabB pabC	gene dihydrofolate reductase 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	Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0562 Rv398c Rv398c	ggtB gorA thiX trxA trxB trxB2 trxC quinone, P dxs grcC1 grcC2 idsA idsA2	y-glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin (QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase leptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase
Rv0808 Rv0957 Rv3276c Rv0803 Rv0809 Rv0956 Rv0788 Rv0389 Rv2964	purF purH purK purL purM purN purN purQ purT purU	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycin-amidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyttransferase I phosphoribosylglycinamide formyttransferase II phosphoribosylglycinamide formyttransferase II formytterahydrofolate deformylase cleotide biosynthesis	2. Folic ac Rv2763c Rv2447c Rv3356c Rv3609c Rv3609c Rv3608c Rv1207 Rv3607c Rv0013 Rv1005c Rv0812 3. Lipoate	id dfrA folC folD folE folK folP folP2 folX pabA pabB pabC	dihydrofolate reductase 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	Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menacterpenoids Rv2682c Rv0562 Rv0989c Rv3398c	ggtB gorA thiX trxA trxB trxB2 trxC quinone, P dxs grcC1 grcC2 idsA	y -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin (QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate geranylgeranyl pyrophosphate
Rv0808 Rv0957 Rv3276c Rv0803 Rv0809 Rv0956 Rv0788 Rv0389 Rv2964	purF purH purK purL purM purN purQ purT purU	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosyldromylglycin-amidine synthase II 5'-phosphoribosylglycinamide phosphoribosylglycinamide formyltransferase I phosphoribosylformylglycin-amidine synthase I phosphoribosylformylglycin-amidine synthase I phosphoribosylformylglycin-amide formyltransferase II phosphoribosylformylglycin-amide formylterahydrofolate deformyltase cleotide biosynthesis carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit	2. Folic ac Rv2763c Rv2447c Rv3356c Rv3609c Rv3609c Rv3609c Rv3607c Rv0013 Rv1005c Rv0812 3. Lipoate Rv2218	id dfrA folC folD folE folK folP folP2 folX pabA pabB pabC	gene dihydrofolate reductase 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	Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0562 Rv398c Rv398c	ggtB gorA thiX trxA trxB trxB2 trxC quinone, P dxs grcC1 grcC2 idsA idsA2	γ-glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase ligeranyldiphosphate synthase II heptaprenyl diphosphate synthase II geranylderanyl gyrophosphate synthase geranylderanyl pyrophosphate synthase geranylderanyl pyrophosphate synthase geranylderanyl pyrophosphate synthase transfergeranyl, similar geranyl
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Rv0808 Rv0957 Rv3276c Rv0803 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381	purF purH purK purL purM purN purQ purT purU interibonu carA carB pyrB pyrC	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycin-amidine synthase II 5'-phosphoribosylformylglycin-amidine synthase I phosphoribosylformylglycin-amidine synthase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II phosphoribosylglycinamide formyltransferase II phosphoribosylglycinamide formyltransferase II comyltetrahydrofolate deformylase carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotase	2. Folic ac Rv2763c Rv2447c Rv3565c Rv3609c Rv3609c Rv3608c Rv1207 Rv0013 Rv1005c Rv0812 3. Lipoate Rv2218 Rv2217 4. Molybdi Rv3109	id dfrA folC folD folE folK folP folP2 folX pabA pabB pabC lipA lipB opterin moaA	dihydrofolate reductase 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	Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0562 Rv0989c Rv3398c Rv2173 Rv3383c Rv0534c Rv0548c	ggtB gorA thiX trxA trxB trxB2 trxC quinone, P dxs grcC1 grcC2 idsA idsA2 idsB menA menB	y -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin (QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase granylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase naphthoate synthase
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Rv0808 Rv0957 Rv3276c Rv0803 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381	purF purH purK purL purM purN purQ purT purU interibonu carA carB pyrB pyrC	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycin-amidine synthase II 5'-phosphoribosylformylglycin-amidine synthase I phosphoribosylformylglycin-amidine synthase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II phosphoribosylglycinamide formyltransferase II phosphoribosylglycinamide formyltransferase II comyltetrahydrofolate deformylase carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotase	2. Folic ac Rv2763c Rv2447c Rv3565c Rv3609c Rv3609c Rv3608c Rv1207 Rv0013 Rv1005c Rv0812 3. Lipoate Rv2218 Rv2217 4. Molybdi Rv3109	id dfrA folC folD folE folK folP folP2 folX pabA pabB pabC lipA lipB opterin moaA	dihydrofolate reductase 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	Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0562 Rv0989c Rv3398c Rv2173 Rv3383c Rv0534c Rv0548c	ggtB gorA thiX trxA trxB trxB2 trxC quinone, P dxs grcC1 grcC2 idsA idsA2 idsB menA menB	y -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin (QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase granylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase naphthoate synthase
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Rv0808 Rv0957 Rv3276c Rv0803 Rv0809 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699 Rv2883c	purF purH purK purL purM purN purQ purT purU iine ribonu carA carB pyrB pyrC pyrC pyrF pyrF pyrF pyrF	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase-phosphoribosylaminoimidazole-carboxylase ATPase subunit phosphoribosylformylglycin-amidine synthase II 5'-phosphoribosylformylglycin-amidine synthase II 5'-phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II formyltransferase dihydroorotase dihydroorotase dihydroorotase dihydroorotase dihydroorotase dihydroorotase CTP synthase uridylate kinase	2. Folic ac Rv2763c Rv2447c Rv3356c Rv2447c Rv3609c Rv3609c Rv3607c Rv0013 Rv1005c Rv0013 3. Lipoate Rv2217 4. Molybde Rv3109 Rv0869c	id dfrA folC folD folE folK folP2 folX pabA pabB pabC lipA lipB opterin moaA2	dihydrofolate reductase 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.	Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0562 Rv0989c Rv3398c Rv2173 Rv3383c Rv0534c Rv0534c Rv0553 Rv0555	ggtB gorA thiX trxA trxB trxB2 trxC quinone, P dxs grcC1 grcC2 idsA idsA2 idsB menA menB menC menD	y -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase li heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase cataprenyltransferase naphthoate octaprenyltransferase naphthoate synthase 2-succinylbenzoate-CoA synthase 2-succinyl-6-hydroxy-2,4-cyclo-hexadiene-1-carboxylate synthase o-succinylbenzoate acid-CoA ligase S-adenosylmethionine:
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Rv0808 Rv0957 Rv3276c Rv0803 Rv0809 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699 Rv2883c Rv0382c	purF purH purK purL purM purN purQ purT purU iine ribonu carA carB pyrB pyrC pyrC pyrF pyrF pyrF pyrF	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase-phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycin-amidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II phosphoribosylglycinamide formyltransferase actionamoyl-phosphate synthase subunit aspartate carbamoyl-phosphate synthase uridylate kinase probable uridine 5'-monophosphate synthase otide metabolism	2. Folic ac Rv2763c Rv2447c Rv3565c Rv3609c Rv3609c Rv3607c Rv0013 Rv1005c Rv0812 3. Lipoate Rv2218 Rv2217 4. Molybdr Rv3109 Rv0869c Rv0438c Rv0438c	id dfrA folC folD folE folK folP2 folX pabA pabB pabC lipA lipB opterin moaA2 moaA3 moaB	dihydrofolate reductase 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	Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0562 Rv0989c Rv3398c Rv2173 Rv3383c Rv0534c Rv0553 Rv0555 Rv0542c Rv0542c Rv3853	ggtB gorA thiX trxA trxB2 trxC quinone, P dxs grcC1 grcC2 idsA idsA2 idsB menA menB menC menD menE menG	y -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin (QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase lapetaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase II geranylgeranyl pyrophosphate synthase uransfergeranyl, similar geranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase aphthoate synthase 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase o-succinylbenzoia cid-CoA ligase S-adenosylmethionine: 2-demethylmenaquinone
Rv0808 Rv0957 Rv3276c Rv0803 Rv0809 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699 Rv2883c Rv0382c	purF purH purK purL purM purN purQ purT purU iine ribonu carA carB pyrB pyrC pyrC pyrF pyrF pyrF pyrF	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosyldromylglycin-amidine synthase II 5'-phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II phosphoribosylglycinamide formylterahydrofolate deformyltase Cleotide biosynthesis 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	2. Folic ac Rv2763c Rv2747c Rv33560 Rv3609c Rv3609c Rv3609c Rv3607c Rv0013 Rv1005c Rv0812 3. Lipoate Rv2217 4. Molybdd Rv3109 Rv0869c Rv0438c Rv3110 Rv0984 Rv3111	id dfrA folC folD folE folK folP folP2 folX pabA pabB pabC lipA lipB opterin moaA moaA2 moaA3 moaB moaB2 moaC	dihydrofolate reductase 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 B molybdenum cofactor biosynthesis, protein C	Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menac terpenoids Rv2682c Rv0562 Rv0562 Rv398c Rv2173 Rv3383c Rv0534c Rv0553 Rv0555 Rv0542c Rv3853 Rv3397c	ggtB gorA thiX trxA trxB trxB2 trxC quinone, P dxs grcC1 grcC2 idsA idsA2 idsB menA menB menC menD menE menG phyA	y -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin lade the synthase liseptapenyl diphosphate synthase II peranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase cotalprenyltransferase naphthoate synthase -succinylbenzoate-CoA synthase 2-succinylbenzoate-CoA synthase 2-succinylbenzoate-CoA synthase synthase o-succinylbenzoate-CoA synthase seachensylmethionine: 2-demethylmenaquinone phytoene synthase coenzyme PQQ synthesis protein Eubliquinone/menaquinone biosyn-
Rv0808 Rv0957 Rv3276c Rv0803 Rv0809 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699 Rv2883c Rv0382c	purF purH purK purL purM purN purQ purT purU iine ribonu carA carB pyrB pyrC pyrF pyrF pyrF pyrF pyrF pyrF pyrF pyrH umpA	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase-phosphoribosylaminoimidazole-carboxylase ATPase subunit phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycin-amidine synthase II 5'-phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II formylterahydrofolate deformylase cleotide biosynthase I lomyltransferase II formylterahydrofolate deformylase cleotide biosynthesis carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit carbamoyl-phosphate decarboxylase CTP synthase uridylate kinase probable uridine 5'-monophosphate synthase synthase uridylate kinase probable uridine 5'-monophosphate synthase cotide metabolism deoxycytidine triphosphate deaminase	2. Folic ac Rv2763c Rv2447c Rv3356c Rv2447c Rv3609c Rv3609c Rv1207 Rv3607c Rv0013 Rv1005c Rv0812 3. Lipoate Rv2217 4. Molybd Rv3109 Rv0869c Rv0438c Rv3110 Rv0984	id dfrA folC folD folE folK folP2 folX pabA pabB pabC lipA lipB opterin moaA2 moaA2 moaA3 moaB2	dihydrofolate reductase 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 B molybdenum cofactor biosynthesis, protein C molybdenum cofactor biosynthesis	Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menacterpenoids Rv2682c Rv0562 Rv0562 Rv0562 Rv398c Rv2173 Rv3383c Rv0534c Rv0553 Rv0555 Rv0542c Rv3853 Rv397c Rv0693	ggtB gorA thiX trxB trxB2 trxC quinone, P dxs grcC1 grcC2 idsA idsA2 idsB menA menB menC menD menE menG phyA pqqE	y -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and ther 1-deoxy-D-xylulose 5-phosphate synthase lineptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase II geranylgeranyl pyrophosphate synthase II geranylgeranyl pyrophosphate synthase II geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase aphthoate synthase 2-succinyl6-hydroxy-2,4-cyclohexadilene-1-carboxylate synthase o-succinylbenzoic acid-CoA ligase S-adenosylmethionine: 2-demethylmenaquinone phytoene synthase coenzyme PQQ synthesis protein E
Rv0808 Rv0957 Rv3276c Rv0803 Rv0809 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699 Rv2883c Rv0382c 3. 2'-deox; Rv0321 Rv2697c	purF purH purK purL purM purN purQ purT purU iine ribonu carA carB pyrB pyrC pyrD pyrF pyrG pyrH umpA yribonucle dcd dut	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase-phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycin-amidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II phosphoribosylglycinamide formyltransferase actionyltransferase 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 deaminase deoxyuridine triphosphatase	2. Folic ac Rv2763c Rv2747c Rv3566c Rv3609c Rv3609c Rv3609c Rv3607c Rv0013 Rv1005c Rv0812 3. Lipoate Rv2218 Rv2217 4. Molybdr Rv3109 Rv0438c Rv0438c Rv3110 Rv0984 Rv3111	id dfrA folC folD folE folK folP2 folX pabA pabB pabC lipA lipB opterin moaA2 moaA2 moaB2 moaB2 moaC2	dihydrofolate reductase 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 B molybdenum cofactor biosynthesis, protein C	Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menacterpenoids Rv2682c Rv0562 Rv0562 Rv398c Rv2173 Rv3383c Rv2173 Rv3383c Rv0553 Rv0555 Rv0542c Rv3853 Rv397c Rv0693 Rv0588	ggtB gorA thiX trxB trxB2 trxC quinone, P dxs grcC1 grcC2 idsA idsA2 idsB menA menB menC menD menE menG phyA pqqE ubiE	y -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX 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 geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase aphthoate synthase 2-succinylbenzoate-CoA synthase 2-succinylbenzoate-CoA synthase 2-succinylbenzoic acid-CoA ligase S-adenosylmethionine: 2-demethylmenaquinone phytoene synthase coenzyme PQQ synthesis protein E ubiquinone/menaquinone biosynthesis methyltransferase
Rv0808 Rv0957 Rv3276c Rv0803 Rv0809 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699 Rv2883c Rv0382c	purF purH purK purL purM purN purQ purT purU iine ribonu carA carB pyrB pyrC pyrF pyrF pyrF pyrF pyrF pyrF pyrF pyrH umpA	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase-phosphoribosylaminoimidazole-carboxylase ATPase subunit phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycin-amidine synthase II 5'-phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II formylterahydrofolate deformylase cleotide biosynthase I lomyltransferase II formylterahydrofolate deformylase cleotide biosynthesis carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit carbamoyl-phosphate decarboxylase CTP synthase uridylate kinase probable uridine 5'-monophosphate synthase synthase uridylate kinase probable uridine 5'-monophosphate synthase cotide metabolism deoxycytidine triphosphate deaminase	2. Folic ac Rv2763c Rv2747c Rv33560 Rv3609c Rv3609c Rv3609c Rv3607c Rv0013 Rv1005c Rv0812 3. Lipoate Rv2217 4. Molybdd Rv3109 Rv0869c Rv0438c Rv3110 Rv0984 Rv3111	id dfrA folC folD folE folK folP folP2 folX pabA pabB pabC lipA lipB opterin moaA moaA2 moaA3 moaB moaB2 moaC	dihydrofolate reductase 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 B molybdenum cofactor biosynthesis, protein C molybdenum cofactor biosynthesis	Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menacterpenoids Rv2682c Rv0562 Rv0562 Rv0562 Rv398c Rv2173 Rv3383c Rv0534c Rv0553 Rv0555 Rv0542c Rv3853 Rv397c Rv0693	ggtB gorA thiX trxB trxB2 trxC quinone, P dxs grcC1 grcC2 idsA idsA2 idsB menA menB menC menD menE menG phyA pqqE ubiE	y -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX 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 geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase aphthoate synthase 2-succinylbenzoate-CoA synthase 2-succinylbenzoate-CoA synthase 2-succinylbenzoic acid-CoA ligase S-adenosylmethionine: 2-demethylmenaquinone phytoene synthase coenzyme PQQ synthesis protein E ubiquinone/menaquinone biosynthesis methyltransferase
Rv0808 Rv0957 Rv3276c Rv0803 Rv0809 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699 Rv2883c Rv0382c 3. 2'-deox; Rv0321 Rv2697c	purF purH purK purL purM purN purQ purT purU iine ribonu carA carB pyrB pyrC pyrD pyrF pyrG pyrH umpA yribonucle dcd dut	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase-phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycin-amidine synthase II 5'-phosphoribosyl-5-aminoimidazole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II phosphoribosylglycinamide subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxylase II phosphate uridine 5'-monophosphate synthase otide metabolism deoxycytidine triphosphate deaminase deoxyuridine triphosphate ribonucleoside-diphosphate	2. Folic ac Rv2763c Rv2747c Rv3566c Rv3609c Rv3609c Rv3609c Rv3607c Rv0013 Rv1005c Rv0812 3. Lipoate Rv2218 Rv2217 4. Molybdr Rv3109 Rv0438c Rv0438c Rv3110 Rv0984 Rv3111	id dfrA folC folD folE folK folP2 folX pabA pabB pabC lipA lipB opterin moaA2 moaA2 moaB2 moaB2 moaC2	dihydrofolate reductase 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 B molybdenum cofactor biosynthesis, protein B molybdenum cofactor biosynthesis, protein B molybdenum cofactor biosynthesis, protein C molybdopterin converting factor	Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menacterpenoids Rv2682c Rv0562 Rv0562 Rv0562 Rv398c Rv2173 Rv3383c Rv0534c Rv0553 Rv0555 Rv0548c Rv0553 Rv0555	ggtB gorA thiX trxB trxB2 trxC quinone, P dxs grcC1 grcC2 idsA idsA2 idsB menA menB menC menD menE menG phyA pqqE ubiE and porph hemA hemB	y -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin (QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase II septaprenyl diphosphate synthase II geranylgeranyl gyrophosphate 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-succinyl-6-hydroxy-2,4-cyclo-hexadiene-1-carboxylate synthase o-succinylbenzoic acid-CoA ligase S-adenosylmethionine: 2-demethylmenaquinone phytoene synthase coenzyme PQQ synthesis protein E ubiquinone/menaquinone biosynthesis methyltransferase nyrin glutamyl-tRNA reductase 8-aminolevulinic acid dehydratase
Rv0808 Rv0957 Rv3276c Rv0803 Rv0809 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699 Rv2883c Rv0382c 3. 2'-deox; Rv0321 Rv2697c Rv0233	purF purH purK purL purM purN purQ purT purU iine ribonu carA carB pyrB pyrC pyrD pyrF pyrG pyrH umpA yribonucle dcd dut nrdB nrdE	phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase-phosphoribosylaminoimidazole-carboxylase ATPase subunit phosphoribosylformylglycin-amidine synthase II 5'-phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II phosphoribosylglycinamide formyltransferase II phosphoribosylglycinamide formyltransferase II formyltetrahydrofolate deformylase cleotide biosynthesis carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit carbamoyl-phosphate decarboxylase cTP synthase uridylate kinase probable uridine 5'-monophosphate synthase uridylate kinase probable uridine 5'-monophosphate synthase deoxycytidine triphosphate deaminase deoxyuridine triphosphate reductase B2 (eukaryotic-like)	2. Folic ac Rv2763c Rv2447c Rv3356c Rv2447c Rv3609c Rv3609c Rv3609c Rv1207 Rv3607c Rv0013 Rv1005c Rv0812 3. Lipoate Rv2217 4. Molybdd Rv3109 Rv0869c Rv0438c Rv3110 Rv0984 Rv3111 Rv0864 Rv3324c	id dfrA folC folD folE folK folP folP2 folX pabA pabB pabC lipA lipB opterin moaA2 moaA2 moaA2 moaB2 moaC2 moaC3	dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehydrogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase 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 molybdenum cofactor biosynthesis, protein C molybdenum cofactor biosynthesis, protein C	Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menacterpenoids Rv2682c Rv0562 Rv0989c Rv3398c Rv2173 Rv3383c Rv0553 Rv0555 Rv0542c Rv3555 Rv0558 Rv0558 Rv397c Rv0693 Rv397c Rv0693	ggtB gorA thiX trxB trxB2 trxC quinone, P dxs grcC1 grcC2 idsA idsA2 idsB menA menB menC menD menE menG phyA pqqE ubiE and porph hemA	y -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> 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 lapetaprenyl diphosphate synthase II peranylgeranyl pyrophosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase cataprenyltransferase notaprenyltransferase naphthoate octaprenyltransferase as o-succinylbenzoate-CoA synthase c-succinylbenzoate-CoA ligase S-adenosylmethionine: 2-demethylmenaquinone phytoene synthase coenzyme PQQ synthesis protein E ubiquinone/menaquinone biosynthesis methyltransferase

Rv1300	hemK	protoporphyrinogen oxidase	Rv0470	c 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		olipid synthe		Rv2935	ppsE	phenolpthiocerol synthesis (pksF)
Rv2677c	hemY'	protoporphyrinogen oxidase ferrochelatase	Rv2289	edh cdh	CDP-diacylglycerol phosphatidyl- hydrolase	Rv2928	tesA -	thioesterase
Rv1485	hemZ	ierrocheialase	Rv288	Ic cdsA	phosphatidate cytidylyltransferase	Rv1544	-	probable ketoacyl reductase
13. Cobala	amin		Rv3804		antigen 85A, mycolyltransferase	J. Broad r	equilatory	functions
Rv2849c	cobA	cob(I)alamin adenosyltransferase	Rv1886		antigen 85B, mycolyltransferase	1. Repres		
Rv2848c	cobB	cobyrinic acid a,c-diamide	Rv3803		antigen 85C, mycolyltransferase	Rv1657	argR	arginine repressor
		synthase	Rv0129	c fbpC2	antigen 85C', mycolytransferase	Rv1267c	embR	regulator of embAB genes
Rv2231c	cobC	aminotransferase	Rv0564	tc gpdA1	glycerol-3-phosphate dehydroge-			(AfsR/DndI/RedD family)
Rv2236c	cobD	cobinamide synthase			nase	Rv1909c	furA	ferric uptake regulatory protein
Rv2064	cobG	percorrin reductase	Rv2982	2c gpdA2	glycerol-3-phosphate dehydroge-	Rv2359	furB	ferric uptake regulatory protein
Rv2065	cobH	precorrin isomerase	D. 001	1	nase	Rv2919c Rv2711	glnB	nitrogen regulatory protein
Rv2066	cobl cobK	Cobl-CobJ fusion protein precorrin reductase	Rv2612	2c pgsA	CDP-diacylglycerol-glycerol-3-	Rv2711 Rv2720	ideR IexA	iron dependent repressor, IdeR
Rv2070c Rv2072c	cobL	probable methyltransferase			phosphate phosphatidyltrans- ferase	Rv1479	moxR	LexA, SOS repressor protein transcriptional regulator, MoxR
Rv2072c	cobL	precorrin-3 methylase	Rv1822	2 pgsA2	CDP-diacylglycerol-glycerol-3-	HV14/3	IIIOXI	homologue
Rv2062c	cobN	cobalt insertion	1111022	- pg0/12	phosphate phosphatidyltrans-	Rv3692	moxR2	transcriptional regulator, MoxR
Rv2208	cobS	cobalamin (5'-phosphate)			ferase			homologue
		synthase	Rv2746	Sc 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 E.coli NadR
Rv0254c	cobU	cobinamide kinase	Rv155	l plsB1	glycerol-3-phosphate acyltrans-	Rv0117	oxyS	transcriptional regulator (LysR
Rv0255c	cobQ	cobyric acid synthase	D. 0 400	n- =/=D0	ferase	D. 1070		family)
Rv3713 Rv0306	cobQ2 -	possible cobyric acid synthase similar to BluB cobalamin synthe-	Rv2482	2c plsB2	glycerol-3-phosphate acyltrans- ferase	Rv1379	pyrR	regulatory protein pyrimidine biosynthesis
HV0300	-	sis protein <i>R. capsulatus</i>	Rv0437	c psd	putative phosphatidylserine	Rv2788	sirR	iron-dependent transcriptional
		olo protoni i i. oapodiatao	1110-101	o pou	decarboxylase	1102700	OII I	repressor
14. Iron ut	ilization		Rv0436	Sc pssA	CDP-diacylglycerol-serine	Rv3082c	virS	putative virulence regulating
Rv1876	bfrA	bacterioferritin		•	o-phosphatidyltransferase			protein (AraC/XyIS family)
Rv3841	bfrB	bacterioferritin	Rv0048	5c -	possible dihydrolipoamide acetyl-	Rv3219	whiB1	WhiB transcriptional activator
Rv3215	entC	probable isochorismate synthase			transferase			homologue
Rv3214	entD	weak similarity to many phospho-	Rv0914		lipid transfer protein	Rv3260c	whiB2	WhiB transcriptional activator
		glycerate mutases	Rv1543		probable fatty-acyl CoA reductase			homologue
Rv2895c	viuB	similar to proteins involved in	Rv1627		lipid carrier protein	Rv3416	whiB3	WhiB transcriptional activator
Rv3525c	_	vibriobactin uptake similar to ferripyochelin binding	Rv1814 Rv1867		possible C-5 sterol desaturase similar to acetyl CoA	Rv3681c	whiB4	homologue WhiB transcriptional activator
NV3525C	-	protein	TV 100	-	synthase/lipid carriers	NV30010	WIIID4	homologue
		protein	Rv226	lc -	apolipoprotein N-acyltrans-	Rv0023	_	putative transcriptional regulator
H. Lipid bi	osvnthesis	3	111220		ferase-a	Rv0043c	_	transcriptional regulator (GntR
		and mycolic acids	Rv2262	2c -	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 Polyl	rotido and no	on-ribosomal peptide synthesis	Rv0081	-	transcriptional regulator (ArsR family)
Rv3280	accD5	acetyl/propionyl CoA carboxylase	Rv2940		mycocerosic acid synthase	Rv0135c	_	putative transcriptional regulator
1110200	иоодо	β subunit	Rv2384		mycobactin/exochelin synthesis	Rv0144	_	putative transcriptional regulator
Rv2247	accD6	acetyl/propionyl CoA carboxylase	()5		(salicylate-AMP ligase)	Rv0158	-	transcriptional regulator
		β subunit	Rv2383	Bc mbtB	mycobactin/exochelin synthesis			(TetR/AcrR family)
Rv2244	асрМ	acyl carrier protein (meromycolate			(serine/threonine ligation)	Rv0165c	-	transcriptional regulator (GntR
		extension)	Rv2382		mycobactin/exochelin synthesis			family)
Rv2523c	acpS	CoA:apo-[ACP] pantethienephos-	Rv238	Ic mbtD	mycobactin/exochelin synthesis	Rv0195	-	transcriptional regulator
D. 0040	6-6D	photransferase	D.,000)b4F	(polyketide synthase)	D. 0100		(LuxR/UhpA family)
Rv2243 Rv0649	fabD fabD2	malonyl CoA-[ACP] transacylase malonyl CoA-[ACP] transacylase	Rv2380	c mbtE	mycobactin/exochelin synthesis (lysine ligation)	Rv0196	-	transcriptional regulator (TetR/AcrR family)
Rv1483	fabG1	3-oxoacyl-[ACP] reductase (aka	Rv2379	e mbtF	mycobactin/exochelin synthesis	Rv0232	_	transcriptional regulator
1111400	abar	MabA)	111207	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	(lysine ligation)	1110202		(TetR/AcrR family)
Rv1350	fabG2	3-oxoacyl-[ACP] Reductase	Rv2378	Bc mbtG	mycobactin/exochelin synthesis	Rv0238	-	transcriptional regulator
Rv2002	fabG3	3-oxoacyl-[ACP] reductase			(lysine hydroxylase)			(TetR/AcrR family)
Rv0242c	fabG4	3-oxoacyl-[ACP] reductase	Rv2377	c mbtH	mycobactin/exochelin synthesis	Rv0273c	-	putative transcriptional regulator
Rv2766c	fabG5	3-oxoacyl-[ACP] reductase	Rv010	l nrp	unknown non-ribosomal peptide	Rv0302	-	transcriptional regulator
Rv0533c	fabH	β-ketoacyl-ACP synthase III			synthase			(TetR/AcrR family)
Rv2524c	fas	fatty acid synthase	Rv1153		PKS o-methyltransferase	Rv0324	-	putative transcriptional regulator transcriptional regulator
Rv1484 Rv2245	inhA kasA	enoyl-[ACP] reductase β-ketoacyl-ACP synthase	Rv3824	tc papA1	PKS-associated protein, unknown function	Rv0328	-	(TetR/AcrR family)
1102243	Rash	(meromycolate extension)	Rv3820	c papA2	PKS-associated protein, unknown	Rv0348	-	putative transcriptional regulator
Rv2246	kasB	β-ketoacyl-ACP synthase		. papite	function	Rv0377	-	transcriptional regulator (LysR
		(meromycolate extension)	Rv1182	2 papA3	PKS-associated protein, unknown			family)
Rv1618	tesB1	thioesterase II			function	Rv0386	-	transcriptional regulator
Rv2605c	tesB2	thioesterase II	Rv1528	3c 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	D. 00 4/	Sa mlind	function	D: :0470a		(PbsX/Xre family)
Rv3221c Rv3472	-	resembles biotin carboxyl carrier possible acyl carrier protein	Rv2946 Rv1660		polyketide synthase polyketide synthase (chalcone	Rv0472c	-	transcriptional regulator (TetR/AcrR family)
NV34/2	-	possible acyl carrier protein	LV 1000) pks10	synthase-like)	Rv0474	_	transcriptional regulator
2 Modifica	ation of fat	ty and mycolic acids	Rv166	5 pks11	polyketide synthase (chalcone	1100-77-7		(PbsX/Xre family)
Rv3391	acrA1	fatty acyl-CoA reductase		, , , , , ,	synthase-like)	Rv0485	-	transcriptional regulator (ROK
Rv3392c	cmaA1	cyclopropane mycolic acid	Rv2048	Bc pks12	polyketide synthase (erythronolide			family)
		synthase 1	_		synthase-like)	Rv0494	-	transcriptional regulator (GntR
Rv0503c	cmaA2	cyclopropane mycolic acid syn-	Rv3800		polyketide synthase	D. 0===		family)
D: 2000 f	4	thase 2	Rv1342	2c pks14	polyketide synthase (chalcone	Rv0552	-	putative transcriptional regulator
Rv0824c	desA1	acyl-[ACP] desaturase	D:-004	70 0115	synthase-like)	Rv0576	-	putative transcriptional regulator
Rv1094	desA2	acyl-[ACP] desaturase	Rv2947		polyketide synthase	Rv0586	-	transcriptional regulator (GntR
Rv3229c	desA3	acyl-[ACP] desaturase	Rv1013		polyketide synthase	Dyneso	_	family)
Rv0645c	mmaA1 mmaA2	methoxymycolic acid synthase 1 methoxymycolic acid synthase 2	Rv1660 Rv1372		polyketide synthase	Rv0650	-	transcriptional regulator (ROK
Rv0644c Rv0643c	mmaA2 mmaA3	methoxymycolic acid synthase 3	Rv3825		polyketide synthase polyketide synthase	Rv0653c	-	family) putative transcriptional regulator
Rv0643c Rv0642c	mmaA4	methoxymycolic acid synthase 4	Rv1180		polyketide synthase	Rv0681	-	transcriptional regulator
Rv0447c	ufaA1	unknown fatty acid methyltrans-	Rv118		polyketide synthase			(TetR/AcrR family)
		ferase	Rv1527		polyketide synthase	Rv0691c	-	transcriptional regulator
Rv3538	ufaA2	unknown fatty acid methyltrans-	Rv0408	pks6	polyketide synthase			(TetR/AcrR family)
		ferase	Rv166	l pks7	polyketide synthase	Rv0737	-	putative transcriptional regulator
Rv0469	umaA1	unknown mycolic acid methyl-	Rv1662		polyketide synthase	Rv0744c	-	putative transcriptional regulator
		transferase	Rv1664	1 pks9	polyketide synthase	Rv0792c	-	transcriptional regulator (GntR

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				D 0400						
	Dunggg	_	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 0001		(TetR/AcrR family)			netabolism	
	Rv1019	-	transcriptional regulator	Rv3291c	-	transcriptional regulator	A. Synthesis and modification of macromolecules			
	Rv1049	_	(TetR/AcrR family) transcriptional regulator (MarR	Rv3295	_	(Lrp/AsnC family) transcriptional regulator	Rv3420c	riml	synthesis and modification ribosomal protein S18 acetyl	
	101043	_	family)	1100233	_	(TetR/AcrR family)	HV3420C	111111	transferase	
	Rv1129c	_	transcriptional regulator	Rv3334	-	transcriptional regulator (MerR	Rv0995	rimJ	acetylation of 30S S5 subunit	
			(PbsX/Xre family)			family)	Rv0641	rpIA	50S ribosomal protein L1	
- 1	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.:1107a		family)	Rv3557c	-	transcriptional regulator (TetR/AcrR family)	Rv0702	rpID	50S ribosomal protein L4	
	Rv1167c Rv1219c	-	putative transcriptional regulator putative transcriptional regulator	Rv3574	_	transcriptional regulator	Rv0716 Rv0719	rpIE rpIF	50S ribosomal protein L5 50S ribosomal protein L6	
		-	transcriptional regulator	1100074		(TetR/AcrR family)	Rv0056	rpll	50S ribosomal protein L9	
			(TetR/AcrR family)	Rv3575c	-	transcriptional regulator (Lacl	Rv0651	rplJ	50S ribosomal protein L10	
	Rv1332	-	putative transcriptional regulator			family)	Rv0640	rpIK	50S ribosomal protein L11	
-	Rv1353c	-	transcriptional regulator	Rv3583c	-	putative transcriptional regulator	Rv0652	rpIL	50S ribosomal protein L7/L12	
	D. 1050	_	(TetR/AcrR family)	Rv3676	-	transcriptional regulator (Crp/Fnr	Rv3443c	rpIM	50S ribosomal protein L13	
	Rv1358	-	transcriptional regulator (LuxR/UhpA family)	Rv3678c	_	family) transcriptional regulator (LysR	Rv0714 Rv0723	rpIN rpIO	50S ribosomal protein L14 50S ribosomal protein L15	
-	Rv1359	_	putative transcriptional regulator	1100700		family)	Rv0708	rpIP	50S ribosomal protein L16	
	Rv1395	-	transcriptional regulator	Rv3736	-	transcriptional regulator	Rv3456c	rpIQ	50S ribosomal protein L17	
			(AraC/XyIS family)			(AraC/XyIS family)	Rv0720	rpIR	50S ribosomal protein L18	
- 1	Rv1404	-	transcriptional regulator (MarR	Rv3744	-	transcriptional regulator (ArsR	Rv2904c	rpIS	50S ribosomal protein L19	
	D1 400		family)	Dv2020a		family)	Rv1643	rpIT	50S ribosomal protein L20	
	Rv1423 Rv1460	-	putative transcriptional regulator putative transcriptional regulator	Rv3830c	-	transcriptional regulator (TetR/AcrR family)	Rv2442c Rv0706	rpIU rpIV	50S ribosomal protein L21 50S ribosomal protein L22	
		-	transcriptional regulator	Rv3833	-	transcriptional regulator	Rv0703	rpIV rpIW	50S ribosomal protein L23	
			(TetR/AcrR family)			(AraC/XyIS family)	Rv0715	rpIX	50S ribosomal protein L24	
- 1	Rv1534	-	transcriptional regulator	Rv3840	-	putative transcriptional regulator	Rv1015c	rpIY	50S ribosomal protein L25	
			(TetR/AcrR family)	Rv3855	-	putative transcriptional regulator	Rv2441c	rpmA	50S ribosomal protein L27	
	Rv1556	-	putative transcriptional regulator	O T			Rv0105c	rpmB	50S ribosomal protein L28	
		-	putative transcriptional regulator	2. Two cor Rv1028c	mponent s <i>kdpD</i>	sensor histidine kinase	Rv2058c Rv0709	rpmB2 rpmC	50S ribosomal protein L28 50S ribosomal protein L29	
		-	putative transcriptional regulator transcriptional regulator (IcIR	Rv10260	kdpE	two-component response	Rv0722	rpmD	50S ribosomal protein L30	
	1111110		family)	11010276	KupL	regulator	Rv1298	rpmE	50S ribosomal protein L31	
-	Rv1773c	-	transcriptional regulator (IcIR	Rv3246c	mtrA	two-component response	Rv2057c	rpmG	50S ribosomal protein L33	
			family)			regulator	Rv3924c	rpmH	50S ribosomal protein L34	
		-	putative transcriptional regulator	Rv3245c	mtrB	sensor histidine kinase	Rv1642	rpml .	50S ribosomal protein L35	
	Rv1816 Rv1846c	-	putative transcriptional regulator	Rv0844c	narL	two-component response	Rv3461c Rv1630	rpmJ	50S ribosomal protein L36	
	Rv1931c		putative transcriptional regulator transcriptional regulator	Rv0757	phoP	regulator two-component response	Rv2890c	rpsA rpsB	30S ribosomal protein S1 30S ribosomal protein S2	
	10010		(AraC/XyIS family)	1100707	prior	regulator	Rv0707	rpsC	30S ribosomal protein S3	
- 1	Rv1956	-	putative transcriptional regulator	Rv0758	phoR	sensor histidine kinase	Rv3458c	rpsD	30S ribosomal protein S4	
		-	putative transcriptional regulator	Rv0491	regX3	two-component response	Rv0721	rpsE	30S ribosomal protein S5	
-	Rv1985c	-	transcriptional regulator (LysR	<u></u>		regulator	Rv0053	rpsF	30S ribosomal protein S6	
	D. 4000-		family)	Rv0490	senX3	sensor histidine kinase	Rv0683	rpsG	30S ribosomal protein S7	
		-	putative transcriptional regulator transcriptional regulator (MerR	Rv0602c	tcrA	two-component response regulator	Rv0718 Rv3442c	rpsH rpsI	30S ribosomal protein S8 30S ribosomal protein S9	
	1013340	-	family)	Rv0260c	_	two-component response	Rv0700	rpsJ	30S ribosomal protein S10	
-	Rv2017	-	putative transcriptional regulator			regulator	Rv3459c	rpsK	30S ribosomal protein S11	
			(PbsX/Xre family)	Rv0600c	-	sensor histidine kinase	Rv0682	rpsL	30S ribosomal protein S12	
	Rv2021c	-	putative transcriptional regulator	Rv0601c	-	sensor histidine kinase	Rv3460c	rpsM	30S ribosomal protein S13	
- 1	Rv2034	-	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	
		_	putative transcriptional regulator	Rv0902c	-	sensor histidine kinase	Rv2909c	rpsP	30S ribosomal protein S16	
			putative transcriptional regulator	Rv0903c	-	two-component response	Rv0710	rpsQ	30S ribosomal protein S17	
	Rv2282c		transcriptional regulator (LysR			regulator	Rv0055	rpsR	30S ribosomal protein S18	
			family)	Rv0981	-	two-component response	Rv2055c	rpsR2	30S ribosomal protein S18	
	Rv2308	-	putative transcriptional regulator	D.,0000		regulator	Rv0705	rpsS	30S ribosomal protein S19	
1	Rv2324	-	transcriptional regulator (Lrp/AsnC family)	Rv0982 Rv1032c	-	sensor histidine kinase sensor histidine kinase	Rv2412 Rv3241c	rpsT -	30S ribosomal protein S20 member of S30AE ribosomal	
- 1	Rv2358	_	transcriptional regulator (ArsR		-	two-component response	11102-110		protein family	
			family)			regulator			•	
- 1	Rv2488c	-	transcriptional regulator	Rv1626	-	two-component response			ation and maturation	
			(LuxR/UhpA family)			regulator	Rv1010	ksgA	16S rRNA dimethyltransferase	
	Rv2506	-	transcriptional regulator (TetR/AcrR family)	Rv2027c Rv2884	-	sensor histidine kinase	Rv2838c Rv2907c	rbfA rimM	ribosome-binding factor A 16S rRNA processing protein	
	Rv2621c	_	putative transcriptional regulator	HV2884	-	two-component response regulator	HV29070	rirnivi	165 TRINA processing protein	
		-	transcriptional regulator (ArsR	Rv3132c	-	sensor histidine kinase	3. Aminoa	cyl tRNA s	synthases and their modification	
			family)	Rv3133c	-	two-component response	Rv2555c	alaS	alanyl-tRNA synthase	
- 1	Rv2642	-	transcriptional regulator (ArsR			regulator	Rv1292	argS	arginyl-tRNA synthase	
			family)	Rv3143	-	putative sensory transduction	Rv2572c	aspS	aspartyl-tRNA synthase	
	Rv2669 Rv2745c	-	putative transcriptional regulator putative transcriptional regulator	Dygggg	-	protein	Rv3580c	cysS	cysteinyl-tRNA synthase	
	Rv27430		transcriptional regulator	Rv3220c Rv3764c	-	sensor histidine kinase sensor histidine kinase	Rv2130c Rv1406	cysS2 fmt	cysteinyl-tRNA synthase methionyl-tRNA formyltransferase	
			(Lrp/AsnC family)	Rv3765c	-	two-component response	Rv3011c	gatA	glu-tRNA-gln amidotransferase,	
-	Rv2887	-	transcriptional regulator (MarR			regulator		-	subunit B	
			family)			•	Rv3009c	gatB	glu-tRNA-gln amidotransferase,	
- 1	Rv2912c	-	transcriptional regulator			protein kinases and phosphoprotein	.		subunit A	
	Dygoon		(TetR/AcrR family)	phosphata		caring through a metals library	Rv3012c	gatC	glu-tRNA-gln amidotransferase,	
	Rv2989	-	transcriptional regulator (IcIR family)	Rv0015c Rv0014c	pknA pknB	serine-threonine protein kinase serine-threonine protein kinase	Rv2992c	gltS	subunit C glutamyl-tRNA synthase	
1	Rv3050c	_	putative transcriptional regulator	Rv00140 Rv0931c	ркпБ pknD	serine-threonine protein kinase serine-threonine protein kinase	Rv29920 Rv2357c	gilS glyS	glycyl-tRNA synthase	
	Rv3055	-	putative transcriptional regulator	Rv1743	pknE	serine-threonine protein kinase	Rv2580c	hisS	histidyl-tRNA synthase	
- 1	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	
	Duance		family)	Rv1266c	pknH	serine-threonine protein kinase	Rv3598c	lysS	lysyl-tRNA synthase	
	Rv3066 Rv3095	-	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	
	Rv3124	_	transcriptional regulator	Rv2088 Rv3080c	pkni pknK	serine-threonine protein kinase serine-threonine protein kinase	Rv1649	pheS	phenylalanyl-tRNA synthase α	
			(AfsR/Dndl/RedD family)	Rv2176	pknL	serine-threonine protein kinase,		٥٥	subunit	
			••							

Rv1650	pheT	phenylalanyl-tRNA synthase β	Rv2090	-	partially similar to DNA poly-	2. DNA		
Rv2845c	proS	subunit	Rv2191	_	merase I similar to both PolC 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 tension and an about	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 later and describe and a 101		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 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	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 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	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 lipL 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 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 hydrolase probable lipase probable lipase probable lipase probable esterase probable acetyl-hydrolase esterase 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 RecBC-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 lipQ lipQ	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 oxodeoxyribonuclease V exodeoxyribonuclease V exodeoxyri	Rv1221 Rv3286c Rv0182c Rv3223c Rv1189 Rv3328c Rv0445c Rv0735 Rv3911 Rv3366 Rv3455c Rv2793c Rv1644 Rv3649	sigF sigG sigH sigJ sigJ 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 carboxlyesterase probable carboxlyesterase probable esterase/lipase probable carboxylesterase probable carboxylesterase probable esterase/lipase probable carboxylesterase probable carboxylesterase
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 Rv203203	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 lesterase probable lipase
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Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv0003 Rv2973c Rv1696 Rv3715c Rv2736c Rv2593c Rv2594c Rv0054 Rv1210 Rv3646c Rv2976c Rv1638 Rv1633 Rv1633 Rv1633 Rv1634 Rv163	polA priA radA recA recB recC recB recF recR recR recR recA ruvA ruvB ruvC ssb tagA topA uvrB 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 DNA replication and SOS induction and SOS induction and DNA repair RecBC-Independent DNA helicase recombination and DNA repair regulatory protein for RecA Holliday junction binding protein, DNA helicase Holliday junction binding protein, DNA helicase single strand binding protein Holliday junction resolvase, endodeoxyribonuclease single strand binding protein DNA-3-methyladenine glycosidase I DNA topoisomerase uracii-DNA glycosylase excinuclease ABC subunit A excinuclease ABC subunit A excinuclease ABC subunit C DNA-dependent ATPase I and helicase III putative UvrD exodeoxyribonuclease III	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 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 exprobable 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 Rv1490c Rv1990c Rv1990c Rv2385 Rv1497 Rv2284 Rv2970c Rv1426c Rv2463 Rv2485c Rv2045c Rv1076 Rv3203 Rv0217c Rv2350c Rv2350c Rv10755c Rv1105 Rv1105 Rv1105 Rv1105 Rv1105 Rv1105 Rv1105 Rv1105 Rv1105 Rv1105 Rv1105 Rv1105 Rv1469c	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 probable probable probable probable probable probable probable probable esterase probable esterase probable esterase probable esterase probable esterase probable procursor phospholipase C precursor partial CDS for phospholipase C probable esterase pseudogene probable esterase pseudogene
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Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv0003 Rv29973c Rv1696 Rv2736c Rv2593c Rv2592c Rv2594c Rv0054 Rv1638 Rv1638 Rv1633 Rv1420 Rv0949 Rv3198c Rv0427c Rv0071	polA priA radA recA recB recC recB recF recR recR recR ruvA ruvB ruvC ssb tagA topA ung uvrA uvrB uvrC uvrD uvrD2 xthA	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 and SOS induction 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 binding protein Holliday junction resolvase, endodeoxyribonuclease single strand binding protein DNA-3-methyladenine glycosidase I DNA topoisomerase uracii-DNA glycosylase excinuclease ABC subunit A excinuclease ABC subunit C DNA-dependent ATPase I and helicase III group II intron maturase probable DNA helicase possible formamidopyrimidine-	Rv1221 Rv3286c Rv0182c Rv3223c Rv1189 Rv3328c Rv0445c Rv0735 Rv3911 Rv3366 Rv3455c Rv2793c Rv1644 Rv3649 8. Polysac Rv1326c Rv1328 Rv1564c Rv1563c Rv1562c Rv0126 Rv1781c Rv2471 B. Degrad 1. RNA Rv1014c Rv2925c Rv2444c Rv2902c	sigF sigG sigH sigH sigH sigH sigK sigK sigK sigL sigM spoU truA truB tsnR - charides (u glgB glgB glgP glgZ - - - - iation of ma	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 grobable rRNA methylase probable pseudouridylate synthase tRNA pseudouridylate synthase tRNA pseudouridylate synthase tRNA pseudouridylate synthase at RNA pseudouridylate synthase tRNA pseudouridylate synthase protable glycogen phoxPlase probable glycogen phosphorylase probable glycogen debranching enzyme putative α-amylase maltooligosyltrehalose trehalohydrolase probable 4-α-glucanotransferase probable maltase α-glucosidase accomolecules peptidyl-tRNA hydrolase RNAse III similar at C-term to ribonuclease Eribonuclease HII	5. Esterase Rv0220 Rv1923 Rv3775 Rv3487c Rv1399c Rv1400c Rv1900c Rv2385 Rv1497 Rv2284 Rv2970c Rv1426c Rv2463 Rv2485c Rv2045c Rv1076 Rv3203 Rv0217c Rv2351c Rv2350c Rv1075 Rv1076 Rv2349c Rv1755c Rv1105 Rv1105 Rv1105 Rv1105 Rv1105 Rv1105 Rv1105 Rv1469c	as and lips lipE lipE lipE lipE lipH lipI lipI lipI lipI lipI lipI lipI lipI	nine amidase ases probable esterase probable esterase probable hydrolase probable hydrolase probable hydrolase probable lipase probable lipase probable lipase probable acetyl-hydrolase esterase probable lipase probable esterase probable carboxylesterase probable esterase partial CDS for phospholipase C probable esterase pseudogene probable esterase pseudogene probable 4-varboxymuconolac-
Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv0003 Rv2973c Rv1696 Rv3715c Rv2593c Rv2593c Rv2594c Rv0054 Rv1103 Rv3646c Rv2976c Rv1638 Rv1633 Rv1420 Rv0949 Rv3198c Rv0427c Rv0071 Rv0861c Rv0944	polA priA radA recA recB recC recC recCN recR recR recX ruvA ruvB ruvC ssb tagA topA ung uvrB uvrC uvrD uvrD2 xthA	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 oxodeoxyribonuclease V exodeoxyribonuclease V oxodeoxyribonuclease V oxodeoxyribonuclease V oxodeoxyribonuclease V oxodeoxyribonuclease V oxodeoxyribonuclease V oxodeoxyribonuclease II putative UvrD exodeoxyribonuclease III group II intron maturase probable DNA helicase possible formamidopyrimidine-DNA glycosylase	Rv1221 Rv3286c Rv0182c Rv3223c Rv1189 Rv3328c Rv0445c Rv0735 Rv3911 Rv3366 Rv3455c Rv2793c Rv1644 Rv3649 8. Polysac Rv1326c Rv1328 Rv1564c Rv1563c Rv1562c Rv1563c Rv1562c Rv1781c Rv2471 B. Degrad 1. RNA Rv1014c Rv2925c Rv2444c	sigF sigG sigH sigJ sigJ sigK sigK sigK sigK sigM spoU truA truB tsnR - charides (i glgB glgP glgZ glgZ - - - ation of ma	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-α-glucan branching enzyme probable glycogen debranching enzyme putative α-amylase maltooligosyltrehalose trehalohydrolase probable alycosyl hydrolase probable maltase α-glucosidase acromolecules peptidyl-tRNA hydrolase RNAse III similar at C-term to ribonuclease E	5. Esterase Rv0220 Rv1923 Rv3775 Rv3487c Rv1490c Rv1490c Rv1490c Rv2385 Rv1497 Rv2284 Rv2970c Rv1426c Rv2463 Rv2485c Rv2045c Rv1076 Rv2045c Rv2045c Rv1076 Rv3203 Rv0217c Rv2351c Rv2350c Rv2349c Rv1104 Rv1105 6. Aromatic Rv3469c Rv0316	es and lipa lipC lipE lipE lipF lipH lipI lipJ lipK lipL lipM lipN lipN lipO lipP lipQ lipP lipP lipQ lipP lipC lipV lipV lipV lipV c lipW c lipW c lipW c lipW c lipC c lipW c l	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 esterase/lipase probable esterase/lipase probable esterase/lipase probable esterase/lipase probable esterase pseudogene probable esterase pseudogene probable 4-hydroxy-2-oxovalerate aldolase probable muconolactone iso- merase probable 4-carboxymuconolac- tone decarboxylase
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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	Dv20770	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>1-lpr0</i>) 65	Rv0507	mmpL2	protein conserved large membrane	Rv0362	mgtE	ATPase protein C putative magnesium ion
2. Surface	polysacch	narides, lipopolysaccharides, pro-	HV0307	mmpLZ	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	ппрсч	protein	Rv2691	trkA	probable potassium uptake pro-
Rv1677	dsbF	highly similar to C-term Mpt53	Rv0676c	mmpL5	conserved large membrane	D. 0000	4-4-0	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-		p20	protein	Rv2287	yjcE	probable Na+/H+ exchanger
Rv3793	embC	thesis	Rv2942	mmpL7	conserved large membrane	Rv2723	-	probable membrane protein, tellurium resistance
HV3/33	embo	involved in arabinogalactan syn- thesis	Rv3823c	mmpL8	protein conserved large membrane	Rv3162c	-	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 probable cation-transporting
Rv0113	gmhA	phosphoheptose isomerase	Rv1183	mmpL10	conserved large membrane	11107 100		ATPase
Rv2965c	kdtB	lipopolysaccharide core biosyn-	D.,0000-		protein	0. Carlaala	. danta a	recuis saids and sleekale
Rv2878c	mpt53	thesis protein secreted protein Mpt53	Rv0202c	mmpL11	conserved large membrane protein	Rv2443	dctA	rganic acids and alcohols C4-dicarboxylate transport protein
Rv1980c	mpt64	secreted immunogenic protein	Rv1522c	mmpL12	conserved large membrane	Rv3476c	kgtP_	sugar transport protein
Rv2875	mpt70	Mpb64/Mpt64 major secreted immunogenic pro-	Rv0403c	mmpS1	protein conserved small membrane	Rv1902c Rv1236	nanT sugA	probable sialic acid transporter membrane protein probably
1102070	mptro	tein Mpt70 precursor	1100-000	mmpor	protein	11/1200	oug/1	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
		protein)			protein	Rv3331	sugl	probable sugar transport protein
Rv3782 Rv1302	rfbE rfe	similar to rhamnosyl transferase undecaprenyl-phosphate α -N-	Rv0451c	mmpS4	conserved small membrane protein	Rv2835c	ugpA	sn-glycerol-3-phosphate permease
HV1302	116	acetylglucosaminyltransferase	Rv0677c	mmpS5	conserved small membrane	Rv2833c	ugpB	sn-glycerol-3-phosphate-binding
Rv2145c	wag31	antigen 84 (aka wag31)		·	protein			periplasmic lipoprotein
Rv0431 Rv0954	-	tuberculin related peptide (AT103) cell envelope antigen	5 Other m	embrane i	proteins 211	Rv2832c	ugpC	sn-glycerol-3-phosphate transport ATP-binding protein
Rv1514c	-	involved in polysaccharide syn-			5.00	Rv2834c	ugpE	sn-glycerol-3-phosphate transport
D.:1510	_	thesis	III. Cell pr			D.:0010		system protein
Rv1518	-	involved in exopolysaccharide synthesis	A. Transpo		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	-	probable secreted protein	Rv1704c	cycA	transport of D-alanine, D-serine	Rv2040c	-	probable sugar transporter
Rv2223c Rv2224c	-	probable exported protease probable exported protease	Rv3666c	dppA	and glycine probable peptide transport system	Rv2041c	-	probable sugar transporter
Rv2301	-	probable cutinase			permease	4. Anions		
Rv2345	-	precursor of probable membrane protein	Rv3665c	dppB	probable peptide transport system permease	Rv2684 Rv2685	arsA arsB	probable arsenical pump probable arsenical pump
Rv2672	-	putative exported protease	Rv3664c	dppC	probable peptide transport system	Rv3578	arsB2	probable arsenical pump
Rv3019c	-	similar to Esat6	D.,0000-	d==D	permease	Rv2643	arsC	probable arsenical pump
Rv3036c Rv3449	-	probable secreted protein probable precursor of serine pro-	Rv3663c Rv0522	dppD gabP	probable ABC-transporter probable 4-amino butyrate trans-	Rv2397c	cysA	sulphate transport ATP-binding protein
D 0454		tease	5		porter	Rv2399c	cysT	sulphate transport system perme-
Rv3451 Rv3452		probable cutinase precursor	Rv0411c Rv2564	glnH glnQ	putative glutamine binding protein probable ATP-binding transport	Rv2398c	cysW	ase protein sulphate transport system perme-
Rv3724	-	probable cutinase precursor		giria	protein		•	ase protein
2 Murain	annoulue a	and peptidoglycan	Rv1280c	oppA	probable oligopeptide transport protein	Rv1857 Rv1858	modA modB	molybdate binding protein
Rv2911	dacB	penicillin binding protein	Rv1283c	оррВ	oligopeptide transport protein	UA 1000	Поив	transport system permease, molybdate uptake
Rv2981c	ddlA	D-alanine-D-alanine ligase A	Rv1282c	oppC	oligopeptide transport system per-	Rv1859	modC	molybdate uptake ABC-
Rv3809c Rv1018c	glf glmU	UDP-galactopyranose mutase UDP-N-acetylglucosamine	Rv1281c	oppD	mease probable peptide transport protein	Rv1860	modD	transporter precursor of Apa (45/47
		pyrophosphorylase	Rv2320c	rocE	arginine/ornithine transporter			kD secreted protein)
Rv3382c Rv1110	lytB lytB'	LytB protein homologue very similar to LytB	Rv3253c	-	probable cationic amino acid transport	Rv2329c Rv1737c	narK1 narK2	probable nitrite extrusion protein nitrite extrusion protein
Rv1315	murA	UDP-N-acetylglucosamine-1-car-	Rv3454	-	possible proline permease	Rv0261c	narK3	nitrite extrusion protein1
D 0400		boxyvinyltransferase				Rv0267	narU	similar to nitrite extrusion
Rv0482		LIDD N analysis and the second of the second						
	murB	UDP-N-acetylenolpyruvoylglu- cosamine reductase	2. Cations By2920c		nutative ammonium transporter	Bv0934	nhoS1	protein 2 PstS component of phosphate
Rv2152c	murB murC	UDP-N-acetylenolpyruvoylglu- 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
	murC	cosamine reductase UDP-N-acetyl-muramate-alanine ligase	Rv2920c	amt	putative calcium/proton antiporter probable magnesium and cobalt	Rv0934 Rv0928	phoS1 phoS2	PstS component of phosphate uptake PstS component of phosphate
Rv2152c Rv2155c		cosamine reductase UDP-N-acetyl-muramate-alanine	Rv2920c Rv1607	amt chaA	putative calcium/proton antiporter		•	PstS component of phosphate uptake
	murC	cosamine reductase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetylmuramoylalanine-D- glutamate ligase meso-diaminopimelate-adding	Rv2920c Rv1607 Rv1239c Rv0092 Rv0103c	amt chaA corA ctpA ctpB	putative calcium/proton antiporter probable magnesium and cobalt transport protein cation-transporting ATPase cation transport ATPase	Rv0928 Rv0820	phoS2 phoT	PstS component of phosphate uptake PstS component of phosphate uptake uptake phosphate transport system ABC transporter
Rv2155c Rv2158c	murC murD murE	cosamine reductase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetylmuramoylalanine-D- glutamate ligase meso-diaminopimelate-adding enzyme	Rv2920c Rv1607 Rv1239c Rv0092 Rv0103c Rv3270	amt chaA corA ctpA ctpB ctpC	putative calcium/proton antiporter probable magnesium and cobalt transport protein cation-transporting ATPase cation transport ATPase cation transport ATPase	Rv0928	phoS2	PstS component of phosphate uptake PstS component of phosphate uptake phosphate transport system ABC transporter phosphate transport system
Rv2155c Rv2158c Rv2157c	murC murD murE murF	cosamine reductase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetylmuramoylalanine-D- glutamate ligase meso-diaminopimelate-adding enzyme D-alanine:D-alanine-adding enzyme	Rv2920c Rv1607 Rv1239c Rv0092 Rv0103c Rv3270 Rv1469	amt chaA corA ctpA ctpB ctpC ctpD	putative calcium/proton antiporter probable magnesium and cobalt transport protein cation-transporting ATPase cation transport ATPase cation transport ATPase cation transport ATPase probable cadmium-transporting ATPase	Rv0928 Rv0820	phoS2 phoT	PstS component of phosphate uptake PstS component of phosphate uptake phosphate transport system ABC transporter phosphate transport system regulator phosphate transport system
Rv2155c Rv2158c	murC murD murE	cosamine reductase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetylmuramoylalanine-D- glutamate ligase meso-diaminopimelate-adding enzyme D-alanine:D-alanine-adding enzyme transferase in peptidoglycan syn-	Rv2920c Rv1607 Rv1239c Rv0092 Rv0103c Rv3270 Rv1469 Rv0908	amt chaA corA ctpA ctpB ctpC ctpD	putative calcium/proton antiporter probable magnesium and cobalt transport protein cation-transporting ATPase cation transport ATPase cation transport ATPase probable cadmium-transporting ATPase probable cation transport ATPase	Rv0928 Rv0820 Rv3301c Rv0821c	phoS2 phoT phoY1 phoY2	PstS component of phosphate uptake PstS component of phosphate uptake phosphate transport system ABC transporter phosphate transport system regulator phosphate transport system regulator
Rv2155c Rv2158c Rv2157c	murC murD murE murF	cosamine reductase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetylmuramoylalanine-D- glutamate ligase meso-diaminopimelate-adding enzyme D-alanine:D-alanine-adding enzyme	Rv2920c Rv1607 Rv1239c Rv0092 Rv0103c Rv3270 Rv1469	amt chaA corA ctpA ctpB ctpC ctpD	putative calcium/proton antiporter probable magnesium and cobalt transport protein cation-transporting ATPase cation transport ATPase cation transport ATPase cation transport ATPase probable cadmium-transporting ATPase	Rv0928 Rv0820 Rv3301c	phoS2 phoT phoY1	PstS component of phosphate uptake PstS component of phosphate uptake phosphate transport system ABC transporter phosphate transport system regulator phosphate transport system
Rv2155c Rv2158c Rv2157c Rv2153c	murC murD murE murF murG	cosamine reductase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetylmuramoylalanine-D- glutamate ligase meso-diaminopimelate-adding enzyme D-alanine:D-alanine-adding enzyme transferase in peptidoglycan synthesis glutamate racemase phospho-N-acetylmuramoyl-	Rv2920c Rv1607 Rv1239c Rv0092 Rv0103c Rv3270 Rv1469 Rv0908 Rv1997	amt chaA corA ctpA ctpB ctpC ctpD ctpE ctpF	putative calcium/proton antiporter probable magnesium and cobalt transport protein cation-transporting ATPase cation transport ATPase cation transport ATPase probable cadmium-transporting ATPase probable cation transport ATPase probable cation transport ATPase probable cation transport ATPase cobable cation transport ATPase cobable cation transport ATPase cobable cation transport ATPase probable cation transport ATPase cobable cation transport ATPase probable cation transport ATPase cobable cation transpo	Rv0928 Rv0820 Rv3301c Rv0821c Rv0545c Rv2281	phoS2 phoT phoY1 phoY2 pitA pitB	PstS component of phosphate uptake PstS component of phosphate uptake phosphate transport system ABC transporter phosphate transport system regulator phosphate transport system regulator low-affinity inorganic phosphate transporter phosphate proposed to the proposed proposed to the proposed
Rv2155c Rv2158c Rv2157c Rv2153c Rv1338 Rv2156c	murC murD murE murF murG murI murX	cosamine reductase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetylmuramoylalanine-D- glutamate ligase meso-diaminopimelate-adding enzyme D-alanine:D-alanine-adding enzyme transferase in peptidoglycan synthesis glutamate racemase phospho-N-acetylmuramoyl- petapeptide transferase	Rv2920c Rv1607 Rv1239c Rv0092 Rv0103c Rv3270 Rv1469 Rv0908 Rv1997 Rv1992c Rv0425c	amt chaA corA ctpA ctpB ctpC ctpD ctpE ctpF ctpG ctpH	putative calcium/proton antiporter probable magnesium and cobalt transport protein cation-transport protein cation-transporting ATPase cation transport ATPase probable cadmium-transporting ATPase probable cation transport ATPase c-terminal region putative cation-transporting ATPase	Rv0928 Rv0820 Rv3301c Rv0821c Rv0545c	phoS2 phoT phoY1 phoY2 pitA	PstS component of phosphate uptake PstS component of phosphate uptake phosphate transport system ABC transporter phosphate transport system regulator phosphate transport system regulator low-affinity inorganic phosphate transporter phosphate transporter phosphate of phosphate permease PstA component of phosphate
Rv2155c Rv2158c Rv2157c Rv2153c Rv1338 Rv2156c Rv3332	murC murD murE murF murG murI murX	cosamine reductase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetylmuramoylalanine-D- glutamate ligase meso-diaminopimelate-adding enzyme D-alanine:D-alanine-adding enzyme transferase in peptidoglycan syn- thesis glutamate racemase phospho-N-acetylmuramoyl- petapeptide transferase N-acetylglucosamine-6-P- deacetylglucosamine-6-P-	Rv2920c Rv1607 Rv1239c Rv0092 Rv0103c Rv3270 Rv1469 Rv0908 Rv1997 Rv1997 Rv1992c Rv0425c	amt chaA corA ctpA ctpB ctpC ctpD ctpE ctpF ctpG ctpH ctpI	putative calcium/proton antiporter probable magnesium and cobalt transport protein cation-transporting ATPase cation transport ATPase cation transport ATPase probable cadmium-transporting ATPase probable cation transport ATPase probable cation transport ATPase probable cation transport ATPase cobable cation transport ATPase C-terminal region putative cationtransporting ATPase probable magnesium transport ATPase	Rv0928 Rv0820 Rv3301c Rv0821c Rv0545c Rv2281	phoS2 phoT phoY1 phoY2 pitA pitB	PstS component of phosphate uptake PstS component of phosphate uptake phosphate transport system ABC transporter phosphate transport system regulator phosphate transport system regulator low-affinity inorganic phosphate transporter phosphate permease PstA component of phosphate uptake PstA component of phosphate
Rv2155c Rv2158c Rv2157c Rv2157c Rv1338 Rv2156c Rv3332 Rv0016c	murC murD murE murF murG murI murX nagA pbpA	cosamine reductase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetylmuramoylalanine-D- glutamate ligase meso-diaminopimelate-adding enzyme D-alanine:D-alanine-adding enzyme transferase in peptidoglycan synthesis glutamate racemase phospho-N-acetylmuramoyl- petapeptide transferase N-acetylglucosamine-6-P- deacetylase penicillin-binding protein	Rv2920c Rv1607 Rv1239c Rv0103c Rv3270 Rv1469 Rv0908 Rv1997 Rv1992c Rv0425c Rv0107c	amt chaA corA ctpA ctpB ctpC ctpD ctpE ctpF ctpG ctpH ctpI ctpV	putative calcium/proton antiporter probable magnesium and cobalt transport protein cation-transport protein cation-transporting ATPase cation transport ATPase probable cadmium-transporting ATPase probable cation transport ATPase probable cation transport ATPase probable cation transport ATPase probable cation transport ATPase probable and protein transport ATPase probable magnesium transport ATPase probable magnesium transport ATPase cation transport ATPase cation transport ATPase	Rv0928 Rv0820 Rv3301c Rv0821c Rv0545c Rv2281 Rv0930 Rv0936	phoS2 phoT phoY1 phoY2 pitA pitB pstA1 pstA2	PstS component of phosphate uptake PstS component of phosphate uptake phosphate transport system ABC transporter phosphate transport system regulator phosphate transport system regulator low-affinity inorganic phosphate transporter phosphate permease PstA component of phosphate uptake PstA component of phosphate uptake
Rv2155c Rv2158c Rv2157c Rv2153c Rv1338 Rv2156c Rv3332	murC murD murE murF murG murI murX	cosamine reductase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetylmuramoylalanine-D- glutamate ligase meso-diaminopimelate-adding enzyme D-alanine:D-alanine-adding enzyme transferase in peptidoglycan syn- thesis glutamate racemase phospho-N-acetylmuramoyl- petapeptide transferase N-acetylglucosamine-6-P- deacetylglucosamine-6-P-	Rv2920c Rv1607 Rv1239c Rv0092 Rv0103c Rv3270 Rv1469 Rv0908 Rv1997 Rv1997 Rv1992c Rv0425c	amt chaA corA ctpA ctpB ctpC ctpD ctpE ctpF ctpG ctpH ctpI	putative calcium/proton antiporter probable magnesium and cobalt transport protein cation-transporting ATPase cation transport ATPase cation transport ATPase probable cadmium-transporting ATPase probable cation transport ATPase probable cation transport ATPase probable cation transport ATPase cobable cation transport ATPase C-terminal region putative cationtransporting ATPase probable magnesium transport ATPase	Rv0928 Rv0820 Rv3301c Rv0821c Rv0545c Rv2281 Rv0930	phoS2 phoT phoY1 phoY2 pitA pitB pstA1	PstS component of phosphate uptake PstS component of phosphate uptake phosphate transport system ABC transporter phosphate transport system regulator phosphate transport system regulator low-affinity inorganic phosphate transporter phosphate permease PstA component of phosphate uptake PstA component of phosphate
Rv2155c Rv2158c Rv2157c Rv2153c Rv1338 Rv2156c Rv3332 Rv0016c Rv2163c Rv0050 Rv3682	murC murD murE murF murG murI murX nagA pbpA pbpA pbpB ponA ponA'	cosamine reductase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetylmuramoylalanine-D- glutamate ligase meso-diaminopimelate-adding enzyme D-alanine:D-alanine-adding enzyme transferase in peptidoglycan synthesis glutamate racemase phospho-N-acetylmuramoyl- petapeptide transferase N-acetylglucosamine-6-P- deacetylglucosamine-6-P- deacetylase penicillin-binding protein penicillin-binding protein class A penicillin binding protein	Rv2920c Rv1607 Rv1239c Rv0103c Rv3270 Rv1469 Rv0908 Rv1997 Rv1992c Rv0425c Rv0107c Rv0969 Rv3044 Rv0265c trate	amt chaA corA ctpA ctpB ctpC ctpC ctpD ctpE ctpF ctpG ctpH ctpI ctpI ctpV fecB fecB2	putative calcium/proton antiporter probable magnesium and cobalt transport protein cation-transport protein cation-transport ATPase cation transport ATPase probable magnesium transport ATPase probable magnesium transport ATPase probable magnesium transport ATPase probable magnesium transport ATPase cation transport ATPase putative Felli-dicitrate transporter iron transport protein Felli dicitransporter	Rv0928 Rv0820 Rv3301c Rv0821c Rv0545c Rv2281 Rv0930 Rv0936	phoS2 phoT phoY1 phoY2 pitA pitB pstA1 pstA2	PstS component of phosphate uptake PstS component of phosphate uptake phosphate transport system ABC transporter phosphate transport system regulator phosphate transport system regulator low-affinity inorganic phosphate transporter phosphate transporter by sphate permease PstA component of phosphate uptake PstA component of phosphate uptake ABC transport component of phosphate uptake PstC component of phosphate
Rv2155c Rv2158c Rv2157c Rv2157c Rv2153c Rv1338 Rv2156c Rv3332 Rv0016c Rv2163c Rv0050	murC murD murE murF murG murI murX nagA pbpA pbpB ponA	cosamine reductase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetylmuramoylalanine-D- glutamate ligase meso-diaminopimelate-adding enzyme D-alanine:D-alanine-adding enzyme transferase in peptidoglycan syn- thesis glutamate racemase phospho-N-acetylmuramoyl- petapeptide transferase N-acetylglucosamine-6-P- deacetylglucosamine-6-P- deacetylase penicillin-binding protein penicillin-bonding protein penicillin-bonding protein	Rv2920c Rv1607 Rv1239c Rv0092 Rv0103c Rv3270 Rv1469 Rv0908 Rv1997 Rv1997 Rv0425c Rv0425c Rv0107c	amt chaA corA ctpA ctpB ctpC ctpD ctpE ctpF ctpG ctpH ctpI ctpV fecB	putative calcium/proton antiporter probable magnesium and cobalt transport protein cation-transport protein cation-transport ATPase cation transport ATPase probable cadmium-transporting ATPase probable cation transport ATPase probable magnesium transport at probable magnesium transport ATPase probable magnesium transport ATPase cation transport ATPase probable magnesium transport ATPase cation transport protein transporter iron transport protein Fell dici-	Rv0928 Rv0820 Rv3301c Rv0821c Rv0545c Rv2281 Rv0930 Rv0936	phoS2 phoT phoY1 phoY2 pitA pitB pstA1 pstA2 pstB	PstS component of phosphate uptake PstS component of phosphate uptake phosphate transport system ABC transporter phosphate transport system regulator phosphate transport system regulator low-affinity inorganic phosphate transporter phosphate permease PstA component of phosphate uptake PstA component of phosphate uptake ABC transport component of phosphate uptake

Rv0932c	pstS	phosphate transport system PstS component of phosphate	Rv1821	secA2	unit SecA, preprotein translocase sub-	Rv3500c - Rv3501c -	part of <i>mce4</i> operon part of <i>mce4</i> operon	
	•	uptake			unit	Rv3896c -	putative p60 homolo	
Rv2400c Rv0143c	subl -	sulphate binding precursor probable chloride channel	Rv2587c Rv0638	secD secE	protein-export membrane protein SecE preprotein translocase	Rv3922c -	possible hemolysin	
Rv1707	-	probable sulphate permease	Rv2586c	secF	protein-export membrane protein	B. IS elements, R	epeated sequences, and	l Phage
Rv1739c Rv3679	-	possible sulphate transporter possible anion transporter	Rv1440	secG	protein-export membrane protein SecG	1. IS elements 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			Rv2462c	tig	chaperone protein, similar to			
Rv2790c Rv3540c	ltp1 ltp2	non-specific lipid transport protein non-specific lipid transport protein	Rv2813	_	trigger factor probable general secretion path-	2. REP13E12 fam	ily 7 copies	
11000400	πρz	non-specific lipid transport protein	1102010		way protein	3. Phage-related		
6. Efflux pi Rv2936	roteins <i>drrA</i>	similar daunorubicin resistance	F Adanta	tions and	atypical conditions	Rv2894c xerC Rv1701 xerD	integrase/recombination	
		ABC-transporter	Rv1901	cinA	competence damage protein	Rv1054 -	integrase-a	
Rv2937	drrB	similar daunorubicin resistance transmembrane protein	Rv3648c	cspA	cold shock protein, transcriptional regulator	Rv1055 - Rv1573 -	integrase-b phiRV1 phage relate	nd protein
Rv2938	drrC	similar daunorubicin resistance	Rv0871	cspB	probable cold shock protein	Rv1574 -	phiRV1 phage relate	
Rv2846c	efpA	transmembrane protein putative efflux protein	Rv3063	cstA	starvation-induced stress response protein	Rv1575 - Rv1576c -	phiRV1 phage relate phiRV1 phage relate	
Rv3065	emrE	resistance to ethidium bromide	Rv3490	otsA	probable α,α -trehalose-phosphate	Rv1577c -	phiRV1 possible prof	
Rv0783c Rv0849	-	multidrug resistance protein possible quinolone efflux pump	Rv2006	otsB	synthase trehalose-6-phosphate phos-	Rv1578c - Rv1579c -	phiRV1 phage relate phiRV1 phage relate	
Rv1145	-	probable drug transporter	HV2000	UISD	phatase	Rv1580c -	phiRV1 phage relate	d protein
Rv1146 Rv1250	-	probable drug transporter probable drug efflux protein	Rv3372	otsB2	trehalose-6-phosphate phos- phatase	Rv1581c - Rv1582c -	phiRV1 phage relate phiRV1 phage relate	
Rv1258c	-	probable multidrug resistance	Rv3758c	proV	osmoprotection ABC transporter	Rv1583c -	phiRV1 phage relate	
Rv1410c	_	pump probable drug efflux protein	Rv3757c Rv3759c	proW	transport system permease similar to osmoprotection proteins	Rv1584c - Rv1585c -	phiRV1 phage relate phiRV1 phage relate	
Rv1634	-	probable drug efflux protein	Rv3756c	proX proZ	transport system permease	Rv1585c - Rv1586c -	phiRV1 integrase	u protein
Rv1819c	-	probable multidrug resistance	Rv1026	-	probable pppGpp-5'phosphohydro-	Rv2309c - Rv2310 -	integrase excisionase	
Rv2136c	_	pump putative bacitracin resistance pro-			lase	Rv2310 - Rv2646 -	phiRV2 integrase	
		tein	F. Detoxific			Rv2647 -	phiRV2 phage relate	
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 relate phiRV2 prohead prof	
		tance protein	Rv2238c	ahpE	member of AhpC/TSA family	Rv2652c -	phiRV2 phage relate	d protein
Rv2994	-	probable fluoroquinolone efflux protein	Rv2521 Rv1608c	bcp bcpB	bacterioferritin comigratory protein probable bacterioferritin comigra-	Rv2653c - Rv2654c -	phiRV2 phage relate phiRV2 phage relate	
Rv1877	-	probable drug efflux protein	11110000	БОРБ	tory protein	Rv2655c -	phiRV2 phage relate	
Rv2459	-	probable drug efflux protein	Rv3473c	bpoA	probable non-heme bromoperoxidase	Rv2656c - Rv2657c -	phiRV2 phage relate similar to gp36 of my	
B. Chaper	ones/Hea	t shock	Rv1123c	bpoB	probable non-heme bromoperoxi-	HV2057C -	phage L5	cobacterio-
Rv0384c Rv0352	clpB dnaJ	heat shock protein acts with GrpE to stimulate DnaK	Rv0554	bpoC	dase probable non-heme bromoperoxi-	Rv2658c - Rv2659c -	phiRV2 phage relate phiRV2 integrase	d protein
NVU332	urias	ATPase	NV0554	bpoc	dase	Rv2830c -	similar to phage P1	phd gene
Rv2373c	dnaJ2	DnaJ homologue	Rv3617	ephA	probable epoxide hydrolase	Rv3750c -	excisionase	
Rv0350	dnaK	70 kD heat shock protein, chromosome replication	Rv1938 Rv1124	ephB ephC	probable epoxide hydrolase probable epoxide hydrolase	Rv3751 -	putative integrase	
Rv3417c	groEL1	60 kD chaperonin 1	Rv2214c	ephD	probable epoxide hydrolase	C. PE and PPE fa	milies	
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 non-heme haloperoxi-	PE_PGRS subfar	nily 61 members	
Rv2374c	hrcA	heat-inducible transcription repressor	Rv1908c	katG	dase catalase-peroxidase	2. PPE family	68 members	
Rv0251c	hsp	possible heat shock protein	Rv3846	sodA	superoxide dismutase	D. Analikinia and	and an area of the same of	
Rv0353 Rv2031c	hspR hspX	heat shock regulator 14kD antigen, heat shock protein	Rv0432	sodC	superoxide dismutase precursor - (Cu-Zn)	D. Antibiotic produ Rv2068c blaC	uction and resistance class A β-lactamase	
		Hsp20 family	Rv1932	tpx	thiol peroxidase	Rv3290c lat	lysine-ε aminotransfe	erase
Rv2299c Rv0563	htpG htpX	heat shock protein Hsp90 family probable (transmembrane) heat	Rv0634c Rv2581c	-	putative glyoxylase II putative glyoxylase II	Rv2043c <i>pncA</i> Rv0133 -	pyrazinamide resista possible puromycin N	
	1.1	shock protein	Rv3177	-	probable non-heme haloperoxi-		ferase	•
Rv2701c	suhB	putative extragenic suppressor protein			dase	Rv0262c -	aminoglycoside 2'-N- ferase	-acetyltrans-
Rv3269	-	probable heat shock protein	IV. Other			Rv0802c -	acetyltransferase	
C. Cell div	ision		A. Viruleno Rv0169	ce mce1	cell invasion protein	Rv1082 - Rv1170 -	similar to S. lincolner similar to S. lincolner	
Rv3641c	fic	possible cell division protein	Rv0589	mce2	cell invasion protein	Rv1347c -	possible aminoglyco:	
Rv3102c Rv3610c	ftsE ftsH	membrane protein inner membrane protein,	Rv1966 Rv3499c	mce3 mce4	cell invasion protein cell invasion protein	Rv2036 -	acetyltransferase similar to lincomycin	production
11000100	11311	chaperone	Rv3100c	smpB	probable small protein b	1102000 -	genes	
Rv2748c Rv2151c	ftsK ftsQ	chromosome partitioning ingrowth of wall at septum	Rv1694 Rv0024	tlyA	cytotoxin/hemolysin homologue putative p60 homologue	Rv2303c -	similar to S. griseus resistance protein	macrotetrolide
Rv2154c	ftsW	membrane protein (shape determi-	Rv0167	-	part of mce1 operon	Rv3225c -	probable aminoglyco	side 3'-phos-
Rv3101c	ftsX	nation) membrane protein	Rv0168 Rv0170	-	part of <i>mce1</i> operon part of <i>mce1</i> operon	Rv3700c -	photransferases probable acetyltrans	foraço
Rv2921c	ftsY	cell division protein FtsY	Rv0171	-	part of <i>mce1</i> operon	Rv3817 -	probable aminoglyco	
Rv2150c	ftsZ	circumferential ring, GTPase	Rv0172	-	part of mce1 operon		photransferase	
Rv3919c Rv3625c	gid mesJ	glucose inhibited division protein B probable cell cycle protein	Rv0174 Rv0587	-	part of <i>mce1</i> operon part of <i>mce2</i> operon	E. Bacteriocin-like	proteins 3	3
Rv3917c	parA	chromosome partitioning; DNA -	Rv0588	-	part of mce2 operon			
Rv3918c	parB	binding possibly involved in chromosome	Rv0590 Rv0591	-	part of <i>mce2</i> operon part of <i>mce2</i> operon	F. Cytochrome P4	50 enzymes 2	22
	•	partitioning	Rv0592	-	part of mce2 operon	G. Coenzyme F42		
Rv2922c	smc	member of Smc1/Cut3/Cut14 family	Rv0594 Rv1085c	-	part of <i>mce2</i> operon possible hemolysin	enzymes	3	}
Rv0012	-	possible cell division protein	Rv1477	-	putative exported p60 protein	H. Miscellaneous	transferases 6	61
Rv0435c Rv2115c	-	ATPase of AAA-family ATPase of AAA-family	Rv1478	_	homologue putative exported p60 protein	I Miscellaneous r	hosphatases, lyases,	
	-	possible role in chromosome seg-			homologue	and hydrolases		18
Rv1708	_	regation possible role in chromosome parti-	Rv1566c	-	putative exported p60 protein homologue	J. Cyclases	6	3
1141700		tioning	Rv1964	-	part of mce3 operon	,		
D Protoi-	and nani	de secretion	Rv1965 Rv1967	-	part of <i>mce3</i> operon part of <i>mce3</i> operon	K. Chelatases	2	2
Rv2916c	ffh	signal recognition particle protein	Rv1967 Rv1968	-	part of <i>mce3</i> operon	V. Conserved hyp	otheticals 9	912
Rv2903c Rv1614	lepB lat	signal peptidase I	Rv1969	-	part of <i>mce3</i> operon part of <i>mce3</i> operon	VI Hakaawaa	,	606
nv 1014	lgt	prolipoprotein diacylglyceryl trans- ferase	Rv1971 Rv2190c	-	putative p60 homologue	VI. Unknowns		100
Rv1539	IspA	lipoprotein signal peptidase	Rv3494c	-	part of mce4 operon	TOTAL	3	3924
Rv0379	sec	probable transport protein SecE/Sec61- γ family	Rv3496c Rv3497c		part of <i>mce4</i> operon part of <i>mce4</i> operon			
Rv3240c	secA	SecA, preprotein translocase sub-	Rv3498c		tu re ® ที่เอากัสเลา คันblishers Ltd 199	8		