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

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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.....GSGAPGGAGGAGGLWGTGGAGGAGGSSAGGGGAGGAGGAGGWLLGDGGAGGIGGAST...

BCG.....GSGAPGGAGGAAGLWGTGGA------GGAGGWLLGDGGAGGIGGAST...

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		ds			superfamily	Rv3562	fadE31	acyl-CoA dehydrogenase
Rv0186	bgİS	β-glucosidase	Rv3039c	echA17	enoyl-CoA hydratase/isomerase	Rv3563	fadE32	acyl-CoA dehydrogenase
Rv2202c	cbhK	carbohydrate kinase			superfamily	Rv3564	fadE33	acyl-CoA dehydrogenase
Rv0727c Rv1731	fucA ach□1	L-fuculose phosphate aldolase succinate-semialdehyde dehydro-	Rv3373	echA18	enoyl-CoA hydratase/isomerase superfamily, N-term	Rv3573c Rv3797	fadE34 fadE35	acyl-CoA dehydrogenase acyl-CoA dehydrogenase
MV1/31	gabD1	genase	Rv3374	echA18'		Rv3761c	fadE36	acyl-CoA dehydrogenase
Rv0234c	gabD2	succinate-semialdehyde dehydro-	110074	0011110	superfamily, C-term	Rv1175c	fadH	2,4-Dienoyl-CoA Reductase
	Ü	genase	Rv3516	echA 19	enoyl-CoA hydratase/isomerase	Rv0855	far	fatty acyl-CoA racemase
Rv0501	galE1	UDP-glucose 4-epimerase			superfamily	Rv1143	mcr	α-methyl acyl-CoA racemase
Rv0536	galE2	UDP-glucose 4-epimerase	Rv3550	echA20		Rv1492	mutA	methylmalonyl-CoA mutase, β
Rv0620 Rv0619	galK galT	galactokinase galactose-1-phosphate uridylyl-	Rv3774	echA21	superfamily enoyl-CoA hydratase/isomerase	Rv1493	mutB	subunit methylmalonyl-CoA mutase, α
1100010	gun	transferase C-term	110774	00111121	superfamily	11111100	mail	subunit
Rv0618	galTʻ	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-
Rv3696c	glpK	transferase ATP:glycerol 3-phosphotrans-	Rv1074c Rv1323	fadA3 fadA4	acetyl-CoA C-acetyltransferase acetyl-CoA C-acetyltransferase	Rv1136	_	unit probable carnitine racemase
11000000	gipit	ferase	1101020	IAU/H+	(aka thiL)	Rv1683	-	possible acyl-CoA synthase
Rv3255c	manA	mannose-6-phosphate isomerase	Rv3546	fadA5	acetyl-CoA C-acetyltransferase			product adji dan dynamad
Rv3441c	mrsA	phosphoglucomutase or phospho-	Rv3556c	fadA6	acetyl-CoA C-acetyltransferase	Phosph		
D 0440		mannomutase	Rv0860	fadB	β oxidation complex, α subunit	Rv2368c	phoH	ATP-binding pho regulon
Rv0118c Rv3068c	oxcA	oxalyl-CoA decarboxylase phosphoglucomutase	Rv0468	fadB2	(multiple activities) 3-hydroxyacyl-CoA dehydroge-	Rv1095	phoH2	component PhoH-like protein
Rv3257c	pgmA pmmA	phosphomannomutase	NV0400	IAUDZ	nase	Rv3628	рпоп2 ppa	probable inorganic pyrophos-
Rv3308	pmmB	phosphomannomutase	Rv1715	fadB3	3-hydroxyacyl-CoA dehydroge-	1110020	ppu	phatase
Rv2702	ppgK	polyphosphate glucokinase			nase	Rv2984	ppk	polyphosphate kinase
Rv0408	pta	phosphate acetyltransferase	Rv3141	fadB4	3-hydroxyacyl-CoA dehydroge-			
Rv0729	xylB	xylulose kinase	D 4040	((0.5	nase	B. Energy		em .
Rv1096	-	carbohydrate degrading enzyme	Rv1912c	fadB5	3-hydroxyacyl-CoA dehydroge- nase	1. Glycoly: Rv1023	sis <i>eno</i>	enolase
2. Amino a	acids and :	amines	Rv1750c	fadD1	acyl-CoA synthase	Rv0363c	eno fba	fructose bisphosphate aldolase
Rv1905c	aao	D-amino acid oxidase	Rv0270	fadD1	acyl-CoA synthase	Rv1436	gap	glyceraldehyde 3-phosphate dehy-
Rv2531c	adi	ornithine/arginine decarboxylase	Rv3561	fadD3	acyl-CoA synthase			drogenase
Rv2780	ald	L-alanine dehydrogenase	Rv0214	fadD4	acyl-CoA synthase	Rv0489	gpm	phosphoglycerate mutase I
Rv1538c	ansA	L-asparaginase	Rv0166	fadD5	acyl-CoA synthase	Rv3010c	pfkA	phosphofructokinase I
Rv1001 Rv0753c	arcA mmsA	arginine deiminase methylmalmonate semialdehyde	Rv1206 Rv0119	fadD6 fadD7	acyl-CoA synthase acyl-CoA synthase	Rv2029c Rv0946c	pfkB pgi	phosphofructokinase II glucose-6-phosphate isomerase
11007500	mmort	dehydrogenase	Rv0551c	fadD7	acyl-CoA synthase	Rv1437	pgi pgk	phosphoglycerate kinase
Rv0751c	mmsB	methylmalmonate semialdehyde	Rv2590	fadD9	acyl-CoA synthase	Rv1617	pykA	pyruvate kinase
		oxidoreductase	Rv0099	fadD10	acyl-CoA synthase	Rv1438	tpi	triosephosphate isomerase
Rv1187	rocA	pyrroline-5-carboxylate dehydro-	Rv1550	fadD11	acyl-CoA synthase, N-term	Rv2419c	-	putative phosphoglycerate mutase
Rv2322c	rocD1	genase ornithine aminotransferase	Rv1549 Rv1427c	fadD11' fadD12	acyl-CoA synthase, C-term acyl-CoA synthase	Rv3837c	-	putative phosphoglycerate mutase
Rv2321c	rocD1	ornithine aminotransferase	Rv3089	fadD12	acyl-CoA synthase	2. Pyruvat	e dehvdro	genase
Rv1848	ureA	urease γ subunit	Rv1058	fadD14	acyl-CoA synthase	Rv2241	aceE	pyruvate dehydrogenase E1 com-
Rv1849	ureB	urease β subunit	Rv2187	fadD15	acyl-CoA synthase			ponent
Rv1850	ureC	urease α subunit	Rv0852	fadD16	acyl-CoA synthase	Rv3303c	lpdA	dihydrolipoamide dehydrogenase
Rv1853 Rv1851	ureD ureF	urease accessory protein	Rv3506 Rv3513c	fadD17 fadD18	acyl-CoA synthase	Rv2497c	pdhA	pyruvate dehydrogenase E1 com-
Rv1852	ureG	urease accessory protein urease accessory protein	Rv3515c	fadD19	acyl-CoA synthase acyl-CoA synthase	Rv2496c	pdhB	ponent α subunit pyruvate dehydrogenase E1 com-
Rv2913c	-	probable D-amino acid	Rv1185c	fadD10	acyl-CoA synthase	1112-1000	punb	ponent β subunit
		aminohydrolase	Rv2948c	fadD22	acyl-CoA synthase	Rv2495c	pdhC	dihydrolipoamide acetyltransferase
Rv3551	-	possible glutaconate CoA-	Rv3826	fadD23	acyl-CoA synthase	Rv0462	-	probable dihydrolipoamide dehy-
		transferase	Rv1529	fadD24	acyl-CoA synthase			drogenase
3. Fatty ac	side		Rv1521 Rv2930	fadD25 fadD26	acyl-CoA synthase acyl-CoA synthase	3. TCA cy	مام	
Rv2501c	accA1	acetyl/propionyl-CoA carboxylase,	Rv0275c	fadD27	acyl-CoA synthase	Rv1475c	acn	aconitate hydratase
		α subunit	Rv2941	fadD28	acyl-CoA synthase	Rv0889c	citA	citrate synthase 2
Rv0973c	accA2	acetyl/propionyl-CoA carboxylase,	Rv2950c	fadD29	acyl-CoA synthase	Rv2498c	citE	citrate lyase β chain
		α subunit	Rv0404	fadD30	acyl-CoA synthase	Rv1098c	fum	fumarase
Rv2502c	accD1	acetyl/propionyl-CoA carboxylase,	Rv1925 Rv3801c	fadD31 fadD32	acyl-CoA synthase	Rv1131 Rv0896	gltA1 gltA2	citrate synthase 1
Rv0974c	accD2	β subunit acetyl/propionyl-CoA carboxylase,	Rv1345	fadD32 fadD33	acyl-CoA synthase acyl-CoA synthase	Rv3339c	icd1	citrate synthase 1 isocitrate dehydrogenase
-11400740	40002	β subunit	Rv0035	fadD34	acyl-CoA synthase	Rv0066c	icd2	isocitrate denydrogenase
Rv3667	acs	acetyl-CoA synthase	Rv2505c	fadD35	acyl-CoA synthase	Rv0794c	lpdB	dihydrolipoamide dehydrogenase
Rv3409c	choD	cholesterol oxidase	Rv1193	fadD36	acyl-CoA synthase	Rv1240	mdh	malate dehydrogenase
Rv0222	echA1	enoyl-CoA hydratase/isomerase	Rv0131c	fadE1	acyl-CoA dehydrogenase	Rv2967c	pca	pyruvate carboxylase
By04EGA	ech 10	superfamily	Rv0154c Rv0215c	fadE2 fadE3	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv3318 Rv3319	sdhA sdhB	succinate dehydrogenase A
Rv0456c	echA2	enoyl-CoA hydratase/isomerase superfamily	Rv02156	тааЕЗ fadE4	acyl-CoA denydrogenase acyl-CoA dehydrogenase	Rv3319	sanB sdhC	succinate dehydrogenase B succinate dehydrogenase C sub-
Rv0632c	echA3	enoyl-CoA hydratase/isomerase	Rv0244c	fadE5	acyl-CoA dehydrogenase	. 140010	54.70	unit
7=0		superfamily	Rv0271c	fadE6	acyl-CoA dehydrogenase	Rv3317	sdhD	succinate dehydrogenase D sub-
Rv0673	echA4	enoyl-CoA hydratase/isomerase	Rv0400c	fadE7	acyl-CoA dehydrogenase			unit
B		superfamily	Rv0672	fadE8	acyl-CoA dehydrogenase	Rv1248c	sucA	2-oxoglutarate dehydrogenase
Rv0675	echA5	enoyl-CoA hydratase/isomerase	Du07504	fadEo	(aka <i>aidB</i>)	Rv2215	sucB	dihydrolipoamide succinyltrans-
Rv0905	echA6	superfamily enoyl-CoA hydratase/isomerase	Rv0752c Rv0873	fadE9 fadE10	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv0951	sucC	ferase succinyl-CoA synthase β chain
. 100000	CONAC	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			a distance of the control of t
		superfamily	Rv1346	fadE14	acyl-CoA dehydrogenase	4. Glyoxyl		
Rv1070c	echA8	enoyl-CoA hydratase/isomerase	Rv1467c	fadE15	acyl-CoA dehydrogenase	Rv0467	aceA	isocitrate lyase
Du4074	aah 40	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	Rv1916	aceAb	isocitrate lyase, β module
Rv1142c	echA10	superтаmily enoyl-CoA hydratase/isomerase	Rv1933c Rv2500c	fadE18 fadE19	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv1837c Rv3323c	glcB gphA	malate synthase phosphoglycolate phosphatase
	COMMIT	superfamily	11120000	MUL 10	(aka <i>mmgC</i>)	. 1000200	Spin	psspriogry coldic priospriatase
Rv1141c	echA11	enoyl-CoA hydratase/isomerase	Rv2724c	fadE20	acyl-CoA dehydrogenase			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	Dudott	mu -f	genase
Rv1935c	ech112	superfamily enoyl-CoA hydratase/isomerase	Rv3140 Rv3139	fadE23 fadE24	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv1844c	gnd	6-phosphogluconate dehydroge- nase (Gram –)
11010000	COLIMIS	superfamily	Rv3274c	fadE25	acyl-CoA denydrogenase acyl-CoA dehydrogenase	Rv1122	gnd2	6-phosphogluconate dehydroge-
Rv2486	echA14	enoyl-CoA hydratase/isomerase	Rv3504	fadE26	acyl-CoA dehydrogenase		J	nase (Gram +)
		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 Rv2465c	rpe rpi	ribulose-phosphate 3-epimerase phosphopentose isomerase	7. Miscella	aneous oxi	doreductases and oxygenases 171	Rv2860c Rv2918c	glnA4 glnD	proable glutamine synthase uridylyltransferase
Rv1448c	tal	transaldolase				Rv2221c	glnE	glutamate-ammonia-ligase
Rv1449c	tkt	transketolase	8. ATP-pro	oton motive	e force			adenyltransferase
Rv1121	zwf	glucose-6-phosphate 1-dehydro-	Rv1308	atpA	ATP synthase α chain	Rv3859c	gltB	ferredoxin-dependent glutamate
Rv1447c	zwf2	genase glucose-6-phosphate 1-dehydro-	Rv1304 Rv1311	atpB atpC	ATP synthase a chain ATP synthase ∈ chain	Rv3858c	gltD	synthase small subunit of NADH-depender
		genase	Rv1310	atpD	ATP synthase β chain		-	glutamate synthase
C Descrive			Rv1305	atpE atpF	ATP synthase c chain	Rv3704c	gshA	possible γ-glutamylcysteine syn-
 Respira a. aerobic 			Rv1306 Rv1309	atpG	ATP synthase b chain ATP synthase γ chain	Rv2427c	proA	thase
Rv0527	ccsA	cytochrome c-type biogenesis	Rv1309	atp U atpH	ATP synthase δ chain	Rv2439c	proA	γ-glutamyl phosphate reductase glutamate 5-kinase
1100027	CCSA	protein	1101307	aipii	All sylidiase o chair	Rv0500	proC	pyrroline-5-carboxylate reductase
Rv0529	ccsB	cytochrome <i>c</i> -type biogenesis	C Central	intermedi	ary metabolism	110000	proc	pyrrolline o darboxyrate reddotase
1140020	0000	protein	1. Genera		ary metabonom	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
	_	peptide I	Rv2211c	gcvT	T protein of glycine cleavage	Rv3565	aspB	aspartate aminotransferase
Rv2193	ctaE	cytochrome c oxidase poly-	D 4040		system	Rv0337c	aspC	aspartate aminotransferase
D. 45.40-	//- A /	peptide III	Rv1213	glgC	glucose-1-phosphate adenylyl-	Rv2753c	dapA	dihydrodipicolinate synthase
Rv1542c	glbN «lbO	hemoglobin-like, oxygen carrier	Du20424	ednO1	transferase	Rv2773c	dapB	dihydrodipicolinate reductase
Rv2470 Rv2249c	glbO glpD1	hemoglobin-like, oxygen carrier glycerol-3-phosphate dehydroge-	Rv3842c	glpQ1	glycerophosphoryl diester phos- phodiesterase	Rv1202	dapE	succinyl-diaminopimelate desuc- cinylase
11022430	gipD i	nase	Rv0317c	glpQ2	glycerophosphoryl diester phos-	Rv2141c	dapE2	ArgE/DapE/Acy1/Cpg2/yscS
Rv3302c	glpD2	glycerol-3-phosphate dehydroge-	11100170	SIPORE	phodiesterase	11721710	Jupie	family
	3	nase	Rv3566c	nhoA	N-hydroxyarylamine <i>o</i> -acetyltrans-	Rv2726c	dapF	diaminopimelate epimerase
Rv0694	IIdD1	L-lactate dehydrogenase			ferase	Rv1293	lysA	diaminopimelate decarboxylase
		(cytochrome)	Rv0155	pntAA	pyridine transhydrogenase sub-	Rv3341	metA	homoserine o-acetyltransferase
Rv1872c	IIdD2	L-lactate dehydrogenase			unit α1	Rv1079	metB	cystathionine γ-synthase
Rv1854c	ndh	probable NADH dehydrogenase	Rv0156	pntAB	pyridine transhydrogenase sub-	Rv3340	metC	cystathionine β-lyase
Rv3145	nuoA	NADH dehydrogenase chain A	D	nr+D	unit α2	Rv1133c	metE	5-methyltetrahydropteroyltrigluta-
Rv3146 Rv3147	nuoB nuoC	NADH dehydrogenase chain B	Rv0157	pntB	pyridine transhydrogenase subunit β			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 denydrogenase chain E	11011210	ppuit	dikinase	11471240	1110111	cysteine methyltransferase
Rv3150	nuoF	NADH dehydrogenase chain F				Rv1392	metK	S-adenosylmethionine synthase
Rv3151	nuoG	NADH dehydrogenase chain G	2. Glucone	eogenesis		Rv0391	metZ	o-succinylhomoserine sulfhy-
Rv3152	nuoH	NADH dehydrogenase chain H	Rv0211	pckA	phosphoenolpyruvate carboxy-			drylase
Rv3153	nuol	NADH dehydrogenase chain I			kinase	Rv1294	thrA	homoserine dehydrogenase
Rv3154	nuoJ	NADH dehydrogenase chain J	Rv0069c	sdaA	L-serine dehydratase 1	Rv1296 Rv1295	thrB thrC	homoserine kinase
Rv3155 Rv3156	nuoK nuoL	NADH dehydrogenase chain K NADH dehydrogenase chain L	3. Sugar r	ucleotides		HV 1293	inic	homoserine synthase
Rv3157	nuoM	NADH dehydrogenase chain M	Rv1512	epiA	nucleotide sugar epimerase	3. Serine f	amily	
Rv3158	nuoN	NADH dehydrogenase chain N	Rv3784	epiB	probable UDP-galactose 4-	Rv0815c	cysA2	thiosulfate sulfurtransferase
Rv2195	gcrA	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-
	_	cytB reductase			transferase			ferase
Rv2194	qcrC	cytochrome b/c component of	Rv3264c	rmlA2	glucose-1-phosphate thymidyl-	Rv2847c	cysG2	multifunctional enzyme, siroheme
		ubiQ-cytB reductase	Rv3464	rmlB	transferase dTDP-glucose 4,6-dehydratase	Rv2334	cysK	synthase cysteine synthase A
b. anaerol	bic		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
		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	rmlD	dTDP-4-dehydrorhamnose	Rv0070c	glyA2	serine hydroxymethyltransferase
Rv1552	frdA	ductase fumarate reductase flavoprotein	Rv0322	udgA	reductase UDP-glucose	Rv2996c	serA	D-3-phosphoglycerate dehydro- genase
1101002	nuA	subunit	110022	uugn	dehydrogenase/GDP-mannose 6-	Rv0505c	serB	probable phosphoserine phos-
Rv1553	frdB	fumarate reductase iron sulphur			dehydrogenase			phatase
		protein	Rv3265c	wbbL	dTDP-rhamnosyl transferase	Rv3042c	serB2	C-term similar to phosphoserine
Rv1554	frdC	fumarate reductase 15kD anchor	Rv1525	wbbL2	dTDP-rhamnosyl transferase		_	phosphatase
Rv1555	frdD	protein fumarate reductase 13kD anchor	Rv3400	-	probable β-phosphoglucomutase	Rv0884c	serC	phosphoserine aminotransferase
UA 1999	Hub	protein	4. Amino s	eliciare		4. Aromati	c amino a	icid family
Rv1161	narG	nitrate reductase α subunit	Rv3436c		glucosamine-fructose-6-	Rv3227	aroA	3-phosphoshikimate
Rv1162	narH	nitrate reductase β chain		9	phosphate aminotransferase		41.07.1	1-carboxyvinyl transferase
Rv1164	narl	nitrate reductase γ chain				Rv2538c	aroB	3-dehydroquinate synthase
Rv1163	narJ	nitrate reductase δ chain	Sulphur			Rv2537c	aroD	3-dehydroquinate dehydratase
Rv1736c	narX	fused nitrate reductase	Rv0711	atsA	arylsulfatase	Rv2552c	aroE	shikimate 5-dehydrogenase
Rv2391	nirA	probable nitrite reductase/sulphite	Rv3299c	atsB	proable arylaulfatase	Rv2540c	aroF	chorismate synthase
Rv0252	nirB	reductase nitrite reductase flavoprotein	Rv0663 Rv3077	atsD atsF	proable arylsulfatase proable arylsulfatase	Rv2178c Rv2539c	aroG aroK	DAHP synthase shikimate kinase I
	nirD	probable nitrite reductase small	Rv0296c	atsG	proable arylsulfatase	Rv3838c	pheA	prephenate dehydratase
		subunit	Rv3796	atsH	proable arylsulfatase	Rv1613	trpA	tryptophan synthase α chain
Rv0253				cysD	ATP:sulphurylase subunit 2	Rv1612	trpB	tryptophan synthase β chain
			Rv1285		ATP:sulphurylase subunit 1	Rv1611	trpC	indole-3-glycerol phosphate
Rv0253 c. Electror			Rv1286	cysN		1101011	,00	
Rv0253 c. Electron Rv0409	ackA	acetate kinase	Rv1286 Rv2131c	cysQ	homologue of M.leprae cysQ			synthase
Rv0253 c. Electror		acetate kinase cytochrome <i>bd-ll</i> oxidase	Rv1286 Rv2131c Rv3248c	cysQ sahH	homologue of <i>M.leprae cysQ</i> adenosylhomocysteinase	Rv2192c	trpD	anthranilate phosphoribosyltrans
Rv0253 c. Electror Rv0409 Rv1623c	ackA appC	acetate kinase cytochrome <i>bd-ll</i> oxidase subunit l	Rv1286 Rv2131c Rv3248c Rv3283	cysQ sahH sseA	homologue of <i>M.leprae cysQ</i> adenosylhomocysteinase thiosulfate sulfurtransferase	Rv2192c	trpD	anthranilate phosphoribosyltrans- ferase
Rv0253 c. Electror Rv0409 Rv1623c	ackA	acetate kinase cytochrome <i>bd-ll</i> oxidase subunit l cytochrome <i>d</i> ubiquinol oxidase	Rv1286 Rv2131c Rv3248c Rv3283 Rv2291	cysQ sahH sseA sseB	homologue of <i>M.leprae cysQ</i> adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase			anthranilate phosphoribosyltrans- ferase anthranilate synthase
Rv0253 c. Electron Rv0409	ackA appC	acetate kinase cytochrome <i>bd-ll</i> oxidase subunit l	Rv1286 Rv2131c Rv3248c Rv3283	cysQ sahH sseA	homologue of <i>M.leprae cysQ</i> adenosylhomocysteinase thiosulfate sulfurtransferase	Rv2192c	trpD	anthranilate phosphoribosyltrans- ferase
c. Electron Rv0409 Rv1623c Rv1622c Rv1620c	ackA appC cydB	acetate kinase cytochrome bd-ll oxidase subunit I cytochrome d ubiquinol oxidase subunit II	Rv1286 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	anthranilate phosphoribosyltrans- ferase anthranilate synthase component I
C. Electron Rv0409 Rv1623c Rv1622c Rv1620c Rv1621c Rv2007c	ackÅ appC cydB cydC cydD fdxA	acetate kinase cytochrome bd-ll oxidase subunit l cytochrome d ubiquinol oxidase subunit ll ABC transporter ABC transporter ferredoxin	Rv1286 Rv2131c Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c	cysQ sahH sseA sseB sseC sseC2	homologue of M.leprae cysQ adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase probable alkyl sulfatase	Rv2192c Rv1609	trpD trpE	anthranilate phosphoribosyltrans- ferase anthranilate synthase component I anthranilate synthase
C. Electror Rv0409 Rv1623c Rv1622c Rv1620c Rv1621c Rv2007c Rv3554	ackÅ appC cydB cydC cydD fdxA fdxB	acetate kinase cytochrome bd-ll oxidase subunit I cytochrome d ubiquinol oxidase subunit II ABC transporter ABC transporter ferredoxin ferredoxin	Rv1286 Rv2131c Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c	cysQ sahH sseA sseB sseC sseC2 -	homologue of M.leprae cysQ adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase probable alkyl sulfatase	Rv2192c Rv1609 Rv2386c Rv3754	trpD trpE trpE2 tyrA	anthranilate phosphoribosyltrans- ferase anthranilate synthase component I anthranilate synthase component I
C. Electron Rv0409 Rv1623c Rv1622c Rv1620c Rv1621c Rv2007c Rv3554 Rv1177	ackA 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	Rv1286 Rv2131c Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c D. Amino 1. Glutama	cysQ sahH sseA sseB sseC sseC2 - acid biosynate family	homologue of M.leprae cysQ adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase probable alkyl sulfatase thiosulfate sulfurtransferase probable alkyl sulfatase	Rv2192c Rv1609 Rv2386c Rv3754 5. Histidine	trpD trpE trpE2 tyrA	anthranilate phosphoribosyltrans- ferase anthranilate synthase component I anthranilate synthase component I prephenate dehydrogenase
C. Electror Rv0409 Rv1623c Rv1622c Rv1620c Rv1621c Rv2007c Rv2007c Rv1177 Rv3503c	ackA appC cydB cydC cydD fdxA fdxB fdxC fdxD	acetate kinase cytochrome bd-ll oxidase subunit I oytochrome d ubiquinol oxidase subunit II ABC transporter ABC transporter ferredoxin ferredoxin ferredoxin 4Fe-4S probable ferredoxin	Rv1286 Rv2131c Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c D. Amino 1. Glutami Rv1654	cysQ sahH sseA sseC sseC2 - acid biosynate 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	anthranilate phosphoribosyltrans- ferase anthranilate synthase component I anthranilate synthase component I prephenate dehydrogenase
C. Electror Rv0409 Rv1623c Rv1622c Rv1620c Rv1621c Rv2007c Rv3554	ackA 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	Rv1286 Rv2131c Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c D. Amino 1. Glutama	cysQ sahH sseA sseB sseC sseC2 - acid biosynate 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. Histidine	trpD trpE trpE2 tyrA	anthranilate phosphoribosyltrans- ferase anthranilate synthase component I anthranilate synthase component I prephenate dehydrogenase
C. Electron Rv0409 Rv1623c Rv1622c Rv1622c Rv1621c Rv2007c Rv3554 Rv1177 Rv3503c Rv3029c	ackÅ appC cydB cydC cydD fdxA fdxB fdxC fdxD fdxA	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	Rv1286 Rv2131c Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c D. Amino 1. Glutam Rv1654 Rv1652	cysQ sahH sseA sseC sseC2 - acid biosyn 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-γ-glutamyl-phosphate reductase	Rv2192c Rv1609 Rv2386c Rv3754 5. Histidine Rv1603	trpD trpE trpE2 tyrA hisA	anthranilate phosphoribosyltrans- ferase anthranilate synthase component I anthranilate synthase component I prephenate dehydrogenase phosphoribosylformimino-5- aminoimidazole carboxamide ribonucleotide isomerase
C. Electror 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 electron transfer flavoprotein	Rv1286 Rv2131c Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c D. Amino 1. Glutami Rv1654	cysQ sahH sseA sseB sseC2 - acid biosyn ate family argB argC argD	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. Histidine	trpD trpE trpE2 tyrA	anthranilate phosphoribosyltrans- ferase anthranilate synthase component I anthranilate synthase component I prephenate dehydrogenase
C. Electron Rv0409 Rv1623c Rv1622c Rv1622c Rv1621c Rv2007c Rv3554 Rv1177 Rv3503c Rv3029c	ackÅ appC cydB cydC cydD fdxA fdxB fdxC fdxD fdxA	acetate kinase cytochrome bd-ll oxidase subunit I cytochrome d ubiquinol oxidase subunit I ABC transporter ABC transporter ferredoxin ferredoxin ferredoxin 4Fe-4S probable ferredoxin electron transfer flavoprotein β subunit electron transfer flavoprotein α subunit adrenodoxin and NADPH ferre-	Rv1286 Rv2131c Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c D. Amino 1. Glutam Rv1654 Rv1655 Rv1655 Rv1656 Rv1658	cysQ sahH sseB sseC sseC2 - acid biosyl 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. Histidine Rv1603	trpD trpE trpE2 tyrA hisA	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-
Rv0253 c. Electror Rv0409 Rv1623c Rv1622c Rv1622c Rv1621c Rv2007c Rv3554 Rv3554 Rv3503c Rv3029c Rv3029c Rv3028c Rv3106	ackA 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 ferredoxin feredoxin feredoxin area flavoprotein β subunit electron transfer flavoprotein α subunit adrenodoxin and NADPH ferredoxin reductase	Rv1286 Rv21316 Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c <i>D. Amino</i> 1. Glutam: Rv1654 Rv1655 Rv1656 Rv1658 Rv1658	oysQ sahH sseA sseB sseC sseC2 - acid biosy, ate family argB argC argD argF argG argH	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	Rv2192c Rv1609 Rv2386c Rv3754 5. Histidine Rv1603 Rv1601 Rv1600	trpD trpE trpE2 tyrA hisA hisB	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
Rv0253 c. Electror Rv0409 Rv1623c Rv1622c Rv1620c Rv1621c Rv2007c Rv3554 Rv1177 Rv3503c Rv3029c Rv3028c	ackA appC cydB cydC cydD fdxA fdxB fdxC fdxD fixA	acetate kinase cytochrome bd-ll oxidase subunit I cytochrome d ubiquinol oxidase subunit II 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 adrenodoxin and NADPH ferredoxin reductase ferredoxin, ferredoxin-NADP	Rv1286 Rv21316 Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c D. Amino 1. Glutam Rv1654 Rv1655 Rv1656 Rv1658 Rv1659 Rv1659 Rv1653	oysQ sahH sseA sseB sseC sseC2 - acid biosy, ate family argB argC argB argG argF argF argH argH	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. Histidine Rv1603	trpD trpE trpE2 tyrA hisA	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
Rv0253 c. Electror Rv0409 Rv1623c Rv1622c Rv1621c Rv2007c Rv3554 Rv1177 Rv3503c Rv3029c Rv3028c Rv3106	ackA 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 ferredoxin feredoxin feredoxin area flavoprotein β subunit electron transfer flavoprotein α subunit adrenodoxin and NADPH ferredoxin reductase	Rv1286 Rv21316 Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c <i>D. Amino</i> 1. Glutam: Rv1654 Rv1655 Rv1656 Rv1658 Rv1658	oysQ sahH sseA sseB sseC sseC2 - acid biosy, ate family argB argC argD argF argG argH	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	Rv2192c Rv1609 Rv2386c Rv3754 5. Histidine Rv1603 Rv1601 Rv1600	trpD trpE trpE2 tyrA hisA hisB	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

Rv1605	hisF	imidazole glycerol-phosphate			subunit			subunit 1
Rv2121c	hisG	synthase ATP phosphoribosyltransferase	Rv3048c	nrdG	ribonucleoside-diphosphate small subunit	Rv3119	moaE	molybdopterin-converting factor subunit 2
Rv1602 Rv2122c	hisH hisl	amidotransferase phosphoribosyl-AMP cyclohydro-	Rv3053c	nrdH	glutaredoxin electron transport component of NrdEF system	Rv0866	moaE2	molybdopterin-converting factor subunit 2
Rv1606	hisl2	lase probable phosphoribosyl-AMP 1,6	Rv3052c Rv3247c	nrdl tmk	Nrdl/YgaO/YmaA family thymidylate kinase	Rv3322c	moaE3	molybdopterin-converting factor 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
6. Pyruvat	e family		Rv3752c	-	probable cytidine/deoxycytidylate deaminase	Rv2338c Rv1681	moeW moeX	molybdopterin biosynthesis weak similarity to <i>E. coli</i> MoaA
Rv3423c		alanine racemase				Rv1355c	moeY	weak similarity to <i>E. coli</i> MoeB
7. Branche	ed amino a		4. Salvage Rv3313c		osides and nucleotides probable adenosine deaminase	Rv3206c	moeZ	probably involved in molybdopterin biosynthesis
Rv1559 Rv3003c	ilvA ilvB	threonine deaminase acetolactate synthase I large sub-	Rv2584c	apt	adenine phosphoribosyltrans- ferases	Rv0865	mog	molybdopterin biosynthesis
Rv3470c	ilvB2	unit acetolactate synthase large sub-	Rv3315c Rv3314c	cdd deoA	probable cytidine deaminase thymidine phosphorylase	5. Pantoth Rv1092c	enate coaA	pantothenate kinase
		unit	Rv0478	deoC	deoxyribose-phosphate aldolase	Rv2225	panB	3-methyl-2-oxobutanoate
Rv3001c Rv0189c	ilvD	ketol-acid reductoisomerase dihydroxy-acid dehydratase	Rv3307	deoD	probable purine nucleoside phos- phorylase	Rv3602c	panC	hydroxymethyltransferase pantoate-β-alanine ligase
Rv2210c	ilvE	branched-chain-amino-acid transaminase	Rv3624c	hpt	probable hypoxanthine-guanine phosphoribosyltransferase	Rv3601c	panD	aspartate 1-decarboxylase
Rv1820 Rv3002c	ilvG ilvN	acetolactate synthase II acetolactate synthase I small sub-	Rv3393	iunH	probable inosine-uridine preferring nucleoside hydrolase	6. Pyridox Rv2607	ine <i>pdxH</i>	pyridoxamine 5'-phosphate
		unit	Rv0535	pnp	phosphorylase from Pnp/MtaP	1112001	Pun.	oxidase
Rv3509c	ilvX	probable acetohydroxyacid syn- thase I large subunit	Rv3309c	ирр	family 2 uracil phophoribosyltransferase	7. Pyridine		
Rv3710 Rv2995c	leuA leuB	α-isopropyl malate synthase 3-isopropylmalate dehydrogenase	5. Miscella	aneous nu	ucleoside/nucleotide reactions	Rv1594 Rv1595	nadA nadB	quinolinate synthase L-aspartate oxidase
Rv2988c	leuC	3-isopropylmalate dehydratase large subunit	Rv0733 Rv2364c	adk bex	probable adenylate kinase GTP-binding protein of Era/ThdF	Rv1596	nadC	nicotinate-nucleotide pyrophos- phatase
Rv2987c	leuD	3-isopropylmalate dehydratase small subunit	Rv1712		family	Rv0423c	thiC	thiamine synthesis, pyrimidine
			Rv2344c	cmk dgt	cytidylate kinase probable deoxyguanosine			moiety
E. Polyam Rv2601	nine synthe speE	esis spermidine synthase	Rv2404c	lepA	triphosphate hydrolase GTP-binding protein LepA	8. Thiamir Rv0422c	ne thiD	phosphomethylpyrimidine kinase
F. Purines	s. pvrimidin	es, nucleosides and nucleotides	Rv2727c	miaA	tRNA δ(2)-isopentenylpyrophos- phate transferase	Rv0414c	thiE	thiamine synthesis, thiazole moiety
		tide biosynthesis putative quanylate kinase	Rv2445c Rv2440c	ndkA obg	nucleoside diphosphate kinase Obg GTP-binding protein	Rv0417	thiG	thiamine synthesis, thiazole moiety
Rv3396c	guaA	GMP synthase	Rv2583c	relA	(p)ppGpp synthase I	Rv2977c	thiL	probable thiamine-monophos-
Rv1843c	guaB1	inosine-5'-monophosphate dehy- drogenase		thesis of d	cofactors, prosthetic groups and			phate kinase
Rv3411c	guaB2	inosine-5'-monophosphate dehy- drogenase	carriers 1. Biotin			9. Riboflav Rv1940	rih <i>ribA</i>	GTP cyclohydrolase II
Rv3410c	guaB3	inosine-5'-monophosphate dehy- drogenase	Rv1568	bioA	adenosylmethionine-8-amino-7- oxononanoate aminotransferase	Rv1415 Rv1412	ribA2 ribC	probable GTP cyclohydrolase II riboflavin synthase α chain
Rv1017c	prsA	ribose-phosphate pyrophosphoki-	Rv1589	bioB	biotin synthase	Rv2671	ribD ribF	probable riboflavin deaminase riboflavin kinase
Rv0357c	purA	nase adenylosuccinate synthase	Rv1570 Rv1569	bioD bioF	dethiobiotin synthase 8-amino-7-oxononanoate	Rv2786c Rv1409	ribG	riboflavin biosynthesis
Rv0777 Rv0780	purB purC	adenylosuccinate lyase phosphoribosylaminoimidazole-	Rv0032	bioF2	synthase C-terminal similar to <i>B. subtilis</i>	Rv1416 Rv3300c	ribH -	riboflavin synthase β chain probable deaminase, riboflavin
Rv0772	purD	succinocarboxamide synthase phosphoribosylamine-glycine lig-	Rv3279c	birA	BioF biotin apo-protein ligase			synthesis
Rv3275c	purE	ase phosphoribosylaminoimidazole	Rv1442 Rv0089	bisC	biotin sulfoxide reductase possible bioC biotin synthesis	10. Thiore Rv0773c	doxin, glut	taredoxin and mycothiol putative γ-glutamyl transpeptidase
		carboxylase	1100009	-	gene	Rv2394	ggtB	γ -glutamyltranspeptidase
Rv0808 Rv0957	purF purH	amidophosphoribosyltransferase- phosphoribosylaminoimidazole-	2. Folic ac	eid		Rv2855	gorA	precursor glutathione reductase homologue
Rv3276c	purK	carboxamide formyltransferase phosphoribosylaminoimidazole	Rv2763c Rv2447c		dihydrofolate reductase folylpolyglutamate synthase	Rv0816c Rv1470	thiX trxA	equivalent to <i>M. leprae</i> ThiX thioredoxin
Rv0803	purL	carboxylase ATPase subunit phosphoribosylformylglycin-	Rv3356c		methylenetetrahydrofolate dehy- drogenase	Rv1471 Rv3913	trxB trxB2	thioredoxin reductase thioredoxin reductase
		amidine synthase II	Rv3609c		GTP cyclohydrolase I	Rv3914	trxC	thioredoxin
Rv0809	purM	5'-phosphoribosyl-5-aminoimida- zole synthase	Rv3606c	folK	7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase			QQ, ubiquinone and other
Rv0956	purN	phosphoribosylglycinamide formyltransferase I	Rv3608c Rv1207	foIP foIP2	dihydropteroate synthase dihydropteroate synthase	terpenoids Rv2682c		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 formyltransferase II	Rv0013	pabA	p-aminobenzoate synthase gluta- mine amidotransferase	Rv0989c	grcC2	synthase II
Rv2964	purU	formyltetrahydrofolate deformy-	Rv1005c	pabB	p-aminobenzoate synthase			heptaprenyl diphosphate synthase II
		lase	Rv0812	pabC	aminodeoxychorismate lyase	Rv3398c	idsA	geranylgeranyl pyrophosphate synthase
2. Pyrimid Rv1383	ine ribonud carA	cleotide biosynthesis carbamoyl-phosphate synthase	3. Lipoate Rv2218	lipA	lipoate biosynthesis protein A	Rv2173	idsA2	geranylgeranyl pyrophosphate synthase
Rv1384	carB	subunit carbamoyl-phosphate synthase	Rv2217	lipB	lipoate biosynthesis protein B	Rv3383c	idsB	transfergeranyl, similar geranyl pyrophosphate synthase
		subunit	4. Molybd		makalahan marakan 1970 di	Rv0534c	menA	4-dihydroxy-2-naphthoate
Rv1380 Rv1381	pyrB pyrC	aspartate carbamoyltransferase dihydroorotase	Rv3109	moaA	molybdenum cofactor biosynthe- sis, protein A	Rv0548c	menB	octaprenyltransferase naphthoate synthase
Rv2139 Rv1385	pyrD pyrF	dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxy-	Rv0869c	moaA2	molybdenum cofactor biosynthe- sis, protein A	Rv0553 Rv0555	menC menD	o-succinylbenzoate-CoA synthase 2-succinyl-6-hydroxy-2,4-cyclo-
Rv1699	pyrG	lase CTP synthase	Rv0438c	moaA3	molybdenum cofactor biosynthe- sis, protein A	Rv0542c	menE	hexadiene-1-carboxylate synthase o-succinylbenzoic acid-CoA ligase
Rv2883c Rv0382c	pyrH umpA	uridylate kinase probable uridine 5'-monophos-	Rv3110	moaB	molybdenum cofactor biosynthe- sis, protein B	Rv3853	menG	S-adenosylmethionine: 2-demethylmenaquinone
HVU3020	ипрА	phate synthase	Rv0984	moaB2	molybdenum cofactor biosynthe-	Rv3397c	phyA	phytoene synthase
	yribonucle	otide metabolism	Rv3111	moaC	sis, protein B molybdenum cofactor biosynthe-	Rv0693	pqqE	coenzyme PQQ synthesis protein E
Rv0321	dcd	deoxycytidine triphosphate deaminase	Rv0864	moaC2	sis, protein C molybdenum cofactor biosynthe-	Rv0558	ubiE	ubiquinone/menaquinone biosyn- thesis methyltransferase
Rv2697c Rv0233	dut nrdB	deoxyuridine triphosphatase ribonucleoside-diphosphate	Rv3324c	moaC3	sis, protein C molybdenum cofactor biosynthe-	12. Heme	and norm!	•
		reductase B2 (eukaryotic-like)			sis, protein C	Rv0509	hemA	glutamyl-tRNA reductase
Rv3051c	nrdE	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

Rv1300 Rv0524	hemK hemL	protoporphyrinogen oxidase glutamate-1-semialdehyde amino-		,	transferase	Rv2931 Rv2932	ppsA ppsB	phenolpthiocerol synthesis (pksB) phenolpthiocerol synthesis (pksC)
Rv2388c	hemN	transferase oxygen-independent copropor-	phosphol	nsterases, ipid synthe	mycolyltransferases and esis	Rv2933 Rv2934	ppsC ppsD	phenolpthiocerol synthesis (<i>pksD</i>) phenolpthiocerol synthesis (<i>pksE</i>)
Rv2677c	hemY'	phyrinogen III oxidase protoporphyrinogen oxidase	Rv2289	cdh	CDP-diacylglycerol phosphatidyl- hydrolase	Rv2935 Rv2928	ppsE tesA	phenolpthiocerol synthesis (pksF) thioesterase
Rv1485	hemZ	ferrochelatase	Rv2881c		phosphatidate cytidylyltransferase	Rv1544	-	probable ketoacyl reductase
13. Cobala	min		Rv3804c Rv1886c		antigen 85A, mycolyltransferase antigen 85B, mycolyltransferase	J. Broad r	ogulatory	functions
Rv2849c	cobA	cob(I)alamin adenosyltransferase	Rv0129c		antigen 85C, mycolytransferase	1. Repres		
Rv2848c	cobB	cobyrinic acid a,c-diamide synthase	Rv3803c	fbpD	antigen MPT51, mycolyltrans-	Rv1657	argR	arginine repressor
Rv2231c Rv2236c	cobC 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 cobl	precorrin isomerase Cobl-CobJ fusion protein	Rv2982c	gpdA2	glycerol-3-phosphate dehydroge- nase	Rv2359 Rv2919c	furB ginB	ferric uptake regulatory protein nitrogen regulatory protein
Rv2070c	cobK	precorrin reductase	Rv2612c	pgsA	CDP-diacylglycerol-glycerol-3-	Rv2711	ideR	iron dependent repressor, IdeR
Rv2072c Rv2071c	cobL cobM	probable methyltransferase precorrin-3 methylase			phosphate phosphatidyltrans- ferase	Rv2720 Rv1479	lexA moxR	LexA, SOS repressor protein transcriptional regulator, MoxR
Rv2062c	cobN	cobalt insertion	Rv1822	pgsA2	CDP-diacylglycerol-glycerol-3-			homologue
Rv2208	cobS	cobalamin (5'-phosphate) synthase			phosphate phosphatidyltrans- ferase	Rv3692	moxR2	transcriptional regulator, MoxR homologue
Rv2207	cobT cobU	nicotinate-nucleotide-dimethyl- benzimidazole transferase cobinamide kinase	Rv2746c	pgsA3	CDP-diacylglycerol-glycerol-3- phosphate phosphatidyltrans- ferase	Rv3164c Rv0212c	moxR3 nadR	transcriptional regulator, MoxR homologue
Rv0254c Rv0255c Rv3713	cobQ cobQ2	cobinarinde kinase cobyric acid synthase possible cobyric acid synthase	Rv1551	plsB1	glycerol-3-phosphate acyltrans- ferase	Rv0117	oxyS	similar to <i>E.coli</i> NadR transcriptional regulator (LysR family)
Rv0306	-	similar to BluB cobalamin synthe-	Rv2482c	plsB2	glycerol-3-phosphate acyltrans-	Rv1379	pyrR	regulatory protein pyrimidine
		sis protein <i>R. capsulatus</i>	Rv0437c	psd	ferase putative phosphatidylserine	Rv2788	sirR	biosynthesis iron-dependent transcriptional
14. Iron uti Rv1876	lization <i>bfrA</i>	bacterioferritin	Rv0436c	pssA	decarboxylase CDP-diacylglycerol-serine	Rv3082c	virS	repressor putative virulence regulating
Rv3841 Rv3215	bfrB entC	bacterioferritin probable isochorismate synthase	Rv0045c	-	o-phosphatidyltransferase possible dihydrolipoamide acetyl-	Rv3219	whiB1	protein (AraC/XyIS family) WhiB transcriptional activator
Rv3214	entD	weak similarity to many phospho- glycerate mutases	Rv0914c		transferase	Rv3260c	whiB2	homologue WhiB transcriptional activator
Rv2895c	viuB	similar to proteins involved in	Rv1543	-	lipid transfer protein probable fatty-acyl CoA reductase			homologue
Rv3525c	-	vibriobactin uptake similar to ferripyochelin binding	Rv1627c Rv1814	-	lipid carrier protein possible C-5 sterol desaturase	Rv3416	whiB3	WhiB transcriptional activator homologue
		protein	Rv1867	-	similar to acetyl CoA synthase/lipid carriers	Rv3681c	whiB4	WhiB transcriptional activator homologue
H. Lipid bid		s and mycolic acids	Rv2261c	: 0	apolipoprotein N-acyltrans- ferase-a	Rv0023 Rv0043c	-	putative transcriptional regulator transcriptional regulator (GntR
Rv3285	accA3	acetyl/propionyl CoA carboxylase	Rv2262c	-	apolipoprotein N-acyltrans-			family)
Rv0904c	accD3	α subunit acetyl/propionyl CoA carboxylase	Rv3523	-	ferase-b lipid carrier protein	Rv0067c	-	transcriptional regulator (TetR/AcrR family)
Rv3799c	accD4	β subunit acetyl/propionyl CoA carboxylase	Rv3720		C-term similar to cyclopropane fatty acid synthases	Rv0078	-	transcriptional regulator (TetR/AcrR family)
Rv3280	accD5	β subunit acetyl/propionyl CoA carboxylase	I Polyket	ide and no	n-ribosomal peptide synthesis	Rv0081	-	transcriptional regulator (ArsR family)
1100200	acces	β subunit	Rv2940c		mycocerosic acid synthase	Rv0135c	_	putative transcriptional regulator
Rv2247	accD6	acetyl/propionyl CoA carboxylase β subunit	Rv2384	mbtA	mycobactin/exochelin synthesis (salicylate-AMP ligase)	Rv0144 Rv0158	-	putative transcriptional regulator transcriptional regulator
Rv2244	асрМ	acyl carrier protein (meromycolate extension)	Rv2383c	mbtB	mycobactin/exochelin synthesis (serine/threonine ligation)	Rv0165c		(TetR/AcrR family) transcriptional regulator (GntR
Rv2523c	acpS	CoA:apo-[ACP] pantethienephos- photransferase	Rv2382c Rv2381c	mbtC mbtD	mycobactin/exochelin synthesis mycobactin/exochelin synthesis	Rv0195		family) transcriptional regulator
Rv2243	fabD	malonyl CoA-[ACP] transacylase			(polyketide synthase)			(LuxR/UhpA family)
Rv0649 Rv1483	fabD2 fabG1	malonyl CoA-[ACP] transacylase 3-oxoacyl-[ACP] reductase (aka	Rv2380c	mbtE	mycobactin/exochelin synthesis (lysine ligation)	Rv0196	-	transcriptional regulator (TetR/AcrR family)
Rv1350	fabG2	MabA) 3-oxoacyl-[ACP] Reductase	Rv2379c	mbtF	mycobactin/exochelin synthesis (lysine ligation)	Rv0232	-	transcriptional regulator (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 Rv1484	fas inhA	fatty acid synthase enoyl-[ACP] reductase	Rv1153c	omt	synthase PKS o-methyltransferase	Rv0324	_	(TetR/AcrR family) putative transcriptional regulator
Rv2245	kasA	β-ketoacyl-ACP synthase	Rv3824c	papA1	PKS-associated protein, unknown	Rv0328	-	transcriptional regulator
Rv2246	kasB	(meromycolate extension) β-ketoacyl-ACP synthase	Rv3820c	papA2	function PKS-associated protein, unknown	Rv0348		(TetR/AcrR family) putative transcriptional regulator
	Kasb	(meromycolate extension)	11000200	papaz	function	Rv0377	-	transcriptional regulator (LysR
Rv1618 Rv2605c	tesB1 tesB2	thioesterase II thioesterase II	Rv1182	papA3	PKS-associated protein, unknown function	Rv0386	_	family) transcriptional regulator
Rv0033	-	possible acyl carrier protein	Rv1528c	papA4	PKS-associated protein, unknown			(LuxR/UhpA family)
Rv1344 Rv1722	-	possible acyl carrier protein possible biotin carboxylase	Rv2939	papA5	function PKS-associated protein, unknown	Rv0452 Rv0465c	-	putative transcriptional regulator transcriptional regulator
Rv3221c Rv3472	-	resembles biotin carboxyl carrier possible acyl carrier protein	Rv2946c	pks1	function polyketide synthase	Rv0472c	_	(PbsX/Xre family) transcriptional regulator
0.14-46	4: 4 4-4	e and moralis saids	Rv3825c	pks2	polyketide synthase	D.:0474		(TetR/AcrR family)
2. Wodings Rv3391	acrA1	ty and mycolic acids fatty acyl-CoA reductase	Rv1180 Rv1181	pks3 pks4	polyketide synthase polyketide synthase	Rv0474	-	transcriptional regulator (PbsX/Xre family)
Rv3392c	cmaA1	cyclopropane mycolic acid	Rv1527c	pks5	polyketide synthase	Rv0485	-	transcriptional regulator (ROK
Rv0503c	cmaA2	synthase 1 cyclopropane mycolic acid syn-	Rv0405 Rv1661	pks6 pks7	polyketide synthase polyketide synthase	Rv0494	-	family) transcriptional regulator (GntR
		thase 2	Rv1662	pks8	polyketide synthase			family)
Rv0824c Rv1094	desA1 desA2	acyl-[ACP] desaturase acyl-[ACP] desaturase	Rv1664 Rv1660	pks9 pks10	polyketide synthase polyketide synthase (chalcone	Rv0552 Rv0576	-	putative transcriptional regulator putative transcriptional regulator
Rv3229c	desA3	acyl-[ACP] desaturase			synthase-like)	Rv0586	-	transcriptional regulator (GntR
Rv0645c Rv0644c	mmaA1 mmaA2	methoxymycolic acid synthase 1 methoxymycolic acid synthase 2	Rv1665	pks11	polyketide synthase (chalcone synthase-like)	Rv0650	_	family) transcriptional regulator (ROK
Rv0643c	mmaA3	methoxymycolic acid synthase 3	Rv2048c	pks 12	polyketide synthase (erythronolide			family)
Rv0642c Rv0447c	mmaA4 ufaA1	methoxymycolic acid synthase 4 unknown fatty acid methyltrans-	Rv3800c	pks 13	synthase-like) polyketide synthase	Rv0653c Rv0681	-	putative transcriptional regulator transcriptional regulator
		ferase	Rv1342c	pks 14	polyketide synthase (chalcone			(TetR/AcrR family)
Rv3538	ufaA2	unknown fatty acid methyltrans- ferase	Rv2947c		synthase-like) polyketide synthase	Rv0691c	-	transcriptional regulator (TetR/AcrR family)
Rv0469	umaA1	unknown mycolic acid methyl- transferase	Rv1013 Rv1663	pks 16 pks 17	polyketide synthase polyketide synthase	Rv0737 Rv0744c	-	putative transcriptional regulator putative transcriptional regulator
Rv0470c	umaA2	unknown mycolic acid methyl-	Rv1372	pks 18	polyketide synthase	Rv0792c	-	transcriptional regulator (GntR

Rv0823	0 -	family) transcriptional regulator	Rv3160c Rv3167c	-	putative transcriptional regulator	Rv0018c	nnn	truncated
HVU023	· ·	(NifR3/Smm1 family)	Rv3173c	-	putative transcriptional regulator transcriptional regulator	HVUUTOU	ppp	putative phosphoprotein phos- phatase
Rv0827	c -	transcriptional regulator (ArsR			(TetR/AcrR family)	Rv2234	ptpA	low molecular weight protein-tyro-
D0000		family)	Rv3183	-	putative transcriptional regulator	D::0450-		sine-phosphatase
Rv0890	·c -	transcriptional regulator (LuxR/UhpA family)	Rv3208	-	transcriptional regulator (TetR/AcrR family)	Rv0153c	-	putative protein-tyrosine-phos- phatase
Rv0891	c -	putative transcriptional regulator	Rv3249c	-	transcriptional regulator			priatase
Rv0894	-	putative transcriptional regulator			(TetR/AcrR family)			metabolism
Rv1019	-	transcriptional regulator	Rv3291c	-	transcriptional regulator			odification of macromolecules
Dudodo		(TetR/AcrR family)	Rv3295	_	(Lrp/AsnC family)	1. Hibosor Rv3420c	nal protei <i>riml</i>	n synthesis and modification
Rv1049	_	transcriptional regulator (MarR family)	HV3293	-	transcriptional regulator (TetR/AcrR family)	HV34200	111111	ribosomal protein S18 acetyl transferase
Rv1129	ic -	transcriptional regulator	Rv3334	-	transcriptional regulator (MerR	Rv0995	rimJ	acetylation of 30S S5 subunit
_		(PbsX/Xre family)	_		family)	Rv0641	rplA	50S ribosomal protein L1
Rv1151		putative transcriptional regulator	Rv3405c	-	putative transcriptional regulator	Rv0704	rplB	50S ribosomal protein L2
Rv1152	-	transcriptional regulator (GntR family)	Rv3522 Rv3557c	-	putative transcriptional regulator transcriptional regulator	Rv0701 Rv0702	rpIC rpID	50S ribosomal protein L3 50S ribosomal protein L4
Rv1167	'c -	putative transcriptional regulator	11000070		(TetR/AcrR family)	Rv0716	rpIE	50S ribosomal protein L5
Rv1219		putative transcriptional regulator	Rv3574	-	transcriptional regulator	Rv0719	rpIF	50S ribosomal protein L6
Rv1255	c -	transcriptional regulator	D-0575		(TetR/AcrR family)	Rv0056	rpll	50S ribosomal protein L9
Rv1332	_	(TetR/AcrR family) putative transcriptional regulator	Rv3575c	-	transcriptional regulator (Lacl family)	Rv0651 Rv0640	rpIJ rpIK	50S ribosomal protein L10 50S ribosomal protein L11
Rv1353		transcriptional regulator	Rv3583c	-	putative transcriptional regulator	Rv0652	rpIL	50S ribosomal protein L7/L12
		(TetR/AcrR family)	Rv3676	-	transcriptional regulator (Črp/Fnr	Rv3443c	rpIM	50S ribosomal protein L13
Rv1358	-	transcriptional regulator			family)	Rv0714	rpIN	50S ribosomal protein L14
Dutan		(LuxR/UhpA family)	Rv3678c	-	transcriptional regulator (LysR	Rv0723	rpIO	50S ribosomal protein L15
Rv1359 Rv1395		putative transcriptional regulator transcriptional regulator	Rv3736	-	family) transcriptional regulator	Rv0708 Rv3456c	rpIP rpIQ	50S ribosomal protein L16 50S ribosomal protein L17
		(AraC/XyIS family)			(AraC/XylS family)	Rv0720	rpIR	50S ribosomal protein L18
Rv1404	-	transcriptional regulator (MarR	Rv3744	-	transcriptional regulator (ArsR	Rv2904c	rpIS	50S ribosomal protein L19
Du4 400		family)	Dugger -		family)	Rv1643	rpIT rpII I	50S ribosomal protein L20
Rv1423 Rv1460		putative transcriptional regulator putative transcriptional regulator	Rv3830c	-	transcriptional regulator (TetR/AcrR family)	Rv2442c Rv0706	rpIU rpIV	50S ribosomal protein L21 50S ribosomal protein L22
Rv1474		transcriptional regulator	Rv3833	-	transcriptional regulator	Rv0703	rplW	50S ribosomal protein L23
		(TetR/AcrR family)			(AraC/XylS family)	Rv0715	rplX	50S ribosomal protein L24
Rv1534	-	transcriptional regulator	Rv3840	-	putative transcriptional regulator	Rv1015c	rplY	50S ribosomal protein L25
Rv1556		(TetR/AcrR family) putative transcriptional regulator	Rv3855	-	putative transcriptional regulator	Rv2441c Rv0105c	rpmA rpmB	50S ribosomal protein L27 50S ribosomal protein L28
Rv1674		putative transcriptional regulator	2. Two cor	nponent s	vstems	Rv2058c	rpmB2	50S ribosomal protein L28
Rv1675		putative transcriptional regulator	Rv1028c	kdpD	sensor histidine kinase	Rv0709	rpmC	50S ribosomal protein L29
Rv1719	-	transcriptional regulator (IcIR	Rv1027c	kdpE	two-component response	Rv0722	rpmD	50S ribosomal protein L30
Du4770	in -	family)	Du2046*	mat v A	regulator	Rv1298	rpmE	50S ribosomal protein L31
Rv1773	·C -	transcriptional regulator (IcIR family)	Rv3246c	mtrA	two-component response regulator	Rv2057c Rv3924c	rpmG rpmH	50S ribosomal protein L33 50S ribosomal protein L34
Rv1776	ic -	putative transcriptional regulator	Rv3245c	mtrB	sensor histidine kinase	Rv1642	rpml	50S ribosomal protein L35
Rv1816	-	putative transcriptional regulator	Rv0844c	narL	two-component response	Rv3461c	ŕpmJ	50S ribosomal protein L36
Rv1846		putative transcriptional regulator	D. 0757	-6-0	regulator	Rv1630	rpsA	30S ribosomal protein S1
Rv1931	c -	transcriptional regulator (AraC/XyIS family)	Rv0757	phoP	two-component response regulator	Rv2890c Rv0707	rpsB rpsC	30S ribosomal protein S2 30S ribosomal protein S3
Rv1956	-	putative transcriptional regulator	Rv0758	phoR	sensor histidine kinase	Rv3458c	rpsD	30S ribosomal protein S4
Rv1963		putative transcriptional regulator	Rv0491	regX3	two-component response	Rv0721	rpsE	30S ribosomal protein S5
Rv1985	c -	transcriptional regulator (LysR	D 0400	1/0	regulator	Rv0053	rpsF	30S ribosomal protein S6
Rv1990	n -	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
Rv1994		transcriptional regulator (MerR	TWOODEO	10//-1	regulator	Rv3442c	rpsi	30S ribosomal protein S9
		family)	Rv0260c	-	two-component response	Rv0700	rpsJ	30S ribosomal protein S10
Rv2017	-	putative transcriptional regulator	D		regulator	Rv3459c	rpsK	30S ribosomal protein S11
Rv2021	0 -	(PbsX/Xre family) putative transcriptional regulator	Rv0600c Rv0601c	-	sensor histidine kinase sensor histidine kinase	Rv0682 Rv3460c	rpsL rpsM	30S ribosomal protein S12 30S ribosomal protein S13
Rv2034		transcriptional regulator (ArsR	Rv0818	-	two-component response	Rv0717	rpsN	30S ribosomal protein S14
		family)			regulator	Rv2056c	rpsN2	30S ribosomal protein S14
Rv2175		putative transcriptional regulator	Rv0845	-	sensor histidine kinase	Rv2785c	rpsO	30S ribosomal protein S15
Rv2250		putative transcriptional regulator	Rv0902c	-	sensor histidine kinase	Rv2909c	rpsP	30S ribosomal protein S16 30S ribosomal protein S17
Rv2258		putative transcriptional regulator transcriptional regulator (LysR	Rv0903c	•	two-component response regulator	Rv0710 Rv0055	rpsQ rpsR	30S ribosomal protein S17
	-	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	Rv0982	-	sensor histidine kinase	Rv2412	rpsT	30S ribosomal protein S20
Rv2358		(Lrp/AsnC family) transcriptional regulator (ArsR	Rv1032c Rv1033c	-	sensor histidine kinase two-component response	Rv3241c	-	member of S30AE ribosomal protein family
2500		family)			regulator			process controlly
Rv2488	c -	transcriptional regulator	Rv1626	-	two-component response			cation and maturation
D. 055		(LuxR/UhpA family)	D 00		regulator	Rv1010	ksgA	16S rRNA dimethyltransferase
Rv2506	-	transcriptional regulator (TetR/AcrR family)	Rv2027c Rv2884	-	sensor histidine kinase two-component response	Rv2838c Rv2907c	rbfA rimM	ribosome-binding factor A 16S rRNA processing protein
Rv2621	c -	putative transcriptional regulator	1 (1/2004		regulator	1145010	ininvi	.50 IT ITAL Processing protein
Rv2640	-	transcriptional regulator (ArsR	Rv3132c		sensor histidine kinase			synthases and their modification
D. co.		family)	Rv3133c	-	two-component response	Rv2555c	alaS	alanyl-tRNA synthase
Rv2642	-	transcriptional regulator (ArsR family)	Rv3143	_	regulator putative sensory transduction	Rv1292 Rv2572c	argS aspS	arginyl-tRNA synthase aspartyl-tRNA synthase
Rv2669		putative transcriptional regulator	1100140		protein	Rv3580c	cysS	cysteinyl-tRNA synthase
Rv2745		putative transcriptional regulator	Rv3220c	-	sensor histidine kinase	Rv2130c	cysS2	cysteinyl-tRNA synthase
Rv2779	·c -	transcriptional regulator		-	sensor histidine kinase	Rv1406	fmt	methionyl-tRNA formyltransferase
Byggoz		(Lrp/AsnC family)	Rv3765c	-	two-component response	Rv3011c	gatA	glu-tRNA-gln amidotransferase, subunit B
Rv2887	-	transcriptional regulator (MarR family)			regulator	Rv3009c	gatB	subunit B glu-tRNA-gln amidotransferase,
Rv2912	c -	transcriptional regulator	3. Serine-t	hreonine i	protein kinases and phosphoprotein		9-10	subunit A
		(TetR/AcrR family)	phosphata	ses		Rv3012c	gatC	glu-tRNA-gln amidotransferase,
Rv2989	-	transcriptional regulator (IcIR		pknA	serine-threonine protein kinase	D. 2227	40	subunit C
BUSINES	ic -	family)		pknB pknD	serine-threonine protein kinase	Rv2992c	gltS alvS	glutamyl-tRNA synthase
Rv3050 Rv3055		putative transcriptional regulator putative transcriptional regulator	Rv0931c Rv1743	pknD pknE	serine-threonine protein kinase serine-threonine protein kinase	Rv2357c Rv2580c	glyS hisS	glycyl-tRNA synthase histidyl-tRNA synthase
Rv3058		putative transcriptional regulator	Rv1746	pknE	serine-threonine protein kinase	Rv1536	ileS	isoleucyl-tRNA synthase
Rv3060		transcriptional regulator (GntR	Rv0410c	pknG	serine-threonine protein kinase	Rv0041	leuS	leucyl-tRNA synthase
D		family)	Rv1266c	pknH	serine-threonine protein kinase	Rv3598c	lysS	lysyl-tRNA synthase
		putative transcriptional regulator putative transcriptional regulator	Rv2914c Rv2088	pknl pknJ	serine-threonine protein kinase serine-threonine protein kinase	Rv1640c Rv1007c	lysX metS	C-term lysyl-tRNA synthase methionyl-tRNA synthase
Rv3066		pulative natiscriptional redutator	LIVEUOO	UNIIU	Schile-threoritie Diotetti Killase	11410076	111010	mounony runiva synthase
Rv3095 Rv3124		transcriptional regulator	Rv3080c	pknK	serine-threonine protein kinase	Rv1649	pheS	phenylalanyl-tRNA synthase α

Rv	/1650	pheT	phenylalanyl-tRNA synthase β	Rv2090	-	partially similar to DNA poly- merase I	2. DNA Rv0670	end	andanualassa IV (anurinasa)
Bv	/2845c	proS	subunit prolyl-tRNA synthase	Rv2191	_	similar to both PolC and UvrC	Rv1108c	xseA	endonuclease IV (apurinase) exonuclease VII large subunit
	/3834c	serS	seryl-tRNA synthase			proteins	Rv1107c	xseB	exonuclease VII small subunit
	/2614c	thrS	threonyl-tRNA synthase	Rv2464c	-	probable DNA glycosylase,	2 Duetaine	n antidaa	and altrapapantidas
HV	/2906c	trmD	tRNA (guanine-N1)-methyltrans- ferase	Rv3201c		endonuclease VIII probable ATP-dependent DNA	Rv3305c	, peptides amiA	and glycopeptides probable aminohydrolase
Rv	/3336c	trpS	tryptophanyl tRNA synthase			helicase	Rv3306c	amiB	probable aminohydrolase
	/1689	tyrS	tyrosyl-tRNA synthase	Rv3202c	-	similar to UvrD proteins	Rv3596c	clpC	ATP-dependent Clp protease
Hv	/2448c	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. 1	Nucleop	roteins		11100110		merase III	Rv2460c	clpP2	ATP-dependent Clp protease pro-
Rv	/1407	fmu	similar to Fmu protein			l le de			teolytic subunit
	/3852 /2986c	hns hupB	HU-histone protein DNA-binding protein II	6. Protein Rv0429c		and modification polypeptide deformylase	Rv2457c	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
	/1388	mIHF	integration host factor	Rv2534c	efp	elongation factor P	Rv2667	clpX'	similar to ClpC from <i>M. leprae</i> but
			_	Rv2882c	frr	ribosome recycling factor	_		shorter
			epair, recombination and restric-	Rv0684 Rv0120c	fusA fusA2	elongation factor G elongation factor G	Rv3419c Rv2725c	gcp hflX	glycoprotease
	n/modifi /1317c		DNA-3-methyladenine glycosi-	Rv1080c	greA	transcription elongation factor G	Rv1223	htrA	GTP-binding protein serine protease
110	/101/0	anot	dase II	Rv3462c	infA	initiation factor IF-1	Rv2861c	mapA1	methionine aminopeptidase
	/2836c	dinF	DNA-damage-inducible protein F	Rv2839c	infB	initiation factor IF-2	Rv0734	mapA2	probable methionine aminopepti-
	/1329c /3056	dinG dinP	probable ATP-dependent helicase DNA-damage-inducible protein	Rv1641 Rv0009	infC ppiA	initiation factor IF-3 peptidyl-prolyl cis-trans isomerase	Rv0319	рср	dase pyrrolidone-carboxylate peptidase
	1537	dinX	probable DNA-damage-inducible	Rv2582	рріВ	peptidyl-prolyl <i>cis-trans</i> isomerase	Rv0125	рерА	probable serine protease
			protein	Rv1299	prfA	peptide chain release factor 1	Rv2213	рерВ	aminopeptidase A/I
Rv	/0001	dnaA	chromosomal replication initiator	Rv3105c Rv2889c	prfB tsf	peptide chain release factor 2 elongation factor EF-Ts	Rv0800 Rv2467	pepC pepD	aminopeptidase I probable aminopeptidase
Bv	/0058	dnaB	protein DNA helicase (contains intein)	Rv0685	tuf	elongation factor EF-Tu	Rv2089c	pepE	cytoplasmic peptidase
Rv	/1547	dnaE1	DNA polymerase III, α subunit				Rv2535c	pepQ	cytoplasmic peptidase
	/3370c	dnaE2	DNA polymerase III α chain			NA modification and DNA	Rv2782c	pepR	protease/peptidase, M16 family
	/2343c /0002	dnaG dnaN	DNA primase DNA polymerase III, β subunit	transcripti Rv1253	on <i>deaD</i>	ATP-dependent DNA/RNA	Rv2109c	prcA	(insulinase) proteasome α-type subunit 1
	/3711c	dnaQ	DNA polymerase III € chain			helicase	Rv2110c	prcB	proteasome β-type subunit 2
	/3721c	dnaZX	DNA polymerase III, γ (dnaZ) and	Rv2783c	gpsl	pppGpp synthase and polyribo-	Rv0782	ptrBa	protease II, α subunit
D.,	/2924c	fpg	τ (dnaX) formamidopyrimidine-DNA glyco-	Rv2841c	nusA	nucleotide phosphorylase transcription termination factor	Rv0781 Rv0724	ptrBb sppA	protease II, β subunit protease IV, signal peptide pepti-
пν	129240	ıρy	svlase	Rv2533c	nusB	N-utilization substance protein B	1100724	σρρη	dase
Rv	/0006	gyrA	DNA gyrase subunit A	Rv0639	nusG	transcription antitermination	Rv0198c	-	probable zinc metalloprotease
	/0005	gyrB	DNA gyrase subunit B	D.:0007-		protein		-	probable peptidase
	/2092c /2101	helY helZ	probable helicase, Ski2 subfamily probable helicase, Shf2/Rad54	Rv3907c Rv3232c	pcnA pvdS	polynucleotide polymerase alternative sigma factor for	Rv0840c Rv0983	-	probable proline iminopeptidase probable serine protease
110	12101	Heiz	family	TIVOLOLO	pruc	siderophore production	Rv1977	-	probable zinc metallopeptidase
Rv	/2756c	hsdM	type I restriction/modification sys-	Rv3211	rhIE	probable ATP-dependent	Rv3668c	-	probable alkaline serine protease
п.,	.0755-	h = 101	tem DNA methylase	Rv1297	rho	RNA helicase transcription termination	Rv3671c Rv3883c	-	probable serine protease
HV	/2755c	hsdS'	type I restriction/modification sys- tem specificity determinant	N/1297	rho	factor rho		-	probable secreted protease protease
Rv	/3296	Ihr	ATP-dependent helicase	Rv3457c	rpoA	α subunit of RNA polymerase			
	/3014c	ligA	DNA ligase	Rv0667	rpoB	β subunit of RNA polymerase		charides, I	ipopolysaccharides and phospho-
	/3062 /3731	ligB ligC	DNA ligase probable DNA ligase	Rv0668 Rv1364c	rpoC rsbU	β' subunit of RNA polymerase SigB regulation protein	lipids Rv0062	celA	cellulase/endoglucanase
	/1020	mfd	transcription-repair coupling factor	Rv3287c	rsbW	anti-sigma B factor	Rv3915	cwlM	hydrolase
Rv	/2528c	mrr	restriction system protein	Rv2703	sigA	RNA polymerase sigma factor	Rv0315	-	probable β-1,3-glucanase
	/2985	mutT1	MutT homologue	Rv2710	sigB	(aka MysA, RpoV) RNA polymerase sigma factor	Rv1090	-	probable inactivated cellulase/endoglucanase
	/1160 /0413	mutT2 mutT3	MutT homologue MutT homologue	NV2710	siyo	(aka MysB)	Rv1327c	_	probable glycosyl hydrolase, α-
	/3589	mutY	probable DNA glycosylase	Rv2069	sigC	ECF subfamily sigma subunit			amylase family
	/3297	nei	probable endonuclease VIII	Rv3414c	sigD	ECF subfamily sigma subunit	Rv1333	-	probable hydrolase
	/3674c /1316c	nth ogt	probable endonuclease III methylated-DNA-protein-cysteine	Rv1221 Rv3286c	sigE sigF	ECF subfamily sigma subunit ECF subfamily sigma subunit	Rv3463 Rv3717	-	probable neuraminidase possible N-acetylmuramoyl-L-ala-
110	710100	ogi	methyltransferase	Rv0182c	sigG	sigma-70 factors ECF subfamily	11.07 17		nine amidase
	/1629	polA	DNA polymerase I	Rv3223c	sigH	ECF subfamily sigma subunit			
Rv	/1402	priA	putative primosomal protein n' (replication factor Y)	Rv1189 Rv3328c	sigl sigJ	ECF family sigma factor similar to Sigl, ECF family	5. Esterase Rv0220	es and lipa <i>lipC</i>	ases probable esterase
Bv	/3585	radA	probable DNA repair RadA homo-	Rv0445c	sigK	ECF-type sigma factor	Rv1923	lipD	probable esterase
			logue	Rv0735	sigL	sigma-70 factors ECF subfamily	Rv3775	lipE	probable hydrolase
	/2737c	recA	recombinase (contains intein)	Rv3911	sigM	probable sigma factor, similar to	Rv3487c	lipF	probable esterase
	/0630c /0631c	recB recC	exodeoxyribonuclease V exodeoxyribonuclease V	Rv3366	spoU	SigE probable rRNA methylase	Rv0646c Rv1399c	lipG lipH	probable hydrolase probable lipase
	/0629c	recD	exodeoxyribonuclease V	Rv3455c	truA	probable pseudouridylate syn-	Rv1400c	lipl	probable lipase
	/0003	recF	DNA replication and SOS induc-	D. 0700	A C	thase	Rv1900c	lipJ	probable esterase
D.,	/2973c	recG	tion ATP-dependent DNA helicase	Rv2793c Rv1644	truB tsnR	tRNA pseudouridine 55 synthase putative 23S rRNA methyltrans-	Rv2385 Rv1497	lipK lipL	probable acetyl-hydrolase esterase
	/1696	recN	recombination and DNA repair		10.11	ferase	Rv2284	lipM	probable esterase
	/3715c	recR	RecBC-Independent process of	Rv3649	-	ATP-dependent DNA/RNA heli-	Rv2970c	lipΝ	probable lipase/esterase
_	,0700	V	DNA repair			case	Rv1426c	lipO linD	probable esterase probable esterase
	/2736c /2593c	recX ruvA	regulatory protein for RecA Holliday junction binding protein,	8. Polysan	charides (cytoplasmic)	Rv2463 Rv2485c	lipP lipQ	probable esterase probable carboxlyesterase
110	0000	/ UVA	DNA helicase	Rv1326c	glgB `	1,4-α-glucan branching enzyme	Rv3084	lipR	probable acetyl-hydrolase
	/2592c	ruvB	Holliday junction binding protein	Rv1328	glgP	probable glycogen phosphory-	Rv3176c	lipS	probable esterase/lipase
Rv	/2594c	ruvC	Holliday junction resolvase, endo-	Rv1564c	glgX	lase probable glycogen debranching	Rv2045c Rv1076	lipT IipU	probable carboxylesterase probable esterase
Rv	0054	ssb	deoxyribonuclease single strand binding protein	11710040	9191	enzyme	Rv3203	lipV	probable esterase probable lipase
	/1210	tagA	DNA-3-methyladenine glycosi-	Rv1563c	glgY	putative α-amylase	Rv0217c	ĺρW	probable esterase
_	10646	tor A	dase I	Rv1562c	glgZ	maltooligosyltrehalose trehalohy- drolase	Rv2351c Rv2350c	plcA plcB	phospholipase C precursor phospholipase C precursor
	/3646c /2976c	topA ung	DNA topoisomerase uracil-DNA glycosylase	Rv0126	-	probable glycosyl hydrolase	Rv2350c Rv2349c	picB plcC	phospholipase C precursor phospholipase C precursor
	/1638	uvrA	excinuclease ABC subunit A	Rv1781c	-	probable 4-α-glucanotransferase	Rv1755c	plcD	partial CDS for phospholipase C
Rv	/1633	uvrB	excinuclease ABC subunit B	Rv2471	-	probable maltase α-glucosidase	Rv1104	-	probable esterase pseudogene
	/1420	uvrC	excinuclease ABC subunit C DNA-dependent ATPase I and	R Denrad	ation of m	acromolecules	Rv1105	-	probable esterase pseudogene
HV	/0949	uvrD	helicase II	1. RNA	anon or me	adioi i diedules	6. Aromatic	hydrocar	bons
Rv	/3198c	uvrD2	putative UvrD	Rv1014c		peptidyl-tRNA hydrolase		mhpE	probable 4-hydroxy-2-oxovalerate
Rv	/0427c	xthA	exodeoxyribonuclease III	Rv2925c	rnc	RNAse III	D::0010		aldolase
	/0071 /0861c	-	group II intron maturase probable DNA helicase	Rv2444c	rne	similar at C-term to ribo- nuclease E	Rv0316	-	probable muconolactone iso- merase
	/0944	-	possible formamidopyrimidine-	Rv2902c	rnhB	ribonuclease HII	Rv0771	-	probable 4-carboxymuconolac-
			DNA glycosylase	Rv3923c	rnpA	ribonuclease P protein compo-			tone decarboxylase
Rv	/1688	-	probable 3-methylpurine DNA	Rv1340	rphA	nent ribonuclease PH	Rv0939 Rv1723	-	probable dehydrase 6-aminohexanoate-dimer hydro-
			glycosylase	1171040	ipin		1141120		5 aminonoxanoate dimer hydro-

Rv2715	-	lase 2-hydroxymuconic semialdehyde	Rv1730c	-	probable penicillin binding protein probable penicillin binding protein	Rv1030	kdpB	potassium-transporting ATPase chain
Rv3530c	_	hydrolase probable <i>cis</i> -diol dehydrogenase	Rv1922 Rv2864c	-	probable penicillin binding protein probable penicillin binding protein	Rv1031	kdpC	potassium-transporting ATPase chain
Rv3534c	-	4-hydroxy-2-oxovalerate aldolase	Rv3330	-	probable penicillin binding protein	Rv3236c	kefB	probable glutathione-regulated
Rv3536c	-	aromatic hydrocarbon degrada- tion	Rv3627c		probable penicillin binding protein	Rv2877c	merT	potassium-efflux protein possible mercury resistance
C. Cell en	velope		4. Conserv Rv0402c	ed memb mmpL1	rane proteins conserved large membrane	Rv1811	mgtC	transport system probable magnesium transport
I. Lipopro	teins (<i>lppA</i>	A-lpr0) 65	Rv0507	mmpL2	protein conserved large membrane	Rv0362	mgtE	ATPase protein C putative magnesium ion
		narides, lipopolysaccharides, pro-		•	protein		-	transporter
eins and a Rv0806c	antigens <i>cpsY</i>	probable UDP-glucose-4-	Rv0206c	mmpL3	conserved large membrane protein	Rv2856 Rv0924c	nicT nramp	probable nickel transport proteir transmembrane protein belongir
Rv3811	csp	epimerase secreted protein	Rv0450c	mmpL4	conserved large membrane protein	Rv2691	trkA	to Nramp family probable potassium uptake pro-
Rv1677 Rv3794	dsbF embA	highly similar to C-term Mpt53 involved in arabinogalactan syn-	Rv0676c	mmpL5	conserved large membrane protein	Rv2692	trkB	tein probable potassium uptake pro-
		thesis	Rv1557	mmpL6	conserved large membrane			tein
Rv3795	embB	involved in arabinogalactan syn- thesis	Rv2942	mmpL7	protein conserved large membrane	Rv2287 Rv2723	yjcE -	probable Na+/H+ exchanger probable membrane protein,
Rv3793	embC	involved in arabinogalactan syn- thesis	Rv3823c	mmpL8	protein conserved large membrane	Rv3162c	-	tellurium resistance probable membrane protein
Rv3875 Rv0112	esat6 gca	early secretory antigen target probable GDP-mannose dehy-	Rv2339	mmpL9	protein conserved large membrane	Rv3237c	C	possible potassium channel protein
Rv0113	gmhA	dratase phosphoheptose isomerase	Rv1183	mmpL10	protein conserved large membrane	Rv3743c		probable cation-transporting ATPase
Rv2965c	kdtB	lipopolysaccharide core biosyn- thesis protein	Rv0202c		protein conserved large membrane	3. Carbobs	drates or	ganic acids and alcohols
Rv2878c	mpt53	secreted protein Mpt53			protein	Rv2443	dctA	C4-dicarboxylate transport prote
Rv1980c	mpt64	secreted immunogenic protein Mpb64/Mpt64	Rv1522c	·	conserved large membrane protein	Rv3476c Rv1902c	kgtP nanT	sugar transport protein 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 Rv0899	mpt83 ompA	surface lipoprotein Mpt83 member of OmpA family	Rv0506	mmpS2	conserved small membrane protein	Rv1237 Rv1238	sugB sugC	sugar transport protein ABC transporter component of
Rv3810	pirG	cell surface protein precursor (Erp	Rv2198c	mmpS3	conserved small membrane		-	sugar uptake system
Rv3782	rfbE	protein) similar to rhamnosyl transferase	Rv0451c	mmpS4	protein conserved small membrane	Rv3331 Rv2835c	sugl ugpA	probable sugar transport protein sn-glycerol-3-phosphate
Rv1302	rfe	undecaprenyl-phosphate α-N- acetylglucosaminyltransferase	Rv0677c	mmpS5	protein conserved small membrane	Rv2833c	ugpB	permease 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 transpo
Rv0954	-	cell envelope antigen involved in polysaccharide syn-	5. Other m	nembrane	proteins 211	Rv2834c		ATP-binding protein sn-glycerol-3-phosphate transpo
		thesis	III. Cell pr				ugpE	system protein
Rv1518	-	involved in exopolysaccharide synthesis	A. Transpo 1. Amino a		proteins	Rv2316 Rv2318	uspA uspC	sugar transport protein sugar transport protein
Rv1758	-	partial cutinase	Rv2127	ansP	L-asparagine permease	Rv2317	uspE	sugar transport protein
	-	probable secreted protein weak similarity to pollen antigens	Rv0346c	aroP2	probable aromatic amino acid permease	Rv1200 Rv2038c	-	probable sugar transporter probable ABC sugar transporter
Rv1984c	-	probable secreted protein	Rv0917	betP	glycine betaine transport	Rv2039c	-	probable sugar transporter
Rv1987 Rv2223c	-	probable secreted protein probable exported protease	Rv1704c	cycA	transport of D-alanine, D-serine and glycine	Rv2040c Rv2041c	-	probable sugar transporter probable sugar transporter
Rv2224c	-	probable exported protease	Rv3666c	dppA	probable peptide transport system			Propapie augai transporter
Rv2301 Rv2345	-	probable cutinase precursor of probable membrane	Rv3665c	dppB	permease probable peptide transport system	4. Anions Rv2684	arsA	probable arsenical pump
∃v2672	_	protein putative exported protease	Rv3664c	dppC	permease probable peptide transport system	Rv2685 Rv3578	arsB arsB2	probable arsenical pump probable arsenical pump
Rv3019c	(similar to Esat6			permease	Rv2643	arsC	probable arsenical pump
Rv3036c Rv3449	11	probable secreted protein probable precursor of serine pro-	Rv3663c Rv0522	dppD gabP	probable ABC-transporter probable 4-amino butyrate trans-	Rv2397c	cysA _	sulphate transport ATP-binding protein
Rv3451		tease probable cutinase	Rv0411c	glnH	porter putative glutamine binding protein	Rv2399c	cysT	sulphate transport system perme ase protein
Rv3452 Rv3724		probable cutinase precursor probable cutinase precursor	Rv2564	glnQ	probable ATP-binding transport	Rv2398c	cysW	sulphate transport system perme ase protein
	onnaul		Rv1280c	оррА	probable oligopeptide transport	Rv1857	modA modB	molybdate binding protein
Rv2911	dacB	and peptidoglycan penicillin binding protein	Rv1283c	оррВ	protein oligopeptide transport protein	Rv1858	modB	transport system permease, molybdate uptake
Rv2981c Rv3809c	ddlA glf	D-alanine-D-alanine ligase A UDP-galactopyranose mutase	Rv1282c	oppC	oligopeptide transport system per- mease	Rv1859	modC	molybdate uptake ABC- transporter
Rv1018c	glmU	UDP-N-acetylglucosamine pyrophosphorylase	Rv1281c Rv2320c	oppD rocE	probable peptide transport protein arginine/ornithine transporter	Rv1860	modD	precursor of Apa (45/47 kD secreted protein)
Rv3382c	lytB1	LytB protein homologue	Rv3253c	-	probable cationic amino acid	Rv2329c	narK1	probable nitrite extrusion protein
Rv1110	lytB2	very similar to LytB			transport	Rv1737c	narK2	nitrite extrusion protein
Rv1315	murA	UDP-N-acetylglucosamine-1-car- boxyvinyltransferase	Rv3454	-	possible proline permease	Rv0261c Rv0267	narK3 narU	nitrite extrusion protein similar to nitrite extrusion
Rv0482	murB	UDP-N-acetylenolpyruvoylglu- cosamine reductase	2. Cations Rv2920c	amt	putative ammonium transporter	Rv0934	phoS1	protein 2 PstS component of phosphate
Rv2152c	murC	UDP-N-acetyl-muramate-alanine ligase	Rv1607 Rv1239c	chaA	putative calcium/proton antiporter probable magnesium and cobalt		phoS2	uptake PstS component of phosphate
Rv2155c	murD	UDP-N-acetylmuramoylalanine-D-		corA	transport protein	Rv0928		uptake
Rv2158c	murE	glutamate ligase meso-diaminopimelate-adding	Rv0092 Rv0103c	ctpA ctpB	cation-transporting ATPase cation transport ATPase	Rv0820	phoT	phosphate transport system AB transporter
Rv2157c	murF	enzyme D-alanine:D-alanine-adding	Rv3270 Rv1469	ctpC ctpD	cation transport ATPase probable cadmium-transporting	Rv3301c	phoY1	phosphate transport system regulator
Rv2153c	murG	enzyme transferase in peptidoglycan syn-	Rv0908	ctpE	ATPase probable cation transport ATPase	Rv0821c	phoY2	phosphate transport system regulator
		thesis	Rv1997	ctpF	probable cation transport ATPase	Rv0545c	pitA	low-affinity inorganic phosphate
Rv1338 Rv2156c	murl murX	glutamate racemase phospho-N-acetylmuramoyl-	Rv1992c Rv0425c	ctpG ctpH	probable cation transport ATPase C-terminal region putative cation-	Rv2281	pitB	transporter phosphate permease
	nagA	petapeptide transferase N-acetylglucosamine-6-P-	Rv0107c	ctpl	transporting ATPase probable magnesium transport	Rv0930	pstA1	PstA component of phosphate uptake
Rv3332		deacetylase penicillin-binding protein	Rv0969	ctpV	ATPase cation transport ATPase	Rv0936	pstA2	PstA component of phosphate uptake
	nnna	pernount origing proteill				Rv0933	pstB	ABC transport component of
Rv0016c	pbpA pbpB	penicillin-binding protein 2	Rv3044	fecB	putative FellI-dicitrate transporter	1100000	PSID	Abo transport component or
Rv0016c Rv2163c Rv0050	pbpB ponA1	penicillin-bonding protein	Rv0265c	тесв fecB2	iron transport protein FeIII dici-			phosphate uptake
Rv3332 Rv0016c Rv2163c Rv0050 Rv3682 Rv0017c	pbpB					Rv0935	pstC	

		phosphate transport system			unit		-	part of <i>mce4</i> oper	
Rv0932c	pstS	PstS component of phosphate uptake	Rv1821	secA2	SecA, preprotein translocase sub- unit	Rv3501c Rv3896c	-	part of mce4 opera putative p60 homo	
Rv2400c Rv0143c	subl -	sulphate binding precursor probable chloride channel	Rv2587c Rv0638	secD secE	protein-export membrane protein SecE preprotein translocase	Rv3922c	-	possible hemolysii	ı ¯
Rv1707	-	probable sulphate permease	Rv2586c	secF	protein-export membrane protein			eated sequences, a	nd Phage
Rv1739c Rv3679	-	possible sulphate transporter possible anion transporter	Rv1440	secG	protein-export membrane protein SecG	1. IS elem IS <i>6110</i>	ents	16 copies	
Rv3680	-	probable anion transporter	Rv0732	secY	SecY subunit of preprotein translo- case	IS 1081 Others		6 copies 34 copies	
5. Fatty ac			Rv2462c	tig	chaperone protein, similar to		E 4 O 4 a maile	·	
Rv2790c Rv3540c	ltp1 ltp2	non-specific lipid transport protein non-specific lipid transport protein	Rv2813	-	trigger factor probable general secretion path-	2. REP 13	·	,	
6. Efflux p	roteins				way protein	3. Phage- Rv2894c		nctions integrase/recombir	nase
Rv2936	drrA	similar daunorubicin resistance ABC-transporter	E. Adapta Rv1901	tions and cinA	atypical conditions competence damage protein	Rv1701 Rv1054	xerD -	integrase/recombinintegrase-a	
Rv2937	drrB	similar daunorubicin resistance	Rv3648c	cspA	cold shock protein, transcriptional	Rv1055	-	integrase-b	. 1
Rv2938	drrC	transmembrane protein similar daunorubicin resistance	Rv0871	cspB	regulator probable cold shock protein	Rv1573 Rv1574	-	phiRV1 phage rela phiRV1 phage rela	
Rv2846c	efpA	transmembrane protein putative efflux protein	Rv3063	cstA	starvation-induced stress response protein	Rv1575 Rv1576c	-	phiRV1 phage rela phiRV1 phage rela	ted protein
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	
Rv1145 Rv1146	-	probable drug transporter probable drug transporter	Rv3372	otsB2	phatase trehalose-6-phosphate phos-	Rv1580c Rv1581c		phiRV1 phage rela phiRV1 phage rela	
Rv1250	-	probable drug efflux protein			phatase	Rv1582c		phiRV1 phage rela	ted protein
Rv1258c	-	probable multidrug resistance pump	Rv3758c Rv3757c	proV proW	osmoprotection ABC transporter transport system permease	Rv1583c Rv1584c		phiRV1 phage rela phiRV1 phage rela	
Rv1410c Rv1634	-	probable drug efflux protein probable drug efflux protein	Rv3759c Rv3756c	proX proZ	similar to osmoprotection proteins transport system permease	Rv1585c Rv1586c		phiRV1 phage rela phiRV1 integrase	ted protein
Rv1819c	-	probable multidrug resistance	Rv1026	-	probable pppGpp-5'phosphohydro-	Rv2309c	-	integrase	
Rv2136c	-	pump putative bacitracin resistance pro-			lase	Rv2310 Rv2646	-	excisionase phiRV2 integrase	
Rv2209	_	tein probable drug efflux protein	F. Detoxific Rv2428	cation ahpC	alkyl hydroperoxide reductase	Rv2647 Rv2650c	-	phiRV2 phage rela phiRV2 phage rela	
Rv2333c	-	probable tetracenomycin C resis- tance protein	Rv2429 Rv2238c	ahpD ahpE	member of AhpC/TSA family member of AhpC/TSA family	Rv2651c Rv2652c	-	phiRV2 prohead p phiRV2 phage rela	rotease
Rv2994	-	probable fluoroquinolone efflux	Rv2521	bcp	bacterioferritin comigratory protein	Rv2653c		phiRV2 phage rela	ted protein
Rv1877		protein probable drug efflux protein	Rv1608c	bcpB	probable bacterioferritin comigra- tory protein	Rv2654c Rv2655c	-	phiRV2 phage rela phiRV2 phage rela	
Rv2459	-	probable drug efflux protein	Rv3473c	bpoA	probable non-heme bromoperoxi- dase	Rv2656c Rv2657c	-	phiRV2 phage rela similar to gp36 of	
B. Chaper			Rv1123c	bpoB	probable non-heme bromoperoxi-			phage L5	
Rv0384c Rv0352	clpB dnaJ	heat shock protein acts with GrpE to stimulate DnaK	Rv0554	bpoC	dase probable non-heme bromoperoxi-	Rv2658c Rv2659c	-	phiRV2 phage rela phiRV2 integrase	
Rv2373c	dnaJ2	ATPase DnaJ homologue	Rv3617	ephA	dase probable epoxide hydrolase	Rv2830c Rv3750c	-	similar to phage P excisionase	1 phd gene
Rv0350	dnaK	70 kD heat shock protein, chromosome replication	Rv1938 Rv1124	ephB ephC	probable epoxide hydrolase probable epoxide hydrolase	Rv3751	-	putative integrase	
Rv3417c Rv0440	groEL1	60 kD chaperonin 1	Rv2214c	ephD ephE	probable epoxide hydrolase	C. PE and		ilies	
Rv3418c	groEL2 groES	60 kD chaperonin 2 10 kD chaperone	Rv3670 Rv0134	ephF	probable epoxide hydrolase probable epoxide hydrolase	PE subfar	nily	38 members	
Rv0351 Rv2374c	grpE hrcA	stimulates DnaK ATPase activity heat-inducible transcription	Rv3171c	hpx	probable non-heme haloperoxi- dase	PE_PGRS	subfamil	y 61 members	
Rv0251c	hsp	repressor possible heat shock protein	Rv1908c Rv3846	katG sodA	catalase-peroxidase superoxide dismutase	2. PPE far	nily	68 members	
Rv0353	hspR	heat shock regulator	Rv0432	sodC	superoxide dismutase precursor -	D. Antibio		tion and resistance	
Rv2031c	hspX	14kD antigen, heat shock protein Hsp20 family	Rv1932	tpx	(Cu-Zn) thiol peroxidase	Rv3290c	lat	class A β-lactama 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 puromycii	
Rv2701c	suhB	shock protein putative extragenic suppressor	Rv3177	-	probable non-heme haloperoxi- dase	Rv0262c		ferase aminoglycoside 2'-	-N-acetvltrans-
		protein	IV Other					ferase acetyltransferase	
Rv3269		probable heat shock protein	IV. Other A. Virulena			Rv0802c Rv1082	-	similar to S. lincolr	
C. Cell div Rv3641c	ision fic	possible cell division protein	Rv0169 Rv0589	mce1 mce2	cell invasion protein cell invasion protein	Rv1170 Rv1347c	-	similar to S. lincolr possible aminogly	
Rv3102c Rv3610c	ftsE ftsH	membrane protein	Rv1966 Rv3499c	mce3 mce4	cell invasion protein	Rv2036	_	acetyltransferase similar to lincomyo	
		chaperone	Rv3100c	smpB	probable small protein b			genes	·
Rv2748c Rv2151c	ftsK ftsQ	chromosome partitioning ingrowth of wall at septum	Rv1694 Rv0024	tiyA -	cytotoxin/hemolysin homologue putative p60 homologue	Rv2303c	-	similar to S. griseu resistance protein	
Rv2154c	ftsW	membrane protein (shape determi- nation)	Rv0167 Rv0168	-	part of <i>mce1</i> operon part of <i>mce1</i> operon		-	probable aminogly photransferases	coside 3'-phos-
Rv3101c Rv2921c	ftsX ftsY	membrane protein cell division protein FtsY	Rv0170 Rv0171	-	part of <i>mce1</i> operon	Rv3700c Rv3817	-	probable acetyltrai	
Rv2150c	ftsZ	circumferential ring, GTPase	Rv0172	-	part of <i>mce1</i> operon	11.0017		photransferase	555.40 O P1100
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. Bacteri	ocin-like p	roteins	3
Rv3917c	parA	chromosome partitioning; DNA - binding	Rv0588 Rv0590	-	part of <i>mce2</i> operon part of <i>mce2</i> operon	F. Cytochr	ome P450) enzvmes	22
Rv3918c	parB	possibly involved in chromosome partitioning	Rv0591 Rv0592	-	part of <i>mce2</i> operon part of <i>mce2</i> operon	-		-dependent	
Rv2922c	smc	member of Smc1/Cut3/Cut14	Rv0594	-	part of mce2 operon	enzyme		аэронаон	3
Rv0012	-	family possible cell division protein	Rv1085c Rv1477	-	possible hemolysin putative exported p60 protein	H. Miscell	aneous tra	ansferases	61
Rv0435c Rv2115c	-	ATPase of AAA-family ATPase of AAA-family	Rv1478	-	homologue putative exported p60 protein	I. Miscella	neous pho	osphatases, lyases,	
Rv3213c	-	possible role in chromosome seg- regation	Rv1566c	_	homologue putative exported p60 protein	and hydro		, 5,	18
Rv1708	-	possible role in chromosome parti-		-	homologue	J. Cyclase	es		6
		tioning	Rv1964 Rv1965	-	part of <i>mce3</i> operon part of <i>mce3</i> operon	K. Chelata	ases		2
D. Protein Rv2916c	and peption	de secretion signal recognition particle protein	Rv1967 Rv1968	-	part of <i>mce3</i> operon part of <i>mce3</i> operon	V. Conser		heticals	912
Rv2903c	lepB	signal peptidase I	Rv1969	-	part of mce3 operon				606
Rv1614	lgt .	prolipoprotein diacylglyceryl trans- ferase	Rv1971 Rv2190c	-	part of <i>mce3</i> operon putative p60 homologue	VI. Unkno	vv115		
Rv1539 Rv0379	lspA sec	lipoprotein signal peptidase probable transport protein	Rv3494c Rv3496c	-	part of <i>mce4</i> operon part of <i>mce4</i> operon	TOTAL			3924
Rv3240c	secA	SecE/Sec61- γ family SecA, preprotein translocase sub-	Rv3497c Rv3498c	-	part of <i>mce4</i> operon part of <i>mce4</i> operon				
32 700		- 13. ij p. sp. stom danoloodoo odo-			part of motor operation				

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

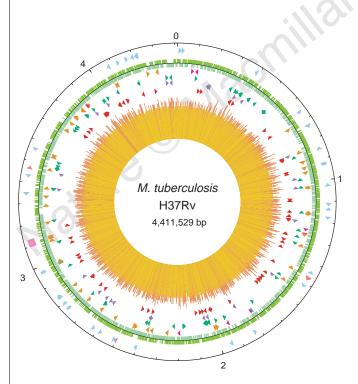


Figure 1 Circular map of the chromosome of M. tuberculosis H37Rv. The outer circle shows the scale in Mb, with 0 representing the origin of replication. The first ring from the exterior denotes the positions of stable RNA genes (tRNAs are blue, others are pink) and the direct repeat region (pink cube);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

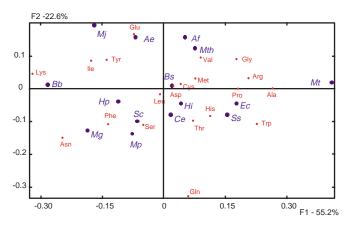


Figure 3 Correspondence analysis of the proteomes from extensively sequenced organisms as a function of amino-acid composition. Note the extreme position of *M. tuberculosis* and the shift in amino-acid preference reflecting increasing G + C content from left to right. Abbreviations used: Ae, Aquifex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

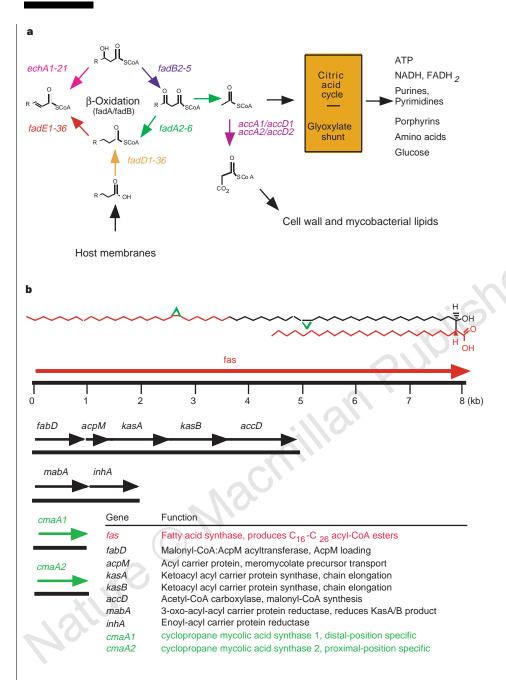
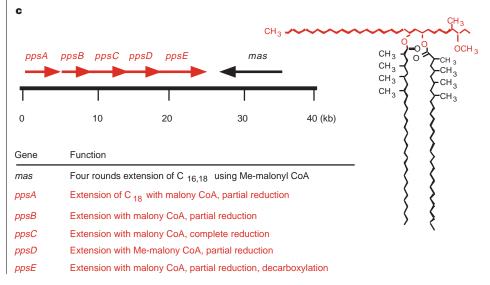


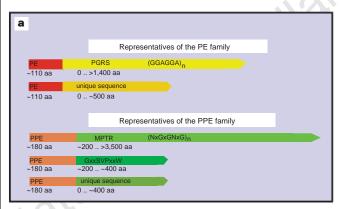
Figure 4 Lipid metabolism. a, Degradation of host-cell lipids is vital in the intracellular life of M. tuberculosis. Host-cell membranes provide precursors for many metabolic processes, as well as potential precursors of mycobacterial cell-wall constituents, through the actions of a broad family of β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



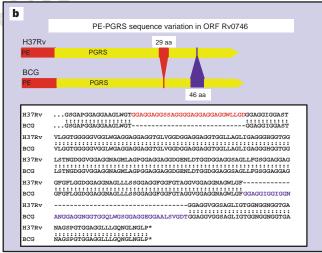


Figure 5 The PE and PPE protein families. **a**, Classification of the PE and PPE protein families. **b**, Sequence variation between *M. tuberculosis* H37Rv and *M. bovis* BCG-Pasteur in the PE-PGRS encoded by open reading frame (ORF) Rv0746.

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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Snider, D. E. Jr, Raviglione, M. & Kochi, A. in Tuberculosis: Pathogenesis, Protection, and Control (ed. Bloom, B. R.) 2–11 (Am. Soc. Microbiol., Washington DC, 1994).

Wheeler, P. R. & Ratledge, C. in Tuberculosis: Pathogenesis, Protection, and Control (ed. Bloom, B. R.) 353–385 (Am. Soc. Microbiol., Washington DC, 1994).

Chan, J. & Kaufmann, S. H. E. in Tuberculosis: Pathogenesis, Protection, and Control (ed. Bloom, B. R.) 271–284 (Am. Soc. Microbiol., Washington DC, 1994).

Brennan, P. J. & Draper, P. in Tuberculosis: Pathogenesis, Protection, and Control (ed. Bloom, B. R.) 271–284 (Am. Soc. Microbiol., Washington DC, 1994).

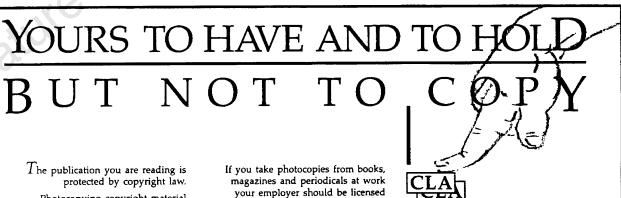
^{5.} Kolattukudy, P. E., Fernandes, N. D., Azad, A. K., Fitzmaurice, A. M. & Sirakova, T. D. Biochemistry

- and molecular genetics of cell-wall lipid biosynthesis in mycobacteria. Mol. Microbiol. 24, 263-270 (1997).
- Sreevatsan, S. et al. Restricted structural gene polymorphism in the Mycobacterium tuberculosis complex indicates evolutionarily recent global dissemination. Proc. Natl Acad. Sci. USA 94, 9869-
- $Brosch, R.\ et\ al.\ Use\ of\ a\ Mycobacterium\ tuberculos is\ H37Rv\ bacterial\ artificial\ chromosome\ library\ for\ bacterial\ bacte$ enome mapping, sequencing and comparative genomics. Infect. Immun. 66, 2221–2229 (1998).
- Philipp, W. J. et al. An integrated map of the genome of the tubercle bacillus, Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium leprae. Proc. Natl Acad. Sci. USA 93, 3132-
- Blattner, F. R. et al. The complete genome sequence of Escherichia coli K-12. Science 277, 1453-1462 (1997)
- 10. Cole, S. T. & Saint-Girons, I. Bacterial genomics. FEMS Microbiol. Rev. 14, 139-160 (1994).
- 11. Freiberg, C. et al. Molecular basis of symbiosis between Rhizobium and legumes. Nature 387, 394-401 (1997).
- 12. Bardarov, S. et al. Conditionally replicating mycobacteriophages: a system for transposon delivery to Mycobacterium tuberculosis. Proc. Natl Acad. Sci. USA 94, 10961-10966 (1997).
- 13. Mahairas, G. G., Sabo, P. J., Hickey, M. J., Singh, D. C. & Stover, C. K. Molecular analysis of genetic differences between Mycobacterium bovis BCG and virulent M. bovis. J. Bacteriol. 178, 1274-1282
- 14. Kunst, F. et al. The complete genome sequence of the gram-positive bacterium Bacillus subtilis. Nature 390, 249-256 (1997)
- 15. Smith, D. R. et al. Multiplex sequencing of 1.5 Mb of the Mycobacterium leprae genome. Genome Res. 7,802-819 (1997).
- Greenacre, M. Theory and Application of Correspondence Analysis (Academic, London, 1984).
- 17. Ratledge, C. R. in The Biology of the Mycobacteria (eds Ratledge, C. & Stanford, J.) 53-94 (Academic, San Diego, 1982).
- 18. Av-Gay, Y. & Davies, J. Components of eukaryotic-like protein signaling pathways in Mycobacterium tuberculosis. Microb. Comp. Genomics 2, 63-73 (1997).
- 19. Cole, S. T. & Telenti, A. Drug resistance in Mycobacterium tuberculosis. Eur. Resp. Rev. 8, 701S-713S (1995).
- 20. Riley, M. & Labedan, B. in Escherichia coli and Salmonella (ed. Neidhardt, F. C.) 2118-2202 (ASM, Washington, 1996).
- 21. Mdluli, K. et al. Inhibition of a Mycobacterium tuberculosis \(\beta \)-ketoacyl ACP synthase by isoniazid. Science 280, 1607-1610 (1998).
- Banerjee, A. et al. inhA, a gene encoding a target for isoniazid and ethionamide in Mycobacterium tuberculosis. Science 263, 227–230 (1994).
- 23. Hopwood, D. A. Genetic contributions to understanding polyketide synthases, Chem. Rev. 97, 2465-
- 24. Minnikin, D. E. in The Biology of the Mycobacteria (eds Ratledge, C. & Stanford, J.) 95-184 (Academic, London, 1982).
- 25. Barry, C. E. III et al. Mycolic acids: structure, biosynthesis, and phsyiological functions. Prog. Lipid
- Res. (in the press). 26. Belisle, J. T. et al. Role of the major antigen of Mycobacterium tuberculosis in cell wall biogenesis.
- Science 276, 1420-1422 (1997). 27. Marahiel, M. A., Stachelhaus, T. & Mootz, H. D. Modular peptide synthetases involved in
- nonribosomal peptide synthesis. Chem. Rev. 97, 2651–2673 (1997) 28. Gobin, J. et al. Iron acquisition by Mycobacterium tuberculosis: isolation and characterization of a
- family of iron-binding exochelins. Proc. Natl Acad. Sci. USA 92, 5189-5193 (1995) 29. Young, D. B. & Fruth, U. in New Generation Vaccines (eds Levine, M., Woodrow, G., Kaper, J. & Cobon,
- G. S.) 631-645 (Marcel Dekker, New York, 1997).
- 30. Sorensen, A. L., Nagai, S., Houen, G., Andersen, P. & Anderson, A. B. Purification and characterization of a low-molecular-mass T-cell antigen secreted by Mycobacterium tuberculosis. Infect. Immun. 63,

- 1710-1717 (1995).
- 31. Hermans, P. W. M., van Soolingen, D. & van Embden, J. D. A. Characterization of a major polymorphic tandem repeat in Mycobacterium tuberculosis and its potential use in the epidemiology of Mycobacterium kansasii and Mycobacterium gordonae. J. Bacteriol. 174, 4157-4165 (1992).
- 32. Poulet, S. & Cole, S. T. Characterisation of the polymorphic GC-rich repetitive sequence (PGRS) present in Mycobacterium tuberculosis. Arch. Microbiol. 163, 87-95 (1995)
- 33. Cole, S. T. & Barrell, B. G. in Genetics and Tuberculosis (eds Chadwick, D. J. & Cardew, G., Novartis Foundation Symp. 217) 160-172 (Wiley, Chichester, 1998).
- 34. Vega-Lopez, F. et al. Sequence and immunological characterization of a serine-rich antigen from Mycobacterium leprae. Infect. Immun. 61, 2145-2153 (1993).
- 35. Abou-Zeid, C. et al. Genetic and immunological analysis of Mycobacterium tuberculosis fibronectinbinding proteins. Infect. Immun. 59, 2712–2718 (1991).
- 36. Robertson, B. D. & Meyer, T. F. Genetic variation in pathogenic bacteria. Trends Genet. 8, 422-427 (1992).
- 37. Levitskaya, J. et al. Inhibition of antigen processing by the internal repeat region of the Epstein-Barr virus nuclear antigen-1. Nature 375, 685-688 (1995).
- 38. Levitskaya, J., Sharipo, A., Leonchiks, A., Ciechanover, A. & Masucci, M. G. Inhibition of ubiquitin/ proteasome-dependent protein degradation by the Gly-Ala repeat domain of the Epstein-Barr virus nuclear antigen 1. Proc. Natl Acad. Sci. USA 94, 12616-12621 (1997)
- 39. Flynn, J. L., Goldstein, M. A., Treibold, K. J., Koller, B. & Bloom, B. R. Major histocompatability complex class-I restricted T cells are required for resistance to Mycobacterium tuberculosis infection. Proc. Natl Acad. Sci. USA 89, 12013–12017 (1992).
- 40. Bloom, B. R. & Fine, P. E. M. in Tuberculosis: Pathogenesis, Protection, and Control (ed. Bloom, B. R.) 531-557 (Am. Soc. Microbiol., Washington DC, 1994).
- 41. Collins, D. M. In search of tuberculosis virulence genes. Trends Microbiol. 4, 426–430 (1996).
- 42. Arruda, S., Bomfim, G., Knights, R., Huima-Byron, T. & Riley, L. W. Cloning of an M. tuberculosis DNA fragment associated with entry and survival inside cells. Science 261, 1454-1457 (1993).
- 43. Baumler, A. J., Kusters, J. G., Stojikovic, I. & Heffron, F. Salmonella typhimurium loci involved in survival within macrophages. Infect. Immun. 62, 1623-1630 (1994).
- 44. McMurray, A. A., Sulston, J. E. & Quail, M. A. Short-insert libraries as a method of problem solving in genome sequencing. Genome Res. 8, 562-566 (1998).
- 45. Bonfield, J. K., Smith, K. F. & Staden, R. A new DNA sequence assembly program. Nucleic Acids Res. 24, 4992-4999 (1995).
- 46. Krogh, A., Mian, I. S. & Haussler, D. A hidden Markov model that finds genes in E. coli DNA. Nucleic Acids Res. 22, 4768-4778 (1994).
- 47. Bairoch, A., Bucher, P. & Hofmann, K. The PROSITE database, its status in 1997. Nucleic Acids Res. 25, 217-221 (1997).
- 48. Altschul, S., Gish, W., Miller, W., Myers, E. & Lipman, D. A basic local alignment search tool. J. Mol. Biol. 215, 403-410 (1990).
- 49. Pearson, W. & Lipman, D. Improved tools for biological sequence comparisons. Proc. Natl Acad. USA **85,** 2444–2448 (1988).
- 50. Lowe, T. M. & Eddy, S. R. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic DNA. Nucleic Acids Res. 25, 955-964 (1997).

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

		netabolism			superfamily	Rv3543c	fadE29	acyl-CoA dehydrogenase
A. Degrad		1-	Rv2831	echA16	enoyl-CoA hydratase/isomerase	Rv3560c	fadE30	acyl-CoA dehydrogenase
1. Carbon			Rv3039c	00h117	superfamily	Rv3562	fadE31 fadE32	acyl-CoA dehydrogenase acyl-CoA dehydrogenase
Rv0186 Rv2202c	bgIS cbhK	β-glucosidase carbohydrate kinase	KV30390	echA17	enoyl-CoA hydratase/isomerase superfamily	Rv3563 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-		00111110	superfamily, N-term	Rv3797	fadE35	acyl-CoA dehydrogenase
	3***	genase	Rv3374	echA18'	enoyl-CoA hydratase/isomerase	Rv3761c	fadE36	acyl-CoA dehydrogenase
Rv0234c	gabD2	succinate-semialdehyde dehydro-			superfamily, C-term	Rv1175c	fadH	2,4-Dienoyl-CoA Reductase
5 0504		genase	Rv3516	echA19	enoyl-CoA hydratase/isomerase	Rv0855	far	fatty acyl-CoA racemase
Rv0501 Rv0536	galE1 galE2	UDP-glucose 4-epimerase UDP-glucose 4-epimerase	Rv3550	echA20	superfamily enoyl-CoA hydratase/isomerase	Rv1143 Rv1492	mcr mutA	α-methyl acyl-CoA racemase methylmalonyl-CoA mutase, β
Rv0620	galK	galactokinase	1773330	CUIAZU	superfamily	111492	muuA	subunit
Rv0619	galT	galactose-1-phosphate uridylyl-	Rv3774	echA21	enoyl-CoA hydratase/isomerase	Rv1493	mutB	methylmalonyl-CoA mutase, α
	3 **	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-
D. 0000		transferase N-term	D. 0040	6-140	(acetyl-CoA C-acetyltransferase)	D. 0500		unit
Rv0993	galU	UTP-glucose-1-phosphate uridylyl- transferase	Rv0243 Rv1074c	fadA2 fadA3	acetyl-CoA C-acetyltransferase acetyl-CoA C-acetyltransferase	Rv2503c	scoB	3-oxo acid:CoA transferase, β sub- unit
Rv3696c	glpK	ATP:glycerol 3-phosphotrans-	Rv1323	fadA4	acetyl-CoA C-acetyltransferase	Rv1136	_	probable carnitine racemase
	3.7	ferase			(aka thiL)	Rv1683	-	possible acyl-CoA synthase
Rv3255c	manA	mannose-6-phosphate isomerase	Rv3546	fadA5	acetyl-CoA C-acetyltransferase			
Rv3441c	mrsA	phosphoglucomutase or phospho-	Rv3556c	fadA6	acetyl-CoA C-acetyltransferase	4. Phospho		
Rv0118c	oxcA	mannomutase oxalyl-CoA decarboxylase	Rv0860	fadB	β oxidation complex, α subunit (multiple activities)	Rv2368c	pnoH	ATP-binding <i>pho</i> regulon component
Rv3068c	pgmA	phosphoglucomutase	Rv0468	fadB2	3-hydroxyacyl-CoA dehydroge-	Rv1095	phoH2	PhoH-like protein
Rv3257c	pmmA	phosphomannomutase			nase	Rv3628	ppa	probable inorganic pyrophos-
Rv3308	pmmB	phosphomannomutase	Rv1715	fadB3	3-hydroxyacyl-CoA dehydroge-			phatase
Rv2702	ppgK	polyphosphate glucokinase	D. 0444	for JD 4	nase	Rv2984	ppk	polyphosphate kinase
Rv0408 Rv0729	pta xylB	phosphate acetyltransferase xylulose kinase	Rv3141	fadB4	3-hydroxyacyl-CoA dehydroge- nase	B. Energy	metaholisi	m
Rv1096	-	carbohydrate degrading enzyme	Rv1912c	fadB5	3-hydroxyacyl-CoA dehydroge-	1. Glycolys		"
		, , , , , , , , , , , , , , , , , , , ,			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 ald	ornithine/arginine decarboxylase	Rv3561	fadD3 fadD4	acyl-CoA synthase acyl-CoA synthase	Dv0490	anm	drogenase
Rv2780 Rv1538c	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
		dehydrogenase	Rv0551c	fadD8	acyl-CoA synthase	Rv1437	pgk	phosphoglycerate kinase
Rv0751c	mmsB	methylmalmonate semialdehyde	Rv2590	fadD9	acyl-CoA synthase	Rv1617	pykA	pyruvate kinase
Rv1187	rocA	oxidoreductase pyrroline-5-carboxylate dehydro-	Rv0099 Rv1550	fadD10 fadD11	acyl-CoA synthase acyl-CoA synthase, N-term	Rv1438 Rv2419c	tpi -	triosephosphate isomerase putative phosphoglycerate mutase
107	TOCA	genase	Rv1549	fadD11	acyl-CoA synthase, C-term	Rv3837c	-	putative phosphoglycerate mutase
Rv2322c	rocD1	ornithine aminotransferase	Rv1427c	fadD12	acyl-CoA synthase			7
Rv2321c	rocD2	ornithine aminotransferase	Rv3089	fadD13	acyl-CoA synthase	Pyruvate		
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	Dy22026	IndA	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	fadD17	acyl-CoA synthase	11124370	punn	ponent α subunit
Rv1852	ureG	urease accessory protein	Rv3515c	fadD19	acyl-CoA synthase	Rv2496c	pdhB	pyruvate dehydrogenase E1 com-
Rv2913c	-	probable D-amino acid	Rv1185c	fadD21	acyl-CoA synthase			ponent β subunit
		aminohydrolase	Rv2948c	fadD22	acyl-CoA synthase	Rv2495c		dihydrolipoamide acetyltransferase
Rv3551	-	possible glutaconate CoA-	Rv3826	fadD23	acyl-CoA synthase	Rv0462	-	probable dihydrolipoamide dehy-
		transferase	Rv1529 Rv1521	fadD24 fadD25	acyl-CoA synthase acyl-CoA synthase			drogenase
3. Fatty ac	cids		Rv2930	fadD26	acyl-CoA synthase	3. TCA cyc	:le	
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
D. 0500-		α subunit	Rv0404	fadD30	acyl-CoA synthase	Rv1098c	fum	fumarase
Rv2502c	accor	acetyl/propionyl-CoA carboxylase, β subunit	Rv1925 Rv3801c	fadD31 fadD32	acyl-CoA synthase acyl-CoA synthase	Rv1131 Rv0896	gltA1 gltA2	citrate synthase 3 citrate synthase 1
Rv0974c	accD2	acetyl/propionyl-CoA carboxylase,	Rv1345	fadD32	acyl-CoA synthase	Rv3339c	icd1	isocitrate dehydrogenase
1		β subunit	Rv0035	fadD34	acyl-CoA synthase		icd2	isocitrate dehydrogenase
Rv3667	acs	acetyl-CoA synthase	Rv2505c	fadD35	acyl-CoA synthase	Rv0794c	lpdB	dihydrolipoamide dehydrogenase
Rv3409c	choD	cholesterol oxidase	Rv1193	fadD36	acyl-CoA synthase	Rv1240	mdh	malate dehydrogenase
Rv0222	echA1	enoyl-CoA hydratase/isomerase	Rv0131c	fadE1	acyl-CoA dehydrogenase	Rv2967c	pca cdb/	pyruvate carboxylase
Rv0456c	echA2	superfamily enoyl-CoA hydratase/isomerase	Rv0154c Rv0215c	fadE2 fadE3	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv3318 Rv3319	sdhA sdhB	succinate dehydrogenase A succinate dehydrogenase B
	00/// 12	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 0070		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	Rv1248c	sucA	unit 2-oxoglutarate dehydrogenase
Rv0675	echA5	enoyl-CoA hydratase/isomerase	11/00/2	IauLo	acyl-CoA dehydrogenase (aka <i>aidB</i>)	Rv2215	sucA	dihydrolipoamide succinyltrans-
		superfamily	Rv0752c	fadE9	acyl-CoA dehydrogenase			ferase
Rv0905	echA6	enoyl-CoA hydratase/isomerase	Rv0873	fadE10	acyl-CoA dehydrogenase	Rv0951	sucC	succinyl-CoA synthase β chain
D. 0074		superfamily (aka eccH)	Rv0972c	fadE12	acyl-CoA dehydrogenase	Rv0952	sucD	succinyl-CoA synthase α chain
Rv0971c	echA7	enoyl-CoA hydratase/isomerase superfamily	Rv0975c Rv1346	fadE13 fadE14	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	4. Glyoxyla	ite hynass	
Rv1070c	echA8	enoyl-CoA hydratase/isomerase	Rv1467c	fadE15	acyl-CoA dehydrogenase	Rv0467	aceA	isocitrate lyase
		superfamily	Rv1679	fadE16	acyl-CoA dehydrogenase	Rv1915	aceAa	isocitrate lyase, α module
Rv1071c	echA9	enoyl-CoA hydratase/isomerase	Rv1934c	fadE17	acyl-CoA dehydrogenase	Rv1916	aceAb	isocitrate lyase, β module
Dv1140-	och 110	superfamily	Rv1933c	fadE18	acyl-CoA dehydrogenase	Rv1837c	glcB aph∆	malate synthase
Rv1142c	echA10	enoyl-CoA hydratase/isomerase superfamily	Rv2500c	fadE19	acyl-CoA dehydrogenase (aka mmgC)	Rv3323c	gphA	phosphoglycolate phosphatase
Rv1141c	echA11	enoyl-CoA hydratase/isomerase	Rv2724c	fadE20	acyl-CoA dehydrogenase	5. Pentose	phosphat	e pathway
		superfamily	Rv2789c	fadE21	acyl-CoA dehydrogenase	Rv1445c	devB	glucose-6-phosphate 1-dehydro-
Rv1472	echA12		Rv3061c	fadE22	acyl-CoA dehydrogenase	5 45		genase
Dv4005 -	00h 110	superfamily	Rv3140	fadE23	acyl-CoA dehydrogenase	Rv1844c	gnd	6-phosphogluconate dehydroge-
Rv1935c	echA13	enoyl-CoA hydratase/isomerase superfamily	Rv3139 Rv3274c	fadE24 fadE25	acyl-CoA dehydrogenase acyl-CoA dehydrogenase	Rv1122	gnd2	nase (Gram –) 6-phosphogluconate dehydroge-
Rv2486	echA14	enoyl-CoA hydratase/isomerase	Rv3504	fadE26	acyl-CoA dehydrogenase		3	nase (Gram +)
		superfamily	Rv3505	fadE27	acyl-CoA dehydrogenase	Rv1446c	opcA	unknown function, may aid
Rv2679	echA15	enoyl-CoA hydratase/isomerase	Rv3544c	fadE28	acyl-CoA dehydrogenase			G6PDH

Rv1448c Rv1449c	rbsK rpe rpi	ribokinase ribulose-phosphate 3-epimerase phosphopentose isomerase	Rv3250c 7. Miscella		rubredoxin B doreductases and oxygenases 171	Rv1878 Rv2860c Rv2918c	glnA3 glnA4 glnD	probable glutamine synthase proable glutamine synthase uridylyltransferase
	tal	transaldolase				Rv2221c	glnE	glutamate-ammonia-ligase
D 4404	tkt	transketolase	8. ATP-pro	oton motive	e force		-	adenyltransferase
Rv1121	zwf	glucose-6-phosphate 1-dehydro-	Rv1308	atpA	ATP synthase α chain	Rv3859c	gltB	ferredoxin-dependent glutamate
		genase	Rv1304	atpB	ATP synthase α chain			synthase
Rv1447c	zwf2	glucose-6-phosphate 1-dehydro-	Rv1311	atpC	ATP synthase ∈ chain	Rv3858c	gltD	small subunit of NADH-depende
		genase	Rv1310	atpD	ATP synthase β chain			glutamate synthase
			Rv1305	atpE	ATP synthase c chain	Rv3704c	gshA	possible γ-glutamylcysteine syn
Respirat	ion		Rv1306	atpF	ATP synthase b chain			thase
a. aerobic			Rv1309	atpG	ATP synthase γ chain	Rv2427c	proA	γ-glutamyl phosphate reductase
Rv0527	ccsA	cytochrome c-type biogenesis	Rv1307	atpH	ATP synthase δ chain	Rv2439c	proB	glutamate 5-kinase
	_	protein				Rv0500	proC	pyrroline-5-carboxylate reductas
Rv0529	ccsB	cytochrome c-type biogenesis			ary metabolism			
		protein	 Genera 			Asparta		
Rv1451	ctaB	cytochrome c oxidase assembly	Rv2589	gabT	4-aminobutyrate aminotransferase	Rv3708c	asd	aspartate semialdehyde dehydr
D. 0000		factor	Rv3432c	gadB	glutamate decarboxylase	D. 0700		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
Dv2102	oto E	peptide I	Rv2211c	gcvT	T protein of glycine cleavage	Rv3565	aspB	aspartate aminotransferase
Rv2193	ctaE	cytochrome c oxidase poly- peptide III	Rv1213	alaC	system glucose-1-phosphate adenylyl-	Rv0337c Rv2753c	aspC dapA	aspartate aminotransferase dihydrodipicolinate synthase
Rv1542c	qlbN	hemoglobin-like, oxygen carrier	IXVIZI3	glgC	transferase	Rv2773c	dapA dapB	dihydrodipicolinate syntiase dihydrodipicolinate reductase
Rv2470	glbO	hemoglobin-like, oxygen carrier	Rv3842c	glpQ1	glycerophosphoryl diester phos-	Rv1202	dapE dapE	succinyl-diaminopimelate desuc
Rv22470	glpD1	glycerol-3-phosphate dehydroge-	17730420	gipQ i	phodiesterase	111202	uapL	cinylase
11122430	gipD i	nase	Rv0317c	glpQ2	glycerophosphoryl diester phos-	Rv2141c	dapE2	ArgE/DapE/Acy1/Cpg2/yscS
Rv3302c	glpD2	glycerol-3-phosphate dehydroge-	1003176	gipaz	phodiesterase	17721410	uapLZ	family
11133020	gipDZ	nase	Rv3566c	nhoA	N-hydroxyarylamine <i>o</i> -acetyltrans-	Rv2726c	dapF	diaminopimelate epimerase
Rv0694	IIdD1	L-lactate dehydrogenase	1.400000	1110/1	ferase	Rv1293	lysA	diaminopimelate decarboxylase
		(cytochrome)	Rv0155	pntAA	pyridine transhydrogenase sub-	Rv3341	metA	homoserine <i>o</i> -acetyltransferase
Rv1872c	IIdD2	L-lactate dehydrogenase		P.10 17	unit α1	Rv1079	metB	cystathionine γ-synthase
Rv1854c	ndh	probable NADH dehydrogenase	Rv0156	pntAB	pyridine transhydrogenase sub-	Rv3340	metC	cystathionine β-lyase
Rv3145	nuoA	NADH dehydrogenase chain A		F	unit α2	Rv1133c	metE	5-methyltetrahydropteroyltrigluta
Rv3146	nuoB	NADH dehydrogenase chain B	Rv0157	pntB	pyridine transhydrogenase			mate-homocysteine methyltrans
Rv3147	nuoC	NADH dehydrogenase chain C		F	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		FF	dikinase			cysteine methyltransferase
Rv3150	nuoF	NADH dehydrogenase chain F				Rv1392	metK	S-adenosylmethionine synthase
Rv3151	nuoG	NADH dehydrogenase chain G	2. Glucon	eogenesis		Rv0391	metZ	o-succinylhomoserine sulfhy-
Rv3152	nuoH	NADH dehydrogenase chain H	Rv0211	pckA	phosphoenolpyruvate carboxy-			drylase
Rv3153	nuol	NADH dehydrogenase chain I		•	kinase	Rv1294	thrA	homoserine dehydrogenase
Rv3154	nuoJ	NADH dehydrogenase chain J	Rv0069c	sdaA	L-serine dehydratase 1	Rv1296	thrB	homoserine kinase
Rv3155	nuoK	NADH dehydrogenase chain K				Rv1295	thrC	homoserine synthase
Rv3156	nuoL	NADH dehydrogenase chain L	Sugar r	nucleotides				•
Rv3157	nuoM	NADH dehydrogenase chain M	Rv1512	epiA	nucleotide sugar epimerase	Serine f	amily	
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-
		cytB reductase			transferase			ferase
Rv2194	qcrC	cytochrome b/c component of	Rv3264c	rmIA2	glucose-1-phosphate thymidyl-	Rv2847c	cysG2	multifunctional enzyme, sirohen
		ubiQ-cytB reductase			transferase			synthase
			Rv3464	rmIB	dTDP-glucose 4,6-dehydratase	Rv2334	cysK	cysteine synthase A
b. anaerob			Rv3634c	rmIB2	dTDP-glucose 4,6-dehydratase	Rv1336	cysM	cysteine synthase B
Rv2392	cysH	3'-phosphoadenylylsulfate (PAPS)	Rv3468c	rmIB3	dTDP-glucose 4,6-dehydratase	Rv1077	cysM2	cystathionine β-synthase
		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
11123000		ductase	D		reductase	Rv2996c	serA	D-3-phosphoglycerate dehydro-
			Rv0322	udgA	UDP-glucose	D 0505	-	genase
Rv1552	frdA	fumarate reductase flavoprotein			dehydrogenase/GDP-mannose 6-	Rv0505c	serB	probable phosphoserine phos-
Rv1552		subunit						
	frdB	subunit fumarate reductase iron sulphur	D 0005		dehydrogenase	D 0010		phatase
Rv1552 Rv1553	frdB	subunit fumarate reductase iron sulphur protein	Rv3265c		dTDP-rhamnosyl transferase	Rv3042c	serB2	C-term similar to phosphoserine
Rv1552	frdB	subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor	Rv1525	wbbl2	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase			C-term similar to phosphoserine phosphatase
Rv1552 Rv1553 Rv1554	frdB frdC	subunit furmarate reductase iron sulphur protein furmarate reductase 15kD anchor protein			dTDP-rhamnosyl transferase	Rv3042c Rv0884c	serB2 serC	C-term similar to phosphoserine
Rv1552 Rv1553	frdB	subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein fumarate reductase 13kD anchor	Rv1525 Rv3400	wbbl2	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase	Rv0884c	serC	C-term similar to phosphoserine phosphatase phosphoserine aminotransferas
Rv1552 Rv1553 Rv1554 Rv1555	frdB frdC frdD	subunit furmarate reductase iron sulphur protein furmarate reductase 15kD anchor protein furmarate reductase 13kD anchor protein	Rv1525 Rv3400 4. Amino :	wbbl2 - sugars	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase	Rv0884c 4. Aromati	serC c amino a	C-term similar to phosphoserine phosphatase phosphoserine aminotransferas acid family
Rv1552 Rv1553 Rv1554 Rv1555 Rv1161	frdB frdC frdD narG	subunit furmarate reductase iron sulphur protein furmarate reductase 15kD anchor protein furmarate reductase 13kD anchor protein nitrate reductase α subunit	Rv1525 Rv3400	wbbl2 - sugars	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase	Rv0884c	serC	C-term similar to phosphoserine phosphatase phosphoserine aminotransferas cid family 3-phosphoshikimate
Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162	frdB frdC frdD narG narH	subunit furmarate reductase iron sulphur protein furmarate reductase 15kD anchor protein furmarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase β chain	Rv1525 Rv3400 4. Amino :	wbbl2 - sugars	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase	Rv0884c 4. Aromati Rv3227	serC c amino a aroA	C-term similar to phosphoserine phosphatase phosphoserine aminotransferas icid family 3-phosphoshikimate 1-carboxyvinyl transferase
Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1164	frdB frdC frdD narG narH narl	subunit furmarate reductase iron sulphur protein furmarate reductase 15kD anchor protein furmarate reductase 13kD anchor protein furmarate reductase α subunit nitrate reductase β chain nitrate reductase γ chain	Rv1525 Rv3400 4. Amino : Rv3436c	wbbl2 - sugars glmS	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase glucosamine-fructose-6-phosphate aminotransferase	Rv0884c 4. Aromati Rv3227 Rv2538c	serC c amino a aroA aroB	C-term similar to phosphosering phosphatase phosphoserine aminotransferas cid family 3-phosphoshikimate 1-carboxyvinyl transferase 3-dehydroquinate synthase
Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1164 Rv1163	frdB frdC frdD narG narH narI narJ	subunit furmarate reductase iron sulphur protein furmarate reductase 15kD anchor protein furmarate reductase 13kD anchor protein furmarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase β chain nitrate reductase β chain nitrate reductase δ chain	Rv1525 Rv3400 4. Amino : Rv3436c 5. Sulphui	wbbl2 - sugars glmS r metabolis	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase glucosamine-fructose-6-phosphate aminotransferase	Rv0884c 4. Aromati Rv3227 Rv2538c Rv2537c	serC c amino a aroA aroB aroD	C-term similar to phosphosering phosphatase phosphoserine aminotransferas acid family 3-phosphoshikimate 1-carboxyvinyl transferase 3-dehydroquinate synthase 3-dehydroquinate dehydratase
Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1164 Rv1163 Rv1736c	frdB frdC frdD narG narH narI narJ narX	subunit furmarate reductase iron sulphur protein furmarate reductase 15kD anchor protein furmarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase β chain nitrate reductase γ chain nitrate reductase δ chain fursed nitrate reductase	Rv1525 Rv3400 4. Amino : Rv3436c 5. Sulphur Rv0711	wbbl2 - sugars glmS r metabolis atsA	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase glucosamine-fructose-6-phosphate aminotransferase	Rv0884c 4. Aromati Rv3227 Rv2538c Rv2537c Rv2552c	serC c amino a aroA aroB aroD aroE	C-term similar to phosphosering phosphatase phosphoserine aminotransferasticid family a-phosphoshikimate 1-carboxyvinyl transferase 3-dehydroquinate synthase 3-dehydroquinate dehydratase shikimate 5-dehydrogenase
Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1164 Rv1163	frdB frdC frdD narG narH narI narJ	subunit furmarate reductase iron sulphur protein furmarate reductase 15kD anchor protein furmarate reductase 13kD anchor protein furmarate reductase α subunit nitrate reductase α subunit nitrate reductase β chain nitrate reductase β chain nitrate reductase β chain fused nitrate reductase probable nitrite reductase/sulphite	Rv1525 Rv3400 4. Amino : Rv3436c 5. Sulphur Rv0711 Rv3299c	wbbl2 - sugars glmS r metabolis atsA atsB	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase glucosamine-fructose-6-phosphate aminotransferase arrylsulfatase proable arrylsulfatase	Rv0884c 4. Aromati Rv3227 Rv2538c Rv2537c Rv2552c Rv2540c	serC c amino a aroA aroB aroD aroE aroF	C-term similar to phosphosering phosphatase phosphoserine aminotransferasticid family 3-phosphoshikimate 1-carboxyvinyl transferase 3-dehydroquinate synthase 3-dehydroquinate dehydratase shikimate 5-dehydrogenase chorismate synthase
Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1164 Rv1163 Rv1736c Rv2391	frdB frdC frdD narG narH narI narI narX nirA	subunit furmarate reductase iron sulphur protein furmarate reductase 15kD anchor protein furmarate reductase 13kD anchor protein furmarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase β chain nitrate reductase δ chain nitrate reductase δ chain fused nitrate reductase probable nitrite reductase/sulphite reductase/sulphite	Rv1525 Rv3400 4. Amino : Rv3436c 5. Sulphui Rv0711 Rv3299c Rv0663	wbbl2 - sugars glmS r metabolis atsA atsB atsD	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase glucosamine-fructose-6-phosphate aminotransferase arm arylsulfatase proable arylsulfatase proable arylsulfatase	Rv0884c 4. Aromati Rv3227 Rv2538c Rv2537c Rv2552c Rv2540c Rv2178c	serC c amino a aroA aroB aroD aroE aroF aroG	C-term similar to phosphoserine phosphatase phosphoserine aminotransferas toid family 3-phosphoshikimate 1-carboxyvinyl transferase 3-dehydroquinate synthase 3-dehydroquinate dehydratase shikimate 5-dehydrogenase chorismate synthase DAHP synthase
Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1163 Rv1736c Rv2391 Rv0252	frdB frdC frdD narG narH narI narJ narX nirA	subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein fumarate reductase 13kD anchor protein fumarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase β chain nitrate reductase γ chain nitrate reductase δ chain fused nitrate reductase probable nitrite reductase probable nitrite reductase nitrite reductase flavoprotein	8. Sulphur Rv3299c Rv3663 Rv3077	wbbl2 - sugars glmS r metabolis atsA atsB atsD atsF	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase glucosamine-fructose-6-phosphate aminotransferase sm arylsulfatase proable arylsulfatase proable arylsulfatase proable arylsulfatase proable arylsulfatase	Rv0884c 4. Aromati Rv3227 Rv2538c Rv2537c Rv2552c Rv2540c Rv2178c Rv2539c	serC c amino a aroA aroB aroD aroE aroF aroG aroK	C-term similar to phosphoserine phosphatase phosphoserine aminotransferas acid family 3-phosphoshikimate 1-carboxyvinyl transferase 3-dehydroquinate synthase 3-dehydroquinate dehydratase shikimate 5-dehydrogenase chorismate synthase DAHP synthase shikimate kinase I
Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1164 Rv1163 Rv1736c Rv2391	frdB frdC frdD narG narH narI narI narX nirA	subunit furmarate reductase iron sulphur protein furmarate reductase 15kD anchor protein furmarate reductase 13kD anchor protein furmarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase β chain nitrate reductase δ chain fused nitrate reductase δ chain fused nitrate reductase probable nitrite reductase probable nitrite reductase flavoprotein probable nitrite reductase small	Rv1525 Rv3400 4. Amino : Rv3436c 5. Sulphui Rv0711 Rv3299c Rv0663 Rv3077 Rv0296c	wbbl2 - sugars glmS r metabolis atsA atsB atsD atsF atsG	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase glucosamine-fructose-6-phosphate aminotransferase arylsulfatase proable arylsulfatase proable arylsulfatase proable arylsulfatase proable arylsulfatase proable arylsulfatase proable arylsulfatase	Rv0884c 4. Aromati Rv3227 Rv2538c Rv2537c Rv2552c Rv2540c Rv2178c Rv2539c Rv3838c	serC c amino a aroA aroB aroD aroE aroF aroG aroK pheA	C-term similar to phosphoserine phosphatase phosphoserine aminotransferas icid family 3-phosphoshikimate 1-carboxyvinyl transferase 3-dehydroquinate synthase 3-dehydroquinate dehydratase shikimate 5-dehydrogenase chorismate synthase DAHP synthase shikimate kinase I prephenate dehydratase
Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1163 Rv1736c Rv2391 Rv0252	frdB frdC frdD narG narH narI narJ narX nirA	subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein fumarate reductase 13kD anchor protein fumarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase β chain nitrate reductase γ chain nitrate reductase δ chain fused nitrate reductase probable nitrite reductase probable nitrite reductase nitrite reductase flavoprotein	Rv1525 Rv3400 4. Amino : Rv3436c 5. Sulphui Rv0711 Rv3299c Rv0663 Rv3077 Rv0296c Rv3796	wbbl2 - sugars glmS r metabolis atsA atsB atsD atsF atsG atsH	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase glucosamine-fructose-6-phosphate aminotransferase sm arylsulfatase proable arylsulfatase proable arylsulfatase proable arylsulfatase proable arylsulfatase proable arylsulfatase	Rv0884c 4. Aromati Rv3227 Rv2538c Rv2537c Rv2552c Rv2540c Rv2178c Rv2539c Rv3838c Rv1613	serC c amino a aroA aroB aroD aroE aroF aroG aroG aroK pheA trpA	C-term similar to phosphoserine phosphatase phosphoserine aminotransferas icid family 3-phosphoshikimate 1-carboxyvinyl transferase 3-dehydroquinate synthase 3-dehydroquinate dehydratase shikimate 5-dehydrogenase chorismate synthase DAHP synthase shikimate kinase I prephenate dehydratase tryptophan synthase α chain
Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1164 Rv1163 Rv1736c Rv2391 Rv0252 Rv0253	frdB frdC frdD narG narH narI narI narX nirA	subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein fumarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase β chain nitrate reductase γ chain nitrate reductase δ chain nitrate reductase δ chain nitrate reductase δ chain nitrate reductase δ chain nitrate reductase probable nitrite reductase/sulphite reductase nitrite reductase flavoprotein probable nitrite reductase small subunit	8v1525 Rv3400 4. Amino: Rv3436c 5. Sulphui Rv0711 Rv3299c Rv0663 Rv3077 Rv0296c Rv3796 Rv1285	wbbl2 - sugars glmS r metabolis atsA atsB atsD atsF atsG atsH cysD	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase glucosamine-fructose-6-phosphate aminotransferase sm arylsulfatase proable arylsulfatase proable arylsulfatase proable arylsulfatase proable arylsulfatase proable arylsulfatase proable arylsulfatase ATP:sulphurylase subunit 2	Rv0884c 4. Aromati Rv3227 Rv2538c Rv2537c Rv2552c Rv2540c Rv2178c Rv2539c Rv3838c Rv1613 Rv1612	serC c amino a aroA aroB aroD aroE aroF aroF aroK pheA trpA trpB	C-term similar to phosphosering phosphatase phosphoserine aminotransferas acid family 3-phosphoshikimate 1-carboxyvinyl transferase 3-dehydroquinate synthase 3-dehydroquinate dehydratase shikimate 5-dehydrogenase chorismate synthase DAHP synthase shikimate kinase I prephenate dehydratase tryptophan synthase α chain tryptophan synthase β chain
Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1164 Rv1163 Rv1736c Rv2391 Rv0252 Rv0253	frdB frdC frdD narG narH narI narX nirA nirB nirD	subunit furmarate reductase iron sulphur protein furmarate reductase 15kD anchor protein furmarate reductase 13kD anchor protein furmarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase β chain nitrate reductase β chain nitrate reductase δ chain fused nitrate reductase probable nitrite reductase probable nitrite reductase sulphite reductase flavoprotein probable nitrite reductase small subunit	8. Sulphul Rv0711 Rv3299c Rv0663 Rv3796 Rv1286 Rv1286 Rv1286	wbbl2 - sugars glmS r metabolis atsA atsB atsD atsF atsG atsH cysD cysN	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase glucosamine-fructose-6-phosphate aminotransferase arylsulfatase proable arylsulfatase ATP:sulphurylase subunit 2 ATP:sulphurylase subunit 1	Rv0884c 4. Aromati Rv3227 Rv2538c Rv2537c Rv2552c Rv2540c Rv2178c Rv2539c Rv3838c Rv1613	serC c amino a aroA aroB aroD aroE aroF aroG aroG aroK pheA trpA	C-term similar to phosphosering phosphatase phosphoserine aminotransferas icid family 3-phosphoshikimate 1-carboxyvinyl transferase 3-dehydroquinate synthase 3-dehydroquinate dehydratase shikimate 5-dehydrogenase chorismate synthase DAHP synthase shikimate kinase I prephenate dehydratase tryptophan synthase α chain tryptophan synthase β chain indole-3-glycerol phosphate
Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1163 Rv1736c Rv2391 Rv0252 Rv0253	frdB frdC frdD narG narH narI narZ nirA nirB nirD	subunit furmarate reductase iron sulphur protein furmarate reductase 15kD anchor protein furmarate reductase 13kD anchor protein furmarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase β chain nitrate reductase δ chain fused nitrate reductase δ chain fused nitrate reductase probable nitrite reductase probable nitrite reductase nitrite reductase small subunit	5. Sulphur Rv3436c 5. Sulphur Rv0711 Rv3299c Rv0663 Rv3077 Rv0296c Rv1285 Rv1286 Rv2131c	wbbl2 - sugars glmS r metabolis atsA atsB atsB atsF atsG atsH cysD cysN cysQ	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase glucosamine-fructose-6-phosphate aminotransferase sm arylsulfatase proable arylsulfatase proable arylsulfatase proable arylsulfatase proable arylsulfatase proable arylsulfatase proable arylsulfatase ATP:sulphurylase subunit 2 ATP:sulphurylase subunit 1 homologue of <i>M.leprae cysQ</i>	Rv0884c 4. Aromati Rv3227 Rv2538c Rv2537c Rv2552c Rv2540c Rv2178c Rv2539c Rv3838c Rv1613 Rv1612 Rv1611	serC c amino a aroA aroB aroD aroE aroF aroF aroK pheA trpA trpB trpC	C-term similar to phosphosering phosphatase phosphoserine aminotransferas icid family 3-phosphoshikimate 1-carboxyvinyl transferase 3-dehydroquinate synthase 3-dehydroquinate dehydratase shikimate 5-dehydrogenase chorismate synthase DAHP synthase shikimate kinase I prephenate dehydratase tryptophan synthase α chain tryptophan synthase α chain indole-3-glycerol phosphate synthase
Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1164 Rv1163 Rv1736c Rv2391 Rv0252 Rv0253	frdB frdC frdD narG narH narI narX nirA nirB nirD	subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein fumarate reductase 13kD anchor protein fumarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase β chain nitrate reductase γ chain nitrate reductase δ chain nitrate reductase δ chain fused nitrate reductase probable nitrite reductase probable nitrite reductase nitrite reductase flavoprotein probable nitrite reductase small subunit	Rv1525 Rv3400 4. Amino : Rv3436c 5. Sulphui Rv0711 Rv3299c Rv0663 Rv33796 Rv1285 Rv1285 Rv1286 Rv2131c Rv3248c	wbbl2 - sugars glmS r metabolis atsA atsB atsD atsF atsG atsH cysD cysN cysQ sahH	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase glucosamine-fructose-6-phosphate aminotransferase sm arylsulfatase proable arylsulfatase proable arylsulfatase proable arylsulfatase proable arylsulfatase proable arylsulfatase proable arylsulfatase ATP:sulphurylase subunit 2 ATP:sulphurylase subunit 1 homologue of M.leprae cysQ adenosylhomocysteinase	Rv0884c 4. Aromati Rv3227 Rv2538c Rv2537c Rv2552c Rv2540c Rv2178c Rv2539c Rv3838c Rv1613 Rv1612	serC c amino a aroA aroB aroD aroE aroF aroF aroK pheA trpA trpB	C-term similar to phosphosering phosphatase phosphoserine aminotransferas told family 3-phosphoshikimate 1-carboxyvinyl transferase 3-dehydroquinate synthase 3-dehydroquinate dehydratase shikimate 5-dehydrogenase chorismate synthase DAHP synthase shikimate kinase I prephenate dehydratase tryptophan synthase α chain tryptophan synthase α chain indole-3-glycerol phosphate synthase anthranilate phosphoribosyltran
Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1164 Rv1736c Rv2391 Rv0252 Rv0253 c. Electron Rv0409 Rv1623c	frdB frdC frdD narG narH narI narI narX nirA nirB nirD	subunit furmarate reductase iron sulphur protein furmarate reductase 15kD anchor protein furmarate reductase 13kD anchor protein furmarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase β chain nitrate reductase β chain nitrate reductase β chain fused nitrate reductase probable nitrite reductase probable nitrite reductase flavoprotein probable nitrite reductase small subunit	8. Rv1525 Rv3400 4. Amino : Rv3436c 5. Sulphui Rv0711 Rv3299c Rv0663 Rv3796 Rv2796 Rv2131c Rv2131c Rv3248c Rv3248c	wbbl2 - sugars glmS r metabolis atsA atsB atsC atsF atsG cysD cysQ sahH sseA	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase glucosamine-fructose-6-phosphate aminotransferase arylsulfatase proable arylsulfatase ATP:sulphurylase subunit 2 ATP:sulphurylase subunit 1 homologue of M.leprae cysQ adenosylhomocysteinase thiosulfate sulfurtransferase	Rv0884c 4. Aromati Rv3227 Rv2538c Rv2537c Rv2536c Rv2540c Rv2178c Rv2539c Rv3838c Rv1613 Rv1612 Rv1611 Rv2192c	serC c amino a aroA aroB aroD aroE aroF aroG aroK pheA trpA trpB trpC trpD	C-term similar to phosphoserin- phosphatase phosphoserine aminotransferas icid family 3-phosphoshikimate 1-carboxyvinyl transferase 3-dehydroquinate synthase 3-dehydroquinate dehydratase shikimate 5-dehydrogenase chorismate synthase DAHP synthase shikimate kinase I prephenate dehydratase tryptophan synthase α chain tryptophan synthase β chain indole-3-glycerol phosphate synthase anthranilate phosphoribosyltran ferase
Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1164 Rv1163 Rv1736c Rv2391 Rv0252 Rv0253 c. Electron Rv0409 Rv1623c	frdB frdC frdD narG narH narI narZ nirA nirB nirD	subunit furmarate reductase iron sulphur protein furmarate reductase 15kD anchor protein furmarate reductase 13kD anchor protein furmarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase β chain nitrate reductase γ chain nitrate reductase γ chain nitrate reductase γ chain fursed nitrate reductase probable nitrite reductase probable nitrite reductase nitrite reductase nitrite reductase sitrite reductase sitrite reductase small subunit acetate kinase cytochrome bd - l I oxidase subunit I cytochrome d ubiquinol oxidase	5. Sulphun Rv9711 Rv97211 Rv97219 Rv0663 Rv3796 Rv1285 Rv1286 Rv2131c Rv3248c Rv3283 Rv2291	wbbl2 - sugars glmS r metabolis atsA atsB atsD atsF atsG atsH cysD cysD cysD sahH sseA	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase glucosamine-fructose-6-phosphate aminotransferase sm arylsulfatase proable arylsulfatase proable arylsulfatase proable arylsulfatase proable arylsulfatase proable arylsulfatase proable arylsulfatase ATP:sulphurylase subunit 2 ATP:sulphurylase subunit 1 homologue of <i>M.leprae cysQ</i> adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase	Rv0884c 4. Aromati Rv3227 Rv2538c Rv2537c Rv2552c Rv2540c Rv2178c Rv2539c Rv3838c Rv1613 Rv1612 Rv1611	serC c amino a aroA aroB aroD aroE aroF aroF aroK pheA trpA trpB trpC	C-term similar to phosphosering phosphatase phosphoserine aminotransferas icid family 3-phosphoshikimate 1-carboxyvinyl transferase 3-dehydroquinate synthase 3-dehydroquinate dehydratase shikimate 5-dehydrogenase chorismate synthase DAHP synthase shikimate kinase I prephenate dehydratase tryptophan synthase α chain tryptophan synthase β chain indole-3-glycerol phosphate synthase anthranilate phosphoribosyltran ferase anthranilate synthase
Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1164 Rv1163 Rv1736c Rv2391 Rv0252 Rv0253 <i>c. Electron</i> Rv1623c Rv1623c	frdB frdC frdD narG narH narI narJ nirA nirB nirD transport aackA appC cydB	subunit furmarate reductase iron sulphur protein furmarate reductase 15kD anchor protein furmarate reductase 13kD anchor protein furmarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase β chain nitrate reductase γ chain nitrate reductase γ chain nitrate reductase β chain fused nitrate reductase probable nitrite reductase probable nitrite reductase nitrite reductase flavoprotein probable nitrite reductase small subunit accetate kinase cytochrome bd-II oxidase subunit I cytochrome d ubiquinol oxidase subunit II	Rv1525 Rv3400 4. Amino : Rv3436c 5. Sulphui Rv0711 Rv3299c Rv0663 Rv33796 Rv1285 Rv1286 Rv2131c Rv3248c Rv3283 Rv2291 Rv3118	wbbl2 - sugars glmS r metabolis atsA atsB atsD atsF atsG cysD cysN cysQ cysN sseA sseB sseC	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase glucosamine-fructose-6-phosphate aminotransferase sm arylsulfatase proable arylsulfatase ATP:sulphurylase subunit 2 ATP:sulphurylase subunit 1 homologue of M.leprae cysQ adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase	Rv0884c 4. Aromatir Rv3227 Rv2538c Rv2539c Rv2540c Rv2540c Rv2539c Rv36338c Rv1612 Rv1611 Rv2192c Rv1609	serC c amino a aroA aroB aroD aroE aroF aroG aroK pheA trpA trpB trpC trpD	C-term similar to phosphosering phosphatase phosphoserine aminotransferas told family 3-phosphoshikimate 1-carboxyvinyl transferase 3-dehydroquinate synthase 3-dehydroquinate dehydratase shikimate 5-dehydrogenase chorismate synthase DAHP synthase shikimate kinase I prephenate dehydratase tryptophan synthase α chain tryptophan synthase α chain indole-3-glycerol phosphate synthase anthranilate phosphoribosyltran ferase anthranilate synthase component I
Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1164 Rv1163 Rv1736c Rv2391 Rv0252 Rv0253 <i>c. Electron</i> Rv0409 Rv1623c Rv1622c Rv1622c	frdB frdC frdD narG narH narI narI narI narX nirA nirB nirD transport ackA appC cydB cydC	subunit furmarate reductase iron sulphur protein furmarate reductase 15kD anchor protein furmarate reductase 13kD anchor protein furmarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase β chain nitrate reductase β chain fused nitrate reductase β chain nitrate reductase β chain fused nitrate reductase probable nitrite reductase subunit reductase flavoprotein probable nitrite reductase small subunit accetate kinase cytochrome bd -II oxidase subunit II cytochrome d ubiquinol oxidase subunit II ABC transporter	8. Rv1525 Rv3400 4. Amino : Rv3436c 5. Sulphui Rv0711 Rv3299c Rv0663 Rv3296 Rv1285 Rv1286 Rv2131c Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c	wbbl2 - sugars glmS r metabolis atsA atsB atsD atsF atsG atsH cysD cysD cysD sahH sseA	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase glucosamine-fructose-6-phosphate aminotransferase arylsulfatase proable arylsulfatase troable arylsulfatase proable arylsulfatase troable arylsulfatase tribulphurylase subunit 2 ATP:sulphurylase subunit 1 homologue of M.leprae cysQ adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase	Rv0884c 4. Aromati Rv3227 Rv2538c Rv2537c Rv2536c Rv2540c Rv2178c Rv2539c Rv3838c Rv1613 Rv1612 Rv1611 Rv2192c	serC c amino a aroA aroB aroD aroE aroF aroG aroK pheA trpA trpB trpC trpD	C-term similar to phosphoserine phosphatase phosphoserine aminotransferas toid family 3-phosphoshikimate 1-carboxyvinyl transferase 3-dehydroquinate synthase 3-dehydroquinate dehydratase shikimate 5-dehydrogenase chorismate synthase DAHP synthase shikimate kinase I prephenate dehydratase tryptophan synthase β chain indole-3-glycerol phosphate synthase anthranilate phosphoribosyltran ferase anthranilate synthase component I anthranilate synthase
Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1163 Rv1736c Rv2391 Rv0252 Rv0253 <i>c. Electron</i> Rv0409 Rv1623c Rv1622c Rv1622c Rv1622c	frdB frdC frdD narG narH narI narJ narX nirA nirB nirD transport ackA appC cydB cydC cydD	subunit furmarate reductase iron sulphur protein furmarate reductase 15kD anchor protein furmarate reductase 13kD anchor protein furmarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase β chain nitrate reductase γ chain nitrate reductase γ chain nitrate reductase γ chain nitrate reductase probable nitrite reductase probable nitrite reductase nitrite reductase nitrite reductase nitrite reductase subunit reductase small subunit acetate kinase cytochrome bd-II oxidase subunit I cytochrome d ubiquinol oxidase subunit I ABC transporter ABC transporter	Rv1525 Rv3400 4. Amino : Rv3436c 5. Sulphui Rv0711 Rv3299c Rv0663 Rv33796 Rv1285 Rv1286 Rv2131c Rv3248c Rv3283 Rv2291 Rv3118	wbbl2 - sugars glmS r metabolis atsA atsB atsD atsF atsG cysD cysN cysQ cysN sseA sseB sseC	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase glucosamine-fructose-6-phosphate aminotransferase sm arylsulfatase proable arylsulfatase ATP:sulphurylase subunit 2 ATP:sulphurylase subunit 1 homologue of M.leprae cysQ adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase	Rv0884c 4. Aromati Rv3227 Rv2538c Rv2537c Rv2552c Rv2540c Rv2178c Rv2539c Rv3838c Rv1613 Rv1611 Rv2192c Rv1609 Rv2386c	serC c amino a aroA aroB aroB aroF aroF aroF aroG aroK pheA trpA trpB trpC trpD trpE	C-term similar to phosphoserine phosphatase phosphoserine aminotransferas icid family 3-phosphoshikimate 1-carboxyvinyl transferase 3-dehydroquinate synthase 3-dehydroquinate dehydratase shikimate 5-dehydrogenase chorismate synthase DAHP synthase shikimate kinase I prephenate dehydratase tryptophan synthase α chain tryptophan synthase α chain indole-3-glycerol phosphate synthase anthranilate phosphoribosyltran ferase anthranilate synthase component I anthranilate synthase component I anthranilate synthase component I anthranilate synthase component I
Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1164 Rv1163 Rv1736c Rv2391 Rv0252 Rv0253 <i>c. Electron</i> Rv0409 Rv1623c Rv1623c Rv1622c Rv1622c Rv1622c Rv1621c Rv1621c Rv1621c	frdB frdC frdD narG narH narI narJ nirA nirB nirD transport ackA appC cydB cydC cydD fdxA	subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein fumarate reductase 13kD anchor protein fumarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase β chain nitrate reductase probable nitrite reductase probable nitrite reductase subunit reductase small subunit accetate kinase cytochrome bd -II oxidase subunit II aBC transporter ABC transporter ferredoxin	Rv1525 Rv3400 4. Amino : Rv3436c 5. Sulphui Rv0711 Rv3299c Rv0663 Rv3796 Rv1285 Rv1286 Rv2131c Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c	wbbl2 - sugars glmS r metabolis atsA atsB atsD atsF atsG cysD cysN cysQ sahH sseA sseB sseC sseC2	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase glucosamine-fructose-6-phosphate aminotransferase sm arylsulfatase proable arylsulfatase ATP:sulphurylase subunit 2 ATP:sulphurylase subunit 1 homologue of M.leprae cysQ adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thosulfate sulfurtransferase	Rv0884c 4. Aromatir Rv3227 Rv2538c Rv2539c Rv2540c Rv2540c Rv2539c Rv36338c Rv1612 Rv1611 Rv2192c Rv1609	serC c amino a aroA aroB aroD aroE aroF aroG aroK pheA trpA trpB trpC trpD	C-term similar to phosphosering phosphatase phosphoserine aminotransferas icid family 3-phosphoshikimate 1-carboxyvinyl transferase 3-dehydroquinate synthase 3-dehydroquinate dehydratase shikimate 5-dehydrogenase chorismate synthase DAHP synthase shikimate kinase I prephenate dehydratase tryptophan synthase β chain indole-3-glycerol phosphate synthase anthranilate phosphoribosyltran ferase anthranilate synthase component I anthranilate synthase
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Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1164 Rv1163 Rv1736c Rv2391 Rv0252 Rv0253 C. Electron Rv0409 Rv1623c Rv1622c Rv1620c Rv1620c Rv1621c Rv1621c Rv2007c Rv3554	frdB frdC frdD narG narH narI narJ nirA nirB nirD transport aackA appC cydB cydC cydD fdxA fdxB fdxC fdxD	subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein fumarate reductase 13kD anchor protein fumarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase β chain nitrate reductase γ chain nitrate reductase γ chain nitrate reductase γ chain nitrate reductase γ chain nitrate reductase β chain fused nitrate reductase probable nitrite reductase probable nitrite reductase small subunit lacetate kinase cytochrome bd-II oxidase subunit I acetate kinase cytochrome bd-II oxidase subunit I ABC transporter ABC transporter ferredoxin ferredoxin ferredoxin ferredoxin ferredoxin lelectron transfer flavoprotein β subunit β su	Rv1525 Rv3400 4. Amino : Rv3436c 5. Sulphui Rv0711 Rv3299c Rv0663 Rv3796 Rv1285 Rv1286 Rv2131c Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c D. Amino 1. Glutam Rv1654 Rv1652	wbbl2 - sugars glmS r metabolis atsA atsB atsD atsF atsG cysD cysN cysQ sahH sseA sseB sseC sseC2 - acid biosy ate family argB argC argD	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase glucosamine-fructose-6-phosphate aminotransferase sm arylsulfatase proable arylsulfatase ATP:sulphurylase subunit 2 ATP:sulphurylase subunit 1 homologue of <i>M.leprae cysQ</i> adenosylhomocysteinase thiosulfate sulfurtransferase acetyl-γ-glutamyl-phosphate reductase acetyl-γ-glutamyl-phosphate reductase	Rv0884c 4. Aromating Rv3227 Rv2538c Rv2537c Rv2552c Rv2540c Rv2539c Rv3838c Rv1612 Rv1611 Rv2192c Rv1609 Rv2386c Rv3754 5. Histidin	serC c amino a aroA aroB aroB aroE aroF aroG aroK pheA trpA trpB trpC trpD trpE trpE2	C-term similar to phosphosering phosphatase phosphoserine aminotransferasicid family 3-phosphoshikimate 1-carboxyvinyl transferase 3-dehydroquinate synthase 3-dehydroquinate dehydratase shikimate 5-dehydrogenase chorismate synthase DAHP synthase shikimate kinase I prephenate dehydratase tryptophan synthase β chain indole-3-glycerol phosphate synthase anthranilate phosphoribosyltran ferase anthranilate synthase component I anthranilate synthase component I prephenate dehydrogenase
Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1164 Rv1163 Rv1736c Rv2391 Rv0252 Rv0253 C. Electron Rv0409 Rv1623c Rv1621c Rv1621c Rv1621c Rv1620c Rv1623c Rv1620c Rv3028c	frdB frdC frdD narG narH narI narI narI nirA nirB nirD transport ackA appC cydB cydC cydB fdxA fdxB fdxC fdxB fdxC fdxA fdxB fdxC fdxA fixB	subunit furmarate reductase iron sulphur protein furmarate reductase 15kD anchor protein furmarate reductase 13kD anchor protein furmarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase α subunit nitrate reductase β chain nitrate reductase β chain fused nitrate reductase β chain ristate reductase probable nitrite reductase probable nitrite reductase subunit reductase flavoprotein probable nitrite reductase small subunit accetate kinase cytochrome d -uliquinol oxidase subunit I cytochrome d -uliquinol oxidase subunit II ABC transporter ABC transporter ferredoxin ferredoxin ferredoxin ferredoxin ferredoxin electron transfer flavoprotein α subunit electron transfer flavoprotein α subunit	8. Rv1525 Rv3400 4. Amino : Rv3436c 5. Sulphui Rv0711 Rv3299c Rv0663 Rv1285 Rv1286 Rv2131c Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c D. Amino 1. Glutam Rv1654 Rv1655 Rv1655 Rv1656	wbbl2 - sugars glmS r metabolis atsA atsB atsD atsF atsG atsH cysD cysN cysQ sahH sseA sseB sseC - acid biosy, ate family argB argC argD argF	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase glucosamine-fructose-6-phosphate aminotransferase and arylsulfatase proable arylsulfatase ATP-sulphurylase subunit 2 ATP-sulphurylase subunit 1 homologue of M.leprae cysQ adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase probable alkyl sulfatase nthesis acetylglutamate kinase N-acetyl-γ-glutamyl-phosphate reductase acetylornithine aminotransferase ornithine carbamoyltransferase	Rv0884c 4. Aromatir Rv3227 Rv2538c Rv2537c Rv2536c Rv2178c Rv2539c Rv3838c Rv1613 Rv1611 Rv2192c Rv1609 Rv2386c Rv3754 5. Histidin Rv1603 Rv1601	serC c amino a aroA aroB aroB aroF aroF aroF aroF aroK pheA trpA trpA trpB trpC trpD trpE trpE tyrA a hisA	C-term similar to phosphoserine phosphatase phosphoserine aminotransferas toid family 3-phosphoshikimate 1-carboxyvinyl transferase 3-dehydroquinate synthase 3-dehydroquinate dehydratase shikimate 5-dehydrogenase chorismate synthase DAHP synthase shikimate kinase I prephenate dehydratase tryptophan synthase α chain tryptophan synthase β chain indole-3-glycerol phosphate synthase anthranilate phosphoribosyltran ferase anthranilate synthase component I anthranilate synthase component I prephenate dehydrogenase
Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1163 Rv1736c Rv2391 Rv0252 Rv0253 C. Electron Rv0409 Rv1623c Rv1623c Rv1621c Rv2007c Rv2057 Rv3503 Rv3503 Rv3503 Rv3503 Rv3503	frdB frdC frdD narG narH narI narJ narX nirA nirB nirD transport ackA appC cydB cydC cydD fdxA fdxB fdxC fdxD fixA	subunit furmarate reductase iron sulphur protein furmarate reductase 15kD anchor protein furmarate reductase 13kD anchor protein furmarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase β chain nitrate reductase β chain nitrate reductase β chain nitrate reductase β chain fursed nitrite reductase probable nitrite reductase probable nitrite reductase small subunit acetate kinase cytochrome bd-II oxidase subunit I acetate kinase cytochrome β -II oxidase subunit I ABC transporter ABC transporter ferredoxin ferredoxin ferredoxin ferredoxin ferredoxin electron transfer flavoprotein β subunit adrenodoxin and NADPH ferre-	Rv1525 Rv3400 4. Amino : Rv3436c 5. Sulphui Rv0711 Rv3299c Rv0663 Rv3077 Rv0296c Rv3796 Rv1285 Rv1285 Rv1285 Rv1284 Rv3248c Rv3248c Rv3248c Rv3248c Rv3762c D. Amino 1. Glutam Rv1654 Rv1655 Rv1655 Rv1656	wbbl2 - sugars glmS r metabolis atsA atsB atsC atsF atsG atsH cysD cysN cysQ sahH sseA sseC sseC2 - acid biosy; ate family argB argC argD argF argG	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase glucosamine-fructose-6-phosphate aminotransferase sm arylsulfatase proable arylsulfatase ATP:sulphurylase subunit 2 ATP:sulphurylase subunit 1 homologue of <i>M.leprae cysQ</i> adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thosulfate sulfurtransferase acetylglutamate kinase N-acetyl-γ-glutamyl-phosphate reductase acetylornithine aminotransferase arginosuccinate synthase	Rv0884c 4. Aromati Rv3227 Rv2538c Rv2537c Rv2552c Rv2540c Rv2539c Rv36333 Rv1612 Rv1611 Rv2192c Rv1609 Rv2386c Rv3754 5. Histidin Rv1603	serC c amino a aroA aroB aroB aroE aroF aroG aroK pheA trpB trpC trpD trpE trpE trpE2 tyrA e hisA	C-term similar to phosphoserine phosphatase phosphoserine aminotransferas phosphoserine aminotransferas deid family 3-phosphoshikimate 1-carboxyvinyl transferase 3-dehydroquinate synthase 3-dehydroquinate dehydratase shikimate 5-dehydrogenase chorismate synthase DAHP synthase shikimate kinase I prephenate dehydratase tryptophan synthase α chain tryptophan synthase β chain indole-3-glycerol phosphate synthase anthranilate phosphoribosyltran ferase anthranilate synthase component I anthranilate synthase component I prephenate dehydrogenase phosphoribosylformimino-5-aminoimidazole carboxamide ribonucleotide isomerase imidazole glycerol-phosphate dehydratase histidinol-phosphate aminotrans
Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1164 Rv1163 Rv1736c Rv2391 Rv0252 Rv0253 C. Electron Rv0409 Rv1623c Rv1623c Rv1621c Rv1620c Rv1621c Rv1620c Rv1621c Rv3554 Rv10207 Rv3554 Rv10203c Rv3029c Rv3028c Rv3028c	frdB frdC frdD narG narH narI narI narI nirA nirB nirD transport ackA appC cydB fdxA fdxB fdxC fdxD fixA fixB fprA	subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein fumarate reductase 13kD anchor protein fumarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase β chain nitrate reductase γ chain fused nitrate reductase probable nitrite reductase subunit reductase sitrate reductase small subunit acetate kinase cytochrome bd-II oxidase subunit I aBC transporter ABC transporter ABC transporter ferredoxin ferredoxin ferredoxin ferredoxin ferredoxin ferredoxin ferredoxin feredoxin feredoxin ferest flavoprotein β subunit lelectron transfer flavoprotein β subunit electron transfer flavoprotein α subunit adrenodoxin and NADPH ferredoxin reductase	Rv1525 Rv3400 4. Amino : Rv3436c 5. Sulphui Rv0711 Rv3299c Rv0663 Rv3296 Rv1285 Rv1286 Rv2131c Rv3248c Rv3283 Rv2291 Rv3118 Rv0814c Rv3762c D. Amino 1. Glutam Rv1654 Rv1655 Rv1656 Rv1658	wbbl2 - sugars glmS r metabolis atsA atsB atsD atsF atsG cysD cysN cysQ cysN cysQ sahH sseA sseB sseC sseC2 - acid biosy atst family argB argC argD argF argG argH	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase glucosamine-fructose-6-phosphate aminotransferase sim arylsulfatase proable arylsulfatase ATP:sulphurylase subunit 2 ATP:sulphurylase subunit 1 homologue of M.leprae cysQ adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase probable alkyl sulfatase nuthesis acetylglutamate kinase N-acetyl-γ-glutamyl-phosphate reductase acetylornithine aminotransferase ornithine carbamoyltransferase arginosuccinate synthase arginosuccinate synthase	Rv0884c 4. Aromatir Rv3227 Rv2538c Rv2537c Rv2552c Rv2540c Rv2578c Rv2539c Rv3838c Rv1613 Rv1612 Rv1601 Rv2192c Rv1609 Rv2386c Rv3754 5. Histidin Rv1603 Rv1601 Rv1600	serC c amino a aroA aroB aroD aroF aroF aroG aroF aroG trpA trpA trpB trpC trpE trpE2 tyrA hisB hisC	C-term similar to phosphoserine phosphatase phosphoserine aminotransferas icid family 3-phosphoshikimate 1-carboxyvinyl transferase 3-dehydroquinate synthase 3-dehydroquinate dehydratase shikimate 5-dehydrogenase chorismate synthase DAHP synthase shikimate kinase I prephenate dehydratase tryptophan synthase β chain indole-3-glycerol phosphate synthase anthranilate phosphoribosyltran ferase anthranilate synthase component I anthranilate synthase component I prephenate dehydrogenase phosphoribosylformimino-5-aminoimidazole carboxamide ribonucleotide isomerase imidazole glycerol-phosphate dehydratase histidinol-phosphate aminotransferase
Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1164 Rv1163 Rv1736c Rv2391 Rv0252 Rv0253 C. Electron Rv0409 Rv1623c Rv1621c Rv1621c Rv1621c Rv1620c Rv1623c Rv1620c Rv3028c	frdB frdC frdD narG narH narI narI narI nirA nirB nirD transport ackA appC cydB cydC cydB fdxA fdxB fdxC fdxD fixA fixB	subunit furmarate reductase iron sulphur protein furmarate reductase 15kD anchor protein furmarate reductase 13kD anchor protein furmarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase β chain nitrate reductase β chain nitrate reductase β chain nitrate reductase β chain fursed nitrite reductase probable nitrite reductase probable nitrite reductase small subunit acetate kinase cytochrome bd-II oxidase subunit I acetate kinase cytochrome β -II oxidase subunit I ABC transporter ABC transporter ferredoxin ferredoxin ferredoxin ferredoxin ferredoxin electron transfer flavoprotein β subunit adrenodoxin and NADPH ferre-	Rv1525 Rv3400 4. Amino : Rv3436c 5. Sulphui Rv0711 Rv3299c Rv0663 Rv3077 Rv0296c Rv3796 Rv1285 Rv1285 Rv1285 Rv1284 Rv3248c Rv3248c Rv3248c Rv3248c Rv3762c D. Amino 1. Glutam Rv1654 Rv1655 Rv1655 Rv1656	wbbl2 - sugars glmS r metabolis atsA atsB atsC atsF atsG atsH cysD cysN cysQ sahH sseA sseC sseC2 - acid biosy; ate family argB argC argD argF argG	dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase dTDP-rhamnosyl transferase probable β-phosphoglucomutase glucosamine-fructose-6-phosphate aminotransferase sm arylsulfatase proable arylsulfatase ATP:sulphurylase subunit 2 ATP:sulphurylase subunit 1 homologue of <i>M.leprae cysQ</i> adenosylhomocysteinase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thiosulfate sulfurtransferase thosulfate sulfurtransferase acetylglutamate kinase N-acetyl-γ-glutamyl-phosphate reductase acetylornithine aminotransferase arginosuccinate synthase	Rv0884c 4. Aromatir Rv3227 Rv2538c Rv2537c Rv2536c Rv2178c Rv2539c Rv3838c Rv1613 Rv1611 Rv2192c Rv1609 Rv2386c Rv3754 5. Histidin Rv1603 Rv1601	serC c amino a aroA aroB aroB aroF aroF aroF aroF aroK pheA trpA trpA trpB trpC trpD trpE trpE tyrA a hisA	C-term similar to phosphoserine phosphatase phosphoserine aminotransferas phosphoserine aminotransferas deid family 3-phosphoshikimate 1-carboxyvinyl transferase 3-dehydroquinate synthase 3-dehydroquinate dehydratase shikimate 5-dehydrogenase chorismate synthase DAHP synthase shikimate kinase I prephenate dehydratase tryptophan synthase α chain tryptophan synthase β chain indole-3-glycerol phosphate synthase anthranilate phosphoribosyltran ferase anthranilate synthase component I anthranilate synthase component I prephenate dehydrogenase phosphoribosylformimino-5-aminoimidazole carboxamide ribonucleotide isomerase imidazole glycerol-phosphate dehydratase 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		model	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. 0004		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
KV0114	-	Similar to hisb	Rv3752c	-	probable cytidine/deoxycytidylate	Rv2338c	тоеЫ	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
					sides and nucleotides	Rv3206c	moeZ	probably involved in
7. Branche			Rv3313c	add	probable adenosine deaminase	D. 000F		molybdopterin biosynthesis
Rv1559 Rv3003c	ilvA ilvB	threonine deaminase acetolactate synthase I large sub-	Rv2584c	apt	adenine phosphoribosyltrans- ferases	Rv0865	mog	molybdopterin biosynthesis
1000000	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. 2004+	h-4	phorylase	Rv3602c	panC	pantoate-β-alanine ligase
Rv2210c	ilvE	branched-chain-amino-acid transaminase	Rv3624c	hpt	probable hypoxanthine-guanine phosphoribosyltransferase	Rv3601c	panD	aspartate 1-decarboxylase
Rv1820	ilvG	acetolactate synthase II	Rv3393	iunH	probable inosine-uridine	6. Pyridoxi	ine	
Rv3002c	ilvN	acetolactate synthase I small sub-			preferring nucleoside hydrolase	Rv2607	pdxH	pyridoxamine 5'-phosphate
		unit	Rv0535	pnp	phosphorylase from Pnp/MtaP			oxidase
Rv3509c	ilvX	probable acetohydroxyacid syn-	B 0000		family 2			
Rv3710	<i>leuA</i>	thase I large subunit α-isopropyl malate synthase	Rv3309c	upp	uracil phophoribosyltransferase	7. Pyridine Rv1594	nucleotid nadA	guinolinate synthase
Rv2995c	leuB	3-isopropylmalate dehydrogenase	5 Miscella	neous nu	cleoside/nucleotide reactions	Rv1595	nadB	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
E. Polyam	sina auntha	ania.	Rv2344c	dgt	probable deoxyguanosine	8. Thiamin	•	
Rv2601	speE	spermidine synthase	Rv2404c	lepA	triphosphate hydrolase GTP-binding protein LepA	Rv0422c	e thiD	phosphomethylpyrimidine kinase
1112001	OPCL	Spormane Synthage	Rv2727c	miaA	tRNA δ(2)-isopentenylpyrophos-	Rv04226	thiE	thiamine synthesis, thiazole
		nes, nucleosides and nucleotides			phate transferase			moiety
		tide biosynthesis	Rv2445c	ndkA	nucleoside diphosphate kinase	Rv0417	thiG	thiamine synthesis, thiazole
Rv1389	gmk	putative guanylate kinase	Rv2440c	obg	Obg GTP-binding protein	D 00==		moiety
Rv3396c Rv1843c	guaA guaB1	GMP synthase inosine-5'-monophosphate dehy-	Rv2583c	relA	(p)ppGpp synthase I	Rv2977c	thiL	probable thiamine-monophos- phate kinase
17710430	yuab i	drogenase	G. Biosyni	hesis of a	ofactors, prosthetic groups and			priate Kiriase
Rv3411c	guaB2	inosine-5'-monophosphate dehy-	carriers		oraciore, presurene greape and	9. Riboflav	rin	
	Ü	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
D::4047a		drogenase	D. 4500	44.0	oxononanoate aminotransferase	Rv1412	ribC	riboflavin synthase α chain
Rv1017c	prsA	ribose-phosphate pyrophosphoki- nase	Rv1589 Rv1570	bioB bioD	biotin synthase dethiobiotin synthase	Rv2671 Rv2786c	ribD ribF	probable riboflavin deaminase 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	C-terminal similar to B. subtilis	Rv3300c	-	probable deaminase, riboflavin
D. 0770		succinocarboxamide synthase	D. 2070*	h:-A	BioF			synthesis
Rv0772	purD	phosphoribosylamine-glycine lig- ase	Rv3279c Rv1442	birA bisC	biotin apo-protein ligase biotin sulfoxide reductase	10 Thiore	doxin alut	taredoxin and mycothiol
Rv3275c	purE	phosphoribosylaminoimidazole	Rv0089	-	possible <i>bioC</i> biotin synthesis	Rv0773c	ggtA	putative γ-glutamyl transpeptidase
	, .	carboxylase			gene	Rv2394	ggtB	γ -glutamyltranspeptidase
Rv0808	purF	amidophosphoribosyltransferase-						precursor
Rv0957	purH	phosphoribosylaminoimidazole-	2. Folic ac			Rv2855	gorA	glutathione reductase homologue
Rv3276c	nurk	carboxamide formyltransferase phosphoribosylaminoimidazole	Rv2763c	dfrA folC	dihydrofolate reductase	Rv0816c Rv1470	thiX	equivalent to <i>M. leprae</i> ThiX thioredoxin
100	purK	carboxylase ATPase subunit	Rv2447c Rv3356c	folD	folylpolyglutamate synthase methylenetetrahydrofolate dehy-	Rv1470	trxA trxB	thioredoxin reductase
Rv0803	purL	phosphoribosylformylglycin-		10.2	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			
Rv0956	purN	zole synthase phosphoribosylglycinamide	Rv3608c	folP	pyrophosphokinase dihydropteroate synthase	 Menacterpenoids 		QQ, ubiquinone and other
KV0956	punv	formyltransferase I	Rv1207	folP2	dihydropteroate synthase	Rv2682c		1-deoxy-D-xylulose 5-phosphate
Rv0788	purQ	phosphoribosylformylglycin-	Rv3607c	folX	may be involved in folate biosyn-		ano	synthase
		amidine synthase I			thesis	Rv0562	grcC1	heptaprenyl diphosphate
Rv0389	purT	phosphoribosylglycinamide	Rv0013	pabA	p-aminobenzoate synthase gluta-	D	0-	synthase II
Rv2964	purU	formyltransferase II formyltetrahydrofolate deformy-	Rv1005c	pabB	mine amidotransferase p-aminobenzoate synthase	Rv0989c	grcC2	heptaprenyl diphosphate synthase II
KV2904	puro	lase	Rv10050	равв равС	aminodeoxychorismate lyase	Rv3398c	idsA	geranylgeranyl pyrophosphate
				P400			,33/1	synthase
Pyrimid	ine ribonu	cleotide biosynthesis	3. Lipoate			Rv2173	idsA2	geranylgeranyl pyrophosphate
Rv1383	carA	carbamoyl-phosphate synthase	Rv2218	<i>lipA</i>	lipoate biosynthesis protein A			synthase
D 4004	-	subunit	Rv2217	lipB	lipoate biosynthesis protein B	Rv3383c	idsB	transfergeranyl, similar geranyl
Rv1384	carB	carbamoyl-phosphate synthase	4 Mohiba	ntorin		Rv0534c	man A	pyrophosphate synthase
Rv1380	pyrB	subunit aspartate carbamoyltransferase	4. Molybdo Rv3109	moaA	molybdenum cofactor biosynthe-	111000340	menA	4-dihydroxy-2-naphthoate octaprenyltransferase
Rv1381	pyrC	dihydroorotase		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	sis, protein A	Rv0548c	menB	naphthoate synthase
Rv2139	pyrD	dihydroorotate dehydrogenase	Rv0869c	moaA2	molybdenum cofactor biosynthe-	Rv0553	menC	o-succinylbenzoate-CoA synthase
Rv1385	pyrF	orotidine 5'-phosphate decarboxy-	D. (0.400		sis, protein A	Rv0555	menD	2-succinyl-6-hydroxy-2,4-cyclo-
D.:4000		lase	Rv0438c	moaA3	molybdenum cofactor biosynthe-	D. 0540+		hexadiene-1-carboxylate synthase
Rv1699 Rv2883c	pyrG pyrH	CTP synthase uridylate kinase	Rv3110	moaB	sis, protein A molybdenum cofactor biosynthe-	Rv0542c Rv3853	menE menG	o-succinylbenzoic acid-CoA ligase S-adenosylmethionine:
Rv0382c	итрА	probable uridine 5'-monophos-		וווטמט	sis, protein B	1110000	mand	2-demethylmenaquinone
		phate synthase	Rv0984	moaB2	molybdenum cofactor biosynthe-	Rv3397c	phyA	phytoene synthase
					sis, protein B	Rv0693	pqqE	coenzyme PQQ synthesis
		otide metabolism	Rv3111	moaC	molybdenum cofactor biosynthe-	D. 0550		protein E
Rv0321	dcd	deoxycytidine triphosphate deaminase	Rv0864	moaC2	sis, protein C molybdenum cofactor biosynthe-	Rv0558	ubiE	ubiquinone/menaquinone biosyn- thesis methyltransferase
Rv2697c	dut	deaminase deoxyuridine triphosphatase	1110004	1110a02	sis, protein C			uloolo illeutyillaitoitiast
Rv0233	nrdB	ribonucleoside-diphosphate	Rv3324c	moaC3	molybdenum cofactor biosynthe-	12. Heme	and porph	nyrin
		reductase B2 (eukaryotic-like)			sis, protein C	Rv0509	hemA	glutamyl-tRNA reductase
Rv3051c				_			t D	Some for a large of the form of the depth of the color of
	nrdE	ribonucleoside diphosphate	Rv3112	moaD	molybdopterin converting factor	Rv0512	hemB	δ-aminolevulinic acid dehydratase
Rv1981c	nrdE nrdF	ribonucleoside diphosphate reductase α chain ribonucleotide reductase small	Rv3112 Rv0868c	moaD moaD2	molybdopterin converting factor subunit 1 molybdopterin converting factor	Rv0512 Rv0510 Rv2678c	nemB hemC hemE	porphobilinogen deaminase uroporphyrinogen decarboxylase

Rv1300	hemK	protoporphyrinogen oxidase	Rv0470c	umaA2	unknown mycolic acid methyl-	Rv2931	ppsA	phenolpthiocerol synthesis (pksB)
Rv0524	hemL	glutamate-1-semialdehyde amino-			transferase	Rv2932	ppsB	phenolpthiocerol synthesis (pksC)
Rv2388c	hemN	transferase	2 A a college		an in a law through a const	Rv2933	ppsC	phenolpthiocerol synthesis (pksD)
IXV2300C	Hellin	oxygen-independent copropor- phyrinogen III oxidase		pid synthe	mycoloyltransferases and	Rv2934 Rv2935	ppsD ppsE	phenolpthiocerol synthesis (<i>pksE</i>) phenolpthiocerol synthesis (<i>pksF</i>)
Rv2677c	hemY'	protoporphyrinogen oxidase	Rv2289	cdh	CDP-diacylglycerol phosphatidyl-	Rv2928	tesA	thioesterase
Rv1485	hemZ	ferrochelatase			hydrolase	Rv1544	-	probable ketoacyl reductase
40.0-1-1			Rv2881c		phosphatidate cytidylyltransferase	1.0		6
13. Cobala Rv2849c	amın <i>cobA</i>	cob(I)alamin adenosyltransferase	Rv3804c Rv1886c	fbpA fbpB	antigen 85A, mycolyltransferase antigen 85B, mycolyltransferase		<i>egulatory i</i> sors/activa	
Rv2848c	cobB	cobyrinic acid a,c-diamide	Rv3803c	тыры fbpC1	antigen 85C, mycolyltransferase	Rv1657	argR	arginine repressor
11120-100	0000	synthase	Rv0129c	fbpC2	antigen 85C', mycolytransferase	Rv1267c	embR	regulator of <i>embAB</i> genes
Rv2231c	cobC	aminotransferase	Rv0564c	gpdA1	glycerol-3-phosphate dehydroge-			(AfsR/DndI/RedD family)
Rv2236c	cobD	cobinamide synthase		•	nase	Rv1909c	furA	ferric uptake regulatory protein
Rv2064	cobG	percorrin reductase	Rv2982c	gpdA2	glycerol-3-phosphate dehydroge-	Rv2359	furB	ferric uptake regulatory protein
Rv2065	cobH	precorrin isomerase	D.:0040a	A	nase	Rv2919c	glnB	nitrogen regulatory protein
Rv2066 Rv2070c	cobl cobK	Cobl-CobJ fusion protein precorrin reductase	Rv2612c	pgsA	CDP-diacylglycerol-glycerol-3- phosphate phosphatidyltrans-	Rv2711 Rv2720	ideR IexA	iron dependent repressor, IdeR LexA, SOS repressor protein
Rv2070c	cobL	probable methyltransferase			ferase	Rv1479	moxR	transcriptional regulator, MoxR
Rv2071c	cobM	precorrin-3 methylase	Rv1822	pgsA2	CDP-diacylglycerol-glycerol-3-		,,,,,,,,,	homologue
Rv2062c	cobN	cobalt insertion		, 0	phosphate phosphatidyltrans-	Rv3692	moxR2	transcriptional regulator, MoxR
Rv2208	cobS	cobalamin (5'-phosphate)			ferase			homologue
D. 2207	bT	synthase	Rv2746c	pgsA3	CDP-diacylglycerol-glycerol-3-	Rv3164c	moxR3	transcriptional regulator, MoxR
Rv2207	cobT	nicotinate-nucleotide-dimethyl- benzimidazole transferase			phosphate phosphatidyltrans- ferase	Rv0212c	nadR	homologue similar to <i>E.coli</i> NadR
Rv0254c	cobU	cobinamide kinase	Rv1551	plsB1	glycerol-3-phosphate acyltrans-	Rv0117	oxyS	transcriptional regulator (LysR
Rv0255c	cobQ	cobyric acid synthase		p	ferase		,-	family)
Rv3713	cobQ2	possible cobyric acid synthase	Rv2482c	plsB2	glycerol-3-phosphate acyltrans-	Rv1379	pyrR	regulatory protein pyrimidine
Rv0306	-	similar to BluB cobalamin synthe-			ferase			biosynthesis
		sis protein R. capsulatus	Rv0437c	psd	putative phosphatidylserine	Rv2788	sirR	iron-dependent transcriptional
14. Iron ut	ilization		Rv0436c	pssA	decarboxylase CDP-diacylglycerol-serine	Rv3082c	virS	repressor putative virulence regulating
Rv1876	bfrA	bacterioferritin	17704300	рээл	o-phosphatidyltransferase	11130020	VIIO	protein (AraC/XyIS family)
Rv3841	bfrB	bacterioferritin	Rv0045c	-	possible dihydrolipoamide acetyl-	Rv3219	whiB1	WhiB transcriptional activator
Rv3215	entC	probable isochorismate synthase			transferase			homologue
Rv3214	entD	weak similarity to many phospho-	Rv0914c	-	lipid transfer protein	Rv3260c	whiB2	WhiB transcriptional activator
D 0005	. 5	glycerate mutases	Rv1543	-	probable fatty-acyl CoA reductase	D 0440		homologue
Rv2895c	viuB	similar to proteins involved in vibriobactin uptake	Rv1627c		lipid carrier protein	Rv3416	whiB3	WhiB transcriptional activator
Rv3525c	_	similar to ferripyochelin binding	Rv1814 Rv1867	-	possible C-5 sterol desaturase similar to acetyl CoA	Rv3681c	whiB4	homologue WhiB transcriptional activator
1000200		protein	1007		synthase/lipid carriers	11130010	WIIIDT	homologue
		F	Rv2261c	-	apolipoprotein N-acyltrans-	Rv0023	-	putative transcriptional regulator
H. Lipid bi	osynthesis	5			ferase-a	Rv0043c	-	transcriptional regulator (GntR
		and mycolic acids	Rv2262c	-	apolipoprotein N-acyltrans-			family)
Rv3285	accA3	acetyl/propionyl CoA carboxylase	D. 2522		ferase-b	Rv0067c	-	transcriptional regulator
Rv0904c	accD3	α subunit acetyl/propionyl CoA carboxylase	Rv3523 Rv3720		lipid carrier protein C-term similar to cyclopropane	Rv0078	_	(TetR/AcrR family) transcriptional regulator
111000-10	асово	β subunit	100720		fatty acid synthases	1110070		(TetR/AcrR family)
Rv3799c	accD4	acetyl/propionyl CoA carboxylase			,,	Rv0081	-	transcriptional regulator (ArsR
		β subunit		de and no	n-ribosomal peptide synthesis			family)
Rv3280	accD5	acetyl/propionyl CoA carboxylase	Rv2940c	mas	mycocerosic acid synthase	Rv0135c	-	putative transcriptional regulator
Rv2247	accD6	β subunit	Rv2384	mbtA	mycobactin/exochelin synthesis	Rv0144 Rv0158	-	putative transcriptional regulator
KV2241	accido	acetyl/propionyl CoA carboxylase β subunit	Rv2383c	mbtB	(salicylate-AMP ligase) mycobactin/exochelin synthesis	KVU136	-	transcriptional regulator (TetR/AcrR family)
Rv2244	асрМ	acyl carrier protein (meromycolate	11120000	morb	(serine/threonine ligation)	Rv0165c	-	transcriptional regulator (GntR
	,	extension)	Rv2382c	mbtC	mycobactin/exochelin synthesis			family)
Rv2523c	acpS	CoA:apo-[ACP] pantethienephos-	Rv2381c	mbtD	mycobactin/exochelin synthesis	Rv0195	-	transcriptional regulator
D 0040		photransferase	D 0000		(polyketide synthase)	D 0400		(LuxR/UhpA family)
Rv2243 Rv0649	fabD fabD2	malonyl CoA-[ACP] transacylase malonyl CoA-[ACP] transacylase	Rv2380c	mbtE	mycobactin/exochelin synthesis (lysine ligation)	Rv0196	-	transcriptional regulator (TetR/AcrR family)
Rv1483	fabG1	3-oxoacyl-[ACP] reductase (aka	Rv2379c	mbtF	mycobactin/exochelin synthesis	Rv0232	_	transcriptional regulator
	10001	MabA)	11120100	,,,,,,,,	(lysine ligation)			(TetR/AcrR family)
Rv1350	fabG2	3-oxoacyl-[ACP] Reductase	Rv2378c	mbtG	mycobactin/exochelin synthesis	Rv0238	-	transcriptional regulator
Rv2002	fabG3	3-oxoacyl-[ACP] reductase			(lysine hydroxylase)			(TetR/AcrR family)
Rv0242c	fabG4	3-oxoacyl-[ACP] reductase	Rv2377c	mbtH	mycobactin/exochelin synthesis	Rv0273c	-	putative transcriptional regulator
Rv2766c Rv0533c	fabG5 fabH	3-oxoacyl-[ACP] reductase β-ketoacyl-ACP synthase III	Rv0101	nrp	unknown non-ribosomal peptide synthase	Rv0302	-	transcriptional regulator (TetR/AcrR family)
Rv2524c	fas	fatty acid synthase	Rv1153c	omt	PKS o-methyltransferase	Rv0324	_	putative transcriptional regulator
Rv1484	inhA	enoyl-[ACP] reductase	Rv3824c	papA1	PKS-associated protein, unknown	Rv0328	-	transcriptional regulator
Rv2245	kasA	β-ketoacyl-ACP synthase			function			(TetR/AcrR family)
		(meromycolate extension)	Rv3820c	papA2	PKS-associated protein, unknown	Rv0348	-	putative transcriptional regulator
Rv2246	kasB	β-ketoacyl-ACP synthase	D.:4400	12	function	Rv0377	-	transcriptional regulator (LysR
Rv1618	tesB1	(meromycolate extension) thioesterase II	Rv1182	papA3	PKS-associated protein, unknown function	Rv0386	_	family) transcriptional regulator
Rv2605c	tesB2	thioesterase II	Rv1528c	papA4	PKS-associated protein, unknown	1110000		(LuxR/UhpA family)
Rv0033	-	possible acyl carrier protein		F-F	function	Rv0452	-	putative transcriptional regulator
Rv1344	-	possible acyl carrier protein	Rv2939	papA5	PKS-associated protein, unknown	Rv0465c	-	transcriptional regulator
Rv1722	-	possible biotin carboxylase	5 0040		function	D 0470		(PbsX/Xre family)
Rv3221c	-	resembles biotin carboxyl carrier	Rv2946c	pks1	polyketide synthase	Rv0472c	-	transcriptional regulator (TetR/AcrR family)
Rv3472	-	possible acyl carrier protein	Rv1660	pks10	polyketide synthase (chalcone synthase-like)	Rv0474	_	transcriptional regulator
2. Modifica	ation of fat	ty and mycolic acids	Rv1665	pks11	polyketide synthase (chalcone			(PbsX/Xre family)
Rv3391	acrA1	fatty acyl-CoA reductase		, -	synthase-like)	Rv0485	-	transcriptional regulator (ROK
Rv3392c	cmaA1	cyclopropane mycolic acid	Rv2048c	pks12	polyketide synthase (erythronolide			family)
D.,0502-	10	synthase 1	D. 2000-	ml-m12	synthase-like)	Rv0494	-	transcriptional regulator (GntR
Rv0503c	cmaA2	cyclopropane mycolic acid syn- thase 2	Rv3800c Rv1342c	pks13	polyketide synthase polyketide synthase (chalcone	Rv0552	_	family) putative transcriptional regulator
Rv0824c	desA1	acyl-[ACP] desaturase	11113420	pks14	synthase-like)	Rv0576	-	putative transcriptional regulator
Rv1094	desA2	acyl-[ACP] desaturase	Rv2947c	pks15	polyketide synthase	Rv0586	-	transcriptional regulator (GntR
Rv3229c	desA3	acyl-[ACP] desaturase	Rv1013	pks16	polyketide synthase			family)
Rv0645c	mmaA1	methoxymycolic acid synthase 1	Rv1663	pks17	polyketide synthase	Rv0650	-	transcriptional regulator (ROK
Rv0644c	mmaA2	methoxymycolic acid synthase 2	Rv1372	pks18	polyketide synthase	D. OCCO		family)
Rv0643c Rv0642c	mmaA3 mmaA4	methoxymycolic acid synthase 3 methoxymycolic acid synthase 4	Rv3825c Rv1180	pks2 pks3	polyketide synthase polyketide synthase	Rv0653c Rv0681	-	putative transcriptional regulator transcriptional regulator
Rv0447c	ufaA1	unknown fatty acid methyltrans-	Rv1181	pks3 pks4	polyketide synthase	1,40001	-	(TetR/AcrR family)
		ferase	Rv1527c	pks5	polyketide synthase	Rv0691c	-	transcriptional regulator
Rv3538	ufaA2	unknown fatty acid methyltrans-	Rv0405	pks6	polyketide synthase			(TetR/AcrR family)
D. 0100		ferase	Rv1661	pks7	polyketide synthase	Rv0737	-	putative transcriptional regulator
Rv0469	umaA1	unknown mycolic acid methyl- transferase	Rv1662 Rv1664	pks8 pks9	polyketide synthase polyketide synthase	Rv0744c Rv0792c	-	putative transcriptional regulator transcriptional regulator (GntR
		110113151035	11/1004	μισσ	polykelide syllilase	1.401.920	-	nanscriptional regulator (Gritk

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		family)	Rv3160c	_	putative transcriptional regulator			truncated
Rv0823c	-	transcriptional regulator	Rv3167c	-	putative transcriptional regulator	Rv0018c	ppp	putative phosphoprotein phos-
Rv0827c		(NifR3/Smm1 family) transcriptional regulator (ArsR	Rv3173c	-	transcriptional regulator (TetR/AcrR family)	Rv2234	ntn A	phatase
11/00276	-	family)	Rv3183	-	putative transcriptional regulator	1112234	ptpA	low molecular weight protein-tyro- sine-phosphatase
Rv0890c	-	transcriptional regulator	Rv3208	-	transcriptional regulator	Rv0153c	-	putative protein-tyrosine-phos-
D: 0004 -		(LuxR/UhpA family)	D. 2040-		(TetR/AcrR family)			phatase
Rv0891c Rv0894	-	putative transcriptional regulator putative transcriptional regulator	Rv3249c	-	transcriptional regulator (TetR/AcrR family)	II. Macron	nolecule i	metabolism
	-	transcriptional regulator	Rv3291c	-	transcriptional regulator	A. Synthe	sis and mo	odification of macromolecules
D: 4040		(TetR/AcrR family)	D. 0005		(Lrp/AsnC family)			n synthesis and modification
Rv1049	-	transcriptional regulator (MarR family)	Rv3295	-	transcriptional regulator (TetR/AcrR family)	Rv3420c	rimI	ribosomal protein S18 acetyl transferase
Rv1129c	-	transcriptional regulator	Rv3334	-	transcriptional regulator (MerR	Rv0995	rimJ	acetylation of 30S S5 subunit
D: 4454 -		(PbsX/Xre family)	Rv3405c		family)	Rv0641	rpIA	50S ribosomal protein L1
	-	putative transcriptional regulator transcriptional regulator (GntR	Rv34050 Rv3522	-	putative transcriptional regulator putative transcriptional regulator	Rv0704 Rv0701	rpIB rpIC	50S ribosomal protein L2 50S ribosomal protein L3
		family)	Rv3557c	-	transcriptional regulator	Rv0702	rpID	50S ribosomal protein L4
Rv1167c		putative transcriptional regulator	D: 0574		(TetR/AcrR family)	Rv0716	rpIE	50S ribosomal protein L5
	-	putative transcriptional regulator transcriptional regulator	Rv3574	-	transcriptional regulator (TetR/AcrR family)	Rv0719 Rv0056	rpIF rpII	50S ribosomal protein L6 50S ribosomal protein L9
1112000		(TetR/AcrR family)	Rv3575c	-	transcriptional regulator (Lacl	Rv0651	rpIJ	50S ribosomal protein L10
	-	putative transcriptional regulator	D: 0500-		family)	Rv0640	rpIK	50S ribosomal protein L11
Rv1353c	-	transcriptional regulator (TetR/AcrR family)	Rv3583c Rv3676	-	putative transcriptional regulator transcriptional regulator (Crp/Fnr	Rv0652 Rv3443c	rpIL rpIM	50S ribosomal protein L7/L12 50S ribosomal protein L13
Rv1358	-	transcriptional regulator			family)	Rv0714	rpIN	50S ribosomal protein L14
D 4050		(LuxR/UhpA family)	Rv3678c	-	transcriptional regulator (LysR	Rv0723	rpIO	50S ribosomal protein L15
Rv1359 Rv1395	-	putative transcriptional regulator transcriptional regulator	Rv3736	_	family) transcriptional regulator	Rv0708 Rv3456c	rpIP rpIQ	50S ribosomal protein L16 50S ribosomal protein L17
		(AraC/XylS family)			(AraC/XyIS family)	Rv0720	rpIR	50S ribosomal protein L18
Rv1404	-	transcriptional regulator (MarR	Rv3744	-	transcriptional regulator (ArsR	Rv2904c	rpIS	50S ribosomal protein L19
Rv1423	_	family) putative transcriptional regulator	Rv3830c	_	family) transcriptional regulator	Rv1643 Rv2442c	rpIT rpIU	50S ribosomal protein L20 50S ribosomal protein L21
Rv1460	-	putative transcriptional regulator			(TetR/AcrR family)	Rv0706	rpIV	50S ribosomal protein L22
Rv1474c	-	transcriptional regulator	Rv3833	-	transcriptional regulator	Rv0703	rpIW	50S ribosomal protein L23
Rv1534	_	(TetR/AcrR family) transcriptional regulator	Rv3840	_	(AraC/XyIS family) putative transcriptional regulator	Rv0715 Rv1015c	rpIX rpIY	50S ribosomal protein L24 50S ribosomal protein L25
		(TetR/AcrR family)	Rv3855	-	putative transcriptional regulator	Rv2441c	rpmA	50S ribosomal protein L27
Rv1556	-	putative transcriptional regulator	2 Two oor	mnonont o	vatama	Rv0105c	rpmB	50S ribosomal protein L28
	-	putative transcriptional regulator putative transcriptional regulator	2. Two cor Rv1028c	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
Rv1773c		family)	Rv3246c		regulator	Rv1298	rpmE rpmG	50S ribosomal protein L31
KV1773C	-	transcriptional regulator (IcIR family)	KV32400	mtrA	two-component response regulator	Rv2057c Rv3924c	rpmH	50S ribosomal protein L33 50S ribosomal protein L34
	-	putative transcriptional regulator	Rv3245c	mtrB	sensor histidine kinase	Rv1642	rpmI	50S ribosomal protein L35
	-	putative transcriptional regulator	Rv0844c	narL	two-component response	Rv3461c Rv1630	rpmJ	50S ribosomal protein L36
	-	putative transcriptional regulator transcriptional regulator	Rv0757	phoP	regulator two-component response	Rv2890c	rpsA rpsB	30S ribosomal protein S1 30S ribosomal protein S2
		(AraC/XylS family)			regulator	Rv0707	rpsC	30S ribosomal protein S3
	-	putative transcriptional regulator	Rv0758	phoR	sensor histidine kinase	Rv3458c	rpsD	30S ribosomal protein S4
	-	putative transcriptional regulator transcriptional regulator (LysR	Rv0491	regX3	two-component response regulator	Rv0721 Rv0053	rpsE rpsF	30S ribosomal protein S5 30S ribosomal protein S6
		family)	Rv0490	senX3	sensor histidine kinase	Rv0683	rpsG	30S ribosomal protein S7
	-	putative transcriptional regulator transcriptional regulator (MerR	Rv0602c	tcrA	two-component response regulator	Rv0718 Rv3442c	rpsH rpsI	30S ribosomal protein S8 30S ribosomal protein S9
1013340	-	family)	Rv0260c	-	two-component response	Rv0700	rpsJ	30S ribosomal protein S10
Rv2017	-	putative transcriptional regulator			regulator	Rv3459c	rpsK	30S ribosomal protein S11
Rv2021c	_	(PbsX/Xre family) putative transcriptional regulator	Rv0600c Rv0601c	-	sensor histidine kinase sensor histidine kinase	Rv0682 Rv3460c	rpsL rpsM	30S ribosomal protein S12 30S ribosomal protein S13
	-	transcriptional regulator (ArsR	Rv0818	-	two-component response	Rv0717	rpsN	30S ribosomal protein S14
		family)			regulator	Rv2056c	rpsN2	30S ribosomal protein S14
Rv2175c Rv2250c	-	putative transcriptional regulator putative transcriptional regulator	Rv0845 Rv0902c	-	sensor histidine kinase sensor histidine kinase	Rv2785c Rv2909c	rpsO rpsP	30S ribosomal protein S15 30S ribosomal protein S16
Rv2258c	- 1	putative transcriptional regulator	Rv0903c	-	two-component response	Rv0710	rpsQ	30S ribosomal protein S17
Rv2282c	-	transcriptional regulator (LysR	D 0004		regulator	Rv0055	rpsR	30S ribosomal protein S18
Rv2308	7	family) putative transcriptional regulator	Rv0981	-	two-component response regulator	Rv2055c Rv0705	rpsR2 rpsS	30S ribosomal protein S18 30S ribosomal protein S19
Rv2324	-	transcriptional regulator	Rv0982	-	sensor histidine kinase	Rv2412	rpsT	30S ribosomal protein S20
D _v 22E0		(Lrp/AsnC family)		-	sensor histidine kinase	Rv3241c	-	member of S30AE ribosomal
Rv2358	-	transcriptional regulator (ArsR family)	Rv1033c	-	two-component response regulator			protein family
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
1112300		(TetR/AcrR family)	Rv2884	-	two-component response	Rv2907c	rimM	16S rRNA processing protein
Rv2621c		putative transcriptional regulator			regulator			
Rv2640c	-	transcriptional regulator (ArsR family)	Rv3132c Rv3133c	-	sensor histidine kinase two-component response	3. Aminoa Rv2555c	cyl tRNA : alaS	synthases and their modification alanyl-tRNA synthase
Rv2642	-	transcriptional regulator (ArsR	11101000		regulator	Rv1292	argS	arginyl-tRNA synthase
D. 0000		family)	Rv3143	-	putative sensory transduction	Rv2572c	aspS	aspartyl-tRNA synthase
	-	putative transcriptional regulator putative transcriptional regulator	Rv3220c	_	protein sensor histidine kinase	Rv3580c Rv2130c	cysS cysS2	cysteinyl-tRNA synthase cysteinyl-tRNA synthase
	-	transcriptional regulator		-	sensor histidine kinase	Rv1406	fmt	methionyl-tRNA formyltransferase
		(Lrp/AsnC family)	Rv3765c	-	two-component response	Rv3011c	gatA	glu-tRNA-gln amidotransferase,
Rv2887	-	transcriptional regulator (MarR family)			regulator	Rv3009c	gatB	subunit B glu-tRNA-gln amidotransferase,
Rv2912c	-	transcriptional regulator			protein kinases and phosphoprotein			subunit A
Dygggg		(TetR/AcrR family)	phosphata		poring throughing protein library	Rv3012c	gatC	glu-tRNA-gln amidotransferase,
Rv2989	-	transcriptional regulator (IcIR family)	Rv0015c Rv0014c	pknA pknB	serine-threonine protein kinase serine-threonine protein kinase	Rv2992c	gltS	subunit C glutamyl-tRNA synthase
Rv3050c	-	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
		family)	Rv1266c	pknH	serine-threonine protein kinase	Rv3598c	lysS	lysyl-tRNA synthase
	-	putative transcriptional regulator	Rv2914c	pknl	serine-threonine protein kinase	Rv1640c	lysX	C-term lysyl-tRNA synthase
Rv3095 Rv3124	-	putative transcriptional regulator transcriptional regulator	Rv2088 Rv3080c	pknJ pknK	serine-threonine protein kinase serine-threonine protein kinase	Rv1007c Rv1649	metS pheS	methionyl-tRNA synthase phenylalanyl-tRNA synthase α
		(AfsR/DndI/RedD family)	Rv2176	pknL	serine-threonine protein kinase,			subunit

	pheT	phenylalanyl-tRNA synthase β	Rv2090	-	partially similar to DNA poly-	2. DNA		
		subunit	D 0101		merase I	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	Rv2464c		proteins probable DNA glycosylase,	Rv1107c	xseB	exonuclease VII small subuni
Rv2614c Rv2906c	thrS trmD	threonyl-tRNA synthase tRNA (guanine-N1)-methyltrans-	KV24040	-	endonuclease VIII	3 Proteins	nentides	and glycopeptides
(VZ300C	שוווט	ferase	Rv3201c	_	probable ATP-dependent DNA	Rv3305c		probable aminohydrolase
Rv3336c	trpS	tryptophanyl tRNA synthase			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
			Rv3644c	-	similar in N-term to DNA poly-			teolytic subunit
I. Nucleop	roteins				merase III	Rv2460c	clpP2	ATP-dependent Clp protease
Rv1407	fmu	similar to Fmu protein	0 D1-1-			D: 0457	-1 V	teolytic subunit
Rv3852	hns	HU-histone protein	Rv0429c		and modification	Rv2457c	clpX	ATP-dependent Clp protease ATP-binding subunit ClpX
Rv2986c	hupB mIHF	DNA-binding protein II	Rv2534c		polypeptide deformylase elongation factor P	Rv2667	clpX'	similar to ClpC from M. leprae
Rv1388	mmr	integration host factor	Rv2882c	frr	ribosome recycling factor	102007	СІРХ	shorter
5 DNA rer	olication r	epair, recombination and restric-	Rv0684	fusA	elongation factor G	Rv3419c	gcp	glycoprotease
ion/modifi		epail, recombination and restric-	Rv0120c		elongation factor G	Rv2725c	hflX	GTP-binding protein
Rv1317c		DNA-3-methyladenine glycosi-	Rv1080c		transcription elongation factor G	Rv1223	htrA	serine protease
		dase II	Rv3462c	infA	initiation factor IF-1	Rv2861c	map	methionine aminopeptidase
Rv2836c	dinF	DNA-damage-inducible protein F	Rv2839c	infB	initiation factor IF-2	Rv0734	map'	probable methionine aminope
Rv1329c	dinG	probable ATP-dependent helicase	Rv1641	infC	initiation factor IF-3			dase
Rv3056	dinP	DNA-damage-inducible protein	Rv0009	ppiA	peptidyl-prolyl cis-trans isomerase	Rv0319	рср	pyrrolidone-carboxylate peption
Rv1537	dinX	probable DNA-damage-inducible	Rv2582	ppiB	peptidyl-prolyl cis-trans isomerase	Rv0125	pepA	probable serine protease
		protein	Rv1299	prfA	peptide chain release factor 1	Rv2213	pepB	aminopeptidase A/I
Rv0001	dnaA	chromosomal replication initiator	Rv3105c Rv2889c	prfB	peptide chain release factor 2	Rv0800	pepC	aminopeptidase I
	D	protein	Rv28890 Rv0685	<i>tsf</i> tuf	elongation factor EF-Ts elongation factor EF-Tu	Rv2467 Rv2089c	pepD	probable aminopeptidase cytoplasmic peptidase
Rv0058	dnaB dnaE1	DNA helicase (contains intein)	170000	tui	elongation lactor E1 - Iu	Rv2535c	pepE pepQ	cytoplasmic peptidase
Rv1547 Rv3370c	dnaE1 dnaE2	DNA polymerase III, α subunit DNA polymerase III α chain	7. RNA sv	nthesis. Rt	NA modification and DNA	Rv2782c	pepQ pepR	protease/peptidase, M16 fam
Rv2343c	dnaG	DNA primase	transcription)	(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 ∈ chain			helicase	Rv2110c	prcB	proteasome β-type subunit 2
Rv3721c	dnaZX	DNA polymerase III, γ (dnaZ) and	Rv2783c	gpsI	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		transcription termination factor	Rv0724	sppA	protease IV, signal peptide pe
		sylase	Rv2533c	nusB	N-utilization substance protein B	D. 0400		dase
Rv0006	gyrA	DNA gyrase subunit A	Rv0639	nusG	transcription antitermination		-	probable zinc metalloproteas
Rv0005	gyrB	DNA gyrase subunit B	Rv3907c	non A	protein	Rv0457c Rv0840c	-	probable peptidase probable proline iminopeptida
Rv2092c	helY	probable helicase, Ski2 subfamily	Rv39070	pcnA pvdS	polynucleotide polymerase alternative sigma factor for	Rv0983	-	probable serine protease
Rv2101	helZ	probable helicase, Snf2/Rad54	KV32320	ρναδ	siderophore production	Rv1977	-	probable zinc metallopeptidas
Rv2756c	hsdM	family type I restriction/modification sys-	Rv3211	rhIE	probable ATP-dependent		_	probable alkaline serine prote
(VZ130C	Houlvi	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		-	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, l	lipopolysaccharides and phosp
Rv3062	ligB	DNA ligase	Rv0668	rpoC	β' subunit of RNA polymerase	lipids		
Rv3731	ligC	probable DNA ligase	Rv1364c	rsbU	SigB regulation protein	Rv0062	celA	cellulase/endoglucanase
Rv1020	mfd	transcription-repair coupling factor	Rv3287c	rsbW	anti-sigma B factor	Rv3915	cwlM	hydrolase
Rv2528c	mrr	restriction system protein	Rv2703	sigA	RNA polymerase sigma factor	Rv0315 Rv1090	-	probable β-1,3-glucanase
Rv2985	mutT1 mutT2	MutT homologue	Rv2710	sigB	(aka MysA, RpoV) RNA polymerase sigma factor	KV1090	-	probable inactivated cellulase/endoglucanase
Rv1160 Rv0413	mutT3	MutT homologue MutT homologue	102710	SigD	(aka MysB)	Rv1327c	_	probable glycosyl hydrolase,
Rv3589	mutY	probable DNA glycosylase	Rv2069	sigC	ECF subfamily sigma subunit	1110270		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	Rv3717	-	possible N-acetylmuramoyl-L-
	- 3	methyltransferase	Rv0182c	sigG	sigma-70 factors ECF subfamily			nine amidase
Rv1629	1 1		Rv3223c	sigH	ECF subfamily sigma subunit			
	polA	DNA polymerase I	11132236				es and lipa	2000
Rv1402	priA	DNA polymerase I putative primosomal protein n'	Rv1189	sigl	ECF family sigma factor			2505
	priA	putative primosomal protein n' (replication factor Y)	Rv1189 Rv3328c	sigJ	similar to SigI, ECF family	Rv0220	lipC	probable esterase
		putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo-	Rv1189 Rv3328c Rv0445c	sigJ sigK	similar to SigI, ECF family ECF-type sigma factor	Rv0220 Rv1923	lipC lipD	probable esterase probable esterase
Rv3585	priA radA	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue	Rv1189 Rv3328c Rv0445c Rv0735	sigJ sigK sigL	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily	Rv0220 Rv1923 Rv3775	lipC lipD lipE	probable esterase probable esterase probable hydrolase
Rv3585 Rv2737c	priA radA recA	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein)	Rv1189 Rv3328c Rv0445c	sigJ sigK	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to	Rv0220 Rv1923 Rv3775 Rv3487c	lipC lipD lipE lipF	probable esterase probable esterase probable hydrolase probable esterase
Rv3585 Rv2737c Rv0630c	priA radA recA recB	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V	Rv1189 Rv3328c Rv0445c Rv0735 Rv3911	sigJ sigK sigL sigM	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE	Rv0220 Rv1923 Rv3775 Rv3487c Rv0646c	lipC lipD lipE lipF lipG	probable esterase probable esterase probable hydrolase probable esterase probable hydrolase
Rv3585 Rv2737c Rv0630c Rv0631c	radA recA recB recC	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V	Rv1189 Rv3328c Rv0445c Rv0735 Rv3911	sigJ sigK sigL sigM spoU	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase	Rv0220 Rv1923 Rv3775 Rv3487c Rv0646c Rv1399c	lipC lipD lipE lipF lipG lipH	probable esterase probable esterase probable hydrolase probable esterase probable hydrolase probable lipase
Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c	radA recA recB recC recD	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V	Rv1189 Rv3328c Rv0445c Rv0735 Rv3911	sigJ sigK sigL sigM	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE	Rv0220 Rv1923 Rv3775 Rv3487c Rv0646c	lipC lipD lipE lipF lipG	probable esterase probable esterase probable hydrolase probable esterase probable hydrolase
Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c	radA recA recB recC	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induc-	Rv1189 Rv3328c Rv0445c Rv0735 Rv3911	sigJ sigK sigL sigM spoU	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate syn-	Rv0220 Rv1923 Rv3775 Rv3487c Rv0646c Rv1399c Rv1400c	lipC lipD lipE lipF lipG lipH lipI	probable esterase probable esterase probable hydrolase probable esterase probable lipase probable lipase
Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv0003	radA recA recB recC recD	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V	Rv1189 Rv3328c Rv0445c Rv0735 Rv3911 Rv3366 Rv3455c	sigJ sigK sigL sigM spoU truA	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate syn- thase	Rv0220 Rv1923 Rv3775 Rv3487c Rv0646c Rv1399c Rv1400c Rv1900c	lipC lipD lipE lipF lipG lipH lipI lipJ	probable esterase probable esterase probable hydrolase probable esterase probable ipase probable lipase probable lipase probable esterase
Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv0003	radA recA recB recC recD recF	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induc- tion	Rv1189 Rv3328c Rv0445c Rv0735 Rv3911 Rv3366 Rv3455c Rv2793c Rv1644	sigJ sigK sigL sigM spoU truA truB	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate syn- thase tRNA pseudouridine 55 synthase putative 23S rRNA methyltrans- ferase	Rv0220 Rv1923 Rv3775 Rv3487c Rv0646c Rv1399c Rv1400c Rv1900c Rv2385 Rv1497 Rv2284	lipC lipD lipE lipF lipG lipH lipI lipJ lipK lipL lipM	probable esterase probable esterase probable hydrolase probable esterase probable esterase probable lipase probable lipase probable esterase probable acetyl-hydrolase esterase probable esterase
Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv0003 Rv2973c Rv1696	radA recA recB recC recD recF	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induc- tion ATP-dependent DNA helicase	Rv1189 Rv3328c Rv0445c Rv0735 Rv3911 Rv3366 Rv3455c Rv2793c	sigJ sigK sigL sigM spoU truA truB	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate syn- thase tRNA pseudouridine 55 synthase putative 23S rRNA methyltrans- ferase ATP-dependent DNA/RNA heli-	Rv0220 Rv1923 Rv3775 Rv3487c Rv0646c Rv1399c Rv1400c Rv1900c Rv2385 Rv1497 Rv2284 Rv2970c	lipC lipD lipE lipF lipG lipH lipI lipJ lipK lipL lipM	probable esterase probable esterase probable hydrolase probable hydrolase probable esterase probable lipase probable lipase probable lipase probable esterase probable esterase probable esterase probable esterase probable esterase probable lipase/esterase
Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv0003 Rv2973c Rv1696 Rv3715c	radA recA recB recC recD recF recG recN recR	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induction ATP-dependent DNA helicase recombination and DNA repair RecBC-Independent process of DNA repair	Rv1189 Rv3328c Rv0445c Rv0735 Rv3911 Rv3366 Rv3455c Rv2793c Rv1644	sigJ sigK sigL sigM spoU truA truB tsnR	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate syn- thase tRNA pseudouridine 55 synthase putative 23S rRNA methyltrans- ferase	Rv0220 Rv1923 Rv3775 Rv3487c Rv0646c Rv1399c Rv1400c Rv1900c Rv2385 Rv1497 Rv2284 Rv2970c Rv1426c	lipC . lipD lipE lipF lipG lipH lipI lipJ lipJ lipK lipM lipM lipM lipN lipN	probable esterase probable esterase probable hydrolase probable hydrolase probable lipase probable lipase probable lipase probable lipase probable esterase probable acetyl-hydrolase esterase probable esterase probable lipase/esterase probable lipase/esterase probable esterase
Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv0003 Rv2973c Rv1696 Rv3715c	priA radA recA recB recC recC recF recG recR recR recX	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induction ATP-dependent DNA helicase recombination and DNA repair RecBC-Independent process of DNA repair regulatory protein for RecA	Rv1189 Rv3328c Rv0445c Rv0735 Rv3911 Rv3366 Rv3455c Rv2793c Rv1644 Rv3649	sigJ sigK sigL sigM spoU truA truB tsnR	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate syn- thase tRNA pseudouridine 55 synthase putative 23S rRNA methyltrans- ferase ATP-dependent DNA/RNA heli- case	Rv0220 Rv1923 Rv3775 Rv3487c Rv0646c Rv1399c Rv1400c Rv1900c Rv2385 Rv1497 Rv2284 Rv2970c Rv1426c Rv2463	lipC lipD lipE lipF lipG lipH lipI lipJ lipK lipL lipM lipN lipO lipP	probable esterase probable esterase probable hydrolase probable esterase probable esterase probable lipase probable lipase probable esterase probable acetyl-hydrolase esterase probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase
Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv0003 Rv2973c Rv1696 Rv3715c	radA recA recB recC recD recF recG recN recR	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V but replication and SOS induc- tion ATP-dependent DNA helicase recombination and DNA repair RecBC-Independent process of DNA repair regulatory protein for RecA Holliday junction binding protein,	Rv1189 Rv3328c Rv0445c Rv0735 Rv3911 Rv3366 Rv3455c Rv2793c Rv1644 Rv3649	sigJ sigK sigL sigM spoU truA truB tsnR	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate syn- thase tRNA pseudouridine 55 synthase putative 23S rRNA methyltrans- ferase ATP-dependent DNA/RNA heli- case cytoplasmic)	Rv0220 Rv1923 Rv3775 Rv3487c Rv0646c Rv1399c Rv1400c Rv2385 Rv1497 Rv2284 Rv2970c Rv1426c Rv2463 Rv2485c	lipC . lipD lipF lipF lipG lipH lipI lipI lipN lipN lipN lipP lipP	probable esterase probable esterase probable esterase probable hydrolase probable hydrolase probable lipase probable lipase probable lipase probable esterase
Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv0003 Rv2973c Rv1696 Rv3715c Rv2736c Rv2593c	priA radA recA recB recC recD recF recG recR recR	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induction ATP-dependent DNA helicase recombination and DNA repair RecBC-Independent process of DNA repair regulatory protein for RecA Holliday junction binding protein, DNA helicase	Rv1189 Rv3328c Rv04735 Rv07735 Rv3911 Rv3366 Rv3455c Rv2793c Rv1644 Rv3649	sigJ sigK sigL sigM spoU truA truB tsnR -	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate syn- thase tRNA pseudouridine 55 synthase putative 23S rRNA methyltrans- ferase ATP-dependent DNA/RNA heli- case cytoplasmic) 1,4-α-glucan branching enzyme	Rv0220 Rv1923 Rv3775 Rv3487c Rv0646c Rv1399c Rv1400c Rv2385 Rv1497 Rv2284 Rv2970c Rv1426c Rv2463 Rv2463 Rv2485c Rv3084	lipC lipD lipE lipE lipG lipH lipI lipJ lipJ lipN lipN lipO lipP lipP lipP	probable esterase probable esterase probable esterase probable hydrolase probable lipase probable lipase probable lipase probable lipase probable esterase probable esterase probable esterase probable lipase/esterase probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase probable catefolyleysterase probable catefolyleysterase probable acetyl-hydrolase
Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv0003 Rv2973c Rv1696 Rv3715c Rv2736c Rv2736c Rv2593c	priA radA recA recB recC recD recF recG recN recK ruvA	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induction ATP-dependent DNA helicase recombination and DNA repair RecBC-Independent process of DNA repair requiatory protein for RecA Holliday junction binding protein, DNA helicase Holliday junction binding protein	Rv1189 Rv3328c Rv0445c Rv0735 Rv3911 Rv3366 Rv3455c Rv2793c Rv1644 Rv3649	sigJ sigK sigL sigM spoU truA truB tsnR	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate syn- thase tRNA pseudouridine 55 synthase putative 23S rRNA methyltrans- ferase ATP-dependent DNA/RNA heli- case cytoplasmic) 1,4-α-glucan branching enzyme probable glycogen phosphory-	Rv0220 Rv1923 Rv3775 Rv3487c Rv0646c Rv1399c Rv1400c Rv2385 Rv1497 Rv2284 Rv2970c Rv1426c Rv2463 Rv2485c Rv3476c	IipC IipD IipD IipF IipG IipH IipJ IipJ IipN IipD IipP IipD IipP IipD IipP IipP IipP IipP IipP IipR IipS	probable esterase probable esterase probable hydrolase probable esterase probable esterase probable lipase probable lipase probable esterase probable esterase probable acetyl-hydrolase esterase probable acetyl-hydrolase probable esterase/lipase
Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv0003 Rv2973c Rv1696 Rv3715c Rv2736c Rv2593c	priA radA recA recB recC recD recF recG recR recR	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induction ATP-dependent DNA helicase recombination and DNA repair RecBC-Independent process of DNA repair regulatory protein for RecA Holliday junction binding protein, DNA helicase Holliday junction binding protein Holliday junction resolvase, endo-	Rv1189 Rv3328c Rv0445c Rv0735 Rv3911 Rv3366 Rv3455c Rv2793c Rv1644 Rv3649 8. Polysac Rv1326c Rv1328	sigJ sigK sigL sigM spoU truA truB tsnR - ccharides (of glgB glgP	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable pseudouridylate syn- thase tRNA pseudouridylate syn- thase tRNA pseudouridine 55 synthase putative 23S rRNA methyltrans- ferase ATP-dependent DNA/RNA heli- case cytoplasmic) 1,4~a~glucan branching enzyme probable glycogen phosphory- lase	Rv0220 Rv1923 Rv3775 Rv3487c Rv1646c Rv1399c Rv1400c Rv2385 Rv1497 Rv2284 Rv2970c Rv1426c Rv2463 Rv2463 Rv2485c Rv3084 Rv3176c Rv2045c	lipC lipD lipE lipF lipG lipH lipI lipJ lipJ lipN lipN lipN lipO lipQ lipC lipD	probable esterase probable esterase probable esterase probable hydrolase probable hydrolase probable lipase probable lipase probable lipase probable esterase probable carbox/yesterase probable esterase/lipase probable esterase/lipase probable carboxylesterase
Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv0629c Rv2973c Rv2973c Rv2736c Rv2736c Rv2592c Rv2594c	priA radA recA recB recC recD recF recG recN recR ruvA ruvB ruvC	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induction ATP-dependent DNA helicase recombination and DNA repair RecBC-Independent process of DNA repair regulatory protein for RecA Holliday junction binding protein, DNA helicase Holliday junction binding protein Holliday junction resolvase, endo- deoxyribonuclease	Rv1189 Rv3328c Rv04735 Rv07735 Rv3911 Rv3366 Rv3455c Rv2793c Rv1644 Rv3649	sigJ sigK sigL sigM spoU truA truB tsnR -	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate syn- thase tRNA pseudouridine 55 synthase putative 23S rRNA methyltrans- ferase ATP-dependent DNA/RNA heli- case cytoplasmic) 1,4-α-glucan branching enzyme probable glycogen phosphory- lase probable glycogen debranching	Rv0220 Rv1923 Rv19275 Rv3487c Rv0646c Rv1399c Rv1400c Rv1900c Rv2485c Rv2485c Rv2485c Rv2485c Rv2485c Rv3084 Rv3176c Rv2045c Rv2045c Rv1076	IipC IipD IipE IipF IipF IipH IipJ IipN IipN IipO IipP IipP IipP IipD IipD IipD IipD IipD IipD IipD IipD	probable esterase probable esterase probable hydrolase probable hydrolase probable lipase probable lipase probable lipase probable lipase probable esterase probable carboxlyesterase probable acetyl-hydrolase probable esterase/lipase probable esterase/lipase probable esterase probable carboxylesterase probable esterase
Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv0003 Rv2973c Rv1696 Rv2736c Rv2736c Rv2593c Rv2592c Rv2594c Rv0054	priA radA recA recB recC recD recF recG recN recR recX ruvA ruvB ruvC ssb	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induction ATP-dependent DNA helicase recombination and DNA repair RecBC-Independent process of DNA repair regulatory protein for RecA Holliday junction binding protein, DNA helicase Holliday junction binding protein Holliday junction resolvase, endodeoxyribonuclease single strand binding protein	RV1189 RV3328c RV0445c RV0735 RV3911 RV3366 RV3455c RV2793c RV1644 RV3649 8. Polysac RV1326c RV1326 RV13264	sigJ sigK sigL sigM spoU truA truB tsnR - ccharides (c glgB glgP glgP	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate syn- thase tRNA pseudouridine 55 synthase putative 23S rRNA methyltrans- ferase ATP-dependent DNA/RNA heli- case cytoplasmic) 1,4-α-glucan branching enzyme probable glycogen phosphory- lase probable glycogen debranching enzyme	Rv0220 Rv1923 Rv19275 Rv3487c Rv0646c Rv1399c Rv1400c Rv2385 Rv1497 Rv2284 Rv2970c Rv2463 Rv2463 Rv2463 Rv2463 Rv3476c Rv2045c Rv2045c Rv1076 Rv2033	lipC lipD lipF lipF lipG lipJ lipJ lipJ lipL lipD lipD lipD lipD lipD lipD lipD lipD	probable esterase probable esterase probable esterase probable hydrolase probable hydrolase probable hydrolase probable lipase probable lipase probable esterase probable carbox/yesterase probable esterase/lipase probable esterase/lipase probable esterase/lipase probable esterase probable esterase probable lipase
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Rv3585 Rv2737c Rv0630c Rv0631c Rv0629c Rv0003 Rv2973c Rv1696 Rv3715c Rv2736c Rv2593c Rv2592c Rv2594c Rv2594c Rv0054 Rv1210	priA radA recA recB recC recD recF recK recN recR recX ruvA ruvB ruvC ssb tagA topA	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induc- tion ATP-dependent DNA helicase recombination and DNA repair RecBC-Independent process of DNA repair regulatory protein for RecA Holliday junction binding protein, DNA helicase Holliday junction binding protein Holliday junction resolvase, endo- deoxyribonuclease single strand binding protein DNA-3-methyladenine glycosi- dase I DNA topoisomerase	Rv1189 Rv3328c Rv0445c Rv0735 Rv3911 Rv3366 Rv3455c Rv2793c Rv1644 Rv3649 8. Polysac Rv1326c Rv1328 Rv1564c Rv1563c	sigJ sigK sigL sigM spoU truA truB tsnR - ccharides (c glgB glgP glgX glgY	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate syn- thase tRNA pseudouridine 55 synthase putative 23S rRNA methyltrans- ferase ATP-dependent DNA/RNA heli- case cytoplasmic) 1,4-α-glucan branching enzyme probable glycogen phosphory- lase probable glycogen debranching enzyme putative α-amylase maltooligosyltrehalose trehalohy-	Rv0220 Rv1923 Rv19275 Rv3487c Rv0646c Rv1399c Rv1400c Rv1900c Rv2485c Rv2485c Rv2485c Rv2485c Rv2485c Rv2485c Rv3084 Rv3176c Rv2045c Rv2045c Rv2045c Rv2045c Rv2045c	lipC lipC lipE lipF lipF lipF lipH lipI lipJ lipW lipO lipV lipV lipV lipW lipV lipW lipW lipU	probable esterase probable esterase probable hydrolase probable hydrolase probable hydrolase probable lipase probable lipase probable lipase probable esterase probable esterase probable esterase probable lipase/esterase probable lipase/esterase probable esterase probable esterase probable esterase probable carboxlyesterase probable acetyl-hydrolase probable acetyl-hydrolase probable esterase/lipase probable esterase probable esterase probable esterase probable lipase probable lipase probable esterase
Rv3585 Rv2737c Rv0630c Rv0631c Rv0631c Rv0629c Rv0629c Rv1696 Rv3715c Rv2736c Rv2592c Rv2592c Rv2592c Rv2594c Rv3646c Rv2596c Rv3646c Rv2976c	priA radA recA recB recC recD recF recK recR recR recX ruvA ruvB ruvC ssb tagA	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induction ATP-dependent DNA helicase recombination and DNA repair ResBC-Independent process of DNA repair regulatory protein for RecA Holliday junction binding protein, DNA helicase Holliday junction binding protein Holliday junction binding protein Holliday junction resolvase, endodeoxyribonuclease single strand binding protein DNA-3-methyladenine glycosidase I	RV1189 RV3328c RV0445c RV0735 RV3911 RV3366 RV3455c RV2793c RV1644 RV3649 8. Polysac RV1326c RV1326c RV1326 RV1564c RV1563c RV1563c	sigJ sigK sigL sigM spoU truA truB tsnR - ccharides (c glgB glgP glgZ glgZ	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate syn- thase tRNA pseudouridine 55 synthase putative 23S rRNA methyltrans- ferase ATP-dependent DNA/RNA heli- case cytoplasmic) 1,4-α-glucan branching enzyme probable glycogen phosphory- lase probable glycogen debranching enzyme putative α-amylase maltooligosyltrehalose trehalohy- drolase	Rv0220 Rv1923 Rv19275 Rv3487c Rv0646c Rv1399c Rv1400c Rv2385 Rv1497 Rv2284 Rv2976 Rv2463 Rv2463 Rv2463 Rv2465 Rv2466 Rv2045c Rv2045c Rv2045c Rv2076 Rv2077 R	IipC IipD IipF IipF IipF IipH IipJ IipJ IipD IipD IipD IipD IipD IipD IipD IipD	probable esterase probable esterase probable esterase probable hydrolase probable hydrolase probable hydrolase probable lipase probable lipase probable lipase probable esterase probable acetyl-hydrolase esterase probable carbox/lyesterase probable carbox/lyesterase probable carbox/lyesterase probable esterase/lipase probable esterase probable processed precursor phospholipase C precursor probable processed precursor probable processed precursor probable processed precursor processed probable precursor processed probable precursor processed probable precursor processed
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RV3585 RV2737c RV0630c RV0631c RV0631c RV0631c RV0631c RV2973c RV2973c RV2593c RV2593c RV2593c RV2594c RV0054 RV1210 RV3646c RV2976c RV1638 RV1638 RV1638 RV1638	priA radA recA recB recC recCF recG recN recR recX ruvA ruvB ruvC ssb tagA topA ung uvrA	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induction ATP-dependent DNA helicase recombination and DNA repair RecBC-Independent process of DNA repair regulatory protein for RecA Holliday junction binding protein, DNA helicase Holliday junction binding protein Holliday junction binding protein Holliday junction resolvase, endodeoxyribonuclease single strand binding protein DNA-3-methyladenine glycosidase I DNA topoisomerase uracil-DNA glycosylase excinuclease ABC subunit A	Rv1189 Rv3328c Rv0445c Rv0735 Rv3911 Rv3366 Rv3455c Rv2793c Rv1644 Rv3649 8. Polysac Rv1326c Rv1328 Rv1564c Rv1563c Rv1563c Rv1563c Rv1563c Rv1781c Rv2471	sigJ sigK sigL sigM spoU truA truB tsnR - - ccharides (c glgB glgP glgZ glgY glgZ - -	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate syn- thase tRNA pseudouridine 55 synthase putative 23S rRNA methyltrans- ferase ATP-dependent DNA/RNA heli- case cytoplasmic) 1,4-α-glucan branching enzyme probable glycogen phosphory- lase probable glycogen debranching enzyme putative α-amylase maltooligosyltrehalose trehalohy- drolase probable glycosyl hydrolase probable maltase α-glucosidase	RV0220 RV1923 RV1927 RV3487c RV0646c RV1399c RV1400c RV1900c RV2485c RV2463 RV2485c RV2463 RV2485c RV2465c RV2045c RV2	lipC lipD lipF lipF lipF lipH lipI lipI lipN lipU lipN lipO lipR lipU lipU lipU lipU lipU lipU lipU lipU	probable esterase probable esterase probable hydrolase probable hydrolase probable hydrolase probable lipase probable lipase probable lipase probable lipase probable esterase probable carboxlyesterase probable carboxlyesterase probable carboxylesterase probable esterase/lipase probable lipase probable lipase probable lipase probable prospholipase C precursor phospholipase C precursor phospholipase C precursor phospholipase C prospholipase C probable probable esterase probable esterase phospholipase C precursor phospholipase C precursor phospholipase C precursor phospholipase C precursor phospholipase Probable esterase pseudoger
RV3585 RV2737c RV0630c RV0630c RV0631c RV0629c RV0629c RV0003 RV2973c RV2736c RV2592c RV2592c RV2594c RV0054 RV1210 RV3646c RV2976c RV1638 RV1	priA radA recA recB recC recD recF recR recX ruvA ruvB ruvC ssb tagA topA ung uvrA uvrB	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induction ATP-dependent DNA helicase recombination and DNA repair RecBC-Independent process of DNA repair regulatory protein for RecA Holliday junction binding protein, DNA helicase Holliday junction binding protein Holliday junction resolvase, endo-deoxyribonuclease single strand binding protein DNA-3-methyladenine glycosi-dase I DNA topoisomerase uracil-DNA glycosylase excinuclease ABC subunit A excinuclease ABC subunit B	RV1189 RV3328c RV0445c RV0735 RV3911 RV3366 RV3455c RV2793c RV1644 RV3649 8. Polysac RV1326c RV1328 RV1563c RV1563c RV1563c RV1563c RV1563c RV1781c RV2471 B. Degrad	sigJ sigK sigL sigM spoU truA truB tsnR - - ccharides (c glgB glgP glgZ glgY glgZ - -	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate syn- thase tRNA pseudouridine 55 synthase putative 23S rRNA methyltrans- ferase ATP-dependent DNA/RNA heli- case cytoplasmic) 1,4-α-glucan branching enzyme probable glycogen debranching enzyme putative α-amylase maltooligosyltrehalose trehalohy- drolase probable glycosyl hydrolase probable glycosyl hydrolase probable glycosyl hydrolase probable glycosyl hydrolase	RV0220 RV1923 RV1927 RV3487c RV0646c RV1399c RV1400c RV1900c RV2485c RV2485c RV2485c RV2485c RV3084 RV3176c RV2045c RV	lipC lipC lipE lipE lipF lipF lipH lipI lipI lipI lipN lipD lipN lipO lipP lipO lipP lipV lipU lipV plcA plcB plcC plcD	probable esterase probable esterase probable hydrolase probable hydrolase probable hydrolase probable lipase probable lipase probable lipase probable lipase probable esterase probable acetyl-hydrolase probable esterase/lipase probable esterase/lipase probable esterase probable esterase probable esterase probable esterase probable esterase probable probable esterase probable probable esterase probable probable esterase probable lipase C precursor phospholipase C precursor phospholipase C precursor partial CDS for phospholipase probable esterase pseudoger probable esterase pseudoger probable esterase pseudoger probable esterase pseudoger
RV3585 RV2737c RV0630c RV0630c RV0631c RV0629c RV0629c RV0003 RV2973c RV2736c RV2592c RV2592c RV2594c RV0054 RV1210 RV3646c RV2976c RV1638 RV1	priA radA recA recB recC recD recF recR recX ruvA ruvB ruvC ssb tagA topA ung uvrA uvrB uvrC uvrD	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induction ATP-dependent DNA helicase recombination and DNA repair RecBC-Independent process of DNA repair regulatory protein for RecA Holliday junction binding protein, DNA helicase Holliday junction binding protein Holliday junction resolvase, endo- deoxyribonuclease single strand binding protein DNA-3-methyladenine glycosi- dase I DNA topoisomerase uracil-DNA glycosylase excinuclease ABC subunit A excinuclease ABC subunit C DNA-dependent ATPase I and helicase II	RV1189 RV3328c RV0445c RV0735 RV3911 RV3366 RV3455c RV2793c RV1644 RV3649 8. POlysac RV1326c RV1328 RV1564c RV1563c RV1562c RV0126 RV1781 RV2471 B. Degradd 1. RNA	sigJ sigK sigL sigM spoU truA truB tsnR - ccharides (c glgB glgP glgX glgY glgZ - - -	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable glycogen phosphory-lase probable glycogen debranching enzyme probable glycogen debranching enzyme putative α-amylase maltooligosyltrehalose trehalohy-drolase probable glycosyl hydrolase probable glycosyl hydrolase probable maltase α-glucosidase probable maltase α-glucosidase	RV0220 RV1923 RV1923 RV3775 RV3487c RV0446c RV1399c RV1400c RV2385 RV1497 RV2284 RV2970c RV1426c RV2463 RV2485c RV3084 RV2176c RV3176c RV3176c RV3176c RV3176c RV3203 RV217c RV3203 RV2485c RV3076 RV3203 RV217c RV3511c RV351	lipC lipD lipE lipF lipF lipH lipI lipJ lipK lipL lipM lipM lipM lipO lipQR lipP lipD lipQR lipP lipU lipV lipV plcA plcD plcD c t hydrocar	probable esterase probable esterase probable esterase probable hydrolase probable hydrolase probable lipase probable lipase probable lipase probable lipase probable esterase probable carboxlyesterase probable esterase/probable esterase/probable esterase/probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase pseudoger probable probable esterase pseudoger probable esterase pseudoger probable esterase pseudoger probable probable esterase pseudoger probable esterase pseudoger probable probable esterase pseudoger probable probable probable esterase pseudoger probable pseudoger probable probable probable probable pseudoger probable probable probable probable pseudoger probable probable probable pseudoger probable probable probable pseudoger probable probable probable pseudoger probable pseudoger probable probable pseudoger probable probable pseudoger probable pseudoger probable pseudoger probable pseudoger probable pseudoger probable probable probable pseudoger pseudoger probable pseudoger probable pseudoger probable pseudoger prob
RV3585 RV2737c RV0630c RV0630c RV0630c RV0629c RV0003 RV2973c RV1696 RV3715c RV2594c RV2594c RV0054 RV1210 RV3646c RV2976c RV1638 RV12976c RV1638 RV1420 RV0949 RV3198c	priA radA recA recB recC recD recF recR recX ruvA ruvB ruvC ssb tagA topA ung uvrA uvrB uvrC uvrD uvrD2	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V but replication and SOS induction ATP-dependent DNA helicase recombination and DNA repair RecBC-Independent process of DNA repair regulatory protein for RecA Holliday junction binding protein, DNA helicase Holliday junction binding protein Holliday junction resolvase, endo- deoxyribonuclease single strand binding protein DNA-3-methyladenine glycosi- dase 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	Rv1189 Rv3328c Rv0445c Rv0735 Rv3911 Rv3366 Rv3455c Rv2793c Rv1644 Rv3649 8. Polysac Rv1326c Rv1328 Rv1564c Rv1563c Rv1563c Rv1563c Rv1781c Rv2471 B. Degrad 1. RNA	sigJ sigK sigL sigM spoU truA truB tsnR - - ccharides (c glgB glgP glgZ glgZ glgY glgZ - - -	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate syn- thase tRNA pseudouridine 55 synthase putative 23S rRNA methyltrans- ferase ATP-dependent DNA/RNA heli- case cytoplasmic) 1,4-α-glucan branching enzyme probable glycogen phosphory- lase probable glycogen debranching enzyme putative α-amylase maltooligosyltrehalose trehalohy- drolase probable glycosyl hydrolase probable glycosyl hydrolase probable maltase α-glucosidase acromolecules peptidyl-tRNA hydrolase	RV0220 RV1923 RV1923 RV3775 RV3487c RV0446c RV1399c RV1400c RV2385 RV1497 RV2284 RV2970c RV1426c RV2463 RV2485c RV3084 RV2176c RV3176c RV3176c RV3176c RV3176c RV3203 RV217c RV3203 RV2485c RV3076 RV3203 RV217c RV3511c RV351	lipC lipC lipE lipE lipF lipF lipH lipI lipI lipI lipN lipD lipN lipO lipP lipO lipP lipV lipU lipV plcA plcB plcC plcD	probable esterase probable esterase probable esterase probable hydrolase probable hydrolase probable lipase probable lipase probable lipase probable lipase probable lipase probable esterase probable earby/systerase probable earby/systerase probable earby/systerase probable earby/systerase probable esterase/lipase probable esterase probable esterase probable lipase probable esterase probable lipase C precursor phospholipase C precursor phospholipase C precursor partial CDS for phospholipase probable esterase pseudoger probable esterase pseudoger probable esterase pseudoger probable esterase pseudoger
RV3585 RV2737c RV0630c RV0630c RV0629c RV0629c RV0003 RV2973c RV1696 RV3715c RV2736c RV2592c RV2592c RV2592c RV0054 RV1100 RV3646c RV1638 RV368 R	priA radA recA recB recC recD recF recR recX ruvA ruvB ruvC ssb tagA topA ung uvrA uvrB uvrC uvrD	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induction ATP-dependent DNA helicase recombination and DNA repair RecBC-Independent process of DNA repair regulatory protein for RecA Holliday junction binding protein, DNA helicase Holliday junction binding protein Holliday junction resolvase, endodeoxyribonuclease single strand binding protein DNA-3-methyladenine glycosidase I DNA topoisomerase uracil-DNA glycosylase excinuclease ABC subunit A excinuclease ABC subunit A excinuclease ABC subunit C DNA-dependent ATPase I and helicase II putative UvrD exodeoxyribonuclease III	RV1189 RV32826 RV03425c RV0735 RV3911 RV3366 RV3455c RV2793c RV1644 RV3649 8. Polysac RV1326c RV1328 RV1563c R	sigJ sigK sigL sigM spoU truA truB tsnR - ccharides (c glgB glgP glgX glgY glgZ - - - lation of ma	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate syn- thase tRNA pseudouridine 55 synthase putative 23S rRNA methyltrans- ferase ATP-dependent DNA/RNA heli- case cytoplasmic) 1,4-α-glucan branching enzyme probable glycogen phosphory- lase probable glycogen debranching enzyme putative α-amylase maltooligosyltrehalose trehalohy- drolase probable glycosyl hydrolase probable d-α-glucanotransferase probable maltase α-glucosidase acromolecules peptidyl-tRNA hydrolase RNAse III	RV0220 RV1923 RV1923 RV3775 RV3487c RV0648c RV13990 RV1400c RV1900c RV2485c RV2485 RV2485c RV2463 RV2485c RV2465 RV20455c RV2045c RV20	lipC lipD lipE lipE lipF lipG lipH lipI lipI lipU lipW lipO lipU lipU lipU lipU lipU lipU lipU lipU	probable esterase probable esterase probable esterase probable hydrolase probable hydrolase probable lipase probable lipase probable lipase probable lipase probable esterase lipase probable esterase/lipase probable esterase pseudoger probable esterase pseudoger probable esterase pseudoger probable 4-hydroxy-2-oxovale aldolase
RV3585 RV2737c RV2737c RV0631c RV0631c RV0631c RV0631c RV0631c RV0631c RV2973c RV2973c RV2593c RV2593c RV2593c RV2594c RV0054 RV1210 RV3646c RV2976c RV1638	priA radA recA recB recC recD recF recR recX ruvA ruvB ruvC ssb tagA topA ung uvrB uvrC uvrD vvrD2 xthA	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induction ATP-dependent DNA helicase recombination and DNA repair RecBC-Independent process of DNA repair regulatory protein for RecA Holliday junction binding protein, DNA helicase Holliday junction binding protein Holliday junction resolvase, endo-deoxyribonuclease single strand binding protein DNA-3-methyladenine glycosi-dase I DNA topoisomerase uracil-DNA glycosylase excinuclease ABC subunit A excinuclease ABC subunit C DNA-dependent ATPase I and helicase I putative UvrD exodeoxyribonuclease III group II intron maturase	Rv1189 Rv3328c Rv0445c Rv0735 Rv3911 Rv3366 Rv3455c Rv2793c Rv1644 Rv3649 8. Polysac Rv1326c Rv1328 Rv1564c Rv1563c Rv1563c Rv1563c Rv1781c Rv2471 B. Degrad 1. RNA	sigJ sigK sigL sigM spoU truA truB tsnR - - ccharides (c glgB glgP glgZ glgZ glgY glgZ - - -	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable pseudouridylate syn- thase tRNA pseudouridine 55 synthase putative 23S rRNA methyltrans- ferase ATP-dependent DNA/RNA heli- case cytoplasmic) 1,4-α-glucan branching enzyme probable glycogen phosphory- lase probable glycogen debranching enzyme putative α-amylase maltooligosyltrehalose trehalohy- drolase probable maltase α-glucosidase acromolecules	RV0220 RV1923 RV1923 RV3775 RV3487c RV0446c RV1399c RV1400c RV2385 RV1497 RV2284 RV2970c RV1426c RV2463 RV2485c RV3084 RV2176c RV3176c RV3176c RV3176c RV3176c RV3203 RV217c RV3203 RV2485c RV3076 RV3203 RV217c RV3511c RV351	lipC lipD lipE lipF lipF lipH lipI lipJ lipK lipL lipM lipM lipM lipO lipQR lipP lipD lipQR lipP lipU lipV lipV plcA plcD plcD c t hydrocar	probable esterase probable esterase probable esterase probable hydrolase probable hydrolase probable lipase probable lipase probable lipase probable lipase probable esterase probable esterase pseudoger probable 4-hydroxy-2-oxovale aldolase probable muconolactone iso-
RV3585 RV2737c RV0630c RV0630c RV0631c RV0629c RV0003 RV2973c RV1696 RV3715c RV2593c RV2592c RV2594c RV0054 RV1210 RV3646c RV2976c RV1638 RV1420 RV0949 RV3198c RV0949 RV3198c RV0949 RV3198c RV00861c	priA radA recA recB recC recD recF recG recN recR ruvA ruvB ruvC ssb tagA topA ung uvrA uvrB uvrC uvrD uvrD uvrD2 xthA	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease recombination and DNA repair RecBC-Independent process of DNA repair regulatory protein for RecA Holliday junction binding protein, DNA helicase Holliday junction binding protein Holliday junction resolvase, endo- deoxyribonuclease single strand binding protein DNA-3-methyladenine glycosi- dase I DNA topoisomerase uracil-DNA glycosylase excinuclease ABC subunit A excinuclease ABC subunit A excinuclease ABC subunit C DNA-dependent ATPase I and helicase II putative UvrD exodeoxyribonuclease III group II intron maturase probable DNA helicase	RV1189 RV3328c RV0445c RV0735 RV3911 RV3366 RV3455c RV2793c RV1644 RV3649 8. Polysac RV1326c RV1328 RV1564c RV1563c RV1563c RV1563c RV1781c RV2471 B. Degrad 1. RNA RV1014c RV2925c RV2444c	sigJ sigK sigL sigM spoU truA truB tsnR - ccharides (c glgB glgP glgZ c tation of map th rmc rne	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate syn- thase tRNA pseudouridine 55 synthase putative 23S rRNA methyltrans- ferase ATP-dependent DNA/RNA heli- case cytoplasmic) 1,4-α-glucan branching enzyme probable glycogen phosphory- lase probable glycogen debranching enzyme putative α-amylase maltooligosyltrehalose trehalohy- drolase probable glycosyl hydrolase probable glycosyl hydrolase probable maltase α-glucosidase acromolecules peptidyl-tRNA hydrolase RNAse III similar at C-term to ribo- nuclease E	RV0220 RV1923 RV1927 RV3487c RV0486c RV1399c RV1400c RV1909c RV2385 RV1497 RV22845 RV2970c RV1426c RV2485c RV3084 RV3176c RV3176c RV31076 RV3203 RV0217c RV3205 RV1104 RV31765 RV3106 RV	lipC lipC lipE lipE lipF lipF lipG lipH lipI lipJ lipU lipM lipO lipO lipO lipO lipO lipC lipU lipU lipU lipU lipU c r lipU lipW c lipU lipW c lipC lipU lipW c lipC lipU lipW c lipU lipW lipW lipC lipU lipW lipU lipW lipU lipW lipU lipW lipU lipW lipU lipW lipU lipU lipU lipU lipU lipU lipU lipU	probable esterase probable esterase probable esterase probable hydrolase probable hydrolase probable lipase probable lipase probable lipase probable lipase probable lipase probable esterase probable earboxlyesterase probable earboxlyesterase probable earboxlyesterase probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase probable lipase probable esterase probable lipase C precursor phospholipase C precursor phospholipase C precursor partial CDS for phospholipase probable esterase pseudoger probable esterase pseudoger probable esterase pseudoger probable 4-hydroxy-2-oxovale aldolase probable muconolactone isomerase
RV3585 RV2737c RV0630c RV0630c RV0631c RV0629c RV0003 RV2973c RV1696 RV3715c RV2593c RV2592c RV2594c RV0054 RV1210 RV3646c RV2976c RV1638 RV1420 RV0949 RV3198c RV0949 RV3198c RV0949 RV3198c RV00861c	priA radA recA recB recC recD recF recR recX ruvA ruvB ruvC ssb tagA topA ung uvrB uvrC uvrD vvrD2 xthA	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induction ATP-dependent DNA helicase recombination and DNA repair RecBC-Independent process of DNA repair regulatory protein for RecA Holliday junction binding protein, DNA helicase Holliday junction binding protein Holliday junction 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 exodeoxyribonuclease III group II intron maturase probable DNA helicase possible formamidopyrimidine-	RV1189 RV32826 RV03445c RV0735 RV3911 RV3366 RV2793c RV1644 RV3649 8. Polysac RV1326c RV1326c RV1563c RV1563c RV1563c RV1563c RV1563c RV1563c RV1563c RV1781c RV2471 B. Degrad 1. RN14 RV10146 RV2925c RV2444c RV2902c	sigJ sigK sigM spoU truA truB tsnR - ccharides (cglgB glgP glgZ lation of map th mc rne rnbB	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate syn- thase tRNA pseudouridine 55 synthase putative 23S rRNA methyltrans- ferase ATP-dependent DNA/RNA heli- case cytoplasmic) 1,4-α-glucan branching enzyme probable glycogen phosphory- lase probable glycogen debranching enzyme putative α-amylase maltooligosyltrehalose trehalohy- drolase probable glycosyl hydrolase probable d-α-glucanotransferase probable maltase α-glucosidase acromolecules peptidyl-tRNA hydrolase RNAse III similar at C-term to ribo- nuclease E ribonuclease HII	RV0220 RV1923 RV1923 RV3775 RV3487c RV0648c RV13990 RV1400c RV1900c RV2485c RV2485 RV2485c RV2463 RV2485c RV2465 RV20455c RV2045c RV20	lipC lipD lipE lipE lipF lipG lipH lipI lipI lipU lipW lipO lipU lipU lipU lipU lipU lipU lipU lipU	probable esterase probable esterase probable hydrolase probable hydrolase probable hydrolase probable lipase probable lipase probable lipase probable lipase probable esterase lipase probable esterase/lipase probable esterase pseudoger probable esterase pseudoger probable 4-hydroxy-2-oxovale aldolase probable 4-carboxymuconola:
RV1402 RV3585 RV2737c RV0630c RV0631c RV0639c RV0629c RV0003 RV2973c RV1696 RV3715c RV2736c RV2593c RV2593c RV2594c RV054 RV110 RV3646c RV1638 RV1633 RV1633 RV1633 RV1694 RV1688	priA radA recA recB recC recD recF recG recN recR ruvA ruvB ruvC ssb tagA topA ung uvrA uvrB uvrC uvrD uvrD uvrD2 xthA	putative primosomal protein n' (replication factor Y) probable DNA repair RadA homologue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease recombination and DNA repair RecBC-Independent process of DNA repair regulatory protein for RecA Holliday junction binding protein, DNA helicase Holliday junction binding protein Holliday junction resolvase, endo- deoxyribonuclease single strand binding protein DNA-3-methyladenine glycosi- dase I DNA topoisomerase uracil-DNA glycosylase excinuclease ABC subunit A excinuclease ABC subunit A excinuclease ABC subunit C DNA-dependent ATPase I and helicase II putative UvrD exodeoxyribonuclease III group II intron maturase probable DNA helicase	RV1189 RV3328c RV0445c RV0735 RV3911 RV3366 RV3455c RV2793c RV1644 RV3649 8. Polysac RV1326c RV1328 RV1564c RV1563c RV1563c RV1563c RV1781c RV2471 B. Degrad 1. RNA RV1014c RV2925c RV2444c	sigJ sigK sigL sigM spoU truA truB tsnR - ccharides (c glgB glgP glgZ c tation of map th rmc rne	similar to Sigl, ECF family ECF-type sigma factor sigma-70 factors ECF subfamily probable sigma factor, similar to SigE probable rRNA methylase probable pseudouridylate syn- thase tRNA pseudouridine 55 synthase putative 23S rRNA methyltrans- ferase ATP-dependent DNA/RNA heli- case cytoplasmic) 1,4-α-glucan branching enzyme probable glycogen phosphory- lase probable glycogen debranching enzyme putative α-amylase maltooligosyltrehalose trehalohy- drolase probable glycosyl hydrolase probable glycosyl hydrolase probable maltase α-glucosidase acromolecules peptidyl-tRNA hydrolase RNAse III similar at C-term to ribo- nuclease E	RV0220 RV1923 RV1927 RV3487c RV0486c RV1399c RV1400c RV1909c RV2385 RV1497 RV22845 RV2970c RV1426c RV2485c RV3084 RV3176c RV3176c RV31076 RV3203 RV0217c RV3205 RV1104 RV31765 RV3106 RV	lipC lipC lipE lipE lipF lipF lipG lipH lipI lipJ lipU lipM lipO lipO lipO lipO lipO lipC lipU lipU lipU lipU lipU c r lipU lipW c lipU lipW c lipC lipU lipW c lipC lipU lipW c lipU lipW lipW lipC lipU lipW lipU lipW lipU lipW lipU lipW lipU lipU lipU lipU lipU lipU lipU lipU	probable esterase probable esterase probable esterase probable hydrolase probable hydrolase probable lipase probable lipase probable lipase probable lipase probable lipase probable esterase probable earboxlyesterase probable earboxlyesterase probable earboxlyesterase probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase probable lipase probable esterase probable lipase C precursor phospholipase C precursor phospholipase C precursor partial CDS for phospholipase probable esterase pseudoger probable esterase pseudoger probable esterase pseudoger probable 4-hydroxy-2-oxovale aldolase probable muconolactone isomerase

D. 0745		lase	Rv1367c	-	probable penicillin binding protein	Rv1030	kdpB	potassium-transporting ATPase B
Rv2715	-	2-hydroxymuconic semialdehyde	Rv1730c	-	probable penicillin binding protein			chain
Rv3530c	_	hydrolase	Rv1922 Rv2864c	-	probable penicillin binding protein probable penicillin binding protein	Rv1031	kdpC	potassium-transporting ATPase C
Rv3534c	-	probable <i>cis</i> -diol dehydrogenase 4-hydroxy-2-oxovalerate aldolase	Rv3330	-	probable penicillin binding protein	Rv3236c	kefB	chain probable glutathione-regulated
Rv3536c	-	aromatic hydrocarbon degrada-	Rv3627c	-	probable penicillin binding protein			potassium-efflux protein
		tion	4 Canaan			Rv2877c	merT	possible mercury resistance
C. Cell en	velone		Rv0402c	mmpL1	rane proteins conserved large membrane	Rv1811	mgtC	transport system probable magnesium transport
1. Lipopro		<i>l-lpr0</i>) 65	11101020	•	protein		g.c	ATPase protein C
			Rv0507	mmpL2	conserved large membrane	Rv0362	mgtE	putative magnesium ion
2. Surface teins and		narides, lipopolysaccharides, pro-	Rv0206c	mmpL3	protein conserved large membrane	Rv2856	nicT	transporter probable nickel transport protein
Rv0806c	cpsY	probable UDP-glucose-4-	11102000	ППРЕЗ	protein	Rv0924c	nramp	transmembrane protein belonging
		epimerase	Rv0450c	mmpL4	conserved large membrane			to Nramp family
Rv3811	csp dsbF	secreted protein	Dv06760	mmpL5	protein	Rv2691	trkA	probable potassium uptake pro-
Rv1677 Rv3794	embA	highly similar to C-term Mpt53 involved in arabinogalactan syn-	Rv0676c	ппрьз	conserved large membrane protein	Rv2692	trkB	tein probable potassium uptake pro-
		thesis	Rv1557	mmpL6	conserved large membrane			tein
Rv3795	embB	involved in arabinogalactan syn-	D 0010		protein	Rv2287	yjcE	probable Na+/H+ exchanger
Rv3793	embC	thesis involved in arabinogalactan syn-	Rv2942	mmpL7	conserved large membrane protein	Rv2723	-	probable membrane protein, tellurium resistance
1110700	cinbo	thesis	Rv3823c	mmpL8	conserved large membrane	Rv3162c	-	probable membrane protein
Rv3875	esat6	early secretory antigen target	D 0000		protein	Rv3237c	-	possible potassium channel
Rv0112	gca	probable GDP-mannose dehy- dratase	Rv2339	mmpL9	conserved large membrane protein	Rv3743c		protein probable cation-transporting
Rv0113	gmhA	phosphoheptose isomerase	Rv1183	mmpL10	conserved large membrane	1007400		ATPase
Rv2965c	kdtB	lipopolysaccharide core biosyn-			protein		OI	
Dv2070a	mntF2	thesis protein	Rv0202c	mmpL11	conserved large membrane			rganic acids and alcohols
Rv2878c Rv1980c	mpt53 mpt64	secreted protein Mpt53 secreted immunogenic protein	Rv1522c	mmnl 12	protein conserved large membrane	Rv2443 Rv3476c	dctA kgtP	C4-dicarboxylate transport protein sugar transport protein
		Mpb64/Mpt64			protein	Rv1902c	nanT	probable sialic acid transporter
Rv2875	mpt70	major secreted immunogenic pro-	Rv0403c	mmpS1	conserved small membrane	Rv1236	sugA	membrane protein probably
Rv2873	mpt83	tein Mpt70 precursor surface lipoprotein Mpt83	Rv0506	mmpS2	protein conserved small membrane	Rv1237	sugB	involved in sugar transport sugar transport protein
Rv0899	ompA	member of OmpA family	1770300	mmpsz	protein	Rv1237	sugC	ABC transporter component of
Rv3810	pirG	cell surface protein precursor (Erp	Rv2198c	mmpS3	conserved small membrane			sugar uptake system
Rv3782	rfbE	protein)	Rv0451c	mmpS4	protein conserved small membrane	Rv3331 Rv2835c	sugl	probable sugar transport protein
Rv1302	rfe	similar to rhamnosyl transferase undecaprenyl-phosphate α-N-	KV04510	ППР34	protein	KV20300	ugpA	sn-glycerol-3-phosphate permease
		acetylglucosaminyltransferase	Rv0677c	mmpS5	conserved small membrane	Rv2833c	ugpB	sn-glycerol-3-phosphate-binding
Rv2145c	wag31	antigen 84 (aka wag31)			protein	D 0000		periplasmic lipoprotein
Rv0431 Rv0954	-	tuberculin related peptide (AT103) cell envelope antigen	5 Other m	embrane i	proteins 211	Rv2832c	ugpC	sn-glycerol-3-phosphate transport ATP-binding protein
Rv1514c	-	involved in polysaccharide syn-	0. 0010111	iombrano _l	STOLENIO ZTT	Rv2834c	ugpE	sn-glycerol-3-phosphate transport
		thesis	III. Cell pr					system protein
Rv1518	-	involved in exopolysaccharide synthesis	A. Transpo		proteins	Rv2316 Rv2318	uspA uspC	sugar transport protein
Rv1758	_	partial cutinase	Rv2127	ansP	L-asparagine permease	Rv2317	uspE	sugar transport protein sugar transport protein
Rv1910c	-	probable secreted protein	Rv0346c	aroP2	probable aromatic amino acid	Rv1200	-	probable sugar transporter
Rv1919c	-	weak similarity to pollen antigens			permease	Rv2038c	-	probable ABC sugar transporter
Rv1984c	-	probable secreted protein	Rv0917	betP	glycine betaine transport	Rv2039c	-	probable sugar transporter
Rv1987	-	probable secreted protein	Rv1704c	cycA	transport of D-alanine, D-serine and glycine	Rv2040c Rv2041c	-	probable sugar transporter probable sugar transporter
	_	probable exported protesse						
Rv2223c Rv2224c	-	probable exported protease probable exported protease	Rv3666c	dppA		KV20410		probable sugar transporter
Rv2223c Rv2224c Rv2301		probable exported protease probable cutinase	Rv3666c	dppA	probable peptide transport system permease	4. Anions		probable sugar transporter
Rv2224c	-	probable exported protease probable cutinase precursor of probable membrane	Rv3666c Rv3665c	dppA dppB	probable peptide transport system permease probable peptide transport system	4. Anions Rv2684	arsA	probable arsenical pump
Rv2224c Rv2301 Rv2345	-	probable exported protease probable cutinase precursor of probable membrane protein	Rv3665c	dppB	probable peptide transport system permease probable peptide transport system permease	4. Anions Rv2684 Rv2685	arsA arsB	probable arsenical pump probable arsenical pump
Rv2224c Rv2301	-	probable exported protease probable cutinase precursor of probable membrane			probable peptide transport system permease probable peptide transport system	4. Anions Rv2684	arsA	probable arsenical pump
Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c	-	probable exported protease probable cutinase precursor of probable membrane protein putative exported protease similar to Esat6 probable secreted protein	Rv3665c Rv3664c Rv3663c	dppB dppC dppD	probable peptide transport system permease probable peptide transport system permease probable peptide transport system permease probable ABC-transporter	4. Anions Rv2684 Rv2685 Rv3578	arsA arsB arsB2	probable arsenical pump probable arsenical pump probable arsenical pump probable arsenical pump sulphate transport ATP-binding
Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c	-	probable exported protease probable cutinase precursor of probable membrane protein putative exported protease similar to Esat6 probable secreted protein probable precursor of serine pro-	Rv3665c Rv3664c	dppB dppC	probable peptide transport system permease probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable 4-amino butyrate trans-	4. Anions Rv2684 Rv2685 Rv3578 Rv2643 Rv2397c	arsA arsB arsB2 arsC cysA	probable arsenical pump probable arsenical pump probable arsenical pump probable arsenical pump sulphate transport ATP-binding protein
Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c Rv3449	-	probable exported protease probable cutinase precursor of probable membrane protein putative exported protease similar to Esat6 probable secreted protein probable precursor of serine protease	Rv3665c Rv3664c Rv3663c Rv0522	dppB dppC dppD gabP	probable peptide transport system permease probable ABC-transporter probable 4-amino butyrate transporter	4. Anions Rv2684 Rv2685 Rv3578 Rv2643	arsA arsB arsB2 arsC	probable arsenical pump probable arsenical pump probable arsenical pump probable arsenical pump sulphate transport ATP-binding protein sulphate transport system perme-
Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c	-	probable exported protease probable cutinase precursor of probable membrane protein putative exported protease similar to Esat6 probable secreted protein probable precursor of serine pro-	Rv3665c Rv3664c Rv3663c	dppB dppC dppD	probable peptide transport system permease probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable 4-amino butyrate trans-	4. Anions Rv2684 Rv2685 Rv3578 Rv2643 Rv2397c	arsA arsB arsB2 arsC cysA	probable arsenical pump probable arsenical pump probable arsenical pump probable arsenical pump sulphate transport ATP-binding protein
Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c Rv3449		probable exported protease probable cutinase precursor of probable membrane protein putative exported protease similar to Esat6 probable secreted protein probable precursor of serine protease probable cutinase	Rv3665c Rv3664c Rv3663c Rv0522 Rv0411c Rv2564	dppB dppC dppD gabP glnH glnQ	probable peptide transport system permease probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable ABC-transporter probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein	4. Anions Rv2684 Rv2685 Rv3578 Rv2643 Rv2397c Rv2399c Rv2398c	arsA arsB arsB2 arsC cysA cysT	probable arsenical pump probable arsenical pump probable arsenical pump probable arsenical pump sulphate transport ATP-binding protein sulphate transport system perme- ase protein sulphate transport system perme- ase protein
Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c Rv3449 Rv3451 Rv3452 Rv3724		probable exported protease probable cutinase precursor of probable membrane protein putative exported protease similar to Esat6 probable secreted protein probable precursor of serine protease probable cutinase probable cutinase probable cutinase precursor probable cutinase precursor	Rv3665c Rv3664c Rv3663c Rv0522 Rv0411c	dppB dppC dppD gabP glnH	probable peptide transport system permease probable ABC-transporter probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport	4. Anions Rv2684 Rv2685 Rv3578 Rv2643 Rv2397c Rv2399c Rv2398c Rv1857	arsA arsB arsB2 arsC cysA cysT cysW modA	probable arsenical pump probable arsenical pump probable arsenical pump probable arsenical pump sulphate transport ATP-binding protein sulphate transport system perme- ase protein sulphate transport system perme- ase protein molybdate binding protein
Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c Rv3449 Rv3451 Rv3452 Rv3724		probable exported protease probable cutinase precursor of probable membrane protein putative exported protease similar to Esat6 probable secreted protein probable precursor of serine protease probable cutinase probable cutinase probable cutinase	Rv3665c Rv3664c Rv3663c Rv0522 Rv0411c Rv2564	dppB dppC dppD gabP glnH glnQ	probable peptide transport system permease probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein	4. Anions Rv2684 Rv2685 Rv3578 Rv2643 Rv2397c Rv2399c	arsA arsB arsB2 arsC cysA cysT	probable arsenical pump probable arsenical pump probable arsenical pump probable arsenical pump sulphate transport ATP-binding protein sulphate transport system perme- ase protein sulphate transport system perme- ase protein
Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv2981c		probable exported protease probable cutinase precursor of probable membrane protein putative exported protease similar to Esat6 probable secreted protein probable secreted protein probable precursor of serine protease probable cutinase precursor land peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A	Rv3665c Rv3664c Rv3663c Rv0522 Rv0411c Rv2564 Rv1280c	dppB dppC dppD gabP glnH glnQ oppA	probable peptide transport system permease probable peptide transport system permease probable peptide transport system permease probable ABC-transporter 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-	4. Anions Rv2684 Rv2685 Rv3578 Rv2643 Rv2397c Rv2399c Rv2398c Rv1857	arsA arsB arsB2 arsC cysA cysT cysW modA	probable arsenical pump probable arsenical pump probable arsenical pump probable arsenical pump probable arsenical pump sulphate transport ATP-binding protein sulphate transport system perme- ase protein sulphate transport system perme- ase protein molybdate binding protein transport system permease, molybdate uptake molybdate uptake
Rv2224c Rv2301 Rv2345 Rv2345 Rv3019c Rv3036c Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv2981c Rv3809c	- - - - - sacculus a dacB ddlA glf	probable exported protease probable cutinase precursor of probable membrane protein putative exported protease similar to Esat6 probable secreted protein probable precursor of serine protease probable cutinase proteinse probable cutinase proteinsor probable cutinase precursor probable cutinase precursor probable cutinase precursor protein D-alanine-D-alanine ligase A UDP-galactopyranose mutase	Rv3665c Rv3664c Rv3663c Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c	dppB dppC dppD gabP glnH glnQ oppA oppB oppC	probable peptide transport system permease probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable ABC-transporter 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	4. Anions Rv2684 Rv2685 Rv3578 Rv2643 Rv2399c Rv2399c Rv2398c Rv1857 Rv1858	arsA arsB arsB2 arsC cysA cysT cysW modA modB	probable arsenical pump probable arsenical pump probable arsenical pump probable arsenical pump probable arsenical pump sulphate transport ATP-binding protein 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
Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv2981c		probable exported protease probable extinase precursor of probable membrane pretein putative exported protease similar to Esat6 probable secreted protein probable secreted protein probable precursor of serine protease probable cutinase probable cutinase probable cutinase precursor probable cutinase precursor und peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-N-acetylglucosamine	Rv3665c Rv3664c Rv3663c Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1281c	dppB dppC dppD gabP ginH glnQ oppA oppB oppC oppD	probable peptide transport system permease probable peptide transport system permease probable peptide transport system permease probable ABC-transporter 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	4. Anions Rv2684 Rv2685 Rv3578 Rv2643 Rv2397c Rv2399c Rv2398c Rv1857 Rv1858	arsA arsB arsB2 arsC cysA cysT cysW modA modB	probable arsenical pump sulphate transport ATP-binding protein 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
Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv2981c Rv3809c Rv1018c	- - - - - - sacculus a dacB ddIA glf glmU	probable exported protease probable cutinase precursor of probable membrane protein putative exported protease similar to Esat6 probable secreted protein probable secreted protein probable precursor of serine protease probable cutinase precursor probable pro	Rv3665c Rv3664c Rv3663c Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1281c Rv2320c	dppB dppC dppD gabP glnH glnQ oppA oppB oppC	probable peptide transport system permease probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable 4-amino butyrate transporter probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport system permease probable peptide transport protein arginine/ornithine transporter	4. Anions Rv2684 Rv2685 Rv3578 Rv2643 Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1859	arsA arsB arsB2 arsC cysA cysT cysW modA modB	probable arsenical pump sulphate transport ATP-binding protein sulphate transport system permease protein sulphate transport system permease protein molybdate binding protein transport system permease, molybdate uptake molybdate uptake MBC-transporter precursor of Apa (45/47 kD secreted protein)
Rv2224c Rv2301 Rv2345 Rv2345 Rv3019c Rv3036c Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv2981c Rv3809c	- - - - - sacculus a dacB ddlA glf	probable exported protease probable extinase precursor of probable membrane pretein putative exported protease similar to Esat6 probable secreted protein probable secreted protein probable precursor of serine protease probable cutinase probable cutinase probable cutinase precursor probable cutinase precursor und peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-N-acetylglucosamine	Rv3665c Rv3664c Rv3663c Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1281c Rv2320c Rv3253c	dppB dppC dppD gabP ginH glnQ oppA oppB oppC oppD	probable peptide transport system permease probable peptide transport system permease probable peptide transport system permease probable ABC-transporter 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	4. Anions Rv2684 Rv2685 Rv3578 Rv2643 Rv2399c Rv2399c Rv2398c Rv1857 Rv1858	arsA arsB arsB2 arsC cysA cysT cysW modA modB	probable arsenical pump sulphate transport ATP-binding protein 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
Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv2981c Rv3809c Rv1018c		probable exported protease probable cutinase precursor of probable membrane protein putative exported protease similar to Esat6 probable secreted protein probable secreted protein probable precursor of serine protease probable cutinase precursor probable pr	Rv3665c Rv3664c Rv3663c Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1281c Rv2320c	dppB dppC dppD gabP ginH glnQ oppA oppB oppC oppD	probable peptide transport system permease probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable ABC-transporter 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	4. Anions Rv2684 Rv2685 Rv3578 Rv2643 Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1859 Rv1860 Rv2329c Rv1737c Rv0261c	arsA arsB arsB2 arsC cysA cysT cysW modA modB modC modD narK1 narK2 narK3	probable arsenical pump sulphate transport ATP-binding protein 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
Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv2981c Rv1018c Rv38809c Rv1018c Rv3882c Rv1110 Rv1315		probable exported protease probable cutinase precursor of probable membrane protein putative exported protease similar to Esat6 probable secreted protein probable secreted protein probable precursor of serine protease probable cutinase precursor probable	Rv3665c Rv3664c Rv3663c Rv0522 Rv0411c Rv1280c Rv1283c Rv1282c Rv1281c Rv2320c Rv3253c	dppB dppC dppD gabP glnH glnQ oppA oppB oppC oppD rocE	probable peptide transport system permease probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable 4-amino butyrate transporter probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport system permease probable peptide transport protein arginine/ornithine transporter probable cationic amino acid transport	4. Anions Rv2684 Rv2685 Rv3578 Rv2643 Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1860 Rv2329c Rv1737c	arsA arsB arsB2 arsC cysA cysA cysT cysW modA modB modC modD	probable arsenical pump sulphate transport ATP-binding protein sulphate transport system perme- ase protein sulphate transport system perme- ase protein molybdate binding protein transport system permease, molybdate uptake aBC- transporter precursor of Apa (45/47 kD secreted protein) probable nitrite extrusion protein nitrite extrusion protein similar to nitrite extrusion
Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv2981c Rv1018c Rv33809c Rv1018c		probable exported protease probable extinase precursor of probable membrane protein putative exported protease similar to Esat6 probable secreted protein probable secreted protein probable precursor of serine protease probable cutinase protable cutinase probable cutinase precursor probable cutinase probable cutinase probable cutinase precursor probable cutinase probable cutinase probable cutinase probable cutinase probable cutinase probable cutin	Rv3665c Rv3664c Rv3663c Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1281c Rv2320c Rv3253c Rv3454 2. Cations	dppB dppC dppD gabP ginH ginQ oppA oppB oppC oppD rocE	probable peptide transport system permease probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable 4-amino butyrate transporter probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport system permease probable peptide transport protein arginine/ornithine transporter probable cationic amino acid transport possible proline permease	4. Anions Rv2684 Rv2685 Rv3578 Rv2643 Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1860 Rv2329c Rv1737c Rv0261c Rv0267	arsA arsB arsBz arsC cysA cysT cysW modA modB modC modD narK1 narK2 narK3 narU	probable arsenical pump sulphate transport ATP-binding protein 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
Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv2981c Rv1018c Rv38809c Rv1018c Rv3882c Rv1110 Rv1315		probable exported protease probable cutinase precursor of probable membrane protein putative exported protease similar to Esat6 probable secreted protein probable secreted protein probable secreted protein probable cutinase precursor probable cutinase pr	Rv3665c Rv3664c Rv3663c Rv0522 Rv0411c Rv1280c Rv1283c Rv1282c Rv1282c Rv3253c Rv3454 2. Cations Rv2920c Rv1607	dppB dppC dppD gabP glnH glnQ oppA oppB oppC amt chaA	probable peptide transport system permease probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable 4-amino butyrate transporter 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	4. Anions Rv2684 Rv2685 Rv3578 Rv2643 Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1859 Rv1860 Rv2329c Rv1737c Rv0261c Rv0261 Rv0267	arsA arsB arsB2 arsC cysA cysT cysW modA modB modC modD narK1 narK2 narU	probable arsenical pump sulphate transport ATP-binding protein 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 similar to nitrite extrusion protein 2 PstS component of phosphate uptake
Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c Rv3449 Rv3451 Rv3452 Rv3724 3. Murein Rv2981c Rv2981c Rv3809c Rv1018c Rv3382c Rv1110 Rv1315 Rv0482		probable exported protease probable extinase precursor of probable membrane protein putative exported protease similar to Esat6 probable secreted protein probable secreted protein probable precursor of serine protease probable cutinase protable cutinase probable cutinase precursor probable cutinase probable cutinase probable cutinase precursor probable cutinase probable cutinase precursor probable cutinase probable	Rv3665c Rv3664c Rv3663c Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1281c Rv2320c Rv3253c Rv3454 2. Cations Rv2920c	dppB dppC dppD gabP glnH glnQ oppA oppB oppC oppC amt	probable peptide transport system permease probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable ABC-transporter probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport system permease probable peptide transport protein arginine/ornithine transporter probable cationic amino acid transport possible proline permease	4. Anions Rv2684 Rv2685 Rv3578 Rv2643 Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1860 Rv2329c Rv1737c Rv0261c Rv0267	arsA arsB arsBz arsC cysA cysT cysW modA modB modC modD narK1 narK2 narK3 narU	probable arsenical pump sulphate transport ATP-binding protein sulphate transport system permease protein sulphate transport system permease protein molybdate binding protein transport system permease, molybdate uptake molybdate uptake MBC-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
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Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c Rv3449 Rv3451 Rv2981c Rv2981c Rv2981c Rv21516 Rv2152c Rv2152c Rv2155c Rv2155c Rv2155c Rv2156c Rv2153c Rv3332 Rv0016c Rv3332 Rv0016c Rv2163c		probable exported protease probable exported protease probable cutinase precursor of probable membrane protein putative exported protease similar to Esat6 probable secreted protein probable precursor of serine protease probable cutinase probable cutinase probable cutinase probable cutinase precursor probable cutinase probable cutinase proposalie probable cutinase probable cutinase A UDP-N-acetylglucosamine probable pr	Rv3665c Rv3664c Rv3663c Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1281c Rv2320c Rv3253c Rv3454 2. Cations Rv2920c Rv1607 Rv1239c Rv0103c Rv3270 Rv1469 Rv0908 Rv1997 Rv1992c Rv0425c Rv0107c	dppB dppC dppD gabP glnH glnQ oppA oppB oppC oppD rocE amt chaA corA ctpB ctpC ctpC ctpD ctpE ctpF ctpG ctpH ctpV fecB	probable peptide transport system permease probable ABC-transporter probable ABC-transporter probable ABC-transporter probable ATP-binding transport protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport system permease probable peptide transport protein arginine/ornithine transporter probable cationic amino acid transport protein arginine/ornithine transporter probable cationic amino acid transport protein arginine/ornithine transporter probable magnesium and cobalt transport protein cation-transport protein cation-transport ATPase cation transport ATPase cation transport ATPase probable cation transport ATPase probable cation transport ATPase probable cation transport ATPase probable magnesium transport ATPase probable magnesium transport ATPase probable magnesium transport ATPase cation transport ATPase probable magnesium transporter	4. Anions Rv2684 Rv2685 Rv3578 Rv2643 Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1860 Rv2329c Rv1737c Rv0261c Rv0267 Rv0934 Rv0928 Rv0820 Rv3301c Rv0821c Rv0821c Rv0821c Rv0821c Rv0821c	arsA arsB arsB2 arsB2 arsC cysA cysT cysW modA modB modC modD narK1 narK2 narK3 narU phoS1 phoT phoY1 phoY2 pitA pitB pstA1	probable arsenical pump sulphate transport ATP-binding protein sulphate transport system permease protein sulphate transport system permease protein molybdate binding protein transport system permease, molybdate uptake MBC-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 phosphate transport system regulator phosphate transport system regulator phosphate transport system regulator phosphate permease PstA component of phosphate uptake ABC transport component of
Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c Rv3449 Rv3451 Rv2981c Rv2981c Rv2981c Rv38809c Rv1018c Rv38809c Rv1018c Rv3882c Rv1110 Rv1315 Rv0482 Rv2155c Rv2155c Rv2155c Rv2157c Rv2153c Rv3382 Rv016c Rv3332 Rv0016c Rv3332	sacculus a dacB ddlA glf glmU lytB lytB' murA murB murC murD murE murF murG murI nagA pbpA pbpA ponA	probable exported protease probable exported protease probable cutinase precursor of probable membrane protein putative exported protease similar to Esat6 probable secreted protein probable secreted protein probable secreted protein probable cutinase precursor probable value probab	Rv3665c Rv3664c Rv3663c Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1282c Rv1282c Rv3250c Rv3253c Rv3454 2. Cations Rv2920c Rv1607 Rv1239c Rv0092 Rv1003c Rv3270 Rv1469 Rv0908 Rv1997 Rv1992c Rv0425c Rv0107c Rv0969	dppB dppC dppD gabP glnH glnQ oppA oppB oppC oppD rocE amt cthaA corA ctpB ctpC ctpC ctpC ctpF ctpG ctpH ctpV	probable peptide transport system permease probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable 4-amino butyrate transporter probable 4-amino butyrate transporter putative glutamine binding protein probable ATP-binding transport protein probable digopeptide transport protein oligopeptide transport protein oligopeptide transport protein oligopeptide transport protein arginine/ornithine transporter probable cationic amino acid transport protein arginine/ornithine transporter probable cationic amino acid transport protein arginine/ornithine transporter probable magnesium and cobalt transport protein cation-transporting ATPase cation transport ATPase cation transport ATPase probable magnesium transport ATPase probable magnesium transport ATPase cation transport atPase probable magnesium transport ATPase cation transport ATPase	4. Anions Rv2684 Rv2685 Rv3578 Rv2643 Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1859 Rv1860 Rv2329c Rv1737c Rv0261c Rv0261 Rv0934 Rv0928 Rv0820 Rv3301c Rv0821c Rv0821c Rv0545c Rv2281 Rv0930 Rv0933	arsA arsB arsB2 arsC cysA cysT cysW modA modB modC modD narK1 narK2 narK3 narU phoS1 phoS1 phoY1 phoY2 pitA pitB pstA1 pstB2	probable arsenical pump sulphate transport ATP-binding protein 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 nitrite extrusion protein similar to nitrite extrusion protein 2 PstS component of phosphate uptake phosphate transport system regulator phosphate transport system regulator low-affinity inorganic phosphate transporter phosphate prmease PstA component of phosphate uptake ABC transport component of phosphate uptake ABC transport component of
Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c Rv3449 Rv3451 Rv2981c Rv2981c Rv2981c Rv2151c Rv2152c Rv2155c Rv2155c Rv2155c Rv2155c Rv2155c Rv2156c Rv2153c Rv3332 Rv0016c Rv3332 Rv0016c Rv2163c Rv0050 Rv3682 Rv0017c		probable exported protease probable exported protease probable cutinase precursor of probable membrane protein putative exported protease similar to Esat6 probable secreted protein probable precursor of serine protease probable cutinase probable cutinase probable cutinase probable cutinase precursor probable cutinase proposed probable cutinase procursor probable cutinase A UDP-N-acetylglucosamine pyrophosphorylase LytB protein homologue very similar to LytB UDP-N-acetylglucosamine-1-carboxyvinyltransferase UDP-N-acetylenolpyruvoylglucosamine reductase UDP-N-acetylmuramotelalinine-Dglutamate ligase UDP-N-acetylmuramotelalinine-Dglutamate ligase UDP-N-acetylmuramotelalinine-dading enzyme capaline-Dalanine-adding enzyme transferase in peptidoglycan synthesis glutamate racemase phospho-N-acetylmuramoyl-petapeptide transferase N-acetylglucosamine-6-P-deacetylase penicillin-binding protein penicillin-binding protein class A penicillin binding protein flstW/RodA/SpovE family	Rv3665c Rv3664c Rv3663c Rv0522 Rv0411c Rv2564 Rv1280c Rv1283c Rv1281c Rv2320c Rv3253c Rv3454 2. Cations Rv2920c Rv1607 Rv1239c Rv0103c Rv3270 Rv1469 Rv0908 Rv1997 Rv1995 Rv0425c Rv0107c Rv0908 Rv0908 Rv1997 Rv1996 Rv0425c Rv0107c	dppB dppC dppD gabP glnH glnQ oppA oppB oppC oppD rocE amt chaA corA ctpB ctpC ctpC ctpD ctpE ctpF ctpG ctpH ctpV fecB	probable peptide transport system permease probable ABC-transporter probable ABC-transporter probable ABC-transporter 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 cationic amino acid transport protein arginine/ornithine transporter probable magnesium and cobalt transport protein cation-transport protein cation-transport ATPase cation transport ATPase cation transport ATPase probable magnesium transport ATPase probable magnesium transport ATPase cation transport ATPase probable magnesium transporter iron transport protein FellI dicitransporter potassium-transporting ATPase A	4. Anions Rv2684 Rv2685 Rv3578 Rv2643 Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1860 Rv2329c Rv1737c Rv0261c Rv0267 Rv0934 Rv0928 Rv0820 Rv3301c Rv0821c Rv0821c Rv0821c Rv0821c Rv0821c Rv0823	arsA arsB arsB2 arsB2 arsC cysA cysT cysW modA modB modC modD narK1 narK2 narK3 narU phoS1 phoS1 phoY1 phoY2 pitA pitB pstA1 pstA2 pstB pstC	probable arsenical pump sulphate transport ATP-binding protein sulphate transport system permease protein sulphate transport system permease protein molybdate binding protein transport system permease, molybdate uptake MBC-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 phosphate transport system regulator phosphate transport system regulator phosphate transport system regulator phosphate permease PstA component of phosphate uptake PstC component of phosphate uptake
Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c Rv3449 Rv3451 Rv2981c Rv2981c Rv2981c Rv3809c Rv1018c Rv3382c Rv1110 Rv1315 Rv0482 Rv2152c Rv2155c Rv2155c Rv2155c Rv2156c Rv2157c Rv2153c Rv3332 Rv0016c Rv2163c Rv33682		probable exported protease probable exported protease probable cutinase precursor of probable membrane protein putative exported protease similar to Esat6 probable secreted protein probable precursor of serine protease probable cutinase protease probable cutinase precursor probable cutinase procursor probable cutinase procursor probable cutinase procursor probable cutinase proposalinie proving probable cutinase probable probable cutinase procursor	Rv3665c Rv3664c Rv3663c Rv3663c Rv0522 Rv0411c Rv2564 Rv1280c Rv1282c Rv1281c Rv2320c Rv3253c Rv3454 2. Cations Rv2920c Rv1607 Rv1239c Rv0103c Rv3270 Rv1409 Rv092 Rv0103c Rv1607 Rv1609	dppB dppC dppD gabP glnH glnQ oppA oppB oppC oppD rocE amt ctpA ctpB ctpC ctpC ctpC ctpC ctpH ctpI ctpV fecB fecB2	probable peptide transport system permease probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable ABC-transporter 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 cationic amino acid transport protein arginine/ornithine transporter probable magnesium and cobalt transport protein cation-transporting ATPase cation transport ATPase cation transport ATPase probable magnesium transport ATPase probable magnesium transport ATPase cation transport ATPase probable magnesium transport ATPase cation transport ATPase putative Felli-dicitrate transporter iron transport protein Felli dicitransporter	4. Anions Rv2684 Rv2685 Rv3578 Rv2643 Rv2397c Rv2399c Rv2398c Rv1857 Rv1858 Rv1859 Rv1860 Rv2329c Rv1737c Rv0261c Rv0261 Rv0934 Rv0928 Rv0820 Rv3301c Rv0821c Rv0821c Rv0545c Rv2281 Rv0930 Rv0933	arsA arsB arsB2 arsC cysA cysT cysW modA modB modC modD narK1 narK2 narK3 narU phoS1 phoS1 phoY1 phoY2 pitA pitB pstA1 pstB2	probable arsenical pump sulphate transport ATP-binding protein sulphate transport system permease protein sulphate transport system permease protein molybdate binding protein transport system permease, molybdate uptake MBC-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 phosphate transport system regulator phosphate permease PstA component of phosphate uptake PstA component of phosphate uptake ABC transport of phosphate uptake ABC transport of phosphate uptake PstA component of phosphate uptake ABC transport of phosphate uptake PstA component of phosphate PstC component of phosphate PstC component of phosphate PstC component of phosphate PstC component of phosphate

		phosphate transport system			unit	Rv3500c -	part of <i>mce4</i> operon
Rv0932c	pstS	PstS component of phosphate uptake	Rv1821	secA2	SecA, preprotein translocase sub- unit	Rv3501c - Rv3896c -	part of <i>mce4</i> operon putative p60 homologue
Rv2400c		sulphate binding precursor	Rv2587c	secD	protein-export membrane protein	Rv3922c -	possible hemolysin
Rv0143c Rv1707	-	probable chloride channel probable sulphate permease	Rv0638 Rv2586c	secE secF	SecE preprotein translocase protein-export membrane protein	R IS elements Rer	peated sequences, and Phage
Rv1739c	-	possible sulphate transporter	Rv1440	secG	protein-export membrane protein	1. IS elements	seated sequences, and I mage
Rv3679 Rv3680	-	possible anion transporter probable anion transporter	Rv0732	secY	SecG SecY subunit of preprotein translo-	IS6110 IS1081	16 copies 6 copies
1773000	-	probable affior transporter		3601	case	Others	37 copies
5. Fatty ac Rv2790c			Rv2462c	tig	chaperone protein, similar to	2. REP13E12 family	/ 7 copies
	пр і ltp2	non-specific lipid transport protein non-specific lipid transport protein	Rv2813	-	trigger factor probable general secretion path-	Z. REF 13E 12 Idillilly	/ Copies
6 Efflux n	rotoino				way protein	3. Phage-related fur	nctions integrase/recombinase
6. Efflux p Rv2936	drrA	similar daunorubicin resistance	E. Adapta	tions and	atypical conditions	Rv2894c xerC Rv1701 xerD	integrase/recombinase
Rv2937	drrB	ABC-transporter similar daunorubicin resistance	Rv1901 Rv3648c	cinA	competence damage protein cold shock protein, transcriptional	Rv1054 - Rv1055 -	integrase-a integrase-b
KV2931	инь	transmembrane protein	KV3040C	cspA	regulator	Rv1573 -	phiRV1 phage related protein
Rv2938	drrC	similar daunorubicin resistance	Rv0871	cspB	probable cold shock protein	Rv1574 - Rv1575 -	phiRV1 phage related protein
Rv2846c	efpA	transmembrane protein putative efflux protein	Rv3063	cstA	starvation-induced stress response protein	Rv1575 - Rv1576c -	phiRV1 phage related protein phiRV1 phage related protein
Rv3065	emrE -	resistance to ethidium bromide	Rv3490	otsA	probable α,α-trehalose-phosphate	Rv1577c - Rv1578c -	phiRV1 possible prohead protease
Rv0783c Rv0849	-	multidrug resistance protein possible quinolone efflux pump	Rv2006	otsB	synthase trehalose-6-phosphate phos-	Rv1578c - Rv1579c -	phiRV1 phage related protein phiRV1 phage related protein
Rv1145	-	probable drug transporter	D. 2272	eteD2	phatase	Rv1580c - Rv1581c -	phiRV1 phage related protein
Rv1146 Rv1250	-	probable drug transporter probable drug efflux protein	Rv3372	otsB2	trehalose-6-phosphate phos- phatase	Rv1581c - Rv1582c -	phiRV1 phage related protein phiRV1 phage related protein
Rv1258c	-	probable multidrug resistance	Rv3758c	proV	osmoprotection ABC transporter	Rv1583c - Rv1584c -	phiRV1 phage related protein
Rv1410c	_	pump probable drug efflux protein	Rv3757c Rv3759c	proW proX	transport system permease similar to osmoprotection proteins	Rv1584c - Rv1585c -	phiRV1 phage related protein phiRV1 phage related protein
Rv1634	-	probable drug efflux protein	Rv3756c	proZ	transport system permease	Rv1586c -	phiRV1 integrase
Rv1819c	-	probable multidrug resistance pump	Rv1026	-	probable pppGpp-5'phosphohydro- lase	Rv2309c - Rv2310 -	integrase excisionase
Rv2136c	-	putative bacitracin resistance pro-				Rv2646 -	phiRV2 integrase
Rv2209		tein probable drug efflux protein	F. Detoxific Rv2428	cation ahpC	alkyl hydroperoxide reductase	Rv2647 - Rv2650c -	phiRV2 phage related protein phiRV2 phage related protein
	-	probable tetracenomycin C resis-	Rv2429	ahpD	member of AhpC/TSA family	Rv2651c -	phiRV2 prohead protease
Rv2994		tance protein probable fluoroquinolone efflux	Rv2238c Rv2521	ahpE bcp	member of AhpC/TSA family bacterioferritin comigratory protein	Rv2652c - Rv2653c -	phiRV2 phage related protein phiRV2 phage related protein
		protein	Rv1608c	bcpB	probable bacterioferritin comigra-	Rv2654c -	phiRV2 phage related protein
Rv1877 Rv2459	-	probable drug efflux protein probable drug efflux protein	Rv3473c	bpoA	tory protein probable non-heme bromoperoxi-	Rv2655c - Rv2656c -	phiRV2 phage related protein phiRV2 phage related protein
1112400	_	probable drug emux protein			dase	Rv2657c -	similar to gp36 of mycobacterio-
B. Chaper Rv0384c	rones/Hear clpB	t shock heat shock protein	Rv1123c	bpoB	probable non-heme bromoperoxidase	Rv2658c -	phage L5 phiRV2 phage related protein
Rv0352	dnaJ	acts with GrpE to stimulate DnaK	Rv0554	bpoC	probable non-heme bromoperoxi-	Rv2659c -	phiRV2 integrase
Rv2373c	d= = 10	ATPase	Rv3617	ephA	dase	Rv2830c - Rv3750c -	similar to phage P1 phd gene
Rv0350	dnaJ2 dnaK	DnaJ homologue 70 kD heat shock protein, chromo-	Rv1938	ephA ephB	probable epoxide hydrolase probable epoxide hydrolase	Rv3750C - Rv3751 -	excisionase putative integrase
D: 0447		some replication	Rv1124	ephC	probable epoxide hydrolase	0.05 / 005 (
Rv3417c Rv0440	groEL1 groEL2	60 kD chaperonin 1 60 kD chaperonin 2	Rv2214c Rv3670	ephD ephE	probable epoxide hydrolase probable epoxide hydrolase	C. PE and PPE fam 1. PE family	illes
Rv3418c	groES	10 kD chaperone	Rv0134	ephF	probable epoxide hydrolase	PE subfamily	38 members
Rv0351 Rv2374c	grpE hrcA	stimulates DnaK ATPase activity heat-inducible transcription	Rv3171c	hpx	probable non-heme haloperoxidase	PE_PGRS subfamil	y 61 members
		repressor	Rv1908c	katG	catalase-peroxidase	2. PPE family	68 members
Rv0251c Rv0353	hsp hspR	possible heat shock protein heat shock regulator	Rv3846 Rv0432	sodA sodC	superoxide dismutase superoxide dismutase precursor -	D. Antibiotic produc	tion and resistance
Rv2031c	hspX	14kD antigen, heat shock protein			(Cu-Zn)	Rv2068c blaC	class A β-lactamase
Rv2299c	htpG	Hsp20 family heat shock protein Hsp90 family	Rv1932 Rv0634c	tpx -	thiol peroxidase putative glyoxylase II	Rv3290c lat Rv2043c pncA	lysine-∈ aminotransferase pyrazinamide resistance/sensitivity
Rv0563	htpX	probable (transmembrane) heat	Rv2581c	-	putative glyoxylase II	Rv0133 -	possible puromycin N-acetyltrans-
Rv2701c	suhB	shock protein putative extragenic suppressor	Rv3177	-	probable non-heme haloperoxi- dase	Rv0262c -	ferase aminoglycoside 2'-N-acetyltrans-
	ouD	protein			4400		ferase
Rv3269		probable heat shock protein	IV. Other A. Virulen	ce		Rv0802c - Rv1082 -	acetyltransferase similar to <i>S. lincolnensis ImbE</i>
C. Cell div			Rv0169	mce1	cell invasion protein	Rv1170 -	similar to S. lincolnensis ImbE
Rv3641c Rv3102c	fic ftsE	possible cell division protein membrane protein	Rv0589 Rv1966	mce2 mce3	cell invasion protein cell invasion protein	Rv1347c -	possible aminoglycoside 6'-N- acetyltransferase
Rv3610c	ftsH	inner membrane protein,	Rv3499c	mce4	cell invasion protein	Rv2036 -	similar to lincomycin production
Rv2748c	ftsK	chaperone chromosome partitioning	Rv3100c Rv1694	smpB tlyA	probable small protein b cytotoxin/hemolysin homologue	Rv2303c -	genes similar to <i>S. griseus</i> macrotetrolide
Rv2151c	ftsQ	ingrowth of wall at septum	Rv0024	-	putative p60 homologue	KV2303C -	resistance protein
Rv2154c	ftsW	membrane protein (shape determination)	Rv0167 Rv0168	-	part of mce1 operon	Rv3225c -	probable aminoglycoside 3'-phos-
Rv3101c		membrane protein	Rv0170	-	part of <i>mce1</i> operon part of <i>mce1</i> operon	Rv3700c -	photransferases probable acetyltransferase
Rv2921c	ftsY	cell division protein FtsY circumferential ring, GTPase	Rv0171	-	part of mce1 operon	Rv3817 -	probable aminoglycoside 3'-phos-
Rv2150c Rv3919c	ftsZ gid	glucose inhibited division protein B	Rv0172 Rv0174	-	part of <i>mce1</i> operon part of <i>mce1</i> operon		photransferase
Rv3625c	mesJ	probable cell cycle protein	Rv0587	-	part of mce2 operon	E. Bacteriocin-like p	proteins 3
Rv3917c	parA	chromosome partitioning; DNA - binding	Rv0588 Rv0590	-	part of <i>mce2</i> operon part of <i>mce2</i> operon	F. Cytochrome P450	0 enzymes 22
Rv3918c	parB	possibly involved in chromosome	Rv0591	-	part of mce2 operon	·	
Rv2922c	smc	partitioning member of Smc1/Cut3/Cut14	Rv0592 Rv0594	-	part of <i>mce2</i> operon part of <i>mce2</i> operon	G. Coenzyme F420 enzymes	l-dependent 3
	01110	family	Rv1085c		possible hemolysin	,	
Rv0012 Rv0435c	-	possible cell division protein ATPase of AAA-family	Rv1477	-	putative exported p60 protein homologue	H. Miscellaneous tra	ansferases 61
Rv2115c	-	ATPase of AAA-family	Rv1478	-	putative exported p60 protein	I. Miscellaneous ph	
Rv3213c	-	possible role in chromosome seg-	Rv1566c		homologue	and hydrolases	18
Rv1708	-	regation possible role in chromosome parti-	KV 1300C	-	putative exported p60 protein homologue	J. Cyclases	6
		tioning	Rv1964	-	part of mce3 operon	•	
D. Protein	and pepti	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	Rv1968	-	part of mce3 operon	V. Conserved hypot	theticals 912
Rv2903c Rv1614	lepB lgt	signal peptidase I prolipoprotein diacylglyceryl trans-	Rv1969 Rv1971	-	part of mce3 operon part of mce3 operon	VI. Unknowns	606
		ferase	Rv2190c	-	putative p60 homologue		
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		to Nature.com
Rv3240c	secA	SecA, preprotein translocase sub-	Rv3498c	- Nat	tuPe®ฟ้าสิติศักดิ์ผลิครับblishers Ltd 1998	В	