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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	<i>ycobacterium tuberculosis</i> protein-c	oding genes

I. Small-m A. Degrad		netabolism	Rv2831	echA16	superfamily enoyl-CoA hydratase/isomerase	Rv3543c Rv3560c	fadE29 fadE30	acyl-CoA dehydrogenase acyl-CoA dehydrogenase
1. Carbon Rv0186	compound bglS	ds β-glucosidase	Rv3039c	echA 17	superfamily enoyl-CoA hydratase/isomerase	Rv3562 Rv3563	fadE31 fadE32	acyl-CoA dehydrogenase acyl-CoA dehydrogenase
Rv2202c	cbhK	carbohydrate kinase	HVSOSSC	ecna ii	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- genase	Rv3374	echA18'	superfamily, N-term enoyl-CoA hydratase/isomerase	Rv3797 Rv3761c	fadE35 fadE36	acyl-CoA dehydrogenase acyl-CoA dehydrogenase
Rv0234c	gabD2	succinate-semialdehyde dehydro-			superfamily, C-term	Rv1175c	fadH	2,4-Dienoyl-CoA Reductase
Rv0501	galE1	genase UDP-glucose 4-epimerase	Rv3516	echA 19	enoyl-CoA hydratase/isomerase superfamily	Rv0855 Rv1143	far mcr	fatty acyl-CoA racemase α-methyl acyl-CoA racemase
Rv0536	galE2	UDP-glucose 4-epimerase	Rv3550	echA20		Rv1492	mutA	methylmalonyl-CoA mutase, β
Rv0620	galK	galactokinase	Dv0774		superfamily	Dud 400	mutB	subunit
Rv0619	galT	galactose-1-phosphate uridylyl- transferase C-term	Rv3774	echA21	enoyl-CoA hydratase/isomerase superfamily	Rv1493	mulb	methylmalonyl-CoA mutase, α subunit
Rv0618	galTʻ	galactose-1-phosphate uridylyl-	Rv0859	fadA	β oxidation complex, β subunit	Rv2504c	scoA	3-oxo acid:CoA transferase, α sub-
Rv0993	galU	transferase N-term UTP-glucose-1-phosphate uridylyl-	Rv0243	fadA2	(acetyl-CoA C-acetyltransferase) acetyl-CoA C-acetyltransferase	Rv2503c	scoB	unit 3-oxo acid:CoA transferase, β sub-
	-	transferase	Rv1074c	fadA3	acetyl-CoA C-acetyltransferase			unit
Rv3696c	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			
Rv3441c	mrsA	phosphoglucomutase or phospho- mannomutase	Rv3556c Rv0860	fadA6 fadB	acetyl-CoA C-acetyltransferase β oxidation complex, α subunit	4. Phosph Rv2368c		
Rv0118c	oxcA	oxalyl-CoA decarboxylase	HV0660	IAUD	(multiple activities)	HV23060	phoH	ATP-binding pho regulon component
Rv3068c	pgm A	phosphoglucomutase	Rv0468	fadB2	3-hydroxyacyl-CoA dehydroge-	Rv1095	phoH2	PhoH-like protein
Rv3257c Rv3308	pmmA pmmB	phosphomannomutase phosphomannomutase	Rv1715	fadB3	nase 3-hydroxyacyl-CoA dehydroge-	Rv3628	ppa	probable inorganic pyrophos- phatase
Rv2702	ppgK	polyphosphate glucokinase			nase	Rv2984	ppk	polyphosphate kinase
Rv0408 Rv0729	pta xylB	phosphate acetyltransferase xylulose kinase	Rv3141	fadB4	3-hydroxyacyl-CoA dehydroge- nase	B. Fnerov	metabolis	m
Rv1096	-	carbohydrate degrading enzyme	Rv1912c	fadB5	3-hydroxyacyl-CoA dehydroge-	1. Glycoly	sis	
2. Amino a	anide 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 Rv0214	fadD3 fadD4	acyl-CoA synthase	Rv0489		drogenase phosphoglycerate mutase I
Rv1538c	aid ansA	L-alanine denydrogenase L-asparaginase	Rv0166	fadD4	acyl-CoA synthase acyl-CoA synthase	Rv3010c	gpm pfkA	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	t pi -	triosephosphate isomerase putative phosphoglycerate mutase
1101107	JOOA	genase	Rv1549	fadD11	acyl-CoA synthase, C-term	Rv3837c	-	putative phosphoglycerate mutase
Rv2322c	rocD1	ornithine aminotransferase	Rv1427c	fadD12 fadD13	acyl-CoA synthase	0 Duminion	معامرة والمامية	
Rv2321c Rv1848	rocD2 ureA	ornithine aminotransferase urease y subunit	Rv3089 Rv1058	fadD14	acyl-CoA synthase acyl-CoA synthase	Pyruvat Rv2241	e deriyaro aceE	pyruvate dehydrogenase E1 com-
Rv1849	ureB	urease β subunit	Rv2187	fadD15	acyl-CoA synthase		t1.8	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		•	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
11020100		aminohydrolase	Rv2948c	fadD21	acyl-CoA synthase	Rv2495c	pdhC	dihydrolipoamide acetyltransferase
Rv3551	•	possible glutaconate CoA- transferase	Rv3826 Rv1529	fadD23 fadD24	acyl-CoA synthase acyl-CoA synthase	Rv0462	-	probable dihydrolipoamide dehy-
		Halisterase	Hv1529	fadD25	acyl-CoA synthase			drogenase
3. Fatty ac			Rv2930	fadD26	acyl-CoA synthase	3. TCA cy		and the state of t
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
Rv2502c	acc∏1	α subunit acetyl/propionyl-CoA carboxylase,	Rv0404 Rv1925	fadD30 fadD31	acyl-CoA synthase acyl-CoA synthase	Rv1098c Rv1131	fum gltA1	fumarase citrate synthase 3
		β subunit	Rv3801c	fadD32	acyl-CoA synthase	Rv0896	gltA2	citrate synthase 1
Rv0974c	accD2	acetyl/propionyl-CoA carboxylase, β subunit	Rv1345 Rv0035	fadD33 fadD34	acyl-CoA synthase acyl-CoA synthase	Rv3339c Rv0066c	icd1 icd2	isocitrate dehydrogenase isocitrate dehydrogenase
Rv3667	acs	acetyl-CoA synthase	Rv2505c	fadD35	acyl-CoA synthase	Rv0794c	lpdB	dihydrolipoamide dehydrogenase
Rv3409c Rv0222	choD	cholesterol oxidase	Rv1193	fadD36 fadE1	acyl-CoA synthase	Rv1240	mdh	malate dehydrogenase
NV0222	echA1	enoyl-CoA hydratase/isomerase superfamily	Rv0131c Rv0154c	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	echA3	superfamily enoyl-CoA hydratase/isomerase	Rv0231 Rv0244c	fadE4 fadE5	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv3316	sdhC	succinate dehydrogenase C sub- unit
		superfamily	Rv0271c	fadE6	acyl-CoA dehydrogenase	Rv3317	sdhD	succinate dehydrogenase D sub-
Rv0673	echA4	enoyl-CoA hydratase/isomerase superfamily	Rv0400c Rv0672	fadE7 fadE8	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv1248c	sucA	unit 2-oxoglutarate dehydrogenase
Rv0675	echA5	enoyl-CoA hydratase/isomerase			(aka <i>aidB</i>)	Rv2215	sucB	dihydrolipoamide succinyltrans-
Rv0905	echA6	superfamily encyl-CoA hydratase/isomerase	Rv0752c Rv0873	fadE9 fadE10	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv0951	sucC	ferase succinyl-CoA synthase β chain
		superfamily (aka <i>eccH</i>)	Rv0972c	fadE12	acyl-CoA dehydrogenase	Rv0952	sucD	succinyl-CoA synthase β chain
Rv0971c	echA7	enoyl-CoA hydratase/isomerase	Rv0975c	fadE13	acyl-CoA dehydrogenase			
Rv1070c	echA8	superfamily enoyl-CoA hydratase/isomerase	Rv1346 Rv1467c	fadE14 fadE15	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	4. Glyoxyl Rv0467	ate bypass aceA	s isocitrate lyase
		superfamily	Rv1679	fadE16	acyl-CoA dehydrogenase	Rv1915	aceAa	isocitrate lyase, α module
Rv1071c	echA9	enoyl-CoA hydratase/isomerase superfamily	Rv1934c Rv1933c	fadE17 fadE18	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv1916 Rv1837c	aceAb glcB	isocitrate lyase, β module malate synthase
Rv1142c	echA10	enoyl-CoA hydratase/isomerase	Rv2500c	fadE 19	acyl-CoA dehydrogenase	Rv3323c	gphA	phosphoglycolate phosphatase
Bu11414	ech A 1 1	superfamily	By2724c	fadEco	(aka mmgC)	5 Donto-	a nhoonb	ta nathway
Rv1141c	echA11	enoyl-CoA hydratase/isomerase superfamily	Rv2724c Rv2789c	fadE20 fadE21	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	5. Pentose Rv1445c	e pnospna devB	te pathway glucose-6-phosphate 1-dehydro-
Rv1472	echA12	enoyl-CoA hydratase/isomerase	Rv3061c	fadE22	acyl-CoA dehydrogenase			genase
Rv1935c	echA13	superfamily enoyl-CoA hydratase/isomerase	Rv3140 Rv3139	fadE23 fadE24	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv1844c	gnd	6-phosphogluconate dehydroge- nase (Gram –)
		superfamily	Rv3274c	fadE25	acyl-CoA dehydrogenase	Rv1122	gnd2	6-phosphogluconate dehydroge-
Rv2486	echA14	enoyl-CoA hydratase/isomerase superfamily	Rv3504 Rv3505	fadE26 fadE27	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv1446c	орсА	nase (Gram +) unknown function, may aid
Rv2679	echA15		Rv3544c	fadE28	acyl-CoA dehydrogenase			G6PDH

Rv2436 Rv1408	rbsK rpe	ribokinase ribulose-phosphate 3-epimerase	Rv3250c	rubB	rubredoxin B	Rv1878 Rv2860c	glnA3 glnA4	probable glutamine synthase proable glutamine synthase
Rv2465c	rpi	phosphopentose isomerase	7. Miscella	neous oxi	doreductases and oxygenases 171	Rv2918c	glnD	uridylyltransferase
Rv1448c Rv1449c	tal tkt	transaldolase transketolase	8. ATP-pro	ton motive	force	Rv2221c	glnE	glutamate-ammonia-ligase adenyltransferase
Rv1121	zwf	glucose-6-phosphate 1-dehydro-	Rv1308	atpA	ATP synthase α chain	Rv3859c	gltB	ferredoxin-dependent glutamate
		genase	Rv1304	atpB	ATP synthase a chain	11100000	9.12	synthase
Rv1447c	zwf2	glucose-6-phosphate 1-dehydro- genase	Rv1311 Rv1310	atpC atpD	ATP synthase ϵ chain ATP synthase β chain	Rv3858c	gltD	small subunit of NADH-depender glutamate synthase
			Rv1305	atpE_	ATP synthase c chain	Rv3704c	gshA	possible γ-glutamylcysteine syn-
6. Respira			Rv1306	atpF	ATP synthase b chain	D.:0407-		thase
a. aerobic Rv0527	ccsA	cytochrome c-type biogenesis	Rv1309 Rv1307	atpG atpH	ATP synthase γ chain ATP synthase δ chain	Rv2427c Rv2439c	proA proB	γ-glutamyl phosphate reductase glutamate 5-kinase
1100027	CCSA	protein	1101001	aupi i	All synthase o chain	Rv0500	proC	pyrroline-5-carboxylate reductase
Rv0529	ccsB	cytochrome <i>c</i> -type biogenesis	C. Central	intermedia	ary metabolism	,,,,,,,,,,	p.00	p) o i u o o o o o o o o o o o o o o o o o
		protein	 General 			Asparta		
Rv1451	ctaB	cytochrome c oxidase assembly	Rv2589	gabT	4-aminobutyrate aminotransferase	Rv3708c	asd	aspartate semialdehyde dehydro
Rv2200c	ctaC	factor cytochrome c oxidase chain II	Rv3432c Rv1832	gadB gcvB	glutamate decarboxylase glycine decarboxylase	Bv3709c	ask	genase aspartokinase
Rv3043c	ctaD	cytochrome c oxidase chair ii	Rv1826	gcvB gcvH	glycine decarboxylase glycine cleavage system H protein	Rv2201	asn asnB	asparagine synthase B
		peptide I	Rv2211c	gcvT	T protein of glycine cleavage	Rv3565	aspB	aspartate aminotransferase
Rv2193	ctaE	cytochrome c oxidase poly-			system	Rv0337c	aspC	aspartate aminotransferase
D: 45.40		peptide III	Rv1213	glgC	glucose-1-phosphate adenylyl-	Rv2753c	dapA	dihydrodipicolinate synthase
Rv1542c Rv2470	glbN glbO	hemoglobin-like, oxygen carrier hemoglobin-like, oxygen carrier	Rv3842c	glpQ1	transferase glycerophosphoryl diester phos-	Rv2773c Rv1202	dapB dapE	dihydrodipicolinate reductase succinyl-diaminopimelate desuc-
Rv2249c	glpD1	glycerol-3-phosphate dehydroge-	11000420	gipari	phodiesterase	1101202	dupL	cinylase
	0,	nase	Rv0317c	glpQ2	glycerophosphoryl diester phos-	Rv2141c	dapE2	ArgE/DapE/Acy1/Cpg2/yscS
Rv3302c	glpD2	glycerol-3-phosphate dehydroge-			phodiesterase			family
Dunco 4	IIAD 4	nase	Rv3566c	nhoA	N-hydroxyarylamine o-acetyltrans-	Rv2726c	dapF	diaminopimelate epimerase
Rv0694	IIdD1	L-lactate dehydrogenase (cytochrome)	Rv0155	pntAA	ferase pyridine transhydrogenase sub-	Rv1293 Rv3341	lysA metA	diaminopimelate decarboxylase homoserine o-acetyltransferase
Rv1872c	IIdD2	L-lactate dehydrogenase		Pinnor	unit a1	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 Rv3148	nuoC nuoD	NADH dehydrogenase chain C NADH dehydrogenase chain D	Rv1127c	ppdK	subunit β similar to pyruvate, phosphate	Rv2124c	metH	ferase 5-methyltetrahydrofolate-homo-
Rv3149	nuoE	NADH dehydrogenase chain E	11011270	ppur	dikinase	11021240	men	cysteine methyltransferase
Rv3150	nuoF	NADH dehydrogenase chain F				Rv1392	metK	Ś-adenosylmethionine synthase
Rv3151	nuoG	NADH dehydrogenase chain G	2. Glucone			Rv0391	metZ	o-succinylhomoserine sulfhy-
Rv3152	nuoH	NADH dehydrogenase chain H	Rv0211	pckA	phosphoenolpyruvate carboxy- kinase	Rv1294	thrA	drylase
Rv3153 Rv3154	nuol nuoJ	NADH dehydrogenase chain I NADH dehydrogenase chain J	Rv0069c	sdaA	L-serine dehydratase 1	Rv1294	thrB	homoserine dehydrogenase homoserine kinase
Rv3155	nuoK	NADH dehydrogenase chain K			7	Rv1295	thrC	homoserine synthase
Rv3156	nuoL	NADH dehydrogenase chain L	3. Sugar n					
Rv3157	nuoM	NADH dehydrogenase chain M	Rv1512	epiA	nucleotide sugar epimerase	3. Serine fa		46 16-4
Rv3158 Rv2195	nuoN qcrA	NADH dehydrogenase chain N Rieske iron-sulphur component of	Rv3784	epiB	probable UDP-galactose 4- epimerase	Rv0815c Rv3117	cysA2 cysA3	thiosulfate sulfurtransferase thiosulfate sulfurtransferase
1102100	guin	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-
	_	cytB reductase			transferase			ferase
Rv2194	qcrC	cytochrome b/c component of ubiQ-cytB reductase	Rv3264c	rmiA2	glucose-1-phosphate thymidyl- transferase	Rv2847c	cysG2	multifunctional enzyme, siroheme synthase
		ubiq-cyib leductase	Rv3464	rmlB	dTDP-glucose 4,6-dehydratase	Rv2334	cysK	cysteine synthase A
b. anaerob	oic		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
Duranna	fdhD	reductase	Rv3465	rmIC	dTDP-4-dehydrorhamnose	Rv0848	cysM3	putative cysteine synthase
Rv2899c Rv2900c	fdhF	affects formate dehydrogenase-N molybdopterin-containing oxidore-	Rv3266c	rmID	3,5-epimerase dTDP-4-dehydrorhamnose	Rv1093 Rv0070c	glyA glyA2	serine hydroxymethyltransferase serine hydroxymethyltransferase
		ductase			reductase	Rv2996c	serA	D-3-phosphoglycerate dehydro-
Rv1552	frdA	fumarate reductase flavoprotein	Rv0322	udgA	UDP-glucose	_	_	genase
D. 4FF0	f(D	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	11000420	SOIDE	phosphatase
		protein	Rv3400	-	probable β-phosphoglucomutase	Rv0884c	serC	phosphoserine aminotransferase
Rv1555	frdD	fumarate reductase 13kD anchor						adal Zamatha
Rv1161	narG	protein	4. Amino s		alungamina fruntasa 6	4. Aromatic Rv3227		cid family 3-phosphoshikimate
Rv1161	narG narH	nitrate reductase α subunit nitrate reductase β chain	Rv3436c	girio	glucosamine-fructose-6- phosphate aminotransferase	HV3ZZ/	aroA	1-carboxyvinyl transferase
Rv1164	narl	nitrate reductase γ chain				Rv2538c	aroB	3-dehydroquinate synthase
Rv1163	narJ	nitrate reductase δ chain	5. Sulphur			Rv2537c	aroD	3-dehydroquinate dehydratase
Rv1736c Rv2391	narX nir ∆	fused nitrate reductase probable nitrite reductase/sulphite	Rv0711 Rv3299c	atsA atsB	arylsulfatase proable arylsulfatase	Rv2552c Rv2540c	aroE aroF	shikimate 5-dehydrogenase chorismate synthase
1172081	nirA	reductase	Rv0663	atsB atsD	proable arylsulfatase	Rv25400 Rv2178c	aror aroG	DAHP synthase
Rv0252	nirB	nitrite reductase flavoprotein	Rv3077	atsF	proable arylsulfatase	Rv2539c	aroK	shikimate kinase l
Rv0253	nirD	probable nitrite reductase small	Rv0296c	atsG	proable arylsulfatase	Rv3838c	pheA	prephenate dehydratase
		subunit	Rv3796	atsH	proable arylsulfatase	Rv1613	trpA trpP	tryptophan synthase α chain
c. Electror	n transnort		Rv1285 Rv1286	cysD cysN	ATP:sulphurylase subunit 2 ATP:sulphurylase subunit 1	Rv1612 Rv1611	trpB trpC	tryptophan synthase β chain indole-3-glycerol phosphate
Rv0409	ackA	acetate kinase	Rv2131c	cysQ	homologue of M.leprae cysQ		., ρυ	synthase
Rv1623c	аррС	cytochrome bd-ll oxidase	Rv3248c	sahH	adenosylhomocysteinase	Rv2192c	trpD	anthranilate phosphoribosyltrans-
D 4000		subunit I	Rv3283	sseA	thiosulfate sulfurtransferase	D 4		ferase
Rv1622c	cydB	cytochrome d ubiquinol oxidase	Rv2291 Rv3118	sseB sseC	thiosulfate sulfurtransferase thiosulfate sulfurtransferase	Rv1609	trpE	anthranilate synthase
Rv1620c	cydC	subunit II ABC transporter	Rv0814c	sseC2	thiosulfate sulfurtransferase	Rv2386c	trpE2	component I anthranilate synthase
Rv1621c	cydD cydD	ABC transporter	Rv3762c	-	probable alkyl sulfatase		,	component I
Rv2007c	fdxA	ferredoxin				Rv3754	tyrA	prephenate dehydrogenase
	fdxB	ferredoxin	D. Amino a		nthesis	- 10 00	_	
Rv3554	fdxC	ferredoxin 4Fe-4S	1. Glutama Rv1654		anetylalutamate kinasa	5. Histidine		phoenharibaeulfarmimina 5
Rv3554 Rv1177		probable ferredoxin electron transfer flavoprotein	Rv1654 Rv1652	argB argC	acetylglutamate kinase N-acetyl-γ-glutamyl-phosphate	Rv1603	hisA	phosphoribosylformimino-5- aminoimidazole carboxamide
Rv3554 Rv1177 Rv3503c	fdxD fixA				reductase			ribonucleotide isomerase
Rv3554 Rv1177 Rv3503c	fixA	β subunit				D 1001	hiaD.	
Rv3554 Rv1177 Rv3503c Rv3029c		electron transfer flavoprotein α	Rv1655	argD_	acetylornithine aminotransferase	Rv1601	hisB	imidazole glycerol-phosphate
Rv3554 Rv1177 Rv3503c Rv3029c Rv3028c	fixA fixB	electron transfer flavoprotein α subunit	Rv1656	argF	ornithine carbamoyltransferase			dehydratase
Rv3554 Rv1177 Rv3503c Rv3029c Rv3028c	fixA	electron transfer flavoprotein α subunit adrenodoxin and NADPH ferre-	Rv1656 Rv1658	argF argG	ornithine carbamoyltransferase arginosuccinate synthase	Hv1601 Rv1600	hisC	dehydratase histidinol-phosphate aminotrans-
Rv3554 Rv1177 Rv3503c Rv3029c Rv3028c Rv3106	fixA fixB	electron transfer flavoprotein α subunit	Rv1656	argF	ornithine carbamoyltransferase			dehydratase
Rv3554 Rv1177 Rv3503c Rv3029c	fixA fixB fprA	electron transfer flavoprotein α subunit adrenodoxin and NADPH ferredoxin reductase	Rv1656 Rv1658 Rv1659	argF argG argH	ornithine carbamoyltransferase arginosuccinate synthase arginosuccinate lyase	Rv1600	hisC	dehydratase histidinol-phosphate aminotrans- ferase

Rv1605	hisF	imidazole glycerol-phosphate synthase	Rv3048c	nrdG	subunit ribonucleoside-diphosphate small	Rv3119	moaE	subunit 1 molybdopterin-converting factor
Rv2121c Rv1602	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
7v1606	hisl2	probable phosphoribosyl-AMP 1,6	Rv3247c	tmk	thymidylate kinase	5		subunit 2
2.0444		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	te family		Rv3752c	-	probable cytidine/deoxycytidylate deaminase	Rv2338c Rv1681	moeW moeX	molybdopterin biosynthesis weak similarity to <i>E. coli</i> MoaA
3. Fyruvai Rv3423c		alanine racemase			deallillase	Rv1355c	moeY	weak similarity to E. coli MoeB
170-1200	un	didililic idocinasc	4. Salvage	of nucleo	osides and nucleotides	Rv3206c	moeZ	probably involved in
7. Branch	ed amino	acid family	Rv3313c		probable adenosine deaminase			molybdopterin biosynthesis
Rv1559	ilvA	threonine deaminase	Rv2584c	apt	adenine phosphoribosyltrans-	Rv0865	mog	molybdopterin biosynthesis
₹v3003c	ilvB	acetolactate synthase I large sub-			ferases			
		unit	Rv3315c	cdd	probable cytidine deaminase	Pantoth		
Rv3470c	ilvB2	acetolactate synthase large sub-	Rv3314c	deoA	thymidine phosphorylase	Rv1092c	coaA	pantothenate kinase
Rv3001c	ilvC	unit	Rv0478	deoC	deoxyribose-phosphate aldolase	Rv2225	panB	3-methyl-2-oxobutanoate
Rv0189c		ketol-acid reductoisomerase dihydroxy-acid dehydratase	Rv3307	deoD	probable purine nucleoside phos- phorylase	Rv3602c	panC	hydroxymethyltransferase pantoate-β-alanine ligase
Rv2210c		branched-chain-amino-acid	Rv3624c	hpt	probable hypoxanthine-guanine	Rv3601c	panD	aspartate 1-decarboxylase
1422100	77 V L	transaminase	11/00240	πρι	phosphoribosyltransferase	11400010	pane	aspartate i decarboxylase
Rv1820	ilvG	acetolactate synthase II	Rv3393	iunH	probable inosine-uridine	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
₹v3509c	ilvX	probable acetohydroxyacid syn-	_		family 2			
70740	(thase I large subunit	Rv3309c	upp	uracil phophoribosyltransferase	7. Pyridine		
Rv3710	leuA	α-isopropyl malate synthase	E Missell	nacus :	alacoido/nualactida vas etissos	Rv1594	nadA	quinolinate synthase
Rv2995c Rv2988c	leuB leuC	3-isopropylmalate dehydrogenase 3-isopropylmalate dehydratase	5. Miscella Rv0733	aneous nu <i>adk</i>	cleoside/nucleotide reactions probable adenylate kinase	Rv1595 Rv1596	nadB nadC	L-aspartate oxidase nicotinate-nucleotide pyrophos-
.v2000	icuo	large subunit	Rv2364c	bex	GTP-binding protein of Era/ThdF	1141090	nauo	phatase
Rv2987c	leuD	3-isopropylmalate dehydratase		~~~	family	Rv0423c	thiC	thiamine synthesis, pyrimidine
		small subunit	Rv1712	cmk	cytidylate kinase			moiety
			Rv2344c	dgt	probable deoxyguanosine			· ·
	nine synthe			•	triphosphate hydrolase	8. Thiamin		
Rv2601	speE	spermidine synthase	Rv2404c	lepA	GTP-binding protein LepA	Rv0422c	thiD	phosphomethylpyrimidine kinase
			Rv2727c	miaA	tRNA 8(2)-isopentenylpyrophos-	Rv0414c	thiE	thiamine synthesis, thiazole
		nes, nucleosides and nucleotides	Duga 45 -	nelle A	phate transferase	Dv0447	thic	moiety
1. Purine Rv1389	ribonuciec gmk	otide biosynthesis putative guanylate kinase	Rv2445c Rv2440c	ndkA obg	nucleoside diphosphate kinase Obg GTP-binding protein	Rv0417	thiG	thiamine synthesis, thiazole moiety
Rv3396c		GMP synthase	Rv2583c	relA	(p)ppGpp synthase I	Rv2977c	thiL	probable thiamine-monophos-
Rv1843c	guaA guaB1	inosine-5'-monophosphate dehy-		7001	(b)bbobb olimpo i			phate kinase
	-	drogenase	G. Biosyn	thesis of d	ofactors, prosthetic groups and			•
Rv3411c	guaB2	inosine-5 -monophosphate dehy-	carriers			9. Riboflav		
D-2115	6-	drogenase	1. Biotin	6: •	and an analysis of the second second	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
1410170	PISM	nase	Rv1589	bioD	dethiobiotin synthase	Rv2786c	ribF	riboflavin kinase
Rv0357c	purA	adenylosuccinate synthase	Rv1569	bioF	8-amino-7-oxononanoate	Rv1409	ribG	riboflavin biosynthesis
Rv0777	purB	adenylosuccinate lyase			synthase	Rv1416	ribH	riboflavin synthase β chain
Rv0780	purC	phosphoribosylaminoimidazole-	Rv0032	bioF2	Ć-terminal similar to <i>B. subtilis</i>	Rv3300c	-	probable deaminase, riboflavin
n	_	succinocarboxamide synthase		,	BioF			synthesis
Rv0772	purD	phosphoribosylamine-glycine lig-	Rv3279c	birA	biotin apo-protein ligase	10 T-:	dovin	torodovin and
Rv3275c	purE	ase phosphoribosylaminoimidazole	Rv1442 Rv0089	bisC -	biotin sulfoxide reductase possible bioC biotin synthesis	10. Thiore Rv0773c	doxin, glui <i>ggtA</i>	taredoxin and mycothiol putative γ-glutamyl transpeptidase
11402100	pur⊏	pnospnoribosylaminolimidazole carboxylase	1140008	-	gene	Rv2394	ggtA ggtB	putative γ-glutamyi transpeptidase γ-glutamyltranspeptidase
Rv0808	purF	amidophosphoribosyltransferase-			3-10		9910	precursor
Rv0957	purH	phosphoribosylaminoimidazole-	2. Folic ac	id		Rv2855	gorA	glutathione reductase homologue
	J 1	carboxamide formyltransferase	Rv2763c		dihydrofolate reductase	Rv0816c	thiX	equivalent to <i>M. leprae</i> ThiX
Rv3276c	purK	phosphoribosylaminoimidazole	Rv2447c	folC	folylpolyglutamate synthase	Rv1470	trxA	thioredoxin
		carboxylase ATPase subunit	Rv3356c	foID	methylenetetrahydrofolate dehy-	Rv1471	t <i>r</i> xB	thioredoxin reductase
R080vF	purL	phosphoribosylformylglycin-			drogenase	Rv3913	trxB2	thioredoxin reductase
		amidine synthase II	Rv3609c	folE	GTP cyclohydrolase I	Rv3914	trxC	thioredoxin
Rv0809	purM	5'-phosphoribosyl-5-aminoimida-	Rv3606c	folK	7,8-dihydro-6-hydroxymethylpterin	44 10	uines: ¬	IOO ubiquiness and attent
Rv0956	purN	zole synthase phosphoribosylglycinamide	Rv3608c	folP	pyrophosphokinase dihydropteroate synthase	11. Menac terpenoids		QQ, ubiquinone and other
140900	puriv	formyltransferase I	Rv1207	foIP2	dinydropteroate synthase dihydropteroate synthase	Rv2682c		1-deoxy-D-xylulose 5-phosphate
Rv0788	purQ	phosphoribosylformylglycin-	Rv3607c	folX	may be involved in folate biosyn-	11420020	una	synthase
	,	amidine synthase I			thesis	Rv0562	grcC1	heptaprenyl diphosphate
Rv0389	purT	phosphoribosylglycinamide	Rv0013	pabA	p-aminobenzoate synthase gluta-			synthase II
	·	formyltransferase II			mine amidotransferase	Rv0989c	grcC2	heptaprenyl diphosphate
	purU	formyltetrahydrofolate deformy-	Rv1005c	pabB	p-aminobenzoate synthase	D		synthase II
Rv2964		lase	Rv0812	pabC	aminodeoxychorismate lyase	Rv3398c	idsA	geranylgeranyl pyrophosphate
Rv2964						Bv2172	idsA2	synthase
	dina ribar:					Rv2173	IUSAZ	geranylgeranyl pyrophosphate synthase
2. Pyrimid		cleotide biosynthesis	3. Lipoate By2218	lin∆	lingate biggynthagig protoin A			
2. Pyrimid	dine ribonu <i>carA</i>	carbamoyl-phosphate synthase	Rv2218	lipA lipB	lipoate biosynthesis protein A	Bv3383c	idsB	transfergeranyl, similar geranyl
2. Pyrimid Rv1383		carbamoyl-phosphate synthase subunit		lipA lipB	lipoate biosynthesis protein A lipoate biosynthesis protein B	Rv3383c	idsB	transfergeranyl, similar geranyl pyrophosphate synthase
2. Pyrimid Rv1383 Rv1384	carA	carbamoyl-phosphate synthase	Rv2218	lipB		Rv3383c Rv0534c	idsB menA	transfergeranyl, sımılar geranyl pyrophosphate synthase 4-dihydroxy-2-naphthoate
2. Pyrimid Rv1383 Rv1384 Rv1380	carA carB pyrB	carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase	Rv2218 Rv2217	lipB	lipoate biosynthesis protein B molybdenum cofactor biosynthe-	Rv0534c	menA	pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase
2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381	carA carB pyrB pyrC	carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotase	Rv2218 Rv2217 4. Molybdo Rv3109	lipB opterin moaA	lipoate biosynthesis protein B molybdenum cofactor biosynthesis, protein A	Rv0534c Rv0548c	menA menB	pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase naphthoate synthase
2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139	carA carB pyrB pyrC pyrD	carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotase dihydroorotate dehydrogenase	Rv2218 Rv2217 4. Molybdo	<i>lipB</i> opterin	lipoate biosynthesis protein B molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthe-	Rv0534c Rv0548c Rv0553	menA menB menC	pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase naphthoate synthase o-succinylbenzoate-CoA synthase
2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139	carA carB pyrB pyrC	carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotase dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxy-	Rv2218 Rv2217 4. Molybdo Rv3109 Rv0869c	lipB opterin moaA moaA2	lipoate biosynthesis protein B molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A	Rv0534c Rv0548c	menA menB	pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase naphthoate synthase o-succinylbenzoate-CoA synthase 2-succinyl-6-hydroxy-2,4-cyclo-
2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385	carA carB pyrB pyrC pyrD pyrF	carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotase dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxylase	Rv2218 Rv2217 4. Molybdo Rv3109	lipB opterin moaA	lipoate biosynthesis protein B molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A	Rv0534c Rv0548c Rv0553 Rv0555	menA menB menC menD	pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase naphthoate synthase o-succinylbenzoate-CoA synthase 2-succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-oarboxylate synthas
2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699	carA carB pyrB pyrC pyrD pyrF	carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotase dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxylase CTP synthase	Rv2218 Rv2217 4. Molybdi Rv3109 Rv0869c Rv0438c	lipB opterin moaA moaA2 moaA3	lipoate biosynthesis protein B molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A	Rv0534c Rv0548c Rv0553 Rv0555	menA menB menC menD	pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase naphthoate synthase o-succinylbenzoate-CoA synthase 2-succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-oarboxylate synthas o-succinylbenzoic acid-CoA ligas
2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699 Rv2883c	carA carB pyrB pyrC pyrD pyrF pyrG pyrG	carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotase dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxylase CTP synthase uridylate kinase	Rv2218 Rv2217 4. Molybdo Rv3109 Rv0869c	lipB opterin moaA moaA2	molybdenum cofactor biosynthesis, protein A	Rv0534c Rv0548c Rv0553 Rv0555	menA menB menC menD	pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase naphthoate synthase o-succinylbenzoate-CoA synthase 2-succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthas o-succinylbenzoic acid-CoA ligas S-adenosylmethionine:
2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699 Rv2883c	carA carB pyrB pyrC pyrD pyrF	carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotase dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxylase CTP synthase	Rv2218 Rv2217 4. Molybde Rv3109 Rv0869e Rv0438e	lipB opterin moaA moaA2 moaA3	lipoate biosynthesis protein B molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A	Rv0534c Rv0548c Rv0553 Rv0555	menA menB menC menD	pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase naphthoate synthase o-succinylbenzoate-CoA synthas 2-succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-oarboxylate synthas o-succinylbenzoic acid-CoA ligas
2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699 Rv2883c Rv0382c	carA carB pyrB pyrC pyrD pyrF pyrF pyrG pyrH umpA	carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotase dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxylase CTP synthase uridylate kinase probable uridine 5'-monophosphate synthase	Rv2218 Rv2217 4. Molybdi Rv3109 Rv0869c Rv0438c Rv3110 Rv0984	ipB opterin moaA moaA2 moaA3 moaB moaB2	Ilipoate biosynthesis protein B molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein B molybdenum cofactor biosynthesis, protein B molybdenum cofactor biosynthesis, protein B	Rv0534c Rv0548c Rv0553 Rv0555 Rv0542c Rv3853	menA menB menC menD menE menG	pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase naphthoate synthase o-succinylbenzoate-CoA synthase 2-succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthas o-succinylbenzoic acid-CoA ligas S-adenosylmethionine: 2-demethylmenaquinone phytoene synthase ocenzyme PQQ synthesis
2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699 Rv2883c Rv0382c	carA carB pyrB pyrC pyrD pyrF pyrG pyrH umpA	carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotase dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxylase CTP synthase uridylate kinase probable uridine 5'-monophosphate synthase	Rv2218 Rv2217 4. Molybdi Rv3109 Rv0869c Rv0438c Rv3110	lipB opterin moaA moaA2 moaA3 moaA3	molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein B	Rv0534c Rv0548c Rv0553 Rv0555 Rv0542c Rv3853 Rv3397c Rv0693	menA menB menC menD menE menG phyA pqqE	pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase naphthoate 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 ocenzyme PQQ synthesis protein E
2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699 Rv2883c Rv0382c	carA carB pyrB pyrC pyrD pyrF pyrF pyrG pyrH umpA	carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotase dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxy-lase CTP synthase uridylate kinase probable uridine 5'-monophosphate synthase	Rv2218 Rv2217 4. Molybdi Rv3109 Rv0869c Rv0438c Rv3110 Rv0984	opterin moaA2 moaA3 moaB3 moaB2 moaC	Ilipoate biosynthesis protein B molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein B molybdenum cofactor biosynthesis, protein B molybdenum cofactor biosynthesis, protein B molybdenum cofactor biosynthesis, protein C	Rv0534c Rv0548c Rv0553 Rv0555 Rv0542c Rv3853 Rv3397c	menA menB menC menD menE menG	pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase naphthoate synthase o-succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-oarboxylate synthase o-succinylbenzoic acid-CoA ligas S-adenosylmethionine: 2-demethylmenaquinone phytoene synthase ocenzyme PQQ synthesis protein E ubiquinone/menaquinone biosyn-
2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699 Rv2883c Rv0382c	carA carB pyrB pyrC pyrC pyrF pyrF pyrG pyrH umpA dyribonucle	carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotase dehydrogenase crotidine 5'-phosphate decarboxylase CTP synthase uridylate kinase probable uridine 5'-monophosphate synthase cotide metabolism deoxycytidine triphosphate deaminase	Rv2218 Rv2217 4. Molybdi Rv3109 Rv0869c Rv0438c Rv3110 Rv0984	ipB opterin moaA moaA2 moaA3 moaB moaB2	Ilipoate biosynthesis protein B molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein B molybdenum cofactor biosynthesis, protein B molybdenum cofactor biosynthesis, protein B molybdenum cofactor biosynthesis, protein C molybdenum cofactor biosynthesis, protein C	Rv0534c Rv0548c Rv0553 Rv0555 Rv0542c Rv3853 Rv3397c Rv0693	menA menB menC menD menE menG phyA pqqE	pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase naphthoate 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 ocenzyme PQQ synthesis protein E
2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1385 Rv1385 Rv1699 Rv2883c Rv0382c Rv0382c	carA carB pyrB pyrC pyrD pyrF pyrG pyrH umpA tyribonucle dcd dut	carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotase dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxylase CTP synthase uridylate kinase probable uridine 5'-monophosphate synthase cotide metabolism deoxycytidine triphosphate deaminase deoxyuridine triphosphatase	Rv2218 Rv2217 4. Molybdi Rv3109 Rv0869c Rv0438c Rv3110 Rv0984 Rv31111	lipB opterin moaA2 moaA3 moaB moaB2 moaC2	Ilipoate 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 molybdenum cofactor biosynthesis, protein C molybdenum cofactor biosynthesis, protein C	Rv0534c Rv0548c Rv0553 Rv0555 Rv0542c Rv3853 Rv3397c Rv0693 Rv0558	menA menB menC menD menE menG phyA pqqE ubiE	pyrophosphate synthase 4-dihydroxy2-anphthoate octaprenyltransferase naphthoate synthase o-succinylbenzoate-CoA synthase o-succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase o-succinylbenzoic acid-CoA ligase S-adenosylmethionine: 2-demethylmenaquinone phytoene synthase ocenzyme PQQ synthesis protein E ubiquinone/menaquinone biosynthesis methyltransferase
2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1385 Rv1385 Rv1699 Rv2883c Rv0382c Rv0382c	carA carB pyrB pyrC pyrC pyrF pyrF pyrG pyrH umpA dyribonucle	carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotase dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxy-lase CTP synthase uridylate kinase probable uridine 5'-monophosphate synthase with the synthase orotide metabolism deoxycytidine triphosphate deaminase deoxycytidine triphosphatase ribonucleoside-diphosphate	Rv2218 Rv2217 4. Molybdi Rv3109 Rv0869c Rv0438c Rv3110 Rv0984	opterin moaA2 moaA3 moaB3 moaB2 moaC	Ilipoate biosynthesis protein B molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein B molybdenum cofactor biosynthesis, protein B molybdenum cofactor biosynthesis, protein C	Rv0534c Rv0548c Rv0553 Rv0555 Rv0542c Rv3853 Rv3397c Rv0693 Rv0558	menA menB menC menD menE menG phyA pqqE ubiE and porph	pyrophosphate synthase 4-dihydroxy-2-aphthoate octaprenyltransferase naphthoate synthase o-succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-oarboxylate synthase o-succinyl-6-hydroxy-2d-cyclo- hexadiene-1-oarboxylate synthase o-succinylbenzoic acid-CoA ligase S-adenosylmethionine: 2-demethylmenaquinone phytoene synthase ocenzyme PQQ synthesis protein E ubiquinone/menaquinone biosyn- thesis methyltransferase
2. Pyrimid Rv1383 Rv1384 Rv1380 Rv1381 Rv1385 Rv1699 Rv2883c Rv0382c Rv0382c Rv0382c Rv0382c	carA carB pyrB pyrC pyrD pyrF pyrG pyrH umpA xyribonucle dcd dut nrdB	carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotase dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxylase CTP synthase uridylate kinase probable uridine 5'-monophosphate synthase votide metabolism deoxycytidine triphosphate deaminase deoxyuridine triphosphatase ribonucleoside-diphosphate reductase B2 (eukaryotic-like)	Rv2218 Rv2217 4. Molybdi Rv3109 Rv0869c Rv0438c Rv3110 Rv0984 Rv3111 Rv0864 Rv3324c	lipB opterin moaA moaA2 moaA3 moaB moaB2 moaC2 moaC3	Ilipoate biosynthesis protein B molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein B molybdenum cofactor biosynthesis, protein B molybdenum cofactor biosynthesis, protein C	Rv0534c Rv0548c Rv0553 Rv0555 Rv0542c Rv3853 Rv3397c Rv0693 Rv0558	menA menB menC menD menE menG phyA pqqE ubiE and porph	pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase naphthoate 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 ocenzyme PQQ synthesis protein E ubiquinone/menaquinone biosyn- thesis methyltransferase nyrin glutamyl-tRNA reductase
Rv1383 Rv1384 Rv1380 Rv1381 Rv2139 Rv1385 Rv1699 Rv2883c Rv0382e	carA carB pyrB pyrC pyrD pyrF pyrG pyrH umpA xyribonucle dcd dut nrdB	carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotase dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxy-lase CTP synthase uridylate kinase probable uridine 5'-monophosphate synthase with the synthase orotide metabolism deoxycytidine triphosphate deaminase deoxycytidine triphosphatase ribonucleoside-diphosphate	Rv2218 Rv2217 4. Molybdi Rv3109 Rv0869c Rv0438c Rv3110 Rv0984 Rv31111	lipB opterin moaA2 moaA3 moaB moaB2 moaC2	Ilipoate biosynthesis protein B molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein A molybdenum cofactor biosynthesis, protein B molybdenum cofactor biosynthesis, protein B molybdenum cofactor biosynthesis, protein C	Rv0534c Rv0548c Rv0553 Rv0555 Rv0542c Rv3853 Rv3397c Rv0693 Rv0558	menA menB menC menD menE menG phyA pqqE ubiE and porph	pyrophosphate synthase 4-dihydroxy-2-aphthoate octaprenyltransferase naphthoate synthase o-succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-oarboxylate synthase o-succinyl-6-hydroxy-2d-cyclo- hexadiene-1-oarboxylate synthase o-succinylbenzoic acid-CoA ligase S-adenosylmethionine: 2-demethylmenaquinone phytoene synthase ocenzyme PQQ synthesis protein E ubiquinone/menaquinone biosyn- thesis methyltransferase

Rv1300 Rv0524	hemK hemL	protoporphyrinogen oxidase glutamate-1-semialdehyde amino-	0. 4		transferase	Rv2931 Rv2932	ppsA ppsB	phenolpthiocerol synthesis (pksB) phenolpthiocerol synthesis (pksC)
Rv2388c	hemN	transferase oxygen-independent copropor-	3. Acyitrar phospholi		mycolyltransferases and esis	Rv2933 Rv2934	ppsC ppsD	phenolpthiocerol synthesis (pksD) phenolpthiocerol synthesis (pksE)
D.,0077-	(\/ (1	phyrinogen III oxidase	Rv2289	cdh	CDP-diacylglycerol phosphatidyl-	Rv2935	ppsE	phenolpthiocerol synthesis (pksF)
Rv2677c Rv1485	hemY' hemZ	protoporphyrinogen oxidase ferrochelatase	Rv2881c Rv3804c	cdsA fbpA	hydrolase phosphatidate cytidylyltransferase	Rv2928 Rv1544	tesA -	thioesterase probable ketoacyl reductase
13. Cobala	amin		Rv1886c	fbpB	antigen 85A, mycolyltransferase antigen 85B, mycolyltransferase	J. Broad i	egulatory	functions
Rv2849c	cobA	cob(I)alamin adenosyltransferase	Rv0129c	fbpC	antigen 85C, mycolytransferase	 Repres 	sors/activa	ators
Rv2848c	cobB cobC	cobyrinic acid a,c-diamide synthase	Rv3803c	fbpD	antigen MPT51, mycolyltrans-	Rv1657	argR	arginine repressor
Rv2231c Rv2236c	cobD	aminotransferase cobinamide synthase	Rv0564c	gpdA1	ferase glycerol-3-phosphate dehydroge-	Rv1267c	embR	regulator of <i>embAB</i> genes (AfsR/Dndl/RedD family)
Rv2064	cobG	percorrin reductase		•	nase	Rv1909c	furA	ferric uptake regulatory protein
Rv2065 Rv2066	cobH	precorrin isomerase	Rv2982c	gpdA2	glycerol-3-phosphate dehydroge-	Rv2359	furB	ferric uptake regulatory protein
Rv2070c	cobl cobK	Cobl-CobJ fusion protein precorrin reductase	Rv2612c	pgsA	nase CDP-diacylglycerol-glycerol-3-	Rv2919c Rv2711	glnB ideR	nitrogen regulatory protein iron dependent repressor, IdeR
Rv2072c	cobL	probable methyltransferase		, 3	phosphate phosphatidyltrans-	Rv2720	lexA	LexA, SOS repressor protein
Rv2071c Rv2062c	cobM cobN	precorrin-3 methylase cobalt insertion	Rv1822	na 10	ferase CDP-diacylglycerol-glycerol-3-	Rv1479	mox <i>R</i>	transcriptional regulator, MoxR
Rv2208	cobS	cobalamin (5'-phosphate) synthase	HV 1022	pgsA2	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
Rv0254c Rv0255c	cobU cobQ	cobinamide kinase cobyric acid synthase	Rv1551	plsB1	ferase glycerol-3-phosphate acyltrans-	Rv0212c Rv0117	nadR oxyS	similar to <i>E.coli</i> NadR transcriptional regulator (LysR
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 ut	tilization		Rv0437c	psd	putative phosphatidylserine decarboxylase	Rv2788	sir⊟	iron-dependent transcriptional repressor
Rv1876	bfrA	bacterioferritin	Rv0436c	pssA	CDP-diacylglycerol-serine	Rv3082c	virS	putative virulence regulating
Rv3841 Rv3215 Rv3214	bfrB entC entD	bacterioferritin probable isochorismate synthase	Rv0045c	-	o-phosphatidyltransferase possible dihydrolipoamide acetyl- transferase	Rv3219	whiB1	protein (AraC/XyIS family) WhiB transcriptional activator
Rv3214		weak similarity to many phospho- glycerate mutases	Rv0914c	-	lipid transfer protein	Rv3260c	whiB2	homologue WhiB transcriptional activator
Rv2895c	viuB	similar to proteins involved in vibriobactin uptake	Rv1543 Rv1627c	-	probable fatty-acyl CoA reductase lipid carrier protein	Rv3416	whiB3	homologue WhiB transcriptional activator
Rv3525c	-	similar to ferripyochelin binding protein	Rv1814 Rv1867	-	possible C-5 sterol desaturase similar to acetyl CoA	Rv3681c	whiB4	homologue WhiB transcriptional activator
H. Lipid bi	iosynthesi:	s	Rv2261c		synthase/lipid carriers apolipoprotein N-acyltrans-	Rv0023	_	homologue putative transcriptional regulator
1. Synthes	sis of fatty	and mycolic acids			ferase-a	Rv0043c	-	transcriptional regulator (GntR
Rv3285	accA3	acetyl/propionyl CoA carboxylase α subunit	Rv2262c		apolipoprotein N-acyltrans- ferase-b	Rv0067c		family) transcriptional regulator
Rv0904c	accD3	acetyl/propionyl CoA carboxylase β subunit	Rv3523 Rv3720	-	lipid carrier protein C-term similar to cyclopropane	Rv0078	_	(TetR/AcrR family) transcriptional regulator
Rv3799c	accD4	acetyl/propionyl CoA carboxylase β subunit	1,10,20		fatty acid synthases	Rv0081	_	(TetR/AcrR family) transcriptional regulator (ArsR
Rv3280	accD5	acetyl/propionyl CoA carboxylase			n-ribosomal peptide synthesis			family)
Rv2247	accD6	β subunit acetyl/propionyl CoA carboxylase	Rv2940c Rv2384	mas mbtA	mycocerosic acid synthase mycobactin/exochelin synthesis	Rv0135c Rv0144	-	putative transcriptional regulator putative transcriptional regulator
Bv2244	асрМ	β subunit acyl carrier protein (meromycolate	Rv2383c	mbtB	(salicylate-AMP ligase) mycobactin/exochelin synthesis	Rv0158	-	transcriptional regulator (TetR/AcrR family)
Rv2523c	acpS	extension) CoA:apo-[ACP] pantethienephos-	Rv2382c	mbtC	(serine/threonine ligation) mycobactin/exochelin synthesis	Rv0165c	-	transcriptional regulator (GntR family)
		photransferase	Rv2381c	mbtD	mycobactin/exochelin synthesis	Rv0195	-	transcriptional regulator
Rv2243 Rv0649	fabD fabD2	malonyl CoA-[ACP] transacylase malonyl CoA-[ACP] transacylase	Rv2380c	mbtE	(polyketide synthase) mycobactin/exochelin synthesis	Rv0196	-	(LuxR/UhpA family) transcriptional regulator
Rv1483	fabG1	3-oxoacyl-[ACP] reductase (aka MabA)	Rv2379c	mbtF	(lysine ligation) mycobactin/exochelin synthesis	Rv0232		(TetR/AcrR family) transcriptional regulator
Rv1350	fabG2	3-oxoacyl-[ACP] Reductase	11023790	mou	(lysine ligation)	1100232	-	(TetR/AcrR family)
Rv2002	fabG3	3-oxoacyl-[ACP] reductase	Rv2378c	mbtG	mycobactin/exochelin synthesis	Rv0238	-	transcriptional regulator
Rv0242c Rv2766c	fabG4 fabG5	3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase	Rv2377c	mbtH	(lysine hydroxylase) mycobactin/exochelin synthesis	Rv0273c	_	(TetR/AcrR family) putative transcriptional regulator
Rv0533c	fabH	β-ketoacyl-ACP synthase III	Rv0101	nrp	unknown non-ribosomal peptide	Rv0302	-	transcriptional regulator
Rv2524c	fas	fatty acid synthase	D 4450		synthase	D 0004		(TetR/AcrR family)
Rv1484 Rv2245	inhA kasA	enoyl-[ACP] reductase β-ketoacyl-ACP synthase	Rv1153c Rv3824c	omt papA1	PKS o-methyltransferase PKS-associated protein, unknown	Rv0324 Rv0328	-	putative transcriptional regulator transcriptional regulator
		(meromycolate extension)			function			(TetR/AcrR family)
Rv2246	kasB	β-ketoacyl-ACP synthase (meromycolate extension)	Rv3820c	papA2	PKS-associated protein, unknown function	Rv0348 Rv0377	-	putative transcriptional regulator transcriptional regulator (LysR
Rv1618	tesB1	thioesterase II	Rv1182	papA3	PKS-associated protein, unknown		-	family)
Rv2605c	tesB2	thioesterase II			function	Rv0386	-	transcriptional regulator
Rv0033 Rv1344	-	possible acyl carrier protein possible acyl carrier protein	Rv1528c	papA4	PKS-associated protein, unknown function	Rv0452	-	(LuxR/UhpA family) putative transcriptional regulator
Rv1722 Rv3221c	-	possible biotin carboxylase resembles biotin carboxyl carrier	Rv2939	papA5	PKS-associated protein, unknown function	Rv0465c	-	transcriptional regulator (PbsX/Xre family)
Rv3472	-	possible acyl carrier protein	Rv2946c	pks1	polyketide synthase	Rv0472c	-	transcriptional regulator
2. Modifica	ation of fat	tty and mycolic acids	Rv3825c Rv1180	pks2 pks3	polyketide synthase polyketide synthase	Rv0474	_	(TetR/AcrR family) transcriptional regulator
Rv3391	acrA1	fatty acyl-CoA reductase	Rv1181	pks4	polyketide synthase			(PbsX/Xre family)
	cmaA1	cyclopropane mycolic acid	Rv1527c Rv0405	pks5 pks6	polyketide synthase	Rv0485	-	transcriptional regulator (ROK family)
Rv3392c	• • •	synthase 1 cyclopropane mycolic acid syn-	Rv1661	pks7	polyketide synthase polyketide synthase	Rv0494	-	transcriptional regulator (GntR
Rv0503c	cmaA2	thase 2	Rv1662	pks8	polyketide synthase	DUARTA		family)
Rv0503c			Rv1664	pks9 pks10	polyketide synthase polyketide synthase (chalcone	Rv0552 Rv0576	-	putative transcriptional regulator putative transcriptional regulator
	desA1	acyl-[ACP] desaturase acyl-[ACP] desaturase	Rv1660					
Rv0503c Rv0824c Rv1094 Rv3229c	desA1 desA2 desA3	acyl-[ACP] desaturase acyl-[ACP] desaturase		·	synthase-like)	Rv0586	-	transcriptional regulator (GntR
Rv0503c Rv0824c Rv1094 Rv3229c Rv0645c	desA1 desA2 desA3 mmaA1	acyl-[ACP] desaturase acyl-[ACP] desaturase methoxymycolic acid synthase 1	Hv1660 Rv1665	pks11	polyketide synthase (chalcone			family)
Rv0503c Rv0824c Rv1094 Rv3229c Rv0645c Rv0644c	desA1 desA2 desA3 mmaA1 mmaA2	acyl-[ACP] desaturase acyl-[ACP] desaturase methoxymycolic acid synthase 1 methoxymycolic acid synthase 2	Rv1665	pks11	polyketide synthase (chalcone synthase-like)	Rv0650		family) transcriptional regulator (ROK
Rv0503c Rv0824c Rv1094 Rv3229c Rv0645c Rv0644c Rv0643c Rv0642c	desA1 desA2 desA3 mmaA1 mmaA2 mmaA3 mmaA4	acyl-[ACP] desaturase acyl-[ACP] desaturase methoxymycolic acid synthase 1 methoxymycolic acid synthase 2 methoxymycolic acid synthase 3 methoxymycolic acid synthase 4	Rv1665 Rv2048c	pks11 pks12	polyketide synthase (chalcone synthase-like) polyketide synthase (erythronolide synthase-like)	Rv0650 Rv0653c		family) transcriptional regulator (ROK family) putative transcriptional regulator
Rv0503c Rv0824c Rv1094 Rv3229c Rv0645c Rv0644c Rv0643c	desA1 desA2 desA3 mmaA1 mmaA2 mmaA3	acyl-[ACP] desaturase acyl-[ACP] desaturase methoxymycolic acid synthase 1 methoxymycolic acid synthase 2 methoxymycolic acid synthase 3 methoxymycolic acid synthase 4 unknown fatty acid methyltrans-	Rv1665 Rv2048c Rv3800c	pks11 pks12 pks13	polyketide synthase (chalcone synthase-like) polyketide synthase (erythronolide synthase-like) polyketide synthase	Rv0650	-	family) transcriptional regulator (ROK family) putative transcriptional regulator transcriptional regulator
Rv0503c Rv0824c Rv1094 Rv3229c Rv0645c Rv0644c Rv0643c Rv0642c	desA1 desA2 desA3 mmaA1 mmaA2 mmaA3 mmaA4	acyl-[ACP] desaturase acyl-[ACP] desaturase methoxymycolic acid synthase 1 methoxymycolic acid synthase 2 methoxymycolic acid synthase 3 methoxymycolic acid synthase 4 unknown fatty acid methyltrans- ferase unknown fatty acid methyltrans-	Rv1665 Rv2048c Rv3800c Rv1342c	pks11 pks12 pks13 pks14	polyketide synthase (chalcone synthase-like) polyketide synthase (erythronolide synthase-like) polyketide synthase polyketide synthase synthase-like)	Rv0650 Rv0653c	-	family) transcriptional regulator (ROK family) putative transcriptional regulator transcriptional regulator (TetR/AcrR family) transcriptional regulator
Rv0503c Rv0824c Rv1094 Rv3229c Rv0645c Rv0644c Rv0643c Rv0642c Rv0447c	desA1 desA2 desA3 mmaA1 mmaA2 mmaA4 ufaA1	acyl-[ACP] desaturase acyl-[ACP] desaturase methoxymycolic acid synthase 1 methoxymycolic acid synthase 2 methoxymycolic acid synthase 3 methoxymycolic acid synthase 4 unknown fatty acid methyltrans- ferase	Rv1665 Rv2048c Rv3800c	pks11 pks12 pks13	polyketide synthase (chalcone synthase-like) polyketide synthase (erythronolide synthase-like) polyketide synthase polyketide synthase (chalcone	Rv0650 Rv0653c Rv0681		family) transcriptional regulator (ROK family) putative transcriptional regulator transcriptional regulator (TetR/AorR family)

Dungga	-	family)		-	putative transcriptional regulator	Ducotes	200	truncated
Rv0823c	-	transcriptional regulator (NifR3/Smm1 family)	Rv3167c Rv3173c	-	putative transcriptional regulator transcriptional regulator	Rv0018c	ppp	putative phosphoprotein phos- phatase
Rv0827c	-	transcriptional regulator (ArsR	D-0400		(TetR/AcrR family)	Rv2234	ptpA	low molecular weight protein-tyre
Rv0890c	-	family) transcriptional regulator	Rv3183 Rv3208	-	putative transcriptional regulator transcriptional regulator	Rv0153c	_	sine-phosphatase putative protein-tyrosine-phos-
		(LuxR/UhpA family)			(TetR/AcrR family)			phatase
Rv0891c Rv0894	-	putative transcriptional regulator putative transcriptional regulator	Rv3249c	-	transcriptional regulator (TetR/AcrR family)	II Maaran	a clasula	metabolism
Rv1019	-	transcriptional regulator	Rv3291c	-	transcriptional regulator			nodification of macromolecules
		(TetR/AcrR family)			(Lrp/AsnC family)	 Ribosor 	nal protei	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
D 4454		(PbsX/Xre family)	D 0405		family)	Rv0641	rplA	50S ribosomal protein L1
Rv1151c Rv1152	-	putative transcriptional regulator transcriptional regulator (GntR	Rv3405c Rv3522	-	putative transcriptional regulator putative transcriptional regulator	Rv0704 Rv0701	rpIB rpIC	50S ribosomal protein L2 50S ribosomal protein L3
		family)	Rv3557c	-	transcriptional regulator	Rv0702	rplD	50S ribosomal protein L4
Rv1167c		putative transcriptional regulator	D-0574		(TetR/AcrR family)	Rv0716	rpIE	50S ribosomal protein L5
Rv1219c Rv1255c		putative transcriptional regulator transcriptional regulator	Rv3574	-	transcriptional regulator (TetR/AcrR family)	Rv0719 Rv0056	rplF rpll	50S ribosomal protein L6 50S ribosomal protein L9
		(TetR/AcrR family)	Rv3575c	-	transcriptional regulator (Lacl	Rv0651	rpIJ	50S ribosomal protein L10
Rv1332 Rv1353c	-	putative transcriptional regulator transcriptional regulator	Rv3583c	_	family) putative transcriptional regulator	Rv0640 Rv0652	rplK rplL	50S ribosomal protein L11
HV 1353C	-	(TetR/AcrR family)	Rv3676	-	transcriptional regulator (Crp/Fnr	Rv3443c	rpiM	50S ribosomal protein L7/L12 50S ribosomal protein L13
Rv1358	-	transcriptional regulator			family)	Rv0714	rplN	50S ribosomal protein L14
Rv1359	_	(LuxR/UhpA family) putative transcriptional regulator	Rv3678c	-	transcriptional regulator (LysR family)	Rv0723 Rv0708	rpIO rpIP	50S ribosomal protein L15 50S ribosomal protein L16
Rv1395	-	transcriptional regulator	Rv3736	-	transcriptional regulator	Rv3456c	rpiQ	50S ribosomal protein L16
		(AraC/XyIS family)			(AraC/XyIS family)	Rv0720	rplR	50S ribosomal protein L18
Rv1404	-	transcriptional regulator (MarR family)	Rv3744	-	transcriptional regulator (ArsR family)	Rv2904c Rv1643	rpIS rpIT	50S ribosomal protein L19 50S ribosomal protein L20
Rv1423	-	putative transcriptional regulator	Rv3830c	-	transcriptional regulator	Rv2442c	rplU	50S ribosomal protein L21
Rv1460	-	putative transcriptional regulator	Duggeon		(TetR/AcrR family)	Rv0706	rplV rplW	50S ribosomal protein L22
Rv1474c	-	transcriptional regulator (TetR/AcrR family)	Rv3833	-	transcriptional regulator (AraC/XyIS family)	Rv0703 Rv0715	rpIW rpIX	50S ribosomal protein L23 50S ribosomal protein L24
Rv1534	-	transcriptional regulator	Rv3840	-	putative transcriptional regulator	Rv1015c	rplY	50S ribosomal protein L25
Dutero		(TetR/AcrR family)	Rv3855	-	putative transcriptional regulator	Rv2441c	rpmA	50S ribosomal protein L27
Rv1556 Rv1674c	-	putative transcriptional regulator putative transcriptional regulator	2. Two cor	nponent s	ystems	Rv0105c Rv2058c	rpmB rpmB2	50S ribosomal protein L28 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	rpm⊆ rpmG	50S ribosomal protein L33
		family)			regulator	Rv3924c	rpmH	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	71700-140	riot L	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	Du0400	00n V2	regulator	Rv0053	rpsF	30S ribosomal protein S6
Rv1990c	-	family) putative transcriptional regulator	Rv0490 Rv0602c	senX3 tcrA	sensor histidine kinase two-component response	Rv0683 Rv0718	rpsG rpsH	30S ribosomal protein S7 30S ribosomal protein S8
Rv1994c		transcriptional regulator (MerR			regulator	Rv3442c	rpsl	30S ribosomal protein S9
Rv2017		family) putative transcriptional regulator	Rv0260c	-	two-component response	Rv0700 Rv3459c	rpsJ rpsK	30S ribosomal protein S10
1142017	-	(PbsX/Xre family)	Rv0600c	-	regulator sensor histidine kinase	Rv0682	rpsk rpsL	30S ribosomal protein S11 30S ribosomal protein S12
Rv2021c	1	putative transcriptional regulator	Rv0601c	-	sensor histidine kinase	Rv3460c	rpsM	30S ribosomal protein S13
Rv2034		transcriptional regulator (ArsR family)	Rv0818	-	two-component response regulator	Rv0717 Rv2056c	rpsN rpsN2	30S ribosomal protein S14 30S ribosomal protein S14
Rv2175c		putative transcriptional regulator	Rv0845	-	sensor histidine kinase	Rv2785c	rpsN2 rpsO	30S ribosomal protein S15
Rv2250c		putative transcriptional regulator	Rv0902c	-	sensor histidine kinase	Rv2909c	rpsP	30S ribosomal protein S16
Rv2258c Rv2282c		putative transcriptional regulator transcriptional regulator (LysR	Rv0903c	-	two-component response regulator	Rv0710 Rv0055	rpsQ rpsR	30S ribosomal protein S17 30S ribosomal protein S18
		family)	Rv0981	-	two-component response	Rv2055c	rpsR2	30S ribosomal protein S18
Rv2308	-	putative transcriptional regulator transcriptional regulator	Ducces		regulator	Rv0705	rpsS rpsT	30S ribosomal protein S19
Rv2324	-		Rv0982	-	sensor histidine kinase	Rv2412	rpsT	30S ribosomal protein S20 member of S30AE ribosomal
				-	sensor histidine kinase		-	
Rv2358	-	(Lrp/AsnC family) transcriptional regulator (ArsR	Rv1032c Rv1033c	-	two-component response	Rv3241c	-	protein family
	-	(Lrp/AsnC family) transcriptional regulator (ArsR family)	Rv1032c Rv1033c	-	two-component response regulator	Rv3241c		protein family
Rv2358 Rv2488c	-	(Lrp/AsnC family) transcriptional regulator (ArsR	Rv1032c	-	two-component response	Rv3241c		
Rv2488c	-	(Lrp/AsnC family) transcriptional regulator (ArsR family) transcriptional regulator (LuxR/UhpA family) transcriptional regulator	Rv1032c Rv1033c Rv1626 Rv2027c	-	two-component response regulator two-component response regulator sensor histidine kinase	2. Ribosor Rv1010 Rv2838c	ne modifi <i>ksgA</i> <i>rbfA</i>	protein family cation and maturation 16S rRNA dimethyltransferase ribosome-binding factor A
Rv2488c Rv2506		(Lrp/AsnC family) transcriptional regulator (ArsR family) transcriptional regulator (LuxR/UhpA family) transcriptional regulator (TetR/AorR family)	Rv1032c Rv1033c Rv1626	-	two-component response regulator two-component response regulator sensor histidine kinase two-component response	Rv3241c 2. Ribosor Rv1010	ne modifi <i>ksgA</i>	protein family cation and maturation 16S rRNA dimethyltransferase
Rv2488c Rv2506 Rv2621c	-	(Lrp/AsnC family) transcriptional regulator (ArsR family) transcriptional regulator (LuxR/UhpA family) transcriptional regulator	Rv1032c Rv1033c Rv1626 Rv2027c Rv2884 Rv3132c	-	two-component response regulator two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase	2. Ribosor Rv1010 Rv2838c Rv2907c	ne modifi ksgA rbfA rimM	protein family cation and maturation 16S rRNA dimethyltransferase ribosome-binding factor A 16S rRNA processing protein synthases and their modification
Rv2488c Rv2506 Rv2621c Rv2640c	-	(Lrp/AsnC family) transcriptional regulator (ArsR family) transcriptional regulator (LuxFl/UhpA family) transcriptional regulator (TetR/AorR family) putative transcriptional regulator transcriptional regulator transcriptional regulator	Rv1032c Rv1033c Rv1626 Rv2027c Rv2884	-	two-component response regulator two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response two-component response	2. Ribosor Rv1010 Rv2838c Rv2907c 3. Aminoa Rv2555c	ne modifi ksgA rbfA rimM cyl tRNA alaS	protein family cation and maturation 16S rRNA dimethyltransferase ribosome-binding factor A 16S rRNA processing protein synthases and their modification alanyl-tRNA synthase
Rv2488c Rv2506 Rv2621c Rv2640c	-	(Lrp/AsnC family) transcriptional regulator (ArsR family) transcriptional regulator (LuxR/UhpA family) transcriptional regulator (TetR/AorR family) putative transcriptional regulator transcriptional regulator (ArsR family) transcriptional regulator (ArsR family)	Rv1032c Rv1033c Rv1626 Rv2027c Rv2884 Rv3132c Rv3133c	-	two-component response regulator two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator	2. Ribosor Rv1010 Rv2838c Rv2907c 3. Aminoa Rv2555c Rv1292	ne modifi ksgA rbfA rimM cyl tRNA alaS argS	protein family cation and maturation 16S rRNA dimethyltransferase ribosome-binding factor A 16S rRNA processing protein synthases and their modification alanyl-tRNA synthase arginyl-tRNA synthase
Rv2488c Rv2506 Rv2621c Rv2640c Rv2642 Rv2669	-	(Lrp/AsnC family) transcriptional regulator (ArsR family) transcriptional regulator (LuxR/UhpA family) transcriptional regulator (TetR/AcrR family) putative transcriptional regulator transcriptional regulator (ArsR family) transcriptional regulator (ArsR family) putative transcriptional regulator (ArsR family) putative transcriptional regulator	Rv1032e Rv1033c Rv1626 Rv2027c Rv2884 Rv3132c Rv3133c Rv3143	- - - - -	two-component response regulator two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator sensor protein sensor y transduction protein	2. Ribosor Rv1010 Rv2838c Rv2907c 3. Aminoa Rv2555c Rv1292 Rv2572c Rv3580c	ne modifi ksgA rbfA rimM cyl tRNA alaS argS aspS cysS	protein family cation and maturation 16S rRNA dimethyltransferase ribosome-binding factor A 16S rRNA processing protein synthases and their modification alanyl-tRNA synthase arginyl-tRNA synthase aspartyl-tRNA synthase cysteinyl-tRNA synthase
Rv2488c Rv2506 Rv2621c Rv2640c Rv2642 Rv2669 Rv2745c	-	(Lrp/AsnC family) transcriptional regulator (ArsR family) transcriptional regulator (LuxR/UhpA family) transcriptional regulator (TetR/AorR family) putative transcriptional regulator transcriptional regulator (ArsR family) transcriptional regulator (ArsR family) putative transcriptional regulator (putative transcriptional regulator (ArsR family)	Rv1032e Rv1033e Rv1626 Rv2027e Rv2884 Rv3132e Rv3133e Rv3143 Rv3220e	- - - - - - -	two-component response regulator two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator putative sensory transduction protein sensor histidine kinase	2. Ribosor Rv1010 Rv2838c Rv2907c 3. Aminoa Rv2555c Rv1292 Rv2572c Rv3580c Rv2130c	ne modifi ksgA rbfA rimM cyl tRNA alaS argS aspS cysS cysS2	protein family cation and maturation 16S rRNA dimethyltransferase ribosome-binding factor A 16S rRNA processing protein synthases and their modification alanyl-tRNA synthase arginyl-tRNA synthase aspartyl-tRNA synthase cysteinyl-tRNA synthase cysteinyl-tRNA synthase
Rv2488c Rv2506 Rv2621c Rv2640c Rv2642 Rv2669 Rv2745c	-	(Lrp/AsnC family) transcriptional regulator (ArsR family) transcriptional regulator (LuxP/UhpA family) transcriptional regulator (TetB/AcrR family) putative transcriptional regulator transcriptional regulator (ArsR family) transcriptional regulator (ArsR family) transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator transcriptional regulator	Rv1032e Rv1033c Rv1626 Rv2027e Rv2884 Rv3132e Rv3133c Rv3143 Rv3220c Rv3764c	- - - - -	two-component response regulator two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator putative sensory transduction protein sensor histidine kinase sensor histidine kinase sensor histidine kinase	2. Ribosor Rv1010 Rv2838c Rv2907c 3. Aminoa Rv2555c Rv1555c Rv1555c Rv2572c Rv3580c Rv2130c Rv1406	ne modifi ksgA rbfA rimM cyl tRNA alaS argS aspS cysS cysS2 fmt	protein family cation and maturation 16S rRNA dimethyltransferase ribosome-binding factor A 16S rRNA processing protein synthases and their modification alanyl-tRNA synthase arginyl-tRNA synthase oysteinyl-tRNA synthase cysteinyl-tRNA synthase methionyl-tRNA formyltransferas
Rv2488c Rv2506 Rv2621c Rv2640c Rv2642 Rv2669 Rv2745c Rv2779c	-	(Lrp/AsnC family) transcriptional regulator (ArsR family) transcriptional regulator (LuxR/UhpA family) transcriptional regulator (TetR/AorR family) putative transcriptional regulator transcriptional regulator (ArsR family) transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator transcriptional regulator (Lrp/AsnC family) transcriptional regulator (Lrp/AsnC family) transcriptional regulator (MarR	Rv1032e Rv1033e Rv1626 Rv2027e Rv2884 Rv3132e Rv3133e Rv3143 Rv3220e		two-component response regulator two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator putative sensory transduction protein sensor histidine kinase	2. Ribosor Rv1010 Rv2838c Rv2907c 3. Aminoa Rv2555c Rv1292 Rv2572c Rv3580c Rv2130c Rv1406 Rv3011c	ne modifi ksgA rbfA rimM eyl tRINA alaS argS aspS cysS cysS2 fmt gatA	protein family cation and maturation 16S rRNA dimethyltransferase ribosome-binding factor A 16S rRNA processing protein synthases and their modification alanyl-tRNA synthase arginyl-tRNA synthase aspartyl-tRNA synthase cysteinyl-tRNA synthase methionyl-tRNA formyltransferas glu-tRNA-gln amidotransferase, subunit B
Rv24886 Rv2506 Rv2621c Rv2640c Rv2642 Rv2669 Rv2745c Rv2779c	-	(Lrp/AsnC family) transcriptional regulator (ArsR family) transcriptional regulator (LuxF/UhpA family) transcriptional regulator (TetF/AcrR family) putative transcriptional regulator transcriptional regulator (ArsR family) transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator transcriptional regulator (Lrp/AsnC family) transcriptional regulator (Lrp/AsnC family) transcriptional regulator (MarR family)	RV1032c RV1033c RV1626 RV2027c RV2884 RV3132c RV3133c RV3143 RV3220c RV3764c RV3765c		two-component response regulator two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator putative sensory transduction protein sensor histidine kinase sensor histidine kinase two-component response regulator	2. Ribosor Rv1010 Rv2838c Rv2907c 3. Aminoa Rv2555c Rv1555c Rv1559c Rv2572c Rv3580c Rv2130c Rv1406	ne modifi ksgA rbfA rimM cyl tRNA alaS argS aspS cysS cysS2 fmt	protein family cation and maturation 16S rRNA dimethyltransferase ribosome-binding factor A 16S rRNA processing protein synthases and their modification alanyl-tRNA synthase arginyl-tRNA synthase aspartyl-tRNA synthase cysteinyl-tRNA synthase cysteinyl-tRNA formyltransferas glu-tRNA-gln amidotransferase, subunit B glu-tRNA-gln amidotransferase,
Rv2488c Rv2506 Rv2621c Rv2640c Rv2642 Rv2669 Rv2745c Rv2779c Rv2887	-	(Lrp/AsnC family) transcriptional regulator (ArsR family) transcriptional regulator (LuxR/UhpA family) transcriptional regulator (TetR/AcrR family) putative transcriptional regulator transcriptional regulator (ArsR family) transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator transcriptional regulator (Lrp/AsnC family) transcriptional regulator (MarR family) transcriptional regulator	Rv1032c Rv1033e Rv1626 Rv2027c Rv2884 Rv3132c Rv3133c Rv3143 Rv3220c Rv3764c Rv3765c		two-component response regulator two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator putative sensory transduction protein sensor histidine kinase sensor histidine kinase two-component response	2. Ribosor Rv1010 Rv2838c Rv2907c 3. Aminoa Rv2555c Rv1292 Rv2572c Rv3580c Rv2130c Rv1406 Rv30011c	ne modifi ksgA rbfA rimM cyl tRNA alaS argS aspS cysS cysS2 fmt gatA	protein family cation and maturation 16S rRNA dimethyltransferase ribosome-binding factor A 16S rRNA processing protein synthases and their modification alanyl-tRNA synthase arginyl-tRNA synthase oysteinyl-tRNA synthase cysteinyl-tRNA synthase cysteinyl-tRNA synthase gusteinyl-tRNA formyltransferas glu-tRNA-gln amidotransferase, subunit B glu-tRNA-gln amidotransferase, subunit A
Rv2488c Rv2506 Rv2621c Rv2640c Rv2642 Rv2669 Rv2745c Rv2779c Rv2887 Rv2912c	-	(Lrp/AsnC family) transcriptional regulator (ArsR family) transcriptional regulator (LuxF/UlpA family) transcriptional regulator (TetF/AcrR family) putative transcriptional regulator transcriptional regulator (ArsR family) transcriptional regulator (ArsR family) transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator transcriptional regulator (Lrp/AsnC family) transcriptional regulator (MarR family) transcriptional regulator (TetR/AcrR family) transcriptional regulator (TetR/AcrR family) transcriptional regulator (IcIR	Rv1032c Rv1033c Rv1626 Rv2027c Rv2884 Rv3132c Rv3133c Rv3143 Rv3220c Rv3764c Rv3765c 3. Serine-t-phosphata Rv00155c	- - - - - - - - - ses pknA	two-component response regulator two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator putative sensory transduction protein sensor histidine kinase sensor histidine kinase two-component response regulator protein kinases and phosphoprotein serine-threonine protein kinase	2. Ribosor Rv1010 Rv2838c Rv2907c 3. Aminoa Rv2555c Rv1292 Rv2572c Rv3580c Rv2130c Rv1406 Rv3011c Rv3009c	ne modific ksgA rbfA rimM cyl tRINA alaS argS aspS cysS cysS2 fmt gatA gatB	protein family cation and maturation 16S rRNA dimethyltransferase ribosome-binding factor A 16S rRNA processing protein synthases and their modification alanyl-tRNA synthase arginyl-tRNA synthase aspartyl-tRNA synthase cysteinyl-tRNA synthase cysteinyl-tRNA synthase methionyl-tRNA formyltransferas glu-tRNA-gln amidotransferase, subunit B glu-tRNA-gln amidotransferase, subunit C
Rv24886 Rv2506 Rv2621c Rv2640c Rv2642 Rv2669 Rv2745c Rv2779c Rv2887 Rv2912c Rv2989		(Lrp/AsnC family) transcriptional regulator (ArsR family) transcriptional regulator (LuxR/UhpA family) transcriptional regulator (TetR/AcrR family) putative transcriptional regulator transcriptional regulator (ArsR family) transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator (Lrp/AsnC family) transcriptional regulator (MarR family) transcriptional regulator (TetR/AcrR family) transcriptional regulator (TetR/AcrR family) transcriptional regulator (IclR family)	Rv1032c Rv1033e Rv1626 Rv2027c Rv2884 Rv3132c Rv3133c Rv3143 Rv3220c Rv3764c Rv3765c 3. Serine-t phosphata Rv0015c Rv0015c Rv0015c	- - - - - - - - ses pknA pknB	two-component response regulator two-component response regulator two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator putative sensory transduction protein sensor histidine kinase sensor histidine kinase two-component response regulator protein kinases and phosphoprotein serine-threonine protein kinase serine-threonine protein kinase serine-threonine protein kinase	2. Ribosor Rv1010 Rv2838c Rv2907c 3. Aminoa Rv2555c Rv1292 Rv2572c Rv3580c Rv2130c Rv1406 Rv3011c Rv3009c Rv3012c Rv2992c	ne modific ksgA rbfA rimM cyl tRINA alaS argS aspS cysS cysS2 fmt gatA gatB gatC gltS	protein family cation and maturation 16S rRNA dimethyltransferase ribosome-binding factor A 16S rRNA processing protein synthases and their modification alanyl-tRNA synthase arginyl-tRNA synthase aspartyl-tRNA synthase oysteinyl-tRNA synthase oysteinyl-tRNA synthase methionyl-tRNA formyltransferase glu-tRNA-gln amidotransferase, subunit B glu-tRNA-gln amidotransferase, subunit A glu-tRNA-gln amidotransferase, subunit C glutamyl-tRNA synthase
Rv2488c Rv2506 Rv2621c Rv2640c Rv2642 Rv2669 Rv2745c Rv2779c Rv2887 Rv2912c Rv2989 Rv3050c		(Lrp/AsnC family) transcriptional regulator (ArsR family) transcriptional regulator (LuxF/UlpA family) transcriptional regulator (TetF/AcrR family) putative transcriptional regulator transcriptional regulator (ArsR family) transcriptional regulator (ArsR family) transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator transcriptional regulator (Lrp/AsnC family) transcriptional regulator (MarR family) transcriptional regulator (TetR/AcrR family) transcriptional regulator (TetR/AcrR family) transcriptional regulator (IcIR	Rv1032c Rv1033c Rv1626 Rv2027c Rv2884 Rv3132c Rv3133c Rv3143 Rv3220c Rv3764c Rv3765c 3. Serine-t-phosphata Rv00155c	- - - - - - - - - ses pknA	two-component response regulator two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator putative sensory transduction protein sensor histidine kinase sensor histidine kinase two-component response regulator protein kinases and phosphoprotein serine-threonine protein kinase	2. Ribosor Rv1010 Rv2838c Rv2907c 3. Aminoa Rv2555c Rv1292 Rv2572c Rv3580c Rv2130c Rv1406 Rv3011c Rv3009c	ne modific ksgA rbfA rimM cyl tRINA alaS argS aspS cysS cysS2 fmt gatA gatB	protein family cation and maturation 16S rRNA dimethyltransferase ribosome-binding factor A 16S rRNA processing protein synthases and their modification alanyl-tRNA synthase arginyl-tRNA synthase aspartyl-tRNA synthase cysteinyl-tRNA synthase cysteinyl-tRNA synthase methionyl-tRNA formyltransferas glu-tRNA-gln amidotransferase, subunit B glu-tRNA-gln amidotransferase, subunit C
Rv2488c Rv2506 Rv2621c Rv2642 Rv2669 Rv2779c Rv2779c Rv2887 Rv2912c Rv2989 Rv2989 Rv3055 Rv3058c		(Lrp/AsnC family) transcriptional regulator (ArsR family) transcriptional regulator (LuxR/UhpA family) transcriptional regulator (TetR/AcrR family) putative transcriptional regulator transcriptional regulator (ArsR family) transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator transcriptional regulator (Lrp/AsnC family) transcriptional regulator (TetR/AcrR family) transcriptional regulator (TetR/AcrR family) transcriptional regulator (IclR family) putative transcriptional regulator	Rv1032c Rv1033e Rv1626 Rv2027c Rv2884 Rv3132c Rv3133c Rv3143 Rv3220c Rv3764c Rv3765c 3. Serine-t phosphata Rv0015c Rv0014c Rv00931c Rv1743 Rv1746	- - - - - - - ses pknA pknB pknB pknB	two-component response regulator two-component response regulator two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator putative sensory transduction protein sensor histidine kinase sensor histidine kinase two-component response regulator protein kinase serine-threonine protein kinase	2. Ribosor Rv1010 Rv2838c Rv2907c 3. Aminoa Rv2555c Rv1292 Rv2572c Rv3580c Rv2130c Rv13009c Rv30011c Rv3009c Rv2992c Rv2357c Rv2580c Rv2580c Rv1536	ne modifii ksgA rbfA rimM cyl tRNA alaS argS cysS cysS2 fmt gatA gatB gatC gltS glyS lieS lieS	protein family cation and maturation 16S rRNA dimethyltransferase ribosome-binding factor A 16S rRNA processing protein synthases and their modification alanyl-tRNA synthase arginyl-tRNA synthase aspartyl-tRNA synthase oysteinyl-tRNA synthase oysteinyl-tRNA synthase methionyl-tRNA formyltransferas glu-tRNA-gln amidotransferase, subunit B glu-tRNA-gln amidotransferase, subunit A glu-tRNA-gln amidotransferase, subunit C glutamyl-tRNA synthase glycyl-tRNA synthase listidyl-tRNA synthase isioleucyl-tRNA synthase
Rv2488c Rv2506 Rv2621c Rv2640c Rv2642 Rv27669 Rv2779c Rv2887 Rv2912c Rv2989 Rv2989 Rv3055 Rv3058c		(Lrp/AsnC family) transcriptional regulator (ArsR family) transcriptional regulator (LuxR/UhpA family) transcriptional regulator (TetR/AcrR family) putative transcriptional regulator transcriptional regulator (ArsR family) transcriptional regulator (ArsR family) transcriptional regulator (ArsR family) transcriptional regulator clarp/AsnC family) transcriptional regulator transcriptional regulator (TetR/AcrR family) transcriptional regulator (TetR/AcrR family) transcriptional regulator (TetR/AcrR family) transcriptional regulator (TetRimily) putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator transcriptional regulator transcriptional regulator	Rv1032c Rv1033c Rv1626 Rv2027c Rv2884 Rv3132c Rv3133c Rv3143 Rv3220c Rv3764c Rv3765c Rv0015c Rv0014c Rv0014c Rv1743 Rv1743 Rv1743 Rv1743 Rv1740	- - - - - ses pknA pknB pknB pknE pknE pknG	two-component response regulator two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator putative sensory transduction protein sensor histidine kinase sensor histidine kinase two-component response regulator protein kinases and phosphoprotein serine-threonine protein kinase	2. Ribosot Rv1010 Rv2838c Rv2907c 3. Aminoa Rv2555c Rv1292 Rv2572c Rv3580c Rv1406 Rv3011c Rv3009c Rv3012c Rv2992c Rv257c Rv2580c Rv1536 Rv1536 Rv0041	ne modifii ksgA rbfA rbfA rbfA cyl tRINA alaS aspS cysS cysS2 fmt gatA gatB gatC gltS glyS liesS leuS	protein family cation and maturation 16S rRNA dimethyltransferase ribosome-binding factor A 16S rRNA processing protein synthases and their modification alanyl-tRNA synthase arginyl-tRNA synthase aspartyl-tRNA synthase oysteinyl-tRNA synthase oysteinyl-tRNA formyltransferas glu-tRNA-gln amidotransferase, subunit B glu-tRNA-gln amidotransferase, subunit A glu-tRNA-gln amidotransferase, subunit C glutamyl-tRNA synthase glyoyl-tRNA synthase histidyl-tRNA synthase isoleucyl-tRNA synthase leucyl-tRNA synthase
Rv24880 Rv2506 Rv2621c Rv2640e Rv2642 Rv2745c Rv2779c Rv2887 Rv2912c Rv2989 Rv3050c Rv3055		(Lrp/AsnC family) transcriptional regulator (ArsR family) transcriptional regulator (LuxR/UhpA family) transcriptional regulator (TetR/AcrR family) putative transcriptional regulator transcriptional regulator (ArsR family) transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator transcriptional regulator (Lrp/AsnC family) transcriptional regulator (TetR/AcrR family) transcriptional regulator (TetR/AcrR family) transcriptional regulator (IclR family) putative transcriptional regulator	Rv1032c Rv1033e Rv1626 Rv2027c Rv2884 Rv3132c Rv3133c Rv3143 Rv3220c Rv3764c Rv3765c 3. Serine-t phosphata Rv0015c Rv0014c Rv00931c Rv1743 Rv1746	- - - - - - - ses pknA pknB pknB pknB	two-component response regulator two-component response regulator two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator putative sensory transduction protein sensor histidine kinase sensor histidine kinase two-component response regulator protein kinase serine-threonine protein kinase	2. Ribosor Rv1010 Rv2838c Rv2907c 3. Aminoa Rv2555c Rv1292 Rv2572c Rv3580c Rv2130c Rv13009c Rv30011c Rv3009c Rv2992c Rv2357c Rv2580c Rv2580c Rv1536	ne modifii ksgA rbfA rimM cyl tRNA alaS argS cysS cysS2 fmt gatA gatB gatC gltS glyS lieS lieS	protein family cation and maturation 16S rRNA dimethyltransferase ribosome-binding factor A 16S rRNA processing protein synthases and their modification alanyl-tRNA synthase arginyl-tRNA synthase aspartyl-tRNA synthase oysteinyl-tRNA synthase oysteinyl-tRNA synthase methionyl-tRNA synthase methionyl-tRNA formyltransferase, subunit B glu-tRNA-gln amidotransferase, subunit A glu-tRNA-gln amidotransferase, subunit C glutamyl-tRNA synthase glycyl-tRNA synthase listidyl-tRNA synthase isioleucyl-tRNA synthase
Rv24880 Rv2506 Rv2621c Rv2640e Rv2642 Rv2745c Rv2779c Rv2887 Rv2912c Rv2989 Rv3050c Rv3055 Rv3058c Rv3060c		(Lrp/AsnC family) transcriptional regulator (ArsR family) transcriptional regulator (LuxF/UhpA family) transcriptional regulator (TetF/AcrR family) putative transcriptional regulator transcriptional regulator (ArsR family) transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator (Lrp/AsnC family) transcriptional regulator (Lrp/AsnC family) transcriptional regulator (TetR/AcrR family) transcriptional regulator (TetR/AcrR family) transcriptional regulator (IclR family) putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator transcriptional regulator putative transcriptional regulator transcriptional regulator (GntR family)	Rv1032c Rv1033c Rv1027c Rv2027c Rv2884 Rv3132c Rv3133c Rv3143 Rv3220c Rv3764c Rv3765c Serine-t-phosphatta Rv0015c Rv0011c Rv0114c Rv1743 Rv17746 Rv1746 Rv1266c	- - - - - - ses pknA pknB pknB pknB pknB pknB pknB	two-component response regulator two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator putative sensory transduction protein sensor histidine kinase sensor histidine kinase two-component response regulator protein kinases and phosphoprotein protein kinases and phosphoprotein serine-threonine protein kinase	2. Ribosor Rv1010 Rv2838c Rv2907c 3. Aminoa Rv2555c Rv1292 Rv2572c Rv3580c Rv2130c Rv1406 Rv3011c Rv3009c Rv2357c Rv2580c Rv1536 Rv041 Rv3598c	ne modifii ksgA rbfA rimM cyl tRINA alaS aspS cysS2 fmt gatA gatB gatC gltS lieS lieS lieS lysS	protein family cation and maturation 16S rRNA dimethyltransferase ribosome-binding factor A 16S rRNA processing protein synthases and their modification alanyl-tRNA synthase arginyl-tRNA synthase oysteinyl-tRNA synthase oysteinyl-tRNA synthase oysteinyl-tRNA synthase glu-tRNA-gln amidotransferase, subunit B glu-tRNA-gln amidotransferase, subunit A glu-tRNA-gln amidotransferase, subunit C glutarmyl-tRNA synthase glycyl-tRNA synthase histidyl-tRNA synthase isoleucyl-tRNA synthase isoleucyl-tRNA synthase leucyl-tRNA synthase leucyl-tRNA synthase

Rv1650	pheT	phenylalanyl-tRNA synthase β subunit	Rv2090	-	partially similar to DNA poly- merase I	2. DNA Rv0670	end	endonuclease IV (apurinase)
Rv2845c	proS	prolyl-tRNA synthase	Rv2191	-	similar to both PolC and UvrC	Rv1108c	xseA	exonuclease VII large subunit
Rv3834c	serS	seryl-tRNA synthase			proteins	Rv1107c	xseB	exonuclease VII small subunit
Rv2614c	thrS	threonyl-tRNA synthase	Rv2464c	-	probable DNA glycosylase,	0 D		and observe while
Rv2906c	trmD	tRNA (guanine-N1)-methyltrans-	Rv3201c		endonuclease VIII probable ATP-dependent DNA	3. Proteins Rv3305c	, peptides <i>amiA</i>	and glycopeptides probable aminohydrolase
Rv3336c	trpS	ferase tryptophanyl tRNA synthase	11002010	-	helicase	Rv3306c	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					merase III	Rv2460c	clpP2	ATP-dependent Clp protease pro-
Rv1407	fmu	similar to Fmu protein			1 120 4	5		teolytic subunit
Rv3852	hns	HU-histone protein	6. Protein Rv0429c		and modification polypeptide deformylase	Rv2457c	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
Rv2986c Rv1388	hupB mIHF	DNA-binding protein II integration host factor	Rv2534c	efp	elongation factor P	Rv2667	clpX'	similar to ClpC from M. leprae bu
HV 1000	1101-11-	integration nost factor	Rv2882c	frr	ribosome recycling factor	1102007	OIDI	shorter
5. DNA rep	olication, i	epair, recombination and restric-	Rv0684	fusA	elongation factor G	Rv3419c	gcp	glycoprotease
tion/modific		opan, recombination and recome	Rv0120c	fusA2	elongation factor G	Rv2725c	hflX	GTP-binding protein
Rv1317c	alkA	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
Rv2836c	dinF	DNA-damage-inducible protein F	Rv2839c	infB infC	initiation factor IF-2	Rv0734	mapA2	probable methionine aminopepti-
Rv1329c	dinG dinP	probable ATP-dependent helicase	Rv1641 Rv0009	ppiA	initiation factor IF-3 peptidyl-prolyl <i>cis-trans</i> isomerase	Rv0319	рср	dase pyrrolidone-carboxylate peptidase
Rv3056 Rv1537	din X	DNA-damage-inducible protein probable DNA-damage-inducible	Rv2582	ppiA ppiB	peptidyl-prolyl <i>cis-trans</i> isomerase	Rv0125	рерА	probable serine protease
10 1007	unix	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
		protein	Rv2889c	tsf	elongation factor EF-Ts	Rv2467	pepD	probable aminopeptidase
Rv0058	dnaB	DNA helicase (contains intein)	Rv0685	tuf	elongation factor EF-Tu	Rv2089c	pepE	cytoplasmic peptidase
Rv1547	dnaE1	DNA polymerase III, α subunit	7 041	mala e de la Pri	NA modification and DATA	Rv2535c	pepQ	cytoplasmic peptidase
Rv3370c	dnaE2	DNA polymerase III α chain			NA modification and DNA	Rv2782c	pepR	protease/peptidase, M16 family (insulinase)
Rv2343c Rv0002	dnaG dnaN	DNA primase DNA polymerase III, β subunit	transcription	on <i>deaD</i>	ATP-dependent DNA/RNA	Rv2109c	prcA	(insulinase) proteasome α-type subunit 1
Rv3711c	anaiv dnaQ	DNA polymerase III, β subunit DNA polymerase III ∈ chain	1141200	JUAN	helicase	Rv21090	prcA	proteasome β-type subunit 2
Rv3721c	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-
		sylase	Rv2533c	nusB	N-utilization substance protein B			dase
Rv0006	gyrA	DNA gyrase subunit A	Rv0639	nusG	transcription antitermination		-	probable zinc metalloprotease
Rv0005	gyrB	DNA gyrase subunit B	Dv2007*		protein	Rv0457c	-	probable peptidase
Rv2092c	helY	probable helicase, Ski2 subfamily	Rv3907c Rv3232c	pcnA pvdS	polynucleotide polymerase alternative sigma factor for	Rv0840c Rv0983	-	probable proline iminopeptidase probable serine protease
Rv2101	helZ	probable helicase, Snf2/Rad54 family	HV32320	pvuo	siderophore production	Rv1977		probable zinc metallopeptidase
Rv2756c	hsdM	type I restriction/modification sys-	Rv3211	rhlE	probable ATP-dependent		_	probable alkaline serine protease
1027300	nsum	tem DNA methylase			RNA helicase	Rv3671c		probable serine protease
Rv2755c	hsdS'	type I restriction/modification sys-	Rv1297	rho	transcription termination	Rv3883c	-	probable secreted protease
		tem specificity determinant			factor rho	Rv3886c	-	protease
Rv3296	lhr	ATP-dependent helicase	Rv3457c	rpoA	α subunit of RNA polymerase			
Rv3014c	ligA	DNA ligase	Rv0667	rpoB	β subunit of RNA polymerase		charides, I	ipopolysaccharides and phospho-
Rv3062	ligB	DNA ligase	Rv0668	rpoC	β' subunit of RNA polymerase	lipids	/4	a allula a a /a n da alua a n a a a
Rv3731	ligC	probable DNA ligase	Rv1364c Rv3287c	rsbU rsbW	SigB regulation protein anti-sigma B factor	Rv0062 Rv3915	celA cwlM	cellulase/endoglucanase hydrolase
Rv1020 Rv2528c	mfd mrr	transcription-repair coupling factor restriction system protein	Rv2703	sigA	RNA polymerase sigma factor	Rv0315	-	probable β-1,3-glucanase
Rv2985	mutT1	MutT homologue	1112700	Uigi i	(aka MysA, RpoV)	Rv1090	-	probable inactivated
Rv1160	mutT2	MutT homologue	Rv2710	sigB	RNA polymerase sigma factor			cellulase/endoglucanase
Rv0413	mutT3	MutT homologue		•	(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	Rv1333	-	probable hydrolase
Rv3674c	nth	probable endonuclease III	Rv1221	sigE	ECF subfamily sigma subunit	Rv3463	-	probable neuraminidase
Rv1316c	ogt	methylated-DNA-protein-cysteine	Rv3286c	sigF	ECF subfamily sigma subunit sigma-70 factors ECF subfamily	Rv3717	-	possible N-acetylmuramoyl-L-ala-
71000		methyltransferase	Rv0182c Rv3223c	sigG cia⊔	ECF subfamily sigma subunit			nine amidase
Rv1629 Rv1402	polA priA	DNA polymerase I putative primosomal protein n'	Rv1189	sigH sigI	ECF sublamily sigma subunit	5. Esterase	es and line	ases
141402	PINA	(replication factor Y)	Rv3328c	sig.i sigJ	similar to Sigl, ECF family	Rv0220	lipC	probable esterase
Rv3585	radA	probable DNA repair RadA homo-	Rv0445c	sigK	ECF-type sigma factor	Rv1923	li p D	probable esterase
		logue	Rv0735	sigL	sigma-70 factors ECF subfamily	Rv3775	lipΕ	probable hydrolase
Rv2737c	recA	recombinase (contains intein)	Rv3911	sigM	probable sigma factor, similar to	Rv3487c	lipF	probable esterase
Rv0630c	recB	exodeoxyribonuclease V	_		SigE	Rv0646c	lipG	probable hydrolase
Rv0631c	recC	exodeoxyribonuclease V	Rv3366	spoU	probable rRNA methylase	Rv1399c	lipH	probable lipase
Rv0629c	recD	exodeoxyribonuclease V	Rv3455c	truA	probable pseudouridylate syn-	Rv1400c	lipl lip l	probable lipase
3v0003	recF	DNA replication and SOS induc-	Rv2793c	truB	thase tRNA pseudouridine 55 synthase	Rv1900c Rv2385	lipJ lipK	probable esterase probable acetyl-hydrolase
Rv2973c	recG	tion ATP-dependent DNA helicase	Rv1644	truB tsnR	putative 23S rRNA methyltrans-	Rv1497	lipk lipL	esterase
7029730 701696	recG recN	recombination and DNA repair			ferase	Rv2284	lipL lipM	probable esterase
Rv3715c	recR	RecBC-Independent process of	Rv3649	-	ATP-dependent DNA/RNA heli-	Rv2970c	lipΝ	probable lipase/esterase
		DNA repair			case	Rv1426c	lipΟ	probable esterase
	recX	regulatory protein for RecA				Rv2463	lip₽	probable esterase
Rv2736c	ruvA	Holliday junction binding protein,			cytoplasmic)	Rv2485c	lipQ	probable carboxlyesterase
	TUVA	DNA helicase	Rv1326c	glgB	1,4-α-glucan branching enzyme	Rv3084	lipR li∞0	probable acetyl-hydrolase
Rv2593c			LU1200	glgP	probable glycogen phosphory-	Rv3176c	lipS linT	probable esterase/lipase
Rv2593c Rv2592c	ruvB	Holliday junction binding protein	Rv1328		lase	Rv2045c	lipΤ	probable carboxylesterase
Rv2593c Rv2592c		Holliday junction binding protein Holliday junction resolvase, endo-		alaY		DUTO70	lin!	
Rv2593c Rv2592c Rv2594c	ruvB ruvC	Holliday junction binding protein Holliday junction resolvase, endo- deoxyribonuclease	Rv1564c	glgX	probable glycogen debranching	Rv1076 Bv3203	lipU linV	probable esterase
Rv2593c Rv2592c Rv2594c Rv0054	ruvB ruvC ssb	Holliday junction binding protein Holliday junction resolvase, endo- deoxyribonuclease single strand binding protein	Rv1564c		probable glycogen debranching enzyme	Rv3203	lipV	probable lipase
Rv2593c Rv2592c Rv2594c Rv0054	ruvB ruvC	Holliday junction binding protein Holliday junction resolvase, endo- deoxyribonuclease single strand binding protein DNA-3-methyladenine glycosi-	Rv1564c Rv1563c	glgY	probable glycogen debranching enzyme putative α -amylase	Rv3203 Rv0217c		probable lipase probable esterase
Rv2593c Rv2592c Rv2594c Rv0054 Rv1210	ruvB ruvC ssb	Holliday junction binding protein Holliday junction resolvase, endo- deoxyribonuclease single strand binding protein	Rv1564c		probable glycogen debranching enzyme	Rv3203	lipV lipW	probable lipase probable esterase phospholipase C precursor phospholipase C precursor
Rv2593c Rv2592c Rv2594c Rv0054 Rv1210	ruvB ruvC ssb tagA	Holliday junction binding protein Holliday junction resolvase, endodeoxyribonuclease single strand binding protein DNA-3-methyladenine glycosidase I DNA topoisomerase uracil-DNA glycosylase	Rv1564c Rv1563c Rv1562c Rv0126	glgY glgZ -	probable glycogen debranching enzyme putative α-amylase maltooligosyltrehalose trehalohy- drolase probable glycosyl hydrolase	Rv3203 Rv0217c Rv2351c Rv2350c Rv2349c	lipV lipW plcA plcB plcC	probable lipase probable esterase phospholipase C precursor phospholipase C precursor phospholipase C precursor
Rv2593c Rv2592c Rv2594c Rv0054 Rv1210 Rv3646c Rv2976c Rv1638	ruvB ruvC ssb tagA topA	Holliday junction binding protein Holliday junction resolvase, endo-deoxyribonuclease single strand binding protein DNA-3-methyladenine glycosidase I DNA topoisomerase uracil-DNA glycosylase excinuclease ABC subunit A	Rv1564c Rv1563c Rv1562c Rv0126 Rv1781c	glgY glgZ -	probable glycogen debranching enzyme putative α-amylase maltooligosyltrehalose trehalohydrolase probable glycosyl hydrolase probable 4-α-glucanotransferase	Rv3203 Rv0217c Rv2351c Rv2350c Rv2349c Rv1755c	lipV lipW plcA plcB	probable lipase probable esterase phospholipase C precursor phospholipase C precursor phospholipase C precursor partial CDS for phospholipase C
Rv2593c Rv2592c Rv2594c Rv0054 Rv1210 Rv3646c Rv2976c Rv1638 Rv1633	ruvB ruvC ssb tagA topA ung uvrA uvrB	Holliday junction binding protein Holliday junction resolvase, endo-deoxyribonuclease single strand binding protein DNA-3-methyladenine glycosidase I DNA topoisomerase uracil-DNA glycosylase excinuclease ABC subunit A excinuclease ABC subunit B	Rv1564c Rv1563c Rv1562c Rv0126	glgY glgZ -	probable glycogen debranching enzyme putative α-amylase maltooligosyltrehalose trehalohy- drolase probable glycosyl hydrolase	Rv3203 Rv0217c Rv2351c Rv2350c Rv2349c Rv1755c Rv1104	lipV lipW plcA plcB plcC plcD	probable lipase probable esterase phospholipase C precursor phospholipase C precursor phospholipase C precursor phospholipase C precursor partial CDS for phospholipase C probable esterase pseudogene
Rv2593c Rv2592c Rv2594c Rv0054 Rv1210 Rv3646c Rv2976c Rv1638 Rv1633 Rv1420	ruvB ruvC ssb tagA topA ung uvrA uvrB uvrC	Holliday junction binding protein Holliday junction resolvase, endodeoxyribonuclease single strand binding protein DNA-3-methyladenine glycosidase! DNA topoisomerase uracil-DNA glycosylase excinuclease ABC subunit A excinuclease ABC subunit B excinuclease ABC subunit C	Rv1564c Rv1563c Rv1562c Rv0126 Rv1781c Rv2471	glgY glgZ - -	probable glycogen debranching enzyme putative α-amylase maltooligosyltrehalose trehalohydrolase probable glycosyl hydrolase probable 4-α-glucanotransferase probable maltase α-glucosidase	Rv3203 Rv0217c Rv2351c Rv2350c Rv2349c Rv1755c	lipV lipW plcA plcB plcC	probable lipase probable esterase phospholipase C precursor phospholipase C precursor phospholipase C precursor partial CDS for phospholipase C
Rv2593c Rv2592c Rv2594c Rv0054 Rv1210 Rv3646c Rv2976c Rv1638 Rv1633 Rv1420	ruvB ruvC ssb tagA topA ung uvrA uvrB	Holliday junction binding protein Holliday junction resolvase, endodeoxyribonuclease single strand binding protein DNA-3-methyladenine glycosidase I DNA topoisomerase uracil-DNA glycosylase excinuclease ABC subunit A excinuclease ABC subunit B excinuclease ABC subunit C DNA-dependent ATPase I and	Rv1564c Rv1563c Rv1562c Rv0126 Rv1781c Rv2471 B. Degrad	glgY glgZ - -	probable glycogen debranching enzyme putative α-amylase maltooligosyltrehalose trehalohydrolase probable glycosyl hydrolase probable 4-α-glucanotransferase	Rv3203 Rv0217c Rv2351c Rv2350c Rv2349c Rv1755c Rv1104 Rv1105	lipV lipW plcA plcB plcC plcD -	probable lipase probable esterase phospholipase C precursor phospholipase C precursor phospholipase C precursor partial CDS for phospholipase C probable esterase pseudogene probable esterase pseudogene
Rv2593c Rv2592c Rv2594c Rv0054 Rv1210 Rv3646c Rv2976c Rv1638 Rv1633 Rv1420 Rv0949	ruvB ruvC ssb tagA topA ung uvrA uvrB uvrC uvrD	Holliday junction binding protein Holliday junction resolvase, endo-deoxyribonuclease 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 II	Rv1564c Rv1563c Rv1562c Rv0126 Rv1781c Rv2471 B. Degrad 1. RNA	glgY glgZ - - - ation of ma	probable glycogen debranching enzyme putative α-amylase maltooligosyltrehalose trehalohydrolase probable glycosyl hydrolase probable 4-α-glucanotransferase probable maltase α-glucosidase acromolecules	Rv3203 Rv0217c Rv2351c Rv2350c Rv2349c Rv1755c Rv1104 Rv1105	lipV lipW plcA plcB plcC plcD c hydrocal	probable lipase probable esterase phospholipase C precursor phospholipase C precursor phospholipase C precursor phospholipase C precursor partial CDS for phospholipase C probable esterase pseudogene probable esterase pseudogene
Rv2593c Rv2592c Rv2594c Rv0054 Rv1210 Rv3646c Rv2976c Rv1633 Rv1633 Rv1420 Rv0949	ruvB ruvC ssb tagA topA ung uvrA uvrB uvrC uvrD	Holliday junction binding protein Holliday junction resolvase, endodeoxyribonuclease single strand binding protein DNA-3-methyladenine glycosidase I DNA topoisomerase uracil-DNA glycosylase excinuclease ABC subunit A excinuclease ABC subunit B excinuclease ABC subunit C DNA-dependent ATPase I and helicase II putative UvrD	Rv1564c Rv1563c Rv1562c Rv0126 Rv1781c Rv2471 B. Degrad 1. RNA Rv1014c	glgY glgZ - - - ation of ma	probable glycogen debranching enzyme putative α-amylase matrooligosyltrehalose trehalohydrolase probable glycosyl hydrolase probable 4-α-glucanotransferase probable maltase α-glucosidase acromolecules peptidyl-tRINA hydrolase	Rv3203 Rv0217c Rv2351c Rv2350c Rv2349c Rv1755c Rv1104 Rv1105	lipV lipW plcA plcB plcC plcD -	probable lipase probable esterase phospholipase C precursor phospholipase C precursor phospholipase C precursor phospholipase C precursor partial CDS for phospholipase C probable esterase pseudogene probable esterase pseudogene bons probable 4-hydroxy-2-oxovalerate
Rv2593c Rv2592c Rv2594c Rv2594c Rv12594c Rv1210 Rv3646c Rv2976c Rv1633 Rv1633 Rv1633 Rv1633 Rv1633 Rv1420 Rv0949	ruvB ruvC ssb tagA topA ung uvrA uvrB uvrC uvrD	Holliday junction binding protein Holliday junction resolvase, endodeoxyribonuclease single strand binding protein DNA-3-methyladenine glycosidase I DNA topoisomerase uracil-DNA glycosylase excinuclease ABC subunit A excinuclease ABC subunit B excinuclease ABC subunit C DNA-dependent ATPase I and helicase II putative UvrD exceleoxyribonuclease III	Rv1564c Rv1563c Rv1562c Rv0126 Rv1781c Rv2471 <i>B. Degrad</i> 1. RNA Rv1014c Rv2925c	glgY glgZ - - - cation of ma	probable glycogen debranching enzyme putative α-amylase maltooligosyltrehalose trehalohydrolase probable glycosyl hydrolase probable 4-α-glucanotransferase probable maltase α-glucosidase acromolecules peptidyl-tRNA hydrolase RNAse III	Rv3203 Rv0217c Rv2351c Rv2350c Rv2349c Rv1755c Rv1104 Rv1105 6. Aromatic Rv3469c	lipV lipW plcA plcB plcC plcD c hydrocal	probable lipase probable esterase probable esterase phospholipase C precursor phospholipase C precursor phospholipase C precursor partial CDS for phospholipase C probable esterase pseudogene probable esterase pseudogene bons probable 4-hydroxy-2-oxovalerate aldolase
Rv2593c Rv2592c Rv2594c Rv1210 Rv1210 Rv3646c Rv2976c Rv1633 Rv1633 Rv1420 Rv0949 Rv3198c Rv0427c Rv0427c	ruvB ruvC ssb tagA topA ung uvrA uvrB uvrC uvrD	Holliday junction binding protein Holliday junction resolvase, endodeoxyribonuclease single strand binding protein DNA-3-methyladenine glycosidase I DNA topoisomerase uracil-DNA glycosylase excinuclease ABC subunit A excinuclease ABC subunit C DNA-dependent ATPase I and helicase II putative UvrD excdeoxyribonuclease III group II intron maturase	Rv1564c Rv1563c Rv1562c Rv0126 Rv1781c Rv2471 B. Degrad 1. RNA Rv1014c	glgY glgZ - - - ation of ma	probable glycogen debranching enzyme putative α-amylase matrooligosyltrehalose trehalohydrolase probable glycosyl hydrolase probable 4-α-glucanotransferase probable maltase α-glucosidase acromolecules peptidyl-tRINA hydrolase	Rv3203 Rv0217c Rv2351c Rv2350c Rv2349c Rv1755c Rv1104 Rv1105	lipV lipW plcA plcB plcC plcD c hydrocal	probable lipase probable esterase phospholipase C precursor phospholipase C precursor phospholipase C precursor phospholipase C precursor partial CDS for phospholipase C probable esterase pseudogene probable esterase pseudogene bons probable 4-hydroxy-2-oxovalerate
Rv2593c Rv2592c Rv2594c Rv2594c Rv1210 Rv3646c Rv2976c Rv1633 Rv1420 Rv0949 Rv3198c Rv0427c Rv0427c Rv0461c	ruvB ruvC ssb tagA topA ung uvrA uvrB uvrC uvrD uvrD	Holliday junction binding protein Holliday junction resolvase, endodeoxyribonuclease single strand binding protein DNA-3-methyladenine glycosidase I DNA topoisomerase uracil-DNA glycosylase excinuclease ABC subunit A excinuclease ABC subunit B excinuclease ABC subunit C DNA-dependent ATPase I and helicase II putative UvrD exceleoxyribonuclease III	Rv1564c Rv1563c Rv1562c Rv0126 Rv1781c Rv2471 <i>B. Degrad</i> 1. RNA Rv1014c Rv2925c	glgY glgZ - - - cation of ma	probable glycogen debranching enzyme putative α-amylase maltooligosyltrehalose trehalohydrolase probable glycosyl hydrolase probable 4-α-glucanotransferase probable maltase α-glucosidase acromolecules peptidyl-tRNA hydrolase RNAse III similar at C-term to ribo-	Rv3203 Rv0217c Rv2351c Rv2350c Rv2349c Rv1755c Rv1104 Rv1105 6. Aromatic Rv3469c	lipV lipW plcA plcB plcC plcD c hydrocal	probable lipase probable esterase phospholipase C precursor phospholipase C precursor phospholipase C precursor phospholipase C precursor partial CDS for phospholipase C probable esterase pseudogene probable esterase pseudogene thons probable 4-hydroxy-2-oxovalerate aldolase probable muconolactone iso-
Rv2593c Rv2592c Rv2594c Rv2594c Rv1210 Rv3646c Rv2976c Rv1633 Rv1420 Rv949 Rv3198c Rv0427c Rv0041 Rv00861c	ruvB ruvC ssb tagA topA ung uvrA uvrB uvrC uvrD uvrD	Holliday junction binding protein Holliday junction resolvase, endodeoxyribonuclease single strand binding protein DNA-3-methyladenine glycosidase I DNA topoisomerase uracil-DNA glycosylase excinuclease ABC subunit A excinuclease ABC subunit B excinuclease ABC subunit C DNA-dependent AT Pase I and helicase II putative UvrD excdeoxyribonuclease III group II intron maturase probable DNA helicase	Rv1564c Rv1563c Rv1562c Rv0126 Rv1781c Rv2471 B. Degrad 1. RNA Rv1014c Rv2925c Rv2444c	glgY glgZ - - - ation of ma pth rnc rne	probable glycogen debranching enzyme putative α-amylase maltooligosyltrehalose trehalohydrolase probable glycosyl hydrolase probable 4-α-glucanotransferase probable maltase α-glucosidase acromolecules peptidyl-tRNA hydrolase RNAse III similar at C-term to ribonuclease E	Rv3203 Rv0217c Rv2351c Rv2350c Rv2349c Rv1755c Rv1104 Rv1105 6. Aromatir Rv3469c Rv0316	lipV lipW plcA plcB plcC plcD c hydrocal	probable lipase probable esterase phospholipase C precursor phospholipase C precursor phospholipase C precursor phospholipase C precursor phospholipase C probable esterase pseudogene probable esterase pseudogene probable 4-hydroxy-2-oxovalerate aldolase probable muconolactone isomerase probable 4-carboxymuconolactone dearrboxylase
Rv0071	ruvB ruvC ssb tagA topA ung uvrA uvrB uvrC uvrD uvrD	Holliday junction binding protein Holliday junction resolvase, endodeoxyribonuclease single strand binding protein DNA-3-methyladenine glycosidase I DNA topoisomerase uracil-DNA glycosylase excinuclease ABC subunit A excinuclease ABC subunit B excinuclease ABC subunit C DNA-dependent ATPase I and helicase II putative UvrD exceleoxyribonuclease III group II intron maturase probable DNA helicase possible formamidopyrimidine-	Rv1564c Rv1563c Rv1562c Rv0126 Rv1781c Rv2471 B. Degrad 1. RNA Rv1014c Rv2925c Rv2444c	glgY glgZ - - cation of ma pth rnc rne rnhB	probable glycogen debranching enzyme putative α-amylase maltooligosyltrehalose trehalohydrolase probable glycosyl hydrolase probable 4-α-glucanotransferase probable maltase α-glucosidase acromolecules peptidyl-tRNA hydrolase RNAse III similar at C-term to ribonuclease E ribonuclease HII	Rv3203 Rv0217c Rv2351c Rv2350c Rv2349c Rv1755c Rv1104 Rv1105 6. Aromatik Rv3469c Rv0316	lipV lipW plcA plcB plcC plcD c hydrocal	probable lipase probable esterase probable esterase phospholipase C precursor phospholipase C precursor phospholipase C precursor partial CDS for phospholipase C probable esterase pseudogene probable esterase pseudogene bons probable 4-hydroxy-2-oxovalerate aldolase probable muconolactone isomerase probable 4-carboxymuconolac-

Modern									
The content of the	Rv2715	-				probable penicillin binding protein probable penicillin binding protein	Rv1030	kdpB	potassium-transporting ATPase B chain
Modern M	Bv3530c	_			-		Rv1031	kdpC	
A. Content weaponed Processor Proces	Rv3534c	-	4-hydroxy-2-oxovalerate aldolase	Rv3330	-	probable penicillin binding protein	Rv3236c	kefB	probable glutathione-regulated
C. C. Cerebrokes BR-05/250 by control by Experimental Septiment Name and Septiment Name	Rv3536c	-					Rv2877c	merT	possible mercury resistance
Package Pack						conserved large membrane	Rv1811	mgtC	probable magnesium transport
## 1848 and adulgers				Rv0507	mmpL2	conserved large membrane	Rv0362	mgtE	putative magnesium ion
Processor Proc			harides, lipopolysaccharides, pro-	Rv0206c	mmpL3		Rv2856	nicT	
Modern Common					,	protein			transmembrane protein belonging
Beels				Rv0676c		protein	Rv2691	trkA	
Proceeds moderation and antimicing before to a process moderation and	Rv3794	embA		Rv1557			Rv2692	trkB	
Modern modern machinerge location sport Modern modern machinerge location Modern Moder	Rv3795	embB		Rv2942	mmpL7				
Publis	Rv3793	embC		Rv3823c	mmpL8		Rv3162c	-	
Prof. Prof				Rv2339	mmpL9		Rv3237c	C	
these process mys. J. Connewvol angle membrane process searced process mys. J. Connewvol angle membrane process mys. J.	Rv0113	gmhA		Rv1183	mmpL10		Rv3743c	•	
Price Pric	Rv2965c	kdtB		Rv0202c	mmpL11		3. Carbohy	/drates, oi	rganic acids and alcohols
Fix2925 myc27 or major secreted immunogenip probably in minimular process of hypothesis				Rv1522c	mmpL12				
beful Margra precision process proce			major secreted immunogenic pro-			protein	Rv1902c	nanT	probable sialic acid transporter membrane protein probably
Processor Proc		·	tein Mpt70 precursor			protein			involved in sugar transport
Portange protein Prote	Rv0899	ompA	member of OmpA family		,	protein			ABC transporter component of
Fig. 24 and experyly-phosphate a N- destylglucosaminythansderase antigen 84 (aka wag31) beroutin retailed prighted (AT103) beroutin retailed (AT103) beroutin retailed prighted (AT103) beroutin retailed		•	protein)			protein			probable sugar transport protein
Product Prod	Rv1302		undecaprenyl-phosphate α-N-	Rv0677c		protein			permease
Fixed Fixe		wag31 -	antigen 84 (aka wag31)			protein			periplasmic lipoprotein
Number Secretary Secreta		-	cell envelope antigen	5. Other n	nembrane	proteins 211			ATP-binding protein
RV1758 - partial cultinase Protein PV1910 - probable secreted protein PV1910 - putsive exported protesses PV1910 - putsive exported protesses PV1910 - putsive exported protesses PV1910 - probable secreted protein PV1910 - putsive exported protesses PV1910 - probable secreted protein PV1910 - pro	Rv1518	-	thesis			proteins			system protein
RV1916 - probable secreted protein Pkr0946 - probable secreted protein Pkr0946 - probable secreted protein Pkr0947 -	Rv1758		synthesis	1. Amino a	acids		Rv2318	uspC	sugar transport protein
Five		-	probable secreted protein		aroP2	probable aromatic amino acid	Rv1200	- '	probable sugar transporter
RV2924 - probable experted protesse PV22240 - probable exported protesse PV22240 - probable exported protesse PV22240 - probable exported protesse probable culmase protested protesse PV22240 - publishe exported protesse PV22240 - pub		-		Rv0917	betP				
Ru2221d probable exported professe probable culinase precursor of probable membrane professe profe		-		Rv1704c	cycA	transport of D-alanine, D-serine			
Fiv2345 - procursor of probable membrane protein probable servered protease probable description probable servered proteins protein probable perpeture or festale probable servered protein probable perpeture or probable durinase precursor probable cutinase precursor probable perpeture probable p	Rv2224c	-	probable exported protease	Rv3666c	dppA	probable peptide transport system		-	probable sugar transporter
Processes protein putative exported protease putative exported protease putative exported protease putative exported protease proteins protein protein probable period for transport system permease probable particle transport system permease probable period transport system permease protein probable period transport protein protein probable for transport system permease protein protein probable cutinase precursor probable cutinase protein probable cutinase protein probable cutinase protein probable cutinase precursor probable cutinase precursor probable cutinase protein probable cutinase precursor probable cutin		-		Bv3665.c	donB			arsA	probable arsenical nump
Ry30366 - similar to Esat6 probable seareted protein Ry30562 dps probable values precursor Ry30562 dps probable utinase precursor Ry2544 probable utinase precursor Ry2564 dps probable utinase precursor Ry2564 dps probable utinase precursor Ry2564 dps Ry2910 dps probable utinase precursor Ry2564 dps Ry2916 dps probable utinase precursor Ry2564 dps probable utinase precursor Ry2565 dps Ry2916 dps probable oligopeptide transport protein P			protein			permease	Rv2685	arsB	probable arsenical pump
Probable precursor of serine proteate tease professor probable cutinase precursor probable probable defined probable attention protein probable attention butyrate transport suphate transport suphate transport system permease probable cutinase precursor probable probable defined probable transport protein probable attention strains and probable pro				HV36640	аррс				
Riv3451								cysA	
Riy352 - probable outinase precursor Riy2564 glnQ probable ATP-binding transport protein protein protein protein as prote	Rv3451			Rv0411c	glnH		Rv2399c	cysT	
3. Murein sacoulus and peptidoglycan Pkv2910 dda Pkv2910 dda D-alanine ligase A Breveillin binding protein Pkv2910 dda D-alanine-D-alanine ligase A Breveillin binding protein Pkv2910 dda D-alanine-D-alanine ligase A Breveillin binding protein Pkv2910 dda D-alanine-D-alanine ligase A Breveillin binding protein Pkv2920 dda D-alanine-D-alanine ligase A Breveillin-binding protein Pkv2920 dapa Pkv21520 dda D-alanine-D-alanine-logilus amate ligase Breveilase Pkv21520 dba Brev			probable cutinase precursor	Rv2564		probable ATP-binding transport	Rv2398c	cysW	sulphate transport system perme-
Rv29810 daCB penicillin binding protein Rv29810 digopeptide transport protein Rv29810 digopeptide transport system per-mease Rv1850 modD Rv28200 modD Rv		sacculus	and peptidoglycan	Rv1280c	oppA	probable oligopeptide transport			molybdate binding protein
RV3890 gff UDP-galactopyranose mutase RV1281c opp probable peptide transport protein pyrophosphorylase RV3230c yB1 LytB protein homologue RV3230c yB2 yB1 LytB protein homologue RV3250c rooE RV3250c rooE RV3250c rooE RV3230c rooE roop roobable rangensium transport ransport ransp	Rv2911	dacB	penicillin binding protein			oligopeptide transport protein			molybdate uptake
pyrophosphorylase pyrophosphor	Rv3809c	glf	UDP-galactopyranose mutase			mease			transporter
RV1315 murA DP-N-acetylglucosamine-1-car-boxyvinyttransferase DP-N-acetylglucosamine-1-car-boxyvinytransferase RV2920c amt putative ammonium transporter Rv0934 phoS1 pstS component of phosphate uptake PstA component of phosphate uptake Uptak		-	pyrophosphorylase	Rv2320c	rocE	arginine/ornithine transporter			kD secreted protein)
Rv04315 murA UDP-N-acetylgluosamine-1-carboxyvinyltransferase Rv2454 - possible proline permease Rv0261c narK3 nitrite extrusion protein				Hv3253c	-				
Rv0482 murB UDP-N-acetylenolpyruvoylglu-cosamine reductase Rv2920c amt Rv1607 chaA putative ammonium transporter probable magnesium and cobalt transport protein probable magnesium and cobalt			UDP-N-acetylglucosamine-1-car-	Rv3454	-		Rv0261c	narK3	nitrite extrusion protein
Rv2152c murD UP-N-acetylmuramoylalanine-D- glutamate ligase Rv2158c murE meso-diaminopimelate-adding enzyme Rv1690 ctpD alanine-D-alanine-D-alanine-adding enzyme Rv2153c murG glutamate racemase Rv1997 ctpF probable cation transport ATPase phosph-acetylmuramoyl- Rv2158c murG balanine-D-alanine-adding enzyme Rv2153c murG glutamate racemase Rv1997 ctpF probable cation transport ATPase phospho-N-acetylmuramoyl- petake probable addinum-transporting ATPase probable cation transport ATPase probable magnesium transport at probable magnesium transport at probable magnesium transport at probable magnesium transport protein probable magnesium transport protein prot	Rv0482	murB	UDP-N-acetylenolpyruvoylglu-			putative ammonium transporter			protein 2
Rv2155c murb UDP-N-acetylmuramoylalanine-D-glutamate ligase meso-diaminopimelate-adding enzyme Pv2157c murb D-alanine-D-alanine-adding enzyme Pv2157c murb D-alanine-adding enzyme Pv2157c murb	Rv2152c	murC	UDP-N-acetyl-muramate-alanine	Rv1607	chaA	putative calcium/proton antiporter			uptake
Rv2158c mur Emso-diaminopimelate-adding enzyme Rv3270 ctpC cation transport ATPase cation transport ATPase repulator regulator regulator regulator repulsion regulator regulator repulsion regulator	Rv2155c	murD	UDP-N-acetylmuramoylalanine-D-			transport protein			uptake
Rv2157c mur	Rv2158c	murE	meso-diaminopimelate-adding	Rv0103c	ctpB	cation transport ATPase		•	transporter
Rv2153c murG transferase in peptidoglycan synthesis Rv1997 ctpF probable cation transport ATPase probable cation transport probable transporter probable transporter probable ration transport pr	Rv2157c	murF	D-alanine:D-alanine-adding			probable cadmium-transporting			regulator
Rv1338 murl glutamate racemase Rv1992c ctpG probable cation transport ATPase C-terminal region putative cation-transport ATPase Rv0930 pstA1 pitB pi	Rv2153c	murG	transferase in peptidoglycan syn-		ctpF	probable cation transport ATPase			regulator
RV332 nagA N-acetylglucosamine-6-P- Rv0107c ctpl probable magnesium transport ATPase Rv0930 pstA1 PstA component of phosphate uptake Rv0016c pbpA penicillin-binding protein Rv0969 ctpV acitor transport ATPase penicillin-binding protein Rv0969 ctpV ponA2 ponA2 ponA2 ponA2 ponA2 class A penicillin binding protein Rv0969 rotein Rv0969 ctpV ponA2 ponA2 ponA2 ponA2 ponA2 class A penicillin binding protein Rv0969 rotein Rv09			glutamate racemase phospho-N-acetylmuramoyl-	Rv1992c	ctpG	probable cation transport ATPase			transporter
deacetylase ATPase ATPase Rv036 pstA2 PstA component of phosphate uptake Rv2163c pbpB penicillin-binding protein Pv3682 ponA2 penicillin-bonding protein Pv3682 ponA2 penicillin-bonding protein Pv3682 ponA2 penicillin-bonding protein Pv3682 ponA2 penicillin-bonding protein Rv3682 ponA2 penicillin-bonding protein Pv3682 ponA2 ponA2 penicillin-bonding protein Pv3682 ponA2 ponA2 penicillin-bonding protein Pv3682 ponA2 penicillin-bonding protein P			petapeptide transferase			transporting ATPase			PstA component of phosphate
Rv2163c pbp8 penicillin-binding protein 2 Rv3044 fecB putative FellI-dicitrate transporter Rv0933 pstB ABC transport component of Pkv3682 ponA2 ponA2 class A penicillin-bonding protein Rv0935 ponA2 class A penicillin-bonding protein Rv0935 pstC PstC component of phosphate uptake Rv0017c rodA FtsW/RodA/SpovE family Rv1029 kdpA potassium-transporting ATPase A	Rv0016c	pbpA	deacetylase penicillin-binding protein	Rv0969	ctpV	ATPase cation transport ATPase		pstA2	PstA component of phosphate uptake
Rv3682 ponA2 class A penicillin binding protein trate transporter Rv0935 pstC PstC component of phosphate Rv0017c rodA FtsW/RodA/SpovE family Rv1029 kdpA potassium-transporting ATPase A uptake		pbpB	penicillin-binding protein 2		fecB	putative FelII-dicitrate transporter	Rv0933	pstB	
	Rv3682	ponA2	class A penicillin binding protein	trate		transporter	Rv0935	pstC	PstC component of phosphate
		rodA -		Hv1029	карА		Rv0929	pstC2	

F F F F F F F F F	Rv2400c Rv0143c Rv1707 Rv1739c	subl -	uptake sulphate binding precursor			unit	Rv3896c	-	putative p60 home	
F F F 5 F F 6	Rv1707 Rv1739c	-	probable chloride channel	Rv2587c Rv0638	secD secE	protein-export membrane protein SecE preprotein translocase	Rv3922c	-	possible hemolysi	
5 F F F F		-	probable sulphate permease	Rv2586c	secF	protein-export membrane protein	B. IS elem	ents, Rep	peated sequences, a	nd Phage
5 F F 6 F		-	possible sulphate transporter	Rv1440	secG	protein-export membrane protein	1. IS elem	ents	16 conico	
F F 6 F	Rv3679 Rv3680	-	possible anion transporter probable anion transporter	Rv0732	secY	SecG SecY subunit of preprotein translo-	IS6110 IS1081		16 copies 6 copies	
F 6 F	. Fatty ac	id transpo	rt	Rv2462c	tig	case chaperone protein, similar to	Others		34 copies	
F	Rv2790c Rv3540c	ltp1 ltp2	non-specific lipid transport protein non-specific lipid transport protein	Rv2813	-	trigger factor probable general secretion path-	2. REP 13		•	
F	6. Efflux pr	otoino				way protein	3. Phage-i Rv2894c		nctions integrase/recombi	
F	. ⊑iiiux pi Rv2936	drrA	similar daunorubicin resistance	E. Adapta	tions and	atypical conditions	Rv1701	xerD xerD	integrase/recombi	
			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 rela	ated protein
F	Rv2938	drrC	similar daunorubicin resistance	Rv0871	cspB	probable cold shock protein	Rv1574	-	phiRV1 phage rela	ated protein
F	Rv2846c	efpA	transmembrane protein putative efflux protein	Rv3063	cstA	starvation-induced stress response protein	Rv1575 Rv1576c	-	phiRV1 phage rela phiRV1 phage rela	
F	Rv3065	emrE	resistance to ethidium bromide	Rv3490	otsA	probable α,α-trehalose-phosphate	Rv1577c	-	phiRV1 possible p	rohead protease
	Rv0783c Rv0849	-	multidrug resistance protein possible quinolone efflux pump	Rv2006	otsB	synthase trehalose-6-phosphate phos-	Rv1578c Rv1579c	-	phiRV1 phage rela phiRV1 phage rela	
F	Rv1 1 45	-	probable drug transporter			phatase	Rv1580c		phiRV1 phage rela	ated protein
	Rv1146 Rv1250	-	probable drug transporter probable drug efflux protein	Rv3372	otsB2	trehalose-6-phosphate phos- phatase	Rv1581c Rv1582c	-	phiRV1 phage rela phiRV1 phage rela	
	Rv1258c	-	probable multidrug resistance	Rv3758c	proV	osmoprotection ABC transporter	Rv1583c		phiRV1 phage rela	
_	Rv1410c	_	pump	Rv3757c Rv3759c	proW proX	transport system permease	Rv1584c Rv1585c		phiRV1 phage rela	
F	Rv1634	-	probable drug efflux protein probable drug efflux protein	Rv3756c	proZ proZ	similar to osmoprotection proteins transport system permease	Rv1586c	<u>.</u>	phiRV1 phage rela phiRV1 integrase	nou protein
F	Rv1819c	-	probable multidrug resistance pump	Rv1026	-	probable pppGpp-5'phosphohydro- lase	Rv2309c Rv2310	-	integrase excisionase	
F	Rv2136c	-	putative bacitracin resistance pro-			iasc	Rv2646	-	phiRV2 integrase	
-	3v2209	_	tein	F. Detoxific Rv2428	cation ahpC	alkyl hydroperoxide reductase	Rv2647 Rv2650c	-	phiRV2 phage rela phiRV2 phage rela	
	1v2209 1v2333c	-	probable drug efflux protein probable tetracenomycin C resis-	Rv2429	ahpD	member of AhpC/TSA family	Rv2651c	-	phiRV2 prohead p	rotease
_	Rv2994		tance protein probable fluoroquinolone efflux	Rv2238c Rv2521	ahpE	member of AhpC/TSA family bacterioferritin comigratory protein	Rv2652c Rv2653c	-	phiRV2 phage rela phiRV2 phage rela	
'	172334	-	protein	Rv1608c	bcp bcpB	probable bacterioferritin comigra-	Rv2654c		phiRV2 phage rela	
	Rv1877 Rv2459	-	probable drug efflux protein probable drug efflux protein	Rv3473c	bpoA	tory protein probable non-heme bromoperoxi-	Rv2655c Rv2656c	-	phiRV2 phage rela phiRV2 phage rela	
			•			dase		-	similar to gp36 of	
	3. Chapero Rv0384c	ones/Heat clpB	t shock heat shock protein	Rv1123c	bpoB	probable non-heme bromoperoxi- dase	Rv2658c	_	phage L5 phiRV2 phage rela	ated protein
	Rv0352	dnaJ	acts with GrpE to stimulate DnaK	Rv0554	bpoC	probable non-heme bromoperoxi-	Rv2659c	-	phiRV2 integrase	
F	Rv2373c	dnaJ2	ATPase DnaJ homologue	Rv3617	ephA	dase probable epoxide hydrolase		-	similar to phage P excisionase	1 phd gene
	Rv0350	dnaK	70 kD heat shock protein, chromo-	Rv1938	ephB	probable epoxide hydrolase	Rv3751	-	putative integrase	
F	Rv3417c	groEL1	some replication 60 kD chaperonin 1	Rv1124 Rv2214c	ephC ephD	probable epoxide hydrolase probable epoxide hydrolase	C. PE and	PPE fam	nilies	
	Rv0440	groEL2	60 kD chaperonin 2	Rv3670	ephE	probable epoxide hydrolase	1. PE fami		22	
	Rv3418c Rv0351	groES grpE	10 kD chaperone stimulates DnaK ATPase activity	Rv0134 Rv3171c	ephF hpx	probable epoxide hydrolase probable non-heme haloperoxi-	PE subfar PE_PGRS		38 members ly 61 members	
F	Rv2374c	hrcA	heat-inducible transcription repressor	Rv1908c	katG	dase catalase-peroxidase	2. PPE far	milu	68 members	
	Rv0251c	hsp	possible heat shock protein	Rv3846	sodA	superoxide dismutase	Z. FFL Idi	illy	00 members	
	Rv0353 Rv2031c	hspR hspX	heat shock regulator 14kD antigen, heat shock protein	Rv0432	sodC	superoxide dismutase precursor - (Cu-Zn)	D. Antibiot Rv2068c		tion and resistance class A β-lactama	00
			Hsp20 family	Rv1932	tpx	thiol peroxidase	Rv3290c	lat	lysine-ε aminotran	sferase
	Rv2299c Rv0563	htpG htpX	heat shock protein Hsp90 family probable (transmembrane) heat	Rv0634c Rv2581c	-	putative glyoxylase II putative glyoxylase II	Rv2043c Rv0133	pncA -	pyrazinamide resis possible puromyci	
			shock protein	Rv3177	-	probable non-heme haloperoxi-			ferase	,
F	Rv2701c	suhB	putative extragenic suppressor protein			dase	Rv0262c	-	aminoglycoside 2' ferase	-N-acetyltrans-
F	Rv3269	-	probable heat shock protein	IV. Other			Rv0802c		acetyltransferase	
C	C. Cell divi	ision		A. Viruleno Rv0169	mce1	cell invasion protein	Rv1082 Rv1170	-	similar to S. lincoli similar to S. lincoli	
F	Rv3641c	fic	possible cell division protein	Rv0589	mce2	cell invasion protein	Rv1347c	-	possible aminogly	coside 6'-N-
	Rv3102c Rv3610c	ftsE ftsH	membrane protein inner membrane protein,	Rv1966 Rv3499c	mce3 mce4	cell invasion protein cell invasion protein	Rv2036	-	acetyltransferase similar to lincomyo	in production
	Rv2748c	ftsK	chaperone chromosome partitioning	Rv3100c Rv1694	smpB tlyA	probable small protein b cytotoxin/hemolysin homologue	Rv2303c	_	genes similar to S. griseu	e macrotetrolide
F	Rv2151c	ftsQ	ingrowth of wall at septum	Rv0024	-	putative p60 homologue			resistance protein	
F	Rv2154c	ftsW	membrane protein (shape determi- nation)	Rv0167 Rv0168	-	part of <i>mce1</i> operon part of <i>mce1</i> operon	Rv3225c	-	probable aminogly photransferases	coside 3'-phos-
	Rv3101c	ftsX	membrane protein	Rv0170	-	part of mce1 operon		-	probable acetyltra	
	Rv2921c Rv2150c	ftsY ftsZ	cell division protein FtsY circumferential ring, GTPase	Rv0171 Rv0172	-	part of <i>mce1</i> operon part of <i>mce1</i> operon	Rv3817	-	probable aminogly photransferase	coside 3'-phos-
F	Rv3919c	gid	glucose inhibited division protein B	Rv0174	-	part of mce1 operon			·	
	Rv3625c Rv3917c	mesJ parA	probable cell cycle protein chromosome partitioning; DNA -	Rv0587 Rv0588	-	part of <i>mce2</i> operon part of <i>mce2</i> operon	E. Bacteri	ocin-like p	proteins	3
			binding	Rv0590	-	part of <i>mce2</i> operon	F. Cytochr	ome P45	0 enzymes	22
F	Rv3918c	parB	possibly involved in chromosome partitioning	Rv0591 Rv0592	-	part of <i>mce2</i> operon part of <i>mce2</i> operon	G. Coenzi	/me F420	-dependent	
F	Rv2922c	smc	member of Smc1/Cut3/Cut14	Rv0594	-	part of mce2 operon	enzyme			3
F	Rv0012	-	family possible cell division protein	Rv1085c Rv1477	-	possible hemolysin putative exported p60 protein	H. Miscell	aneous tr	ansferases	61
	Rv0435c	-	ATPase of AAA family	Du4470	_	homologue	/ Micaella		aankataana kaana	
	Rv2115c Rv3213c	-	ATPase of AAA-family possible role in chromosome seg-	Rv1478	-	putative exported p60 protein homologue	and hydro		osphatases, lyases,	18
_	8v1708	_	regation	Rv1566c	-	putative exported p60 protein	I Cyplace	ne.		6
r	Rv1708	•	possible role in chromosome parti- tioning	Rv1964	-	homologue part of <i>mce3</i> operon	J. Cyclase			6
-) Protoin	and panti	de secretion	Rv1965 Rv1967	-	part of <i>mce3</i> operon part of <i>mce3</i> operon	K. Chelata	ases		2
F	Rv2916c	ffh	signal recognition particle protein	Rv1968	-	part of mce3 operon	V. Conser	ved hypot	heticals	912
	Rv2903c Rv1614	lepB Igt	signal peptidase I prolipoprotein diacylglyceryl trans-	Rv1969 Rv1971	-	part of <i>mce3</i> operon part of <i>mce3</i> operon	VI. Unkno			606
		-	ferase	Rv2190c	-	putative p60 homologue		** 110		
	Rv1539 Rv0379	IspA sec	lipoprotein signal peptidase probable transport protein	Rv3494c Rv3496c	-	part of <i>mce4</i> operon part of <i>mce4</i> operon	TOTAL			3924
			SecE/Sec61- γ family	Rv3497c	-	part of mce4 operon				
	Rv3240c	secA	SecA, preprotein translocase sub-	Rv3498c	-	part of <i>mce4</i> operon				

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

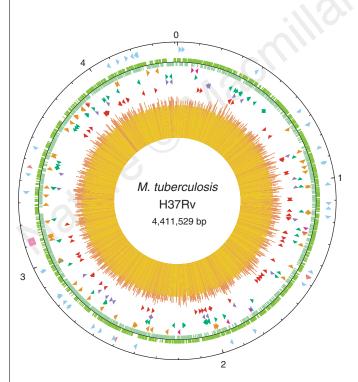


Figure 1 Circular map of the chromosome of M. tuberculosis H37Rv. The outer circle shows the scale in Mb, with 0 representing the origin of replication. The first ring from the exterior denotes the positions of stable RNA genes (tRNAs are blue, others are pink) and the direct repeat region (pink cube);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

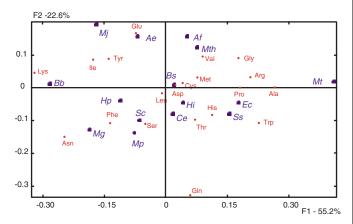


Figure 3 Correspondence analysis of the proteomes from extensively sequenced organisms as a function of amino-acid composition. Note the extreme position of *M. tuberculosis* and the shift in amino-acid preference reflecting increasing G + C content from left to right. Abbreviations used: Ae, Aquifex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

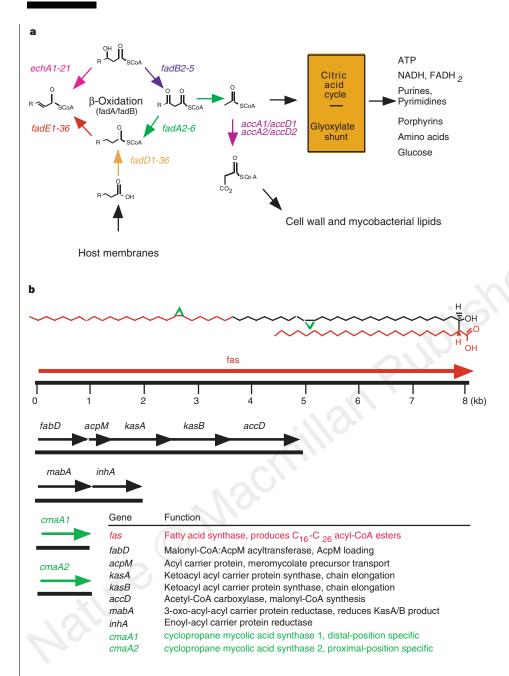
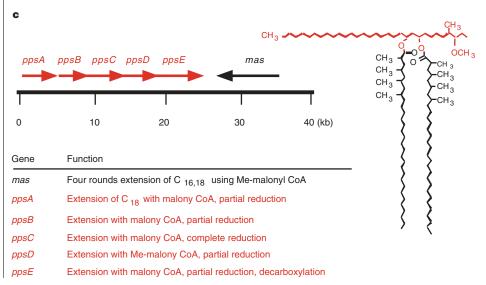


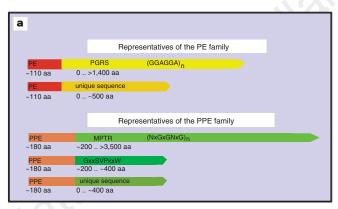
Figure 4 Lipid metabolism. a, Degradation of host-cell lipids is vital in the intracellular life of M. tuberculosis. Host-cell membranes provide precursors for many metabolic processes, as well as potential precursors of mycobacterial cell-wall constituents, through the actions of a broad family of β -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. $colt^{20}$.

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



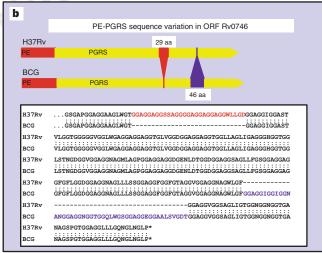


Figure 5 The PE and PPE protein families. **a**, Classification of the PE and PPE protein families. **b**, Sequence variation between *M. tuberculosis* H37Rv and *M. bovis* BCG-Pasteur in the PE-PGRS encoded by open reading frame (ORF) Rv0746.

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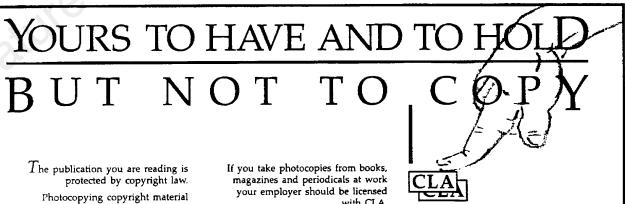
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Table 1. Functional classification of Mycobacterium tuberculosis protein-coding genes

		netabolism	D. 0004		superfamily	Rv3543c	fadE29	acyl-CoA dehydrogenase
A. Degrad		da.	Rv2831	echA16	enoyl-CoA hydratase/isomerase	Rv3560c	fadE30	acyl-CoA dehydrogenase
1. Carbon			D0000	117	superfamily	Rv3562	fadE31	acyl-CoA dehydrogenase acyl-CoA dehydrogenase
Rv0186	bgIS	β-glucosidase	Rv3039c	echA17	enoyl-CoA hydratase/isomerase	Rv3563	fadE32	
Rv2202c		carbohydrate kinase	D. 0070		superfamily	Rv3564	fadE33	acyl-CoA dehydrogenase
Rv0727c		L-fuculose phosphate aldolase	Rv3373	echA18	enoyl-CoA hydratase/isomerase	Rv3573c Rv3797	fadE34 fadE35	acyl-CoA dehydrogenase
Rv1731	gabD1	succinate-semialdehyde dehydro- genase	Rv3374	echA18'	superfamily, N-term enoyl-CoA hydratase/isomerase	Rv3761c	fadE36	acyl-CoA dehydrogenase acyl-CoA dehydrogenase
Rv0234c	gabD2	succinate-semialdehyde dehydro-	HV3374	echa io	superfamily, C-term	Rv1175c	fadH	2,4-Dienoyl-CoA Reductase
11002040	gabbz	genase	Rv3516	echA19	enoyl-CoA hydratase/isomerase	Rv0855	far	fatty acyl-CoA racemase
Rv0501	galE1	UDP-glucose 4-epimerase		00111110	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
		transferase C-term			superfamily			subunit
Rv0618	galT'	galactose-1-phosphate uridylyl-	Rv0859	fadA	β oxidation complex, β subunit	Rv2504c	scoA	3-oxo acid:CoA transferase, α sub-
		transferase N-term			(acetyl-CoA C-acetyltransferase)			unit
Rv0993	galU	UTP-glucose-1-phosphate uridylyl-	Rv0243	fadA2	acetyl-CoA C-acetyltransferase	Rv2503c	scoB	3-oxo acid:CoA transferase, β sub-
D 0000		transferase	Rv1074c	fadA3	acetyl-CoA C-acetyltransferase	D 4400		unit
Rv3696c	glpK	ATP:glycerol 3-phosphotrans-	Rv1323	fadA4	acetyl-CoA C-acetyltransferase	Rv1136 Rv1683	-	probable carnitine racemase possible acyl-CoA synthase
Rv3255c	man A	ferase	Rv3546	fadA5	(aka thiL) acetyl-CoA C-acetyltransferase	NV 1003	-	possible acyl-coa synthase
Rv3441c	manA mrsA	mannose-6-phosphate isomerase phosphoglucomutase or phospho-	Rv3556c	fadA6	acetyl-CoA C-acetyltransferase	4. Phosph	orous com	prounds
11734410	IIIISA	mannomutase	Rv0860	fadB	β oxidation complex, α subunit	Rv2368c	phoH	ATP-binding pho regulon
Rv0118c	oxcA	oxalyl-CoA decarboxylase	1100000	IAUD	(multiple activities)	11020000	priori	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-		1.1	phatase
Rv2702	ppgK	polyphosphate glucokinase			nase	Rv2984	ppk	polyphosphate kinase
Rv0408	pta	phosphate acetyltransferase	Rv3141	fadB4	3-hydroxyacyl-CoA dehydroge-			
Rv0729	xylB	xylulose kinase			nase	B. Energy		em .
Rv1096	-	carbohydrate degrading enzyme	Rv1912c	fadB5	3-hydroxyacyl-CoA dehydroge-	 Glycoly 		
			D 4	:	nase	Rv1023	eno	enolase
2. Amino a			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 fadD4	acyl-CoA synthase acyl-CoA synthase	D. 0400		drogenase
Rv2780 Rv1538c	ald ansA	L-alanine dehydrogenase L-asparaginase	Rv0214 Rv0166	fadD5	acyl-CoA synthase	Rv0489 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	Rv0119	fadD7	acyl-CoA synthase	Rv0946c	pgi	glucose-6-phosphate isomerase
1107000	111111071	dehydrogenase	Rv0551c	fadD8	acyl-CoA synthase	Rv1437	pgk	phosphoglycerate kinase
Rv0751c	mmsB	methylmalmonate semialdehyde	Rv2590	fadD9	acyl-CoA synthase	Rv1617	pykA	pyruvate kinase
		oxidoreductase	Rv0099	fadD10	acyl-CoA synthase	Rv1438	tpi	triosephosphate isomerase
Rv1187	rocA	pyrroline-5-carboxylate dehydro-	Rv1550	fadD11	acyl-CoA synthase, N-term	Rv2419c	-	putative phosphoglycerate mutase
D 0000	5.4	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 dobudro	gonooo
Rv1848	ureA	urease γ subunit	Rv1058	fadD14	acyl-CoA synthase	Rv2241	aceE	pyruvate dehydrogenase E1 com-
Rv1849	ureB	urease β subunit	Rv2187	fadD15	acyl-CoA synthase			ponent
Rv1850	ureC	urease α subunit	Rv0852	fadD16	acyl-CoA synthase	Rv3303c	<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	_		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	fadD24	acyl-CoA synthase			drogenase
			Rv1521	fadD25	acyl-CoA synthase			·
Fatty ac	cids		Rv2930	fadD26	acyl-CoA synthase	TCA cy	cle	
Rv2501c	accA1	acetyl/propionyl-CoA carboxylase,	Rv0275c	fadD27	acyl-CoA synthase	Rv1475c	acn	aconitate hydratase
		α subunit	Rv2941	fadD28	acyl-CoA synthase	Rv0889c	citA	citrate synthase 2
Rv0973c	accA2	acetyl/propionyl-CoA carboxylase,	Rv2950c	fadD29	acyl-CoA synthase	Rv2498c	citE	citrate lyase β chain
Rv2502c	D1	α subunit acetyl/propionyl-CoA carboxylase,	Rv0404 Rv1925	fadD30 fadD31	acyl-CoA synthase	Rv1098c	fum gltA1	fumarase
NV25020	accor	β subunit	Rv3801c	fadD32	acyl-CoA synthase acyl-CoA synthase	Rv1131 Rv0896	gltA2	citrate synthase 3 citrate synthase 1
Rv0974c	accD2	acetyl/propionyl-CoA carboxylase,	Rv1345	fadD32	acyl-CoA synthase	Rv3339c	icd1	isocitrate dehydrogenase
11003740	accoz	β subunit	Rv0035	fadD34	acyl-CoA synthase	Rv0066c	icd2	isocitrate dehydrogenase
Rv3667	acs	acetyl-CoA synthase	Rv2505c	fadD34	acyl-CoA synthase	Rv0794c	lpdB	dihydrolipoamide dehydrogenase
Rv3409c	choD	cholesterol oxidase	Rv1193	fadD36	acyl-CoA synthase	Rv1240	mdh	malate dehydrogenase
Rv0222	echA1	enoyl-CoA hydratase/isomerase	Rv0131c	fadE1	acyl-CoA dehydrogenase	Rv2967c	pca	pyruvate carboxylase
		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	acyl-CoA dehydrogenase			unit
D. 00=0		superfamily	Rv0271c	fadE6	acyl-CoA dehydrogenase	Rv3317	sdhD	succinate dehydrogenase D sub-
Rv0673	echA4	enoyl-CoA hydratase/isomerase superfamily	Rv0400c Rv0672	fadE7 fadE8	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv1248c	sucA	unit 2-oxoglutarate dehydrogenase
Rv0675	echA5	enoyl-CoA hydratase/isomerase	1100072	IAULU	(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
		superfamily (aka eccH)	Rv0972c	fadE12	acyl-CoA dehydrogenase	Rv0952	sucD	succinyl-CoA synthase α chain
Rv0971c	echA7	enoyl-CoA hydratase/isomerase	Rv0975c	fadE13	acyl-CoA dehydrogenase			
D. 4070		superfamily	Rv1346	fadE14	acyl-CoA dehydrogenase	4. Glyoxyl		
Rv1070c	echA8	enoyl-CoA hydratase/isomerase	Rv1467c	fadE15	acyl-CoA dehydrogenase	Rv0467	aceA	isocitrate lyase
Rv1071c	echA9	superfamily enoyl-CoA hydratase/isomerase	Rv1679 Rv1934c	fadE16 fadE17	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv1915 Rv1916	aceAa aceAb	isocitrate lyase, α module isocitrate lyase, β module
HV1071C	ECHAS	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
		superfamily	0000		(aka mmgC)		3F."'	F E 3-7 prisoprimaso
Rv1141c	echA11		Rv2724c	fadE20	acyl-CoA dehydrogenase	5. Pentose	phospha	te pathway
		superfamily	Rv2789c	fadE21	acyl-CoA dehydrogenase	Rv1445c	devB	glucose-6-phosphate 1-dehydro-
Rv1472	echA12	enoyl-CoA hydratase/isomerase	Rv3061c	fadE22	acyl-CoA dehydrogenase			genase
D. 4005		superfamily	Rv3140	fadE23	acyl-CoA dehydrogenase	Rv1844c	gnd	6-phosphogluconate dehydroge-
Rv1935c	echA13	enoyl-CoA hydratase/isomerase	Rv3139	fadE24	acyl-CoA dehydrogenase	Dv1100	anda	nase (Gram –)
Rv2486	echA14	superfamily enoyl-CoA hydratase/isomerase	Rv3274c Rv3504	fadE25 fadE26	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv1122	gnd2	6-phosphogluconate dehydroge- nase (Gram +)
	33.7114	superfamily	Rv3505	fadE27	acyl-CoA dehydrogenase	Rv1446c	opcA	unknown function, may aid
Rv2679	echA15	enoyl-CoA hydratase/isomerase	Rv3544c	fadE28	acyl-CoA dehydrogenase			G6PDH

Rv2436	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	7. Miscella	aneous ox	doreductases and oxygenases 171	Rv2918c	glnD	uridylyltransferase
Rv1448c Rv1449c	tal tkt	transaldolase transketolase	Q ATD pr	oton motiv	o force	Rv2221c	glnE	glutamate-ammonia-ligase adenyltransferase
Rv1121	zwf	glucose-6-phosphate 1-dehydro-	8. ATF-PIO Rv1308	atpA	ATP synthase α chain	Rv3859c	gltB	ferredoxin-dependent glutamate
1101121	2111	genase	Rv1304	atpB	ATP synthase α chain	11000000	gnD	synthase
Rv1447c	zwf2	glucose-6-phosphate 1-dehydro-	Rv1311	atpC	ATP synthase ε chain	Rv3858c	gltD	small subunit of NADH-dependent
		genase	Rv1310	atpD	ATP synthase β chain		Ü	glutamate synthase .
			Rv1305	atpE	ATP synthase c chain	Rv3704c	gshA	possible γ-glutamylcysteine syn-
Respira			Rv1306	atpF	ATP synthase b chain			thase
a. aerobic		and a decrease of the second of	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
Rv0529	ccsB	protein cytochrome c-type biogenesis	C Centra	l intermedi	iary metabolism	Rv0500	proC	pyrroline-5-carboxylate reductase
1100525	CC3D	protein	1. Genera		ary metabolism	2. Asparta	te family	
Rv1451	ctaB	cytochrome c oxidase assembly	Rv2589	gabT	4-aminobutyrate aminotransferase	Rv3708c	asd	aspartate semialdehyde dehydro-
		factor	Rv3432c	gadB	glutamate decarboxylase			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	-1	peptide I	Rv2211c	gcvT	T protein of glycine cleavage	Rv3565	aspB	aspartate aminotransferase
Rv2193	ctaE	cytochrome <i>c</i> oxidase poly- peptide III	Rv1213	alaC	system glucose-1-phosphate adenylyl-	Rv0337c Rv2753c	aspC dapA	aspartate aminotransferase dihydrodipicolinate synthase
Rv1542c	glbN	hemoglobin-like, oxygen carrier	HVIZIO	glgC	transferase	Rv2773c	dapA	dihydrodipicolinate reductase
Rv2470	glbO	hemoglobin-like, oxygen carrier	Rv3842c	glpQ1	glycerophosphoryl diester phos-	Rv1202	dapE	succinyl-diaminopimelate desuc-
Rv2249c	glpD1	glycerol-3-phosphate dehydroge-		3	phodiesterase			cinylase
	01	nase	Rv0317c	glpQ2	glycerophosphoryl diester phos-	Rv2141c	dapE2	ArgE/DapE/Acy1/Cpg2/yscS
Rv3302c	glpD2	glycerol-3-phosphate dehydroge-			phodiesterase			family
		nase	Rv3566c	nhoA	N-hydroxyarylamine o-acetyltrans-	Rv2726c	dapF	diaminopimelate epimerase
Rv0694	IIdD1	L-lactate dehydrogenase	5 04==		ferase	Rv1293	lysA	diaminopimelate decarboxylase
Dv1970c	IIdD2	(cytochrome)	Rv0155	pntAA	pyridine transhydrogenase sub-	Rv3341	metA motB	homoserine o-acetyltransferase
Rv1872c Rv1854c	ndh	L-lactate dehydrogenase probable NADH dehydrogenase	Rv0156	pntAB	unit α1 pyridine transhydrogenase sub-	Rv1079 Rv3340	metB metC	cystathionine γ-synthase cystathionine β-lyase
Rv3145	nuoA	NADH dehydrogenase chain A	1100100	PITAL	unit α2	Rv1133c	metE	5-methyltetrahydropteroyltrigluta-
Rv3146	nuoA	NADH denydrogenase chain B	Rv0157	pntB	pyridine transhydrogenase		···otL	mate-homocysteine methyltrans-
Rv3147	nuoC	NADH dehydrogenase chain C		<i>µ</i> ···-	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				Rv1392	metK	S-adenosylmethionine synthase
Rv3151	nuoG	NADH dehydrogenase chain G		eogenesis		Rv0391	metZ	o-succinylhomoserine sulfhy-
Rv3152	nuoH	NADH dehydrogenase chain H	Rv0211	pckA	phosphoenolpyruvate carboxy-	D: 1004	464	drylase
Rv3153	nuol	NADH dehydrogenase chain I	By0060a	ada A	kinase	Rv1294	thrA	homoserine dehydrogenase
Rv3154 Rv3155	nuoJ nuoK	NADH dehydrogenase chain J NADH dehydrogenase chain K	Rv0069c	sdaA	L-serine dehydratase 1	Rv1296 Rv1295	thrB thrC	homoserine kinase homoserine synthase
Rv3156	nuoL	NADH dehydrogenase chain L	3 Sugar r	nucleotides		1101233	uno	nomosenne synthase
Rv3157	nuoM	NADH dehydrogenase chain M	Rv1512	epiA	nucleotide sugar epimerase	3. Serine	family	
Rv3158	nuoN	NADH dehydrogenase chain N	Rv3784	epiB	probable UDP-galactose 4-	Rv0815c	cysA2	thiosulfate sulfurtransferase
Rv2195	qcrA	Rieske iron-sulphur component of			epimerase	Rv3117	cysA3	thiosulfate sulfurtransferase
		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 c-methyltrans-
D 0101	_	cytB reductase			transferase	D 00.1=		ferase
Rv2194	qcrC	cytochrome b/c component of	Rv3264c	rmIA2	glucose-1-phosphate thymidyl-	Rv2847c	cysG2	multifunctional enzyme, siroheme
		ubiQ-cytB reductase	Rv3464	rmIB	transferase dTDP-glucose 4,6-dehydratase	Rv2334	cysK	synthase cysteine synthase A
b. anaerob	nic		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
	-,	reductase	Rv3465	rmIC	dTDP-4-dehydrorhamnose	Rv0848	cysM3	putative cysteine synthase
Rv2899c	fdhD	affects formate dehydrogenase-N			3,5-epimerase	Rv1093	glyA	serine hydroxymethyltransferase
Rv2900c	fdhF	molybdopterin-containing oxidore-	Rv3266c	rmID	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
D: 4550	(ID	subunit			dehydrogenase/GDP-mannose 6-	Rv0505c	serB	probable phosphoserine phos-
Rv1553	frdB	fumarate reductase iron sulphur protein	Rv3265c		dehydrogenase	Rv3042c	D0	phatase C-term similar to phosphoserine
Rv1554	frdC	fumarate reductase 15kD anchor	Rv1525	wbbL wbbl2	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase	NV30420	serB2	
HV 1554	IIUC	protein	Rv3400	-	probable β-phosphoglucomutase	Rv0884c	serC	phosphatase phosphoserine aminotransferase
Rv1555	frdD	fumarate reductase 13kD anchor	. 140-400		F. 1545.5 P Prioopriogracomatase		23,0	poopoociio aliiilollallolelase
		protein	4. Amino	sugars		4. Aromati	ic amino a	acid family
Rv1161	narG	nitrate reductase α subunit	Rv3436c	glmS	glucosamine-fructose-6-	Rv3227	aroA	3-phosphoshikimate
Rv1162	narH	nitrate reductase β chain			phosphate aminotransferase	B	_	1-carboxyvinyl transferase
Rv1164	narl	nitrate reductase γ chain	F 0 · ·			Rv2538c	aroB	3-dehydroquinate synthase
Rv1163	narJ	nitrate reductase δ chain		r metabolis		Rv2537c	aroD	3-dehydroquinate dehydratase
Rv1736c	narX nirA	fused nitrate reductase probable nitrite reductase/sulphite	Rv0711 Rv3299c	atsA atsB	arylsulfatase	Rv2552c	aroE aroF	shikimate 5-dehydrogenase chorismate synthase
Rv2391	IIIIA	reductase	Rv32990 Rv0663	atsB atsD	proable arylsulfatase proable arylsulfatase	Rv2540c Rv2178c	aro⊦ aroG	DAHP synthase
Rv0252	nirB	nitrite reductase flavoprotein	Rv3077	atsF	proable arylsulfatase	Rv2539c	aroK	shikimate kinase I
Rv0253	nirD	probable nitrite reductase small	Rv0296c	atsG	proable arylsulfatase	Rv3838c	pheA	prephenate dehydratase
		subunit	Rv3796	atsH	proable arylsulfatase	Rv1613	trpA	tryptophan synthase α chain
			Rv1285	cysD	ATP:sulphurylase subunit 2	Rv1612	trpB	tryptophan synthase β chain
c Flectron			D 4000	cysN	ATP:sulphurylase subunit 1	Rv1611	trpC	indole-3-glycerol phosphate
	n transpor		Rv1286					
Rv0409	ackÁ	acetate kinase	Rv2131c	cysQ	homologue of M.leprae cysQ			synthase
		acetate kinase cytochrome bd-II oxidase	Rv2131c Rv3248c	cysQ sahH	homologue of <i>M.leprae cysQ</i> adenosylhomocysteinase	Rv2192c	trpD	synthase anthranilate phosphoribosyltrans-
Rv0409 Rv1623c	ackÁ appC	acetate kinase cytochrome <i>bd-II</i> oxidase subunit I	Rv2131c Rv3248c Rv3283	cysQ sahH sseA	homologue of <i>M.leprae cysQ</i> adenosylhomocysteinase thiosulfate sulfurtransferase	Rv2192c	trpD	synthase anthranilate phosphoribosyltrans- ferase
Rv0409	ackÁ	acetate kinase cytochrome <i>bd-II</i> oxidase subunit I cytochrome <i>d</i> ubiquinol oxidase	Rv2131c Rv3248c Rv3283 Rv2291	cysQ sahH sseA sseB	homologue of <i>M.leprae cysQ</i> adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase			synthase anthranilate phosphoribosyltrans- ferase anthranilate synthase
Rv0409 Rv1623c Rv1622c	ackA appC cydB	acetate kinase cytochrome bd-II oxidase subunit I cytochrome d ubiquinol oxidase subunit II	Rv2131c Rv3248c Rv3283 Rv2291 Rv3118	cysQ sahH sseA sseB sseC	homologue of M.leprae cysQ adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase	Rv2192c Rv1609	trpD trpE	synthase anthranilate phosphoribosyltrans- ferase anthranilate synthase component I
Rv0409 Rv1623c Rv1622c Rv1620c	ackÁ appC cydB cydC	acetate kinase cytochrome bd-II oxidase subunit I cytochrome d ubiquinol oxidase subunit II ABC transporter	Rv2131c Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c	cysQ sahH sseA sseB	homologue of M.leprae cysQ adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase	Rv2192c	trpD	synthase anthranilate phosphoribosyltrans- ferase anthranilate synthase component I anthranilate synthase
Rv0409 Rv1623c Rv1622c	ackA appC cydB	acetate kinase cytochrome bd-II oxidase subunit I cytochrome d ubiquinol oxidase subunit II	Rv2131c Rv3248c Rv3283 Rv2291 Rv3118	cysQ sahH sseA sseB sseC	homologue of M.leprae cysQ adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase	Rv2192c Rv1609	trpD trpE	synthase anthranilate phosphoribosyltrans- ferase anthranilate synthase component I
Rv0409 Rv1623c Rv1622c Rv1620c Rv1621c	ackÁ appC cydB cydC cydD	acetate kinase cytochrome bd-II oxidase subunit I cytochrome d ubiquinol oxidase subunit I ABC transporter ABC transporter	Rv2131c Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c	cysQ sahH sseA sseB sseC	homologue of M.leprae cysQ adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase probable alkyl sulfatase	Rv2192c Rv1609 Rv2386c	trpD trpE trpE2	synthase anthranilate phosphoribosyltrans- ferase anthranilate synthase component I anthranilate synthase component I
Rv0409 Rv1623c Rv1622c Rv1620c Rv1621c Rv2007c Rv3554 Rv1177	ackÁ appC cydB cydC cydD fdxA fdxB fdxC	acetate kinase cytochrome bd-II oxidase subunit I cytochrome d ubiquinol oxidase subunit IABC transporter ABC transporter ferredoxin ferredoxin ferredoxin 4Fe-4S	Rv2131c Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c <i>D. Amino</i> 1. Glutam	cysQ sahH sseA sseB sseC sseC2 - acid biosy ate family	homologue of M.leprae cysQ adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase probable alkyl sulfatase	Rv2192c Rv1609 Rv2386c Rv3754 5. Histidin	trpD trpE trpE2 tyrA	synthase anthranilate phosphoribosyltrans- ferase anthranilate synthase component I anthranilate synthase component I prephenate dehydrogenase
Rv0409 Rv1623c Rv1622c Rv1620c Rv1621c Rv2007c Rv3554 Rv1177 Rv3503c	ackA appC cydB cydC cydD fdxA fdxB fdxC fdxD	acetate kinase cytochrome bd-ll oxidase subunit I cytochrome d ubiquinol oxidase subunit II ABC transporter ABC transporter ferredoxin ferredoxin ferredoxin 4Fe-4S probable ferredoxin	Rv2131c Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c <i>D. Amino</i> 1. Glutam Rv1654	cysQ sahH sseA sseB sseC sseC2 - acid biosy ate family argB	homologue of M.leprae cysQ adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase probable alkyl sulfatase nthesis acetylglutamate kinase	Rv2192c Rv1609 Rv2386c Rv3754	trpD trpE trpE2 tyrA	synthase anthranilate phosphoribosyltrans- ferase anthranilate synthase component I anthranilate synthase component I prephenate dehydrogenase
Rv0409 Rv1623c Rv1622c Rv1620c Rv1621c Rv2007c Rv3554 Rv1177	ackÁ appC cydB cydC cydD fdxA fdxB fdxC	acetate kinase cytochrome bd-ll oxidase subunit I cytochrome d ubiquinol oxidase subunit II ABC transporter ABC transporter ferredoxin ferredoxin ferredoxin 4Fe-4S probable ferredoxin electron transfer flavoprotein	Rv2131c Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c <i>D. Amino</i> 1. Glutam	cysQ sahH sseA sseB sseC sseC2 - acid biosy ate family	homologue of M.leprae cysQ adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase probable alkyl sulfatase probable alkyl sulfatase nthesis acetylglutamate kinase N-acetyl-y-glutamyl-phosphate	Rv2192c Rv1609 Rv2386c Rv3754 5. Histidin	trpD trpE trpE2 tyrA	synthase anthranilate phosphoribosyltrans- ferase anthranilate synthase component I anthranilate synthase component I prephenate dehydrogenase phosphoribosylformimino-5- aminoimidazole carboxamide
Rv0409 Rv1623c Rv1622c Rv1620c Rv1621c Rv2007c Rv3554 Rv1177 Rv3503c Rv3029c	ackA appC cydB cydC cydD fdxA fdxB fdxC fdxD fixA	acetate kinase cytochrome bd-II oxidase subunit I cytochrome d ubiquinol oxidase subunit IA ABC transporter ABC transporter ferredoxin ferredoxin ferredoxin ferredoxin 4Fe-4S probable ferredoxin electron transfer flavoprotein β subunit	Rv2131c Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c <i>D. Amino</i> 1. Glutam Rv1654 Rv1652	cysQ sahH sseA sseB sseC sseC2 - acid biosy ate family argB argC	homologue of M.leprae cysQ adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase probable alkyl sulfatase nthesis acetylglutamate kinase N-acetylglutamate kinase N-acetyl-y-glutamyl-phosphate reductase	Rv2192c Rv1609 Rv2386c Rv3754 5. Histidin Rv1603	trpD trpE trpE2 tyrA e hisA	synthase anthranilate phosphoribosyltrans- ferase anthranilate synthase component I anthranilate synthase component I prephenate dehydrogenase phosphoribosylformimino-5- aminoimidazole carboxamide ribonucleotide isomerase
Rv0409 Rv1623c Rv1622c Rv1620c Rv1621c Rv2007c Rv3554 Rv1177 Rv3503c	ackA appC cydB cydC cydD fdxA fdxB fdxC fdxD	acetate kinase cytochrome bd-II oxidase subunit I cytochrome d ubiquinol oxidase subunit I ABC transporter ABC transporter ferredoxin ferredoxin ferredoxin ferredoxin 4Fe-4S probable ferredoxin electron transfer flavoprotein β subunit electron transfer flavoprotein α	Rv2131c Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c <i>D. Amino</i> 1. Glutam Rv1654 Rv1652	cysQ sahH sseA sseB sseC2 - acid biosy ate family argB argC argD	homologue of M.leprae cysQ adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase probable alkyl sulfatase nthesis acetylglutamate kinase N-acetyl-y-glutamyl-phosphate reductase acetylornithine aminotransferase	Rv2192c Rv1609 Rv2386c Rv3754 5. Histidin	trpD trpE trpE2 tyrA	synthase anthranilate phosphoribosyltrans- ferase anthranilate synthase component I anthranilate synthase component I prephenate dehydrogenase phosphoribosylformimino-5- aminoimidazole carboxamide ribonucleotide isomerase imidazole glycerol-phosphate
Rv0409 Rv1623c Rv1622c Rv1620c Rv1621c Rv2007c Rv3554 Rv1177 Rv3503c Rv3029c Rv3028c	ackÁ appC cydB cydC cydD fdxA fdxB fdxC fdxD fixA	acetate kinase cytochrome bd-ll oxidase subunit I cytochrome d ubiquinol oxidase subunit II ABC transporter ABC transporter ferredoxin ferredoxin ferredoxin 4Fe-4S probable ferredoxin electron transfer flavoprotein β subunit electron transfer flavoprotein α subunit	Rv2131c Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c D. Amino 1. Glutam Rv1654 Rv1652 Rv1655 Rv1656	cysQ sahH sseA sseB sseC sseC2 - acid biosy ate family argB argC argD argF	homologue of M.leprae cysQ adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase probable alkyl sulfatase probable alkyl sulfatase nthesis acetylglutamate kinase N-acetyl-y-glutamyl-phosphate reductase acetylornithine aminotransferase ornithine carbamoyltransferase	Rv2192c Rv1609 Rv2386c Rv3754 5. Histidin Rv1603	trpD trpE trpE2 tyrA e hisA	synthase anthranilate phosphoribosyltrans- ferase anthranilate synthase component I anthranilate synthase component I prephenate dehydrogenase phosphoribosylformimino-5- aminoimidazole carboxamide ribonucleotide isomerase imidazole glycerol-phosphate dehydratase
Rv0409 Rv1623c Rv1622c Rv1620c Rv1621c Rv2007c Rv3554 Rv1177 Rv3503c Rv3029c	ackA appC cydB cydC cydD fdxA fdxB fdxC fdxD fixA	acetate kinase cytochrome bd-II oxidase subunit I cytochrome d ubiquinol oxidase subunit I ABC transporter ABC transporter ferredoxin ferredoxin ferredoxin ferredoxin 4Fe-4S probable ferredoxin electron transfer flavoprotein β subunit electron transfer flavoprotein α	Rv2131c Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c D. Amino 1. Glutam Rv1654 Rv1655 Rv1656 Rv1656 Rv1656	cysQ sahH sseA sseB sseC sseC2 - acid biosy ate family argB argC argD argF argG	homologue of M.leprae cysQ adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase probable alkyl sulfatase nthesis acetylglutamate kinase N-acetyl-y-glutamyl-phosphate reductase acetylornithine aminotransferase ornithine carbamoyltransferase arginosuccinate synthase	Rv2192c Rv1609 Rv2386c Rv3754 5. Histidin Rv1603	trpD trpE trpE2 tyrA e hisA	synthase anthranilate phosphoribosyltrans- ferase anthranilate synthase component I anthranilate synthase component I prephenate dehydrogenase phosphoribosylformimino-5- aminoimidazole carboxamide ribonucleotide isomerase imidazole glycerol-phosphate
Rv0409 Rv1623c Rv1622c Rv1620c Rv1621c Rv2007c Rv3554 Rv1177 Rv3503c Rv3029c Rv3028c	ackÁ appC cydB cydC cydD fdxA fdxB fdxC fdxD fixA	acetate kinase cytochrome bd-ll oxidase subunit 1 cytochrome d ubiquinol oxidase subunit 1 ABC transporter ABC transporter ferredoxin ferredoxin ferredoxin ferredoxin 4Fe-4S probable ferredoxin electron transfer flavoprotein β subunit electron transfer flavoprotein α subunit adrenodoxin and NADPH ferre-	Rv2131c Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c D. Amino 1. Glutam Rv1654 Rv1652 Rv1655 Rv1656	cysQ sahH sseA sseB sseC sseC2 - acid biosy ate family argB argC argD argF	homologue of M.leprae cysQ adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase probable alkyl sulfatase probable alkyl sulfatase nthesis acetylglutamate kinase N-acetyl-y-glutamyl-phosphate reductase acetylornithine aminotransferase ornithine carbamoyltransferase	Rv2192c Rv1609 Rv2386c Rv3754 5. Histidin Rv1603	trpD trpE trpE2 tyrA e hisA	synthase anthranilate phosphoribosyltrans- ferase anthranilate synthase component I anthranilate synthase component I prephenate dehydrogenase phosphoribosylformimino-5- aminoimidazole carboxamide ribonucleotide isomerase imidazole glycerol-phosphate dehydratase histidinol-phosphate aminotrans-
Rv0409 Rv1623c Rv1622c Rv1620c Rv1621c Rv2007c Rv3554 Rv1177 Rv3503c Rv3029c Rv3028c Rv3106 Rv0886	ackÁ appC cydB cydC cydD fdxA fdxB fdxC fdxD fixA fixB	acetate kinase cytochrome bd-ll oxidase subunit 1 cytochrome d ubiquinol oxidase subunit 1 ABC transporter ABC transporter ferredoxin ferredoxin ferredoxin ferredoxin subunit 1 subunit electron transfer flavoprotein β subunit electron transfer flavoprotein α subunit adrenodoxin and NADPH ferredoxin reductase ferredoxin, ferredoxin, ferredoxin, NADP reductase	Rv2131c Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c D. Amino 1. Glutam Rv1654 Rv1655 Rv1655 Rv1656 Rv1658 Rv1659 Rv1653 Rv2220	cysQ sahH sseA sseB sseC sseC2 - acid biosy atte family argB argC argD argF argG argH argJ glnA1	homologue of M.leprae cysQ adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase probable alkyl sulfatase nthesis acetylglutamate kinase N-acetyl-y-glutamyl-phosphate reductase acetylornithine aminotransferase ornithine carbamoyltransferase arginosuccinate synthase arginosuccinate synthase glutamine synthase class I	Rv2192c Rv1609 Rv2386c Rv3754 5. Histidin Rv1603 Rv1601 Rv1600 Rv3772	trpD trpE trpE2 tyrA e hisA hisB hisC	synthase anthranilate phosphoribosyltrans- ferase anthranilate synthase component I anthranilate synthase component I prephenate dehydrogenase phosphoribosylformimino-5- aminoimidazole carboxamide ribonucleotide isomerase imidazole glycerol-phosphate dehydratase histidinol-phosphate aminotrans- ferase histidinol-phosphate aminotrans- ferase anthranilate properties of the properties of t
Rv0409 Rv1623c Rv1622c Rv1620c Rv1621c Rv2007c Rv3554 Rv1177 Rv3503c Rv3029c Rv3028c Rv3106	ackÁ appC cydB cydC cydD fdxA fdxB fdxC fdxD fixA fixB	acetate kinase cytochrome bd-ll oxidase subunit I cytochrome d ubiquinol oxidase subunit II ABC transporter ABC transporter ferredoxin ferredoxin ferredoxin ferredoxin sprobable ferredoxin electron transfer flavoprotein β subunit electron transfer flavoprotein α subunit adrenodoxin and NADPH ferredoxin reductase ferredoxin, ferredoxin, ferredoxin, ferredoxin-NADP	Rv2131c Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c D. Amino 1. Glutam Rv1654 Rv1652 Rv1656 Rv1658 Rv1658 Rv1658 Rv1658	cysQ sahH sseA sseB sseC sseC2 - acid biosy argB argC argD argF argG argH argJ	homologue of M.leprae cysQ adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase probable alkyl sulfatase probable alkyl sulfatase nthesis acetylglutamate kinase N-acetyl-y-glutamyl-phosphate reductase acetylornithine aminotransferase ornithine carbamoyltransferase arginosuccinate synthase arginosuccinate lyase glutamate N-acetyltransferase	Rv2192c Rv1609 Rv2386c Rv3754 5. Histidin Rv1603 Rv1601 Rv1600	trpD trpE trpE2 tyrA e hisA hisB	synthase anthranilate phosphoribosyltrans- ferase anthranilate synthase component I anthranilate synthase component I prephenate dehydrogenase phosphoribosylformimino-5- aminoimidazole carboxamide ribonucleotide isomerase imidazole glycerol-phosphate dehydratase histidinol-phosphate aminotrans- ferase histidinol-phosphate aminotrans-

Rv1605	hisF	imidazole glycerol-phosphate	D 0010	10	subunit	D 0440	_	subunit 1
Rv2121c	hisG	synthase ATP phosphoribosyltransferase	Rv3048c	nrdG	ribonucleoside-diphosphate small subunit	Rv3119	moaE	molybdopterin-converting factor subunit 2
Rv1602	hisH	amidotransferase	Rv3053c	nrdH	glutaredoxin electron transport	Rv0866	moaE2	molybdopterin-converting factor
Rv2122c	hisl	phosphoribosyl-AMP cyclohydro-			component of NrdEF system		moull	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	D: 000.4		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
NV0114	-	Similar to HISB	Rv3752c	-	probable cytidine/deoxycytidylate	Rv2338c	тоеБ	molybdopterin biosynthesis
6. Pyruvat	e family				deaminase	Rv1681	moeX	weak similarity to <i>E. coli</i> MoaA
	alr	alanine racemase				Rv1355c	moeY	weak similarity to E. coli MoeB
					osides and nucleotides	Rv3206c	moeZ	probably involved in
7. Branch			Rv3313c	add	probable adenosine deaminase	D. 0005		molybdopterin biosynthesis
Rv1559 Rv3003c	ilvA ilvB	threonine deaminase acetolactate synthase I large sub-	Rv2584c	apt	adenine phosphoribosyltrans- ferases	Rv0865	mog	molybdopterin biosynthesis
HV3003C	IIVD	unit	Rv3315c	cdd	probable cytidine deaminase	5. Pantoth	enate	
Rv3470c	ilvB2	acetolactate synthase large sub-	Rv3314c	deoA	thymidine phosphorylase	Rv1092c	coaA	pantothenate kinase
		unit	Rv0478	deoC	deoxyribose-phosphate aldolase	Rv2225	panB	3-methyl-2-oxobutanoate
Rv3001c		ketol-acid reductoisomerase	Rv3307	deoD	probable purine nucleoside phos-			hydroxymethyltransferase
Rv0189c	ilvD	dihydroxy-acid dehydratase	D 0004		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. Pyridox	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-			family 2			
D. 0740	/A	thase I large subunit	Rv3309c	ирр	uracil phophoribosyltransferase	7. Pyridine		
Rv3710 Rv2995c	leuA leuB	α-isopropyl malate synthase 3-isopropylmalate dehydrogenase	5 Miscells	nanue nu	cleoside/nucleotide reactions	Rv1594 Rv1595	nadA 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			family	Rv0423c	thiC	thiamine synthesis, pyrimidine
		small subunit	Rv1712	cmk	cytidylate kinase			moiety
5 D-1	to a south		Rv2344c	dgt	probable deoxyguanosine	O This was to		
E. Polyam Rv2601	nine synthe speE	esis spermidine synthase	Rv2404c	lepA	triphosphate hydrolase GTP-binding protein LepA	8. Thiamin Rv0422c	e thiD	phosphomethylpyrimidine kinase
1102001	SPEL	spermane synthase	Rv2727c	miaA	tRNA δ(2)-isopentenylpyrophos-	Rv0414c	thiE	thiamine synthesis, thiazole
F. Purines	s, pyrimidir	nes, nucleosides and nucleotides			phate transferase			moiety
1. Purine		tide biosynthesis	Rv2445c	ndkA	nucleoside diphosphate kinase	Rv0417	thiG	thiamine synthesis, thiazole
Rv1389	gmk	putative guanylate kinase	Rv2440c	obg	Obg GTP-binding protein			moiety
Rv3396c	guaA	GMP synthase	Rv2583c	relA	(p)ppGpp synthase I	Rv2977c	thiL	probable thiamine-monophos-
Rv1843c	guaB1	inosine-5'-monophosphate dehy- drogenase	G Riocyn	thocic of c	pofactors, prosthatic groups and			phate kinase
Rv3411c	guaB2	inosine-5'-monophosphate dehy-	carriers	u lesis oi c	cofactors, prosthetic groups and	9. Riboflav	/in	
	3	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
		drogenase			oxononanoate aminotransferase	Rv1412	ribC	riboflavin synthase α chain
Rv1017c	prsA	ribose-phosphate pyrophosphoki-	Rv1589	bioB	biotin synthase	Rv2671	ribD	probable riboflavin deaminase
Rv0357c	purA	nase adenylosuccinate synthase	Rv1570 Rv1569	bioD bioF	dethiobiotin synthase 8-amino-7-oxononanoate	Rv2786c Rv1409	ribF ribG	riboflavin kinase riboflavin biosynthesis
Rv0777	purB	adenylosuccinate lyase	1101303	DIOI	synthase	Rv1416	ribH	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			
D. 0075-		ase	Rv1442	bisC	biotin sulfoxide reductase			taredoxin and mycothiol
Rv3275c	purE	phosphoribosylaminoimidazole carboxylase	Rv0089	-	possible bioC biotin synthesis gene	Rv0773c Rv2394	ggtA ggtB	putative γ-glutamyl transpeptidase γ-glutamyltranspeptidase
Rv0808	purF	amidophosphoribosyltransferase-			gene	1102004	ggib	precursor
Rv0957	purH	phosphoribosylaminoimidazole-	2. Folic ac	id		Rv2855	gorA	glutathione reductase homologue
	•	carboxamide formyltransferase	Rv2763c		dihydrofolate reductase	Rv0816c	thiX	equivalent to M. leprae ThiX
Rv3276c	purK	phosphoribosylaminoimidazole	Rv2447c	folC	folylpolyglutamate synthase	Rv1470	trxA	thioredoxin
D. 0000		carboxylase ATPase subunit	Rv3356c	folD	methylenetetrahydrofolate dehy-	Rv1471	trxB	thioredoxin reductase
Rv0803	purL	phosphoribosylformylglycin- amidine synthase II	Rv3609c	folE	drogenase GTP cyclohydrolase I	Rv3913 Rv3914	trxB2 trxC	thioredoxin reductase thioredoxin
Rv0809	purM	5'-phosphoribosyl-5-aminoimida-	Rv3606c	folK	7,8-dihydro-6-hydroxymethylpterin	1100014	uxo	unoredoxin
	7	zole synthase			pyrophosphokinase	11. Menad	quinone, P	QQ, ubiquinone and other
Rv0956	purN	phosphoribosylglycinamide	Rv3608c	folP	dihydropteroate synthase	terpenoids		
D.:0700	n	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-	1140002	9,001	synthase II
	,	formyltransferase II		,	mine amidotransferase	Rv0989c	grcC2	heptaprenyl diphosphate
Rv2964	purU	formyltetrahydrofolate deformy-	Rv1005c	pabB	p-aminobenzoate synthase			synthase II
		lase	Rv0812	pabC	aminodeoxychorismate lyase	Rv3398c	idsA	geranylgeranyl pyrophosphate
9 Dunlant-	ino riba	cleotide biosynthesis	2 linaata			Rv2173	idsA2	synthase geranylgeranyl pyrophosphate
2. Fyriiliu Rv1383	carA	carbamoyl-phosphate synthase	Lipoate Rv2218	lipA	lipoate biosynthesis protein A	NV21/3	IUSAZ	synthase
1101000	Cair	subunit	Rv2217	lipB	lipoate biosynthesis protein B	Rv3383c	idsB	transfergeranyl, similar geranyl
Rv1384	carB	carbamoyl-phosphate synthase			р-сы.с,			pyrophosphate synthase
		subunit	Molybde			Rv0534c	menA	4-dihydroxy-2-naphthoate
Rv1380	pyrB	aspartate carbamoyltransferase	Rv3109	moaA	molybdenum cofactor biosynthe-	D. 05.10		octaprenyltransferase
Rv1381	pyrC	dihydroorotase	Dyneco	maa 12	sis, protein A	Rv0548c	menB menC	naphthoate synthase
Rv2139 Rv1385	pyrD pyrF	dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxy-	Rv0869c	moaA2	molybdenum cofactor biosynthe- sis, protein A	Rv0553 Rv0555	menD	o-succinylbenzoate-CoA synthase 2-succinyl-6-hydroxy-2,4-cyclo-
	F)	lase	Rv0438c	moaA3	molybdenum cofactor biosynthe-			hexadiene-1-carboxylate synthase
Rv1699	pyrG	CTP synthase		-	sis, protein A	Rv0542c	menE	o-succinylbenzoic acid-CoA ligase
Rv2883c	pyrH	uridylate kinase	Rv3110	moaB	molybdenum cofactor biosynthe-	Rv3853	menG	S-adenosylmethionine:
Rv0382c	umpA	probable uridine 5'-monophos-	D. 0001	25	sis, protein B	D. 0000		2-demethylmenaquinone
		phate synthase	Rv0984	moaB2	molybdenum cofactor biosynthe-	Rv3397c	phyA pagE	phytoene synthase
3 2'-deev	vrihonuclo	otide metabolism	Rv3111	moaC	sis, protein B molybdenum cofactor biosynthe-	Rv0693	pqqE	coenzyme PQQ synthesis protein E
Rv0321	dcd	deoxycytidine triphosphate	1100111	moao	sis, protein C	Rv0558	ubiE	ubiquinone/menaquinone biosyn-
	-	deaminase	Rv0864	moaC2	molybdenum cofactor biosynthe-			thesis methyltransferase
Rv2697c	dut	deoxyuridine triphosphatase			sis, protein C			•
Rv0233	nrdB	ribonucleoside-diphosphate	Rv3324c	moaC3	molybdenum cofactor biosynthe-	12. Heme		
By2051a	nrdE	reductase B2 (eukaryotic-like)	By2112	moaD	sis, protein C	Rv0509	hemA hemB	glutamyl-tRNA reductase
Rv3051c	muE	ribonucleoside diphosphate reductase α chain	Rv3112	moaD	molybdopterin converting factor subunit 1	Rv0512 Rv0510	hemB hemC	δ-aminolevulinic acid dehydratase porphobilinogen deaminase
Rv1981c	nrdF	ribonucleotide reductase small	Rv0868c	moaD2	molybdopterin converting factor	Rv2678c	hemE	uroporphyrinogen decarboxylase
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Rv1300	hemK	protoporphyrinogen oxidase	Rv0470	umaA2	unknown mycolic acid methyl-	Rv2931	ppsA	phenolpthiocerol synthesis (pksB)
Rv0524	hemL	glutamate-1-semialdehyde amino-			transferase	Rv2932	ppsB	phenolpthiocerol synthesis (pksC)
D. 0000		transferase		,		Rv2933	ppsC	phenolpthiocerol synthesis (pksD)
Rv2388c	hemN	oxygen-independent copropor-			mycoloyltransferases and	Rv2934	ppsD	phenolphicoerol synthesis (pksE)
Rv2677c	hemY'	phyrinogen III oxidase protoporphyrinogen oxidase	Rv2289	olipid synthe cdh	CDP-diacylglycerol phosphatidyl-	Rv2935 Rv2928	ppsE tesA	phenolpthiocerol synthesis (<i>pksF</i>) thioesterase
Rv1485	hemZ	ferrochelatase	1102203	curi	hydrolase	Rv1544	-	probable ketoacyl reductase
			Rv2881	c cdsA	phosphatidate cytidylyltransferase			p
13. Cobala	amin		Rv3804		antigen 85A, mycolyltransferase	J. Broad r	egulatory	functions
Rv2849c	cobA	cob(I)alamin adenosyltransferase	Rv1886		antigen 85B, mycolyltransferase	 Repress 		
Rv2848c	cobB	cobyrinic acid a,c-diamide	Rv3803		antigen 85C, mycolyltransferase	Rv1657	argR	arginine repressor
D.:0001 a		synthase	Rv0129		antigen 85C', mycolytransferase	Rv1267c	embR	regulator of <i>embAB</i> genes
Rv2231c Rv2236c	cobC cobD	aminotransferase cobinamide synthase	Rv0564	gpdA1	glycerol-3-phosphate dehydroge- nase	Rv1909c	furA	(AfsR/DndI/RedD family) ferric uptake regulatory protein
Rv2064	cobG	percorrin reductase	Rv2982	gpdA2	glycerol-3-phosphate dehydroge-	Rv2359	furB	ferric uptake regulatory protein
Rv2065	cobH	precorrin isomerase		. Jr	nase	Rv2919c	glnB	nitrogen regulatory protein
Rv2066	cobl	Cobl-CobJ fusion protein	Rv2612	pgsA	CDP-diacylglycerol-glycerol-3-	Rv2711	ideR	iron dependent repressor, IdeR
Rv2070c	cobK	precorrin reductase			phosphate phosphatidyltrans-	Rv2720	<i>lexA</i>	LexA, SOS repressor protein
Rv2072c	cobL	probable methyltransferase	D 4000		ferase	Rv1479	moxR	transcriptional regulator, MoxR
Rv2071c Rv2062c	cobM cobN	precorrin-3 methylase cobalt insertion	Rv1822	pgsA2	CDP-diacylglycerol-glycerol-3- phosphate phosphatidyltrans-	Rv3692	moxR2	homologue transcriptional regulator, MoxR
Rv2208	cobS	cobalamin (5'-phosphate)			ferase	HV3032	IIIUXI1Z	homologue
		synthase	Rv2746	pgsA3	CDP-diacylglycerol-glycerol-3-	Rv3164c	moxR3	transcriptional regulator, MoxR
Rv2207	cobT	nicotinate-nucleotide-dimethyl-		, 0	phosphate phosphatidyltrans-			homologue
_		benzimidazole transferase			ferase	Rv0212c	nadR	similar to <i>E.coli</i> NadR
Rv0254c	cobU	cobinamide kinase	Rv1551	plsB1	glycerol-3-phosphate acyltrans-	Rv0117	oxyS	transcriptional regulator (LysR
Rv0255c	cobQ cobQ2	cobyric acid synthase	Rv24820	plsB2	ferase glycerol-3-phosphate acyltrans-	Rv1379	nurD.	family)
Rv3713 Rv0306	-	possible cobyric acid synthase similar to BluB cobalamin synthe-	NV24020	; pisbz	ferase	NV13/9	pyrR	regulatory protein pyrimidine biosynthesis
1110000		sis protein <i>R. capsulatus</i>	Rv0437	psd	putative phosphatidylserine	Rv2788	sirR	iron-dependent transcriptional
					decarboxylase			repressor
14. Iron ut			Rv0436	pssA	CDP-diacylglycerol-serine	Rv3082c	virS	putative virulence regulating
Rv1876	bfrA	bacterioferritin	D. 0045		o-phosphatidyltransferase	D 0010		protein (AraC/XyIS family)
Rv3841	bfrB	bacterioferritin	Rv0045	-	possible dihydrolipoamide acetyl-	Rv3219	whiB1	WhiB transcriptional activator
Rv3215 Rv3214	entC entD	probable isochorismate synthase weak similarity to many phospho-	Rv0914	-	transferase lipid transfer protein	Rv3260c	whiB2	homologue WhiB transcriptional activator
1100214	GIILD	glycerate mutases	Rv1543		probable fatty-acyl CoA reductase	11002000	WIIIDZ	homologue
Rv2895c	viuB	similar to proteins involved in	Rv1627		lipid carrier protein	Rv3416	whiB3	WhiB transcriptional activator
		vibriobactin uptake	Rv1814	-	possible C-5 sterol desaturase			homologue
Rv3525c	-	similar to ferripyochelin binding	Rv1867	-	similar to acetyl CoA	Rv3681c	whiB4	WhiB transcriptional activator
		protein	D. 0004		synthase/lipid carriers	D. 0000		homologue
H. Lipid bi	iocunthocia		Rv2261	-	apolipoprotein N-acyltrans- ferase-a	Rv0023 Rv0043c	-	putative transcriptional regulator transcriptional regulator (GntR
		and mycolic acids	Rv22620		apolipoprotein N-acyltrans-	11000400	_	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
Rv3799c	accD4	β subunit			fatty acid synthases	Rv0081	_	(TetR/AcrR family) transcriptional regulator (ArsR
HV37990	accD4	acetyl/propionyl CoA carboxylase β subunit	I Polyke	tide and no	n-ribosomal peptide synthesis	1,00001	-	family)
Rv3280	accD5	acetyl/propionyl CoA carboxylase	Rv2940		mycocerosic acid synthase	Rv0135c	-	putative transcriptional regulator
		β subunit	Rv2384	mbtA	mycobactin/exochelin synthesis	Rv0144	-	putative transcriptional regulator
Rv2247	accD6	acetyl/propionyl CoA carboxylase			(salicylate-AMP ligase)	Rv0158	-	transcriptional regulator
D.:0044	11	β subunit	Rv2383	c mbtB	mycobactin/exochelin synthesis	D::0105+		(TetR/AcrR family)
Rv2244	acpM	acyl carrier protein (meromycolate extension)	Rv2382	mbtC	(serine/threonine ligation) mycobactin/exochelin synthesis	Rv0165c	-	transcriptional regulator (GntR family)
Rv2523c	acpS	CoA:apo-[ACP] pantethienephos-	Rv2381		mycobactin/exochelin synthesis	Rv0195	_	transcriptional regulator
	шоро	photransferase		, ,,,,,,,,	(polyketide synthase)			(LuxR/UhpA family)
Rv2243	fabD	malonyl CoA-[ACP] transacylase	Rv2380	mbtE	mycobactin/exochelin synthesis	Rv0196	-	transcriptional regulator
Rv0649	fabD2	malonyl CoA-[ACP] transacylase			(lysine ligation)			(TetR/AcrR family)
Rv1483	fabG1	3-oxoacyl-[ACP] reductase (aka	Rv2379	mbtF	mycobactin/exochelin synthesis	Rv0232	-	transcriptional regulator
Rv1350	fabG2	MabA) 3-oxoacyl-[ACP] Reductase	Bv2378	mbtG	(lysine ligation) mycobactin/exochelin synthesis	Rv0238	_	(TetR/AcrR family) transcriptional regulator
Rv2002	fabG3	3-oxoacyl-[ACP] reductase	11020700	mota	(lysine hydroxylase)	1100200		(TetR/AcrR family)
Rv0242c	fabG4	3-oxoacyl-[ACP] reductase	Rv23770	mbtH	mycobactin/exochelin synthesis	Rv0273c	-	putative transcriptional regulator
Rv2766c	fabG5	3-oxoacyl-[ACP] reductase	Rv0101	nrp	unknown non-ribosomal peptide	Rv0302	-	transcriptional regulator
Rv0533c	fabH	β-ketoacyl-ACP synthase III	D 4450		synthase	5		(TetR/AcrR family)
Rv2524c	fas	fatty acid synthase	Rv11536 Rv38246		PKS o-methyltransferase PKS-associated protein, unknown	Rv0324 Rv0328	-	putative transcriptional regulator transcriptional regulator
Rv1484 Rv2245	inhA kasA	enoyl-[ACP] reductase β-ketoacyl-ACP synthase	NV30240	papA1	function	NVU320	-	(TetR/AcrR family)
	7101071	(meromycolate extension)	Rv3820	papA2	PKS-associated protein, unknown	Rv0348	-	putative transcriptional regulator
Rv2246	kasB	β-ketoacyl-ACP synthase			function	Rv0377	-	transcriptional regulator (LysR
		(meromycolate extension)	Rv1182	papA3	PKS-associated protein, unknown	_		family)
Rv1618	tesB1	thioesterase II	D. 4500	4.4	function	Rv0386	-	transcriptional regulator
Rv2605c Rv0033	tesB2	thioesterase II possible acyl carrier protein	Rv1528	papA4	PKS-associated protein, unknown function	Rv0452		(LuxR/UhpA family) putative transcriptional regulator
Rv1344	-	possible acyl carrier protein	Rv2939	papA5	PKS-associated protein, unknown	Rv0452	-	transcriptional regulator
Rv1722	-	possible biotin carboxylase		pp	function			(PbsX/Xre family)
Rv3221c	-	resembles biotin carboxyl carrier	Rv2946	pks1	polyketide synthase	Rv0472c	-	transcriptional regulator
Rv3472	-	possible acyl carrier protein	Rv1660	pks10	polyketide synthase (chalcone			(TetR/AcrR family)
O Madifia		tu and musclin asida	D. 4 CCE	mlend d	synthase-like)	Rv0474	-	transcriptional regulator
2. Modifica Rv3391	acrA1	ty and mycolic acids fatty acyl-CoA reductase	Rv1665	pks11	polyketide synthase (chalcone synthase-like)	Rv0485	_	(PbsX/Xre family) transcriptional regulator (ROK
Rv3392c	cmaA1	cyclopropane mycolic acid	Rv2048	pks12	polyketide synthase (erythronolide	1110-100		family)
		synthase 1		,	synthase-like)	Rv0494	-	transcriptional regulator (GntR
Rv0503c	cmaA2	cyclopropane mycolic acid syn-	Rv3800		polyketide synthase			family)
D 007	4	thase 2	Rv1342	pks14	polyketide synthase (chalcone	Rv0552	-	putative transcriptional regulator
Rv0824c	desA1	acyl-[ACP] desaturase	Du0047	nko1F	synthase-like)	Rv0576	-	putative transcriptional regulator
Rv1094 Rv3229c	desA2 desA3	acyl-[ACP] desaturase acyl-[ACP] desaturase	Rv29470 Rv1013	pks15 pks16	polyketide synthase polyketide synthase	Rv0586	-	transcriptional regulator (GntR family)
Rv0645c	mmaA1	methoxymycolic acid synthase 1	Rv1663	pks16 pks17	polyketide synthase	Rv0650	-	transcriptional regulator (ROK
Rv0644c	mmaA2	methoxymycolic acid synthase 2	Rv1372	pks18	polyketide synthase			family)
Rv0643c	mmaA3	methoxymycolic acid synthase 3	Rv3825	pks2	polyketide synthase	Rv0653c	-	putative transcriptional regulator
Rv0642c	mmaA4	methoxymycolic acid synthase 4	Rv1180	pks3	polyketide synthase	Rv0681	-	transcriptional regulator
Rv0447c	ufaA1	unknown fatty acid methyltrans-	Rv1181	pks4	polyketide synthase	By06010	_	(TetR/AcrR family) transcriptional regulator
Rv3538	ufaA2	ferase unknown fatty acid methyltrans-	Rv15276 Rv0405	pks5 pks6	polyketide synthase polyketide synthase	Rv0691c	-	(TetR/AcrR family)
	G.G. 12	ferase	Rv1661	pks7	polyketide synthase	Rv0737	-	putative transcriptional regulator
Rv0469	umaA1	unknown mycolic acid methyl-	Rv1662	pks8	polyketide synthase	Rv0744c	-	putative transcriptional regulator
		transferase	Rv1664	pks9	polyketide synthase	Rv0792c	-	transcriptional regulator (GntR

		family)	Rv3160c	_	putative transcriptional regulator			truncated
Rv0823c	-	transcriptional regulator	Rv3167c	-	putative transcriptional regulator	Rv0018c	ppp	putative phosphoprotein phos-
D 000=		(NifR3/Smm1 family)	Rv3173c	-	transcriptional regulator	D 0004		phatase
Rv0827c	-	transcriptional regulator (ArsR	Rv3183	_	(TetR/AcrR family)	Rv2234	ptpA	low molecular weight protein-tyro-
Rv0890c	_	family) transcriptional regulator	Rv3208	-	putative transcriptional regulator transcriptional regulator	Rv0153c	-	sine-phosphatase putative protein-tyrosine-phos-
11000000		(LuxR/UhpA family)	1110200		(TetR/AcrR family)	11001000		phatase
Rv0891c		putative transcriptional regulator	Rv3249c	-	transcriptional regulator			·
Rv0894	-	putative transcriptional regulator	D. 0004		(TetR/AcrR family)			metabolism
Rv1019	-	transcriptional regulator (TetR/AcrR family)	Rv3291c	-	transcriptional regulator (Lrp/AsnC family)			odification of macromolecules n synthesis and modification
Rv1049	-	transcriptional regulator (MarR	Rv3295	-	transcriptional regulator	Rv3420c	rimI	ribosomal protein S18 acetyl
		family)			(TetR/AcrR family)			transferase
Rv1129c	-	transcriptional regulator	Rv3334	-	transcriptional regulator (MerR	Rv0995	rimJ	acetylation of 30S S5 subunit
Rv1151c	_	(PbsX/Xre family)	Rv3405c	_	family) putative transcriptional regulator	Rv0641 Rv0704	rpIA rpIB	50S ribosomal protein L1 50S ribosomal protein L2
	-	putative transcriptional regulator transcriptional regulator (GntR	Rv3522	-	putative transcriptional regulator	Rv0704	грIБ rpIC	50S ribosomal protein L3
		family)	Rv3557c	-	transcriptional regulator	Rv0702	rpID	50S ribosomal protein L4
	-	putative transcriptional regulator			(TetR/AcrR family)	Rv0716	rpIE	50S ribosomal protein L5
	-	putative transcriptional regulator	Rv3574	-	transcriptional regulator	Rv0719	rpIF	50S ribosomal protein L6
NV12550	-	transcriptional regulator (TetR/AcrR family)	Rv3575c	_	(TetR/AcrR family) transcriptional regulator (Lacl	Rv0056 Rv0651	rpII rpIJ	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	rpIL	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
HV 1000	-	(LuxR/UhpA family)	Rv3678c	_	transcriptional regulator (LysR	Rv0714	rpIO	50S ribosomal protein L15
Rv1359	-	putative transcriptional regulator			family)	Rv0708	rpIP	50S ribosomal protein L16
Rv1395	-	transcriptional regulator	Rv3736	-	transcriptional regulator	Rv3456c	rpIQ	50S ribosomal protein L17
Rv1404	_	(AraC/XyIS family) transcriptional regulator (MarR	Rv3744	_	(AraC/XyIS family) transcriptional regulator (ArsR	Rv0720 Rv2904c	rpIR rpIS	50S ribosomal protein L18 50S ribosomal protein L19
NV1404	-	family)	11007-4-4		family)	Rv1643	rpIT	50S ribosomal protein L20
Rv1423	-	putative transcriptional regulator	Rv3830c	-	transcriptional regulator	Rv2442c	rpIU	50S ribosomal protein L21
Rv1460	-	putative transcriptional regulator	D0000		(TetR/AcrR family)	Rv0706	rpIV	50S ribosomal protein L22
Rv1474c	-	transcriptional regulator (TetR/AcrR family)	Rv3833	-	transcriptional regulator (AraC/XyIS family)	Rv0703 Rv0715	rpIW rpIX	50S ribosomal protein L23 50S ribosomal protein L24
Rv1534	-	transcriptional regulator	Rv3840	-	putative transcriptional regulator	Rv1015c	rpiX rplY	50S ribosomal protein L25
		(TetR/AcrR family)	Rv3855	-	putative transcriptional regulator	Rv2441c	rpmA	50S ribosomal protein L27
Rv1556	-	putative transcriptional regulator	0 T		tom.	Rv0105c	rpmB	50S ribosomal protein L28
Rv1674c Rv1675c	-	putative transcriptional regulator putative transcriptional regulator	2. Two cor Rv1028c	mponent s kdpD	sensor histidine kinase	Rv2058c Rv0709	rpmB2 rpmC	50S ribosomal protein L28 50S ribosomal protein L29
Rv1719	-	transcriptional regulator (IcIR	Rv1027c	kdpE	two-component response	Rv0722	rpmD	50S ribosomal protein L30
		family)			regulator	Rv1298	rpmE	50S ribosomal protein L31
Rv1773c	-	transcriptional regulator (IcIR	Rv3246c	mtrA	two-component response	Rv2057c	rpmG	50S ribosomal protein L33
Rv1776c	-	family) putative transcriptional regulator	Rv3245c	mtrB	regulator sensor histidine kinase	Rv3924c Rv1642	rpmH rpmI	50S ribosomal protein L34 50S ribosomal protein L35
Rv1816	-	putative transcriptional regulator	Rv0844c	narL	two-component response	Rv3461c	rpmJ	50S ribosomal protein L36
Rv1846c	-	putative transcriptional regulator			regulator	Rv1630	rpsA	30S ribosomal protein S1
Rv1931c	-	transcriptional regulator	Rv0757	phoP	two-component response	Rv2890c	rpsB	30S ribosomal protein S2
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
D: 4000-		family)	Rv0490	senX3	sensor histidine kinase	Rv0683	rpsG	30S ribosomal protein S7
Rv1990c Rv1994c	-	putative transcriptional regulator transcriptional regulator (MerR	Rv0602c	tcrA	two-component response regulator	Rv0718 Rv3442c	rpsH rpsI	30S ribosomal protein S8 30S ribosomal protein S9
11013340	_	family)	Rv0260c	_	two-component response	Rv0700	rpsJ	30S ribosomal protein S10
Rv2017	-	putative transcriptional regulator			regulator	Rv3459c	rpsK	30S ribosomal protein S11
D: 0004 -		(PbsX/Xre family)	Rv0600c	-	sensor histidine kinase	Rv0682	rpsL	30S ribosomal protein S12
Rv2021c Rv2034	-	putative transcriptional regulator transcriptional regulator (ArsR	Rv0601c Rv0818	-	sensor histidine kinase two-component response	Rv3460c Rv0717	rpsM rpsN	30S ribosomal protein S13 30S ribosomal protein S14
1102004		family)	1100010		regulator	Rv2056c	rpsN2	30S ribosomal protein S14
Rv2175c		putative transcriptional regulator	Rv0845	-	sensor histidine kinase	Rv2785c	rpsO	30S ribosomal protein S15
Rv2250c Rv2258c	-	putative transcriptional regulator	Rv0902c	-	sensor histidine kinase	Rv2909c	rpsP	30S ribosomal protein S16
Rv2282c		putative transcriptional regulator transcriptional regulator (LysR	Rv0903c	-	two-component response regulator	Rv0710 Rv0055	rpsQ rpsR	30S ribosomal protein S17 30S ribosomal protein S18
		family)	Rv0981	-	two-component response	Rv2055c	rpsR2	30S ribosomal protein S18
Rv2308	-	putative transcriptional regulator			regulator	Rv0705	rpsS	30S ribosomal protein S19
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
Rv2358	-	transcriptional regulator (ArsR	Rv1032c	-	two-component response	11402410		protein family
		family)			regulator			
Rv2488c	-	transcriptional regulator	Rv1626	-	two-component response			cation and maturation
Rv2506	-	(LuxR/UhpA family) transcriptional regulator	Rv2027c	_	regulator sensor histidine kinase	Rv1010 Rv2838c	ksgA rbfA	16S rRNA dimethyltransferase ribosome-binding factor A
		(TetR/AcrR family)	Rv2884	-	two-component response	Rv2907c	rimM	16S rRNA processing protein
Rv2621c		putative transcriptional regulator			regulator			
Rv2640c	-	transcriptional regulator (ArsR	Rv3132c	-	sensor histidine kinase two-component response		cyl tRNA:	synthases and their modification
Rv2642	_	family) transcriptional regulator (ArsR	Rv3133c	-	regulator	Rv2555c Rv1292	argS	alanyl-tRNA synthase arginyl-tRNA synthase
		family)	Rv3143	-	putative sensory transduction	Rv2572c	aspS	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)	Rv3764c Rv3765c	-	sensor histidine kinase two-component response	Rv1406 Rv3011c	fmt gatA	methionyl-tRNA formyltransferase glu-tRNA-gln amidotransferase,
Rv2887	-	transcriptional regulator (MarR			regulator		3	subunit B
		family)			-	Rv3009c	gatB	glu-tRNA-gln amidotransferase,
Rv2912c	-	transcriptional regulator			protein kinases and phosphoprotein	D-0010	ac+0	subunit A
Rv2989	_	(TetR/AcrR family) transcriptional regulator (IcIR	phosphata Rv0015c		serine-threonine protein kinase	Rv3012c	gatC	glu-tRNA-gln amidotransferase, subunit C
		family)	Rv0013c	pknA pknB	serine-threonine protein kinase	Rv2992c	gltS	glutamyl-tRNA synthase
	-	putative transcriptional regulator	Rv0931c	pknD	serine-threonine protein kinase	Rv2357c	glyS	glycyl-tRNA synthase
Rv3055	-	putative transcriptional regulator	Rv1743	pknE	serine-threonine protein kinase	Rv2580c	hisS	histidyl-tRNA synthase
Rv3058c Rv3060c	-	putative transcriptional regulator transcriptional regulator (GntR	Rv1746 Rv0410c	pknF pknG	serine-threonine protein kinase serine-threonine protein kinase	Rv1536 Rv0041	ileS leuS	isoleucyl-tRNA synthase leucyl-tRNA synthase
11400000		family)	Rv1266c	pknH pknH	serine-threonine protein kinase	Rv3598c	lysS	lysyl-tRNA synthase
Rv3066	-	putative transcriptional regulator	Rv2914c	pknl	serine-threonine protein kinase	Rv1640c	ĺysX	C-term lysyl-tRNA synthase
Rv3095	-	putative transcriptional regulator	Rv2088	pknJ pknK	serine-threonine protein kinase	Rv1007c	metS pheS	methionyl-tRNA synthase
Rv3124	-	transcriptional regulator (AfsR/Dndl/RedD family)	Rv3080c Rv2176	pknK pknL	serine-threonine protein kinase serine-threonine protein kinase,	Rv1649	μιισο	phenylalanyl-tRNA synthase α subunit
		, , , , , , , , , , , , , , , , , , , ,		,				

Rv1650	pheT	phenylalanyl-tRNA synthase β	Rv2090	-	partially similar to DNA poly-	2. DNA	,	
Rv2845c	proS	subunit prolyl-tRNA synthase	Rv2191		merase I similar to both PolC and UvrC	Rv0670 Rv1108c	end xseA	endonuclease IV (apurinase) exonuclease VII large subunit
Rv3834c	serS	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-	Rv3201c		endonuclease VIII probable ATP-dependent DNA	3. Proteins Rv3305c	s, peptides <i>amiA</i>	and glycopeptides probable aminohydrolase
Rv3336c	trpS	ferase tryptophanyl tRNA synthase	HV32010	-	helicase	Rv3306c	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 Rv3644c	-	probable DNA methylase similar in N-term to DNA poly-	Rv2461c	clpP	ATP-dependent Clp protease pro- teolytic subunit
4. Nucleon	oroteins		NV30440	-	merase III	Rv2460c	clpP2	ATP-dependent Clp protease pro-
Rv1407	fmu	similar to Fmu protein			meraee m	1112-1000	OIPI Z	teolytic subunit
Rv3852	hns	HU-histone protein			and modification	Rv2457c	clpX	ATP-dependent Clp protease
Rv2986c	hupB	DNA-binding protein II	Rv0429c Rv2534c	def efp	polypeptide deformylase elongation factor P	Rv2667	clpX'	ATP-binding subunit ClpX similar to ClpC from <i>M. leprae</i> but
Rv1388	mIHF	integration host factor	Rv2882c	frr	ribosome recycling factor	NV2007	CIPA	shorter
5. DNA re	plication, i	repair, recombination and restric-	Rv0684	fusA	elongation factor G	Rv3419c	gcp	glycoprotease
tion/modif		•	Rv0120c	fusA2	elongation factor G	Rv2725c	hflX	GTP-binding protein
Rv1317c	alkA	DNA-3-methyladenine glycosi-	Rv1080c Rv3462c	greA infA	transcription elongation factor G initiation factor IF-1	Rv1223 Rv2861c	htrA map	serine protease methionine aminopeptidase
Rv2836c	dinF	dase II DNA-damage-inducible protein F	Rv2839c	infB	initiation factor IF-2	Rv0734	тар'	probable methionine aminopepti-
Rv1329c	dinG	probable ATP-dependent helicase	Rv1641	infC	initiation factor IF-3		- 1	dase
Rv3056	dinP	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 Rv1299	ppiB prfA	peptidyl-prolyl <i>cis-trans</i> isomerase peptide chain release factor 1	Rv0125 Rv2213	pepA pepB	probable serine protease aminopeptidase A/I
Rv0001	dnaA	protein chromosomal replication initiator	Rv3105c	prfB	peptide chain release factor 2	Rv0800	pepC	aminopeptidase I
		protein	Rv2889c	tsf	elongation factor EF-Ts	Rv2467	pepD	probable aminopeptidase
Rv0058	dnaB	DNA helicase (contains intein)	Rv0685	tuf	elongation factor EF-Tu	Rv2089c	pepE	cytoplasmic peptidase
Rv1547 Rv3370c	dnaE1 dnaE2	DNA polymerase III, α subunit DNA polymerase III α chain	7 RNA ev	nthacic RI	NA modification and DNA	Rv2535c Rv2782c	pepQ pepR	cytoplasmic peptidase protease/peptidase, M16 family
Rv2343c	dnaG	DNA primase in a chain	transcription		TO THOUSE CALCULATION AND DIVI	11020	роргі	(insulinase)
Rv0002	dnaN	DNA polymerase III, β subunit	Rv1253	deaD	ATP-dependent DNA/RNA	Rv2109c	prcA	proteasome α-type subunit 1
Rv3711c	dnaQ	DNA polymerase III ϵ chain	D 0700		helicase	Rv2110c	prcB	proteasome β-type subunit 2
Rv3721c	dnaZX	DNA polymerase III, γ (dnaZ) and	Rv2783c	gpsl	pppGpp synthase and polyribo- nucleotide phosphorylase	Rv0782 Rv0781	ptrBa ptrBb	protease II, α subunit protease II, β subunit
Rv2924c	fpg	τ (dnaX) formamidopyrimidine-DNA glyco-	Rv2841c	nusA	transcription termination factor	Rv0724	sppA	protease IV, signal peptide pepti-
	.49	sylase	Rv2533c	nusB	N-utilization substance protein B			dase
Rv0006	gyrA	DNA gyrase subunit A	Rv0639	nusG	transcription antitermination	Rv0198c	-	probable zinc metalloprotease
Rv0005	gyrB	DNA gyrase subunit B	Rv3907c	pcnA	protein polymerase	Rv0457c Rv0840c	-	probable peptidase probable proline iminopeptidase
Rv2092c Rv2101	helY helZ	probable helicase, Ski2 subfamily probable helicase, Snf2/Rad54	Rv3232c	pvdS	alternative sigma factor for	Rv0983	-	probable serine protease
1102101	11012	family		,	siderophore production	Rv1977	-	probable zinc metallopeptidase
Rv2756c	hsdM	type I restriction/modification sys-	Rv3211	rhIE	probable ATP-dependent	11000000	-	probable alkaline serine protease
Rv2755c	hsdS'	tem DNA methylase	Rv1297	rho	RNA helicase transcription termination	Rv3671c Rv3883c	-	probable serine protease probable secreted protease
HV2/550	risas	type I restriction/modification sys- tem specificity determinant	HV1231	IIIO	factor rho	Rv3886c	-	protease
Rv3296	lhr	ATP-dependent helicase	Rv3457c	rpoA	α subunit of RNA polymerase			p
Rv3014c	ligA	DNA ligase	Rv0667	rpoB	β subunit of RNA polymerase		charides, l	lipopolysaccharides 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	cwlM	hydrolase
Rv2528c	mrr	restriction system protein	Rv2703	sigA	RNA polymerase sigma factor	Rv0315	-	probable β-1,3-glucanase
Rv2985	mutT1	MutT homologue	D 0710		(aka MysA, RpoV)	Rv1090	-	probable inactivated
Rv1160	mutT2	MutT homologue	Rv2710	sigB	RNA polymerase sigma factor (aka MysB)	Rv1327c	_	cellulase/endoglucanase probable glycosyl hydrolase, α-
Rv0413 Rv3589	mutT3 mutY	MutT homologue probable DNA glycosylase	Rv2069	sigC	ECF subfamily sigma subunit	11010270	_	amylase family
Rv3297	nei	probable endonuclease VIII	Rv3414c	sigD	ECF subfamily sigma subunit	Rv1333	-	probable hydrolase
Rv3674c	nth	probable endonuclease III	Rv1221	sigE	ECF subfamily sigma subunit	Rv3463	-	probable neuraminidase
Rv1316c	ogt	methylated-DNA-protein-cysteine	Rv3286c Rv0182c	sigF sigG	ECF subfamily sigma subunit sigma-70 factors ECF subfamily	Rv3717	-	possible N-acetylmuramoyl-L-ala- nine amidase
Rv1629	polA	methyltransferase DNA polymerase I	Rv3223c	sigH	ECF subfamily sigma subunit			Time arridase
Rv1402	priA	putative primosomal protein n'	Rv1189	sigl	ECF family sigma factor	Esteras		ases
		(replication factor Y)	Rv3328c	sigJ	similar to Sigl, ECF family	Rv0220	lipC	probable esterase
Rv3585	radA	probable DNA repair RadA homo-	Rv0445c Rv0735	sigK sigL	ECF-type sigma factor sigma-70 factors ECF subfamily	Rv1923 Rv3775	lipD lipE	probable esterase probable hydrolase
Rv2737c	recA	logue recombinase (contains intein)	Rv3911	sigM	probable sigma factor, similar to	Rv3487c	lipF	probable esterase
Rv0630c	recB	exodeoxyribonuclease V			SigE	Rv0646c	lipG	probable hydrolase
Rv0631c		exodeoxyribonuclease V	Rv3366	spoU truA	probable rRNA methylase	Rv1399c	lipH	probable lipase
Rv0629c Rv0003	recD recF	exodeoxyribonuclease V	Rv3455c	IruA	probable pseudouridylate syn- thase	Rv1400c Rv1900c	lipl lipJ	probable lipase probable esterase
1140000	1001	DNA replication and SOS induction	Rv2793c	truB	tRNA pseudouridine 55 synthase	Rv2385	lipK	probable acetyl-hydrolase
Rv2973c	recG	ATP-dependent DNA helicase	Rv1644	tsnR	putative 23S rRNA methyltrans-	Rv1497	lipL	esterase
Rv1696	recN	recombination and DNA repair	Dv2640	_	ferase	Rv2284	lipM	probable esterase
Rv3715c	recR	RecBC-Independent process of DNA repair	Rv3649	-	ATP-dependent DNA/RNA heli- case	Rv2970c Rv1426c	lipN lipO	probable lipase/esterase probable esterase
Rv2736c	recX	regulatory protein for RecA			5455	Rv2463	lipP	probable esterase
Rv2593c	ruvA	Holliday junction binding protein,			cytoplasmic)	Rv2485c	lipQ	probable carboxlyesterase
D 0=00	-	DNA helicase	Rv1326c	glgB	1,4-α-glucan branching enzyme probable glycogen phosphory-	Rv3084	lipR	probable acetyl-hydrolase
Rv2592c Rv2594c	ruvB ruvC	Holliday junction binding protein Holliday junction resolvase, endo-	Rv1328	glgP	lase	Rv3176c Rv2045c	lipS lipT	probable esterase/lipase probable carboxylesterase
HV23340	TUVC	deoxyribonuclease	Rv1564c	glgX	probable glycogen debranching	Rv1076	lipU	probable esterase
Rv0054	ssb	single strand binding protein			enzyme	Rv3203	lipV	probable lipase
Rv1210	tagA	DNA-3-methyladenine glycosi-	Rv1563c	glgY ala7	putative α-amylase	Rv0217c	lipW	probable esterase
Rv3646c	topA	dase I DNA topoisomerase	Rv1562c	glgZ	maltooligosyltrehalose trehalohy- drolase	Rv2351c Rv2350c	plcA plcB	phospholipase C precursor phospholipase C precursor
Rv2976c	ung	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	R Deared	ation of m	acromolecules	Rv1105	-	probable esterase pseudogene
HV0949	uviD	helicase II	1. RNA	anon or me		6. Aromati	c hydrocai	rbons
Rv3198c	uvrD2	putative UvrD	Rv1014c	pth	peptidyl-tRNA hydrolase	Rv3469c		probable 4-hydroxy-2-oxovalerate
Rv0427c	xthA	exodeoxyribonuclease III	Rv2925c	rnc	RNAse III	D ₁ 0040		aldolase
Rv0071 Rv0861c	-	group II intron maturase probable DNA helicase	Rv2444c	rne	similar at C-term to ribo- nuclease E	Rv0316	-	probable muconolactone iso- merase
Rv0944	-	possible formamidopyrimidine-	Rv2902c	rnhB	ribonuclease HII	Rv0771	-	probable 4-carboxymuconolac-
		DNA glycosylase	Rv3923c	rnpA	ribonuclease P protein compo-			tone decarboxylase
Rv1688	-	probable 3-methylpurine DNA	Rv1340	rphA	nent ribonuclease PH	Rv0939 Rv1723	-	probable dehydrase 6-aminohexanoate-dimer hydro-
		glycosylase	1141040	IPIIA		1141120		aminonoxanoate-uniter flyuro-

D 0745		lase	Rv1367c	-	probable penicillin binding protein	Rv1030	kdpB	potassium-transporting ATPase B
Rv2715	-	2-hydroxymuconic semialdehyde		-	probable penicillin binding protein	D: 4004		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	D: 0077		potassium-efflux protein
		tion	4 Consen	red memb	rane proteins	Rv2877c	merT	possible mercury resistance transport system
C. Cell en	velope		Rv0402c	mmpL1	conserved large membrane	Rv1811	mgtC	probable magnesium transport
 Lipoprof 		A-lpr0) 65		·	protein			ATPase protein C
O Curtono	nalvaaad	narides, lipopolysaccharides, pro-	Rv0507	mmpL2	conserved large membrane protein	Rv0362	mgtE	putative magnesium ion transporter
teins and		larides, lipopolysaccilarides, pro-	Rv0206c	mmpL3	conserved large membrane	Rv2856	nicT	probable nickel transport protein
Rv0806c		probable UDP-glucose-4-			protein	Rv0924c	nramp	transmembrane protein belonging
Dv2011	200	epimerase secreted protein	Rv0450c	mmpL4	conserved large membrane	Rv2691	trkA	to Nramp family
Rv3811 Rv1677	csp dsbF	highly similar to C-term Mpt53	Rv0676c	mmpL5	protein conserved large membrane	HV2091	IIKA	probable potassium uptake pro- tein
Rv3794	embA	involved in arabinogalactan syn-			protein	Rv2692	trkB	probable potassium uptake pro-
D 0705		thesis	Rv1557	mmpL6	conserved large membrane	D 000=		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-	1102072	mmpLi	protein	111/2/20		tellurium resistance
D 00==		thesis	Rv3823c	mmpL8	conserved large membrane	Rv3162c	-	probable membrane protein
Rv3875 Rv0112	esat6 gca	early secretory antigen target probable GDP-mannose dehy-	Rv2339	mmpL9	protein conserved large membrane	Rv3237c	-	possible potassium channel protein
1100112	gca	dratase	1102000	mmpL3	protein	Rv3743c		probable cation-transporting
Rv0113	gmhA	phosphoheptose isomerase	Rv1183	mmpL10	conserved large membrane			ATPase
Rv2965c	kdtB	lipopolysaccharide core biosyn- thesis protein	Rv0202c	mmnl 11	protein	2 Carbabi	dratas a	rannia asida and alashala
Rv2878c	mpt53	secreted protein Mpt53	NV02020	mmpLTT	conserved large membrane protein	8. Carbony	dctA	rganic acids and alcohols C4-dicarboxylate transport protein
Rv1980c	mpt64	secreted immunogenic protein	Rv1522c	mmpL12	conserved large membrane	Rv3476c	kgtP	sugar transport protein
D. 0075		Mpb64/Mpt64	D: 0400-		protein	Rv1902c	nanT	probable sialic acid transporter
Rv2875	mpt70	major secreted immunogenic pro- tein Mpt70 precursor	Rv0403c	mmpS1	conserved small membrane protein	Rv1236	sugA	membrane protein probably involved in sugar transport
Rv2873	mpt83	surface lipoprotein Mpt83	Rv0506	mmpS2	conserved small membrane	Rv1237	sugB	sugar transport protein
Rv0899	ompA	member of OmpA family			protein	Rv1238	sugC	ABC transporter component of
Rv3810	pirG	cell surface protein precursor (Erp protein)	Rv2198c	mmpS3	conserved small membrane protein	Rv3331	oual	sugar uptake system
Rv3782	rfbE	similar to rhamnosyl transferase	Rv0451c	mmpS4	conserved small membrane	Rv2835c	sugl ugpA	probable sugar transport protein sn-glycerol-3-phosphate
Rv1302	rfe	undecaprenyl-phosphate α-N-			protein			permease
5 0445		acetylglucosaminyltransferase	Rv0677c	mmpS5	conserved small membrane	Rv2833c	ugpB	sn-glycerol-3-phosphate-binding
Rv2145c Rv0431	wag31 -	antigen 84 (aka wag31) tuberculin related peptide (AT103)			protein	Rv2832c	ugpC	periplasmic lipoprotein sn-glycerol-3-phosphate transport
Rv0954	-	cell envelope antigen	5. Other m	nembrane i	proteins 211	11120020	ugpo	ATP-binding protein
Rv1514c	-	involved in polysaccharide syn-				Rv2834c	ugpE	sn-glycerol-3-phosphate transport
Rv1518	_	thesis involved in exopolysaccharide	III. Cell pr A. Transpo		protoine	Rv2316	uspA	system protein sugar transport protein
HVISIO	-	synthesis	1. Amino a		proteiris	Rv2318	uspA uspC	sugar transport protein
Rv1758	-	partial cutinase	Rv2127	ansP	L-asparagine permease	Rv2317	uspE	sugar transport protein
Rv1910c		probable secreted protein	Rv0346c	aroP2	probable aromatic amino acid	Rv1200	-	probable sugar transporter
Rv1919c Rv1984c	-	weak similarity to pollen antigens probable secreted protein	Rv0917	betP	permease glycine betaine transport	Rv2038c Rv2039c	-	probable ABC sugar transporter probable sugar transporter
Rv1987	-	probable secreted protein	Rv1704c	cycA	transport of D-alanine, D-serine	Rv2040c	-	probable sugar transporter
Rv2223c	-	probable exported protease			and glycine	Rv2041c	-	probable sugar transporter
Rv2224c Rv2301	-	probable exported protease probable cutinase	Rv3666c	dppA	probable peptide transport system permease	4. Anions		
Rv2345	-	precursor of probable membrane	Rv3665c	dppB	probable peptide transport system	Rv2684	arsA	probable arsenical pump
		protein			permease	Rv2685	arsB	probable arsenical pump
Rv2672 Rv3019c	-	putative exported protease similar to Esat6	Rv3664c	dppC	probable peptide transport system	Rv3578 Rv2643	arsB2	probable arsenical pump
HV30190					permease		arsC	probable arsenical pump sulphate transport ATP-binding
Bv3036c	-		Bv3663c	dnnD				protein
Rv3036c Rv3449	-	probable secreted protein probable precursor of serine pro-	Rv3663c Rv0522	dppD gabP	probable ABC-transporter probable 4-amino butyrate trans-	Rv2397c	cysA	protein
Rv3449	Ι.,	probable secreted protein probable precursor of serine pro- tease	Rv0522	gabP	probable 4-amino butyrate trans- porter			sulphate transport system perme-
Rv3449 Rv3451	:	probable secreted protein probable precursor of serine pro- tease probable cutinase	Rv0522 Rv0411c	gabP glnH	probable 4-amino butyrate trans- porter putative glutamine binding protein	Rv2397c Rv2399c	cysA cysT	sulphate transport system perme- ase protein
Rv3449 Rv3451 Rv3452	Ι.,	probable secreted protein probable precursor of serine pro- tease probable cutinase probable cutinase precursor	Rv0522	gabP	probable 4-amino butyrate trans- porter	Rv2397c	cysA	sulphate transport system perme-
Rv3449 Rv3451 Rv3452 Rv3724		probable secreted protein probable precursor of serine pro- tease probable cutinase probable cutinase precursor probable cutinase precursor	Rv0522 Rv0411c	gabP glnH	probable 4-amino butyrate trans- porter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport	Rv2397c Rv2399c Rv2398c Rv1857	cysA cysT cysW modA	sulphate transport system perme- ase protein sulphate transport system perme- ase protein molybdate binding protein
Rv3449 Rv3451 Rv3452 Rv3724 3. Murein	- - - - sacculus a	probable secreted protein probable precursor of serine pro- tease probable cutinase probable cutinase precursor probable cutinase precursor and peptidoglycan	Rv0522 Rv0411c Rv2564 Rv1280c	gabP gInH gInQ oppA	probable 4-amino butyrate trans- porter putative glutamine binding protein probable ATP-binding transport probable oligopeptide transport probable oligopeptide transport protein	Rv2397c Rv2399c Rv2398c	cysA cysT cysW	sulphate transport system perme- ase protein sulphate transport system perme- ase protein molybdate binding protein transport system permease,
Rv3449 Rv3451 Rv3452 Rv3724 3. Murein : Rv2911	- - - - sacculus a	probable secreted protein probable precursor of serine pro- tease probable cutinase probable cutinase precursor probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein	Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c	gabP gInH gInQ oppA oppB	probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport protein	Rv2397c Rv2399c Rv2398c Rv1857 Rv1858	cysA cysT cysW modA modB	sulphate transport system perme- ase protein sulphate transport system perme- ase protein molybdate binding protein transport system permease, molybdate uptake
Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv2981c Rv3809c	- - - - sacculus a dacB ddlA glf	probable secreted protein probable precursor of serine protease probable cutinase precursor probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-galactopyranose mutase	Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c	gabP glnH glnQ oppA oppB oppC	probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport protein oligopeptide transport system per- mease	Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1859	cysA cysT cysW modA modB	sulphate transport system perme- ase protein sulphate transport system perme- ase protein molybdate binding protein transport system permease, molybdate uptake molybdate uptake ABC- transporter
Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv2981c	- - - - - sacculus a dacB ddlA	probable secreted protein probable precursor of serine pro- tease probable cutinase probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-galactopyranose mutase UDP-N-acetylglucosamine	Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1281c	gabP glnH glnQ oppA oppB oppC	probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport protein oligopeptide transport system permease probable peptide transport protein	Rv2397c Rv2399c Rv2398c Rv1857 Rv1858	cysA cysT cysW modA modB	sulphate transport system perme- ase protein sulphate transport system perme- ase protein molybdate binding protein transport system permease, molybdate uptake molybdate uptake ABC- transporter precursor of Apa (45/47
Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv2981c Rv3809c Rv1018c	sacculus a dacB ddlA glf glmU	probable secreted protein probable precursor of serine protease probable cutinase precursor probable cutinase precursor probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-galactopyranose mutase UDP-N-acetylglucosamine pyrophosphorylase	Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1281c Rv2320c	gabP glnH glnQ oppA oppB oppC	probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport protein oligopeptide transport system permease probable peptide transport protein arginine/ornithine transporter	Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1859 Rv1860	cysA cysT cysW modA modB modC	sulphate transport system perme- ase protein sulphate transport system perme- ase protein molybdate binding protein transport system permease, molybdate uptake molybdate uptake ABC- transporter precursor of Apa (45/47 kD secreted protein)
Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv2981c Rv3809c	- - - - sacculus a dacB ddlA glf	probable secreted protein probable precursor of serine pro- tease probable cutinase probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-galactopyranose mutase UDP-N-acetylglucosamine pyrophosphorylase LytB protein homologue very similar to LytB	Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1281c	gabP glnH glnQ oppA oppB oppC	probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport protein oligopeptide transport system permease probable peptide transport protein	Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1859	cysA cysT cysW modA modB	sulphate transport system perme- ase protein sulphate transport system perme- ase protein molybdate binding protein transport system permease, molybdate uptake molybdate uptake ABC- transporter precursor of Apa (45/47
Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv2981c Rv3809c Rv1018c Rv3382c	- - - - sacculus a dacB ddIA glf glmU lytB	probable secreted protein probable precursor of serine protease probable cutinase precursor probable cutinase precursor probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-galactopyranose mutase UDP-N-acetylglucosamine pyrophosphorylase LytB protein homologue very similar to LytB UDP-N-acetylglucosamine-1-car-	Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1281c Rv2320c	gabP glnH glnQ oppA oppB oppC	probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport protein oligopeptide transport system per- mease probable peptide transport protein arginine/ornithine transporter probable cationic amino acid	Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1859 Rv1860 Rv2329c Rv2329c Rv0261c	cysA cysT cysW modA modB modC modD narK1 narK2 narK3	sulphate transport system perme- ase protein sulphate transport system perme- ase protein molybdate binding protein transport system permease, molybdate uptake molybdate uptake ABC- transporter precursor of Apa (45/47 kD secreted protein) probable nitrite extrusion protein nitrite extrusion protein in itrite extrusion protein
Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv3809c Rv1018c Rv3382c Rv1110 Rv1315	sacculus a dacB dalA glf glmU lytB lytB' murA	probable secreted protein probable precursor of serine protease probable cutinase precursor penicillin binding protein D-alanine-D-alanine ligase A UDP-qalactopyranose mutase UDP-N-acetylglucosamine pyrophosphorylase LytB protein homologue very similar to LytB UDP-N-acetylglucosamine-1-carboxyvinyltransferase	Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1282c Rv12820c Rv3253c Rv3454	gabP glnH glnQ oppA oppB oppC oppD rocE -	probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport protein oligopeptide transport system permease probable peptide transport protein arginine/ornithine transporter probable cationic amino acid transport	Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1859 Rv1860 Rv2329c Rv1737c	cysA cysT cysW modA modB modC modD	sulphate transport system perme- ase protein sulphate transport system perme- ase protein molybdate binding protein transport system permease, molybdate uptake molybdate uptake molybdate uptake ABC- transporter precursor of Apa (45/47 kD secreted protein) probable nitrite extrusion protein nitrite extrusion protein similar to nitrite extrusion
Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv2981c Rv38809c Rv1018c Rv3882c Rv1110	- - - - sacculus a dacB ddlA glf glmU lytB lytB'	probable secreted protein probable precursor of serine protease probable cutinase precursor probable cutinase precursor probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-galactopyranose mutase UDP-N-acetylglucosamine pyrophosphorylase LytB protein homologue very similar to LytB UDP-N-acetylglucosamine-1-car-	Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1281c Rv2320c Rv3253c	gabP glnH glnQ oppA oppB oppC oppD rocE -	probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport protein oligopeptide transport system permease probable peptide transport protein arginine/ornithine transporter probable cationic amino acid transport	Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1859 Rv1860 Rv2329c Rv2329c Rv0261c	cysA cysT cysW modA modB modC modD narK1 narK2 narK3	sulphate transport system perme- ase protein sulphate transport system perme- ase protein molybdate binding protein transport system permease, molybdate uptake molybdate uptake ABC- transporter precursor of Apa (45/47 kD secreted protein) probable nitrite extrusion protein nitrite extrusion protein in itrite extrusion protein
Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv3809c Rv1018c Rv3382c Rv1110 Rv1315	sacculus a dacB dalA glf glmU lytB lytB' murA	probable secreted protein probable precursor of serine protease probable cutinase precursor penicillin binding protein pr	Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1282c Rv3253c Rv3454 2. Cations Rv2920c Rv1607	gabP glnH glnQ oppA oppB oppC oppD rocE amt chaA	probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport protein oligopeptide transport system per- mease probable peptide transport protein arginine/ornithine transporter probable cationic amino acid transport possible proline permease putative ammonium transporter putative calcium/proton antiporter	Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1859 Rv1860 Rv2329c Rv1737c Rv0261c Rv0267	cysA cysT cysW modA modB modC modD narK1 narK2 narU	sulphate transport system permease protein sulphate transport system permease protein molybdate binding protein transport system permease, molybdate uptake molybdate uptake molybdate uptake ABC-transporter precursor of Apa (45/47 kD secreted protein) probable nitrite extrusion protein nitrite extrusion protein similar to nitrite extrusion protein 2 PstS component of phosphate uptake
Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv2981c Rv3809c Rv1018c Rv3382c Rv1110 Rv1315 Rv0482 Rv2152c	sacculus a dacB ddlA glf glmU lytB lytB' murA murB	probable secreted protein probable precursor of serine protease probable cutinase probable cutinase probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-galactopyranose mutase UDP-N-acetylglucosamine pyrophosphorylase LytB protein homologue very similar to LytB UDP-N-acetylgucosamine-1-carboxyvinyltransferase UDP-N-acetylenolpyruvoylglucosamine reductase UDP-N-acetyl-muramate-alanine ligase	Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1281c Rv2320c Rv3253c Rv3454 2. Cations Rv2920c	gabP glnH glnQ oppA oppB oppC oppD rocE amt	probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein arginine/ornithine transporter probable peptide transporter probable cationic amino acid transport possible proline permease putative ammonium transporter putative calcium/proton antiporter probable magnesium and cobalt	Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1859 Rv1860 Rv2329c Rv1737c Rv0261c Rv0267	cysA cysT cysW modA modB modC modD narK1 narK2 narK3 narU	sulphate transport system permease protein sulphate transport system permease protein molybdate binding protein transport system permease, molybdate uptake molybdate uptake ABC- transporter precursor of Apa (45/47 kD secreted protein) probable nitrite extrusion protein nitrite extrusion protein similar to nitrite extrusion protein 2 PatS component of phosphate uptake PstS component of phosphate
Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv2981c Rv3809c Rv1018c Rv3382c Rv1110 Rv1315 Rv0482	sacculus a dacB ddlA glf glmU lytB' murA	probable secreted protein probable precursor of serine protease probable cutinase precursor penicillin binding protein pr	Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1281c Rv2320c Rv3253c Rv3454 2. Cations Rv2920c Rv1607 Rv1239c	gabP glnH glnQ oppA oppB oppC oppD rocE - amt chaA corA	probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport protein oligopeptide transport system permease probable peptide transport protein arginine/ornithine transporter probable cationic amino acid transport protein possible proline permease protein arginine/ornithine transporter probable cationic amino acid transport possible proline permease	Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1859 Rv1860 Rv2329c Rv1737c Rv0261c Rv0267	cysA cysT cysW modA modB modC modD narK1 narK2 narK3 narU phoS1	sulphate transport system permease protein sulphate transport system permease protein molybdate binding protein transport system permease, molybdate uptake molybdate uptake molybdate uptake ABC-transporter precursor of Apa (45/47 kD secreted protein) probable nitrite extrusion protein nitrite extrusion protein similar to nitrite extrusion protein 2 PstS component of phosphate uptake
Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv2981c Rv3809c Rv1018c Rv3382c Rv1110 Rv1315 Rv0482 Rv2152c	sacculus a dacB ddlA glf glmU lytB lytB' murA murB	probable secreted protein probable precursor of serine protease probable cutinase probable cutinase probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-N-acetylglucosamine pyrophosphorylase LytB protein homologue very similar to LytB UDP-N-acetylglucosamine-1-carboxyvinyltransferase UDP-N-acetylenolpyruvoylglucosamine reductase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetylmuramoylalanine-D-glutamate ligase meso-diaminopimelate-adding	Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1281c Rv2320c Rv3253c Rv3454 2. Cations Rv2920c Rv1607 Rv1239c Rv0092 Rv0092 Rv0103c	gabP glnH glnQ oppA oppB oppC oppD rocE - amt chaA corA ctpA	probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport protein oligopeptide transport system permease probable peptide transport protein arginine/ornithine transporter probable cationic amino acid transport protein protein protein arginine/ornithine transporter probable protein permease putative ammonium transporter putative calcium/proton antiporter probable magnesium and cobalt transport protein cation-transporting ATPase cation transport ATPase	Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1859 Rv1860 Rv2329c Rv1737c Rv0261c Rv0267 Rv0934 Rv0928	cysA cysT cysW modA modB modC modD narK1 narK2 narK3 narU phoS1 phoS2	sulphate transport system permease protein sulphate transport system permease protein molybdate binding protein transport system permease, molybdate uptake molybdate uptake ABC- transporter precursor of Apa (45/47 kD secreted protein) probable nitrite extrusion protein nitrite extrusion protein nitrite extrusion protein similar to nitrite extrusion protein 2 PatS component of phosphate uptake PstS component of phosphate uptake phosphate transport system ABC transporter
Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv3809c Rv1018c Rv3382c Rv1110 Rv1315 Rv0482 Rv2152c Rv2155c Rv2158c	sacculus a dacB ddIA glf glmU lytB lytB' murA murB murC murD	probable secreted protein probable precursor of serine protease probable cutinase precursor probable cutinase precursor probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-9alactopyranose mutase UDP-N-acetlyglucosamine pyrophosphorylase LytB protein homologue very similar to LytB UDP-N-acetylglucosamine-1-carboxyvinyltransferase UDP-N-acetylenolpyruvoylglucosamine reductase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetylmuramoylalanine-D-glutamate ligase meso-diaminopimelate-adding enzyme	Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1281c Rv2320c Rv3253c Rv3454 2. Cations Rv2920c Rv1607 Rv1239c Rv0092 Rv0092 Rv0103c Rv3270	gabP glnH glnQ oppA oppB oppC oppD rocE - amt chaA corA ctpA ctpB ctpC	probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport protein oligopeptide transport system permease probable peptide transport protein arginine/ornithine transporter probable cationic amino acid transport protein protein protein protein arginine/ornithine transporter probable proline permease putative calcium/proton antiporter probable magnesium and cobalt transport protein cation-transporting ATPase cation transport ATPase cation transport ATPase	Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1859 Rv1860 Rv2329c Rv1737c Rv0261c Rv0267 Rv0934	cysA cysT cysW modA modB modC modD narK1 narK2 narK3 narU phoS1	sulphate transport system permease protein sulphate transport system permease protein molybdate binding protein transport system permease, molybdate uptake molybdate uptake molybdate uptake ABC-transporter precursor of Apa (45/47 kD secreted protein) probable nitrite extrusion protein nitrite extrusion protein itritie extrusion protein 2 PstS component of phosphate uptake PstS component of phosphate uptake phosphate transporter phosphate transporter phosphate transporter
Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv3809c Rv1018c Rv3382c Rv1110 Rv1315 Rv0482 Rv2152c Rv2155c	sacculus a dacB ddIA glf glmU lytB lytB' murA murB murC murD	probable secreted protein probable precursor of serine protease probable cutinase probable cutinase probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-Qualctopyranose mutase UDP-N-acetylglucosamine pyrophosphorylase LytB protein homologue very similar to LytB UDP-N-acetylglucosamine-1-carboxyvinyttransferase UDP-N-acetylenolpyruvoylglucosamine reductase UDP-N-acetylenolpyruvoylglucosamine reductase UDP-N-acetylmuramate-alanine ligase UDP-N-acetylmuramoylalanine-D-glutamate ligase meso-diaminopimelate-adding enzyme D-alanine:D-alanine-adding	Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1281c Rv2320c Rv3253c Rv3454 2. Cations Rv2920c Rv1607 Rv1239c Rv0092 Rv0092 Rv0103c	gabP glnH glnQ oppA oppB oppC oppD rocE - amt chaA corA ctpA	probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport protein oligopeptide transport system per- mease probable peptide transport protein arginine/ornithine transporter probable cationic amino acid transport possible proline permease putative ammonium transporter putative calcium/proton antiporter probable magnesium and cobalt transport protein cation-transporting ATPase cation transport ATPase cation transport ATPase probable cadmium-transporting	Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1859 Rv1860 Rv2329c Rv1737c Rv0261c Rv0267 Rv0934 Rv0928 Rv0820 Rv3301c	cysA cysT cysW modA modB modC modD narK1 narK2 narK3 narU phoS1 phoS2 phoT	sulphate transport system permease protein sulphate transport system permease protein molybdate binding protein transport system permease, molybdate uptake molybdate uptake molybdate uptake ABC- transporter precursor of Apa (45/47 kD secreted protein) probable nitrite extrusion protein nitrite extrusion protein nitrite extrusion protein similar to nitrite extrusion protein 2 PstS component of phosphate uptake PstS component of phosphate uptake phosphate transport system ABC transporter phosphate transport system regulator
Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv2981c Rv3809c Rv1018c Rv3382c Rv1110 Rv1315 Rv0482 Rv2152c Rv2155c Rv2155c	sacculus a dacB ddIA glf glmU lytB lytB' murA murB murC murD	probable secreted protein probable precursor of serine protease probable cutinase precursor probable cutinase precursor probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-9alactopyranose mutase UDP-N-acetlyglucosamine pyrophosphorylase LytB protein homologue very similar to LytB UDP-N-acetylglucosamine-1-carboxyvinyltransferase UDP-N-acetylenolpyruvoylglucosamine reductase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetylmuramoylalanine-D-glutamate ligase meso-diaminopimelate-adding enzyme	Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1281c Rv2320c Rv3253c Rv3454 2. Cations Rv2920c Rv1607 Rv1239c Rv0092 Rv0092 Rv0103c Rv3270	gabP glnH glnQ oppA oppB oppC oppD rocE - amt chaA corA ctpA ctpB ctpC	probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport protein oligopeptide transport system permease probable peptide transport protein arginine/ornithine transporter probable cationic amino acid transport protein protein protein protein arginine/ornithine transporter probable proline permease putative calcium/proton antiporter probable magnesium and cobalt transport protein cation-transporting ATPase cation transport ATPase cation transport ATPase	Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1859 Rv1860 Rv2329c Rv1737c Rv0261c Rv0267 Rv0934 Rv0928	cysA cysT cysW modA modB modC modD narK1 narK2 narK3 narU phoS1 phoS1 phoY1 phoY1	sulphate transport system permease protein sulphate transport system permease protein molybdate binding protein transport system permease, molybdate uptake molybdate uptake molybdate uptake ABC-transporter precursor of Apa (45/47 kD secreted protein) probable nitrite extrusion protein nitrite extrusion protein itritie extrusion protein 2 PstS component of phosphate uptake PstS component of phosphate uptake phosphate transporter phosphate transporter phosphate transporter
Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv3809c Rv1018c Rv3382c Rv1110 Rv1315 Rv0482 Rv2155c Rv2155c Rv2155c Rv2157c Rv2153c	sacculius a dacB ddlA glf glmU lytB' murA murB murC murD murE murF	probable secreted protein probable precursor of serine protease probable cutinase probable cutinase probable cutinase probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-N-acetylglucosamine pyrophosphorylase LyfB protein homologue very similar to LyfB UDP-N-acetylglucosamine-1-carboxyvinyttransferase UDP-N-acetylenolpyruvoylglucosamine reductase UDP-N-acetylmuramate-alanine ligase UDP-N-acetylmuramoylalanine-D-glutamate ligase meso-diaminopimelate-adding enzyme D-alanine:D-alanine-adding enzyme transferase in peptidoglycan synthesis	Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1281c Rv2320c Rv3253c Rv3454 2. Cations Rv2920c Rv1607 Rv1239c Rv0103c Rv3270 Rv1469 Rv0908 Rv1997	gabP glnH glnQ oppA oppB oppC oppD rocE amt chaA corA ctpA ctpB ctpC ctpC ctpF	probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport protein oligopeptide transport system per- mease probable peptide transport protein arginine/ornithine transporter probable cationic amino acid transport possible proline permease putative ammonium transporter putative calcium/proton antiporter probable magnesium and cobalt transport protein cation-transporting ATPase cation transport ATPase probable cadmium-transporting ATPase probable cation transport ATPase probable cation transport ATPase	Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1859 Rv1860 Rv2329c Rv1737c Rv0261c Rv0267 Rv0934 Rv0928 Rv0820 Rv3301c	cysA cysT cysW modA modB modC modD narK1 narK2 narK3 narU phoS1 phoS2 phoT	sulphate transport system permease protein sulphate transport system permease protein molybdate binding protein transport system permease, molybdate uptake molybdate uptake molybdate uptake ABC- transporter precursor of Apa (45/47 kD secreted protein) probable nitrite extrusion protein nitrite extrusion protein nitrite extrusion protein similar to nitrite extrusion protein 2 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
Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv2981c Rv3809c Rv1018c Rv3382c Rv1110 Rv1315 Rv0482 Rv2152c Rv2155c Rv2157c Rv2157c Rv2153c Rv1338	sacculus a dacB ddlA glf glmU lytB lytB' murA murB murC murD murF murF murG murl	probable secreted protein probable precursor of serine protease probable cutinase probable cutinase probable cutinase probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-N-acetylglucosamine pyrophosphorylase LytB protein homologue very similar to LytB UDP-N-acetylglucosamine-1-carboxyvinyltransferase UDP-N-acetylenolpyruvoylglucosamine reductase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetylmuramoylalanine-D-glutamate ligase UDP-N-acetylmuramoylalanine-D-glutamate ligase mso-diaminopimelate-adding enzyme D-alanine:D-alanine-adding enzyme transferase in peptidoglycan synthesis glutamate racemase	Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1281c Rv2320c Rv3253c Rv3454 2. Cations Rv2920c Rv1607 Rv1239c Rv0103c Rv0103c Rv3270 Rv1469 Rv0908 Rv0908 Rv1997 Rv1992c	gabP glnH glnQ oppA oppB oppC oppD rocE - amt chaA corA ctpB ctpC ctpC ctpC ctpE ctpF ctpG	probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport protein oligopeptide transport system permease probable peptide transport protein arginine/ornithine transporter probable cationic amino acid transport possible proline permease putative ammonium transporter putative calcium/proton antiporter probable magnesium and cobalt transport protein cation-transport ATPase cation transport ATPase probable cation transport ATPase	Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1860 Rv2329c Rv1737c Rv0261c Rv0267 Rv0934 Rv0928 Rv0928 Rv3301c Rv0821c Rv0821c	cysA cysT cysW modA modB modC modD narK1 narK2 narK3 narU phoS1 phoS2 phoT phoY1 phoY2 pitA	sulphate transport system permease protein sulphate transport system permease protein molybdate binding protein transport system permease, molybdate uptake molybdate uptake molybdate uptake ABC- transporter precursor of Apa (45/47 kD secreted protein) probable nitrite extrusion protein nitrite extrusion protein nitrite extrusion protein similar to nitrite extrusion protein 2 PatS component of phosphate uptake PstS component of phosphate uptake PstS component of phosphate uptake phosphate transport system regulator phosphate transport system regulator low-affinity inorganic phosphate transporter
Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv3809c Rv1018c Rv3382c Rv1110 Rv1315 Rv0482 Rv2155c Rv2155c Rv2155c Rv2157c Rv2153c	sacculius a dacB ddlA glf glmU lytB' murA murB murC murD murE murF	probable secreted protein probable precursor of serine protease probable cutinase precursor probable cutinase precursor probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-9alactopyranose mutase UDP-N-acetylglucosamine pyrophosphorylase LytB protein homologue very similar to LytB UDP-N-acetylglucosamine-1-carboxyvinyltransferase UDP-N-acetylenolpyruvoylglucosamine reductase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetylmuramoylalanine-D-glutamate ligase UDP-N-acetylmuramoylalanine-D-glutamate ligase meso-diaminopimelate-adding enzyme transferase in peptidoglycan synthesis glutamate racemase phospho-N-acetylmuramoyl-	Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1281c Rv2320c Rv3253c Rv3454 2. Cations Rv2920c Rv1607 Rv1239c Rv0103c Rv3270 Rv1469 Rv0908 Rv1997	gabP glnH glnQ oppA oppB oppC oppD rocE amt chaA corA ctpA ctpB ctpC ctpC ctpF	probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport protein oligopeptide transport protein oligopeptide transport system permease probable peptide transport protein arginine/ornithine transporter probable cationic amino acid transport possible proline permease putative ammonium transporter putative calcium/proton antiporter probable magnesium and cobalt transport protein cation-transporting ATPase cation transport ATPase probable cation transport ATPase probable cation transport ATPase probable cation transport ATPase probable cation transport ATPase cation transport ATPase probable cation transport ATPase cobable cation transport ATPase cobable cation transport ATPase C-terminal region putative cation.	Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1859 Rv1860 Rv2329c Rv1737c Rv0261c Rv0267 Rv0934 Rv0928 Rv0820 Rv3301c Rv0821c Rv0545c Rv2281	cysA cysT cysW modA modB modC modD narK1 narK2 narK3 narU phoS1 phoS1 phoY1 phoY2 pitA pitB	sulphate transport system permease protein sulphate transport system permease protein molybdate binding protein transport system permease, molybdate uptake molybdate uptake molybdate uptake ABC- transporter precursor of Apa (45/47 kD secreted protein) probable nitrite extrusion protein nitrite extrusion protein similar to nitrite extrusion protein 2 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
Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv2981c Rv3809c Rv1018c Rv3382c Rv1110 Rv1315 Rv0482 Rv2152c Rv2155c Rv2157c Rv2157c Rv2153c Rv1338	sacculus a dacB ddlA glf glmU lytB lytB' murA murB murC murD murF murF murG murl	probable secreted protein probable precursor of serine protease probable cutinase probable cutinase probable cutinase probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-N-acetylglucosamine pyrophosphorylase LytB protein homologue very similar to LytB UDP-N-acetylglucosamine-1-carboxyvinyltransferase UDP-N-acetylenolpyruvoylglucosamine reductase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetylmuramoylalanine-Dglutamate ligase UDP-N-acetylmuramoylalanine-Dglutamate 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-	Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1281c Rv2320c Rv3253c Rv3454 2. Cations Rv2920c Rv1607 Rv1239c Rv0103c Rv0103c Rv3270 Rv1469 Rv0908 Rv0908 Rv1997 Rv1992c	gabP glnH glnQ oppA oppB oppC oppD rocE - amt chaA corA ctpB ctpC ctpC ctpC ctpE ctpF ctpG	probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport protein oligopeptide transport system permease probable peptide transport protein arginine/ornithine transporter probable cationic amino acid transport protein arginine/ornithine transporter probable proline permease putative ammonium transporter putative ammonium transporter putative calcium/proton antiporter probable magnesium and cobalt transport protein cation-transport ATPase cation transport ATPase probable cation transport ATPase probable cation transport ATPase probable cation transport ATPase probable cation transport ATPase creminal region putative cation-transporting ATPase C-terminal region putative cation-transporting ATPase probable magnesium transport	Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1859 Rv1860 Rv2329c Rv1737c Rv0261c Rv0267 Rv0934 Rv0928 Rv0820 Rv3301c Rv0821c Rv0821c Rv0821c Rv0821c Rv08231	cysA cysT cysW modA modB modC modD narK1 narK2 narK3 narU phoS1 phoS1 phoY2 pitA pitB pstA1	sulphate transport system permease protein sulphate transport system permease protein molybdate binding protein transport system permease, molybdate uptake molybdate uptake molybdate uptake ABC- transporter precursor of Apa (45/47 kD secreted protein) probable nitrite extrusion protein nitrite extrusion protein nitrite extrusion protein similar to nitrite extrusion protein 2 PatS component of phosphate uptake PstS component of phosphate uptake PstS component system ABC transporter phosphate transport system regulator low-affinity inorganic phosphate transporter phosphate permease PstA component of phosphate transporter phosphate PstA component of phosphate transporter
Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv3809c Rv1018c Rv3382c Rv1110 Rv1315 Rv0482 Rv2152c Rv2155c Rv2155c Rv2157c Rv2153c Rv2153c Rv2153c Rv2153c Rv3338 Rv2156c Rv3332	sacculus a dacB ddlA glf glmU lytB murA murB murC murD murE murF murG murl murX nagA	probable secreted protein probable precursor of serine protease probable cutinase precursor probable cutinase precursor probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-9alactopyranose mutase UDP-N-acetylglucosamine pyrophosphorylase LytB protein homologue very similar to LytB UDP-N-acetylglucosamine-1-car-boxyvinyltransferase UDP-N-acetylenopyruvoylglucosamine reductase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetylmuramoylalanine-D-glutamate ligase UDP-N-acetylmuramoylalanine-D-glutamate procession peningen procession peningen	Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1281c Rv2320c Rv3253c Rv3454 2. Cations Rv2920c Rv1607 Rv1239c Rv0092 Rv0103c Rv3270 Rv1469 Rv0908 Rv1997 Rv1992c Rv01925c Rv0107c	gabP glnH glnQ oppA oppB oppC oppD rocE - amt chaA corA ctpA ctpB ctpC ctpC ctpC ctpC ctpC ctpC ctpC ctpC	probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport protein oligopeptide transport protein oligopeptide transport system permease probable peptide transport protein arginine/ornithine transporter probable cationic amino acid transport protein experience probable proline permease probable proline permease probable proline permease probable proline permease probable magnesium and cobalt transport protein cation-transporting ATPase cation transport ATPase probable magnesium transport ATPase probable magnesium transport ATPase probable magnesium transport ATPase probable magnesium transport ATPase	Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1859 Rv1860 Rv2329c Rv1737c Rv0261c Rv0267 Rv0934 Rv0928 Rv0820 Rv3301c Rv0821c Rv0545c Rv2281	cysA cysT cysW modA modB modC modD narK1 narK2 narK3 narU phoS1 phoS1 phoY1 phoY2 pitA pitB	sulphate transport system permease protein sulphate transport system permease protein molybdate binding protein transport system permease, molybdate uptake molybdate uptake molybdate uptake ABC- transporter precursor of Apa (45/47 kD secreted protein) probable nitrite extrusion protein nitrite extrusion protein similar to nitrite extrusion protein 2 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 premease PstA component of phosphate uptake PstS component of phosphate
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Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv3809c Rv1018c Rv3382c Rv1110 Rv1315 Rv0482 Rv2152c Rv2155c Rv2155c Rv2157c Rv2153c Rv2153c Rv2153c Rv2153c Rv3338 Rv2156c Rv3332	sacculus a dacB ddlA glf glmU lytB murA murB murC murD murE murF murG murl murX nagA	probable secreted protein probable precursor of serine protease probable cutinase precursor probable cutinase precursor probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-galactopyranose mutase UDP-N-acetylglucosamine pyrophosphorylase LytB protein homologue very similar to LytB UDP-N-acetylglucosamine-1-carboxyvinyltransferase UDP-N-acetylenopyruvoylglucosamine reductase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetylmuramoylalanine-D-glutamate 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-deacetylgase penicillin-binding protein protein	Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1281c Rv2320c Rv3253c Rv3454 2. Cations Rv2920c Rv1607 Rv1239c Rv0092 Rv0103c Rv3270 Rv1469 Rv0908 Rv1997 Rv1992c Rv01925c Rv0107c	gabP glnH glnQ oppA oppB oppC oppD rocE - amt chaA corA ctpA ctpB ctpC ctpC ctpC ctpC ctpC ctpC ctpC ctpC	probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport protein oligopeptide transport protein oligopeptide transport system permease probable peptide transport protein arginine/ornithine transporter probable cationic amino acid transport protein experience probable proline permease probable proline permease probable proline permease probable proline permease probable magnesium and cobalt transport protein cation-transporting ATPase cation transport ATPase probable magnesium transport ATPase probable magnesium transport ATPase probable magnesium transport ATPase probable magnesium transport ATPase	Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1859 Rv1860 Rv2329c Rv1737c Rv0261c Rv0267 Rv0934 Rv0928 Rv0820 Rv3301c Rv0821c Rv0821c Rv0821c Rv0821c Rv08231	cysA cysT cysW modA modB modC modD narK1 narK2 narK3 narU phoS1 phoS1 phoY2 pitA pitB pstA1	sulphate transport system permease protein sulphate transport system permease protein molybdate binding protein transport system permease, molybdate uptake molybdate uptake molybdate uptake ABC- transporter precursor of Apa (45/47 kD secreted protein) probable nitrite extrusion protein nitrite extrusion protein similar to nitrite extrusion protein 2 PstS component of phosphate uptake phosphate transport system ABC transporter phosphate transport system regulator low-affinity inorganic phosphate transporter phosphate transport system regulator low-affinity inorganic phosphate transporter phosphate transport of phosphate transporter phosphate transport system regulator low-affinity inorganic phosphate transporter Phosphate permease PstA component of phosphate uptake ABC transport component of phosphate uptake
Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv3809c Rv1018c Rv3382c Rv1110 Rv1315 Rv0482 Rv2155c Rv2155c Rv2155c Rv2155c Rv2155c Rv2153c Rv1338 Rv2156c Rv3332 Rv0016c Rv2163c Rv0050 Rv3682	sacculus a dacB ddlA gif gimU lytB lytB' murA murB murC murF murF murG murl murX nagA pbpA pbpA ponA'	probable secreted protein probable precursor of serine protease probable cutinase probable cutinase probable cutinase probable cutinase precursor probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-N-acetylglucosamine pyrophosphorylase LytB protein homologue very similar to LytB UDP-N-acetylglucosamine-1-carboxyvinyttransferase UDP-N-acetylenolpyruvoylglucosamine reductase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetylmuramoylalanine-D-glutamate ligase UDP-N-acetylmuramoylalanine-D-glutamate ligase meso-diaminopimelate-adding enzyme D-alanine:D-alanine-doglycan synthesis glutamate racemase phospho-N-acetylmuramoyl-petapeptide transferase N-acetylglucosamine-6-P-deacetylase penicillin-binding protein 2 penicillin-binding protein class A penicillin binding protein	Rv0522 Rv0411c Rv2564 Rv1283c Rv1283c Rv1282c Rv1281c Rv2320c Rv3253c Rv3454 2. Cations Rv2920c Rv1607 Rv1239c Rv0103c Rv3270 Rv1469 Rv0908 Rv1997 Rv1992c Rv0425c Rv0107c Rv0969 Rv3044 Rv0266c trate	gabP glnH glnQ oppA oppB oppC oppD rocE - amt chaA corA ctpA ctpC ctpC ctpC ctpC ctpC ctpH ctpI ctpV fecB fecB2	probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport protein oligopeptide transport protein oligopeptide transport system permease probable peptide transport protein arginine/ornithine transporter probable cationic amino acid transport protein exporter probable proline permease probable proline permease probable proline permease probable magnesium and cobalt transport protein cation-transporting ATPase cation transport ATPase probable magnesium transport ATPase probable magnesium transport ATPase cation transport ATPase probable magnesium transport ATPase cation transport ATPase probable magnesium transport ATPase cation transport ATPase probable magnesium transport ATPase probable magnesium transport ATPase cation transport ATPase protein Falli-dicitrate transporter iron transport protein Falli dicitrates protein	Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1859 Rv1860 Rv2329c Rv1737c Rv0261c Rv0267 Rv0934 Rv0928 Rv0820 Rv3301c Rv0821c Rv0821c Rv0821c Rv0845c Rv2281 Rv0936	cysA cysT cysW modA modB modC modD narK1 narK2 narK3 narU phoS1 phoT phoY1 phoY2 pitA pitB pstA1 pstA2	sulphate transport system permease protein sulphate transport system permease protein molybdate binding protein transport system permease, molybdate uptake molybdate uptake ABC- transporter precursor of Apa (45/47 kD secreted protein) probable nitrite extrusion protein nitrite extrusion protein nitrite extrusion protein similar to nitrite extrusion protein 2 PstS component of phosphate uptake PstS component of phosphate uptake phosphate transport system ABC transporter phosphate transport system regulator 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 ABC transport component of
Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv3809c Rv1018c Rv3382c Rv1110 Rv1315 Rv2152c Rv2155c Rv2155c Rv2157c Rv2157c Rv2153c Rv2157c Rv2153c Rv3332 Rv0016c Rv3332 Rv0016c Rv2163c Rv0050	sacculus a dacB ddlA glf glmU lytB lytB' murA murB murC murD murE murF murG murl murX nagA pbpA pppA ppnA	probable secreted protein probable precursor of serine protease probable cutinase precursor probable cutinase precursor probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-galactopyranose mutase UDP-N-acetylglucosamine pyrophosphorylase LytB protein homologue very similar to LytB UDP-N-acetylglucosamine-1-carboxyvinyltransferase UDP-N-acetylenopyruvoylglucosamine reductase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetylmuramoylalanine-D-glutamate 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-deacetylgase penicillin-binding protein protein	Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1281c Rv2320c Rv3253c Rv3454 2. Cations Rv2920c Rv1607 Rv1239c Rv0092 Rv0103c Rv3270 Rv1469 Rv0908 Rv1997 Rv1992c Rv0425c Rv0107c Rv0969 Rv3044 Rv0265c	gabP glnH glnQ oppA oppB oppC oppD rocE amt chaA corA ctpA ctpB ctpC ctpD ctpE ctpG ctpH ctpl ctpt fecB	probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport protein oligopeptide transport protein oligopeptide transport system permease probable peptide transport protein arginine/ornithine transporter probable cationic amino acid transport protein acid transport protein arginine/ornithine transporter probable proline permease putative calcium/proton antiporter probable magnesium and cobalt transport protein cation-transporting ATPase cation transport ATPase probable cadmium-transporting ATPase probable cation transport ATPase probable cation transport ATPase colombia proling ATPase colombia proling at produce to the probable cation transport ATPase probable cation transport ATPase colombia magnesium transport ATPase cation transport ATPase probable magnesium transport ATPase cation transport ATPase cation transport ATPase cation transport ATPase probable magnesium transport ATPase cation transport ATPase cation transport ATPase cation transport ATPase probable magnesium transport ATPase cation transport ATPase cation transport ATPase probable magnesium transport ATPase pr	Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1859 Rv1860 Rv2329c Rv1737c Rv0261c Rv0267 Rv0934 Rv0928 Rv3301c Rv0821c Rv0821c Rv0545c Rv2281 Rv0930 Rv0936 Rv0933	cysA cysT cysW modA modB modC modD narK1 narK2 narK3 narU phoS1 phoS2 phoT phoY1 phoY2 pitA pitB pstA1 pstA2 pstB	sulphate transport system permease protein sulphate transport system permease protein molybdate binding protein transport system permease, molybdate uptake molybdate uptake molybdate uptake ABC- transporter precursor of Apa (45/47 kD secreted protein) probable nitrite extrusion protein nitrite extrusion protein similar to nitrite extrusion protein 2 PstS component of phosphate uptake phosphate transport system ABC transporter phosphate transport system regulator low-affinity inorganic phosphate transporter phosphate transport system regulator low-affinity inorganic phosphate transporter phosphate transport of phosphate transporter phosphate transport system regulator low-affinity inorganic phosphate transporter Phosphate permease 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> opero part of <i>mce4</i> opero	
		uptake			unit	Rv3896c -	putative p60 homol	ogue
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, an	nd 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	nily 7 copies	
11000400	npz	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/recombin integrase/recombin	
		ABC-transporter	Rv1901	cinA	competence damage protein	Rv1054 -	integrase-a	ase
Rv2937	drrB	similar daunorubicin resistance transmembrane protein	Rv3648c	cspA	cold shock protein, transcriptional regulator	Rv1055 - Rv1573 -	integrase-b phiRV1 phage relat	ted protein
Rv2938	drrC	similar daunorubicin resistance	Rv0871	cspB	probable cold shock protein	Rv1574 -	phiRV1 phage relat	
Rv2846c	efpA	transmembrane protein putative efflux protein	Rv3063	cstA	starvation-induced stress response protein	Rv1575 - Rv1576c -	phiRV1 phage relat phiRV1 phage relat	
Rv3065	emrE	resistance to ethidium bromide	Rv3490	otsA	probable α, α -trehalose-phosphate	Rv1577c -	phiRV1 possible pr	
Rv0783c Rv0849	-	multidrug resistance protein possible quinolone efflux pump	Rv2006	otsB	synthase trehalose-6-phosphate phos-	Rv1578c - Rv1579c -	phiRV1 phage relat phiRV1 phage relat	
Rv1145	-	probable drug transporter	1102000	Olad	phatase	Rv1580c -	phiRV1 phage relat	
Rv1146 Rv1250	-	probable drug transporter probable drug efflux protein	Rv3372	otsB2	trehalose-6-phosphate phos- phatase	Rv1581c - Rv1582c -	phiRV1 phage relat phiRV1 phage relat	
Rv1258c	-	probable multidrug resistance	Rv3758c	proV	osmoprotection ABC transporter	Rv1583c -	phiRV1 phage relat	
Rv1410c	_	pump	Rv3757c	proW	transport system permease similar to osmoprotection proteins	Rv1584c - Rv1585c -	phiRV1 phage relat	
Rv1634	-	probable drug efflux protein probable drug efflux protein	Rv3759c Rv3756c	proX proZ	transport system permease	Rv1585c - Rv1586c -	phiRV1 phage relat phiRV1 integrase	lea protein
Rv1819c	-	probable multidrug resistance	Rv1026	1	probable pppGpp-5'phosphohydro-	Rv2309c -	integrase	
Rv2136c	_	pump putative bacitracin resistance pro-			lase	Rv2310 - Rv2646 -	excisionase phiRV2 integrase	
		tein	F. Detoxific			Rv2647 -	phiRV2 phage relat	
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 relat phiRV2 prohead pro	
		tance protein	Rv2238c	ahpE	member of AhpC/TSA family	Rv2652c -	phiRV2 phage relat	ted protein
Rv2994	-	probable fluoroquinolone efflux protein	Rv2521 Rv1608c	bcp bcpB	bacterioferritin comigratory protein probable bacterioferritin comigra-	Rv2653c - Rv2654c -	phiRV2 phage relat phiRV2 phage relat	
Rv1877	-	probable drug efflux protein	1101000	БОРБ	tory protein	Rv2655c -	phiRV2 phage relat	
Rv2459	-	probable drug efflux protein	Rv3473c	bpoA	probable non-heme bromoperoxidase	Rv2656c - Rv2657c -	phiRV2 phage relat similar to gp36 of n	
B. Chaper	ones/Heat	shock	Rv1123c	bpoB	probable non-heme bromoperoxi-		phage L5	nycobacterio-
Rv0384c Rv0352	clpB dnaJ	heat shock protein acts with GrpE to stimulate DnaK	Rv0554	bpoC	dase probable non-heme bromoperoxi-	Rv2658c - Rv2659c -	phiRV2 phage relat phiRV2 integrase	ted protein
HV0332	unao	ATPase	HV0554	bpoc	dase	Rv2830c -	similar to phage P1	phd gene
Rv2373c Rv0350	dnaJ2 dnaK	DnaJ homologue	Rv3617 Rv1938	ephA	probable epoxide hydrolase	Rv3750c - Rv3751 -	excisionase	
nvussu	unan	70 kD heat shock protein, chromo- some replication	Rv1124	ephB ephC	probable epoxide hydrolase probable epoxide hydrolase	NV3/31 -	putative integrase	
Rv3417c	groEL1	60 kD chaperonin 1	Rv2214c	ephD	probable epoxide hydrolase	C. PE and PPE fa	amilies	
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		
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-lactamas	e
		Hsp20 family	Rv1932	tpx	thiol peroxidase	Rv3290c lat	lysine-ϵ aminotrans	ferase
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 resist possible puromycin	
		shock protein	Rv3177	-	probable non-heme haloperoxi-		ferase	•
Rv2701c	suhB	putative extragenic suppressor protein			dase	Rv0262c -	aminoglycoside 2'-I ferase	N-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. lincolne similar to S. lincolne	
Rv3641c	fic	possible cell division protein	Rv0589	mce2	cell invasion protein	Rv1347c -	possible aminoglyc	
Rv3102c Rv3610c	ftsE ftsH	membrane protein inner membrane protein,	Rv1966 Rv3499c	mce3 mce4	cell invasion protein cell invasion protein	Rv2036 -	acetyltransferase similar to lincomyci	n 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	s macrotetrolide
Rv2154c	ftsW	membrane protein (shape determi-	Rv0167	-	part of mce1 operon	Rv3225c -	probable aminoglyo	coside 3'-phos-
Rv3101c	ftsX	nation) membrane protein	Rv0168 Rv0170	-	part of <i>mce1</i> operon part of <i>mce1</i> operon	Rv3700c -	photransferases probable acetyltran	eferace
Rv2921c	ftsY	cell division protein FtsY	Rv0171	-	part of <i>mce1</i> operon	Rv3817 -	probable aminoglyo	
Rv2150c	ftsZ	circumferential ring, GTPase	Rv0172	-	part of <i>mce1</i> operon part of <i>mce1</i> 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	e proteins	3
Rv3917c	parA	chromosome partitioning; DNA -	Rv0588	-	part of mce2 operon	5 O to the second D		00
Rv3918c	parB	binding possibly involved in chromosome	Rv0590 Rv0591	-	part of <i>mce2</i> operon part of <i>mce2</i> operon	F. Cytochrome P4	150 enzymes	22
		partitioning	Rv0592	-	part of mce2 operon	G. Coenzyme F42	20-dependent	
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	61
Rv0435c Rv2115c	-	ATPase of AAA-family ATPase of AAA-family	Rv1478	_	homologue putative exported p60 protein	I Miscellaneous r	phosphatases, 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
1750		tioning	Rv1964	-	part of mce3 operon	,		
D Protoin	and north	de secretion	Rv1965 Rv1967	-	part of <i>mce3</i> operon part of <i>mce3</i> operon	K. Chelatases		2
Rv2916c	ffh	signal recognition particle protein	Rv1967 Rv1968	-	part of <i>mce3</i> operon	V. Conserved hyp	otheticals	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		000
Rv1539	IspA	lipoprotein signal peptidase	Rv3494c	-	part of mce4 operon	TOTAL		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		tuPe ® ที่ม <i>ลิธัสส์</i> ปลิกิศ Publishers Ltd 199	8		