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errata

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

Rohan Mahadevan

Nature 394, 651–653 (1998)

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

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

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

Nature 393, 537-544 (1998)

New Haven, 1987).

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.....GSGAPGGAGGAAGLWGTGGAGGAGGAGGSSAGGGGAGGAGGAGGWLLGDGGAGGIGGAST...

BCGGSGAPGGAGGAAGLWGTGGA	-GGAGGWLLGDGGAGGIGGAST.

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

I. Small-n A. Degrad	nolecule n lation	netabolism	Rv2831	echA16	superfamily enoyl-CoA hydratase/isomerase
1. Carbon	compound	ds			superfamily
Rv0186	bglS	β-glucosidase	Rv3039c	echA17	enoyl-CoA hydratase/isomerase
Rv2202c	cbhK	carbohydrate kinase	D. 0070		superfamily
Rv1731	gabD1	succinate-semialdehyde dehydro-	HV3373	echA 18	superfamily, N-term
Rv0234c	gabD2	succinate-semialdehyde dehydro-	Dv3516	echA 19	superfamily, C-term
Bv0501	aalE1	UDP-glucose 4-epimerase	HV3510	echa is	superfamily
Rv0536	galE2	UDP-glucose 4-epimerase	Rv3550	echA20	enovl-CoA hvdratase/isomerase
Rv0620	galK	galactokinase			superfamily
Rv0619	galT	galactose-1-phosphate uridylyl-	Rv3774	echA21	enoyl-CoA hydratase/isomerase
	-	transferase C-term			superfamily
Rv0618	galT'	galactose-1-phosphate uridylyl-	Rv0859	fadA	β oxidation complex, β subunit
		transferase N-term			(acetyl-CoA C-acetyltransferase)
Rv0993	galU	UTP-glucose-1-phosphate uridylyl-	Rv0243	fadA2	acetyl-CoA C-acetyltransferase
		transferase	Rv1074c	fadA3	acetyl-CoA C-acetyltransferase
Rv3696c	glpK	ATP:glycerol 3-phosphotrans-	Rv1323	fadA4	acetyl-CoA C-acetyltransferase
Ducorra		terase	D: 05 40	6	(aka IniL)
Dv24410	manA	namose-o-prospirate isomerase	Dv25560	fadAG	acetyl-CoA C-acetyltransferase
11034410	misA	mannomutase	Rv0860	fadR	B oxidation complex a subunit
Bv0118c	oveA	oxalvi-CoA decarboxviase	HV0600	Idud	p oxidation complex, α subunit (multiple activities)
Bv3068c	namA	phosphoglucomutase	Bv0468	fadB2	3-hydroxyacyl-CoA dehydroge-
Rv3257c	pmmA	phosphomannomutase			nase
Rv3308	pmmB	phosphomannomutase	Rv1715	fadB3	3-hydroxyacyl-CoA dehydroge-
Rv2702	, ppgK	polyphosphate glucokinase			nase
Rv0408	pta	phosphate acetyltransferase	Rv3141	fadB4	3-hydroxyacyl-CoA dehydroge-
Rv0729	xylB	xylulose kinase			nase
Rv1096	-	carbohydrate degrading enzyme	Rv1912c	fadB5	3-hydroxyacyl-CoA dehydroge-
·			D :==	6. (5.)	nase
2. Amino a	acids and a	amines	Hv1750c	fadD1	acyl-CoA synthase
HV19050	aao	D-amino acid oxidase	HV0270	fadD2	acyl-CoA synthase
HV25310	adi	ornitnine/arginine decarboxylase	HV3561	fadD3	acyl-CoA synthase
HV2780	alo	L-alanine denydrogenase	HV0214	fadD4	acyl-CoA synthase
By1001	ansA	argining deiminace	Pv1206	fadD6	acyl-CoA synthase
By0753c	mme A	methylmalmonate semialdehyde	By0119	fadD7	acyl-CoA synthase
11007000	mmora	dehvdrogenase	Bv0551c	fadD8	acyl-CoA synthase
Bv0751c	mmsB	methylmalmonate semialdehyde	Bv2590	fadD9	acyl-CoA synthase
		oxidoreductase	Rv0099	fadD10	acyl-CoA synthase
Rv1187	rocA	pyrroline-5-carboxylate dehydro-	Rv1550	fadD11	acyl-CoA synthase, N-term
		genase	Rv1549	fadD11'	acyl-CoA synthase, C-term
Rv2322c	rocD1	ornithine aminotransferase	Rv1427c	fadD12	acyl-CoA synthase
Rv2321c	rocD2	ornithine aminotransferase	Rv3089	fadD13	acyl-CoA synthase
Rv1848	ureA	urease γ subunit	Rv1058	fadD14	acyl-CoA synthase
Hv1849	ureB	urease β subunit	Hv2187	fadD15	acyl-CoA synthase
HV1850	ureC	urease α subunit	HV0852	180D15	acyl-CoA synthase
Dv1053	ureD	urease accessory protein	Dv25120	fadD17	acyl-CoA synthase
By1852	ureG	urease accessory protein	Bv35150	fadD 10	acyl-CoA synthase
By2913c	-	probable D-amino acid	By1185c	fadD21	acyl-CoA synthase
11020100		aminohydrolase	By2948c	fadD22	acyl-CoA synthase
Bv3551	-	possible glutaconate CoA-	Bv3826	fadD23	acvl-CoA synthase
		transferase	Rv1529	fadD24	acyl-CoA synthase
			Rv1521	fadD25	acyl-CoA synthase
3. Fatty ac	ids		Rv2930	fadD26	acyl-CoA synthase
Rv2501c	accA1	acetyl/propionyl-CoA carboxylase,	Rv0275c	fadD27	acyl-CoA synthase
_		α subunit	Rv2941	fadD28	acyl-CoA synthase
Rv0973c	accA2	acetyl/propionyl-CoA carboxylase,	Rv2950c	fadD29	acyl-CoA synthase
D. 0500-		α subunit	HV0404	fadD30	acyl-CoA synthase
HV25020	accor	acety/propionyi-CoA carboxylase,	HV1925	fadD31	acyl-CoA synthase
By09740	20002	p suburnit apatyl/propionyl-CoA parboxylase	Dv1245	fadD32	acyl-CoA synthase
11003740	accoz	B subunit	By0035	fadD34	acyl-CoA synthase
Rv3667	acs	acetyl-CoA svnthase	Rv2505c	fadD35	acyl-CoA synthase
Rv3409c	choD	cholesterol oxidase	Rv1193	fadD36	acvl-CoA synthase
Rv0222	echA1	enoyl-CoA hydratase/isomerase	Rv0131c	fadE1	acyl-CoA dehydrogenase
		superfamily	Rv0154c	fadE2	acyl-CoA dehydrogenase
Rv0456c	echA2	enoyl-CoA hydratase/isomerase	Rv0215c	fadE3	acyl-CoA dehydrogenase
		superfamily	Rv0231	fadE4	acyl-CoA dehydrogenase
Rv0632c	echA3	enoyl-CoA hydratase/isomerase	Rv0244c	fadE5	acyl-CoA dehydrogenase
Ducoza		supertamily	Hv0271c	tadE6	acyl-CoA dehydrogenase
Hv0673	echA4	enoyl-CoA hydratase/isomerase	Hv0400c	fadE7	acyl-CoA dehydrogenase
Duceze	ach AE	superramily	HV0672	TAGE8	acyl-CoA denydrogenase
UA0012	ecnA5	enoyi-ooa nyuratase/isomerase superfamily	Bu07504	fadEn	(ana alud) acyl-CoA debydrogenoco
Bungos	ACHAG	enovl-CoA hydratase/isomerase	RVU1920	iau⊑∂ fadE10	acyl-CoA debydrogenase
1100905	CUIND	superfamily (aka eccH)	BV0070	fadE 10	acyl-CoA debydrogenase
Bv0971c	echA7	enovl-CoA hydratase/isomerase	Bv09750	fadE 12	acyl-CoA dehvdrogenase
		superfamily	Rv1346	fadE 14	acyl-CoA dehvdrogenase
Rv1070c	echA8	enoyl-CoA hydratase/isomerase	Rv1467c	fadE15	acyl-CoA dehydrogenase
		superfamily	Rv1679	fadE16	acyl-CoA dehydrogenase
Rv1071c	echA9	enoyl-CoA hydratase/isomerase	Rv1934c	fadE17	acyl-CoA dehydrogenase
_		superfamily	Rv1933c	fadE18	acyl-CoA dehydrogenase
Rv1142c	echA10	enoyl-CoA hydratase/isomerase	Rv2500c	fadE 19	acyl-CoA dehydrogenase
-		superfamily	D 4		(aka mmgC)
Hv1141c	echA11	enoyl-CoA hydratase/isomerase	Hv2724c	tadE20	acyl-CoA dehydrogenase
Du4 470	0.0- 1.1.0	superramily	HV2/890	tadE21	acyl-CoA dehydrogenase
HV14/2	ecnA12	enoyi-CoA riyaratase/isomerase	HV30610	tadE22	acyl-CoA denydrogenase
Bv1025c	Ach112	enovi-CoA bydratase/isomeraes	Rv3130	iau⊆23 fadE94	acy-CoA debydrogenase
11010000	001/410	superfamily	Rv3274n	fadF25	acyl-CoA dehvdrogenase
Rv2486	echA14	enoyl-CoA hydratase/isomerase	Rv3504	fadE26	acyl-CoA dehvdrogenase
	• • • •	superfamily	Rv3505	fadE27	acyl-CoA dehydrogenase
Rv2679	echA15	enoyl-CoA hydratase/isomerase	Rv3544c	fadE28	acyl-CoA dehydrogenase

Dv25420	fodE20	anyl CoA dobydrogonaco
Bv3560c	fadE30	acyl-CoA dehydrogenase
By3562	fadE31	acyl-CoA dehydrogenase
Rv3563	fadE32	acyl-CoA dehydrogenase
Rv3564	fadE33	acvl-CoA dehvdrogenase
Rv3573c	fadE34	acyl-CoA dehydrogenase
Rv3797	fadE35	acyl-CoA dehydrogenase
Rv3761c	fadE36	acyl-CoA dehydrogenase
Rv1175c	fadH	2,4-Dienoyl-CoA Reductase
Rv0855	far	fatty acyl-CoA racemase
Rv1143	mcr	α-methyl acyl-CoA racemase
Rv1492	mutA	methylmalonyl-CoA mutase, β
D / /00		subunit
HV1493	mutB	methylmalonyl-CoA mutase, α
Duceode		subunit
HV23040	SCOA	unit
Bv2503c	scoB	3-oxo acid:CoA transferase ß sub-
11020000	3000	unit
Rv1136	-	probable carnitine racemase
Rv1683	-	possible acyl-CoA synthase
4. Phospho	orous com	pounds
Rv2368c	phoH	ATP-binding pho regulon
		component
Rv1095	phoH2	PhoH-like protein
Rv3628	ppa	probable inorganic pyrophos-
B 0004		phatase
Hv2984	ррк	polyphosphate kinase
P Energy	motobolio	m
 Energy Choolyr 	netabolisi	n
By1023	eno	enclase
By0363c	fha	fructose bisphosphate aldolase
Bv1436	nan	dvceraldehvde 3-phosphate dehv-
	3-1-	drogenase
Rv0489	apm	phosphoglycerate mutase I
Rv3010c	pfkA	phosphofructokinase I
Rv2029c	pfkB	phosphofructokinase II
Rv0946c	pgi	glucose-6-phosphate isomerase
Rv1437	pgk	phosphoglycerate kinase
Rv1617	pykA	pyruvate kinase
Hv1438	tpi	triosephosphate isomerase
Hv2419c	-	putative phosphoglycerate mutase
HV3837c	-	putative phosphoglycerate mutase
2 Durinuet	- dobudror	100000
2. Fyluvale	e denyaroų	pyruvata dahydrogonaca E1 aam
TV2241	acer	ponent
Bv3303c	IndA	dihvdrolipoamide dehvdrogenase
Bv2497c	pdhA	pyruvate dehydrogenase E1 com-
	pan	ponent α subunit
Rv2496c	pdhB	pyruvate dehydrogenase E1 com-
		ponent β subunit
Rv2495c	pdhC	dihydrolipoamide acetyltransferase
Rv0462	-	probable dihydrolipoamide dehy-
		drogenase
2 TO 4 101		
S. TCA Cyc	ie ogo	acchitata hydrotoca
RV14750	acri oitA	aconitate nyuratase
Bv2498c	citE	citrate lyase 8 chain
Rv1098c	fum	fumarase
Bv1131	altA1	citrate synthase 3
Rv0896	altA2	citrate synthase 1
Rv3339c	icd1	isocitrate dehydrogenase
Rv0066c	icd2	isocitrate dehydrogenase
Rv0794c	lpdB	dihydrolipoamide dehydrogenase
Rv1240	mdh	malate dehydrogenase
Hv2967c	pca	pyruvate carboxylase
HV3318	sahA	succinate denydrogenase A
HV3319	sanB odbC	succinate dehydrogenase B
1100010	Suno	unit
Bv3317	sdhD	succinate dehydrogenase D sub-
	June	unit
Rv1248c	sucA	2-oxoglutarate dehydrogenase
Rv2215	sucB	dihydrolipoamide succinyltrans-
		ferase
Rv0951	sucC	succinyl-CoA synthase β chain
Rv0952	sucD	succinyl-CoA synthase α chain
	4 - I	
4. Giyoxyla	ue pypass	inneitrate lunne
HV0467	aceA	isocitrate lyase
RV1010	aceAa aceAh	isocitrate lyase, a module
Bv18370	alcR	malate synthase
Bv33230	aphA	phosphoglycolate phosphatase
	31-111	springly source principlication
5. Pentose	phosphat	e pathway
Rv1445c	devB	glucose-6-phosphate 1-dehydro-
Rv1844c		genase
	gnd	genase 6-phosphogluconate dehydroge-
	gnd	genase 6-phosphogluconate dehydroge- nase (Gram –)
Rv1122	gnd gnd2	genase 6-phosphogluconate dehydroge- nase (Gram –) 6-phosphogluconate dehydroge-
Rv1122	gnd gnd2	genase 6-phosphogluconate dehydroge- nase (Gram –) 6-phosphogluconate dehydroge- nase (Gram +)

Rv2436	rbsK	ribokinase	Rv3250
Rv1408	rpe	ribulose-phosphate 3-epimerase	7 14
HV24650 By1448c	rpi tal	prospropentose isomerase	7. WIISCE
Rv1449c	tkt	transketolase	8. ATP-p
Rv1121	zwf	glucose-6-phosphate 1-dehydro-	Rv1308
_		genase	Rv1304
Rv1447c	zwł2	glucose-6-phosphate 1-dehydro-	Hv1311
		genase	By1305
6. Respirat	ion		Rv1306
a. aerobic			Rv1309
Rv0527	ccsA	cytochrome <i>c</i> -type biogenesis	Rv1307
Ductor		protein	0.0
HV0529	CCSB	cytochrome c-type biogenesis	1 Gene
Bv1451	ctaB	cvtochrome c oxidase assembly	Rv2589
		factor	Rv3432
Rv2200c	ctaC	cytochrome c oxidase chain II	Rv1832
Rv3043c	ctaD	cytochrome <i>c</i> oxidase poly-	Rv1826
Bv2193	ctaE	ovtochrome c oxidase poly-	HV2211
1102100	oluc	peptide III	Rv1213
Rv1542c	glbN	hemoglobin-like, oxygen carrier	
Rv2470	glbO	hemoglobin-like, oxygen carrier	Rv3842
Rv2249c	glpD1	glycerol-3-phosphate dehydroge-	D. 0047
Bv3302c	alnD2	nase alveerol-3-phosphate debydroge-	HV0317
11000020	gipbz	nase	Rv3566
Rv0694	lldD1	L-lactate dehydrogenase	
		(cytochrome)	Rv0155
Rv1872c	lldD2	L-lactate dehydrogenase	-
Hv18540	ndh	probable NADH dehydrogenase	Hv0156
HV3145 Bv3146	nuoA nuoR	NADH dehydrogenase chain A	Bv0157
Rv3147	nuoC	NADH dehydrogenase chain C	1100107
Rv3148	nuoD	NADH dehydrogenase chain D	Rv1127
Rv3149	nuoE	NADH dehydrogenase chain E	
Rv3150	nuoF	NADH dehydrogenase chain F	0.01
HV3151 Bv3152	nuoG nuoH	NADH denydrogenase chain G	2. Gluco
Bv3153	nuol	NADH dehydrogenase chain I	1100211
Rv3154	nuoJ	NADH dehydrogenase chain J	Rv0069
Rv3155	nuoK	NADH dehydrogenase chain K	
Rv3156	nuoL	NADH dehydrogenase chain L	3. Sugar
Hv3157	nuoM	NADH dehydrogenase chain M	Hv1512
Rv2195	nuon acr A	Rieske iron-sulphur component of	TV3/04
1102100	yon	ubiQ-cvtB reductase	Rv1511
Rv2196	qcrB	cytochrome β component of <i>ubiQ</i> -	Rv0334
		cytB reductase	
Rv2194	qcrC	cytB reductase cytochrome b/c component of	Rv3264
Rv2194	qcrC	cytB reductase cytochrome b/c component of ubiQ-cytB reductase	Rv3264
Rv2194 b. anaerob	qcrC ic	cytB reductase cytochrome <i>b/c</i> component of <i>ubiQ-cytB</i> reductase	Rv3264 Rv3464 Rv3634
Rv2194 <i>b. anaerob</i> Rv2392	qcrC ic cysH	cytB reductase sytochrome b/c component of ub/Q-cytB reductase 3'-phosphoadenylylsulfate (PAPS)	Rv3264 Rv3464 Rv3634 Rv3634
Rv2194 <i>b. anaerob</i> Rv2392	qcrC ic cysH	cytB reductase cytochrome b/c component of ubiQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase	Rv3264 Rv3464 Rv3634 Rv3468 Rv3465
Rv2194 b. anaerob. Rv2392 Rv2899c	qcrC ic cysH fdhD	cytB reductase cytochrome b/c component of ubiQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N	Rv3264 Rv3464 Rv36344 Rv3468 Rv3465
Rv2194 <i>b. anaerob.</i> Rv2392 Rv2899c Rv2900c	qcrC ic cysH fdhD fdhF	cytB reductase cytochrome b/c component of ubiQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase	Rv32644 Rv3464 Rv36344 Rv34684 Rv3465 Rv3465
Rv2194 <i>b. anaerob.</i> Rv2392 Rv2899c Rv2900c Rv1552	qcrC ic cysH fdhD fdhF frdA	cytB reductase cytochrome b/c component of ubiQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein	Rv3264 Rv3464 Rv3634 Rv3468 Rv3465 Rv3266 Rv3226
Rv2194 <i>b. anaerob.</i> Rv2392 Rv2899c Rv2900c Rv1552	qerC ic cysH fdhD fdhF frdA	cytB reductase sytochrome b/c component of ubiQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit	Rv3264 Rv3464 Rv3634 Rv3465 Rv3465 Rv3266 Rv3226
Rv2194 b. anaerob. Rv2392 Rv2899c Rv2900c Rv1552 Rv1553	qcrC ic cysH fdhD fdhF frdA frdB	cytB reductase cytochrome b/c component of ubiQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molydopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase iron sulphur	Rv32644 Rv3464 Rv36344 Rv34684 Rv3465 Rv32664 Rv32664 Rv0322
Rv2194 b. anaerob Rv2392 Rv2899c Rv2900c Rv1552 Rv1553	qcrC ic cysH fdhD fdhF frdA frdB	cytB reductase cytochrome b/c component of ubiQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein	Rv3264/ Rv3464 Rv34634 Rv3465 Rv3465 Rv3266/ Rv0322
Rv2194 b. anaerob Rv2392 Rv2899c Rv2900c Rv1552 Rv1553 Rv1554	qcrC ic cysH fdhD fdhF frdA frdB frdC	cytB reductase cytochrome b/c component of ubiQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor	Rv3264/ Rv3464 Rv3634/ Rv3465 Rv3465 Rv3266/ Rv0322 Rv3265/ Rv1525
Rv2194 <i>b. anaerob.</i> Rv2392 Rv2899c Rv2900c Rv1552 Rv1553 Rv1554 Rv1555	qcrC ic cysH fdhD fdhF frdA frdA frdB frdC trdD	cytB reductase cytochrome b/c component of ubiQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein	Rv3264/ Rv3464 Rv3634/ Rv3465 Rv3465 Rv3266/ Rv0322 Rv3265/ Rv1525 Rv1525 Rv3400
Rv2194 <i>b. anaerob.</i> Rv2392 Rv28990 Rv29000 Rv1552 Rv1553 Rv1554 Rv1555	qcrC cysH fdhD fdhF frdA frdB frdB frdC frdD	cytB reductase sytochrome b/c component of ubiQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molydopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein fumarate reductase 15kD anchor protein fumarate reductase 13kD anchor protein	Rv3264/ Rv3464 Rv3634/ Rv3468 Rv3465 Rv3266/ Rv0322 Rv3265/ Rv1525 Rv3400 4, Aming
Rv2194 b. anaerob Rv2392 Rv2899c Rv2900c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG	cytB reductase cytochrome b/c component of ubiQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molyddopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein fumarate reductase 13kD anchor protein fumarate reductase α subunit	Rv3264/ Rv3464 Rv3634/ Rv3468/ Rv3266/ Rv3266/ Rv3265/ Rv1525 Rv3400 4. Amin(Rv3436/
Rv2194 b. anaerob Rv2392 Rv2899c Rv2900c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162	qcrC ic cysH fdhD fdhF frdA frdA frdB frdC frdD narG narH	cytB reductase cytochrome b/c component of ubiQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein fumarate reductase ion sulphur protein fumarate reductase 15kD anchor protein fumarate reductase 13kD anchor protein fumarate reductase a subunit nitrate reductase β chain	Rv32644 Rv3464 Rv346834 Rv34665 Rv32666 Rv03222 Rv32655 Rv1525 Rv1525 Rv15400 4. Amino Rv3436
Rv2194 <i>b. anaerob</i> Rv2392 Rv2899c Rv2900c Rv1552 Rv1553 Rv1554 Rv1155 Rv1161 Rv1162 Rv1162	qcrC cysH fdhD fdhF frdA frdB frdC frdD narG narH narl	cytB reductase cytochrome b/c component of ubiQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein grotein fumarate reductase 15kD anchor protein fumarate reductase 15kD anchor protein nitrate reductase α subunit nitrate reductase α subunit nitrate reductase α y chain	Rv3264/ Rv3464 Rv3468/ Rv3468 Rv3465 Rv3266/ Rv3226 Rv32265/ Rv1525 Rv3400 4. Amino Rv3436
Rv2194 b. anaerob Rv2392 Rv28990 Rv29000 Rv1552 Rv1553 Rv1554 Rv1155 Rv1162 Rv1164 Rv1164 Rv1164 Rv1164	qcrC ic cysH fdhD fdhF frdA frdA frdB frdC frdD narG narH narI narI narI narI narY	cytB reductase sytochrome b/c component of ubiQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molydopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein fumarate reductase flavoprotein fumarate reductase 15kD anchor protein nitrate reductase 0 skiD anchor protein nitrate reductase α subunit nitrate reductase α subunit nitrate reductase α chain nitrate reductase α chain nitrate reductase α chain nitrate reductase α chain	Rv3264 Rv3464 Rv3468 Rv3468 Rv3468 Rv3266 Rv0322 Rv3265 Rv1525 Rv1525 Rv1525 Rv1525 Rv3400 4. Amina Rv3436
Rv2194 b. anaerob Rv2899c Rv2890c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1163 Rv1736c Rv7391	qcrC cysH fdhD fdhF frdA frdA frdC frdD narG narH narI narI narI narJ narX narX	cytB reductase sytochrome b/c component of ubiQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molydopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein grotein fumarate reductase 15kD anchor protein fumarate reductase 15kD anchor protein fumarate reductase 15kD anchor protein fumarate reductase 3kD anchor protein nitrate reductase β chain nitrate reductase β chain nitrate reductase β chain nitrate reductase β chain nitrate reductase δ chain fused nitrate reductase δ chain fused nitrate reductase δ chain fused nitrate reductase	Rv3264 Rv3464 Rv34634 Rv3465 Rv3465 Rv3266 Rv0322 Rv3265 Rv1525 Rv1525 Rv3400 4. Amina Rv3436 5. Sulph Rv0711 Rv0721
Rv2194 b. anaerob Rv2392 Rv28990 Rv29000 Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1164 Rv1163 Rv17360 Rv2391	qorC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narI narJ narX nirA	cytB reductase cytochrome b/c component of ubiQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molyddopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein fumarate reductase a Subunit nitrate reductase α Subunit nitrate reductase β chain nitrate reductase β chain nitrate reductase β chain nitrate reductase β chain nitrate reductase β chain fuse flavoprotectase probable nitrite reductase/sulphite reductase	Rv3264 Rv3464 Rv3468 Rv3465 Rv3266 Rv32265 Rv32265 Rv32265 Rv3220 4. Amina Rv3436 S. Sulph Rv3436
Rv2194 b. anaerob Rv2392 Rv2890c Rv2900c Rv1552 Rv1553 Rv1554 Rv1161 Rv1162 Rv1164 Rv1163 Rv17366 Rv2391 Rv0252	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narI narJ narX nirA nirB	cytB reductase cytochrome b/c component of ubiQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molydopterin-containing oxidore- ductase fumarate reductase flavoprotein fumarate reductase flavoprotein fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein fumarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase α subunit nitrate reductase β chain nitrate reductase probable nitrite reductase/ protectase probable nitrite reductase/ subplier	Rv32644 Rv3464 Rv34648 Rv3465 Rv3465 Rv32666 Rv0322 Rv3265 Rv1525 Rv3400 4. Amina Rv34366 S. Sulph Rv0711 Rv3299 Rv0663 Rv30711
Rv2194 b. anaerob Rv2392 Rv28990c Rv2900c Rv1552 Rv1553 Rv11554 Rv11555 Rv1161 Rv1162 Rv1163 Rv17360 Rv17360 Rv1391 Rv2391 Rv2391	qcrC ic cysH fdhD fdhF frdA frdB frdA frdB frdC frdD narH narH narH narH narX nirA nirA nirB nirD	cytB reductase sytochrome b/c component of ubiQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein grotein fumarate reductase 15kD anchor protein fumarate reductase 15kD anchor protein nitrate reductase α subunit nitrate reductase α subunit nitrate reductase α subunit nitrate reductase β chain nitrate reductase β subunit reductase probable nitrite reductase small	Rv3264 Rv3464 Rv3464 Rv3465 Rv3266 Rv3266 Rv3265 Rv3265 Rv3265 Rv3400 4. Amine Rv3436 S. Sulph Rv0711 Rv3299 Rv0663 Rv327 Rv3296
Rv2194 b. anaerob Rv2399 Rv28990 Rv29000 Rv1552 Rv1553 Rv1554 Rv1164 Rv1162 Rv1164 Rv1163 Rv17360 Rv2391 Rv0252 Rv0252	qcrC ic cysH fdhD fdhF frdA frdA frdB frdC frdD narG narH narI narI narJ narX nirA nirB nirD	<i>cytB</i> reductase sytochrome <i>b/c</i> component of <i>ubiQ-cytB</i> reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molyddopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein grotein nitrate reductase 15kD anchor protein nitrate reductase a Subunit nitrate reductase β chain nitrate reductase β chain	Rv32644 Rv3464 Rv3465 Rv3465 Rv3465 Rv32666 Rv1525 Rv32656 Rv1525 Rv3400 4. Amind Rv34360 5. Sulph Rv040 S. Sulph Rv0711 Rv3299 Rv0296 Rv3796 Rv3796
Rv2194 b. anaerob Rv23992 Rv2899c Rv2900c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1163 Rv1736c Rv2391 Rv0252 Rv0253	qcrC ic cysH fdhD fdhF fdhF frdA frdB frdC frdD narH narl narl narl narl narl narl narl narl	cytB reductase sytochrome b/c component of ubiQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molydopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein grotein fumarate reductase 15kD anchor protein fumarate reductase 15kD anchor protein fumarate reductase 13kD anchor protein nitrate reductase β chain nitrate reductase β subunit	Rv3264 Rv3464 Rv3463 Rv3465 Rv3266 Rv3226 Rv32265 Rv1525 Rv3400 4. Amina Rv3436 S. Sulph Rv0711 Rv3299 Rv3299 Rv3299 Rv3299 Rv3295 Rv3296 Rv329 Rv349 Rv
Rv2194 b. anaerob Rv2392 Rv28990c Rv29000c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1164 Rv1163 Rv1736c Rv2391 Rv0252 Rv0253 c. Electron Rv0409	qorC ic cysH fdhD fdhF frdA frdA frdB frdC frdD narG narH narI narJ narX nirA nirA nirB nirD transport transport	<i>cytB</i> reductase sytochrome <i>b/c</i> component of <i>ubiQ-cytB</i> reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molyddopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein fumarate reductase a subunit nitrate reductase β chain nitrate reductase β chain fused nitrate reductase probable nitrite reductase/sulphite reductase nitrite reductase flavoprotein probable nitrite reductase small subunit	Rv32644 Rv3464 Rv34648 Rv3465 Rv3465 Rv32666 Rv0322 Rv3265 Rv1525 Rv3265 Rv1525 Rv3400 4. Amina Rv34366 S. Sulph Rv0711 Rv3299 Rv0633 Rv0771 Rv0668 Rv3796 Rv1285 Rv1285 Rv1286 Rv1285 Rv1286 Rv1285 Rv1286 Rv1285 Rv1286 Rv1285 Rv1286 Rv1285 Rv1286 Rv1285 Rv1285 Rv1286 Rv1285 Rv2185 R
Rv2194 b. anaerob Rv2392 Rv2392 Rv2800c Rv1552 Rv1553 Rv1155 Rv1161 Rv1162 Rv1163 Rv1736c Rv2391 Rv0252 Rv0253 c. Electron Rv0409 Rv1623c	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narl narl narl narR nirB nirD transport ackA appC	cytB reductase cytochrome b/c component of ubiQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein grotein fumarate reductase 15kD anchor protein fumarate reductase 15kD anchor protein nitrate reductase α subunit nitrate reductase α subunit nitrate reductase β chain nitrate reductase β subunit nitrate reductase β subunit nitrate reductase β subunit nitrate reductase small subunit	Rv32644 Rv3464 Rv3465 Rv3465 Rv32666 Rv32667 Rv1525 Rv3400 4. Amina Rv3436 S. Sulph Rv07111 Rv3299 Rv0663 Rv3796 Rv3796 Rv3796 Rv1286 Rv1286 Rv1286 Rv1286
Rv2194 b. anaerob Rv2392 Rv2392 Rv1552 Rv1553 Rv1554 Rv1555 Rv1164 Rv1164 Rv1163 Rv1703 Rv2391 Rv2391 Rv2252 Rv2253 c. Electron Rv0409 Rv1623c	qcrC ic cysH fdhD fdhF frdA frdA frdB frdC frdD narG narH narJ narJ narJ narJ narJ narJ narZ nirB nirD transport ackA appC	cytB reductase sytochrome <i>b/c</i> component of <i>ubiQ-cytB</i> reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molydopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein protein fumarate reductase 15kD anchor protein nitrate reductase a Subunit nitrate reductase α subunit nitrate reductase α subunit nitrate reductase β chain nitrate reductase β chain fused nitrate reductase β subunit acetate kinase cytochrome <i>bd-ll</i> oxidase subunit l	Rv3264/ Rv3464 Rv3463 Rv3465 Rv3266/ Rv3265/ Rv3265/ Rv3265/ Rv3265/ Rv3265/ Rv3265/ Rv3265/ Rv3265/ Rv3265/ Rv3265/ Rv3265/ Rv3265/ Rv3265/ Rv3265/ Rv3276/ Rv3276/ Rv3276/ Rv3276/ Rv3276/ Rv3276/ Rv3276/ Rv3276/ Rv3276/ Rv3276/ Rv3276/ Rv3276/ Rv3276/ Rv3276/ Rv3276/ Rv3276/ Rv3228/ Rv348/ Rv38
Rv2194 b. anaerob Rv2899c Rv2990c Rv1552 Rv1553 Rv1554 Rv1555 Rv1164 Rv1164 Rv1163 Rv1736c Rv2391 Rv0252 Rv0253 c. Electron Rv0409 Rv1622c	qcrC ic cysH fdhD fdhF frdA frdA frdA frdC frdD narH narJ narJ narJ narJ narJ narJ narJ narJ	cytB reductase sytochrome <i>b/c</i> component of <i>ubiQ-cytB</i> reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molydopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase a subplur protein nitrate reductase 15kD anchor protein nitrate reductase 15kD anchor protein nitrate reductase 3kD anchor protein nitrate reductase 3kD anchor protein nitrate reductase 9 chain nitrate reductase 9 chain nitrate reductase 9 chain nitrate reductase 8 chain fused nitrate reductase 9 chain nitrate reductase 9 subunit subunit	Rv32644 Rv3464 Rv34634 Rv3465 Rv32666 Rv32656 Rv1525 Rv3400 4. Amind Rv32650 Rv32650 Rv1285 Rv3400 4. Amind Rv3299 Rv02966 Rv1285 Rv1286 Rv1285 Rv1286 Rv1285 Rv185 Rv1285
Rv2194 b. anaerob Rv2392 Rv2899c Rv2900c Rv1552 Rv1553 Rv1555 Rv1555 Rv1161 Rv1163 Rv1164 Rv1163 Rv1736c Rv2391 Rv0252 Rv0253 c. <i>Electron</i> Rv0409 Rv1622c Rv1622c	qcrC ic cysH fdhD fdhF frdA frdA frdB frdC frdD narG narH narI narI narI narI narI narI narI narJ transport tackA appC cydB	cytB reductase sytochrome b/c component of ubiQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molydopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein fumarate reductase a 15kD anchor protein fumarate reductase 15kD anchor protein fumarate reductase 3kD anchor protein fumarate reductase 3kD anchor protein nitrate reductase β chain nitrate reductase β chain nitrate reductase β chain nitrate reductase β chain nitrate reductase β chain fused nitrate reductase probable nitrite reductase subunit acetate kinase cytochrome <i>bd-ll</i> oxidase subunit II dBC tarearceter	Rv32644 Rv3464 Rv34648 Rv3465 Rv32666 Rv0322 Rv3265 Rv1525 Rv1525 Rv1525 Rv1525 Rv1525 Rv1525 Rv1525 Rv1525 Rv1226 S.Sulph Rv0663 Rv3296 Rv0711 Rv3299 Rv0603 Rv0771 Rv0296 Rv1285 Rv1285 Rv1286 Rv3299 Rv1285 Rv1285 Rv1281 Rv3299 Rv1285 Rv285
Rv2194 b. anaerob Rv2392 Rv2392 Rv2900c Rv1552 Rv1553 Rv1554 Rv1161 Rv1162 Rv1164 Rv1163 Rv17366 Rv2391 Rv0252 Rv0253 c. Electron Rv1623c Rv1622c Rv1622c	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narJ narJ narJ narX nirA nirB nirD transport ackA appC cydB cydC cydC	<i>cytB</i> reductase sytochrome <i>b/c</i> component of <i>ubiQ-cytB</i> reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein protein fumarate reductase 15kD anchor protein fumarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase α subunit nitrate reductase β chain nitrate reductase scale probable nitrite reductase subunit acetate kinase cytochrome <i>bd-ll</i> oxidase subunit I ABC transporter	Rv32644 Rv3464 Rv3464 Rv3465 Rv32666 Rv3265 Rv1525 Rv3265 Rv1525 Rv3400 4. Amina Rv34366 S. Sulph Rv0711 Rv3299 Rv0607 Rv3796 Rv1285 Rv1286 Rv110 Rv110 Rv110 Rv110 Rv110 Rv1286 Rv110 Rv1286 Rv128
Rv2194 b. anaerob Rv2392 Rv2392 Rv1352 Rv1552 Rv1553 Rv11554 Rv11554 Rv11555 Rv1161 Rv1162 Rv1163 Rv17360 Rv17360 Rv17360 Rv17360 Rv17360 Rv17360 Rv1623 Rv16200 Rv16200 Rv16210 Rv16210	qcrC ic cysH fdhD fdhF frdA frdB frdA frdB frdC frdD narG narH narJ narJ narX nirA nirA nirA nirB nirD transport ackA appC cydB cydD fdxA	<i>cytB</i> reductase sytochrome <i>b/c</i> component of <i>ubiQ-cytB</i> reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein subunit fumarate reductase a t5kD anchor protein fumarate reductase 15kD anchor protein nitrate reductase a Subunit nitrate reductase & chain nitrate reductase & subunit nitrate reductase & subunit nitrate reductase & subunit nitrate reductase & subunit nitrate reductase so probable nitrite reductase subunit acetate kinase cytochrome <i>bd-ll</i> oxidase subunit II ABC transporter ABC transporter	Rv32644 Rv3464 Rv3465 Rv3465 Rv32666 Rv3265 Rv1525 Rv3400 4. Amind Rv3436 S. Sulph Rv07111 Rv3299 Rv0663 Rv3796 Rv3796 Rv1285 Rv1286 Rv32131 Rv3294 Rv3283 Rv3283 Rv2291 Rv3284 Rv3283 Rv3283 Rv3294 Rv3283 Rv3283 Rv3294 Rv3283 Rv3283 Rv3283 Rv3283 Rv3283 Rv3283 Rv3283 Rv3283 Rv3283 Rv3283 Rv3284 Rv3283 Rv3285 R
Rv2194 b. anaerob Rv2392 Rv28900 Rv1552 Rv1553 Rv1554 Rv1555 Rv1164 Rv1164 Rv1163 Rv17360 Rv2391 Rv2391 c. Electron Rv0409 Rv16220 Rv16220 Rv16220 Rv16220 Rv16220 Rv16220 Rv16220	qcrC ic cysH fdhD fdhF frdA frdA frdB frdC frdD narH narH narH narH narH narH narD transport ackA appC cydD fdxA fdxB	<i>cytB</i> reductase sytochrome <i>b/c</i> component of <i>ubiQ-cytB</i> reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molyddopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein subunit fumarate reductase ion sulphur protein nitrate reductase 15kD anchor protein nitrate reductase a subunit nitrate reductase g chain nitrate re	Rv32644 Rv3464 Rv3465 Rv3465 Rv32666 Rv3265 Rv32796 Rv3265 Rv3276
Rv2194 b. anaerob Rv23990 Rv28990 Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1164 Rv1163 Rv17360 Rv2391 Rv0252 Rv0253 c. Electron Rv0409 Rv16230 Rv16220 Rv16220 Rv16210 Rv3554 Rv16210 Rv3654 Rv16210 Rv16210 Rv16210 Rv3654 Rv16210 Rv3654 Rv16210 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv165 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv165 Rv1655 Rv165 Rv1655 Rv165 R	qcrC ic cysH fdhD fdhF frdA frdA frdA frdC frdD narG nard narJ narJ narJ narJ narJ narJ narJ narJ	cytB reductase sytochrome <i>b/c</i> component of <i>ubiQ-cytB</i> reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase a subput protein nitrate reductase 15kD anchor protein nitrate reductase 3kD anchor protein nitrate reductase 3kD anchor protein nitrate reductase 9 chain nitrate 1 chain nitrate 9 chain nitrate 9 chain nitrate 1 chain nitrate 9	Rv32644 Rv3464 Rv3465 Rv3465 Rv32666 Rv0322 Rv32655 Rv3400 4. Amind Rv3465 Rv32656 Rv1256 Rv3400 4. Amind Rv34360 Rv3265 Rv3400 4. Amind Rv3400 Rv3296 Rv3266 Rv3265 Rv320 Rv3266 Rv3265 Rv326 Rv3265 Rv326 Rv3265 Rv326 Rv3265 Rv326 Rv3265 Rv3265 Rv3265 Rv3265 Rv3265 Rv3265 Rv3265 Rv3265 Rv3265 Rv3265 Rv3265 Rv326 Rv326 Rv3265 Rv326 Rv326 Rv326 Rv326 Rv326 Rv326 Rv326 Rv326
Rv2194 b. anaerob Rv2899c Rv2899c Rv2900c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1164 Rv1163 Rv1736c Rv2391 Rv0252 Rv0253 c. Electron Rv0409 Rv1623c Rv1622c Rv1622c Rv1622c Rv1622c Rv1622c Rv1622c Rv1622c Rv1622c Rv1622c	, qcrC cysH fdhD fdhF frdA frdB frdC frdD narG narH narJ narJ narX nirA nirB nirD transport ackA appC cydB cydC cydD fdxA fdxD fdxC fdxC fdxC	<i>cytB</i> reductase sytochrome <i>b/c</i> component of <i>ubIQ-cytB</i> reductase affects formate dehydrogenase-N molydopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein fumarate reductase 15kD anchor protein nitrate reductase 0 subunit nitrate reductase 0 subunit nitrate reductase 9 chain nitrate reductase 8 chain nitrate reductase 8 chain nitrate reductase 8 chain nitrate reductase 8 chain nitrate reductase 9 chain nitrate reductase 8 chain nitrate reductase 8 chain nitrate reductase 9 chain nitrate reductase 9 chain nitrate reductase 8 chain subunit acetate kinase cytochrome <i>bd-ll</i> oxidase subunit 1 ABC transporter ABC transporter ABC transporter ferredoxin ferredoxin 4Fe-4S probable firefox in ferredoxin affer fluvencredin	Rv3264/ Rv3464 Rv3465 Rv3465 Rv3266/ Rv3265/ Rv1525 Rv3265/ Rv1525 Rv3400 4. Amin(Rv3436) S. Sulph Rv0711 Rv3299 Rv0637 Rv1285 Rv1285 Rv1285 Rv1286 Rv3796 Rv1285 Rv1285 Rv1285 Rv1286 Rv3298 Rv3298 Rv3298 Rv3299 Rv3298 Rv3298 Rv3298 Rv3299 Rv3298 Rv328 Rv38 Rv38 Rv38 Rv38 Rv38 Rv38 Rv38 Rv3
Rv2194 b. anaerob Rv2392 Rv2392 Rv28900 Rv1552 Rv1553 Rv1155 Rv1161 Rv1162 Rv1163 Rv17366 Rv2391 Rv0252 Rv0253 c. Electron Rv0409 Rv16220 Rv1655 Rv1755 Rv1655	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narI narJ narJ narJ narJ narJ narZ nirA nirB nirD transport ackA appC cydB cydB fdxA fdxB fdxD fdxA fdxD fdxA fdxD fdxA	<i>cytB</i> reductase sytochrome <i>b/c</i> component of <i>ubiQ-cytB</i> reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein grotein fumarate reductase 13kD anchor protein fumarate reductase 13kD anchor protein nitrate reductase 0 subunit nitrate reductase 13kD anchor probable nitrite reductase probable nitrite reductase subunit accetate kinase cytochrome <i>bd-ll</i> oxidase subunit II ABC transporter ABC transporter ferredoxin ferredoxin ferredoxin ferredoxin electon transfer flavoprotein 8 subunit	Rv32644 Rv3464 Rv3465 Rv3465 Rv32666 Rv3265 Rv1525 Rv3400 4. Amina Rv3436 S. Sulph Rv07111 Rv3299 Rv0663 Rv3796 Rv3796 Rv1285 Rv1286 Rv32131 Rv3293 Rv1286 Rv3291 Rv3294 Rv3283 Rv2291 Rv3283 Rv2291 Rv3283 Rv3291 Rv3284 Rv3283 Rv2291 Rv3284 Rv3283 Rv3294 Rv3284 Rv3283 Rv2291 Rv3284 Rv3284 Rv3284 Rv3284 Rv3284 Rv3284 Rv3295 Rv1286 Rv3295 Rv325 Rv35 Rv35 Rv35 Rv35 Rv35 Rv35 Rv35 Rv3
Rv2194 b. anaerob Rv2392 Rv2392 Rv1552 Rv1553 Rv1554 Rv1155 Rv1154 Rv1155 Rv1161 Rv1162 Rv1163 Rv17366 Rv2391 Rv2391 Rv252 Rv253 c. <i>Electron</i> Rv0409 Rv16220 Rv2620 Rv16220 Rv2520	qcrC ic cysH fdhD fdhF frdA frdB frdA frdB frdC frdD narG narH narI narJ narX nirA nirA nirA nirA cydC cydB cydC cydB cydC cydB fdxA fdxB fdxA fdxB fdxA fdxB fdxA fdxB fdxA fdxD fdxA fdxB fdxC fdxA fdxB fdxC fdxA fdxB fdxC fdxA fdxB fdxC fdxA fdxB fdxC fdxA fdxB fdxC fdxA fdxB fdxC fdxA fdxB fdxC fdxB fdxC fdxA fdxB fdxC fdxA fdxB fdxC fdxA fdxB fdxC fdxA fdxB fdxC fdxA fdxA fdxA fdxA fdxC fdxA fdxA fdxA fdxC fdxA fdxA fdxA fdxA fdxA fdxA fdxA fdxA	<i>cytB</i> reductase sytochrome <i>b/c</i> component of <i>ubiQ-cytB</i> reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein protein fumarate reductase a t5kD anchor protein nitrate reductase a t5kD anchor protein nitrate reductase a subunit nitrate reductase a subunit nitrate reductase β chain nitrate reductase β subunit used nitrate reductase small subunit	Rv3264/ Rv3464 Rv3463 Rv3465 Rv3266/ Rv3265/ Rv3265/ Rv3265/ Rv3265/ Rv3265/ Rv3265/ Rv3265/ Rv3265/ Rv3265/ Rv3265/ Rv3265/ Rv3265/ Rv3265/ Rv3265/ Rv3265/ Rv3265/ Rv3266/ Rv3265/ Rv3265/ Rv3266/ Rv3265/ Rv3265/ Rv3265/ Rv3266/ Rv3265/ Rv3266/ Rv3266/ Rv3266/ Rv3266/ Rv3266/ Rv327/ Rv326/ Rv36/ Rv326/
Rv2194 b. anaerob Rv23990 Rv28990 Rv1752 Rv1552 Rv1553 Rv1554 Rv1555 Rv1164 Rv1163 Rv2391 Rv252 Rv0252 Rv162cc Rv3028c Rv3028c	qcrC ic cysH fdhD fdhF frdA frdA frdB frdC frdD narG narH narJ narJ narJ narJ narJ narJ narJ narJ	<i>cytB</i> reductase sytochrome <i>b/c</i> component of <i>ubiQ-cytB</i> reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molyddopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein protein fumarate reductase 15kD anchor protein nitrate reductase a SkD anchor protein nitrate reductase a SkD anchor protein nitrate reductase g chain nitrate reductase & chain tused nitrate reductase g chain nitrate reductase & chain tused nitrate reductase schain fused nitrate reductase schain subunit acetate kinase cytochrome <i>du</i> biquinol oxidase subunit l other apporter ABC transporter ferredoxin ferredoxin aFe-4S probable ferredoxin electron transfer flavoprotein β subunit electron transfer flavoprotein α subunit	Rv32644 Rv3464 Rv3465 Rv3465 Rv3465 Rv3265 Rv3265 Rv3265 Rv3265 Rv3400 4. Amind Rv321 Rv3265 Rv3400 4. Amind Rv3299 Rv663 Rv3299 Rv6663 Rv3299 Rv6663 Rv3299 Rv6663 Rv3291 Rv3299 Rv6663 Rv3299 Rv6663 Rv3299 Rv6663 Rv3295 Rv3299 Rv6663 Rv3299 Rv6663 Rv3295 Rv3299 Rv6663 Rv329 Rv1655 Rv329 Rv1655 Rv1655 Rv1655
Rv2194 b. anaerob Rv2899c Rv2900c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1164 Rv1163 Rv1736c Rv2391 Rv0252 Rv0253 c. Electron Rv0409 Rv1622c Rv1620c Rv1620c Rv1620c Rv1620c Rv3028c Rv3028c Rv3106	qcrC ic cysH fdhD fdhF frdA frdA frdC frdD narG narH narJ narJ narJ narJ narJ narJ narJ narJ	<i>cytB</i> reductase sytochrome <i>b/c</i> component of <i>ubiQ-cytB</i> reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molydopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase a subput protein nitrate reductase 15kD anchor protein nitrate reductase 15kD anchor protein nitrate reductase 3kD anchor protein nitrate reductase 3kD anchor protein nitrate reductase 9 chain nitrate 9 chain nitrate 10 chain nitrate 9 chain ni	Rv32644 Rv3464 Rv34648 Rv3465 Rv32666 Rv32265 Rv1525 Rv1525 Rv1525 Rv1525 Rv1525 Rv1525 Rv1525 Rv1525 Rv1525 Rv1226 Sv167 Rv2431 Rv3299 Rv0663 Rv2131 Rv3299 Rv06711 Rv3299 Rv0663 Rv1285 Rv1285 Rv1286 Rv21311 Rv3248 Rv3248 Rv3248 Rv3248 Rv3248 Rv3248 Rv3248 Rv3248 Rv3248 Rv3248 Rv3248 Rv3248 Rv3248 Rv3248 Rv3265 Rv1285 Rv1285 Rv1655 Rv16
Rv2194 b. anaerob Rv2392 Rv2392 Rv2900c Rv1552 Rv1553 Rv1554 Rv1155 Rv1161 Rv1162 Rv1164 Rv1163 Rv17366 Rv2391 Rv0252 Rv0253 c. <i>Electron</i> Rv1621c Rv1622c Rv1625 Rv165 Rv1625 Rv165 Rv	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narJ narJ narJ narJ narJ narZ nirB nirD transport ackA appC cydB fdxC fdxD fdxD fdxC fdxD fdxC fdxD fdxC fdxC fdxD fdxA fdxB fdxC fdxC fdxA fdxB fdxC fdxD fdxA fdxB fdxC fdxC fdxD fdxC fdxD fdxC fdxD fdxC fdxD fdxC fdx	<i>cytB</i> reductase sytochrome <i>b/c</i> component of <i>ubiQ-cytB</i> reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein protein fumarate reductase 15kD anchor protein fumarate reductase 13kD anchor protein nitrate reductase 0 subunit nitrate reductase 3 subunit nitrate reductase 3 subunit nitrate reductase 3 chain nitrate reductase 3 chain nitrate reductase 8 chain subunit acetate kinase cytochrome <i>bd-ll</i> oxidase subunit I asectate kinase cytochrome <i>du</i> biquinol oxidase subunit I ABC transporter ferredoxin ferredoxin ferredoxin 4Fe-4S probable ferredoxin electron transfer flavoprotein β subunit electron transfer flavoprotein α subunit electron transfer flavoprotein α subunit	Rv32644 Rv3464 Rv3464 Rv3465 Rv3465 Rv32666 Rv3265 Rv1525 Rv3400 4. Amina Rv34366 S. Sulph Rv0711 Rv3299 Rv0607 Rv3796 Rv3796 Rv3796 Rv3796 Rv3796 Rv21311 Rv32484 Rv3244 Rv3244 Rv3244 Rv3244 Rv3244 Rv3244 Rv3244 Rv3244 Rv3244 Rv3244 Rv3244 Rv3244 Rv3444 Rv3444 R
Rv2194 b. anaerob Rv2392 Rv2392 Rv1352 Rv1552 Rv1553 Rv1155 Rv1155 Rv1162 Rv1162 Rv1163 Rv17366 Rv2391 Rv0252 Rv0253 c. Electron Rv0409 Rv16230 Rv16230 Rv16230 Rv16230 Rv16200 Rv16207 Rv1607	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narJ narJ narA nirA nirB nirD transport ackA appC cydB cydB cydC cydB fdxA fdxB fdxC fdxC fdxA fdxB fdxC fdxA fdxB fdxA fdxB fdxC fdxA fdxB fdxA fdxB fdxA fdxB fdxA fdxB fdxA fdxB fdxA fdxB fdxA fdxB fdxA fdxB fdxA fdxB fdxA fdxB fdxA fdxB fdxA fdxB fdxA fdxB fdxF fxA fdxB fdxF fxA fdxB fdxF fxA fdxB fdxF fxA fdxB fdxF fxA fdxB fdxF fxA fdxB fdxF fxA fdxB fdxB fdxB fdxC fdxC fdxA fdxB fdxC fdxA fdxB fdxB fdxB fdxA fdxB fdxB fdxB fdxB fdxB fdxB fdxB fdxB	<i>cytB</i> reductase sytochrome <i>b/c</i> component of <i>ubiQ-cytB</i> reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein protein fumarate reductase 15kD anchor protein fumarate reductase 13kD anchor protein nitrate reductase a subunit nitrate reductase 3 subunit nitrate reductase 4 subunit nitrate reductase 5 chain nitrate reductase 6 chain nitrate reductase 8 chain nitrate reductase 8 chain fused nitrate reductase probable nitrite reductase probable nitrite reductase probable nitrite reductase small subunit acetate kinase cytochrome <i>bd-ll</i> oxidase subunit II ABC transporter ABC transporter ABC transporter ABC transporter ferredoxin ferredoxin ferredoxin ferredoxin electron transfer flavoprotein α subunit adternodoxin and NADPH ferre- doxin reductase ferredoxin, ferredoxin-NADP	Rv32644 Rv3464 Rv3465 Rv3465 Rv32666 Rv32667 Rv3265 Rv1525 Rv3400 4. Amina Rv3436 S. Sulph Rv07111 Rv3299 Rv0711 Rv3299 Rv0762 Rv3796 Rv32796 Rv32796 Rv32796 Rv3279 Rv1286 Rv3291 Rv3291 Rv3293 Rv3291 Rv3293 Rv3291 Rv3293 Rv3291 Rv3293 Rv3291 Rv3293 Rv3291 Rv3293 Rv329 Rv3293 Rv3293 Rv329 Rv
Rv2194 b. anaerob Rv2392 Rv2390 Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1164 Rv1163 Rv1755 Rv252 Rv253 c. Electron Rv0252 Rv0253 Rv0253 Rv1622c Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1655 Rv1755 Rv1655 Rv1755 Rv1655 Rv1755 Rv	qcrC ic cysH fdhD fdhF frdA frdB frdA frdB frdC frdD narG narH narH narH narH narH narH narK nirB transport ackA appC cydB cydC cydB cydC cydB fdxB fdxA fdxB fdxA fdxB fdxA fdxB fdxA fdxB fdxA fdxB fdxA fdxB fdxA fdxB fdxA fdxB fdxA fdxB fdxA fdxB fdxA fdxB fdxA fdxB fdxB fdxC rulbA fdxB fdxB fdxC rulbA fdxB fdxB fdxB fdxB fdxB frdC rulbA frdB frdD frdD frdD frdD frdD frdD frdD frdD	<i>cytB</i> reductase sytochrome <i>b/c</i> component of <i>ubiQ-cytB</i> reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein protein fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein nitrate reductase a subunit nitrate reductase β chain nitrate reductase β subunit subunit acetate kinase cytochrome <i>bd-ll</i> oxidase subunit ABC transporter ABC transporter	Rv3264/ Rv3464 Rv3464 Rv3465 Rv3465 Rv3266/ Rv3265/ Rv3266/ Rv3265/ Rv326/ Rv

v3250c	rubB	rubredoxin B
Miscellar	neous oxic	loreductases and oxygenases 171
. ATP-prot	on motive	force
v1308	atpA	ATP synthase α chain
v1304 v1311	aipo atnC	ATP synthase a chain
v1310	atpD	ATP synthase 6 chain
v1305	atpE	ATP synthase c chain
v1306	atpF	ATP synthase b chain
v1309	atpG	ATP synthase γ chain
V1307	атрн	AIP synthase & chain
. Central i	intermedia	rv metabolism
General		,
v2589	gabT	4-aminobutyrate aminotransferase
v3432c	gadB	glutamate decarboxylase
v1832 v1826	gcvB acvH	glycine decarboxylase
v2211c	acvT	T protein of glycine cleavage
	J	system
v1213	glgC	glucose-1-phosphate adenylyl-
	-1-01	transferase
V3842C	gipuri	phodiesterase
v0317c	alpQ2	glycerophosphoryl diester phos-
	J	phodiesterase
v3566c	nhoA	N-hydroxyarylamine o-acetyltrans-
		ferase
VU155	pntAA	unit a1
v0156	pntAB	pyridine transhydrogenase sub-
	,	unit α2
v0157	pntB	pyridine transhydrogenase
		subunit β
V1127C	ррак	dikinase
		dikilase
Glucone	ogenesis	
v0211	pckA	phosphoenolpyruvate carboxy-
		kinase
V0069c	sdaA	L-serine dehydratase 1
Sugar ni	cleotides	
v1512	epiA	nucleotide sugar epimerase
v3784	epíB	probable UDP-galactose 4-
		epimerase
V1511	gmaA miA	GDP-mannose 4,6 denydratase
00004	1111A	transferase
v3264c	rmlA2	glucose-1-phosphate thymidyl-
		transferase
v3464	rmlB	dTDP-glucose 4,6-dehydratase
v3634c	rmlB2	dTDP-glucose 4,6-dehydratase
V3468C	rmiB3 rmiC	dTDP-glucose 4,6-denydratase
V3403	mic	3.5-epimerase
v3266c	rmlD	dTDP-4-dehydrorhamnose
		reductase
v0322	udgA	UDP-glucose
		dehydrogenase/GDP-mannose 6-
v3265c	wbbl	dTDP-rhamnosyl transferase
v1525	wbbL2	dTDP-rhamnosyl transferase
v3400	-	probable β-phosphoglucomutase
. Amino si	ugars	aluana antia a faunta a a O
V3436C	yinis	phosphate aminotransferase
. Sulphur	metabolisr	n
v0711	atsA	arylsulfatase
V32990	atsB ataD	proable aryisultatase
v0663 v3077	atsE	proable aryisultatase
v0296c	atsG	proable aryisulfatase
v3796	atsH	proable arylsulfatase
v1285	cysD	ATP:sulphurylase subunit 2
v1286	cysN	ATP:sulphurylase subunit 1
V2131C	cysQ cabU	adoposylhomosysteinaso
v3283	sseA	thiosulfate sulfurtransferase
v2291	sseB	thiosulfate sulfurtransferase
v3118	sseC	thiosulfate sulfurtransferase
v0814c	sseC2	thiosulfate sulfurtransferase
v3762c	-	probable alkyl sulfatase
Amino a	cid binevn	thesis
. Glutamat	te familv	
v1654	argB	acetylglutamate kinase
v1652	argC	N-acetyl-y-glutamyl-phosphate
		reductase
v1655	argD ara⊑	acetylornithine aminotransferase
v1658	argr argG	arginosuccinate synthase
v1659	argH	arginosuccinate lyase
v1653	argJ	glutamate N-acetyltransferase
v2220	gInA1	glutamine synthase class I
v2222c	ginA2	giutamine synthase class II

Bv1878	alnA3	probable glutamine synthase
By2860c	alnA4	proable dutamine synthase
Bv2918c	ainD	uridvlvltransferase
Rv2221c	alnE	glutamate-ammonia-ligase
	3	adenvltransferase
Bv3859c	altB	ferredoxin-dependent dutamate
	3=	synthase
Bv3858c	altD	small subunit of NADH-dependent
111000000	gne	dutamate synthase
Bv3704c	ashA	possible a-dutamyloysteine syn-
11107040	90111	thase
By2427c	nroA	v-glutamvl phosphate reductase
Bv2439c	proR	glutamate 5-kinase
By0500	proC	pyrroline-5-carboxylate reductase
	<i>pioo</i>	pyrioline e salbergiale readelase
2. Aspartat	te family	
Bv3708c	asd	aspartate semialdehyde dehydro-
11107000	400	deparate comunicity de denyare
Bv3709c	ask	aspartokinase
Bv2201	aenR	asparadine synthase B
Bv3565	aenB	aspartate aminotransferase
By0337c	aspD aspC	aspartate aminotransferase
Bv2753c	dan A	dibydrodinicolinate synthase
By2773c	danB	dihydrodipicolinate reductase
By1202	danE	succinvl-diaminonimelate desuc-
TRIECE	dupt	cinvlase
Bv2141c	danE2	ArgE/DapE/Acy1/Cpg2/vscS
11021410	GUPEL	family
By27260	danE	diaminonimelate enimerase
By1293	h/sA	diaminopimelate decarboxulase
BV33/11	ny sri met∆	homoserine a-saetultransferses
Rv1070	met ^p	overathioning accurates
EV1079	metC	cystathionine y-synthase
HV3340	meic	cystatnionine β-iyase
HV11330	metE	5-metnyitetranydropteroyitrigiuta-
		mate-nomocysteine metnyitrans-
		terase
Hv2124c	metH	5-methyltetrahydrofolate-homo-
_		cysteine methyltransferase
Rv1392	metK	S-adenosylmethionine synthase
Rv0391	metZ	o-succinylhomoserine sulfhy-
		drylase
Rv1294	thrA	homoserine dehydrogenase
Rv1296	thrB	homoserine kinase
Rv1295	thrC	homoserine synthase
Serine fa	amily	
Rv0815c	cysA2	thiosulfate sulfurtransferase
Rv3117	cysA3	thiosulfate sulfurtransferase
Rv2335	cysE	serine acetyltransferase
Rv0511	cysG	uroporphyrin-III c-methyltrans-
		ferase
Rv2847c	cysG2	multifunctional enzyme, siroheme
		synthase
Rv2334	cvsK	cysteine synthase A
Rv1336	cvsM	cysteine synthase B
Rv1077	cvsM2	cvstathionine β-synthase
Bv0848	cvsM3	putative cysteine synthase
Bv1093	alvA	serine hydroxymethyltransferase
Rv0070c	alvA2	serine hydroxymethyltransferase
Bv2996c	serA	D-3-phosphoglycerate dehydro-
		genase
Rv0505c	serB	probable phosphoserine phos-
		phatase
Rv3042c	serB2	C-term similar to phosphoserine
		phosphatase
Rv0884c	serC	phosphoserine aminotransferase
4. Aromatic	c amino ac	bid family
Rv3227	aroA	3-phosphoshikimate
		1-carboxyvinyl transferase
Rv2538c	aroB	3-dehydroquinate synthase
Rv2537c	aroD	3-dehvdroquinate dehvdratase
Rv2552c	aroE	shikimate 5-dehvdrogenase
Bv2540c	aroF	chorismate synthase
Bv21780	aroG	DAHP synthase
Rv2539c	aroK	shikimate kinase l
By3838c	nheA	prephenate debydratase
Bv1613	trnA	tryptophan synthase a chain
By1612	trnB	tryptophan synthase ß chain
By1611	trnC	indole-3-alveerol phosphate
		synthase
By2192c	trnD	anthranilate phosphoribosyltrans-
		ferase
Bv1609	troF	anthranilate synthase
	·· /	component I
Rv2386c	trpE2	anthranilate synthase
	··	component
Rv3754	tvrA	prephenate dehvdrogenase
5 Histidine	`	
Bv1603	hisA	phosphoribosylformimino-5-
		aminoimidazole carboxamide
		ribonucleotide isomerase
By1601	hisR	imidazole diverol-phoephato
	1130	debudratase
Buteoo	hieC	histidinal-nhosnhate aminatrana
10000	1150	ferase
Bv3772	hisCo	histidinol-phosphate aminotrans-
1100/72	11502	foraço
Bv1500	hie₽	istidinal debudragensee
1111000	mer	meranner denyarogenase

Rv1605	hisF	imidazole glycerol-phosphate	D::0040-		subunit
Bv2121c	hisG	ATP phosphoribosyltransferase	HV3048C	nraG	ribonucieoside-dipnosphate small
Rv1602	hisH	amidotransferase	Rv3053c	nrdH	glutaredoxin electron transport
Rv2122c	hisl	phosphoribosyl-AMP cyclohydro-	Ducorda	mrall	component of NrdEF system
Bv1606	hisl2	probable phosphoribosyl-AMP 1.6	Rv3247c	tmk	thymidylate kinase
1111000	mone	cyclohydrolase	Rv2764c	thyA	thymidylate synthase
Rv0114	-	similar to HisB	Rv0570	nrdZ	ribonucleotide reductase, class II
6 Durimote	family		Rv3752c	-	probable cytidine/deoxycytidylate
Rv3423c	alr	alanine racemase			dearminase
			4. Salvage	of nucleos	sides and nucleotides
7. Branche	d amino a	cid family	Rv3313c	add	probable adenosine deaminase
HV1559 Bv3003c	iNA iNB	threonine deaminase	HV2584C	apt	adenine phosphoribosyltrans-
11000000	IIVD	unit	Rv3315c	cdd	probable cvtidine deaminase
Rv3470c	ilvB2	acetolactate synthase large sub-	Rv3314c	deoA	thymidine phosphorylase
D. cood .	11-0	unit	Rv0478	deoC	deoxyribose-phosphate aldolase
HV30010 Bv0189c	iNC iND	dibydrozy-acid debydratase	HV3307	aeoD	probable purine nucleoside phos-
Rv2210c	ilvE	branched-chain-amino-acid	Rv3624c	hpt	probable hypoxanthine-guanine
_		transaminase	_		phosphoribosyltransferase
Rv1820	ilvG	acetolactate synthase II	Rv3393	iunH	probable inosine-uridine
HV30020	IIVIN	unit	Bv0535	nnn	phosphorylase from Pnp/MtaP
Rv3509c	ilvX	probable acetohydroxyacid syn-		<i>aa</i>	family 2
-		thase I large subunit	Rv3309c	upp	uracil phophoribosyltransferase
Hv3/10	leuA leuR	α-isopropyl malate synthase	E Misseller		laasida/suelastida raastiana
Rv2988c	leuC	3-isopropylmalate dehydrogenase	Bv0733	adk	probable adenvlate kinase
	1040	large subunit	Rv2364c	bex	GTP-binding protein of Era/ThdF
Rv2987c	leuD	3-isopropylmalate dehydratase	_		family
		small subunit	Rv1712	cmk dat	cytidylate kinase
E Polvami	ne synthe	sis	HV2344C	agi	triphosphate bydrolase
Rv2601	speE	spermidine synthase	Rv2404c	lepA	GTP-binding protein LepA
			Rv2727c	miaA	tRNA δ(2)-isopentenylpyrophos-
F. Purines,	pyrimidine	es, nucleosides and nucleotides	D. O.LIE		phate transferase
1. Purine ri By1389	amk	ide biosynthesis putative quanylate kinase	HV2445C Bv2440c	пака ора	Obd GTP-binding protein
Rv3396c	guaA	GMP synthase	Rv2583c	relA	(p)ppGpp synthase I
Rv1843c	guaB1	inosine-5'-monophosphate dehy-			
Diam'r		drogenase	G. Biosynti	hesis of co	factors, prosthetic groups and
HV3411C	guaB2	drogenase	1 Biotin		
Rv3410c	guaB3	inosine-5'-monophosphate dehy-	Rv1568	bioA	adenosylmethionine-8-amino-7-
Bv1017c	orsA	ribose-phosphate pyrophosphoki-	Bv1589	hinB	oxononanoate aminotransferase
11110110	prort	nase	Rv1570	bioD	dethiobiotin synthase
Rv0357c	purA	adenylosuccinate synthase	Rv1569	bioF	8-amino-7-oxononanoate
HV0777	purB purC	adenylosuccinate lyase	Bv0032	bioE2	synthase
110700	puio	succinocarboxamide synthase	1100002	0101 2	BioF
Rv0772	purD	phosphoribosylamine-glycine lig-	Rv3279c	birA	biotin apo-protein ligase
Bv2275a	ourE	ase phosphoribosylaminoimidazole	Hv1442	bisC	biotin sulfoxide reductase
11002700	puit	carboxylase	1100000		gene
Rv0808	purF	amidophosphoribosyltransferase-			-
Rv0957	purH	phosphoribosylaminoimidazole-	2. Folic aci	d affer 0	dila selvada la da un du seda a a
Bv3276c	nurK	phosphoribosylaminoimidazole	HV2763C Bv2447c	arrA folC	folvorologi and reductase
TWOLTOO	punt	carboxylase ATPase subunit	Rv3356c	folD	methylenetetrahydrofolate dehy-
Rv0803	purL	phosphoribosylformylglycin-			drogenase
Buosee		amidine synthase II	Rv3609c	folE	GTP cyclohydrolase I
HV0809	punn	5-phosphoribosyl-5-aminoimida- zole synthase	HV3606C	IOIN	pyrophosphokinase
Rv0956	purN	phosphoribosylglycinamide	Rv3608c	folP	dihydropteroate synthase
D 0700	~	formyltransferase I	Rv1207	folP2	dihydropteroate synthase
HV0788	purQ	amidine synthase l	HV3607C	τοιχ	thesis
Rv0389	purT	phosphoribosylglycinamide	Rv0013	pabA	<i>p</i> -aminobenzoate synthase gluta-
D-0004	and t	formyltransferase II	Dud oor -		mine amidotransferase
HV2964	purU	formyltetranydrofolate deformy-	HV10050 Bv0812	pabB nahC	p-aminobenzoate synthase
			110012	pubb	annihodeoxyononsmate lyase
2. Pyrimidi	ne ribonuc	leotide biosynthesis	3. Lipoate		
Rv1383	carA	carbamoyl-phosphate synthase	Rv2218	lipA lin B	lipoate biosynthesis protein A
Bv1384	carB	carbamovl-phosphate synthase	HV2217	прв	lipoate biosynthesis protein B
	04.2	subunit	4. Molybdo	pterin	
Rv1380	pyrB	aspartate carbamoyltransferase	Rv3109	moaA	molybdenum cofactor biosynthe-
Rv1381	pyrC	dihydroorotase	Ducaco.		sis, protein A
Bv1385	pyrD pyrE	orotidine 5'-phosphate decarboxy-	HV08690	moaaz	sis, protein A
	121	lase	Rv0438c	moaA3	molybdenum cofactor biosynthe-
Rv1699	pyrG	CTP synthase		_	sis, protein A
HV28830 Bv03820	pyrH umpA	uriayiate kinase probable uridine 5'-monophos-	HV3110	тоаВ	molypdenum cotactor biosynthe-
1100020	uniori	phate synthase	Rv0984	moaB2	molybdenum cofactor biosvnthe-
				-	sis, protein B
3. 2'-deoxy	ribonuclec	deoxyoutidine triphocohoto	HV3111	moaC	molybdenum cotactor biosynthe-
110021	404	deaminase	Rv0864	moaC2	molybdenum cofactor biosynthe-
Rv2697c	dut	deoxyuridine triphosphatase		-	sis, protein C
Hv0233	nrdB	ribonucleoside-diphosphate	Hv3324c	moaC3	molybdenum cofactor biosynthe-
Rv3051c	nrdE	ribonucleoside diphosphate	Rv3112	moaD	molybdopterin converting factor
_		reductase α chain	_		subunit 1
Bv1981c	nrdF	ribonucleotide reductase small	Rv0868c	moaD2	molybdopterin converting factor

		subunit 1
Rv3119	moaE	molybdopterin-converting factor
		subunit 2
Rv0866	moaE2	molybdopterin-converting factor
		subunit 2
Rv3322c	moaE3	molybdopterin-converting factor
		subunit 2
Rv0994	moeA	molybdopterin biosynthesis
Rv3116	moeB	molybdopterin biosynthesis
Rv2338c	moeW	molybdopterin biosynthesis
Rv1681	moeX	weak similarity to E. coli MoaA
Rv1355c	moeY	weak similarity to E. coli MoeB
Rv3206c	moeZ	probably involved in
		molybdopterin biosynthesis
Rv0865	moa	molybdopterin biosynthesis
	0	
5. Pantothe	enate	
Rv1092c	coaA	pantothenate kinase
Rv2225	panB	3-methyl-2-oxobutanoate
	,	hydroxymethyltransferase
Rv3602c	panC	pantoate-B-alanine ligase
Rv3601c	panD	aspartate 1-decarboxylase
6. Pyridoxir	ne	
Rv2607	pdxH	pyridoxamine 5'-phosphate
		oxidase
7. Pyridine	nucleotide	•
Rv1594	nadA	quinolinate synthase
Rv1595	nadB	L-aspartate oxidase
Rv1596	nadC	nicotinate-nucleotide pyrophos-
		phatase
Rv0423c	thiC	thiamine synthesis, pyrimidine
		moiety
8. Thiamine	è	
Rv0422c	thíD	phosphomethylpyrimidine kinase
Rv0414c	thiE	thiamine synthesis, thiazole
		moiety
Rv0417	thiG	thiamine synthesis, thiazole
		moiety
Rv2977c	thiL	probable thiamine-monophos-
		phate kinase
 Riboflavi 	n	
Rv1940	ribA	GTP cyclohydrolase II
Rv1415	ribA2	probable GTP cyclohydrolase II
Rv1412	ribC	riboflavin synthase α chain
Rv2671	ribD	probable riboflavin deaminase
Rv2786c	ribF	riboflavin kinase
Rv1409	ribG	riboflavin biosynthesis
Rv1416	ribH	riboflavin synthase β chain
Rv3300c	-	probable deaminase, riboflavin
		synthesis
10. I hiored	loxin, gluta	aredoxin and mycothiol
Hv0773c	ggtA	putative γ-glutamyl transpeptidase
	aatu	γ -glutamyltranspeptidase
Rv2394	yyıD	precursor
Rv2394	yyın.	
Rv2394 Rv2855	gorA	glutathione reductase homologue
Rv2394 Rv2855 Rv0816c	gorA thiX	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX
Rv2394 Rv2855 Rv0816c Rv1470	gorA thiX trxA	equivalent to <i>M. leprae</i> ThiX thioredoxin
Rv2394 Rv2855 Rv0816c Rv1470 Rv1471	gorA thiX trxA trxB	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase
Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv2914	gorA thiX trxA trxB trxB2 trxC	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase
Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914	gorA thiX trxA trxB trxB2 trxC	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin
Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914	gorA thiX trxA trxB trxB2 trxC	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin
Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menaq	gorA thiX trxA trxB trxB2 trxC uinone, PC	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin ductase
Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menaqi terpenoids	gorA thiX trxA trxB trxB2 trxC uinone, PC	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin 2Q, ubiquinone and other
Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menaqi terpenoids Rv2682c	gorA thiX trxA trxB trxB2 trxC uinone, PC dxs	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate
Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menaqi terpenoids Rv2682c	gorA thiX trxA trxB trxB2 trxC uinone, PC dxs	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin 2Q, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase
Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menaqi terpenoids Rv2682c Rv0562	gorA thiX trxA trxB trxB2 trxC uinone, PC dxs grcC1	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin tribioredoxin reductase thioredoxin reductase thioredoxin aductase thioredoxin QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase
Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menaqi terpenoids Rv2682c Rv0562 Bv0982a	gorA thiX trxA trxB2 trxC uinone, PC dxs grcC1 arcC2	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin 2Q, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II bentaprenyl diphosphate
Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menaqi terpenoids Rv2682c Rv0562 Rv0989c	gorA thiX trxA trxB trxC uinone, PC dxs grcC1 grcC2	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin 2Q, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II
Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menaqi terpenoids Rv2682c Rv0562 Rv089c	gorA thiX trxA trxB trxB2 trxC uinone, PC dxs groC1 groC2 ir(cA	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin 2Q, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II synthase II
Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menaq terpenoids Rv2682c Rv0562 Rv0989c Rv3398c	gorA thiX trxA trxB trxC ulinone, PC dxs grcC1 grcC2 idsA	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase
Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menaq terpenoids Rv2682c Rv0562 Rv0989c Rv398c Bv2173	gorA thiX trxA trxB2 trxC uinone, PC dxs grcC1 grcC2 idsA ir(sA2	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin 2Q, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase
Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menaq terpenoids Rv2682c Rv0562 Rv0562 Rv0989c Rv3398c Rv2173	gorA thiX trxA trxB trxB2 trxC uinone, PC dxs grcC1 grcC2 idsA idsA2	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase
Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menaq terpenoids Rv2682c Rv0989c Rv0562 Rv0989c Rv3398c Rv2173 Rv2382c	gorA thiX trxA trxB trxB2 trxC disa grcC1 grcC2 idsA idsA2 idsA2	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin 2Q, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase tansferreranyl cimilar geranyl
Rv2394 Rv2855 Rv0816c Rv1471 Rv3913 Rv2682c Rv2682c Rv0562 Rv0989c Rv3398c Rv2173 Rv3383c	gorA thiX trxA trxB trxB2 trxC dxs groC1 groC2 idsA idsA2 idsB	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin 2Q, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase
Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv2914 11. Menaq terpenoids Rv2682c Rv0562 Rv0562 Rv3398c Rv2173 Rv3383c Bv0534c	ggiD gorA thiX trxA trxB trxC uinone, PC dxs groC1 groC2 idsA idsA2 idsB menA	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin QQ, ubiquinone and other 1-deoxy-D-xy/ulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase synthase geranylgeranyl pyrophosphate synthase synthase definition of the synthase definition of the synthase
Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 Rv3914 Rv2682c Rv0562 Rv0989c Rv0398c Rv2173 Rv3383c Rv3383c	ggiD gorA thiX trxA trxB trxC ulinone, PC dxs groC1 groC2 idsA idsA2 idsB menA	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin 2Q, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase Igeranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase 4-dihydroxy-2-naphthoate octanrend/transferase
Rv2394 Rv2855 Rv0816c Rv1471 Rv3913 Rv3914 11. Menaqterpenoids Rv2682c Rv0562 Rv398c Rv2173 Rv3383c Rv0534c Rv0542c	gorA thiX trxA trxB trxB2 trxC dxs groC1 drsA idsA2 idsA idsB menA menR	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase naphthoate synthase
Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv2914 11. Menaq terpenoids Rv2682c Rv0562 Rv0562 Rv3398c Rv2173 Rv3383c Rv0534c Rv0534c	ggiD gorA thiX trxA trxB trxC uinone, PC dxs groC1 groC2 idsA idsA2 idsB menA menB menC	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin QQ, ubiquinone and other 1-deoxy-D-xy/ulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase geranylgeranyl pyrophosphate synthase yunthase synthase transfergeranyl, similar geranyl pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase naphthoate synthase
Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 Rv3913 Rv3914 Rv0562 Rv0582 Rv0582 Rv0582 Rv2173 Rv3383c Rv2173 Rv3383c Rv0534c Rv0548c Rv0555	ggiD gorA thiX trxA trxB trxC dxs groC1 groC2 idsA idsA2 idsA2 idsB menA menB menC menC	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin 2Q, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase Il geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase naphthoate synthase
Rv2394 Rv2855 Rv0816c Rv1471 Rv3913 Rv1471 Rv3913 Rv0562 Rv0582c Rv398c Rv2173 Rv0538c Rv0542c Rv0542c Rv0542c	gorA thiX trxA trxB trxB2 trxC dxs groC1 drsA idsA2 idsA idsA2 idsB menA menB menC menD	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase -dihydroxy-2-naphthoate octaprenyltransferase naphthoate synthase 2-succinyl-6-hydroxy-2,4-cyclo- bavadinae t synthase
Rv2394 Rv2855 Rv0816c Rv1470 Rv1470 Rv1471 Rv3913 Rv2914 11. Menaq terpenoids Rv2682c Rv0562 Rv0989c Rv3398c Rv2173 Rv3383c Rv0534c Rv0555 Rv0555 Rv0555	ggiD gorA thiX trxA trxB trxC uinone, PC dxs groC1 groC2 idsA idsA2 idsA idsA2 idsB menA menD menD menE	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xy/ulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase geranylgeranyl pyrophosphate synthase transfergeranyl pyrophosphate synthase transfergeranyl similar geranyl pyrophosphate synthase octaprenyltransferase naphthoate synthase 2-succinyl6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase
Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 Rv3913 Rv2682c Rv0562 Rv0989c Rv0582 Rv2173 Rv3383c Rv2173 Rv3383c Rv0534c Rv0534c Rv05425 Rv05425 Rv05425	ggiD gorA thiX trxA trxB trxC dxs groC1 groC2 idsA idsA2 idsA2 idsB menA menB menC menB menG	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thi
Rv2394 Rv2855 Rv0816c Rv1471 Rv3913 Rv3914 11. Menaqterpenoids Rv2682c Rv0989c Rv3398c Rv2173 Rv0548c Rv0548c Rv0548c Rv0553 Rv0542c	ggiD gorA thiX trxA trxB trxB2 trxC dxs groC1 dxs groC2 idsA idsA2 idsA menA menB menC menD menE menG	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase o-sucoinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase o-sucoinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase o-sucoinylbenzoic acid-CoA ligase <i>S</i> -adenosylmethionine:
Rv2394 Rv2855 Rv0816c Rv1471 Rv3913 Rv3914 11. Menagt terpenoids Rv2682c Rv0562 Rv398c Rv2173 Rv0534c Rv0534c Rv0553 Rv0555 Rv0542c Rv3853	ggiD gorA thiX trxA trxB trxC uinone, PC dxs groC1 groC2 idsA idsA2 idsA idsA2 idsB menA menB menD menE menG nhvA	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xy/ulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase -dihydroxy-2-naphthoate octaprenyltransferase naphthoate synthase -ssuccinylbenzoite -CoA synthase 2-succinylbenzoite -CoA synthase -ssuccinylbenzoite -CoA synthase -ssuccinylbenzoite -CoA synthase -ssuccinylbenzoite -CoA synthase -succinylbenzoite -CoA synthase -succinylbenzoite -CoA synthase -succinylbenzoite -CoA synthase -succinylbenzoite -CoA synthase
Rv2394 Rv2855 Rv0816c Rv1471 Rv3913 Rv3914 11. Menaq terpenoids Rv0562 Rv0398c Rv2173 Rv0533c Rv0553 Rv0542c	ggiD gorA thiX trxA trxB trxC dxs groC1 groC2 idsA idsA2 idsA2 idsB menA menB menC menB menC menE menE menE menA	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin 2Q, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase 1 heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase II geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase naphthoate synthase 2-succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase 5-adenosylmethionine: 2-demethylmenaquinone phytoene synthase
Rv2394 Rv2855 Rv0816c Rv1471 Rv3913 Rv1471 Rv3913 Rv0562 Rv088c Rv3398c Rv2173 Rv0548c Rv0548c Rv0548c Rv0553 Rv0542c Rv3397c Rv3397c	ggiD gorA thiX trxA trxB trxB2 trxC dxs groC1 dxs groC2 idsA idsA2 idsA menA menB menC menD menE menG phyA pqqE	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase deranylgeranyl pyrophosphate synthase synthase deranylgeranyl pyrophosphate synthase synthase deranylgeranyl pyrophosphate synthase deranylgeranyl pyrophosphate synthase deranylgeranyl pyrophosphate synthase deranylgeranyl pyrophosphate synthase oscionyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase o-succinylbenzoic acid-CoA ligase S-adenosylmethionine: 2-demethylmenaquinone phytoene synthase coenzyme PQQ synthesis portein F
Rv2394 Rv2855 Rv0816c Rv1471 Rv3913 Rv1471 Rv3913 Rv2682c Rv0562 Rv398c Rv2173 Rv05398c Rv0534c Rv0553 Rv0555 Rv0542c Rv387c Rv387c Rv0553 Rv0553 Rv0553 Rv0593 Rv0693 Rv0558	ggiD gorA thiX trxA trxB trxC uinone, PC dxs groC1 groC2 idsA idsA2 idsA idsA2 idsB menA menB menD menB menG phyA pqqE uhE	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II synthase II heptaprenyl diphosphate synthase geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase octaprenyltransferase naphthoate synthase o-succinylbenzoite -CoA synthase 2-succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase o-succinylbenzoite -CoA synthase S-adenosylmethionine: 2-demethylmenaquinone phytoene synthase ocenzyme PQQ synthesis protein E ubiquinone/menaquinone biosup-
Rv2394 Rv2855 Rv0816c Rv1471 Rv3913 Rv1471 Rv3913 Rv0562 Rv0562 Rv3398c Rv2173 Rv0533c Rv0553 Rv0542c Rv0542c Rv3397c Rv3585 Rv0542c	ggiD gorA thiX trxA trxB trxC dxs groC1 groC2 idsA idsA2 idsA2 idsB menA menB menC menB menC menE menG phyA pqqE ubiE	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin 2Q, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase 1 heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase II geranylgeranyl pyrophosphate synthase I geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase naphthoate synthase 2-succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase S-adenosylmethionine: 2-demethylimenaquinone phytoene synthase coenzyme PQQ synthesis protein E ubiquinone/menaquinone biosyn- thesis methyltransferase
Rv2394 Rv2855 Rv0816c Rv1471 Rv3913 Rv3914 11. Menaqterpenoids Rv2682c Rv0989c Rv3398c Rv2173 Rv0548c Rv0548c Rv0548c Rv0553 Rv0542c Rv3997c Rv0693 Rv0558	ggiD gorA thiX trxA trxB trxC dxs groC1 dxs groC2 idsA idsA2 idsA menA menB menC menD menE menG phyA pqqE ubiE	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase defaulgeranyl pyrophosphate synthase synthase soutinylbenzoate-CoA synthase 2-succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase o-succinylbenzoic acid-CoA ligase S-adenosylmethionine: 2-demethylmenaquinone phytoene synthase coenzyme PQQ synthesis protein E ubiquinone/menaquinone biosyn- thesis methyltransferase
Rv2394 Rv2855 Rv0816c Rv1470 Rv1470 Rv1471 Rv3913 Rv3914 11. Menaq terpenoids Rv2682c Rv0989c Rv398c Rv398c Rv398c Rv398c Rv398c Rv3383c Rv0542c Rv0553 Rv0555 Rv0542c Rv3853 Rv0558 Rv397c Rv0558	gyrD gorA thiX trxA trxB trxC uinone, PC dxs groC1 groC2 idsA idsA2 idsA idsA2 idsB menA menB menC menD menC menG phyA pqqE ubiE	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase - octoorylbenzoate-CoA synthase 2-succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase o-succinylBenzoic acid-CoA ligase <i>S</i> -adenosylmethionine: 2-demethylmenaquinone phytoene synthase coenzyme PQQ synthesis protein E ubiquinone/menaquinone biosyn- thesis methyltransferase
Rv2394 Rv2855 Rv0816c Rv1471 Rv1471 Rv3913 Rv1470 Rv3914 11. Menaq terpenoids Rv088c Rv0562 Rv0398c Rv2173 Rv0534c Rv0553 Rv0542c Rv0542c Rv3387c Rv3873 Rv3853 Rv3875 Rv3875 Rv0542c Rv0598 12. Heme a Rv0509	ggrA thiX trxA trxB trxC dxs grcC1 grcC2 idsA idsA2 idsA2 idsB menA menB menC menB menC phyA pqqE ubiE and porphy	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase II geranylgeranyl pyrophosphate synthase Il geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase naphthoate synthase -succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase s-adenosylmethionine: 2-demethylimenaquinone phytoene synthase protein E ubiquinone/menaquinone biosyn- thesis methyltransferase ragitamyl-tRNA reductase
Rv2394 Rv2855 Rv0816c Rv1471 Rv3913 Rv3914 11. Menaqterpenoids Rv2682c Rv0989c Rv3398c Rv2173 Rv3398c Rv0548c Rv0553 Rv0548c Rv3997c Rv0588 12. Heme at Nv059 Rv0512	ggiD gorA thiX trxA trxB trxB2 trxC dxs groC1 dxs groC2 idsA idsA2 idsA2 idsB menA menB menC menD menE menG phyA pqqE ubiE and porphy hemA	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase synthase label{eq:synthase} synthase li heptaprenyl diphosphate synthase li geranylgeranyl pyrophosphate synthase li geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase o-succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase o-succinylbenzoic acid-CoA ligase <i>S</i> -adenosylimethionine: 2-demethylmenaquinone phytoene synthase coenzyme PQQ synthesis protein E ubiquinone/menaquinone biosyn- thesis methyltransferase <i>r</i> in glutamyl-tRNA reductase <i>s</i> -aminolevulinic acid dehvdratase
Rv2394 Rv2855 Rv0816c Rv1471 Rv3913 Rv1471 Rv3914 11. Menagterpenoids Rv2682c Rv0989c Rv3398c Rv2173 Rv0533 Rv0553 Rv0553 Rv0558 12. Heme r Rv0559 Rv0559	ggiD gorA thiX trxA trxB trxB2 trxC uinone, PC dxs groC1 groC2 idsA idsA2 idsA idsA2 idsB menA menB menC menD menE menG phyA pqqE ubiE	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase - ostucoinylbenzoate-CoA synthase 2-succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase o-succinylbenzoic acid-CoA ligase <i>S</i> -adenosylmethionine: 2-demethylmenaquinone phytoene synthase coenzyme PQQ synthesis protein E ubiquinone/menaquinone biosyn- thesis methyltransferase rin glutamyl-tRINA reductase &-aminolevulinic acid dehydratase porphobilinogen deaminase
Rv2394 Rv2855 Rv0816c Rv1471 Rv1471 Rv3913 Rv3914 11. Menaq terpenoids Rv0682c Rv0562 Rv3398c Rv2173 Rv0534c Rv0553 Rv0542c Rv0542c Rv0542c Rv0542c Rv0542c Rv0553 Rv0558 12. Heme # Rv0512 Rv0512 Rv0512 Rv0510	ggiD gorA thiX trxA trxB trxC dxs groC1 groC2 idsA idsA2 idsA2 idsA2 idsA2 idsB menA menB menC menB menC phyA pqqE ubiE and porphy hemA hemB hemC	glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase 1-deoxy-D-xylulose 5-phosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase II geranylgeranyl pyrophosphate synthase Iransfergeranyl, similar geranyl pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase naphthoate synthase 2-succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase cosuccinylbenzoit a cid-CoA ligase 5-adenosylmethionine: 2-demethylmenaquinone phytoene synthase coenzyme PQQ synthesis protein E ubiquinone/menaquinone biosyn- thesis methyltransferase a-aminolevulinic acid dehydratase porphobilinogen dearboxylase

Rv1300	hemK	protoporphyrinogen oxidase			transferase
NV0524	nemL	transferase	3 Acyltran	sferases	mycolyltransferases and
Rv2388c	hemN	oxygen-independent copropor-	phospholip	oid synthes	sis
		phyrinogen III oxidase	Rv2289	cdĥ	CDP-diacylglycerol phosphatidyl-
Rv2677c	hemY'	protoporphyrinogen oxidase			hydrolase
Rv1485	hemZ	ferrochelatase	Rv2881c	cdsA	phosphatidate cytidylyltransferase
10.0.1.1.			Hv3804c	tbpA	antigen 85A, mycolyltransferase
13. Cobala	min		HV18860	fbpB fbmC	antigen 85B, mycolyltransferase
HV28490	cobR	cob(i)alamin adenosyltransierase	RV01290	ibpC fbpD	antigen MDT51 mycolytransierase
Bv2231c	cobC	aminotransferase	11000000	юрD	ferase
Rv2236c	cobD	cobinamide synthase	Rv0564c	apdA 1	glycerol-3-phosphate dehydroge-
Rv2064	cobG	percorrin reductase		J.	nase
Rv2065	cobH	precorrin isomerase	Rv2982c	gpdA2	glycerol-3-phosphate dehydroge-
Rv2066	cobl	Cobl-CobJ fusion protein			nase
Hv2070c	CODK	precorrin reductase	Hv2612c	pgsA	CDP-diacylglycerol-glycerol-3-
RV20720	copL	propable methyltransferase			phosphate phosphatidyitrans-
By2062c	cobN	cobalt insertion	Bv1822	nasA2	CDP-diacylglycerol-glycerol-3-
Rv2208	cobS	cobalamin (5'-phosphate)		pgc, 12	phosphate phosphatidyltrans-
		synthase			ferase
Rv2207	cobT	nicotinate-nucleotide-dimethyl-	Rv2746c	pgsA3	CDP-diacylglycerol-glycerol-3-
		benzimidazole transferase			phosphate phosphatidyltrans-
Rv0254c	cobU	cobinamide kinase	D		ferase
HV02550	copQ	cobyric acid synthase	HV1551	pisB1	glycerol-3-phosphate acyltrans-
Rv0306	-	similar to BluB ochalamin synthe-	Bv24820	nlcB2	dvoerol-3-phosphate apyltraps-
1100000	-	sis protein <i>R</i> cansulatus	11024020	pisoz	ferase
		olo protoni i ni odpodratao	Rv0437c	psd	putative phosphatidvlserine
14. Iron util	lization			/	decarboxylase
Rv1876	bfrA	bacterioferritin	Rv0436c	pssA	CDP-diacylglycerol-serine
Rv3841	bfrB	bacterioferritin	_		o-phosphatidyltransferase
Rv3215	entC	probable isochorismate synthase	Rv0045c	-	possible dihydrolipoamide acetyl-
Hv3214	entD	weak similarity to many phospho-	Duco14+		transferase
Bv2895c	viuR	similar to proteins involved in	HV09140 Bv15/3		probable fatty-acyl CoA reductase
11020300	VIUD	vibriobactin uptake	Bv1627c	-	lipid carrier protein
Rv3525c	-	similar to ferripyochelin binding	Rv1814	-	possible C-5 sterol desaturase
		protein	Rv1867	-	similar to acetyl CoA
					synthase/lipid carriers
H. Lipid bio	osynthesis	:	Rv2261c		apolipoprotein N-acyltrans-
1. Synthesi	is of fatty a	and mycolic acids	D. 0000		ferase-a
HV3285	accA3	acety/propionyl CoA carboxylase	HV22620	· C	apolipoprotein N-acyltrans-
Bv0904c	ассЛЗ	a suburit acetyl/propionyl CoA carboxylase	Bv3523	_	lipid carrier protein
1100040	40020	ß subunit	Rv3720		C-term similar to cyclopropane
Rv3799c	accD4	acetyl/propionyl CoA carboxylase			fatty acid synthases
		β subunit			
Rv3280	accD5	acetyl/propionyl CoA carboxylase	I. Polyketia	le and nor	n-ribosomal peptide synthesis
D-0047		β subunit	Rv2940c	mas	mycocerosic acid synthase
HV2247	accD6	acety/propionyl CoA carboxylase	HV2384	motA	mycopactin/exochelin synthesis
Bv2244	acnM	acyl carrier protein (meromycolate	Bv2383c	mhtB	(salicylate-AMF ligase)
1102244	иорт	extension)	11020000	more	(serine/threonine ligation)
Rv2523c	acpS	CoA:apo-[ACP] pantethienephos-	Rv2382c	mbtC	mycobactin/exochelin synthesis
		photransferase	Rv2381c	mbtD	mycobactin/exochelin synthesis
Rv2243	fabD	malonyl CoA-[ACP] transacylase			(polyketide synthase)
Rv0649	fabD2	malonyl CoA-[ACP] transacylase	Rv2380c	mbtE	mycobactin/exochelin synthesis
HV1483	TADGT	3-oxoacyl-[ACP] reductase (aka	Dv2270a	mb+E	(lysine ligation)
Bv1350	fahG2	3-oroacyl-[ACP] Beductase	HV23/90	mor	(lysine ligation)
Rv2002	fabG3	3-oxoacyl-[ACP] reductase	Rv2378c	mbtG	mycobactin/exochelin synthesis
Rv0242c	fabG4	3-oxoacyl-[ACP] reductase			(lysine hydroxylase)
Rv2766c	fabG5	3-oxoacyl-[ACP] reductase	Rv2377c	mbtH	mycobactin/exochelin synthesis
Rv0533c	fabH	β-ketoacyl-ACP synthase III	Rv0101	nrp	unknown non-ribosomal peptide
Rv2524c	fas	fatty acid synthase	Durate		synthase
HV1484	INNA	enoyi-[ACP] reductase	HV11530	omt	PKS o-methyltransterase
HV2240	NASA	(meromycolate extension)	HV36240	рарнт	function
Rv2246	kasB	β-ketoacvl-ACP synthase	Rv3820c	papA2	PKS-associated protein, unknown
		(meromycolate extension)			function
Rv1618	tesB1	thioesterase II	Rv1182	рарАЗ	PKS-associated protein, unknown
Rv2605c	tesB2	thioesterase II	D /		function
Rv0033	-	possible acyl carrier protein	Hv1528c	papA4	PKS-associated protein, unknown
rhv 1344 By1799	-	possible biotin carboxylase	Bv2030	nan45	PKS-associated protein unknown
Bv3221c	_	resembles biotin carboxylase	1102303	рарно	function
Rv3472	-	possible acvl carrier protein	Rv2946c	pks1	polyketide synthase
			Rv3825c	pks2	polyketide synthase
2. Modificat	tion of fatt	y and mycolic acids	Rv1180	pks3	polyketide synthase
Hv3391	acrA1	tatty acyl-CoA reductase	Rv1181	pks4	polyketide synthase
HV33920	cmaA1	cyclopropane mycolic acid	HV15270	pks5	polyketide synthase
By0503a	cma10	synmase i ovelopropane mycolic acid syn-	HV0405	pkso nke7	polyketide synthase
. 1000000	JIIIaAZ	thase 2	Rv1662	pks8	polyketide synthase
Rv0824c	desA1	acyl-[ACP] desaturase	Rv1664	pks9	polyketide synthase
Rv1094	desA2	acyl-[ACP] desaturase	Rv1660	pks10	polyketide synthase (chalcone
Rv3229c	desA3	acyl-[ACP] desaturase			synthase-like)
Rv0645c	mmaA1	methoxymycolic acid synthase 1	Rv1665	pks11	polyketide synthase (chalcone
HV06440	mmaA2	methoxymycolic acid synthase 2	Du0040-	nka 10	synthase-like)
nv06430 Bv06436	mmaA3	memoxymycolic acid synthase 3	∩v20480	pks 12	porykenne synthase (erythronolide
Rv0447o	ufaA1	unknown fatty acid methyltrans-	Bv38000	oks 13	polyketide synthase
	a.a. 1	ferase	Rv1342c	pks 14	polyketide synthase (chalcone
Rv3538	ufaA2	unknown fatty acid methyltrans-			synthase-like)
_		ferase	Rv2947c	pks15	polyketide synthase
Rv0469	umaA1	unknown mycolic acid methyl-	Rv1013	pks16	polyketide synthase
_		transterase	HV1663	pks17	polyketide synthase
BV04700	10mg nr	1 1 F 1 M F 1/2 MARTEL F F 10 / / / / / / / / / / / / / / / / / /		F 100 A 1 1 10	E MANAGEMENT REAL BOARD FOR

Rv2931	ppsA	phenolpthiocerol synthesis (<i>pksB</i>)
Rv2932	ppsB	phenolpthiocerol synthesis (pksC)
HV2933 BV2024	ppsC	phenolpthiocerol synthesis (<i>pksD</i>)
Rv2934	ppsD ppsE	phenolphilocerol synthesis (<i>pksE</i>)
Rv2928	tesA	thioesterase
Rv1544	-	probable ketoacyl reductase
1 Bread a		
1. Repress	ors/activa	tors
Rv1657	argR	arginine repressor
Rv1267c	embR	regulator of embAB genes
Dut000-	6 A	(AfsR/Dndl/RedD family)
HV19090	furA furB	ferric uptake regulatory protein
Rv2919c	alnB	nitrogen regulatory protein
Rv2711	<i>ideR</i>	iron dependent repressor, IdeR
Rv2720	lexA	LexA, SOS repressor protein
HV1479	тохн	transcriptional regulator, MoxH
Rv3692	moxR2	transcriptional regulator. MoxR
		homologue
Rv3164c	moxR3	transcriptional regulator, MoxR
By02126	nadB	homologue
Rv0117	oxvS	transcriptional regulator (LvsR
		family)
Rv1379	pyrR	regulatory protein pyrimidine
Du0700	-	biosynthesis
HV2788	sirH	repressor
Rv3082c	virS	putative virulence regulating
		protein (AraC/XyIS family)
Rv3219	whiB1	WhiB transcriptional activator
D 0000	(100	homologue
HV32600	whiB2	while transcriptional activator
Rv3416	whiB3	WhiB transcriptional activator
		homologue
Rv3681c	whiB4	WhiB transcriptional activator
D: 0000		homologue
HV0023 Bv0043c	2	transcriptional regulator (GntB
11100100		family)
Rv0067c	-	transcriptional regulator
D 0070		(TetR/AcrR family)
HV0078	-	transcriptional regulator
Rv0081	-	transcriptional regulator (ArsR
		family)
Rv0135c	-	putative transcriptional regulator
Rv0144	-	putative transcriptional regulator
HVU156	-	(TetB/AcrB family)
Rv0165c	-	transcriptional regulator (GntR
		family)
Rv0195	-	transcriptional regulator
Bv0196		(LUXH/UNPA TAMIIy) transcriptional regulator
1100100		(TetR/AcrR family)
Rv0232	-	transcriptional regulator
		(TetR/AcrR family)
Rv0238	-	transcriptional regulator
Bv0273c		putative transcriptional regulator
Rv0302	-	transcriptional regulator
_		(TetR/AcrR family)
Rv0324	-	putative transcriptional regulator
HV0326	-	(TetB/AcrB family)
Rv0348	-	putative transcriptional regulator
Rv0377	-	transcriptional regulator (LysR
Ducade		family)
HV0366	-	(LuxB/LlbpA family)
Rv0452	-	putative transcriptional regulator
Rv0465c	-	transcriptional regulator
D: 0470 -		(PbsX/Xre family)
HV04720	-	(TetB/AcrB family)
Rv0474	-	transcriptional regulator
		(PbsX/Xre family)
Rv0485	-	transcriptional regulator (ROK
Bv0494	_	tamily) transprintional regulator (CotB
1100484		family)
Rv0552	-	putative transcriptional regulator
Rv0576	-	putative transcriptional regulator
Rv0586	-	transcriptional regulator (GntR
Bv0650	-	transcriptional regulator /ROK
. 100000		family)
Rv0653c	-	putative transcriptional regulator
Rv0681	-	transcriptional regulator
BV0601A		(Tech/ACrH tamily) transcriptional regulator
		(TetR/AcrR family)
Rv0737	-	putative transcriptional regulator
Rv0744c	-	putative transcriptional regulator
HVU/920	-	transcriptional regulator (GntH

		family)	Bv3160c		nutative transcriptional regulator
Bv08230	_	transcriptional regulator	By3167c		putative transcriptional regulator
11000200	-	(Nifp2/Smm1 family)	Dv21720	-	transcriptional regulator
Bu09276		(NIIFIG/STITTET TATTING)	HV31730	-	(TotP/A orP formily)
11000270	-	family)	Dv2192		(Tell (Ach Transprintional regulator
Du00000		transportational regulator	Du2200	-	transcriptional regulator
HV06900	-	(LuxD) (John & femily)	NV3200	-	(TetD/AerD femily)
Dv09010		(Euxin/OnpA family)	Dv2240a		transprintional regulator
By0894		putative transcriptional regulator	1102430	-	(TetP/AorP family)
RV0094	-	transcriptional regulator	Du2201a		(Tech/Acin faithiy)
HV1019	-	(TotP/A orP formily)	HV32910	-	(I rp/A ppC formily)
Dut 040		(Teth/Actin tathiny)	Duccor		(LIP/ASIC latility)
HV1049	-	familu)	HV3295	-	(TetP/AerD femily)
Dut 120a		transprintional regulator	Ducco4		(Teth/Actin tarrily)
NV11290	-	(Dhe V(Vre femily)	NV3334	-	family
DuttEta		(PDSA/Are farmily)	Ductor a		ramily)
HVI 151C	-	putative transcriptional regulator	HV34050	-	putative transcriptional regulator
HV1152	-	transcriptional regulator (Grith	Duorrz.	-	putative transcriptional regulator
D. 4407.		tamily)	HV3557C	-	transcriptional regulator
HV1167C	-	putative transcriptional regulator	D. 0574		(TetH/AcrH family)
HV12190	-	putative transcriptional regulator	HV3574	-	transcriptional regulator
HV12550	-	transcriptional regulator	D 0575		(TetH/AcrH family)
-		(TetH/AcrH family)	Hv3575c	-	transcriptional regulator (Laci
HV1332	-	putative transcriptional regulator	B 9599		tamily)
Hv1353c	-	transcriptional regulator	Hv3583c	-	putative transcriptional regulator
		(TetR/AcrR family)	Rv3676	-	transcriptional regulator (Crp/Fnr
Rv1358	-	transcriptional regulator			family)
		(LuxR/UhpA family)	Rv3678c	-	transcriptional regulator (LysR
Rv1359	-	putative transcriptional regulator			family)
Rv1395	-	transcriptional regulator	Rv3736	-	transcriptional regulator
		(AraC/XyIS family)			(AraC/XyIS family)
Rv1404	-	transcriptional regulator (MarR	Rv3744	-	transcriptional regulator (ArsR
		family)			family)
Rv1423	-	putative transcriptional regulator	Rv3830c	-	transcriptional regulator
Rv1460	-	putative transcriptional regulator			(TetR/AcrR family)
Rv1474c	-	transcriptional regulator	Rv3833	-	transcriptional regulator
		(TetR/AcrR family)			(AraC/XyIS family)
Rv1534	-	transcriptional regulator	Rv3840	-	putative transcriptional regulator
		(TetR/AcrR family)	Rv3855	-	putative transcriptional regulator
Rv1556	-	putative transcriptional regulator			
Rv1674c	-	putative transcriptional regulator	2. Two cor	mponent sy	vstems
Rv1675c	-	putative transcriptional regulator	Rv1028c	kdpD	sensor histidine kinase
Rv1719	-	transcriptional regulator (IcIR	Rv1027c	kdpE	two-component response
		family)			regulator
Rv1773c	-	transcriptional regulator (IcIR	Rv3246c	mtrA	two-component response
		family)			regulator
Rv1776c	-	putative transcriptional regulator	Rv3245c	mtrB	sensor histidine kinase
Rv1816	-	putative transcriptional regulator	Rv0844c	narL	two-component response
Rv1846c	-	putative transcriptional regulator			regulator
Rv1931c		transcriptional regulator	Rv0757	phoP	two-component response
		(AraC/XvIS family)		,	regulator
Rv1956	-	putative transcriptional regulator	Rv0758	phoR	sensor histidine kinase
D. 4000.		putativa transprintional regulator	Bv0/91	1 1/2	And a summariant users are a
HV1963C	-			reax3	two-component response
Rv1963c Rv1985c	-	transcriptional regulator (LvsR	1100401	regX3	regulator
Rv1963c Rv1985c	-	transcriptional regulator (LysR family)	Bv0490	regX3 senX3	regulator sensor histidine kinase
Rv1963c Rv1985c Rv1990c	-	transcriptional regulator family) putative transcriptional regulator	Rv0490 Rv0602c	regX3 senX3 tcrA	regulator sensor histidine kinase two-component response
Rv1963c Rv1985c Rv1990c Rv1994c	-	transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator	Rv0490 Rv0602c	regX3 senX3 tcrA	regulator sensor histidine kinase two-component response regulator
Rv1963c Rv1985c Rv1990c Rv1994c	-	family) putative transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family)	Rv0490 Rv0602c Rv0260c	regX3 senX3 tcrA -	regulator sensor histidine kinase two-component response regulator two-component response
Rv1985c Rv1990c Rv1994c Rv2017	-	transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator	Rv0490 Rv0602c Rv0260c	regX3 senX3 tcrA -	regulator sensor histidine kinase two-component response regulator two-component response regulator
Rv1993c Rv1985c Rv1990c Rv1994c Rv2017	-	family) putative transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (PbsX/Xre family)	Rv0490 Rv0602c Rv0260c	regX3 senX3 tcrA -	two-component response regulator sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase
Rv1990c Rv1990c Rv1994c Rv2017 Rv2021c	: :	family) putative transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (PbsX/Xre family) putative transcriptional regulator	Rv0490 Rv0602c Rv0260c Rv0600c Rv0600c	regX3 senX3 tcrA - -	two-component response regulator sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase sensor histidine kinase
Rv1990c Rv1990c Rv1994c Rv2017 Rv2021c Rv2034	: : : :,0	family) putative transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (PbsX/Xre family) putative transcriptional regulator transcriptional regulator (ArsR	Rv0490 Rv0602c Rv0260c Rv0600c Rv0601c Rv0818	regX3 senX3 tcrA - - -	regulator sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase sensor histidine kinase two-component response
Rv1983c Rv1985c Rv1990c Rv1994c Rv2017 Rv2021c Rv2021c Rv2034		transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (PbsX/Xre family) putative transcriptional regulator transcriptional regulator (ArsR family)	Rv0490 Rv0602c Rv0260c Rv0600c Rv0601c Rv0818	regX3 senX3 tcrA - - -	two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase sensor histidine kinase two-component response redulator sensor histidine kinase
Rv1990c Rv1990c Rv1994c Rv2017 Rv2021c Rv2034 Rv2175c		putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator (mark) putative transcriptional regulator (PbsX/Xre family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator	Rv0490 Rv0602c Rv0602c Rv0600c Rv0601c Rv0818 Bv0845	regX3 senX3 tcrA - - - -	two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase sensor histidine kinase two-component response regulator sensor histidine kinase
Rv1990c Rv1990c Rv1990c Rv1994c Rv2017 Rv2021c Rv2034 Rv2175c Rv2250c		putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (Pbs/X/re family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator	Rv0490 Rv0602c Rv0260c Rv0600c Rv0601c Rv0845 Rv0902c	regX3 senX3 tcrA - - - - -	two-component response regulator sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase sensor histidine kinase
Rv199030 Rv199000 Rv199000 Rv2017 Rv20210 Rv20210 Rv2034 Rv217500 Rv225000 Rv22500		putative transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (PbsX/Xre family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator	Rv0490 Rv0602c Rv0260c Rv0601c Rv0601c Rv0845 Rv0902c	regX3 senX3 tcrA - - - - - -	two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase
Rv199030 Rv19900 Rv19900 Rv19940 Rv2017 Rv20210 Rv20210 Rv2034 Rv21750 Rv22500 Rv22580 Rv22580		putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator	Rv0490 Rv0260c Rv0260c Rv0600c Rv0801c Rv0818 Rv0845 Rv0902c	regX3 senX3 tcrA - - - - - - - - - - - - -	two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase sensor histidine kinase two-component response regulator sensor histidine kinase sensor histidine kinase sensor histidine kinase
Rv1983c Rv1990c Rv1990c Rv1990c Rv2017 Rv2021c Rv2034 Rv2175c Rv2250c Rv2258c Rv2282c		putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (Pbs X/Xre family) putative transcriptional regulator family) putative transcriptional regulator putative transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator	Rv0490 Rv0260c Rv0260c Rv0600c Rv0601c Rv0818 Rv0845 Rv0902c Rv0903c	regX3 senX3 torA - - - - - - -	two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase sensor histidine kinase two-component response regulator sensor histidine kinase sensor histidine kinase sensor histidine kinase two-component response regulator
Hv199630 Rv19950 Rv19900 Rv19940 Rv2017 Rv2021c Rv2034 Rv21750 Rv22500 Rv22820 Rv2308		putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (PbsX/Xre family) putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator transcriptional regulator (LysR family)	Rv0490 Rv0602c Rv0260cc Rv0260cc Rv0601c Rv0818 Rv0845 Rv0902cc Rv0903cc	regX3 senX3 tcrA - - - - - - - -	two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase two-component response regulator two-component response regulator
Rv199030 Rv19906 Rv19906 Rv2017 Rv20210 Rv2034 Rv21750 Rv22500 Rv22500 Rv22820 Rv22820 Rv2308 Rv2308		putative transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (PbsX/Xre family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator family)	Rv0490 Rv0602c Rv0602c Rv0600c Rv0600c Rv0601c Rv0845 Rv0902c Rv0903c Rv0981 Rv0982	regX3 senX3 torA - - - - - - - - -	two-component response regulator sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase two-component response regulator two-component response regulator two-component response regulator
HV1963c Rv1985c Rv1990c Rv1990c Rv2017 Rv2017 Rv2016 Rv2034 Rv2175c Rv2250c Rv2258c Rv282c Rv208 Rv2324		putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (Pbs X/Xre family) putative transcriptional regulator family) putative transcriptional regulator putative transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator family) putative transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator	Rv0490 Rv0602c Rv0602c Rv0600c Rv0600c Rv0600c Rv0818 Rv0845 Rv0902c Rv0903c Rv0981 Rv0982 Rv1032c	regX3 senX3 torA - - - - - - - - - -	two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase sensor histidine kinase two-component response regulator sensor histidine kinase sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase sensor histidine kinase
HV1963c RV1985c RV1994c RV2994c RV2017 RV2021c RV2034 RV2175c RV2250c RV2250c RV2250c RV2250c RV2250c RV2258c RV2308 RV2324 RV2358	316	putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (PbsX/Xre family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (Lrg/AsnC family)	RV0490 RV0490 RV0602c RV0260c RV0600c RV0601c RV0818 RV0902c RV0903c RV0903c RV0981 RV0982 RV1032c RV1032c	regX3 senX3 torA - - - - - - - - - - - - - - - -	two-component response regulator sensor histidine kinase two-component response regulator two-component response sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase sensor histidine kinase sensor histidine kinase
HV1963c Rv1985c Rv1990c Rv21990c Rv2017 Rv2017 Rv2017 Rv2034 Rv2175c Rv2250c Rv2250c Rv2282c Rv2328 Rv2324 Rv2358		putative transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (PbsX/Xre family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator (Lrp/AsnC family) transcriptional regulator (Lrp/AsnC family)	Rv0490 Rv0602c Rv0602c Rv0600c Rv0600c Rv0601c Rv0845 Rv0902c Rv0903c Rv0981 Rv0982 Rv1032c Rv1032c Rv1032c	regX3 senX3 tcrA - - - - - - - - - - - - - - - - - - -	two-component response regulator sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase two-component response regulator two-component response regulator two-component response regulator sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase
HV1963c RV1985c RV1990c RV1990c RV2017 RV2021c RV2034 RV2175c RV2258c RV2282c RV2282c RV2282c RV2282c RV2324 RV2324 RV2388 RV2388		putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (Pbs X/Xre family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator (Lrp/AsnC family) transcriptional regulator family) putative transcriptional regulator transcriptional regulator (Lrp/AsnC family) transcriptional regulator	Rv0490 Rv0490 Rv0602c Rv0260c Rv0600c Rv0601c Rv0845 Rv0981 Rv0982 Rv1033c Rv1033c	regX3 senX3 tcrA - - - - - - - - - - -	two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase sensor histidine kinase two-component response regulator
HV1963c RV1985c RV1990c RV1990c RV2017 RV2021c RV2034 RV2250c RV2250c RV2250c RV2282c RV2282c RV2308 RV2324 RV2358 RV2358		putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (PbsX/Xre family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator (Lrp/AsnC family) transcriptional regulator (ArsR family) transcriptional regulator (LuxR/Uhpa family)	Rv0490 Rv0490 Rv0602c Rv0600c Rv0600c Rv0601c Rv0845 Rv0902c Rv0903c Rv0981 Rv0982 Rv1032c Rv1032c Rv1032c Rv1032c Rv1032c	regX3 senX3 tarA - - - - - - - - - - - - - - - - - - -	two-component response regulator sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase two-component response regulator two-component response regulator two-component response regulator two-component response regulator
HV1963c Rv1985c Rv1990c Rv21990c Rv2017 Rv2017 Rv2014 Rv2175c Rv2250c Rv2250c Rv2282c Rv2282c Rv2324 Rv2358 Rv2488c Rv2506		putative transcriptional regulator (LysR family) putative transcriptional regulator (transcriptional regulator (MerR family) putative transcriptional regulator (PbsX/Xre family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (Lrp/AsnC family) transcriptional regulator (ArsR family) transcriptional regulator (ArsR family) transcriptional regulator (LysR family) transcriptional regulator (LysR family)	Rv0490 Rv0602c Rv0260c Rv0600c Rv0601c Rv0818 Rv0845 Rv0903c Rv0993c Rv0993 Rv0992 Rv1032c Rv1032c Rv1032c Rv1032c Rv10260	regX3 senX3 torA - - - - - - - - - - - - - - - - - - -	two-component response regulator sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase sensor histidine kinase sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase sensor histidine kinase two-component response regulator two-component response regulator
HV1963c RV1985c RV1990c RV1990c RV2017 RV20217 RV20216 RV2034 RV2175c RV2250c RV2250c RV2250c RV2282c RV2282c RV2282c RV2324 RV2324 RV2328 RV2488c RV2506		putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (Pbs X/Xre family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (Lyz/AsnC family) transcriptional regulator (LuxR/UhpA family) transcriptional regulator (LuxR/UhpA family)	Rv0490 Rv0490 Rv0602c Rv0260c Rv0805c Rv0818 Rv0845 Rv0981 Rv0982 Rv1033c Rv1626 Rv2627c	regX3 senX3 torA - - - - - - - - - - - - - - - - - - -	two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase sensor histidine kinase sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase
HV1963c RV1983c RV1994c RV2017 RV2017 RV2017 RV2017 RV2014 RV2175c RV2250c RV2250c RV2250c RV2250c RV2282c RV2324 RV2358 RV2488c RV2506 RV261c		putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (PbsX/Xre family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator transcriptional regulator transcriptional regulator (LysR family) transcriptional regulator (LysR family) transcriptional regulator (LusR/JpAs family) transcriptional regulator (LusR/JpA family) transcriptional regulator (LusR/JpA family) transcriptional regulator (LusR/JpA family) transcriptional regulator (TetF/AcrR family)	Rv0490 Rv0490 Rv0602c Rv0600c Rv0600c Rv0601c Rv0845 Rv0902c Rv0903c Rv0981 Rv032c Rv1032c Rv1032c Rv1032c Rv1032c Rv1032c Rv1626 Rv2027c Rv2884	regX3 senX3 tarA - - - - - - - - - - - - - - - - - - -	two-component response regulator sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase two-component response regulator sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase two-component response regulator two-component response regulator two-component response regulator two-component response regulator two-component response regulator two-component response regulator sensor histidine kinase two-component response regulator
HV1993c RV1993c RV1990c RV1990c RV2017 RV2017 RV2021c RV2034 RV2250c RV2250c RV2250c RV2308 RV2308 RV2308 RV2358 RV2506 RV2506 RV2506		putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (Pbs/X/re family) putative transcriptional regulator (Pbs/X/re family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator transcriptional regulator transcriptional regulator (Lp/AsnC family) transcriptional regulator (Lp/AsnC family) transcriptional regulator (Lp/AsnC family) transcriptional regulator (Lp/AsnC family) transcriptional regulator (LpCASNC family) transcriptional regulator (LucASNC family) transcriptional regulator (LucASNC family) transcriptional regulator (LucASNC family)	Rv0490 Rv0490 Rv0602c Rv0260c Rv0600c Rv0818 Rv0845 Rv0903c Rv0981 Rv1032c Rv2027c Rv2844	regX3 senX3 tcrA - - - - - - - - - - - - - - - - - - -	two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator two-component response regulator two-component response regulator sensor histidine kinase two-component response regulator two-component response regulator two-component response regulator two-component response regulator two-component response regulator two-component response regulator two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator
HV1963c RV1985c RV1990c RV1990c RV2017 RV2017 RV2021c RV2034 RV2250c RV2250c RV2282c RV2282c RV2324 RV2382 RV2488c RV2506 RV2506 RV2506 RV2506 RV2621c RV2621c RV2621c		putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (Pbs X/Xre family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (LyrAsnC family) transcriptional regulator (LuxR/UhpA family) transcriptional regulator (TetR/AcrR family) putative transcriptional regulator (TetR/AcrR family)	RV0400 RV0602c RV0602c RV0600c RV0600c RV0600c RV0601c RV0818 RV0845 RV0981 RV0981 RV1033c RV1033c RV1626 RV2027c RV3122c	regX3 senX3 torA - - - - - - - - - - - - - - - - - - -	two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase sensor histidine kinase two-component response regulator sensor histidine kinase sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase
HV1963c RV1993c RV1994c RV2017 RV2017 RV2017 RV2017 RV2014 RV2175c RV2250c RV2250c RV2250c RV2250c RV2282c RV2324 RV2358 RV2488c RV2506 RV2621c RV2621c RV2640c		putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (PbsX/Xre family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator transcriptional regulator transcriptional regulator (LysR family) transcriptional regulator (LysR family) transcriptional regulator (LusR/JpAnC family) transcriptional regulator (LusR/JpA family) putative transcriptional regulator (LusR/JpA family) putative transcriptional regulator (TetF/AcrR family) putative transcriptional regulator (TetF/AcrR family) putative transcriptional regulator transcriptional regulator (ArsR family)	Rv0490 Rv0490 Rv0602c Rv0600c Rv0600c Rv0845 Rv0902c Rv0902c Rv0903c Rv0981 Rv0982 Rv1032c Rv1032c Rv1032c Rv1032c Rv1626 Rv2027c Rv3132c Rv3132c	regX3 senX3 tarA - - - - - - - - - - - - - - - - - - -	two-component response regulator sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase sensor histidine kinase sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator
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		truncated
Rv0018c	ppp	putative phosphoprotein phos-
		phatase
Rv2234	ptpA	low molecular weight protein-tyro-
	, ,	sine-phosphatase
Bv0153c	-	putative protein-tyrosine-phos-
11001000		nhatace
		priatase
II Maarom		etabolism
A Supthea	io and mo	dification of magramalagulas
A. Synanes	is and mo	authoric and modification
T. HIDOSON	ai protein	synthesis and modification
HV34200	THEM	houseful protein S to acetyr
Duccor	star i	transferase
RV0995	rimj	acetylation of 305 55 subunit
Hv0641	rpiA	50S ribosomal protein L1
Hv0704	rplB	50S ribosomal protein L2
Rv0701	rpIC	50S ribosomal protein L3
Rv0702	rplD	50S ribosomal protein L4
Rv0716	rplE	50S ribosomal protein L5
Rv0719	rplF	50S ribosomal protein L6
Rv0056	rpll	50S ribosomal protein L9
Rv0651	rplJ	50S ribosomal protein L10
Rv0640	rplK	50S ribosomal protein L11
Rv0652	rplL	50S ribosomal protein L7/L12
Rv3443c	rpIM	50S ribosomal protein L13
Rv0714	rpIN	50S ribosomal protein L14
Rv0723	rplO	50S ribosomal protein L15
Rv0708	rpIP	50S ribosomal protein L16
Rv3456c	rplQ	50S ribosomal protein L17
Rv0720	rplR	50S ribosomal protein L18
Bv2904c	rolS	50S ribosomal protein L19
Rv1643	rpIT	50S ribosomal protein L20
Bv2442c	rolU	50S ribosomal protein I 21
Bv0706	rolV	50S ribosomal protein L22
Rv0703	rplW	50S ribosomal protein 23
Bv0715	rnIX	50S ribosomal protein L24
By1015c	rnlY	50S ribosomal protein L25
Bv2441c	rnmA	50S ribosomal protein L27
Bv0105c	rnmR	50S ribosomal protein L28
Bv2058c	rnmB2	50S ribosomal protein L28
By0709	rpmC	50S ribosomal protein L29
Bv0722	rnmD	50S ribosomal protein L30
By1298	rnmE	50S ribosomal protein L31
By2057c	rnmG	50S ribosomal protein L33
By3924c	romH	50S ribosomal protein L34
Bv1642	rnml	50S ribosomal protein L35
Bv3461c	romJ	50S ribosomal protein L36
Bv1630	rosA	30S ribosomal protein S1
Bv2890c	rosB	30S ribosomal protein S2
Rv0707	rpsC	30S ribosomal protein S3
Bv3458c	rpsD	30S ribosomal protein S4
Bv0721	rpsE	30S ribosomal protein S5
Rv0053	rpsF	30S ribosomal protein S6
Rv0683	rpsG	30S ribosomal protein S7
Rv0718	rpsH	30S ribosomal protein S8
Rv3442c	rpsl	30S ribosomal protein S9
Rv0700	rpsJ	30S ribosomal protein S10
Rv3459c	rpsK	30S ribosomal protein S11
Rv0682	rpsL	30S ribosomal protein S12
Rv3460c	rpsM	30S ribosomal protein S13
Rv0717	rpsN	30S ribosomal protein S14
Rv2056c	rpsN2	30S ribosomal protein S14
Rv2785c	rpsO	30S ribosomal protein S15
Rv2909c	rpsP	30S ribosomal protein S16
Rv0710	rpsQ	30S ribosomal protein S17
Rv0055	rpsR	30S ribosomal protein S18
Rv2055c	rpsR2	30S ribosomal protein S18
Rv0705	rpsS	30S ribosomal protein S19
Rv2412	rpsT	30S ribosomal protein S20
Rv3241c	-	member of S30AE ribosomal
		protein family
2. Ribosom	e modifica	ation and maturation
Rv1010	ksgA	16S rRNA dimethyltransferase
Rv2838c	rbfA	ribosome-binding factor A
Rv2907c	rimM	16S rRNA processing protein
3. Aminoad	yl tRNA sv	ynthases and their modification
Rv2555c	alaS	alanyl-tRNA synthase
Rv1292	argS	arginyl-tRNA synthase
Rv2572c	aspS	aspartyl-tRNA synthase
Rv3580c	cysS	cysteinyl-tRNA synthase
Rv2130c	cysS2	cysteinyl-tRNA synthase
Rv1406	fmt	methionyl-tRNA formyltransferase
Rv3011c	gatA	glu-tRNA-gln amidotransferase.
	-	subunit B
Rv3009c	gatB	glu-tRNA-gln amidotransferase,
		subunit A
Rv3012c	gatC	glu-tRNA-gln amidotransferase,
	-	subunit C
Rv2992c	gltS	glutamyl-tRNA synthase
Rv2357c	glyS	glycyl-tRNA synthase
Rv2580c	hisS	histidyl-tRNA synthase
Rv1536	ileS	isoleucyl-tRNA synthase
Rv0041	leuS	leucyl-tRNA synthase
Rv3598c	lysS	lysyl-tRNA synthase
Rv1640c	ÍvsX	C-term lysyl-tRNA synthase
Rv1007c	metS	methionyl-tRNA synthase
Rv1649	pheS	phenylalanyl-tRNA synthase a
		subunit

Rv1650	pheT	phenylalanyl-tRNA synthase β	Rv2090	-	partially similar to DNA poly-
Rv2845c	proS	prolyI-tRNA synthase	Rv2191	-	similar to both PoIC and UvrC
Rv3834c	serS	seryl-tRNA synthase	Bv2464c	-	proteins probable DNA glycosylase
Rv2906c	trmD	tRNA (guanine-N1)-methyltrans-	11024040		endonuclease VIII
Duccoco.	true C		Rv3201c	-	probable ATP-dependent DNA
Rv1689	tvrS	tyrosyl-tRNA synthase	Rv3202c	-	similar to UvrD proteins
Rv2448c	valS	valyl-tRNA synthase	Rv3263	-	probable DNA methylase
4 Nucleon	rotoina		Rv3644c	-	similar in N-term to DNA poly-
Rv1407	fmu	similar to Fmu protein			
Rv3852	hns	HU-histone protein	6. Protein t	ranslation	and modification
HV29860 Bv1388	пирв mIHF	integration host factor	Rv2534c	efp	elongation factor P
			Rv2882c	frr	ribosome recycling factor
5. DNA rep	dication, re	epair, recombination and restric-	Hv0684 Bv0120c	tusA fusA2	elongation factor G
Rv1317c	alkA	DNA-3-methyladenine glycosi-	Rv1080c	greA	transcription elongation factor G
Duggge	din F	dase II DNA demose indusible protein E	Rv3462c	infA infB	initiation factor IF-1
Rv1329c	dinG	probable ATP-dependent helicase	Rv1641	infC	initiation factor IF-3
Rv3056	dinP	DNA-damage-inducible protein	Rv0009	ppiA	peptidyl-prolyl cis-trans isomerase
Hv1537	dınX	probable DNA-damage-inducible	Rv1299	ppiB prfA	peptidyi-prolyi <i>cis-trans</i> isomerase peptide chain release factor 1
Rv0001	dnaA	chromosomal replication initiator	Rv3105c	prfB	peptide chain release factor 2
DUCCES	da e D	protein	Rv2889c	tsf tuf	elongation factor EF-Ts
Rv1547	dnaE1	DNA polymerase III, α subunit	1100000	107	
Rv3370c	dnaE2	DNA polymerase III α chain	7. RNA syr	thesis, Rh	NA modification and DNA
Rv2343c Bv0002	dnaG dnaN	DNA primase	Rv1253	n deaD	ATP-dependent DNA/BNA
Rv3711c	dnaQ	DNA polymerase III ϵ chain	1111200	Goub	helicase
Rv3721c	dnaZX	DNA polymerase III, γ (dnaZ) and	Rv2783c	gpsl	pppGpp synthase and polyribo-
Rv2924c	fpa	formamidopyrimidine-DNA glyco-	Rv2841c	nusA	transcription termination factor
_	, 0	sylase	Rv2533c	nusB	N-utilization substance protein B
Rv0006 Bv0005	gyrA avrB	DNA gyrase subunit A	Hv0639	nusG	transcription antitermination protein
Rv2092c	helY	probable helicase, Ski2 subfamily	Rv3907c	pcnA	polynucleotide polymerase
Rv2101	helZ	probable helicase, Snf2/Rad54	Rv3232c	pvdS	alternative sigma factor for
Rv2756c	hsdM	type I restriction/modification sys-	Rv3211	rhIE	probable ATP-dependent
D-0755	h	tem DNA methylase	But 207	rha	RNA helicase
HV2/550	nsas	tem specificity determinant	HV1297	mo	factor rho
Rv3296	lhr	ATP-dependent helicase	Rv3457c	rpoA	α subunit of RNA polymerase
Rv3014c	ligA ligP	DNA ligase	Rv0667 Bv0668	rpoB rpoC	β subunit of RNA polymerase β' subunit of RNA polymerase
Rv3731	ligC	probable DNA ligase	Rv1364c	rsbU	SigB regulation protein
Rv1020	mfd	transcription-repair coupling factor	Rv3287c	rsbW	anti-sigma B factor
Hv2528c Bv2985	mrr mutT1	restriction system protein	HV2703	sigA	(aka MvsA, RpoV)
Rv1160	mutT2	MutT homologue	Rv2710	sigB	RNA polymerase sigma factor
Rv0413	mutT3	MutT homologue	Bv2069	eiaC	(aka MysB) ECE subfamily sigma subunit
Rv3297	nei	probable endonuclease VIII	Rv3414c	sigD	ECF subfamily sigma subunit
Rv3674c	nth	probable endonuclease III	Rv1221	sigE	ECF subfamily sigma subunit
Hv13160	ogt	methylated-DNA-protein-cysteine methyltransferase	Rv0182c	sigr siaG	sigma-70 factors ECF subfamily
Rv1629	polA	DNA polymerase I	Rv3223c	sigH	ECF subfamily sigma subunit
Rv1402	priA	putative primosomal protein n'	Rv1189 Bv3328c	sigi sia.l	ECF family sigma factor similar to Sigl_ECE family
Rv3585	radA	probable DNA repair RadA homo-	Rv0445c	sigK	ECF-type sigma factor
Du07074		logue	Rv0735	sigL sigM	sigma-70 factors ECF subfamily
Rv0630c	recA recB	exodeoxvribonuclease V	1100911	sigivi	SigE
Rv0631c	recC	exodeoxyribonuclease V	Rv3366	spoU	probable rRNA methylase
Hv0629c Bv0003	recD recE	exodeoxyribonuclease V DNA replication and SOS induc-	HV34550	truA	thase
		tion	Rv2793c	truB	tRNA pseudouridine 55 synthase
Rv2973c	recG recN	ATP-dependent DNA helicase	Hv1644	tsnH	putative 23S rHNA methyltrans- ferase
Rv3715c	recR	RecBC-Independent process of	Rv3649	-	ATP-dependent DNA/RNA heli-
D 0700	V	DNA repair			case
Rv27360 Rv2593c	recx ruvA	Holliday junction binding protein.	8. Polysaco	harides (d	ytoplasmic)
		DNA helicase	Rv1326c	glgB	1,4-α-glucan branching enzyme
Rv2592c	ruvB ruvC	Holliday junction binding protein	Hv1328	gigP	probable glycogen phosphory- lase
11020340	1000	deoxyribonuclease	Rv1564c	glgX	probable glycogen debranching
Rv0054	ssb	single strand binding protein	Du1562a	alaV	enzyme
HV1210	tagA	dase I	Rv1562c	gigZ	maltooligosyltrehalose trehalohy-
Rv3646c	topA	DNA topoisomerase	B a i a		drolase
Rv2976c Bv1638	ung uwrA	uracil-DNA glycosylase	Bv1781c	-	probable glycosyl hydrolase probable 4-α-glucanotransferase
Rv1633	uvrB	excinuclease ABC subunit A	Rv2471	-	probable maltase α-glucosidase
Rv1420	uvrC	excinuclease ABC subunit C	P. Downad	tion of	aromologuloo
HVU949	uvrD	helicase II	1. RNA	ation of ma	an on lorgeures
Rv3198c	uvrD2	putative UvrD	Rv1014c	pth	peptidyl-tRNA hydrolase
Rv0427c	xthA	exodeoxyribonuclease III group II intron maturase	Hv2925c Bv2444c	rnc rne	HNAse III similar at C-term to ribo-
Rv0861c	-	probable DNA helicase			nuclease E
Rv0944	-	possible formamidopyrimidine-	Rv2902c	rnhB rnnA	ribonuclease HII ribonuclease P protein compo
Rv1688	-	probable 3-methylpurine DNA	. 1002.00	pr	nent
		glycosylase	Rv1340	rphA	ribonuclease PH

2. DNA	and	andonuologoo IV (anuringgo)
Rv1108c	ena xseA	exonuclease VII large subunit
Rv1107c	xseB	exonuclease VII small subunit
3. Proteins	. peptides	and glycopeptides
Rv3305c	amiA	probable aminohydrolase
Rv3306c	amiB	probable aminohydrolase
HV35960 Bv2461c	cipC cipP	ATP-dependent Cip protease
	e .,	teolytic subunit
Rv2460c	clpP2	ATP-dependent Clp protease pro-
Bv2457c	cloX	ATP-dependent Clp protease
	.,	ATP-binding subunit ClpX
Rv2667	clpX'	similar to ClpC from <i>M. leprae</i> but
Bv3419c	aco	glycoprotease
Rv2725c	hflX	GTP-binding protein
Rv1223	htrA	serine protease
Rv0734	mapA1 mapA2	probable methionine aminopepti-
_		dase
Rv0319	pcp	pyrrolidone-carboxylate peptidase
Bv2213	pepA	aminopeptidase A/I
Rv0800	pepC	aminopeptidase I
Rv2467	pepD	probable aminopeptidase
Rv2089c	pepE	cytoplasmic peptidase
Rv2535c	pepQ	cytoplasmic peptidase
HV27820	рерн	(insulinase)
Rv2109c	prcA	proteasome α -type subunit 1
Rv2110c	prcB	proteasome β-type subunit 2
Rv0782	ptrBa	protease II, α subunit
Rv0781	ptrBb	protease II, β subunit
Hv0724	sppA	protease IV, signal peptide pepti-
Rv0198c	-	probable zinc metalloprotease
Rv0457c	-	probable peptidase
Rv0840c	-	probable proline iminopeptidase
HV0983 By1977	-	probable serine protease
Bv3668c	-	probable alkaline serine protease
Rv3671c	-	probable serine protease
Rv3883c	-	probable secreted protease
Rv3886c	-	protease
4 Polycacc	baridee li	inon-olygacebarides and phospho-
lipids	manues, n	popolysacchances and phospho-
Rv0062	celA	cellulase/endoglucanase
Rv3915	cwlM	hydrolase
Rv0315	-	probable β-1,3-glucanase
HV1090	-	cellulase/endoducanase
Rv1327c	-	probable glycosyl hydrolase, α-
		amylase family
Rv1333	-	probable hydrolase
HV3463 By3717	-	propable neuraminidase
1100/17	-	nine amidase
5. Esterase	es and lipa	ses
HV0220 Bv1923	lipC linD	probable esterase
Bv3775	linE	probable esterase
Rv3487c	lipF	probable esterase
Rv0646c	lipG	probable hydrolase
Rv1399c	lipH	probable lipase
Hv1400c	lini	probable lipase
Bv2385	lint	probable octorade
Rv1497	lipJ linK	probable esterase
-	lipJ lipK lipL	probable esterase probable acetyl-hydrolase esterase
Hv2284	lipJ lipK lipL lipM	probable esterase probable acetyl-hydrolase esterase probable esterase
Hv2284 Rv2970c	lipJ lipK lipL lipM lipN	probable esterase probable acetyl-hydrolase esterase probable esterase probable lipase/esterase
Hv2284 Rv2970c Rv1426c Bv2462	lipJ lipK lipL lipM lipN lipO	probable esterase probable acetyl-hydrolase esterase probable esterase probable lipase/esterase probable esterase
Hv2284 Rv2970c Rv1426c Rv2463 Rv24850	lipJ lipK lipL lipM lipN lipP lipQ	probable esterase probable acetyl-hydrolase esterase probable esterase probable esterase probable esterase probable esterase
Hv2284 Rv2970c Rv1426c Rv2463 Rv2485c Rv3084	lipJ lipK lipL lipM lipN lipP lipP lipR	probable esterase probable acetyl-hydrolase esterase probable esterase probable esterase probable esterase probable esterase probable carboxilyesterase probable carboxilyesterase probable carboxilyesterase
Hv2284 Rv2970c Rv1426c Rv2463 Rv2485c Rv3084 Rv3176c	lipJ lipK lipL lipM lipN lipO lipP lipR lipS	probable esterase probable acetyl-hydrolase esterase probable esterase probable esterase probable esterase probable esterase probable carboxlyesterase probable acetyl-hydrolase probable acetyl-hydrolase probable esterase/lipase
Hv2284 Rv2970c Rv1426c Rv2463 Rv2485c Rv3084 Rv3176c Rv2045c	lipJ lipK lipL lipN lipN lipP lipP lipR lipS lipT	probable esterase probable acetyl-hydrolase esterase probable esterase probable esterase probable esterase probable esterase probable carboxlyesterase probable acetyl-hydrolase probable acetrase/lipase probable carboxylesterase
Hv2284 Rv2970c Rv1426c Rv2463 Rv2485c Rv3084 Rv3176c Rv2045c Rv1076	lipJ lipJ lipK lipK lipM lipN lipP lipP lipR lipS lipT lipU	probable esterase probable acetyl-hydrolase esterase probable esterase probable esterase probable esterase probable esterase probable carbox/yesterase probable acetyl-hydrolase probable esterase/lipase probable esterase/ probable esterase
HV2284 RV2970c RV1426c RV2463 RV2485c RV3084 RV3176c RV2045c RV1076 RV3203 RV203	lipJ lipJ lipK lipK lipM lipN lipP lipP lipP lipF lipT lipV lipV	probable esterase probable acetyl-hydrolase esterase probable esterase probable esterase probable esterase probable esterase probable acetyl-hydrolase probable acetyl-hydrolase probable acetyl-hydrolase probable esterase/lipase probable esterase probable esterase probable esterase
HV2284 Rv2970c Rv1426c Rv2463 Rv2463 Rv2485c Rv3084 Rv3176c Rv3045c Rv1076 Rv3203 Rv0217c Rv2217c Rv2351c	lipJ lipJ lipK lipL lipN lipO lipP lipP lipS lipT lipV lipV lipV lipW ocA	probable esterase probable acetyl-hydrolase esterase probable esterase probable esterase probable esterase probable esterase probable carboxlyesterase probable carboxlyesterase probable esterase/lipase probable esterase probable esterase probable esterase probable esterase probable esterase
HV2284 Rv2970c Rv1426c Rv2463 Rv2463 Rv2485c Rv3084 Rv3176c Rv1076 Rv3203 Rv0217c Rv20351c Rv2350c	ip: JipJ lipK lipK lipA lipA lipP lipP lipQ lipV lipV lipV lipV plcA plcB	probable esterase probable acetyl-hydrolase esterase probable esterase probable esterase probable esterase probable esterase probable acetyl-hydrolase probable acetyl-hydrolase probable esterase/lipase probable esterase probable esterase probable esterase probable esterase probable esterase phospholipase C precursor
HV2284 Rv2970c Rv1426c Rv2463 Rv2485c Rv3084 Rv3176c Rv2045c Rv1076 Rv2045c Rv1076 Rv2203 Rv0217c Rv2351c Rv2351c Rv2350c Rv2349c	ip) IIpJ IIpK IIpK IIpM IIpN IIpO IIpP IIpR IIpS IIpV IIpV IIpW IIpW IIpW IIPA IIPV IIPA IIPV IIPO IIPV IIPO IIPJ	probable esterase probable acetyl-hydrolase esterase probable esterase probable esterase probable esterase probable esterase probable carboxylesterase probable carboxylesterase probable esterase/lipase probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase phospholipase C precursor phospholipase C precursor
HV2284 Rv2970c Rv1426c Rv2463 Rv2485c Rv3084 Rv3176c Rv2045c Rv1076 Rv2203 Rv0217c Rv22351c Rv2350c Rv2350c Rv2349c Rv2349c	ipJ IIpJ IIpK IIpK IIpM IIpM IIpN IIpP IIpP IIpS IIpV IIpV IIpV IIpV IIpV IIpV IIpV	probable esterase probable acetyl-hydrolase esterase probable esterase probable esterase probable esterase probable esterase probable catboxlyesterase probable acetyl-hydrolase probable acetyl-hydrolase probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase phospholipase C precursor phospholipase C precursor phospholipase C precursor
HV2284 Rv2970c Rv1426c Rv2463 Rv2485c Rv3084 Rv3176c Rv3045c Rv1076 Rv3203 Rv0217c Rv2351c Rv2350c Rv2350c Rv2349c Rv1755c Rv1104	IIPJ IIPJ IIPK IIPN IIPN IIPP IIPP IIPR IIPT IIPU IIPV IIPV IIPV IIPV IIPW IIPW IIPW IIPW	probable esterase probable acetyl-hydrolase esterase probable esterase probable esterase probable esterase probable esterase probable carbox/yesterase probable carbox/yesterase probable carbox/yesterase probable carbox/yesterase probable esterase/lipase probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase phospholipase C precursor phospholipase C precursor phospholipase C precursor partial CDS for phospholipase C probable esterase pseudogene
HV2284 RV2970c RV1426c RV2463 RV2463 RV3084 RV3084 RV3045c RV1076 RV3203 RV0217c RV2351c RV2351c RV2350c RV2349c RV1755c RV1104 RV1105	ipJ lipJ lipK lipN lipN lipP lipR lipR lipR lipT lipU lipV lipV lipV lipV lipV lipV lipV lipC - -	probable esterase probable acetyl-hydrolase esterase probable esterase probable esterase probable esterase probable esterase probable carboxlyesterase probable carboxlyesterase probable carboxlyesterase probable esterase/lipase probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase probable carboxylesteros phospholipase C precursor phospholipase C precursor
HV22870 RV2970c RV2463 RV24863 RV2485c RV3084 RV3176c RV3084 RV1076 RV3070 RV2045c RV1075 RV2045c RV1075c RV2045c RV1075c RV1075c RV1075c RV1075c RV1075c RV1075c RV1075c RV1075c RV1075c RV1075c RV1075c RV1005c RV1005c RV1005c RV1005c RV1005c RV1005c RV1005c RV2005c RV1005c RV2005c RV2005c RV2005c RV2005c RV2005c RV2005c RV1005c RV2005c RV10	IIPJ IIPJ IIPK IIPL IIPN IIPN IIPN IIPN IIPN IIPV IIPV IIPV	probable esterase probable acetyl-hydrolase esterase probable esterase probable esterase probable esterase probable esterase probable esterase/lipase probable esterase/lipase probable esterase/lipase probable esterase probable esterase probable esterase probable esterase phospholipase C precursor phospholipase C precursor partial CDS for phospholipase C probable esterase pseudogene probable esterase pseudogene
HV2284 RV2970c RV1426c RV2463c RV2463c RV2463c RV2483c RV2485c RV2045c RV2045c RV2047c RV2045c RV2017c RV20217c	IIPJ IIPJ IIPK IIPL IIPN IIPN IIPP IIPQ IIPR IIPS IIPT IIPV IIPV IIPV IIPV IIPV IIPV IIPV	probable esterase probable acetyl-hydrolase esterase probable esterase probable esterase probable esterase probable esterase probable carboxlyesterase probable acetyl-hydrolase probable acetyl-hydrolase probable acetyl-hydrolase probable esterase probable esterase probable esterase probable esterase probable esterase phospholipase C precursor phospholipase C precursor phospholipase C precursor partial CDS for phospholipase C probable esterase pseudogene probable esterase pseudogene probable esterase pseudogene
HV2284 RV2970c RV1426c RV2463 RV24663 RV2485c RV2485c RV2045c RV1076 RV2045c RV1076 RV2037 RV20176 RV2037 RV20176 RV20176 RV20176 RV20176 RV1105 6. Aromatic RV20469 RV2010	IIPJ IIPJ IIPK IIPL IIPN IIPN IIPP IIPQ IIPR IIPS IIPT IIPU IIPV IIPV IIPV IIPV IIPV IIPV IIPV	probable esterase probable acetyl-hydrolase esterase probable esterase probable esterase probable esterase probable esterase probable acetyl-hydrolase probable acetyl-hydrolase probable acetyl-hydrolase probable esterase probable esterase probable esterase probable esterase phospholipase C precursor phospholipase C precursor phospholipase C precursor partial CDS for phospholipase C probable esterase pseudogene probable esterase pseudogene probable esterase pseudogene probable esterase pseudogene
HV2284 RV2970c RV1426c RV2463 RV24663 RV2485c RV2485c RV2045c RV2045c RV2045c RV2045c RV2076 RV2027 RV2037 RV2037 RV2037 RV2034 RV1755c RV1104 RV1755c 6. Aromatic RV3469c RV3469c RV0316	IIIPJ IIIPJ IIIPK IIIPA IIIPA IIIPA IIIPA IIIPA IIIPA IIIPU IIIPU IIIPU IIIPU IIIPU IIIPU IIIPU IIIPU IIIPU IIIPU IIIPU IIIPU IIIPA IIII IIIPA I	probable esterase probable acetyl-hydrolase esterase probable esterase probable esterase probable esterase probable carboxlyesterase probable carboxlyesterase probable caetyl-hydrolase probable caetyl-hydrolase probable esterase/lipase probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase phospholipase C precursor phospholipase C precursor phospholipase C precursor phospholipase C precursor partial CDS for phospholipase C probable esterase pseudogene probable esterase pseudogene probable esterase pseudogene probable 4-hydroxy-2-oxovalerate aldolase probable muconolactone iso- merase
HV2287 RV2970c RV1426c RV2465c RV2465c RV2465c RV20455c RV1076 RV2045c RV1076 RV2017c RV200	IIPJ IIPJ IIPK IIPA IIPA IIPO IIPO IIPO IIPO IIPO IIPV IIPW IIPW IIPW IIPW IIPW IIPW IIPW	probable esterase probable acetyl-hydrolase esterase probable esterase probable esterase probable esterase probable esterase probable carboxlyesterase probable carboxlyesterase probable carboxlyesterase probable carboxlyesterase probable esterase/lipase probable esterase/lipase probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase phospholipase C precursor phospholipase C precursor phospholipase C precursor phospholipase C precursor partial CDS for phospholipase C probable esterase pseudogene probable esterase pseudogene probable 4-nydroxy-2-oxovalerate aldolase probable 4-carboxymuconolac-
HV2284 RV2970c RV2462c RV2463c RV2465c RV20455c RV20455c RV20455c RV20455c RV20455c RV20245c RV20217c RV20202 RV20217c RV20202 RV20217c RV20202 RV20217c RV20202 RV2020 RV200 RV	IIPJ IIPJ IIPK IIPJ IIPA IIPO IIPQ IIPQ IIPQ IIPQ IIPV IIPW IIPW IIPW IIPW IIPW IIPW IIPW	probable esterase probable acetyl-hydrolase esterase probable esterase probable esterase probable esterase probable esterase probable esterase probable acetyl-hydrolase probable acetyl-hydrolase probable esterase/lipase probable esterase/lipase probable esterase probable esterase pseudogene probable esterase pseudogene probable esterase pseudogene probable 4-hydroxy-2-oxovalerate aldolase probable 4-carboxymuconolac- tone decarboxylase
HV2287 RV2970c RV2970c RV24803 RV24853 RV2485c RV3084 RV3176c RV3084 RV3176c RV20457 RV20457 RV20470 RV20170 RV203500 RV23510c RV20490 RV1105 6. Aromatic RV3469c RV0316 RV0771 RV0939 RV1722	ipJ ipJ ipK ipL ipL ipL ipL ipL ipN ipP ipQ ipP ipQ ipF ipV ipV ipV plcA plcB plcA plcA plcA plcA - - - - - - - -	probable esterase probable acetyl-hydrolase esterase probable esterase probable esterase probable esterase probable esterase probable carboxlyesterase probable carboxlyesterase probable esterase/lipase probable esterase/lipase probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase probable esterase pseudogene probable desterase pseudogene probable 4-hydroxy-2-oxovalerate aldolase probable muconolactone iso- merase probable 4-carboxymuconolac- tone decarboxylase probable dehydrase

letters	to	nature
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		lase	Rv1367c	-	probable penicillin binding protein
Rv2715	-	2-hydroxymuconic semialdehyde	Rv1730c	-	probable penicillin binding protein
_		hydrolase	Rv1922	-	probable penicillin binding protein
Rv3530c	-	probable <i>cis</i> -diol dehydrogenase	Rv2864c	-	probable penicillin binding protein
Hv3534c	-	4-hydroxy-2-oxovalerate aldolase	Hv3330	-	probable penicillin binding protein
Hv3536c	-	aromatic hydrocarbon degrada-	Hv3627c	-	probable penicillin binding protein
		uon	4 Concon	od mamb	rano protoino
C. Cellen	velone		By0402c	mmnl 1	conserved large membrane
1. Lipopro	teins (InnA	- <i>lpr(</i>) 65	11004020	ninpe i	protein
11 Elbobro	(10)	(p. c) co	Bv0507	mmpL2	conserved large membrane
2. Surface	polysacch	narides, lipopolysaccharides, pro-		,	protein
teins and	antigens		Rv0206c	mmpL3	conserved large membrane
Rv0806c	cpsY	probable UDP-glucose-4-			protein
		epimerase	Rv0450c	mmpL4	conserved large membrane
Rv3811	csp	secreted protein			protein
Rv1677	dsbF	highly similar to C-term Mpt53	Rv0676c	mmpL5	conserved large membrane
Hv3794	embA	involved in arabinogalactan syn-	Dutrez		protein
Dv2705	omhB	inesis	HV1557	ттргө	protoin
1103793	eniod	thesis	Bv2942	mmnl 7	conserved large membrane
Bv3793	embC	involved in arabinogalactan syn-	1112012	in inper	protein
		thesis	Rv3823c	mmpL8	conserved large membrane
Rv3875	esat6	early secretory antigen target			protein
Rv0112	gca	probable GDP-mannose dehy-	Rv2339	mmpL9	conserved large membrane
		dratase			protein
Rv0113	gmhA	phosphoheptose isomerase	Rv1183	mmpL10	conserved large membrane
Hv2965c	kdtB	lipopolysaccharide core biosyn-	B. 0000		protein
D: 0070		thesis protein	Hv0202c	mmpL11	conserved large membrane
Hv2878c	mpt53	secreted protein Mpt53	Duteooa	manage 10	protein
HV19800	трю4	Mobe4/Mote4	HV15220	mmpL12	protein
Bv2875	mot70	major secreted immunoranic pro-	Bv0403c	mmnS1	conserved small membrane
1102075	mptro	tein Mpt70 precursor	11004000	mmpor	protein
Bv2873	mot83	surface lipoprotein Mpt83	Bv0506	mmoS2	conserved small membrane
Rv0899	ompA	member of OmpA family		····· p	protein
Rv3810	pirĠ	cell surface protein precursor (Erp	Rv2198c	mmpS3	conserved small membrane
		protein)		•	protein
Rv3782	rfbE	similar to rhamnosyl transferase	Rv0451c	mmpS4	conserved small membrane
Rv1302	rfe	undecaprenyl-phosphate α-N-		_	protein
		acetylglucosaminyltransferase	Rv0677c	mmpS5	conserved small membrane
Rv2145c	wag31	antigen 84 (aka wag31)			protein
HV0431	-	tuberculin related peptide (A1103)	E. Other m		avataina 011
Rv15140	-	involved in polycapeharida cyp.	5. Other m	iembrane j	broteins 211
11013140	-	thesis	III. Cell pr	ocesses	
Bv1518	-	involved in exopolysaccharide	A. Transpo	ort/binding	proteins
		synthesis	1. Amino a	cids	
Rv1758	-	partial cutinase	Rv2127	ansP	L-asparagine permease
Dutotos		· · · · · · · · · · · · · · · · · · ·	D 0040		
HV1910C	-	probable secreted protein	HV0346C	arop2	probable aromatic amino acid
Rv1910c Rv1919c	-	weak similarity to pollen antigens	HV03460	arop2	probable aromatic amino acid permease
Rv1910c Rv1919c Rv1984c	-	probable secreted protein weak similarity to pollen antigens probable secreted protein	Rv0346c	arop2 betP	probable aromatic amino acid permease glycine betaine transport
Rv1910c Rv1919c Rv1984c Rv1987	-	probable secreted protein weak similarity to pollen antigens probable secreted protein probable secreted protein	Rv0346c Rv0917 Rv1704c	aroP2 betP cycA	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine
Rv1910c Rv1919c Rv1984c Rv1987 Rv2223c	- - -	probable secreted protein weak similarity to pollen antigens probable secreted protein probable secreted protein probable exported protease	Rv0917 Rv1704c	betP cycA	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine
Rv1910c Rv1919c Rv1984c Rv1987 Rv2223c Rv2224c	-	probable secreted protein weak similarity to polien antigens probable secreted protein probable secreted protein probable exported protease probable exported protease	Rv0917 Rv1704c Rv3666c	aroP2 betP cycA dppA	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine probable peptide transport system
Rv19106 Rv1919c Rv1984c Rv1987 Rv2223c Rv2224c Rv2301	- - - - -	probable secreted protein weak similarity to polien antigens probable secreted protein probable secreted protein probable exported protease probable exported protease probable cutinase	Rv0917 Rv1704c Rv3666c	aroP2 betP cycA dppA	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine probable peptide transport system permease
Rv19106 Rv19196 Rv19846 Rv1987 Rv22236 Rv22246 Rv22301 Rv2345	-	probable secreted protein weak similarity to pollen antigens probable secreted protein probable secreted protein probable exported protease probable exported protease probable extinase precursor of probable membrane protein	Rv0917 Rv1704c Rv3666c Rv3665c	aroP2 betP cycA dppA dppB	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine probable peptide transport system permease probable peptide transport system nermease
Rv19106 Rv19196 Rv19846 Rv1987 Rv22236 Rv22246 Rv22301 Rv2345 Rv2672	-	probable secreted protein weak similarity to pollen antigens probable secreted protein probable secreted protein probable exported protease probable exported protease probable cutinase precursor of probable membrane protein putative exported protease	Rv0917 Rv1704c Rv3666c Rv3665c Bv3664c	arop2 betP cycA dppA dppB dppC	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine probable peptide transport system permease probable peptide transport system permease
Rv1910c Rv1919c Rv1984c Rv1987 Rv2223c Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c	· · · · · · · · · · · · · · · · · · ·	probable secreted protein weak similarity to pollen antigens probable secreted protein probable secreted protein probable exported protease probable exported protease probable cutinase precursor of probable membrane protein putative exported protease similar to Esat6	Rv0346c Rv0917 Rv1704c Rv3666c Rv3665c Rv3664c	arop2 betP cycA dppA dppB dppC	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine probable peptide transport system permease probable peptide transport system permease probable peptide transport system permease
Rv1910c Rv1919c Rv1984c Rv1987 Rv2223c Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c		probable secreted protein weak similarity to pollen antigens probable secreted protein probable secreted protein probable exported protease probable exported protease probable cutinase precursor of probable membrane protein putative exported protease similar to Esat6 probable secreted protein	Rv0346c Rv0917 Rv1704c Rv3666c Rv3665c Rv3665c Rv3665c Rv3665c Rv3665c	arop2 betP cycA dppA dppB dppC dppD	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine probable peptide transport system permease probable peptide transport system permease probable peptide transport system permease
Rv1910c Rv1919c Rv1984c Rv2223c Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv30036c Rv3036c Rv3449		probable secreted protein weak similarity to pollen antigens probable secreted protein probable secreted protein probable exported protease probable exported protease probable cutinase protein protein putative exported protease similar to Esat6 probable secreted protein probable precursor of serine pro-	Rv0346c Rv0917 Rv1704c Rv3666c Rv3665c Rv3664c Rv3663c Rv3663c Rv0522	arop2 betP cycA dppA dppB dppC dppD gabP	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine 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 trans-
Rv1910c Rv1919c Rv1984c Rv223c Rv2224c Rv2224c Rv2301 Rv2672 Rv3019c Rv3036c Rv3449		probable secreted protein weak similarity to polien antigens probable secreted protein probable secreted protein 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 pro- tease	Rv0346c Rv0917 Rv1704c Rv3666c Rv3665c Rv3664c Rv3664c Rv3663c Rv0522	aror2 betP cycA dppA dppB dppC dppD gabP	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine probable peptide transport system permease probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable 4-amino butyrate trans- porter
Rv1910c Rv1919c Rv1984c Rv1987 Rv2223c Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c Rv30449 Rv3451		probable secreted protein weak similarity to pollen antigens probable secreted protein probable secreted protein probable exported protease probable exported protease procursor of probable membrane protein putative exported protease similar to Esat6 probable secreted protein probable secreted protein probable secreted protein probable precursor of serine pro- tease probable cutinase	Rv0346c Rv0917 Rv1704c Rv3666c Rv3665c Rv3665c Rv3663c Rv3663c Rv0522 Rv0411c	aror2 betP cycA dppA dppB dppC dppD gabP glnH	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable ABC-transporter probable ABC-transporter probable ABC-transporter probable ABC-transporter protable ABC-transporter
Rv1910c Rv1910c Rv1987 Rv2223c Rv2224c Rv2201 Rv2345 Rv2672 Rv3019c Rv3019c Rv3036c Rv3449 Rv3451 Rv3452		probable secreted protein weak similarity to pollen antigens probable secreted protein probable secreted protein 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 pro- tease probable cutinase probable cutinase	Rv0346c Rv0917 Rv1704c Rv3666c Rv3665c Rv3664c Rv3663c Rv0522 Rv0411c Rv2564	arop2 betP cycA dppA dppB dppC dppD gabP ginH ginQ	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable ABC-transporter probable ABC-transporter probable ABC-transporter putative glutamine binding protein probable ATP-binding transport
HV1910c RV1919c RV1987 RV2223c RV2224c RV2301 RV2345 RV2672 RV3019c RV3036c RV3451 RV3451 RV3452 RV3451		probable secreted protein weak similarity to pollen antigens probable secreted protein probable secreted protein probable exported protease probable exported protease probable cutinase protein putative exported protease similar to Esat6 probable secreted protein probable secreted protein probable secrets of serine pro- tease probable cutinase precursor probable cutinase precursor	Rv0346c Rv0917 Rv1704c Rv3666c Rv3665c Rv3664c Rv3663c Rv0522 Rv0411c Rv2564	arop2 betP cycA dppA dppB dppC dppD gabP glnH glnQ	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable ABC-transporter probable 4-amino butyrate trans- porter putative glutamine binding protein probable ATP-binding transport protein
Rv1910c Rv1910c Rv1987 Rv2984c Rv2901 Rv2204c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c Rv30459 Rv3451 Rv3451 Rv3452 Rv3724	X	probable secreted protein weak similarity to pollen antigens probable secreted protein probable secreted protein probable exported protease probable exported protease probable exported protease protable cutinase protein putative exported protease similar to Esat6 probable secreted protein probable secreted protein probable precursor of serine pro- tease probable cutinase precursor probable cutinase precursor	Rv0346c Rv0917 Rv1704c Rv3666c Rv3665c Rv3664c Rv3663c Rv0522 Rv0411c Rv2864 Rv1280c	arop2 betP cycA dppA dppB dppC dppD gabP glnH glnQ oppA	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable ABC-transporter probable ABC-transporter probable ABC-transporter probable ATP-binding transport protein protein protein on protein protein on transport transport
HV1910c RV1910c RV1987 RV2984c RV2987 RV2224c RV2224c RV22345 RV2672 RV3019c RV30019c RV3036c RV3451 RV3452 RV3724 3. Murein	- - - - - - - - - - - - - - - - - - -	probable secreted protein weak similarity to pollen antigens probable secreted protein probable secreted protein 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 precursor of serine pro- tease probable cutinase precursor probable cutinase precursor probable cutinase precursor and peptidoglycan pensidili biding protein	HV03466 Rv0917 Rv1704c Rv3666c Rv3665c Rv1280c Rv1280c	arop2 betP cycA dppA dppB dppC dppD gabP glnH glnQ oppA	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable ABC-transporter protein butyrate transport protein
HV1910c RV1910c RV1987 RV2984c RV2987 RV2224c RV2224c RV22345 RV2672 RV3019c RV3019c RV3036c RV3451 RV3452 RV3724 3. Murein RV2981c	- - - - - - - - - - - - - - - - - - -	probable secreted protein weak similarity to pollen antigens probable secreted protein probable secreted protein 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 pro- tease probable cutinase precursor probable cutinase precursor probable cutinase precursor probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine linase A	HV03466 Rv0917 Rv1704c Rv3666c Rv3665c Rv3665c Rv3663c Rv0522 Rv0411c Rv1280c Rv1280c Rv1282c	aron2 betP cycA dppA dppB dppC dppD gabP glnH glnQ oppA oppB oppB oppC	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable ABC-transport protein probable oligopeptide transport protein
HV1910c RV1919c RV1987c RV1987c RV2223c RV2224c RV22345 RV3019c RV3019c RV3036c RV3451 RV34551 RV32911 RV22911 RV2981c RV3809c	- - - - - - - - - - - - - - - - - - -	probable secreted protein weak similarity to pollen antigens probable secreted protein probable secreted protein probable exported protease 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 pro- tease probable cutinase precursor probable cutinase precursor probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-galadopyranose mutase	HV03466 RV0917 RV17040 RV36660 RV36650 RV36640 RV36630 RV0522 RV04110 RV12800 RV128300 RV128300	aron2 betP cycA dppA dppB dppC dppD gabP glnH glnQ oppA oppA oppB oppC	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable ABC-transporter probable ABC-transporter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport pystem per- mease
HV1910c RV1910c RV1987 RV1987 RV2223c RV2224c RV2224c RV2301 RV3036c RV3036c RV30451 RV3451 RV3724 3. Murein RV2911 RV281c RV3809c RV1018c	- - - - - - - - - - - - - - - - - - -	probable secreted protein weak similarity to pollen antigens probable secreted protein probable secreted protein 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 secreted protein probable cutinase precursor probable cutinase precursor probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-N-acetlydlucosamine	HVU3466 RV0917 RV17040 RV3666c RV3665c RV36640 RV3663c RV3663c RV522 RV0411c RV2564 RV1280c RV1283c RV1283c RV1283c	aron2 betP cycA dppA dppB dppC dppD gabP glnH glnQ oppA oppA oppB oppC	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable ABC-transporter probable ABC-transporter probable ABC-transporter probable ABC-transporter probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport protein oligopeptide transport system per- mease probable peptide transport protein oligopeptide transport system per- mease
Rv1910c Rv1910c Rv1987 Rv2981c Rv2224c Rv2224c Rv2224c Rv2345 Rv2672 Rv3019c Rv3036c Rv30452 Rv3451 Rv3452 Rv3452 Rv3724 3. Murein Rv2911 Rv2911 Rv2981c Rv3809c Rv1018c	- - - - - - - - - - - - - - - - - - -	probable secreted protein weak similarity to pollen antigens probable secreted protein probable secreted protein 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 probable cutinase precursor probable cutinase precursor probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-N-acetylglucosamine pyrophosphorylase	HV03466 Rv0917 Rv17040 Rv36660 Rv36650 Rv36640 Rv36630 Rv0522 Rv04110 Rv12800 Rv12830 Rv12820 Rv12810 Rv12810	aron2 betP cycA dppA dppB dppC dppD gabP ginH ginQ oppA oppA oppB oppD rocE	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable ABC-transporter protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport system per- mease probable peptide transport protein arginine/ornithine transporter
HV1910c RV1919c RV1986 RV1987 RV2223c RV2224c RV2224c RV22301 RV3019c RV3036c RV3451 RV3451 RV2911 RV2981c RV3809c RV1018c RV3382c	- - - - - - - - - - - - - - - - - - -	probable secreted protein weak similarity to pollen antigens probable secreted protein probable secreted protein 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 cutinase probable cutinase precursor probable cutinase precursor und peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-galactopyranose mutase UDP-N-acety/glucosamine pyrophosphorylase LytB protein homologue	HV03466 Rv0917 Rv1704c Rv3666c Rv3665c Rv3665c Rv3665c Rv3663c Rv0522 Rv0411c Rv1280c Rv1283c Rv2320c Rv3253c	aror2 betP cycA dppA dppB dppC dppD gabP glnQ oppA oppA oppB oppC oppD rocE	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable oligopeptide transport protein oligopeptide transport protein oligopeptide transport protein arginine/ornithine transporter probable cationic amino acid
HV1910c RV1919c RV1987 RV1987 RV2223c RV2224c RV2231 RV2672 RV3019c RV3036c RV3452 RV3452 RV3724 3. Murein RV2911 RV3809c RV1018c RV3382cc RV1110	- - - - - - - - - - - - - - - - - - -	probable secreted protein weak similarity to polion antigens probable secreted protein probable secreted protein 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 pro- tease probable cutinase precursor probable cutinase precursor UDP-N-acetylglucosamine pyrophosphorylase LytB protein homologue very similar to LytB	HV03466 RV0917 RV17040 RV36660 RV36650 RV36640 RV36632 RV04110 RV2564 RV12800 RV128300 RV32200 RV32200 RV32300 RV32300	aron2 betP cycA dppA dppB dppC dppD gabP glnH glnQ oppA oppA oppB oppC oppD rocE	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable ABC-transporter probable ABC-transporter probable ABC-transporter probable ABC-transporter probable ABC-transporter probable ABC-transporter probable ABC-transporter probable ABC-transport probable ABC-transport probable ABC-transport probable ABC-transport probable ABC-transport probable ABC-transport probable ABC-transport probable ABC-transport probable ABC-transport protein oligopeptide transport protein oligopeptide transport protein arginine/ornithine transport probable cationic amino acid transport
Rv1910c Rv1910c Rv1987 Rv2987 Rv2223c Rv2224c Rv2301 Rv2345 Rv3019c Rv3036c Rv30459 Rv3451 Rv3452 Rv3724 3. Murein Rv2911 Rv2981c Rv3809c Rv1018c Rv3382c Rv1110 Rv1315	- - - - - - - - - - - - - - - - - - -	probable secreted protein weak similarity to pollen antigens probable secreted protein probable secreted protein probable exported protease probable exported protease protein putative exported protease similar to Esat6 probable secreted protein probable secreted protein probable secreted protein probable secreted protein probable cutinase probable cutinase precursor probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-N-acety/glucosamine pyrophosphorylase LytB protein homologue very similar to LytB UDP-N-acety/glucosamine-1-car-	HV03466 RV0917 RV17040 RV36660 RV36660 RV36640 RV36630 RV0522 RV04110 RV2564 RV12800 RV128300 RV128300 RV128300 RV128300 RV128300 RV128300 RV128300 RV32530 RV32530 RV32530	aron2 betP cycA dppA dppB dppC dppD gabP ginH ginQ oppA oppA oppB oppC rocE -	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine probable peptide transport system permease probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable ABC-transporter probable ABC-transporter probable ATP-binding transport protein probable digopeptide transport protein oligopeptide transport protein oligopeptide transport protein oligopeptide transport system per- mease probable peptide transport protein oligopeptide transport protein arginine/ornithine transporter probable cationic amino acid transport possible proline permease
HV1910c RV1910c RV1910c RV1987 RV2223c RV2224c RV22345 RV2672 RV3019c RV3036c RV30451 RV3452 RV3451 RV2911 RV2911 RV2981c RV3809c RV1018c RV3382c RV1110 RV1315	- - - - - - - - - - - - - - - - - - -	probable secreted protein probable secreted protein probable secreted protein probable secreted protein probable exported protease probable exported protease probable exported protease protein putative exported protease similar to Esat6 probable secreted protein probable secreted protein probable secreted protein probable cutinase probable cutinase precursor probable cutinase precursor proba	HV03466 HV03466 HV0917 HV17040 RV36650 HV36650 RV36630 RV0522 RV04110 RV2564 RV12800 RV128300 RV128300 RV128200 RV128200 RV128100 RV325300 RV325300 RV3454	aron2 betP cycA dppA dppB dppC dppD gabP ginH ginQ oppA oppA oppB oppC -	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable ABC-transporter protein probable ABC-transporter protein oligopeptide transport protein oligopeptide transport protein oligopeptide transport protein arginine/conithine transporter probable cationic amino acid transport possible proline permease
Rv1910c Rv1919c Rv1987 Rv1987 Rv2223c Rv2224c Rv224b Rv3019c Rv3019c Rv3036c Rv3451 Rv3452 Rv3724 3. Murein Rv2981c Rv3809c Rv1018c Rv3382cc Rv1110 Rv1315 Rv0482	- - - - - - - - - - - - - - - - - - -	probable secreted protein probable secreted protein probable secreted protein probable secreted protein probable sexported protease probable exported protease probable exported protease probable catinase precursor of probable membrane protein putative exported protease similar to Esat6 probable secreted protein probable precursor of serine pro- tease probable cutinase precursor probable cutinase precursor und peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-N-acety/glucosamine LytB protein homologue very similar to LytB UDP-N-acety/glucosamine-1-car- boxyvinylitransferase UDP-N-acety/encore	HV03466 HV03466 HV0917 RV17046 HV36666 RV36656 RV36646 RV36632 RV04110 RV2564 RV12806 RV128306 RV128302 RV128302 RV128303 RV128304 RV128305 RV32532 RV3454 2. Cations	aror2 betP cycA dppA dppB dppC dppD gabP glnH glnQ oppA oppA oppB oppC - -	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine probable peptide transport system permease probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable 4-amino butyrate trans- porter putative glutamine binding protein probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport protein oligopeptide transport protein oligopeptide transport protein arginine/ornithine transporter probable peptide transport probable peptide transport probable peptide transport probable cationic amino acid transport possible proline permease
HV1910c RV1910c RV1910c RV1987 RV2987 RV2224c RV2224c RV22345 RV2672 RV3019c RV3036c RV3451 RV3452 RV3451 RV3452 RV3724 3. Murein RV2911 RV2981c RV3809c RV1018c RV3382c RV110 RV1315 RV0482 RV2152c	- - - - - - - - - - - - - - - - - - -	probable secreted protein probable secreted protein probable secreted protein probable secreted protein probable exported protease probable exported protease probable exported protease probable exported protease similar to Esat6 probable secreted protein probable secreted protein probable secreted protein probable secreted protein probable cutinase precursor probable cutinase precursor probable cutinase precursor probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-N-acety/glucosamine pyrophosphorylase LytB protein homologue very similar to LytB UDP-N-acety/glucosamine-1-car- boxyvinyltransferase UDP-N-acety/glucosamine	HV03466 HV03466 HV0917 HV17040 HV36666 HV36666 HV36666 HV36666 HV36666 HV36666 HV36666 HV36666 HV36667 HV36668 HV3664 HV12800 HV12830 HV12830 HV12830 HV12830 HV12830 HV12810 HV32320 HV3454 2. Cations HV4802	articita appA dppA dppB dppC dppD gabP glnH glnQ oppA oppA oppB oppC - -	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable ABC-transporter probable ABC-transporter probable ABC-transporter probable ABC-transporter probable ABC-transporter probable ABC-transporter probable ABC-transporter probable ABC-transport protein probable ATP-binding transport protein oligopeptide transport protein oligopeptide transport protein oligopeptide transport protein oligopeptide transport protein arginine/ornithine transporter probable optide transport protein arginine/ornithine transporter probable proline permease
Rv1910c Rv1910c Rv1987 Rv2987 Rv2223c Rv2224c Rv2301 Rv2345 Rv3019c Rv3036c Rv30459 Rv3452 Rv3452 Rv3452 Rv3452 Rv3452 Rv3452 Rv3452 Rv3452 Rv3809c Rv1018c Rv3809c Rv1018c Rv1018c Rv1110 Rv1315 Rv0482 Rv2152c	- - - - - - - - - - - - - - - - - - -	probable secreted protein weak similarity to pollen antigens probable secreted protein probable secreted protein probable exported protease probable exported protease probable exported protease protein putative exported protease similar to Esat6 probable secreted protein probable secreted protein probable secreted protein probable secreted protein probable cutinase probable cutinase precursor probable cutinase precursor probable cutinase precursor probable cutinase precursor and peptidoglycan penicillin binding protein D-alanine-D-alanine ligase A UDP-N-acety/glucosamine pyrophosphorylase LytB protein homologue very similar to LytB UDP-N-acety/glucosamine-1-car- boxyvinyltransferase UDP-N-acetylenolpyruvoylglu- cosamine reductase UDP-N-acetylenolpyruvoylglu- cosamine reductase	HV03466 HV03466 HV0917 HV17040 HV36666 HV36666 HV36666 HV36667 HV36668 HV36640 HV36640 HV12800 HV12800 HV12820 HV12810 HV12820 HV12810	artor2 betP cycA dppA dppB dppC dppD gabP ginH ginQ oppA oppA oppA oppB oppC - -	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable ABC-transporter probable ABC-transporter probable ABC-transporter probable ABC-transporter probable ATP-binding transport protein probable oligopeptide transport protein oligopeptide transport protein oligopeptide transport protein optobable peptide transport protein probable peptide transport protein probable peptide transport protein optobable cationic amino acid transport possible proline permease
HV1910c RV1910c RV1910c RV1987 RV2223c RV2223c RV2224c RV22345 RV2672 RV30019c RV30019c RV30019c RV3036c RV30452 RV30452 RV3451 RV2911 RV2911 RV2981c RV3809c RV1018c RV3382c RV1100 RV1315 RV0482 RV2152c RV2155c	- - - - - - - - - - - - - - - - - - -	probable secreted protein probable secreted protein probable secreted protein probable secreted protein probable exported protease probable exported protease probable exported protease protein putative exported protease similar to Esat6 probable secreted protein probable secreted protein probable secreted protein probable cutinase probable cutinase precursor probable cutinase precursor DP-N-acetylglucosamine pyrophosphorylase LytB protein homologue very similar to LytB UDP-N-acetylglucosamine-1-car- boxyvinyltransferase UDP-N-acetylglucosamine-1-car- boxyvinyltransferase UDP-N-acetyl-muramate-alanine ligase	HV03466 Rv0917 Rv17040 Rv36650 Rv36650 Rv36640 Rv36652 Rv0522 Rv04110 Rv12800 Rv12800 Rv128300 Rv12840 Rv12840 Rv12810 Rv3454 2. Cations Rv292000 Rv1607 Rv12390	arot2 betP cycA dppA dppB dppC dppD gabP ginH ginQ oppA oppA oppA oppB oppC - -	probable aromatic amino acid permease glycine betaine transport transport of D-alanine, D-serine and glycine probable peptide transport system permease probable peptide transport system permease probable ABC-transporter probable ABC-transporter protein probable ATP-binding transport protein oligopeptide transport protein oligopeptide transport protein oligopeptide transport protein arginine/conithine transporter probable peptide transport protein possible proline permease
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Rv1030	kdpВ	potassium-transporting ATPase B
Rv1031	kdpC	chain potassium-transporting ATPase C
Rv3236c	kefB	chain probable glutathione-regulated
Rv2877c	merT	potassium-efflux protein possible mercury resistance
Rv1811	mgtC	transport system probable magnesium transport
Rv0362	mgtE	ATPase protein C putative magnesium ion
Rv2856	nicT	transporter probable nickel transport protein
Rv0924c	nramp	transmembrane protein belonging to Nramp family
Rv2691	trkA	probable potassium uptake pro- tein
Rv2692	trkB	probable potassium uptake pro- tein
Rv2287 Rv2723	yjcE -	probable Na+/H+ exchanger probable membrane protein,
Bv3162c		tellurium resistance probable membrane protein
Rv3237c	-	possible potassium channel
Rv3743c		protein probable cation-transporting
		ATPase
3. Carbohy	drates, or	ganic acids and alcohols
Rv2443	dctA	C4-dicarboxylate transport protein
Rv3476c	kgtP nanT	sugar transport protein
HV19020 Bv1236	nan sunA	membrane protein probably
1111200	e agri	involved in sugar transport
Rv1237	sugB	sugar transport protein
Hv1238	sugC	ABC transporter component of sugar uptake system
Rv3331	sugl	probable sugar transport protein
Rv2835c	ugpA	sn-glycerol-3-phosphate
Dv29220	uanP	permease
NV20000	uypь	periplasmic lipoprotein
Rv2832c	ugpC	sn-glycerol-3-phosphate transport
Rv2834c	ugpE	sn-glycerol-3-phosphate transport
Bv2316	uenA	system protein
Rv2318	uspC	sugar transport protein
Rv2317	uspE	sugar transport protein
Rv1200	-	probable sugar transporter
Rv2038c	-	probable ABC sugar transporter
Rv20390		probable sugar transporter
Rv2041c	-	probable sugar transporter
4. Anions By2684	areA	probable arsenical nump
Rv2685	arsB	probable arsenical pump
Rv3578	arsB2	probable arsenical pump
Rv2643	arsC	probable arsenical pump
HV2397C	cysA	protein
Rv2399c	cysT	sulphate transport system perme-
Rv2398c	cysW	sulphate transport system perme-
Rv1857	modA	molybdate binding protein
Rv1858	modB	transport system permease,
Rv1859	modC	molybdate uptake ABC-
Rv1860	modD	precursor of Apa (45/47
Bv2329c	narK1	probable nitrite extrusion protein
Rv1737c	narK2	nitrite extrusion protein
Rv0261c	narK3	nitrite extrusion protein
Rv0267	narU	similar to nitrite extrusion protein 2
Rv0934	phoS1	PstS component of phosphate uptake
Rv0928	phoS2	PstS component of phosphate uptake
Rv0820	phoT	phosphate transport system ABC transporter
Rv3301c	phoY1	phosphate transport system regulator
Rv0821c	phoY2	phosphate transport system regulator
Rv0545c	pitA	low-affinity inorganic phosphate transporter
Rv2281 Rv0930	pitB pstA1	phosphate permease PstA component of phosphate
Rv0936	pstA2	uptake PstA component of phosphate
Rv0933	pstB	ABC transport component of
Rv0935	pstC	Pitc component of phosphate
Rv0929	pstC2	membrane-bound component of

Rv0932c	pstS	phosphate transport system PstS component of phosphate	Rv1821	secA2	unit SecA, preprotein translocase sub-	Rv3500c - Rv3501c -		part of mce4 opero	on on
Bu2400a	aubl	uptake	Du0597a		unit	Rv3896c -		putative p60 homo	logue
Rv0143c	-	probable chloride channel	Rv0638	secE	SecE preprotein translocase	HV39220 -		possible nerrolysir	1
Rv1707 Bv1739c	-	probable sulphate permease	Rv2586c Bv1440	secF secG	protein-export membrane protein	B. IS element	ts, Repe	eated sequences, a	nd Phage
Rv3679	-	possible anion transporter	1101440	3000	SecG	IS6110	.5	16 copies	
Rv3680	-	probable anion transporter	Rv0732	secY	SecY subunit of preprotein translo- case	IS1081 Others		6 copies 34 copies	
5. Fatty a	cid transpo	rt	Rv2462c	tig	chaperone protein, similar to				
Rv3540c	ltp1 ltp2	non-specific lipid transport protein non-specific lipid transport protein	Rv2813	-	trigger factor probable general secretion path-	2. REP 13E12	? family	7 copies	
0.54	, 				way protein	3. Phage-rela	ted fund	ctions	
8. Elliux p Rv2936	drrA	similar daunorubicin resistance	E. Adapta	ions and	atypical conditions	Rv1701 X	ərC ərD	integrase/recombin	nase
Bv2037	drrB	ABC-transporter	Rv1901	cinA cspA	competence damage protein	Rv1054 -		integrase-a	
1102307	und	transmembrane protein	11000400	Сэрл	regulator	Rv1573 -		phiRV1 phage rela	ted protein
Rv2938	drrC	similar daunorubicin resistance	Rv0871 Bv3063	cspB cstA	probable cold shock protein starvation-induced stress	Rv1574 - Bv1575 -		phiRV1 phage rela	ted protein ted protein
Rv2846c	efpA	putative efflux protein			response protein	Rv1576c -		phiRV1 phage rela	ted protein
Rv3065 Rv0783c	emr⊨ -	multidrug resistance protein	HV3490	otsA	probable α,α-trenalose-phosphate synthase	Rv1577c - Rv1578c -		phiRV1 possible pl phiRV1 phage rela	ted protein
Rv0849 Bv1145	-	possible quinolone efflux pump	Rv2006	otsB	trehalose-6-phosphate phos-	Rv1579c -		phiRV1 phage rela	ted protein
Rv1146	-	probable drug transporter	Rv3372	otsB2	trehalose-6-phosphate phos-	Rv1581c -		phiRV1 phage rela	ted protein
Rv1250 Rv1258c	-	probable drug efflux protein probable multidrug resistance	Rv3758c	proV	phatase osmoprotection ABC transporter	Rv1582c - Rv1583c -		phiRV1 phage rela phiRV1 phage rela	ted protein ted protein
5		pump	Rv3757c	proW	transport system permease	Rv1584c -		phiRV1 phage rela	ted protein
Rv1410c Rv1634	-	probable drug efflux protein	Rv3759c Rv3756c	pro X pro Z	similar to osmoprotection proteins transport system permease	Rv15850 -		phiRV1 phage rela phiRV1 integrase	ted protein
Rv1819c	-	probable multidrug resistance	Rv1026	-	probable pppGpp-5'phosphohydro-	Rv2309c -		integrase	
Rv2136c	-	putative bacitracin resistance pro-			lase	Rv2646 -		phiRV2 integrase	
Bv2209	_	tein probable drug efflux protein	F. Detoxific Bv2428	ation abnC	alkyl hydroneroxide reductase	Rv2647 -		phiRV2 phage rela	ted protein
Rv2333c	-	probable tetracenomycin C resis-	Rv2429	ahpD	member of AhpC/TSA family	Rv2651c -		phiRV2 prohead p	rotease
Rv2994	_	tance protein probable fluoroquinolone efflux	Rv2238c Rv2521	ahpE bcp	member of AhpC/TSA family bacterioferritin comigratory protein	Rv2652c - Rv2653c -		phiRV2 phage rela phiRV2 phage rela	ted protein ted protein
D.::1077		protein	Rv1608c	bcpB	probable bacterioferritin comigra-	Rv2654c -		phiRV2 phage rela	ted protein
Rv2459	-	probable drug efflux protein probable drug efflux protein	Rv3473c	bpoA	tory protein probable non-heme bromoperoxi-	Rv26550 -		phiRV2 phage rela	ted protein ted protein
R Chapa	range/Heat	chack	By11220	bnoR.	dase probable pop home bromoporovi	Rv2657c -		similar to gp36 of r	mycobacterio-
Rv0384c	clpB	heat shock protein	11011230	бров	dase	Rv2658c -		phiRV2 phage rela	ted protein
Rv0352	dnaJ	acts with GrpE to stimulate DnaK ATPase	Rv0554	bpoC	probable non-heme bromoperoxi-	Rv2659c - Bv2830c -		phiRV2 integrase similar to phage P	1 <i>phd</i> gene
Rv2373c	dnaJ2	DnaJ homologue	Rv3617	ephA	probable epoxide hydrolase	Rv3750c -		excisionase	·
HV0350	anaK	some replication	Rv1938 Rv1124	ерnв ephC	probable epoxide hydrolase probable epoxide hydrolase	HV3/51 -		putative integrase	
Rv3417c	groEL1	60 kD chaperonin 1	Rv2214c	ephD	probable epoxide hydrolase	C. PE and PF	PE famil	lies	
Rv3418c	groES	10 kD chaperone	Rv0134	ephE ephF	probable epoxide hydrolase	PE subfamily		38 members	
Rv0351 Rv2374c	grpE hrcA	stimulates DnaK ATPase activity heat-inducible transcription	Rv3171c	hpx	probable non-heme haloperoxi- dase	PE_PGRS su	ubfamily	61 members	
Du0051-	h	repressor	Rv1908c	katG	catalase-peroxidase	2. PPE family	,	68 members	
Rv02510	nsp hspR	heat shock regulator	Rv0432	sodA sodC	superoxide dismutase superoxide dismutase precursor -	D. Antibiotic p	oroducti	on and resistance	
Rv2031c	hspX	14kD antigen, heat shock protein Hsp20 family	Bv1932	trax	(Cu-Zn) thiol peroxidase	Rv2068c bi Bv3290c la	laC it	class A β-lactamas	se sferase
Rv2299c	htpG	heat shock protein Hsp90 family	Rv0634c	-	putative glyoxylase II	Rv2043c p	ncA	pyrazinamide resis	tance/sensitivity
Hv0563	htpX	probable (transmembrane) heat shock protein	Hv2581c Rv3177	-	putative glyoxylase II probable non-heme haloperoxi-	Hv0133 -		possible puromycii ferase	n N-acetyltrans-
Rv2701c	suhB	putative extragenic suppressor			dase	Rv0262c -		aminoglycoside 2'-	N-acetyltrans-
Rv3269	-	probable heat shock protein	IV. Other			Rv0802c -		acetyltransferase	
C. Cell di	vision		A. Viruleno By0169	mce1	cell invasion protein	Rv1082 - Bv1170 -		similar to S. lincolr	nensis ImbE Densis ImbE
Rv3641c	fic	possible cell division protein	Rv0589	mce2	cell invasion protein	Rv1347c -		possible aminogly	coside 6'-N-
Rv3102c Rv3610c	ftsE ftsH	inner membrane protein,	Rv1966 Rv3499c	mce3 mce4	cell invasion protein cell invasion protein	Rv2036 -		similar to lincomyc	in production
Dv0749a	ftoK	chaperone	Rv3100c	smpB thrA	probable small protein b	Bv22020		genes	a maaratatralida
Rv2151c	ftsQ	ingrowth of wall at septum	Rv0024	-	putative p60 homologue	11020000 -		resistance protein	3 macrotetronde
Rv2154c	ftsW	membrane protein (shape determi- nation)	Rv0167 Rv0168	-	part of <i>mce1</i> operon part of <i>mce1</i> operon	Rv3225c -		probable aminogly photransferases	coside 3'-phos-
Rv3101c	ftsX	membrane protein	Rv0170	-	part of <i>mce1</i> operon	Rv3700c -		probable acetyltrar	nsferase
Rv2921c Rv2150c	fts7 ftsZ	cell division protein Fisir circumferential ring, GTPase	Rv0171 Rv0172	-	part of <i>mce1</i> operon part of <i>mce1</i> operon	HV3817 -		probable aminogly photransferase	coside 3 -prios-
Rv3919c	gid moc l	glucose inhibited division protein B	Rv0174	-	part of mce1 operon	E Ractoriaci	n liko pr	rataina	2
Rv3917c	parA	chromosome partitioning; DNA -	Rv0588	-	part of mce2 operon	E. Daoterioon	r inc pr	0101113	0
Rv3918c	parB	binding possibly involved in chromosome	Rv0590 Rv0591	-	part of <i>mce2</i> operon part of <i>mce2</i> operon	F. Cytochrom	e P450	enzymes	22
D . 00000	J	partitioning	Rv0592	-	part of <i>mce2</i> operon	G. Coenzyme	₹F420-0	dependent	2
HV29220	smc	family	Rv1085c	-	part of <i>mce2</i> operon possible hemolysin	enzymes			3
Rv0012 Rv04355	-	possible cell division protein	Rv1477	-	putative exported p60 protein	H. Miscellane	ous trai	nsferases	61
Rv2115c	-	ATPase of AAA-family	Rv1478	-	putative exported p60 protein	I. Miscellaned	ous pho	sphatases, lyases,	10
HV3213c	-	possible role in chromosome seg- regation	Rv1566c	-	nomologue putative exported p60 protein	and hydrolas	es		18
Rv1708	-	possible role in chromosome parti-	Butoot		homologue	J. Cyclases			6
		uoning	Rv1965	-	part of <i>mce3</i> operon	K. Chelatase	s		2
D. Proteir By29160	and peptic	de secretion	Rv1967 Bv1968	-	part of mce3 operon	V Concerver	l hvnath	eticals	912
Rv2903c	lepB	signal peptidase I	Rv1969	-	part of mce3 operon				
Hv1614	lgt	prolipoprotein diacylglyceryl trans- ferase	Hv1971 Rv2190c	-	part of <i>mce3</i> operon putative p60 homoloque	VI. Unknown	s		606
Rv1539	lspA	lipoprotein signal peptidase	Rv3494c	-	part of <i>mce4</i> operon	TOTAL			3924
HVU379	500	propable transport protein SecE/Sec61- γ family	nv34960 Rv3497c	-	part of <i>mce4</i> operon part of <i>mce4</i> operon				
Bv3240c	secA	SecA preprotein translocase sub-	Bv3498c	-	part of mce4 operon				

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

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

Figure 1 shows the most up-to-date observations of the Galactic Centre¹⁸. The spectrum rises at radio and submillimetre frequencies $\nu \approx 10^9 - 10^{12}$ Hz, where most of the emission occurs, and has a sharp drop in the infrared. The X-ray observations consist of a possible detection at soft X-ray energies, and firm upper limits in the hard X-rays. The X-ray error-box corresponds to uncertainties in the observed photon index which lies between 1.0 and 2.0 (ref. 18). At very high energies, the EGRET satellite has observed γ -ray emission from the Galactic Centre region⁸. But owing to the low angular resolution of the measurements, $\sim 1^\circ$, the observations should perhaps be considered as upper limits.

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

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

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

case, a rather *ad hoc* electron-temperature profile might be needed to account for the excess radio emission¹⁸, which probably does not correspond to physical conditions. More importantly, recent high-resolution measurements constrain the actual size of the emitting region^{5,22}. These observations require large brightness temperatures (in excess of 10^{10} K) to explain the observed flux at 43 GHz and 86 GHz. In an ADAF, however, the electron temperature is always well below 10^{10} K at all radii¹¹, and therefore cannot account for these high temperatures.

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



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

emission¹⁹

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

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

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

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



Figure 2 The energy spectrum, R(E), of positrons and electrons that are created by colliding power-law protons with energy index s = 2.75. The vertical axis is the logarithm of number of positron and electrons created per unit volume, per second, per energy interval, and the horizontal axis is the logarithm of the energy. The scale on the vertical axis corresponds to a number density of protons equal to unity. For a number density N, the vertical axis must be multiplied by N^2 . The particles that are responsible for most of the emission are determined by the energy at which the function $E^2R(E)$ peaks, which occurs in the range 100 MeV < E < 500 MeV. The shape of the spectrum depends only on the physics of particle collisions and decays^{65,26}, and at high energies has the spectral shape $R(E) \propto E^{-s}$ (ref. 25). The spectrum therefore contains information about the parent proton distribution, as well as determining the shape of the resulting synchrotron spectrum. It therefore acts as a link between the form of the proton energy distribution and the observed synchrotron spectrum.

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

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

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

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

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

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

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

Although past work has attempted to answer both these questions theoretically²⁸⁻³³, the results here provide indirect observational evidence that these assumptions are probably valid. Further, theoretical models which reach contrary conclusions are probably based on assumptions that are not valid in ADAF^{18,34}. The present results could therefore be used as tools to aid future theoretical work in resolving these complex questions in plasma physics.

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

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

We stress that there is no fine tuning in the present results. Whereas previous work on ADAFs has not included the e^{\pm} synchrotron radiation, the results presented here show that this process is essential to explaining the observed non-uniform radio spectrum. The model used is identical to that presented in ref. 18, and we have simply taken into account an additional physical process and emission mechanism in the two-temperature ADAF. It is remarkably that, using the same parameters as in ref. 18, an emission mechanism associated with the protons is able to naturally reproduce the entire radio spectrum including the observed spectral break at ~86 GHz. The agreement of the theory with the observations encourages us to take the natural explanation, and conclude that Sgr A* is in fact a 2 × 10⁶ solar-mass black hole that is accreting by way of a two-temperature ADAF.

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

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

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

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

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

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

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

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

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

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

Organization and sequence of the genome

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

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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*)⁹. 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 horizon-tally 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 replication¹⁰. 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 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 ~ 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 $\sim 91\%$ 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 \sim 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 $\sim 40\%$ 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 ~250 distinct enzymes involved in fatty acid metabolism in *M. tuberculosis* compared with only 50 in *E. coli*²⁰.

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



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

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

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

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

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

Much of the subsequent structural diversity in mycolic acids is

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

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

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

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

Siderophores. Peptides that are not ribosomally synthesized are

made by a process that is mechanistically analogous to polyketide synthesis^{23,27}. These peptides include the structurally related ironscavenging 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 salicylateactivating 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 nonribosomal 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 \sim 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 \sim 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. \square

Methods

Sequence analysis. Initially, $\sim 3.2 \text{ Mb}$ 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 non-coding 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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Correspondence and requests for materials should be addressed to B.G.B. (barrell@sanger.ac.uk) or S.T.C. (stcole@pasteur.fr). The complete sequence has been deposited in EMBL/GenBank/DDBJ as MTBH37RV, accession number AL123456.

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

I. Small-m A. Degrada	olecule m ation	etabolism	Rv2
1. Carbon	compound	IS	
Rv0186	bgIS	β-glucosidase	Rv3
Rv2202c	cbhK	carbohydrate kinase	
Rv0727c	fucA	L-fuculose phosphate aldolase	Rv3
Rv1731	gabD1	succinate-semialdehyde dehydro-	
Rv0234c	- gabD2	genase succinate-semialdehyde dehydro-	Rv3
Rv0501	galE1	genase UDP-glucose 4-epimerase	Rv3
Rv0536 Rv0620	galE2 galK	UDP-glucose 4-epimerase galactokinase	Rv3
Rv0619	galT	galactose-1-phosphate uridylyl- transferase C-term	Rv3
Rv0618	galT'	galactose-1-phosphate uridylyl- transferase N-term	Rv0
Rv0993	galU	UTP-glucose-1-phosphate uridylyl- transferase	Rv0 Rv1
Rv3696c	glpK	ATP:glycerol 3-phosphotrans- ferase	Rv1
Rv3255c	manA	mannose-6-phosphate isomerase	Rv3
Rv3441c	mrsA	phosphoglucomutase or phospho- mannomutase	Rv3 Rv0
Rv0118c	oxcA	oxalyl-CoA decarboxylase	
Rv3068c	pqmA	phosphoglucomutase	Rv0
Rv3257c	pmmA	phosphomannomutase	
Bv3308	nmmB	phosphomannomutase	Bv1
By2702	nnaK	polyphosphate dlucokinase	
Dv0409	ppgi	phosphate acetultransforase	Dv2
RV0400	pia vul		HV3
Du1000	луір	Aylulose Killase	D. 2
Rv1096	-	carbohydrate degrading enzyme	Rv1
2. Amino a	cids and a	amines	Rv1
Rv1905c	aao	D-amino acid oxidase	Rv0
Rv2531c	adi	ornithine/arginine decarboxylase	Rv3
Rv2780	ald	L-alanine dehydrogenase	Rv0
By1538c	ansA	L-asparaginase	Bv0
By1001	arcA	arginine deiminase	By1
Dv07520	mmcA	mothylmalmonato comialdobydo	Dv0
HV0753C	IIIIISA	debudre sesses	
D. 0754		denydrogenase	RVU Du0
RV0751C	mmsB	metnyimaimonate semiaidenyde	RV2
		oxidoreductase	RVU
Rv1187	rocA	pyrroline-5-carboxylate dehydro-	Rv1
		genase	Rv1
Rv2322c	rocD1	ornithine aminotransferase	Rv1
Rv2321c	rocD2	ornithine aminotransferase	Rv3
Rv1848	ureA	urease v subunit	Bv1
Bv1849	ureB	urease ß subunit	Bv2
Dv1950	uroC		Dv0
RV1050	uiec	urease a suburni	
RV1853	ureD	urease accessory protein	RV3
RV1851	urer	urease accessory protein	RV3
Rv1852	ureG	urease accessory protein	Rv3
Rv2913c	-	probable D-amino acid	Rv1
		aminohydrolase	Rv2
Rv3551	-	possible glutaconate CoA-	Rv3
		transferase	Rv1
			Rv1
3 Eatty aci	ds		Bv2
By2501c	accA1	acetyl/propionyl-CoA carboxylase	By0
		a subunit	Bv2
Bv0973c	20042	acetyl/propionyl-CoA carboxylase	Bv2
11003700	accaz	a cubupit	Dv0
Dv25020	200D1	a subulin	Dv1
11023020	accor	R cubupit	Dv2
Bv0074a	222002	p suburni	Dut
1009740	20002	acety/propionyr-COA carboxyiase,	
D. 0007		p suburiit	HV0
Rv3667	acs	acetyl-CoA synthase	Rv2
Hv3409c	choD	cholesterol oxidase	Rv1
Rv0222	echA1	enoyl-CoA hydratase/isomerase	Rv0
		superfamily	Rv0
Rv0456c	echA2	enoyl-CoA hydratase/isomerase	Rv0
		superfamily	Rv0
Rv0632c	echA3	enoyl-CoA hydratase/isomerase	Rv0
Rv0673	echA4	enoyl-CoA hydratase/isomerase	Rv0
		superfamily	Rv0
Rv0675	echA5	enoyl-CoA hydratase/isomerase	By0
Rv0905	echA6	enoyl-CoA hydratase/isomerase	Rv0
Bv0971c	echA7	enovi-CoA hydratase/isomerase	Rv0
		superfamily	Rv1
HV10/0C	ecnA8	enoyi-GOA nydratase/isomerase superfamily	Rv1 Rv1
Rv1071c	echA9	enoyl-CoA hydratase/isomerase superfamily	Rv1 Rv1
Rv1142c	echA10	enoyl-CoA hydratase/isomerase	Rv2
Rv1141c	echA11	enoyl-CoA hydratase/isomerase	Rv2
Rv1472	echA12	enoyl-CoA hydratase/isomerase	Rv3
Rv1935c	echA13	enoyl-CoA hydratase/isomerase	Rv3
Rv2486	echA14	superiamily enoyl-CoA hydratase/isomerase	Rv3
Rv2679	echA15	superramily enovl-CoA hvdratase/isomerase	HV3 RV3

		superfamily
2831	echA16	enoyl-CoA hydratase/isomerase
		superfamily
3039c	echA17	enoyl-CoA hydratase/isomerase
3373	och418	superfamily
575	CUIATO	superfamily. N-term
3374	echA18'	enoyl-CoA hydratase/isomerase
0510	aab 4 10	superfamily, C-term
010	ecnA 19	superfamily
3550	echA20	enoyl-CoA hydratase/isomerase
		superfamily
3774	echA21	enoyl-CoA hydratase/isomerase
0859	fadA	β oxidation complex. β subunit
		(acetyl-CoA C-acetyltransferase)
0243	fadA2	acetyl-CoA C-acetyltransferase
1074C	fadA3	acetyl-CoA C-acetyltransferase
1323	IauA4	(aka thiL)
3546	fadA5	acetyl-CoA C-acetyltransferase
3556c	fadA6	acetyl-CoA C-acetyltransferase
0860	fadB	β oxidation complex, α subunit
1468	fadR2	3-bydroxyacyl-CoA debydroge-
	TRODE	nase
715	fadB3	3-hydroxyacyl-CoA dehydroge-
	fodP4	nase
5141	IAUB4	ase
912c	fadB5	3-hydroxyacyl-CoA dehydroge-
750	(ID (nase
1/5UC	iaaレ1 fadD2	acyl-CoA synthese
3561	fadD3	acyl-CoA synthase
)214	fadD4	acyl-CoA synthase
0166	fadD5	acyl-CoA synthase
206	tadD6	acyl-CoA synthase
0119 05510	tadD7 fadD9	acyl-CoA synthase
2590	fadD9	acyl-CoA synthase
0099	fadD10	acyl-CoA synthase
550	fadD11	acyl-CoA synthase, N-term
549	fadD11'	acyl-CoA synthase, C-term
427c	fadD12	acyl-CoA synthase
058	fadD13	acyl-CoA synthase
2187	fadD15	acyl-CoA synthase
0852	fadD16	acyl-CoA synthase
3506	fadD17	acyl-CoA synthase
3513c	fadD18	acyl-CoA synthase
1850	fadD21	acyl-CoA synthase
2948c	fadD22	acyl-CoA synthase
3826	fadD23	acyl-CoA synthase
529	fadD24	acyl-CoA synthase
020	fadD25	acyl-CoA synthase
2930 275c	fadD20	acyl-CoA synthase
2941	fadD28	acyl-CoA synthase
2950c	fadD29	acyl-CoA synthase
0404	fadD30	acyl-CoA synthase
1925	tadD31 fadD32	acyl-CoA synthase
345	fadD33	acvI-CoA synthase
0035	fadD34	acyl-CoA synthase
2505c	fadD35	acyl-CoA synthase
193	fadD36	acyl-CoA synthase
1310	ia0E1 fadE2	acyl-CoA denydrogenase
)215c	fadE3	acyl-CoA dehvdrogenase
0231	fadE4	acyl-CoA dehydrogenase
)244c	fadE5	acyl-CoA dehydrogenase
)271c	fadE6	acyl-CoA dehydrogenase
)400C)672	iauE7 fadE8	acyl-CoA dehydrogenase
		(aka <i>aidB</i>)
)752c	fadE9	acyl-CoA dehydrogenase
073	tadE10	acyl-CoA dehydrogenase
1972C	idUE12 fadE12	acyl-CoA dehydrogenase
346	fadE14	acyl-CoA dehvdrogenase
467c	fadE15	acyl-CoA dehydrogenase
679	fadE16	acyl-CoA dehydrogenase
1934c	tadE17	acyl-CoA dehydrogenase
1933C 2500c	iauE18 fadE19	acyl-CoA dehydrogenase
	.au 17	(aka mmqC)
2724c	fadE20	acyl-CoA dehydrogenase
2789c	fadE21	acyl-CoA dehydrogenase
3061c	tadE22	acyl-CoA dehydrogenase
8139	iau⊑23 fadF24	acyl-CoA dehydrogenase
3274c	fadE25	acyl-CoA dehydrogenase
3504	fadE26	acyl-CoA dehydrogenase
3505	fadE27	acyl-CoA dehydrogenase
3544c	fadE28	acyl-CoA dehydrogenase

Bv3543c	fadE29	acyl-CoA dehydrogenase
Bv3560c	fadE30	acyl-CoA dehydrogenase
Rv3562	fadE31	acyl-CoA dehydrogenase
Rv3563	fadE32	acvl-CoA dehvdrogenase
Rv3564	fadE33	acyl-CoA dehydrogenase
Rv3573c	fadE34	acvl-CoA dehvdrogenase
Rv3797	fadE35	acvl-CoA dehvdrogenase
Rv3761c	fadE36	acyl-CoA dehydrogenase
Rv1175c	fadH	2,4-Dienoyl-CoA Reductase
Rv0855	far	fatty acyl-CoA racemase
Rv1143	mcr	α-methyl acyl-CoA racemase
Rv1492	mutA	methylmalonyl-CoA mutase, β
		subunit
Rv1493	mutB	methylmalonyl-CoA mutase, α
D 050/		subunit
Rv2504c	SCOA	3-oxo acid:CoA transferase, α sub-
Dv25020	ccoR	2 oxo acid:CoA transforaço, 8 sub
HV25050	SCOD	unit
Rv1136	-	probable carnitine racemase
Rv1683	-	possible acyl-CoA synthase
4. Phospho	prous com	pounds
Rv2368c	phoH	ATP-binding pho regulon
D 1005		component
Rv1095	phoH2	PhoH-like protein
Rv3628	ppa	probable inorganic pyrophos-
Dv0094	nnk	prialase
RV2984	ррк	polyphosphale kinase
	motaholier	7
1 Glycolys	is	
Rv1023	eno	enolase
Rv0363c	fba	fructose bisphosphate aldolase
Rv1436	gap	glyceraldehyde 3-phosphate dehy-
		drogenase
Rv0489	gpm	phosphoglycerate mutase I
Rv3010c	pfkA	phosphofructokinase I
Rv2029c	pfkB	phosphofructokinase II
Rv0946c	pgi	glucose-6-phosphate isomerase
Rv1437	pgk	phosphoglycerate kinase
Rv1617	pykA	pyruvate kinase
Rv1438	tpi	triosephosphate isomerase
Rv2419c	-	putative phosphoglycerate mutase
Rv3837c	-	putative phosphoglycerate mutase
	م ما م ام ، ، ما م م	
2. Fyruvale		pyruvata dabydrogonaso E1.com
1102241	acel	ponent
Rv3303c	IpdA	dihydrolipoamide dehydrogenase
Rv2497c	, pdhA	pyruvate dehydrogenase E1 com-
		ponent α subunit
Rv2496c	pdhB	pyruvate dehydrogenase E1 com-
B 0 405	" 0	ponent β subunit
Rv2495c	panC	dihydrolipoamide acetyltransferase
NV0402	-	drogenase
		arogenado
3. TCA cyc	le	
Rv1475c	acn	aconitate hydratase
Rv0889c	citA	citrate synthase 2
Rv2498c		
	citE	citrate lyase β chain
Rv1098c	citE fum	citrate lyase β chain fumarase
Rv1098c Rv1131	citE fum gltA1	citrate Iyase β chain fumarase citrate synthase 3
Rv1098c Rv1131 Rv0896	citE fum gltA1 gltA2	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1
Rv1098c Rv1131 Rv0896 Rv3339c	citE fum gltA1 gltA2 icd1	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase
Rv1098c Rv1131 Rv0896 Rv3339c Rv0066c	citE fum gltA1 gltA2 icd1 icd2	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase
Rv1098c Rv1131 Rv0896 Rv3339c Rv0066c Rv0794c	citE fum gltA1 gltA2 icd1 icd2 lpdB	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase
Rv1098c Rv1131 Rv0896 Rv3339c Rv0066c Rv0794c Rv1240 Rv1240	citE fum gltA1 gltA2 icd1 icd2 lpdB mdh	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase malate dehydrogenase
Rv1098c Rv1131 Rv0896 Rv3339c Rv0066c Rv0794c Rv1240 Rv2967c Bv2319	citE fum gltA1 gltA2 icd1 icd2 lpdB mdh pca schA	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase malate dehydrogenase pyruvate carboxylase
Rv1098c Rv1131 Rv0896 Rv3339c Rv0066c Rv0794c Rv1240 Rv2967c Rv3318 Rv3319	citE fum gltA1 gltA2 icd1 icd2 lpdB mdh pca sdhA sdhB	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase dihydrolipoamide dehydrogenase malate dehydrogenase pyruvate carboxylase succinate dehydrogenase A succinate dehydrogenase B
Rv1098c Rv1131 Rv0896 Rv3339c Rv0066c Rv0794c Rv1240 Rv2967c Rv3318 Rv3319 Rv3316	citE fum gltA1 gltA2 icd1 icd2 lpdB mdh pca sdhA sdhB sdhB	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase malate dehydrogenase pyruvate carboxylase succinate dehydrogenase A succinate dehydrogenase C sub-
Rv1098c Rv1131 Rv0896 Rv3339c Rv0066c Rv0794c Rv1240 Rv2967c Rv3318 Rv3319 Rv3316	citE fum gltA1 gltA2 icd1 icd2 lpdB mdh pca sdhA sdhA sdhC	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase malate dehydrogenase pyruvate carboxylase succinate dehydrogenase A succinate dehydrogenase B succinate dehydrogenase C sub- unit
Rv1098c Rv1131 Rv0896 Rv3339c Rv0066c Rv0794c Rv1240 Rv2967c Rv3318 Rv3319 Rv3316	citE fum gltA1 gltA2 icd1 icd2 lpdB mdh pca sdhA sdhB sdhC sdhD	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase malate dehydrogenase succinate dehydrogenase A succinate dehydrogenase B succinate dehydrogenase C sub- unit succinate dehydrogenase D sub-
Rv1098c Rv1131 Rv0896 Rv3339c Rv0066c Rv0794c Rv2967c Rv3318 Rv3319 Rv3316	citE fum gltA1 jicd1 icd2 lpdB mdh pca sdhA sdhB sdhC sdhD	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase pyruvate carboxylase succinate dehydrogenase A succinate dehydrogenase B succinate dehydrogenase C sub- unit
Rv1098c Rv1131 Rv0896 Rv3339c Rv0066c Rv0794c Rv1240 Rv3318 Rv3319 Rv3316 Rv3317 Rv1248c	citE fum gltA1 gltA2 icd1 icd2 lpdB mdh pca sdhA sdhB sdhC sdhD sucA	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase malate dehydrogenase pyruvate carboxylase succinate dehydrogenase A succinate dehydrogenase C sub- unit succinate dehydrogenase D sub- unit 2-oxoglutarate dehydrogenase
Rv1098c Rv1131 Rv0896 Rv3339c Rv0066c Rv1240 Rv2967c Rv3318 Rv3319 Rv3316 Rv3317 Rv1248c Rv2215	citE fum gltA1 gltA2 icd1 icd2 lpdB mdh pca sdhA sdhA sdhC sdhD sucA sucA	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase malate dehydrogenase succinate dehydrogenase A succinate dehydrogenase B succinate dehydrogenase C sub- unit succinate dehydrogenase D sub- unit 2-oxoglutarate dehydrogenase dihydrolipoamide succinyltrans-
Rv1098c Rv1131 Rv0896 Rv3339c Rv0794c Rv1240 Rv2967c Rv3318 Rv3319 Rv3316 Rv3317 Rv1248c Rv2215	citE fum gltA1 gltA2 icd1 icd2 lpdB mdh pca sdhA sdhB sdhC sdhD sucA sucB	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase malate dehydrogenase succinate dehydrogenase A succinate dehydrogenase B succinate dehydrogenase C sub- unit 2-oxoglutarate dehydrogenase D sub- unit 2-oxoglutarate dehydrogenase dihydrolipoamide succinyttrans- ferase succinate Gehydrogenase
Rv1098c Rv1131 Rv0896 Rv0896 Rv0896 Rv0794c Rv1240 Rv297c Rv319 Rv3318 Rv3319 Rv3316 Rv3317 Rv1248c Rv2215 Rv0951	citE fum gltA1 gltA2 icd1 icd2 lpdB mdh pca sdhA sdhB sdhC sdhD sucA sucB sucC	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase malate dehydrogenase A succinate dehydrogenase A succinate dehydrogenase B succinate dehydrogenase C sub- unit 2-oxoglutarate dehydrogenase dihydrolipoamide succinyltrans- ferase succinyl-CoA synthase β chain succinate
Rv1098c Rv1131 Rv0896 Rv0396 Rv0066c Rv1240 Rv2967c Rv318 Rv3319 Rv3316 Rv3317 Rv1248c Rv2215 Rv0951 Rv0952	citE fum gltA1 gltA2 icd1 icd2 lpdB mdh pca sdhA sdhB sdhC sdhD sucA sucB sucC sucD	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase malate dehydrogenase succinate dehydrogenase A succinate dehydrogenase A succinate dehydrogenase C sub- unit 2-oxoglutarate dehydrogenase D sub- unit 2-oxoglutarate dehydrogenase dihydrolipoamide succinyltrans- ferase succinyl-CoA synthase α chain succinyl-CoA synthase α chain
Rv1098c Rv1131 Rv0896 Rv3339c Rv0096c Rv1240 Rv2967c Rv3318 Rv3318 Rv3317 Rv1248c Rv2215 Rv0951 Rv0952 4. Glyoxyla	citE fum gltA1 gltA2 icd1 icd2 lpdB mdh pca sdhA sdhB sdhC sdhD sucA sucB sucC sucD te bypass	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase malate dehydrogenase succinate dehydrogenase A succinate dehydrogenase B succinate dehydrogenase C sub- unit succinate dehydrogenase D sub- unit 2-oxoglutarate dehydrogenase dihydrolipoamide succinyltrans- ferase succinyl-CoA synthase α chain
Rv1098c Rv1131 Rv0896 Rv3339c Rv00966c Rv1240 Rv2967c Rv318 Rv3318 Rv3318 Rv3317 Rv1248c Rv2215 Rv0951 Rv0951 Rv0952 4. Glyoxyla Rv0467	citE fum gltA1 gltA2 icd1 icd2 lpdB mdh pca sdhA sdhB sdhB sdhC sucA sucB sucA sucB sucC sucD te bypass aceA	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase pyruvate carboxylase succinate dehydrogenase A succinate dehydrogenase B succinate dehydrogenase C sub- unit 2-oxoglutarate dehydrogenase D sub- unit 2-oxoglutarate dehydrogenase succinyl-CoA synthase β chain succinyl-CoA synthase α chain
Rv1098c Rv1131 Rv0896 Rv0396 Rv0066c Rv1240 Rv2967c Rv318 Rv3319 Rv3316 Rv3317 Rv1248c Rv2215 Rv0951 Rv0951 Rv0952 4. Glyoxyla Rv0467 Rv0467 Rv0495	citE fum gltA1 gltA1 gltA2 icd1 icd2 lpdB mdh pca sdhA sdhA sdhA sucA sucA sucA sucC sucD te bypass aceA	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase malate dehydrogenase A succinate dehydrogenase A succinate dehydrogenase A succinate dehydrogenase C sub- unit 2-oxoglutarate dehydrogenase D sub- unit 2-oxoglutarate dehydrogenase B succinyt-CoA synthase β chain succinyl-CoA synthase β chain succinyl-CoA synthase α chain
Rv1098c Rv1131 Rv0896 Rv0396 Rv0096c Rv1240 Rv2967c Rv3318 Rv3319 Rv3317 Rv1248c Rv2215 Rv0951 Rv0951 Rv0952 4. Glyoxyla Rv0957 Rv1916	citE fum gltA1 gltA2 icd1 icd2 lpdB mdh pca sdhA sdhB sdhC sdhD sucA sucB sucC sucD te bypass aceA aceAa aceAa	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase malate dehydrogenase pyruvate carboxylase succinate dehydrogenase A succinate dehydrogenase C sub- unit succinate dehydrogenase D sub- unit 2-oxoglutarate dehydrogenase dihydrolipoamide succinyltrans- ferase succinyl-CoA synthase β chain succinate lyase isocitrate lyase isocitrate lyase, α module isocitrate lyase, β module
Rv1098c Rv1131 Rv0896 Rv3339c Rv0096c Rv1240 Rv2967c Rv3318 Rv3318 Rv3317 Rv3316 Rv3317 Rv1248c Rv2215 Rv0951 Rv0952 4. Glyoxyla Rv0467 Rv1915 Rv1915 Rv1985 Rv1985	citE fum gltA1 gltA2 icd1 icd2 lpdB mdh pca sdhA sdhB sdhB sdhC sucA sucB sucA sucB sucC sucD te bypass aceA aceAa aceAb glcB	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase pyruvate carboxylase succinate dehydrogenase A succinate dehydrogenase B succinate dehydrogenase D succinate dehydrogenase D succinate dehydrogenase D succinate dehydrogenase D succinate dehydrogenase D succinate dehydrogenase C sub- unit 2-oxoglutarate dehydrogenase dihydrolipoamide succinyltrans- ferase succinyl-CoA synthase β chain succinate lyase isocitrate lyase isocitrate lyase, β module isocitrate lyase, β module malate synthase
Rv1098c Rv1131 Rv0896 Rv03936 Rv03930c Rv0794c Rv1240 Rv1240 Rv3118 Rv3119 Rv3318 Rv3317 Rv1248c Rv2215 Rv0951 Rv0952 4. Glyoxyla Rv0952 4. Glyoxyla Rv1915 Rv1915 Rv1915 Rv1937c Rv1837c Rv1837c	citE furm gltA1 gltA1 gltA2 icd1 icd2 lpdB mdh pca sdhA sdhB sdhA sdhB sucA sucA sucA sucC sucD te bypass aceA aceAa aceAb glcB glpA	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase pyruvate carboxylase succinate dehydrogenase A succinate dehydrogenase A succinate dehydrogenase C sub- unit 2-oxoglutarate dehydrogenase D sub- unit 2-oxoglutarate dehydrogenase succinyl-CoA synthase β chain succinyl-CoA synthase β chain succinate lyase isocitrate lyase, α module isocitrate lyase, β module malate synthase phosphoglycolate phosphatase
Rv1098c Rv1131 Rv0896 Rv0396 Rv0398c Rv1240 Rv2967c Rv318 Rv3319 Rv3316 Rv3317 Rv1248c Rv2215 Rv0951 Rv0951 Rv0951 Rv0952 4. Glyoxyla Rv0951 Rv1915 Rv1916 Rv1916 Rv1932c Rv1932 Rv1916 Rv1932c Rv1932 Rv193	citE fum gltA1 gltA1 gltA2 icd1 icd2 lpdB mdh pca sdhA sdhA sdhA sdhA sucA sucA sucC sucD te bypass aceAa aceAa glcB gphA	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase malate dehydrogenase A succinate dehydrogenase A succinate dehydrogenase A succinate dehydrogenase C sub- unit 2-oxoglutarate dehydrogenase D sub- unit 2-oxoglutarate dehydrogenase B succinyl-CoA synthase β chain succinyl-CoA synthase β chain succinyl-CoA synthase α chain succintate lyase isocitrate lyase, α module isocitrate lyase, β module malate synthase
Rv1098c Rv1131 Rv0896 Rv0396 Rv0096c Rv1240 Rv2967c Rv1240 Rv3318 Rv3319 Rv3317 Rv1248c Rv2215 Rv0951 Rv0951 Rv0952 4. Glyoxyla Rv0952 4. Glyoxyla Rv0951 Rv0952 5. Pentosz 5. Pentosz 5. Pentosz 5. Pentosz 5. Pentosz	citE fum gltA1 gltA1 gltA2 icd1 icd2 lpdB mdh scdA sdhB sdhA sdhB sdhC sucA sucB sucC sucD te bypass aceAa aceAb glcB gphA	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase malate dehydrogenase succinate dehydrogenase A succinate dehydrogenase A succinate dehydrogenase D sub- unit succinate dehydrogenase D sub- unit 2-oxoglutarate dehydrogenase dihydrolipoamide succinyltrans- ferase succinyl-CoA synthase β chain succinyl-CoA synthase β chain succinate lyase isocitrate lyase, β module malate synthase phosphoglycolate phosphatase
Rv1098c Rv1131 Rv0896 Rv3339c Rv0896C Rv1240 Rv294C Rv1240 Rv3318 Rv3318 Rv3317 Rv3316 Rv3317 Rv1248c Rv2215 Rv0951 Rv0952 4. Glyoxyla Rv0951 Rv0952 4. Glyoxyla Rv0951 Rv1915 Rv1915 Rv1915 Rv1915 S. Pentose Rv1445c	citE fum gltA1 gltA1 gltA2 icd1 icd2 lpdB mdh pca sdhA sdhB sdhA sdhB sucA sucB sucA sucB sucC sucD te bypass aceA aceAa aceAb glcB glhA phosphate devB	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase pyruvate carboxylase succinate dehydrogenase A succinate dehydrogenase B succinate dehydrogenase D succinate dehydrogenase dehydrogen
Rv1098c Rv1131 Rv0896 Rv0896 Rv0896 Rv1240 Rv2967c Rv1240 Rv3318 Rv3319 Rv3317 Rv3317 Rv1248c Rv2215 Rv0951 Rv0951 Rv0951 Rv0952 4. Gly0xyla Rv0467 Rv1915 Rv1916 Rv1837c S. Pentose Rv1445c Rv1844c	citE furm gltA1 gltA1 gltA2 icd1 icd2 lpdB mdh pca sdhA sdhB sdhC sdhD sucA sucA sucB sucC sucD te bypass aceA aceAa aceAb glcB glpA glnB glnB aceA aceAa aceAb glnB glnA1 sucA sucC sucD aceA aceAa aceAb glnB glnB glnB sucC sucD aceA aceAa ac ac ac ac ac ac ac ac ac ac ac ac ac	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase pyruvate carboxylase succinate dehydrogenase A succinate dehydrogenase B succinate dehydrogenase B succinate dehydrogenase D succinate dehydrogenase D succinate dehydrogenase D succinate dehydrogenase D succinate dehydrogenase B succinate dehydrogenase B succinate dehydrogenase B succinate dehydrogenase B succinate dehydrogenase C succinyl-CoA synthase β chain succinyl-CoA synthase β chain succinate lyase, β module isocitrate lyase, β module malate synthase phosphoglycolate phosphatase e pathway glucose-6-phosphate 1-dehydro- genase
Rv1098c Rv1131 Rv0896 Rv0396 Rv03339c Rv0794c Rv1240 Rv2967c Rv3318 Rv3319 Rv3317 Rv1248c Rv2215 Rv0951 Rv0951 Rv0951 Rv0951 Rv1915 Rv1916 Rv1916 Rv1916 Rv1916 S. Pentose Rv1445c Rv1844c	citE fum gltA1 gltA1 gltA2 icd1 icd2 lpdB mdh sdhA sdhA sdhA sucA sucA sucA sucC sucD te bypass accAa accAa glcB gphA phosphate devB	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase malate dehydrogenase A succinate dehydrogenase A succinate dehydrogenase A succinate dehydrogenase C sub- unit 2-oxoglutarate dehydrogenase D sub- unit 2-oxoglutarate dehydrogenase B succinate dehydrogenase C sub- unit succinate dehydrogenase B succinyl-CoA synthase β chain succinyl-CoA synthase α chain succinyl-CoA synthase α chain succintate lyase, α module isocitrate lyase, β module malate synthase phosphoglycolate phosphatase e pathway glucose-6-phosphate 1-dehydro- genase 6-phosphogluconate dehydroge- nase (Gram –)
Rv1098c Rv1131 Rv0896 Rv3339c Rv0096c Rv1240 Rv1240 Rv3318 Rv3319 Rv3317 Rv3317 Rv1248c Rv2215 Rv0951 Rv0951 Rv0951 Rv0952 4. Glyoxyla Rv0951 Rv0952 4. Glyoxyla Rv10457 Rv1916 Rv1837c Rv1945c S. Pentose Rv1445c Rv1445c Rv1844c Rv1122	citE fum gltA1 gltA1 gltA2 icd1 icd2 lpdB mdh pca sdhA sdhB sdhA sdhB sdhC sucA sucB sucC sucD te bypass aceAa aceAb glcB gphA phosphate devB gnd gnd2	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase malate dehydrogenase 8 succinate dehydrogenase A succinate dehydrogenase C sub- unit succinate dehydrogenase D sub- unit 2-oxoglutarate dehydrogenase D sub- unit 2-oxoglutarate dehydrogenase succinytate dehydrogenase succinytate dehydrogenase d isocitrate lyase isocitrate lyase, β module isocitrate lyase, β module malate synthase phosphoglycolate phosphatase 6-phosphogluconate dehydroge- nase (Gram –) 6-phosphogluconate dehydroge-
Rv1098c Rv1131 Rv0896 Rv3339c Rv0896C Rv1240 Rv294C Rv1240 Rv3318 Rv3318 Rv3318 Rv3317 Rv1248c Rv2215 Rv0951 Rv0952 4. Glyoxyla Rv0951 Rv1915 Rv195 Rv195 Rv195 Rv195 Rv195 Rv195 Rv195 Rv195 Rv195 Rv195 Rv195 Rv195 Rv195 Rv195 Rv195 Rv195 Rv195 Rv1	citE fum gltA1 gltA2 licd1 licd2 lpdB mdh pca sdhA sdhB sdhC sdhD sucA sucA sucB sucC sucD te bypass aceA aceAa aceAb glcB gphA phosphate devB	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase pyruvate carboxylase succinate dehydrogenase A succinate dehydrogenase B succinate dehydrogenase D succinate dehydrogenase C succinate dehydrogenase D succinate dehydrogenase D succinate dehydrogenase D succinate dehydrogenase d dihydrolipoamide succinyltrans- ferase succinyl-CoA synthase β chain succinyl-CoA synthase α chain suc
Rv1098c Rv1131 Rv0896 Rv3339c Rv0896 Rv3339c Rv0794c Rv1240 Rv2967c Rv3318 Rv3318 Rv3318 Rv3317 Rv1248c Rv2215 Rv0951 Rv0952 4. Glyoxyla Rv0467 Rv1915 Rv1945 Rv1945 S. Pentose Rv1445c Rv144c Rv1122 Rv1446c	citE fum gltA1 gltA1 gltA2 icd1 icd2 lpdB mdh pca sdhA sdhB sdhC sdhD sucA sucB sucC sucD te bypass aceA aceAa aceAa glcB glpA glnB glnA glnB glnA1 sucC sucD glnA1 sucA sucC sucD glnA1 sucA sucC glnA1 sucA sucC glnA1 sucA sucC glnA1 sucA sucC sucD glnA1 sucA sucC glnA1 sucA sucC glnA2 glnA2 sucA sucC glnA2 glnA2 sucA sucC glnA2 glnA2 sucA sucC glnA2 sucA sucC glnA2 sucA glnA2 sucA sucC glnA2 sucA glnA2 sucA glnA2 sucA sucC glnA2 sucC glnA3 sucA sucC glnA3 glnA3	citrate lyase β chain fumarase citrate synthase 3 citrate synthase 1 isocitrate dehydrogenase isocitrate dehydrogenase dihydrolipoamide dehydrogenase pyruvate carboxylase succinate dehydrogenase A succinate dehydrogenase B succinate dehydrogenase B succinate dehydrogenase D succinate dehydrogenase d inydrolipoamide succinyltrans- ferase succinyl-CoA synthase β chain succinyl-CoA synthase α chain succintate lyase, α module isocitrate lyase, β module malate synthase phosphoglycolate phosphatase e pathway glucose-6-phosphate 1-dehydro- genase 6-phosphogluconate dehydroge- nase (Gram +) unknown function, may aid

Bv2436	IDSK	UUUNIIIdSE
By1408	rne	ribulose-phosphate 3-enimerase
Dv0405+	npe mi	
RV2465C	rpi	phosphopentose isomerase
Rv1448c	tal	transaldolase
Bv1449c	tkt	transketolase
Dv1101	TIAC	glucoso 6 phosphato 1 dobudro
HV1121	2 001	glucose-o-priospriate 1-deriyuro-
_		genase
Rv1447c	zwf2	glucose-6-phosphate 1-dehydro-
		genase
		-
6 Pospirat	ion	
o. nespirai	1011	
a. aerobic		
Rv0527	ccsA	cytochrome c-type biogenesis
		protein
Bv0520	cceR	cytochrome c-type biogenesis
110023	CUSD	cytochionie c-type biogenesis
		protein
Rv1451	ctaB	cytochrome <i>c</i> oxidase assembly
		factor
Bv2200c	ctaC	cytochrome c oxidase chain II
Dv2042e	otaD	outoohromo o ovidase onalir n
HV30430	CIAD	cytochrome c oxidase poly-
		peptide I
Rv2193	ctaE	cytochrome c oxidase poly-
		peptide III
By1542c	albN	hemoglobin-like oxygen carrier
Dv0470	gibia	hemeslekia like, oxygen camer
RV2470	gibO	nemoglobin-like, oxygen carrier
Rv2249c	glpD1	glycerol-3-phosphate dehydroge-
		nase
Bv3302c	alnD2	alvcerol-3-phosphate dehydroge-
	9.002	
Duoco t	11-10-1	
HV0694	ιιαυ1	L-lactate denydrogenase
		(cytochrome)
Rv1872c	lldD2	L-lactate dehydrogenase
Bv1854c	ndh	probable NADH debydrogenase
Dv2145	nuo 4	NADU dobudrogenese sheir *
1110140	nuoA	NADIT derivarogenase chain A
Rv3146	nuoB	NADH dehydrogenase chain B
Rv3147	nuoC	NADH dehydrogenase chain C
Bv3148	nuoD	NADH dehvdrogenase chain D
Dv2140	nuoE	NADH dohydrogonaso chain E
Du0150	nuoL	
RV3150	nuor	NADH denydrogenase chain F
Rv3151	nuoG	NADH dehydrogenase chain G
Rv3152	nuoH	NADH dehvdrogenase chain H
By3153	nual	NADH debydrogenase chain I
Du0154	nuor	
RV3154	nuoj	NADH denydrogenase chain J
Rv3155	nuoK	NADH dehydrogenase chain K
Rv3156	nuoL	NADH dehydrogenase chain L
Bv3157	nuoM	NADH dehvdrogenase chain M
By3158	nuoN	NADH debydrogenase chain N
Du0105	nuorv mar A	Disalia iran aulahur aamaanan of
RV2195	qcrA	Rieske iron-sulphur component of
		ubiQ-cytB reductase
Rv2196	<i>qcrB</i>	cytochrome β component of ubiQ-
		cvtB reductase
Dv2104	aarC	autochromo b/c component of
Rv2194	qcrC	cytochrome <i>b/c</i> component of
Rv2194	qcrC	cytochrome <i>b/c</i> component of <i>ubiQ-cytB</i> reductase
Rv2194	qcrC	cytochrome <i>b/c</i> component of <i>ubiQ-cytB</i> reductase
Rv2194 b. anaerob	qcrC ic	cytochrome <i>b/c</i> component of <i>ubiQ-cytB</i> reductase
Rv2194 <i>b. anaerob</i> Rv2392	qcrC ic cvsH	cytochrome <i>b/c</i> component of <i>ubiQ-cytB</i> reductase 3'-phosphoadenvtVlsulfate (PAPS)
Rv2194 <i>b. anaerob</i> Rv2392	qcrC ic cysH	cytochrome b/c component of ubiQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS)
Rv2194 b. anaerob Rv2392	qcrC ic cysH	 cytochrome b/c component of ubiQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase
Rv2194 <i>b. anaerob</i> Rv2392 Rv2899c	qcrC ic cysH fdhD	3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N
Rv2194 <i>b. anaerob</i> Rv2392 Rv2899c Rv2900c	qcrC ic cysH fdhD fdhF	 School and School and Schol and School and School and School and School and School and
Rv2194 <i>b. anaerob</i> Rv2392 Rv2899c Rv2900c	qcrC ic cysH fdhD fdhF	3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase
Rv2194 <i>b. anaerob</i> Rv2392 Rv2899c Rv2900c Rv1552	qcrC ic cysH fdhD fdhF frdA	 Substitute System b/c component of ubiQ-cytB reductase Si-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein
Rv2194 <i>b. anaerob</i> Rv2392 Rv2899c Rv2900c Rv1552	qcrC ic cysH fdhD fdhF frdA	 3'-phosphoadenylylsulfate (PAPS) reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molyddopterin-containing oxidore- ductase fumarate reductase flavoprotein othorit
Rv2194 <i>b. anaerob</i> Rv2392 Rv2899c Rv2900c Rv1552	qcrC ic cysH fdhD fdhF frdA	 Stochame b/c component of ubiQ-cytB reductase Si-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit
Rv2194 <i>b. anaerob</i> Rv2392 Rv2899c Rv2900c Rv1552 Rv1553	qcrC cysH fdhD fdhF frdA frdB	 Structure b/c component of ubiQ-cytB reductase S'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase iron sulphur
Rv2194 <i>b. anaerob</i> Rv2392 Rv2899c Rv2900c Rv1552 Rv1553	qcrC ic cysH fdhD fdhF frdA frdB	3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein
Rv2194 <i>b. anaerob</i> Rv2392 Rv2899c Rv2900c Rv1552 Rv1553 Rv1554	qcrC cysH fdhD fdhF frdA frdB frdC	3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor
Rv2194 <i>b. anaerob</i> Rv2392 Rv2899c Rv2900c Rv1552 Rv1553 Rv1554	qcrC ic cysH fdhD fdhF frdA frdB frdC	3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor orotain
Rv2194 b. anaerob Rv2392 Rv2899c Rv2900c Rv1552 Rv1553 Rv1554	qcrC ic cysH fdhD fdhF frdA frdB frdB frdC	3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein
Rv2194 <i>b. anaerob</i> Rv2392 Rv2899c Rv2900c Rv1552 Rv1553 Rv1554 Rv1555	qcrC cysH fdhD fdhF frdA frdB frdB frdC frdD	3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein fumarate reductase 15kD anchor
Rv2194 b. anaerob Rv2392 Rv2899c Rv2900c Rv1552 Rv1553 Rv1554 Rv1555	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD	3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein fumarate reductase 13kD anchor protein
Rv2194 <i>b. anaerob</i> Rv2392 Rv2899c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161	qcrC ic cysH fdhD fdhF frdA frdB frdB frdC frdD narG	3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein fumarate reductase α subunit
Rv2194 b. anaerob Rv2392 Rv2899c Rv1552 Rv1553 Rv1555 Rv1161 Rv1162	qcrC ic cysH fdhD fdhF frdA frdA frdC frdD narG narH	3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein fumarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase β chain
Rv2194 b. anaerob Rv2392 Rv2899c Rv2900c Rv1552 Rv1554 Rv1555 Rv1554 Rv1161 Rv1162 Rv1164	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narI	 Substitute System b/c component of ubiQ-cytB reductase Si-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein fumarate reductase ion sulphur protein fumarate reductase 15kD anchor protein nitrate reductase α subunit nitrate reductase α subunit
Rv2194 b. anaerob Rv2392 Rv2899c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1164	qcrC cysH fdhD fdhF frdA frdB frdC frdD narG narH narl narl	 Statute b/c component of ub/Q-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein fumarate reductase 13kD anchor protein nitrate reductase β chain nitrate reductase β chain nitrate reductase β chain
Rv2194 b. anaerob Rv2392 Rv2899c Rv2900c Rv1552 Rv1554 Rv1555 Rv1161 Rv1164 Rv1164 Rv1164	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narI narJ	3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein nitrate reductase α subunit nitrate reductase α subunit nitrate reductase α chain nitrate reductase β chain nitrate reductase δ chain
Rv2194 b. anaerob Rv2392 Rv2899c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1164 Rv1736c	qcrC cysH fdhD fdhF frdA frdB frdC frdD narG narH narI narJ narX	 Standard Component of ubIQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein nitrate reductase 0 subunit nitrate reductase 0 chain
Rv2194 b. anaerob Rv2392 Rv2899c Rv2900c Rv1552 Rv1553 Rv1554 Rv11655 Rv1161 Rv1164 Rv1163 Rv2164 Rv2163	qcrC cysH fdhD fdhF frdA frdB frdC frdD narG narH narH narH narX nirA	3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein fumarate reductase 15kD anchor protein fumarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase β chain nitrate reductase β chain nitrate reductase β chain nitrate reductase β chain fused nitrate reductase probable nitrate reductase pr
Rv2194 b. anaerob Rv2392 Rv2899c Rv1552 Rv1553 Rv1554 Rv1155 Rv1161 Rv1162 Rv1164 Rv1736c Rv2393	qcrC cysH fdhD fdhF frdA frdB frdC frdD narG narH narI narX nirA	3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein fumarate reductase flavoprotein fumarate reductase flavoprotein fumarate reductase flavoprotein fumarate reductase flavoprotein nitrate reductase 25kD anchor protein nitrate reductase α subunit nitrate reductase α subunit nitrate reductase α subunit nitrate reductase α chain nitrate reductase α chain fused nitrate reductase / schain fused nitrate reductase/sulphite reductase α
Rv2194 b. anaerob Rv2392 Rv2990c Rv1552 Rv1553 Rv1555 Rv1161 Rv1162 Rv1163 Rv17366 Rv17366 Rv17366 Rv2391	qcrC cysH fdhD fdhF frdA frdB frdB frdC frdD narG narH narI narJ narX nirA nirR	Si-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein fumarate reductase iron sulphur protein fumarate reductase 13kD anchor protein fumarate reductase a Subunit nitrate reductase α subunit nitrate reductase α subunit nitrate reductase α chain nitrate reductase α chain fused nitrate reductase probable nitrite reductase flavoprotein
Rv2194 b. anaerob Rv2392 Rv2899c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1163 Rv1164 Rv1736c Rv2392	qcrC cysH fdhD fdhF frdA frdB frdC frdD narG narH narI narJ narX nirA nirB	3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein fumarate reductase $13kD$ anchor protein nitrate reductase α subunit nitrate reductase α subunit nitrate reductase α subunit nitrate reductase β chain nitrate reductase β chain fused nitrate reductase β subunit fused nitrate reductase β subunit nitrate reductase β chain fused nitrate reductase flavoprotein
Rv2194 b. anaerob Rv2392 Rv2899c Rv1552 Rv1553 Rv1555 Rv1161 Rv1162 Rv1163 Rv17365 Rv2393	qcrC cysH fdhD fdhF frdA frdB frdB frdC frdD narG narH narJ narJ narX nirA nirB nirD	Si-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein 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 so probable nitrite reductase small
Rv2194 b. anaerob Rv2392 Rv2899c Rv2900c Rv1552 Rv1554 Rv1155 Rv1161 Rv1164 Rv1163 Rv1736c Rv2391 Rv0252	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narI narJ narX nirA nirB nirD	Si-based ovpochrome b/c component of ubIQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase ifavoprotein fumarate reductase ifavoprotein fumarate reductase 15kD anchor protein fumarate reductase 0 subunit nitrate reductase 0 subunit nitrate reductase 0 subunit nitrate reductase 0 chain nitrate reductase 0 chain fused nitrate reductase 0 chain fused nitrate reductase probable nitrite reductase probable nitrite reductase nitrite reductase 0 subunit fused nitrate reductase probable nitrite reductase small subunit
Rv2194 b. anaerob Rv2392 Rv2899c Rv1552 Rv1553 Rv1554 Rv1161 Rv1162 Rv1164 Rv1163 Rv1736C Rv2391 Rv0252 Rv0253	qcrC cysH fdhD fdhF frdA frdB frdC frdD narG narH narH narJ narX nirA nirB nirD	Si-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molyddopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein nitrate reductase a subunit nitrate reductase β chain nitrate reductase so chain nitrate reductase flavoprotein probable nitrite reductase small subunit
Rv2194 b. anaerob Rv2392 Rv2899c Rv1552 Rv1553 Rv1554 Rv11655 Rv1164 Rv1163 Rv2391 Rv2020c Rv1164 Rv2164 Rv2163 Rv2523 c. Electron	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narH narH narJ narX nirA transport	Si-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein fumarate reductase a Subunit nitrate reductase α subunit nitrate reductase β chain nitrate reductase β chain fused nitrate reductase probable nitrite reductase small subunit
Rv2194 b. anaerob Rv2392 Rv2899c Rv2900c Rv1552 Rv1553 Rv1554 Rv1155 Rv1161 Rv1162 Rv1163 Rv1164 Rv1736c Rv0252 Rv0253	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narJ narX nirA nirB nirD transport transport	Si-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein fumarate reductase iron sulphur protein nitrate reductase ox subunit nitrate reductase 0 schain nitrate reductase φ schain nitrate reductase φ schain nitrate reductase φ schain fused nitrate reductase probable nitrite reductase probable nitrite reductase small subunit acetate kinase
Rv2194 b. anaerob Rv2392 Rv2990c Rv1552 Rv1553 Rv1554 Rv1162 Rv1163 Rv1163 Rv17366 Rv1163 Rv17366 Rv2391 Rv0252 Rv0253 c. Electron Rv0409 Rv04920	qcrC ic cysH fdhD fdhF frdA frdB frdB frdC frdD narG narH narI narJ narJ nirA nirB nirD transport ackA	 Stochame b/c component of ub/Q-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore-ductase flavoprotein subunit fumarate reductase flavoprotein fumarate reductase iron sulphur protein fumarate reductase 13kD anchor protein nitrate reductase a subunit nitrate reductase φ chain nitrate reductase β chain nitrate reductase φ chain nitrate reductase φ chain nitrate reductase β chain η η η η η η η η η η η η η η η η η η η
Rv2194 b. anaerob Rv2392 Rv2399c Rv1552 Rv1553 Rv1554 Rv1155 Rv1161 Rv1162 Rv1163 Rv1164 Rv1736c Rv2391 Rv0252 Rv0409 Rv0409 Rv04025	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narI narJ narX nirA nirB nirD transport tackA appC	Si-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein fumarate reductase 13kD anchor protein nitrate reductase α subunit nitrate reductase α subunit nitrate reductase α subunit nitrate reductase β chain nitrate reductase β chain nitrate reductase β chain nitrate reductase β chain nitrate reductase β chain fused nitrate reductase β chain fused nitrate reductase β chain fused nitrate reductase β chain fused nitrate reductase β subunit nitrate reductase β chain fused nitrite reductase small subunit
Rv2194 b. anaerob Rv2392 Rv2899c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv17365 Rv163 Rv17365 Rv2391 Rv0252 Rv0252 Rv0269 Rv0269 Rv0269	qcrC ic cysH fdhD fdhF frdA frdB frdB frdC frdD narG narH narI narJ narJ narX nirB nirD transport ackA appC	Si-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein nitrate reductase 13kD anchor protein nitrate reductase 0 subunit nitrate reductase % chain nitrate % chain n
Rv2194 b. anaerob Rv2392 Rv2899c Rv1552 Rv1553 Rv1554 Rv1155 Rv1161 Rv1162 Rv1163 Rv1164 Rv1736c Rv0252 Rv0252 Rv0409 Rv1623cc Rv1622c	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narI narJ narX nirA nirB nirD transport tackA appC cydB	Si-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein fumarate reductase 0 subunit nitrate reductase 0 subunit fuse reductase 0 subunit fuse reductase 0 subunit fuse reductase 1 subunit fuse reductase 1 subunit fuse reductase 0 subunit fuse reductase 1 subunit subunit acetate kinase cytochrome <i>bd-ll</i> oxidase subunit 1 oytochrome <i>d</i> ubiquinol oxidase
Rv2194 b. anaerob Rv2392 Rv2899c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv17355 Rv1163 Rv17365 Rv2391 Rv0252 Rv0252 Rv0252 Rv1625c Rv1625c Rv1625c	qcrC ic cysH fdhD fdhF frdA frdB frdB frdC frdD narG narH narH narJ narK nirB nirD transport ackA appC cydB	 Standard Component of ub/Q-cytB reductase S'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore-ductase flavoprotein subunit fumarate reductase flavoprotein fumarate reductase iron sulphur protein fumarate reductase a subunit nitrate reductase 3kD anchor protein nitrate reductase y chain nitrate reductase y chain nitrate reductase y chain nitrate reductase y chain nitrate reductase b chain nitrate reductase β chain nitrate reductase y chain nitrate reductase y chain nitrate reductase glavoprotein probable nitrite reductase small subunit acetate kinase cytochrome bd-II oxidase subunit I
Rv2194 b. anaerob Rv2392 Rv2899c Rv1552 Rv1553 Rv1554 Rv1155 Rv1161 Rv1162 Rv1163 Rv1736c Rv0252 Rv0252 Rv0409 Rv162cc Rv162cc	qcrC ic cysH fdhD fdhF frdA frdB frdB frdC frdD narG narH narJ narY narX nirB nirD transport ackA appC cydB cydC	 Structure b/c component of ub/Q-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore-ductase flumarate reductase flavoprotein subunit fumarate reductase ison sulphur protein fumarate reductase 15kD anchor protein nitrate reductase 0 chain nitrate reductase β chain fused nitrate reductase subunit acetate kinase cytochrome bd-II oxidase subunit I cytochrome dubiquinol oxidase subunit I
Rv2194 b. anaerob Rv2392 Rv2899c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1163 Rv17356 Rv2392 Rv2393 c. Electron Rv1623c Rv1623c Rv1622c Rv1622c	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narH narJ narX nirA nirB nirD transport appC cydB cydC	 Standard Component of ubIQ-cytB reductase S'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore-ductase flavoprotein subunit fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein nitrate reductase 13kD anchor protein nitrate reductase 0 chain nitrate reductase 18avoprotein probable nitrite reductase small subunit
Rv2194 b. anaerob Rv2392 Rv2899c Rv1552 Rv1553 Rv1554 Rv11655 Rv1164 Rv1163 Rv2392 Rv200c Rv1164 Rv2194 Rv2155 Rv1163 Rv2523 c. Electron Rv40292 Rv1623c Rv1623c Rv1623c	qcrC ic cysH fdhD fdhF frdA frdB frdC frdC frdD narG narH narJ narX nirB nirD transport ackA appC cydB cydC cydC cydC	 Standard Component of ubiQ-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore-ductase flumarate reductase flavoprotein subunit fumarate reductase is subunit fumarate reductase is subunit nitrate reductase 15kD anchor protein nitrate reductase 0 chain nitrate reductase 1 flavoprotein probable nitrite reductase small subunit acetate kinase cytochrome bd-II oxidase subunit I ABC transporter ABC transporter
Rv2194 b. anaerob Rv2392 Rv2899c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1163 Rv17356 Rv2392 Rv2393 c. Electron Rv1623c Rv1623c Rv1623c Rv1623c Rv1623c Rv1623c Rv1623c Rv1620c Rv2007c	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narH narJ narX nirA nirB nirD transport ackA appC cydB cydC	Si-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein fumarate reductase flavoprotein fumarate reductase iron sulphur protein fumarate reductase a SkD anchor protein nitrate reductase 13kD anchor protein nitrate reductase 0 chain nitrate reductase 1 subunit nitrate reductase 1 subunit 1 ABC transporter farredoxin
Rv2194 b. anaerob Rv2392 Rv2899c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1755 Rv1163 Rv17365 Rv2391 Rv2391 Rv20252 Rv16252 Rv16252 Rv16252 Rv16253	qcrC ic cysH fdhD fdhF frdA frdB frdC frdC frdD narG narH narJ narX nirB nirD transport ackA appC cydB cydC cydC cydC fdxA	Si-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein fumarate reductase i SkD anchor protein fumarate reductase 15kD anchor protein nitrate reductase 0 chain nitrate reductase 0 chain fused nitrate reductase small subunit acetate kinase cytochrome <i>bd-II</i> oxidase subunit I ABC transporter ABC transporter ferredoxin
Rv2194 b. anaerob Rv2392 Rv2399c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv17556 Rv1162 Rv1163 Rv1736c Rv2391 Rv0252 Rv1625c Rv3554 Rv177	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narJ narJ narJ narJ narX nirB nirD transport ackA appC cydC cydC fdxA fdxA fdxA	 J-bostnae b/c component of ub/Q-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore-ductase flavoprotein subunit fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein nitrate reductase 0 subunit nitrate reductase 0 subunit nitrate reductase 0 schain nitrate reductase 18voprotein probable nitrite reductase/sulphite reductase small subunit acetate kinase cytochrome <i>du</i>-<i>ll</i> oxidase subunit II ABC transporter ABC transporter ABC transporter ABC transporter
Rv2194 b. anaerob Rv2392 Rv2899c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv17356 Rv1163 Rv17366 Rv2391 Rv0252 Rv1623c Rv162c Rv36c3c	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narJ narJ narJ narJ narJ narJ narJ cydD transport ackA appC cydD fdxA fdxB fdxC	Si-phosphoadenylylsulfate (PAPS) eductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein fumarate reductase i SkD anchor protein fumarate reductase 15kD anchor protein nitrate reductase a subunit nitrate reductase β chain nitrate reductase β chain fused nitrate reductase β chain fused nitrate reductase β chain fused nitrate reductase β chain fused nitrate reductase subunit acetate kinase cytochrome <i>bd-II</i> oxidase subunit I oytochrome <i>d</i> ubiquinol oxidase subunit II ABC transporter ABC transporter ferredoxin ferredoxin 4Fe-4S probable firzedoxin
Rv2194 b. anaerob Rv2392 Rv2399c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv17556 Rv1162 Rv17365 Rv1736c Rv0252 Rv0409 Rv162cc Rv1777 Rv3554	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narJ narX nirA nirB nirD transport ackA appC cydB cydC cydC fdxB fdxC fdxC fdxB fdxC fdxC fdxB fdxC	 Stochame b/c component of ub/Q-cytB reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore-ductase flavoprotein subunit fumarate reductase flavoprotein subunit fumarate reductase flavoprotein fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein nitrate reductase 0 chain nitrate reductase 13kD anchor probable nitrite reductase/sulphite reductase 0 chain nitrate reductase 0 chain nitrate reductase 0 chain nitrate reductase 0 chain fused nitrite reductase small subunit acetate kinase cytochrome <i>bd-ll</i> oxidase subunit II ABC transporter ABC transporter ABC transporter ferredoxin 4Fe-4S probable firedoxin affec-4S
Rv2194 b. anaerob Rv2392 Rv2392 Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv17355 Rv1163 Rv17356 Rv2391 Rv2252 Rv1623c Rv1622c Rv1622c Rv1622c Rv1622c Rv1622c Rv1622c Rv1623c Rv1623c Rv303c Rv303c Rv303c	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narI narJ narJ narX nirA nirB nirD transport ackA appC cydB cydC cydC cydC cydC fdxA fdx	 Statutation b/c component of ub/Q-cytB reductase S'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore-ductase flavoprotein subunit fumarate reductase flavoprotein fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein fumarate reductase 3 chain nitrate reductase 0 chain nitrate reductase 9 chain nitrate reductase 8 chain futare futare reductase 8 chain fused nitrate reductase subunit acetate kinase cytochrome bd-II oxidase subunit I ABC transporter ABC transporter ABC transporter ABC transporter Chain State Fredoxin ferredoxin 4Fe-4S probable foredoxin
Rv2194 b. anaerob Rv2392 Rv2399c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1655 Rv1161 Rv17355 Rv1161 Rv162 Rv1736c Rv0252 Rv0409 Rv162cc Rv1777 Rv3503c Rv1777	qcrC cysH fdhD fdhF frdA frdB frdC frdD narG narH narI narJ narX nirA nirB nirD transport tassport cydB cydC cydD fdxB fdxC fdxD fdxB fdxC fdxD	Si-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein fumarate reductase 15kD anchor protein fumarate reductase 0 shain nitrate reductase 0 shain nitrate reductase 0 shain nitrate reductase 0 shain fused nitrate reductase 13kD anchor probable nitrite reductase/sulphite reductase subunit 1 acetate kinase cytochrome <i>bd-ll</i> oxidase subunit 1 ABC transporter ABC transporter ABC transporter ferredoxin ferredoxin ferredoxin 4Fe-4S probable firedoxin electron transfer flavoprotein β subunit
Rv2194 b. anaerob Rv2392 Rv2899c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv17356 Rv1163 Rv17366 Rv2392 Rv2393 c. Electron Rv16252 Rv30254 Rv30254 Rv30254 Rv30254	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narH narH narJ narK nirB nirD transport ackA appC cydB cydC cydB fdxC fdxD fixA fixA	2)-biotechambe b/c component of <i>ubIQ-cytB</i> reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molyddopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein nitrate reductase 0 subunit nitrate reductase 1 subunit acetate kinase cytochrome <i>bd-ll</i> oxidase subunit I ABC transporter ABC transporter ABC transporter ferredoxin ferredoxin ferredoxin ferredoxin ferredoxin electron transfer flavoprotein α
Rv2194 b. anaerob Rv2392 Rv2399c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1163 Rv1164 Rv1736c Rv0252 Rv0252 Rv164 Rv162 Rv162 Rv162 Rv162 Rv1622c Rv1622c Rv1620c Rv1620c Rv1620c Rv1620c Rv3028c Rv3028c	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narI narJ narX nirA nirB nirD transport transport transport cydB cydC cydD fdxA fdxE fdxC fdxD fdxA fdxA	2) - Discrete cytochrome <i>b/c</i> component of <i>ubIQ-cytB</i> reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein fumarate reductase iron sulphur protein fumarate reductase 15kD anchor protein fumarate reductase 0 subunit nitrate reductase 0 subunit subunit subunit acetate kinase cytochrome <i>bd-ll</i> oxidase subunit I ABC transporter ABC transporter ABC transporter ABC transporter electron transfer flavoprotein α subunit
Rv2194 b. anaerob Rv2392 Rv2899c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1163 Rv17365 Rv2392 Rv2393 c. Electron Rv1623c Rv3025c Rv302c Rv302c Rv302c Rv302c Rv302c	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narH narJ narX nirA nirB nirD transport ackA appC cydB cydB fdxC fdxD fixA fixB fnxB fnxB	2)-biotecharacteristic component of <i>ubIQ-cytB</i> reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein fumarate reductase a flavo protein fumarate reductase 15kD anchor protein nitrate reductase 13kD anchor protein nitrate reductase 0 chain nitrate reductase 13kD anchor probable nitrite reductase/sulphite reductase subunit acetate kinase cytochrome <i>du</i> - <i>l</i> / oxidase subunit I ABC transporter ferredoxin ferredoxin ferredoxin ferredoxin 4Fe-4S probable ferredoxin electron transfer flavoprotein α subunit
Rv2194 b. anaerob Rv2392 Rv2399c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv1162 Rv1163 Rv1164 Rv1736c Rv0252 Rv1642c Rv162c Rv162c Rv162c Rv162cc Rv302cc Rv302cc Rv302cc Rv302cc Rv302cc Rv302cc	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narG narH narJ narJ narX nirB nirD transport ackA appC cydB cydC cydD fdxB fdxC fdxB fdxC fdxB fdxC fdxC fdxB fdxC fdxC fdxB fdxC fdxB fdxC fdxB fdxC fdxB fdxC fdxB fdxC fdxB fdxC fdxB fdxC fdxB fdxC fdxB fdxC fdxC fdxB fdxC fdxC fdxC fdxB fdxC fdxC fdxB fdxC fdxB fdxC fdxC fdxC fdxC fdxB fdxC fdxC fdxB fdxC fdxB fdxC fdxB fdxC fdxC fdxB fdxC fdxC fdxB fdxC fdxC fdxC fdxA ffxA	2) - Discrete cytochrome <i>b/c</i> component of <i>ubIQ-cytB</i> reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein fumarate reductase i SkD anchor protein fumarate reductase 15kD anchor protein nitrate reductase 0 chain nitrate reductase 0 chain nitrate reductase 0 chain nitrate reductase 0 chain fused nitrate reductase small subunit acetate kinase cytochrome <i>bd-II</i> oxidase subunit 1 oytochrome <i>du</i> biquinol oxidase subunit 1 electron transfer flavoprotein β subunit electron transfer flavoprotein α subunit adrenodoxin and NADPH ferre- dovin reductase
Rv2194 b. anaerob Rv2392 Rv2899c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv17556 Rv1162 Rv1163 Rv1736c Rv2391 Rv0252 Rv1625c Rv3025c Rv3025c Rv3025c Rv3026c Rv3026c Rv3026c	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narJ narJ narJ narX nirB nirD transport ackA appC cydC cydC fdxD fdxA fdxC fdxD fdxA fdxA fdxB fdxC fdxC fdxD fdxC fdxC fdxD fdxC fdx	Si-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein fumarate reductase a subput protein nitrate reductase 25kD anchor protein nitrate reductase 0 chain nitrate reductase 0 chain fused nitrite reductase / subunit nitrate reductase 0 chain fused nitrite reductase / subunit acetate kinase cytochrome <i>bd-ll</i> oxidase subunit I ABC transporter ABC transporter ferredoxin 4Fe-4S probable ferredoxin electron transfer flavoprotein α subunit electron transfer flavoprotein α subunit electron transfer flavoprotein α subunit
Rv2194 b. anaerob Rv2392 Rv2899c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv17356 Rv1163 Rv17356 Rv17366 Rv2393 <i>c. Electron</i> Rv1622c Rv1623c Rv1623c Rv1622c Rv1623c Rv1623c Rv3028c Rv3028c Rv3028c Rv3028c Rv3106 Rv0886	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narJ narJ narX nirB nirD transport ackA appC cydB cydC cydC fdxA fdxB fdxC fdxB fdxA fixB fprA fprB	Si-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase iron sulphur protein fumarate reductase i SkD anchor protein fumarate reductase 15kD anchor protein nitrate reductase 0 subunit nitrate reductase 0 subunit subunit acetate kinase cytochrome <i>bd-ll</i> oxidase subunit 1 cytochrome <i>bd-ll</i> oxidase subunit 1 cytochrome <i>du</i> -ll oxidase subunit 1 electron transfer flavoprotein β subunit electron transfer flavoprotein α subunit adrenodoxin and NADPH ferre- doxin reductase ferredoxin, ferredoxin-NADP
Rv2194 b. anaerob Rv2392 Rv2399c Rv1552 Rv1553 Rv1554 Rv1555 Rv1161 Rv17556 Rv1162 Rv1163 Rv1736c Rv2391 Rv0252 Rv0409 Rv162cc Rv162cc Rv162cc Rv162cc Rv3029c Rv3029c Rv3028c Rv3048	qcrC ic cysH fdhD fdhF frdA frdB frdC frdD narG narH narJ narJ narX nirA nirB nirD transport ackA appC cydB cydC cydB fdxC fdxC fdxD fdxC fdx	2) - Discrete cytochrome <i>b/c</i> component of <i>ubIQ-cytB</i> reductase 3'-phosphoadenylylsulfate (PAPS) reductase affects formate dehydrogenase-N molybdopterin-containing oxidore- ductase fumarate reductase flavoprotein subunit fumarate reductase flavoprotein fumarate reductase a subput protein nitrate reductase 0 subunit nitrate reductase 0 subunit fused nitrite reductase/sulphite reductase nitrite reductase small subunit acetate kinase cytochrome <i>bd-ll</i> oxidase subunit ABC transporter ABC transporter ABC transporter ABC transporter ferredoxin ferredoxin 4Fe-4S probable firredoxin electron transfer flavoprotein α subunit electron transfer flavoprotein α subunit

7. Miscella	neous oxio	doreductases and oxygenases 171	Rv2860C Rv2918c Bv2221c	gii gli gli
8. ATP-pro	ton motive	force	By3850c	ali
Bv1304	atpA	ATP synthase a chain	11000330	gn
Bv1311	atpC	ATP synthase ϵ chain	Bv3858c	ali
Rv1310	atpD	ATP synthase ß chain		9.
Rv1305	atpE	ATP synthase c chain	Rv3704c	gs
Rv1306	atpF	ATP synthase b chain		-
Rv1309	atpG	ATP synthase γ chain	Rv2427c	pr
Rv1307	atpH	ATP synthase δ chain	Rv2439c	pr
			Rv0500	pr
C. Central	intermedia	ary metabolism	0.4	
1. General	achT	1 aminabuturata aminatranafaraaa	2. Asparta	e ta
RV2089	gabi	4-aminobulyrate aminotransierase	RV3708C	as
Rv1832	gaub	diverse decarboxylase	By3709c	20
Bv1826	acvH	glycine cleavage system H protein	Bv2201	as
Rv2211c	qcvT	T protein of glycine cleavage	Rv3565	as
	0	system	Rv0337c	as
Rv1213	glgC	glucose-1-phosphate adenylyl-	Rv2753c	da
Rv3842c	glpQ1	transferase glycerophosphoryl diester phos-	Rv2773c Rv1202	da da
Bv0317c	alpQ2	phodiesterase glycerophosphoryl diester phos-	Bv2141c	da
Bv3566c	nho4	phodiesterase	By2726c	da
11000000	nnoA	ferase	Bv1293	Ive
Rv0155	pntAA	pyridine transhydrogenase sub-	Rv3341	m
	1	unit α1	Rv1079	m
Rv0156	pntAB	pyridine transhydrogenase sub-	Rv3340	m
		unit α2	Rv1133c	m
Rv0157	pntB	pyridine transhydrogenase		
D. 1107.		subunit β	D. 0101.	
Rv112/c	ррак	similar to pyruvate, phosphate	Rv2124c	m
		dikinase	Dv1202	m
2 Glucone	ogenesis		Bv0391	m
Rv0211	pckA	phosphoenolpyruvate carboxy-		
	,	kinase	Rv1294	th
Rv0069c	sdaA	L-serine dehydratase 1	Rv1296	th
_			Rv1295	th
3. Sugar ni	ucleotides		0. Carina f	
RV1512 Rv3784	epiA eniB	nucleolide sugar epimerase	3. Serine la By0815c	
1100704	ерів	enimerase	Bv3117	CV
Rv1511	amdA	GDP-mannose 4.6 dehydratase	Rv2335	cv
Rv0334	rmIA	glucose-1-phosphate thymidyl-	Rv0511	cy
		transferase		
Rv3264c	rmIA2	glucose-1-phosphate thymidyl-	Rv2847c	су
		transferase		
Rv3464	rmlB	dTDP-glucose 4,6-dehydratase	Rv2334	су
RV3634C	rmIB2	dTDP-glucose 4,6-denydratase	RV1336	cy
Rv3466	rmIC	dTDP-glucose 4,0-denydralase	Rv08/8	CY
1103403	111110	3 5-epimerase	Bv1093	alı
Rv3266c	rmID	dTDP-4-dehydrorhamnose	Rv0070c	gly
		reductase	Rv2996c	se
Rv0322	udgA	UDP-glucose		
		dehydrogenase/GDP-mannose 6-	Rv0505c	se
Bv3265c	wbbl	dTDP-rhamposyl transferase	By3042c	60
Rv1525	wbbL whhl2	dTDP-rhamnosyl transferase	11000420	30
Rv3400	-	probable β-phosphoglucomutase	Bv0884c	se
		h i i i h h i h i h i h i h i h i h i h		
4. Amino s	ugars		4. Aromatio	c ar
Rv3436c	glmS	glucosamine-fructose-6-	Rv3227	ar
		phosphate aminotransferase	D. 0500.	
5 Sulphur	motabolia	m	nv∠0380 By2527¢	dľ
Bv0711	atsA	arvlsulfatase	Rv2552c	an
Rv3299c	atsB	proable arvisulfatase	Rv2540c	ar
Rv0663	atsD	proable arylsulfatase	Rv2178c	ar
Rv3077	atsF	proable arylsulfatase	Rv2539c	ar
Rv0296c	atsG	proable arylsulfatase	Rv3838c	ph
Rv3796	atsH	proable arylsulfatase	Rv1613	trp
Rv1285	cysD	AI P:sulphurylase subunit 2	Rv1612	trp
RV1286	cysin	AI P:sulphurylase subunit 1	RV1611	trp
By3248c	sahH	adenosylhomocysteinase	By2192c	trr
Rv3283	sseA	thiosulfate sulfurtransferase	11020	υp
Rv2291	sseB	thiosulfate sulfurtransferase	Rv1609	trp
Rv3118	sseC	thiosulfate sulfurtransferase		
Rv0814c	sseC2	thiosulfate sulfurtransferase	Rv2386c	trp
Rv3762c	-	probable alkyl sulfatase	_	
D. Andrea	-1-1-1-1		Rv3754	tyı
D. Amino a	to formily	itnesis	E Lliotiding	
Rv1654	araR	acetylalutamate kinase	5. HISUUITE By1603	; hii
Rv1652	araC	N-acetyl-v-glutamyl-phosphate		1112
		reductase		
Rv1655	argD	acetylornithine aminotransferase	Rv1601	his
Rv1656	aroF	ornithine carbamoyltransferase		
	u.g.			la i i
Rv1658	argG	arginosuccinate synthase	Rv1600	rn:
Rv1658 Rv1659	argG argH	arginosuccinate synthase arginosuccinate lyase	Rv1600	ти: ,,
Rv1658 Rv1659 Rv1653 Bv2220	argG argH argJ alpA1	arginosuccinate synthase arginosuccinate lyase glutamate N-acetyltransferase	Rv1600 Rv3772	his
Rv1658 Rv1659 Rv1653 Rv2220 Rv2222c	argG argH argJ glnA1 alnA2	arginosuccinate synthase arginosuccinate lyase glutamate N-acetyltransferase glutamine synthase class I glutamine synthase class I	Rv1600 Rv3772 Rv1599	hi:

Rv3250c rubB

rubredoxin B

Rv1878 probable glutamine synthase alnA3 nA4 nD proable glutamine synthase uridylyltransferase glutamate-ammonia-ligase nE adenyltransferase tΒ ferredoxin-dependent glutamate synthase small subunit of NADH-dependent tD glutamate synthase :hA possible γ-glutamylcysteine synthase γ-glutamyl phosphate reductase glutamate 5-kinase оA σВ ъС pyrroline-5-carboxylate reductase amily aspartate semialdehyde dehydrosd genase sk aspartokinase asparagine synthase B snB spВ aspartate aminotransferase aspartate aminotransferase . DC арА dihydrodipicolinate synthase apB apE dihydrodipicolinate reductase succinyl-diaminopimelate desuccinylase ArgE/DapE/Acy1/Cpg2/yscS apE2 family diaminopimelate epimerase apF sA diaminopimelate decarboxylase homoserine o-acetyltransferase cystathionine γ -synthase cystathionine β -lyase etA etB ətC 5-methyltetrahydropteroyltriglutaetE mate-homocysteine methyltransferase 5-methyltetrahydrofolate-homoetH cysteine methyltransferase S-adenosylmethionine synthase etK etZ o-succinylhomoserine sulfhydrvlase homoserine dehydrogenase rA rВ homoserine kinase rC homoserine synthase ily /sA2 /sA3 thiosulfate sulfurtransferase thiosulfate sulfurtransferase νsΕ serine acetyltransferase 'sG uroporphyrin-III c-methyltransferase multifunctional enzyme, siroheme sG2 svnthase cysteine synthase A sK cysteine synthase B cystathionine β -synthase 'sM sM2 sM3 putative cysteine synthase serine hydroxymethyltransferase /A /A2 serine hydroxymethyltransferase . erA D-3-phosphoglycerate dehydrogenase erΒ probable phosphoserine phos-. phatase C-term similar to phosphoserine ərB2 phosphatase rC phosphoserine aminotransferase nino acid family 3-phosphoshikimate 1-carboxyvinyl transferase 'nΑ 'nΒ 3-dehydroquinate synthase 3-dehydroquinate dehydratase оD οE οF shikimate 5-dehydrogenase chorismate synthase roG roK heA DAHP synthase shikimate kinase I prephenate dehydratase tryptophan synthase α chain tryptophan synthase β chain oA oB С indole-3-glycerol phosphate synthase anthranilate phosphoribosyltransэD ferase anthranilate synthase ЪЕ component I anthranilate synthase bE2 component I prephenate dehydrogenase rΑ phosphoribosylformimino-5sA aminoimidazole carboxamide ribonucleotide isomerase sВ imidazole glycerol-phosphate dehvdratase sC histidinol-phosphate aminotransferase sC2 histidinol-phosphate aminotransferase sD histidinol dehydrogenase

Rv1605	hisF	imidazole glycerol-phosphate
Rv2121c	hisG	synthase ATP phosphoribosyltransferase
Rv1602	hisH	amidotransferase
Rv2122c	hisi	phosphoribosyl-AMP cyclohydro- lase
Rv1606	hisl2	probable phosphoribosyl-AMP 1,6
Rv0114	-	similar to HisB
6. Pyruvate Rv3423c	alr	alanine racemase
7. Branche Rv1559	d amino a <i>ilvA</i>	threonine deaminase
Rv3003c	ilvB	acetolactate synthase I large sub-
Rv3470c	ilvB2	unit acetolactate synthase large sub-
		unit
Rv3001c Bv0189c	ilvC ilvD	ketol-acid reductoisomerase dihydroxy-acid dehydratase
Rv2210c	ilvE	branched-chain-amino-acid
Bv1820	ilvG	transaminase acetolactate synthase II
Rv3002c	ilvN	acetolactate synthase I small sub-
Bv3509c	ilvX	unit probable acetohydroxyacid syn-
		thase I large subunit
Rv3710 Bv2995c	leuA leuB	α-isopropyl malate synthase
Rv2988c	leuC	3-isopropylmalate dehydratase
Bv2987c	leuD	large subunit 3-isopropylmalate debydratase
11023070	lead	small subunit
E Polvami	ina svntha	sis
Rv2601	speE	spermidine synthase
E Durinoc	nyrimidin	as nucleosides and nucleotides
1. Purine r	ibonucleot	ide biosynthesis
Rv1389	gmk	putative guanylate kinase
Rv33960 Rv1843c	guaA auaB1	inosine-5'-monophosphate dehv-
		drogenase
Rv3411c	guaB2	inosine-5'-monophosphate dehy- drogenase
Rv3410c	guaB3	inosine-5'-monophosphate dehy-
Bv1017c	nrsA	drogenase ribose-phosphate pyrophosphoki-
	pron	inpose buogbuate bytobuogbuott
		nase
Rv0357c	purA purB	nase adenylosuccinate synthase
Rv0357c Rv0777 Rv0780	purA purB purC	nase adenylosuccinate synthase adenylosuccinate lyase phosphoribosylaminoimidazole-
Rv0357c Rv0777 Rv0780	purA purB purC	nase adenylosuccinate synthase adenylosuccinate lyase phosphoribosylaminoimidazole- succinocarboxamide synthase phosphoribosylamine dhoine lin
Rv0357c Rv0777 Rv0780 Rv0772	purA purB purC purD	nase adenylosuccinate synthase adenylosuccinate lyase phosphoribosylaminoimidazole- succinocarboxamide synthase phosphoribosylamine-glycine lig- ase
Rv0357c Rv0777 Rv0780 Rv0772 Rv3275c	purA purB purC purD purE	nase adenylosuccinate synthase adenylosuccinate lyase phosphoribosylaminoimidazole- succinocarboxamide synthase phosphoribosylamino-glycine lig- ase phosphoribosylaminoimidazole carboxulase
Rv0357c Rv0777 Rv0780 Rv0772 Rv3275c Rv0808	purA purB purC purD purE purF	nase adenylosuccinate synthase adenylosuccinate lyase phosphoribosylaminoimidazole- succinocarboxamide synthase phosphoribosylamino-glycine lig- ase phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase-
Rv0357c Rv0777 Rv0780 Rv0772 Rv3275c Rv0808 Rv0957	purA purB purC purD purE purF purH	nase adenylosuccinate synthase adenylosuccinate lyase phosphoribosylaminoimidazole- succinocarboxamide synthase phosphoribosylamino-glycine lig- ase phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase- phosphoribosylaminoimidazole- oraboxymic formytransferase
Rv0357c Rv0777 Rv0780 Rv0772 Rv3275c Rv0808 Rv0957 Rv3276c	purA purB purC purD purE purF purH purK	nase adenylosuccinate synthase adenylosuccinate lyase phosphoribosylaminoimidazole- succinocarboxamide synthase phosphoribosylamino-glycine lig- ase phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase- phosphoribosylaminoimidazole- carboxamide formyltransferase phosphoribosylaminoimidazole
Rv0357c Rv0777 Rv0780 Rv0772 Rv3275c Rv0808 Rv0957 Rv3276c	purA purB purC purD purE purF purH purK	nase adenylosuccinate synthase adenylosuccinate lyase phosphoribosylaminoimidazole- succinocarboxamide synthase phosphoribosylamino-glycine lig- ase phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase- phosphoribosylaminoimidazole- carboxylase ATPase subunit
Rv0357c Rv0777 Rv0780 Rv0772 Rv3275c Rv0808 Rv0957 Rv3276c Rv0803	purA purB purC purD purE purF purH purK purL	nase adenylosuccinate synthase adenylosuccinate lyase phosphoribosylaminoimidazole- succinocarboxamide synthase phosphoribosylamino-glycine lig- ase phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase- phosphoribosylaminoimidazole- carboxylase ATPase subunit phosphoribosylformylglycin- amidine synthase II
Rv0357c Rv0777 Rv0780 Rv3275c Rv0808 Rv0957 Rv3276c Rv0803 Rv0803	purA purB purC purD purE purH purH purK purL purM	nase adenylosuccinate synthase adenylosuccinate lyase phosphoribosylaminoimidazole- succinocarboxamide synthase phosphoribosylamino-glycine lig- ase phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase- phosphoribosylaminoimidazole- carboxylase ATPase subunit phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycin- amidine synthase II 5'-phosphoribosyl-5-aminoimida-
Rv0357c Rv0777 Rv0772 Rv3275c Rv3275c Rv0808 Rv0957 Rv3276c Rv0803 Rv0809 Rv0809	purA purB purC purD purF purH purH purK purL purL	nase adenylosuccinate synthase adenylosuccinate lyase phosphoribosylaminoimidazole- succinocarboxamide synthase phosphoribosylamino-glycine lig- ase phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase- phosphoribosylaminoimidazole- carboxylase ATPase subunit phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycin- amidine synthase II 5'-phosphoribosyl-5-aminoimida- zole synthase
Rv0357c Rv0777 Rv0780 Rv072 Rv3275c Rv0808 Rv0957 Rv0803 Rv0809 Rv0805 Rv0805	purA purB purC purD purE purF purH purK purL purM	nase adenylosuccinate synthase adenylosuccinate lyase phosphoribosylaminoimidazole- succinocarboxamide synthase phosphoribosylamino-glycine lig- ase phosphoribosylaminoimidazole carboxylase amidophosphoribosylaminoimidazole- carboxylase forsphoribosylaminoimidazole- carboxylase ATPase subunit phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycin- amidine synthase II 5'-phosphoribosyl-5-aminoimida- zole synthase phosphoribosylglycinamide formyltransferase I
Rv0357c Rv0777 Rv0780 Rv0722 Rv3275c Rv0808 Rv0957 Rv0803 Rv0809 Rv08956 Rv0788	purA purB purC purD purE purF purH purK purL purM purN purQ	nase adenylosuccinate synthase adenylosuccinate lyase phosphoribosylaminoimidazole- succinocarboxamide synthase phosphoribosylamino-glycine lig- ase phosphoribosylaminoimidazole carboxylase amidophosphoribosylaminoimidazole carboxylase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycin- amidine synthase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase I phosphoribosylformylglycin- amidine synthase I
Rv0357c Rv0777 Rv0780 Rv3275c Rv3275c Rv3276c Rv0803 Rv0803 Rv0803 Rv08956 Rv0788 Rv0389	purA purB purC purD purE purF purH purK purL purM purN purQ purT	nase adenylosuccinate synthase adenylosuccinate lyase phosphoribosylaminoimidazole- succinocarboxamide synthase phosphoribosylamino-glycine lig- ase phosphoribosylaminoimidazole carboxylase amidophosphoribosylaminoimidazole carboxylase phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosyl5-aminoimida- zole synthase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide phosphoribosylglycinamide phosphoribosylglycinamide
Rv0357c Rv0777 Rv3275c Rv3275c Rv3276c Rv0957 Rv3276c Rv0956 Rv0956 Rv0380 Rv0956 Rv0380 Rv0380	purA purB purC purD purF purH purK purK purK purK purN purQ purQ purT	nase adenylosuccinate synthase adenylosuccinate lyase phosphoribosylaminoimidazole- succinocarboxamide synthase phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase- phosphoribosylaminoimidazole carboxyase ATPase subunit phosphoribosylaminoimidazole carboxyase ATPase subunit phosphoribosylarinoimidazole carboxylase ATPase subunit phosphoribosylformylglycin- amidine synthase II 5'-phosphoribosylfycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II phosphoribosylglycinamide formyltransferase II phosphoribosylglycinamide formyltransferase II phosphoribosylglycinamide formyltransferase II
Rv0357c Rv0777 Rv0780 Rv3275c Rv3275c Rv3276c Rv0803 Rv0803 Rv0809 Rv0956 Rv0956 Rv0788 Rv0389 Rv2964	purA purB purC purD purF purH purH purK purK purL purM purN purQ purT purU	nase adenylosuccinate synthase adenylosuccinate lyase phosphoribosylaminoimidazole- succinocarboxamide synthase phosphoribosylamine-glycine lig- ase phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase- phosphoribosylaminoimidazole carboxyase ATPase subunit phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylglycin- amidine synthase II 5'-phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II phosphoribosylglycinamide formyltransferase II formyltansferase II formyltansferase II formyltansferase II formyltansferase II formyltansferase II formyltansferase II formyltansferase II
Rv0357c Rv0777 Rv0772 Rv3275c Rv3275c Rv3276c Rv0803 Rv0803 Rv0803 Rv0956 Rv0956 Rv0788 Rv0389 Rv2964	purA purB purC purD purF purH purK purK purK purK purN purN purQ purT purU	nase adenylosuccinate synthase adenylosuccinate lyase phosphoribosylaminoimidazole- succinocarboxamide synthase phosphoribosylamine-glycine lig- ase phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase- phosphoribosylaminoimidazole carboxyase ATPase subunit phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylarinoimidazole carboxylase ATPase subunit phosphoribosylsylayicin- amidine synthase II 5'-phosphoribosyl5-aminoimida- zole synthase phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II formyltansferase II formyltarsferase II
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Rv0357c Rv0777 Rv0772 Rv3275c Rv3275c Rv3276c Rv0803 Rv0803 Rv0803 Rv0956 Rv0956 Rv0788 Rv0389 Rv2964 2. Pyrimidi Rv1384	purA purB purD purE purF purH purK purK purK purK purK purK purV purV purQ purT purU carA	nase adenylosuccinate synthase adenylosuccinate lyase phosphoribosylaminoimidazole- succinocarboxamide synthase phosphoribosylamine-glycine lig- ase phosphoribosylaminoimidazole carboxylase amidophosphoribosyltransferase- phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycin- amidine synthase II 5'-phosphoribosylformylglycin- amidine synthase II phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltransferase II formyltansferase II formyltansferase II formyltansferase II formyltansferase II formyltansferase II formyltatetrahydrofolate deformy- lase
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Rv0357c Rv0777 Rv0778 Rv0780 Rv3275c Rv3275c Rv0808 Rv0957 Rv0803 Rv0809 Rv0809 Rv0956 Rv0788 Rv0389 Rv0788 Rv0389 Rv2964 2. Pyrimidi Rv1383 Rv1384 Rv1381 Rv2139 Rv2385	purA purB purC purE purF purH purK purK purL purM purN purQ purT purU me ribonuc carA pyrC pyrC pyrC pyrC pyrF	nase adenylosuccinate synthase adenylosuccinate lyase phosphoribosylamine-glycine lig- ase phosphoribosylamine-glycine lig- ase phosphoribosylamine-glycine lig- ase amidophosphoribosyltransferase- phosphoribosylaminoimidazole carboxylase ATPase subunit phosphoribosylformylglycin- amidine synthase II 5-phosphoribosylformylglycin- amidine synthase II 5-phosphoribosylformylglycin- amidine synthase II 5-phosphoribosylformylglycin- amidine synthase II 5-phosphoribosylformylglycin- amidine synthase II phosphoribosylformylglycin- amidine synthase I phosphoribosylformylglycin- amidine synthase I phosphoribosylformylglycin- amidine synthase I phosphoribosylformylglycin- amidine synthase subunit carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxy- lase
Rv0357c Rv0777 Rv0778 Rv0780 Rv3275c Rv3275c Rv0808 Rv0957 Rv0803 Rv0809 Rv0809 Rv0956 Rv0389 Rv0389 Rv2964 2. Pyrimidi Rv1383 Rv1381 Rv1381 Rv2139 Rv1385 Rv2139 Rv2139	purA purB purC purE purF purH purH purK purL purM purN purQ purT purU carA purU carB pyrC pyrC pyrC pyrF pyrG	nase adenylosuccinate synthase adenylosuccinate lyase phosphoribosylamine-glycine lig- ase phosphoribosylamine-glycine lig- ase phosphoribosylamine-glycine lig- ase phosphoribosylamine/glycine amidophosphoribosyltransferase- phosphoribosylamine/midazole carboxylase ATPase subunit phosphoribosylformylglycin- amidine synthase II 5'-phosphoribosylformylglycin- amidine synthase II 5'-phosphoribosylformylglycin- amidine synthase II 5'-phosphoribosylformylglycin- amidine synthase II phosphoribosylformylglycin- amidine synthase I phosphoribosylformylglycin- amidine synthase I phosphoribosylformylglycin- amidine synthase I phosphoribosylformylglycin- amidine synthase I phosphoribosylformylglycin- amidine synthase synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxy- lase CTP synthase
Rv0357c Rv0777 Rv0778 Rv0780 Rv0722 Rv3275c Rv0808 Rv0957 Rv0803 Rv0809 Rv0809 Rv0956 Rv0389 Rv0389 Rv2964 2. Pyrimidi Rv1383 Rv1384 Rv1380 Rv1385 Rv1399 Rv2883c	purA purB purC purE purF purH purH purK purL purM purN purQ purT purU carA carB pyrC pyrC pyrF pyrF pyrF pyrF	nase adenylosuccinate synthase adenylosuccinate lyase phosphoribosylamine-glycine lig- ase phosphoribosylamine-glycine lig- ase phosphoribosylamine-glycine lig- ase phosphoribosylamine-glycine lig- ase phosphoribosylaminemidazole carboxylase amidophosphoribosyltransferase- phosphoribosylaminemidazole carboxylase ATPase subunit phosphoribosylformylglycin- amidine synthase II 5'-phosphoribosylformylglycin- amidine synthase II 5'-phosphoribosylformylglycin- amidine synthase II phosphoribosylformylglycin- amidine synthase I phosphoribosylformylglycin- amidine synthase I phosphoribosylformylglycin- amidine synthase I phosphoribosylformylglycin- amidine synthase I phosphoribosylformylglycin- amidine synthase I phosphoribosylformylglycin- amidine synthase synthase subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxy- lase CTP synthase uridylate kinase
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Rv0357c Rv0777 Rv0778 Rv0772 Rv3275c Rv3275c Rv0808 Rv0957 Rv0809 Rv0809 Rv0809 Rv0809 Rv0956 Rv0389 Rv0389 Rv2964 2. Pyrimidi Rv1383 Rv1384 Rv1380 Rv1381 Rv1383 Rv1385 Rv1385 Rv2883c Rv0382c	purA purB purC purE purF purH purH purK purL purM purN purQ purT purU carB pyrC pyrD pyrF pyrF pyrF pyrF pyrF	nase adenylosuccinate synthase adenylosuccinate lyase phosphoribosylamine-glycine lig- ase phosphoribosylamine-glycine lig- ase phosphoribosylamine-glycine lig- ase phosphoribosylamine-glycine lig- ase phosphoribosylamine-glycine lig- ase phosphoribosylamine-glycine amidophosphoribosylamine phosphoribosylamine phosphoribosylamine phosphoribosylamine phosphoribosylformylglycin- amidine synthase II 5'-phosphoribosylformylglycin- amidine synthase phosphoribosylformylglycin- amidine synthase II formyltransferase I phosphoribosylformylglycin- amidine synthase I phosphoribosylformylglycin- amidine synthase I phosphoribosylformylglycin- amidine synthase I phosphoribosylformylglycin- amidine synthase I formyltransferase I formyltransferase I formyltransferase I formyltarsferase I subunit carbamoyl-phosphate synthase subunit aspartate carbamoyltransferase dihydroorotase dihydroorotate dehydrogenase orotidine 5'-phosphate decarboxy- lase CTP synthase probable uridine 5'-monophos- phate synthase
Rv0357c Rv0777 Rv0778 Rv0772 Rv3275c Rv3275c Rv3276c Rv0808 Rv0809 Rv0809 Rv0809 Rv0809 Rv0956 Rv0389 Rv2964 2. Pyrimidi Rv1380 Rv1384 Rv1380 Rv1381 Rv1383 Rv1385 Rv1385 Rv2883c Rv0382c	purA purB purC purE purF purH purH purK purL purM purQ purV purQ purT purU carB pyrC pyrD pyrF pyrF pyrF pyrF pyrF pyrF pyrF pyrF	nase adenylosuccinate synthase adenylosuccinate lyase phosphoribosylamine-glycine lig- ase phosphoribosylamine-glycine lig- ase phosphoribosylamine-glycine lig- ase phosphoribosylamine-glycine lig- ase phosphoribosylamine-glycine lig- ase phosphoribosylaminoimidazole carboxamide formyltransferase phosphoribosylaminoimidazole carboxamide formyltransferase phosphoribosylformylglycin- amidine synthase II 5'-phosphoribosylformylglycin- amidine synthase II 5'-phosphoribosylformylglycin- amidine synthase I phosphoribosylformylglycin- amidine synthase I phosphoribosylformylglycin- amidine synthase I phosphoribosylformylglycin- amidine synthase I phosphoribosylformylglycin- amidite synthase I phosphoribosylformylglycin- amidite synthase I phosphoribosylformylglycin- amidite synthase I phosphoribosylformylglycin- amidite synthase synthase subunit carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit carbamoyl-phosphate decarboxy- lase CTP synthase probable uridine 5'-monophos- phate synthase
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Rv0357c Rv0777 Rv0777 Rv0772 Rv3275c Rv0803 Rv0957 Rv0803 Rv0803 Rv0804 Rv0956 Rv0389 Rv2964 2. Pyrimidi Rv1380 Rv1384 Rv1385 Rv1386 Rv1387 Rv1388 Rv1388 Rv1388 Rv1388 Rv2883c Rv0321 Rv2697c Rv2697c	purA purB purC purE purF purH purK purL purM purN purQ purT purU me ribonuc carA pyrB pyrC pyrB pyrC pyrB pyrC pyrB pyrC pyrH umpA	nase adenylosuccinate synthase adenylosuccinate lyase phosphoribosylamine-glycine lig- ase phosphoribosylamine-glycine lig- ase phosphoribosylamine-glycine lig- ase phosphoribosylamine-glycine lig- ase amidophosphoribosyltransferase- phosphoribosylaminoimidazole carboxyanide formyltransferase phosphoribosylaminoimidazole carboxyalae ATPase subunit phosphoribosylformylglycin- amidine synthase II 5'-phosphoribosylformylglycin- amidine synthase II 5'-phosphoribosylformylglycin- amidine synthase II phosphoribosylformylglycin- amidine synthase I phosphoribosylformylglycin- amidine synthase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltetrahydrofolate deformy- lase leotide biosynthesis carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit carbamoyl-phosphate decarboxy- lase CTP synthase probable uridine 5'-monophos- phate synthase probable uridine 5'-monophos- phate synthase tide metabolism deoxycytidine triphosphate deaxinase deoxyuridine triphosphate deaxinase deoxyuridine triphosphate deaxinase deoxyuridine triphosphates ribonucleoside-diphosphate ribonucleoside-diphosphate
Rv0357c Rv0777 Rv0777 Rv0772 Rv3275c Rv0803 Rv0957 Rv0803 Rv0803 Rv0803 Rv0803 Rv0956 Rv0778 Rv0956 Rv0788 Rv2964 2. Pyrimidi Rv1380 Rv1380 Rv1380 Rv1381 Rv2139 Rv2883c Rv03821 3. 2'-deoxy Rv2697c Rv20321c	purA purB purC purE purF purH purH purK purL purM purQ purT purQ purT purQ carB pyrC pyrD pyrF pyrF pyrF pyrF pyrF pyrF pyrF pyrF	nase adenylosuccinate synthase adenylosuccinate lyase phosphoribosylamine-glycine lig- ase phosphoribosylamine-glycine lig- ase phosphoribosylamine-glycine lig- ase phosphoribosylamine-glycine lig- ase amidophosphoribosyltransferase- phosphoribosylaminoimidazole carboxyanide formyltransferase phosphoribosylaminoimidazole carboxyanide formyltransferase phosphoribosylformylglycin- amidine synthase II 5'-phosphoribosylformylglycin- amidine synthase II 5'-phosphoribosylformylglycin- amidine synthase phosphoribosylformylglycin- amidine synthase I phosphoribosylformylglycin- amidine synthase I phosphoribosylglycinamide formyltransferase I phosphoribosylglycinamide formyltetrahydrofolate deformy- lase leotide biosynthesis carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit carbamoyl-phosphate synthase subunit carbamoyl-phosphate decarboxy- lase CTP synthase probable uridine 5'-monophos- phate synthase tide metabolism deoxycytidine triphosphate deaxinase deoxyuridine triphosphate ribonucleoside-diphosphate reductase B2 (eukaryotic-like) ribonucleoside diphosphate

Rv3048c	nrdG	subunit ribonucleoside-diphosphate small	Rv311
Rv3053c	nrdH	subunit glutaredoxin electron transport	Rv086
		component of NrdEF system	
Rv3052c	nrdl	Nrdl/YgaO/YmaA family	Rv332
Rv3247c	tmk	thymidylate kinase	D 000
Rv2/64c	thyA	thymidylate synthase	Rv099
Rv0570	nrdZ	ribonucleotide reductase, class II	Rv311
Rv3752c	-	probable cytidine/deoxycytidylate	Rv233
		deaminase	Rv168
			Rv135
4. Salvage	of nucleo	sides and nucleotides	Rv320
RV3313C	add	probable adenosine deaminase	D. 000
RV2584C	apt	adenine phosphoribosyltrans-	HV086
D. OOM F.		terases	5 D.
RV3315C	caa	probable cytidine deaminase	5. Par
RV3314C	deoA	tnymidine phosphorylase	RV105
RV0478	aeoC	deoxyribose-phosphate aldolase	RVZZZ
RV3307	aeoD	probable purine nucleoside phos-	Dunce
D: 0004a	h m t	priorylase	RV300
NV30240	πρι	probable hypoxaninine-guarine	nv300
D.2202	iunU		6 Dur
NV3393	IUIIII	probable mosilie-unume	D. Fyi
DUCEDE		pheterning nucleoside hydrolase	
RV0535	prip	family 0	
D. 0000 a		tamily 2	7 D
RV3309C	upp	uracii prioprioribosyltransierase	7. Pyr
		lesside /	RV159
5. Miscella	neous nuc		RV155
RV0733	auk	CTD hinding protein of Fre/ThdE	RVISS
RV2364C	Dex	GIP-binding protein of Era/IndF	Diate
D. 1710		tamily	RV042
RV1712	стк	cytidylate kinase	
Rv2344c	dgt	probable deoxyguanosine	
B <i>a i a i</i>		triphosphate hydrolase	8. Thi
Rv2404c	IepA	GTP-binding protein LepA	Rv042
Rv2/2/c	miaA	tRNA 8(2)-isopentenylpyrophos-	Rv041
D. O.L.		phate transferase	D. O.
RV2445C	пака	nucleoside dipnosphate kinase	RV04
RV2440C	obg	Obg GTP-binding protein	D. 007
RV2583C	reiA	(p)ppGpp synthase I	RV297
C Discust		fasters susstingting and	
G. BIOSYIII	nesis oi co	naciors, prosinetic groups and	
1 Diotin			9. DU
Du1569	high	adapagulmathianing 8 aming 7	Dv141
RV1568	DIDA	adenosymethionine-8-amino-7-	RV14
Dv1500	hisD	biolin ourthage	DV141
RV1589	DIOB	DIOTIN SYNTASE	RV20/
BV1570			80278
D (500	DIOD	det liobiotini synthase	
Rv1569	bioF	8-amino-7-oxononanoate	Rv140
Rv1569	bioF	8-amino-7-oxononanoate synthase	Rv140 Rv141
Rv1569 Rv0032	bioF bioF2	8-amino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i>	Rv140 Rv141 Rv330
Rv1569 Rv0032	bioF bioF2	8-amino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF	Rv140 Rv141 Rv330
Rv1569 Rv0032 Rv3279c	bioF2 birA	S-amino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF biotin apo-protein ligase biotin ago-protein ligase	Rv140 Rv141 Rv330
Rv1569 Rv0032 Rv3279c Rv1442	bioF2 birA bisC	S-amino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF biotin apo-protein ligase biotin sulfoxide reductase	Rv140 Rv141 Rv330
Rv1569 Rv0032 Rv3279c Rv1442 Rv0089	bioF2 bioF2 birA bisC	S-amino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF biotin apo-protein ligase biotin sulfoxide reductase possible <i>bioC</i> biotin synthesis	Rv140 Rv141 Rv330 10. Th Rv077
Rv1569 Rv0032 Rv3279c Rv1442 Rv0089	bioF bioF2 birA bisC	Samino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF biotin apo-protein ligase biotin sulfoxide reductase possible <i>bioC</i> biotin synthesis gene	10. Tr Rv077 Rv239
Rv1569 Rv0032 Rv3279c Rv1442 Rv0089	bioF bioF2 birA bisC -	Samino-T-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF biotin apo-protein ligase biotin sulfoxide reductase possible <i>bioC</i> biotin synthesis gene	10. Tr Rv077 Rv239
Rv1569 Rv0032 Rv3279c Rv1442 Rv0089 2. Folic aci	bioF bioF2 birA bisC -	s-amino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF biotin apo-protein ligase biotin sulfoxide reductase possible <i>bioC</i> biotin synthesis gene	Rv140 Rv141 Rv330 10. Th Rv077 Rv239 Rv285
Rv1569 Rv0032 Rv3279c Rv1442 Rv0089 2. Folic aci Rv2763c Rv2763c	bioF bioF2 birA bisC - d dfrA	A-amino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF biotin apo-protein ligase biotin sulfoxide reductase possible <i>bioC</i> biotin synthesis gene	Rv140 Rv141 Rv330 10. Th Rv077 Rv239 Rv285 Rv081 Rv140
Rv1569 Rv0032 Rv3279c Rv1442 Rv0089 2. Folic aci Rv2763c Rv2763c Rv247c	bioF bioF2 birA bisC - d dfrA folC	deinioolain syntasse 8-amino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF biotin apo-protein ligase biotin sulfoxide reductase possible <i>bioC</i> biotin synthesis gene dihydrofolate reductase folylpolyglutamate synthase mathularottarba vidrolate dabu	Rv140 Rv141 Rv330 10. Th Rv077 Rv235 Rv285 Rv081 Rv147
Rv1569 Rv0032 Rv3279c Rv1442 Rv0089 2. Folic aci Rv2763c Rv2447c Rv3356c	bioF bioF2 birA bisC - d dfrA folC folD	demotodant synthase 8-amino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF biotin sufoxide reductase possible <i>bioC</i> biotin synthesis gene dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- dragemore	Rv140 Rv141 Rv330 10. Th Rv077 Rv235 Rv235 Rv285 Rv081 Rv147 Rv147 Rv147
Rv1569 Rv0032 Rv3279c Rv1442 Rv0089 2. Folic aci Rv2763c Rv2447c Rv3356c	bioD bioF bioF2 birA bisC - d dfrA folC folD	deinolocim syntasie 8-amino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF biotin apo-protein ligase biotin sulfoxide reductase possible <i>bioC</i> biotin synthesis gene dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase CTD exclusionaria	Rv144 Rv141 Rv330 10. Tr Rv077 Rv235 Rv285 Rv081 Rv147 Rv147 Rv147 Rv147
Rv1569 Rv0032 Rv3279c Rv1442 Rv0089 2. Folic aci Rv2763c Rv2447c Rv3356c Rv3609c Rv3609c	bioD bioF bioF2 birA bisC - d dfrA folC folD folE	deinioolain syntasie 8-amino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF biotin apo-protein ligase biotin sulfoxide reductase possible <i>bioC</i> biotin synthesis gene dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I S. e dihude & bidrewemathylateria	Rv14(Rv141 Rv330 10. Th Rv077 Rv235 Rv085 Rv085 Rv081 Rv147 Rv147 Rv147 Rv391
Rv1569 Rv0032 Rv3279c Rv1442 Rv0089 2. Folic aci Rv2763c Rv247c Rv3356c Rv3609c Rv3609c	bioD bioF bioF2 birA bisC - d dfrA folC folD folE folK	deimolocim synthase 8-amino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF biotin sufoxide reductase possible <i>bioC</i> biotin synthesis gene dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin werobroeb chiocoe	Rv14(Rv141 Rv33(10. Th Rv077 Rv239 Rv239 Rv147 Rv147 Rv147 Rv147 Rv147 Rv141 Rv391
Rv1569 Rv0032 Rv3279c Rv1442 Rv0089 2. Folic aci Rv2763c Rv2447c Rv3356c Rv3609c Rv3609c Rv3606c	bioF bioF2 birA bisC - d dfrA folC folD folE folK folR	demotodam synthase 8-amino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF biotin apo-protein ligase biotin sulfoxide reductase possible <i>bioC</i> biotin synthesis gene dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase	Rv14(Rv141 Rv330 10. Th Rv077 Rv235 Rv081 Rv147 Rv391 Rv391 Rv391 11. M
Rv1569 Rv0032 Rv3279c Rv1442 Rv0089 2. Folic aci Rv2763c Rv2763c Rv2447c Rv3356c Rv3609c Rv3609c Rv3609c	bioF bioF2 birA bisC - d dfrA foIC foID foIE foIK foIP foIP2	deinioolain syntase 8-amino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF biotin apo-protein ligase biotin sulfoxide reductase possible <i>bioC</i> biotin synthesis gene dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase	Rv14(Rv141 Rv33(10. Tr Rv235 Rv285 Rv285 Rv285 Rv285 Rv147 Rv147 Rv147 Rv391 11. M terper Rv295
Rv1569 Rv0032 Rv3279c Rv1442 Rv0089 2. Folic aci Rv2763c Rv247c Rv2447c Rv24356c Rv2409c Rv3609c Rv3609c Rv1609c Rv1609c	bioF bioF2 birA bisC - d dfrA foIC foID foIE foIK foIP foIP2 foIY	dihydrofolate reductase folylpolyglutamate synthase dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase methylenetetra synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase may be involved in folta bioeyn-	Rv14(Rv141 Rv33(10. Tř Rv077 Rv235 Rv081 Rv147 Rv147 Rv147 Rv147 Rv391 Rv391 11. M terper Rv265
Rv1569 Rv0032 Rv3279c Rv1442 Rv0089 2. Folic aci Rv2763c Rv2447c Rv3556c Rv3606c Rv3606c Rv3606c Rv3606c Rv3606c Rv3606c	bioF bioF2 birA bisC - d dfrA foIC foID foIE foIK foIP2 foIX	dinydrofolate reductase folylpolyglutamate synthase dihydrofolate reductase possible <i>bioC</i> biotin synthesis gene dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase may be involved in folate biosyn- thasis	Rv14(Rv141 Rv33(10. Tr Rv077 Rv285 Rv085 Rv147 Rv391 Rv391 11. M terper Rv265 Rv265
Rv1569 Rv0032 Rv3279c Rv1442 Rv0089 2. Folic aci Rv2763c Rv2447c Rv3609c Rv3609c Rv3609c Rv3609c Rv3609c Rv3609c Rv3609c Rv3609c Rv3607c Rv3607c	bioF bioF2 birA bisC - d dfrA folC folD folE folP2 folP2 folP2 folX pach4	demotodani syntase S-amino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF biotin apo-protein ligase biotin sulfoxide reductase possible <i>bioC</i> biotin synthesis gene dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosyn- thesis	Rv14(Rv14(Rv14) Rv33(Rv23) Rv235 Rv081 Rv147 Rv147 Rv391 11. M terper Rv268 Rv056
Rv1569 Rv0032 Rv3279c Rv1442 Rv0089 2. Folic aci Rv247c Rv3356c Rv3609c Rv3609c Rv3609c Rv3609c Rv3609c Rv3609c Rv3609c Rv3609c Rv3607c Rv3607c Rv0013	bioF bioF2 birA bisC - - d dfrA folC folD folE folK folP2 folY2 folX pabA	demotodan synthase 8-amino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF biotin apo-protein ligase biotin sulfoxide reductase possible <i>bioC</i> biotin synthesis gene dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosyn- thesis <i>p</i> -aminobenzoate synthase gluta- ping amictorate synthase	Rv14(Rv141 Rv33() 10. Th Rv077 Rv235 Rv081 Rv147 Rv147 Rv391 11. M terper Rv266 Rv056
Rv1569 Rv0032 Rv279c Rv1442 2. Folic aci Rv2763c Rv247c Rv356c Rv3506c Rv3609c Rv3608c Rv1207 Rv3607c Rv0013 Rv1055c	bioF bioF2 bioF2 birA bisC - - dfrA folC folD folE folD folE folP2 folX pabA pabB	dinydrofolate reductase folylpolyglutamate ynthase dihydrofolate reductase folylpolyglutamate ynthase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase may be involved in folate biosyn- thesis p-aminobenzoate synthase gluta- mine amidotransferase	Rv14(Rv141 Rv33(10. Th Rv23(Rv23(Rv23(Rv147 Rv147 Rv391 Rv147 Rv391 11. M terper Rv266 Rv056 Rv056
Rv1569 Rv0032 Rv3279c Rv1442 Rv0089 2. Folic aci Rv2763c Rv2763c Rv2763c Rv2763c Rv3609c Rv3609c Rv3609c Rv3609c Rv3609c Rv3609c Rv3609c Rv1207 Rv3607c Rv0013 Rv0052c Rv0812	bioF bioF2 bioF2 birA bisC - d drA folC folD folE folK folP2 folX pabB pabB pabB	dihydrofolate reductase folydrofolate reductase biotin sulfoxide reductase possible <i>bioC</i> biotin synthesis gene dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosyn- thesis <i>p</i> -aminobenzoate synthase gluta- mine amiotherase by a second <i>p</i> -aminobenzoate synthase <i>p</i> -aminobenzoate synthase	Rv14(Rv141 Rv33(10. Th Rv077 Rv235 Rv081 Rv147 Rv147 Rv147 Rv391 11. Mt terper Rv265 Rv056 Rv0956 Rv0956
Rv1569 Rv0032 Rv279c Rv1442 Rv0089 2. Folic aci Rv247c Rv3356c Rv3609c Rv3607c	bioF bioF2 birA bisC - - d dfrA folC folD folE folK folP2 folY2 folX pabA pabB pabC	dihydrofolate reductase folypolyglutamate synthase dihydrofolate reductase folypolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase may be involved in folate biosyn- thesis <i>p</i> -aminobenzoate synthase aminodeoxychorismate lyase	Rv14(Rv14) Rv33(10. Tr Rv23(Rv23) Rv23(Rv23) Rv23(Rv33) 11. M terper Rv26(Rv05(Rv05(Rv05(Rv05(Rv33)
Rv1569 Rv0032 Rv279c Rv1442 2. Folic aci Rv2763c Rv247c Rv356c Rv2447c Rv3506c Rv3609c Rv3608c Rv1207 Rv3608c Rv1207 Rv3607c Rv0013 Rv1005c Rv0012 3. Linoste	bioF bioF2 bioF2 birA bisC - - d drA folC folD folE folD folP2 folX pabA pabB pabC	Samino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF biotin apo-protein ligase biotin sulfoxide reductase possible <i>bioC</i> biotin synthesis gene dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase may be involved in folate biosyn- thesis <i>p</i> -aminobenzoate synthase gluta- mino benzoate synthase aminodeoxychorismate lyase	Rv14(Rv141 Rv33(10. Th Rv23(Rv23(Rv23(Rv147 Rv391 Rv147 Rv391 11. M terper Rv26(Rv05(Rv05(Rv05(Rv05(Rv05(Rv33(Rv3(
Rv1569 Rv0032 Rv3279c Rv1442 Rv0089 2. Folic aci Rv2763c Rv263c Rv247c Rv356c Rv356c Rv3606c Rv3606c Rv3606c Rv1207 Rv3607c Rv10013 Rv1005c Rv0013 S. Lipo2ta	bioF bioF2 bioF2 birA bisC - d drA folC folD folE folK folP folP2 folX pabA pabB pabC	demotodum syntase S-amino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF biotin apo-protein ligase biotin sulfoxide reductase possible <i>bioC</i> biotin synthesis gene dihydrofolate reductase folyloplyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosyn- thesis <i>p</i> -aminobenzoate synthase aminodenzychorismate lyase lipoate biosynthesis protein A	Rv14(Rv141 Rv33(10. Th Rv077 Rv235 Rv081 Rv147 Rv147 Rv147 Rv391 11. Mt terper Rv265 Rv056 Rv056 Rv035 Rv335
Rv1569 Rv0032 Rv279c Rv1442 Rv0089 2. Folic aci Rv2763c Rv247c Rv247c Rv247c Rv3556c Rv247c Rv3609c Rv3600 Rv300 Rv30	bioF bioF bioF2 birA bisC - - d dfrA folC folD folE folK folP2 folK folP2 folX pabA pabB pabC	dihydrofolate reductase folypolyglutamate synthase dihydrofolate reductase folypolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase may be involved in folate biosyn- thesis <i>p</i> -aminobenzoate synthase aminodeoxychorismate lyase	Rv14(Rv14) Rv33(10. Th Rv077 Rv233 Rv28 Rv081 Rv147 Rv391 11. M terper Rv266 Rv096 Rv096 Rv335 Rv217 Rv335
Rv1569 Rv0032 Rv279c Rv1442 Rv0089 2. Folic aci Rv279c Rv247c Rv356c Rv3609c Rv3606c Rv3606c Rv3607c Rv0013 Rv1005c Rv2218 Rv2217	bioF bioF2 bioF2 birA bisC - dfrA folC folD folE folD folP2 folX pabA pabB pabC	Samino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF biotin apo-protein ligase biotin sulfoxide reductase possible <i>bioC</i> biotin synthesis gene dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase may be involved in folate biosyn- thesis <i>p</i> -aminobenzoate synthase gluta- mino denzoate synthase aminodenzoate synthase aminodenzoate lyase lipoate biosynthesis protein A lipoate biosynthesis protein B	Rv14(Rv141 Rv33(10. Th Rv23(Rv23(Rv23(Rv147 Rv391 Rv147 Rv391 11. M terper Rv26(Rv05(Rv05(Rv05(Rv05(Rv33(Rv217 Rv33)
Rv1569 Rv0032 Rv279c Rv1442 Rv0089 2. Folic aci Rv2763c Rv247c Rv247c Rv247c Rv3356c Rv2407c Rv3609c Rv3609c Rv3609c Rv1207 Rv3607c Rv3607c Rv0013 Rv1005c Rv0013 Rv1005c Rv2217 3. Lipoate Rv2217	bioF bioF2 bioF2 birA bisC - d drA folC folD folE folK folP folP2 folP2 folP2 folX pabA pabB pabC lipA lipB	dinydrofolate reductase folydrofolate reductase possible <i>bioC</i> biotin synthesis gene dihydrofolate reductase possible <i>bioC</i> biotin synthesis gene dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase dihydropteroate synthase gene dihydropteroate synthase gene dihydropteroate synthase dihydropteroate synthase gene p-aminobenzoate synthase aminodenzychorismate lyase	Rv14(Rv14) Rv33(10. Tr Rv23(Rv28) Rv28(Rv28) Rv23(Rv24) Rv31(Rv31) Rv31(Rv31) Rv31(Rv33(Rv32) Rv33(Rv21) Rv33(Rv21)
Rv1569 Rv0032 Rv279c Rv1442 Rv0089 2. Folic aci Rv2763c Rv247c Rv247c Rv247c Rv3556c Rv247c Rv3609c Rv3600 Rv3	bioF bioF bioF2 birA bisC - - d dfrA folC folD folE folR folP2 folR folP2 folX pabA pabB pabC lipA lipB pterin maaA	Samino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF biotin apo-protein ligase biotin sulfoxide reductase possible <i>bioC</i> biotin synthesis gene dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase may be involved in folate biosyn- thesis <i>p</i> -aminobenzoate synthase aminodenzoate synthase aminodeoxychorismate lyase	Rv14(Rv14) Rv33(10. Th Rv077 Rv233 Rv285 Rv081 Rv147 Rv147 Rv147 Rv391 11. M terper Rv266 Rv096 Rv096 Rv335 Rv217 Rv336 Rv336
Rv1569 Rv0032 Rv279c Rv1442 2. Folic aci Rv2763c Rv247c Rv3506c Rv3609c Rv3606c Rv3609c Rv3608c Rv1207 Rv3607c Rv0013 Rv1005c Rv0013 Rv1005c Rv2217 3. Lipoate Rv2217 4. Molybdc Rv3109	bioF bioF2 bioF2 birA bisC - - d dfrA folC folD folE folD folE folK folP2 folX pabA pabB pabC lipA lipB opterin moaA	Samino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF biotin apo-protein ligase biotin sulfoxide reductase possible <i>bioC</i> biotin synthesis gene dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase may be involved in folate biosyn- thesis <i>p</i> -aminobenzoate synthase gluta- mino benzoate synthase aminodeoxychorismate lyase lipoate biosynthesis protein A lipoate biosynthesis protein B	Rv14(Rv141 Rv33(10. Th Rv23(Rv23(Rv23(Rv147 Rv37) Rv23(Rv147 Rv391 Rv147 Rv391 11. M terper Rv26(Rv05(Rv05(Rv217 Rv33(Rv217 Rv33(Rv217) Rv33(Rv217)
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Rv1569 Rv032 Rv279c Rv1442 Rv0089 2. Folic aci Rv2763c Rv247c Rv2607c	bioF bioF bioF2 birA bisC - - d dfrA folC folD folE folK folP2 folV folP2 folX pabA pabB pabC lipA lipB ppterin moaA2	Samino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF biotin apo-protein ligase biotin sulfoxide reductase possible <i>bioC</i> biotin synthesis gene dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase may be involved in folate biosyn- thesis <i>p</i> -aminobenzoate synthase aminodenzoate synthase aminodeoxychorismate lyase lipoate biosynthesis protein A lipoate biosynthesis protein B molybdenum cofactor biosynthe- sis, protein A	Rv14(Rv14) Rv33(10. Th Rv077 Rv233 Rv285 Rv081 Rv147 Rv147 Rv147 Rv147 Rv147 Rv391 11. M terper Rv266 Rv096 Rv335 Rv217 Rv336 Rv217 Rv336 Rv054 Rv055 Rv055
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Rv1569 Rv0032 Rv279c Rv1442 Rv1442 Rv24763c Rv24763c Rv24763c Rv2476 Rv2476 Rv2476 Rv2477 Rv3606c Rv2477 Rv3608c Rv2013 Rv0013 Rv0050c Rv0013 Rv0050 Rv0050 Rv0013 Rv0050	bioD bioF bioF2 birA bisC - - d dfrA folD folE folD folP folP2 folX pabA pabB pabC lipA lipB pabC lipA lipB opterin moaA3 moaA2 moaA2 moaC2 moaC3 moaD	Samino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF biotin apo-protein ligase biotin apo-protein ligase biotin sulfoxide reductase possible <i>bioC</i> biotin synthesis gene dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase gene biotin sulfoxide reductase paninobenzoate synthase gihydropteroate synthase aminodenzoate synthase p-aminobenzoate synthase aminodeoxychorismate lyase lipoate biosynthesis protein A lipoate biosynthesis protein A lipoate biosynthesis protein B molybdenum cofactor biosynthe- sis, protein A molybdenum cofactor biosynthe- sis, protein B molybdenum cofactor biosynthe- sis, protein B molybdenum cofactor biosynthe- sis, protein C molybdenum cofactor biosynthe- sis, protein C	Rv14(Rv141 Rv33(10, Th Rv235 Rv235 Rv235 Rv235 Rv237 Rv391 11, M terper Rv266 Rv056 Rv056 Rv056 Rv056 Rv056 Rv055 Rv05
Rv1569 Rv032 Rv279c Rv1442 Rv0089 2. Folic aci Rv2763c Rv247c Rv2607c Rv2607c Rv3607c Rv0013 Rv1005c Rv2218 Rv2218 Rv2217 4. Molybdc Rv3109 Rv0869c Rv3100 Rv0984 Rv3111 Rv0864 Rv3324c Rv3112	bioF bioF2 bioF2 birA bisC - - d dfrA folC folD folE folK folP folP2 folX pabA pabB pabC lipA lipB pabC lipA lipB moaA2 moaA2 moaA2 moaA2 moaA2 moaC2 moaC3 moaD	Samino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF biotin sufoxide reductase possible <i>bioC</i> biotin synthesis gene dihydrofolate reductase folylpolyglutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase may be involved in folate biosyn- thesis <i>p</i> -aminobenzoate synthase aminodenzythesis protein A lipoate biosynthesis protein B molybdenum cofactor biosynthe- sis, protein A molybdenum cofactor biosynthe- sis, protein B molybdenum cofactor biosynthe- sis, protein C molybdenum cofactor biosynthe- sis, protein C	Rv14(Rv141 Rv33(Rv285 Rv285 Rv285 Rv285 Rv285 Rv235 Rv285 Rv285 Rv285 Rv285 Rv395
Rv1569 Rv032 Rv279c Rv1442 Rv0089 2. Folic aci Rv2763c Rv247c Rv247c Rv247c Rv247c Rv247c Rv247c Rv247c Rv247c Rv247c Rv247c Rv247c Rv247c Rv247c Rv247c Rv247c Rv247c Rv247c Rv2607c Rv2607c Rv2607c Rv2013 Rv1005c Rv2218 Rv2218 Rv2217 3. Lipoate Rv2218 Rv2217 4. Molybdc Rv3100 Rv0869c Rv0438c Rv3110 Rv0984 Rv3111 Rv0864 Rv3112 Rv0868c	bioF bioF2 bioF2 birA bisC - - d dfrA folC folD folE folK folP folP2 folX pabA pabB pabC lipA lipB pabC lipA lipB moaA2 moaA3 moaB2 moaC2 moaC3 moaD2	Seamino-7-oxononanoate synthase C-terminal similar to <i>B. subtilis</i> BioF biotin apo-protein ligase biotin sulfoxide reductase possible <i>bioC</i> biotin synthesis gene dihydrofolate reductase folylpolydutamate synthase methylenetetrahydrofolate dehy- drogenase GTP cyclohydrolase I 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase dihydropteroate synthase dihydropteroate synthase gene zihydropteroate synthase dihydropteroate synthase gene zihydropteroate synthase dihydropteroate synthase dihydropteroate synthase dihydropteroate synthase dihydropteroate synthase dihydropteroate synthase dihydropteroate synthase dihydroptenzoate synthase aminobenzoate synthase aminodeoxychorismate lyase zipoate biosynthesis protein A lipoate biosynthesis protein B molybdenum cofactor biosynthe- sis, protein A molybdenum cofactor biosynthe- sis, protein B molybdenum cofactor biosynthe- sis, protein B molybdenum cofactor biosynthe- sis, protein B molybdenum cofactor biosynthe- sis, protein C molybdenum cofactor biosynthe- sis, protein C	Rv14(Rv14) Rv33(10. Tr Rv233 Rv285 Rv081 Rv141 Rv31 Rv141 Rv31 Rv142 Rv31 Rv142 Rv31 Rv31 Rv32 Rv056 Rv056 Rv055 Rv05

Bv3110	moaE	subunit 1
	moal	subunit 2
Rv0866	moaE2	molybdopterin-converting factor subunit 2
Rv3322c	moaE3	molybdopterin-converting factor subunit 2
Rv0994	moeA	molybdopterin biosynthesis
Rv3116	moeB	molybdopterin biosynthesis
Rv2338c	moeW	molybdopterin biosynthesis
Rv1681	moeX	weak similarity to E. coli MoaA
Rv1355c	moeY	weak similarity to E. coli MoeB
Rv3206c	moeZ	probably involved in
Bv0865	moa	molybdopterin biosynthesis
1100000	mog	
5. Pantothe	nate	
Rv1092c	coaA	2 mother ate kinase
NV2220	рапь	hydroxymethyltransferase
Rv3602c	panC	pantoate-β-alanine ligase
Rv3601c	panD	aspartate 1-decarboxylase
6 Pyridoxir	he	
By2607	ndyH	pyridoxamine 5'-phosphate
1112007	puxii	oxidase
Pyridine	nucleotide	
Rv1594	nadA	quinolinate synthase
Rv1595	nadB	L-aspartate oxidase
Rv1596	nadC	nicotinate-nucleotide pyrophos-
Rv0423c	thiC	thiamine synthesis, pyrimidine
		moiety
8. Thiamine		a la secola succesta das solas fallas en latas e se
Rv0422C	thiD thiE	phosphomethylpyrimidine kinase
1104140	unc	moietv
Rv0417	thiG	thiamine synthesis, thiazole
		moiety
Rv2977c	thiL	probable thiamine-monophos-
		phate kinase
9. Riboflavi	n	
Bv1940	ribA	GTP cyclohydrolase II
Bv1415	ribA2	probable GTP cyclohydrolase II
Bv1412	rihC	riboflavin synthase α chain
Bv2671	rihD	probable riboflavin deaminase
By2786c	rihF	riboflavin kinase
Rv1409	rihG	riboflavin biosynthesis
Bv1416	ribH	riboflavin synthase ß chain
Rv3300c	-	probable deaminase, riboflavin synthesis
Rv3300c	-	probable deaminase, riboflavin synthesis
Rv3300c	- loxin, gluta	probable deaminase, riboflavin synthesis aredoxin and mycothiol
Rv3300c 10. Thiored Rv0773c	- loxin, gluta ggtA	probable deaminase, riboflavin synthesis aredoxin and mycothiol putative γ-glutamyl transpeptidase
Rv3300c 10. Thiored Rv0773c Rv2394	- loxin, gluta ggtA ggtB	probable deaminase, riboflavin synthesis aredoxin and mycothiol putative γ-glutamyl transpeptidase γ -glutamyltranspeptidase
Rv3300c 10. Thiored Rv0773c Rv2394	- loxin, gluta ggtA ggtB	probable déaminase, riboflavin synthesis aredoxin and mycothiol putative γ-glutamyl transpeptidase γ-glutamyltranspeptidase precursor
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855	- loxin, gluta ggtA ggtB gorA	probable deaminase, riboflavin synthesis aredoxin and mycothiol putative γ-glutamyl transpeptidase γ -glutamyltranspeptidase precursor glutathione reductase homologue
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c	- loxin, gluta ggtA ggtB gorA thiX	probable déaminase, riboflavin synthesis rredoxin and mycothiol putative γ-glutamyl transpeptidase γ -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. lepra</i> e ThiX
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470	- loxin, gluta ggtA ggtB gorA thiX trxA	probable déaminase, riboflavin synthesis aredoxin and mycothiol putative γ -glutamyl transpeptidase γ -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv1471	- loxin, gluta ggtA ggtB gorA thiX trxA trxA trxB	probable deaminase, riboflavin synthesis aredoxin and mycothiol putative γ-glutamyl transpeptidase γ -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913	oxin, gluta ggtA ggtB gorA thiX trxA trxB trxB2	probable deaminase, riboflavin synthesis aredoxin and mycothiol putative γ-glutamyl transpeptidase γ -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914	loxin, gluta ggtA ggtB gorA thiX trxA trxB trxB2 trxC	probable doaminase, riboflavin synthesis rredoxin and mycothiol putative y-glutamyl transpeptidase y-glutamyl transpeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menagi	- loxin, gluta ggtA ggtB gorA thiX trxA trxB trxB2 trxC uinone, PC	probable deaminase, riboflavin synthesis aredoxin and mycothiol putative γ-glutamyl transpeptidase γ-glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menaqu terpenoids	- loxin, gluta ggtA ggtB gorA thiX trxA trxB trxB2 trxC uinone, PC	probable deaminase, riboflavin synthesis aredoxin and mycothiol putative γ-glutamyl transpeptidase γ-glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin ductase thioredoxin
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menaqu terpenoids Rv2682c	- loxin, gluta ggtA ggtB gorA thiX trxA trxB trxB trxC uinone, PC dxs	probable deaminase, riboflavin synthesis aredoxin and mycothiol putative γ-glutamyl transpeptidase γ-glutamyltranspeptidase grecursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin ductase thioredoxin 2Q, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menaqu terpenoids Rv2682c B:0552	- loxin, gluta ggtA ggtB gorA thiX trxA trxB trxB trxC uinone, PC dxs graC1	probable deaminase, riboflavin synthesis aredoxin and mycothiol putative γ-glutamyl transpeptidase γ-glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin thioredoxin reductase thioredoxin reductase thioredoxin 2Q, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menaqt terpenoids Rv2682c Rv0562	loxin, gluta ggtA ggtB gorA thiX trxA trxB trxB2 trxC uinone, PC dxs grcC1	probable deaminase, riboflavin synthesis aredoxin and mycothiol putative y-glutamyl transpeptidase y-glutamyl transpeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin 2Q, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3913 Rv3914 11. Menaqu terpenoids Rv2682c Rv0562 Rv0989c	loxin, gluta ggtA ggtB gorA thiX trxA trxB trxB2 trxC uinone, PC dxs grcC1 grcC2	probable deaminase, riboflavin synthesis aredoxin and mycothiol putative y-glutamyl transpeptidase y-glutamyl transpeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin 2Q, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3913 Rv3914 11. Menaqu terpenoids Rv2682c Rv0562 Rv0989c	loxin, gluta ggtA ggtB gorA thiX trxA trxB trxC uinone, PC dxs grcC1 grcC2	probable deaminase, riboflavin synthesis aredoxin and mycothiol putative γ-glutamyl transpeptidase γ -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin AQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3913 Rv3914 11. Menaqu terpenoids Rv2682c Rv0562 Rv0989c Rv3398c	loxin, gluta ggtA ggtB gorA thiX trxA trxB trxB2 trxC uinone, PC dxs grcC1 grcC2 idsA	probable deaminase, riboflavin synthesis aredoxin and mycothiol putative γ-glutamyl transpeptidase γ -glutamyltranspeptidase grecursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase II
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2895 Rv0816c Rv1470 Rv3913 Rv3913 Rv3914 11. Menaqu terpenoids Rv2682c Rv0562 Rv0989c Rv3398c Rv2173	loxin, gluta ggtA ggtB gorA thiX thX thX trxB trxC uinone, PC dxs grcC1 grcC2 idsA idsA2	probable deaminase, riboflavin synthesis aredoxin and mycothiol putative γ-glutamyl transpeptidase γ -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin extuctase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase II geranylgeranyl pyrophosphate
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2895 Rv0816c Rv1470 Rv1471 Rv3914 11. Menaqu terpenoids Rv2682c Rv0969c Rv0989c Rv3398c Rv2173 Rv2173	loxin, gluta ggtA ggtB gorA thiX trxA trxB trxB2 trxC uinone, PC dxs grcC1 grcC2 idsA idsA2	probable deaminase, riboflavin synthesis aredoxin and mycothiol putative γ-glutamyl transpeptidase γ -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin dother 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menaqu terpenoids Rv2682c Rv0562 Rv0989c Rv3398c Rv2173 Rv3383c	loxin, gluta ggtA ggtB gorA thiX trxA trxB trxB trxC uinone, PC dxs grcC1 grcC2 idsA idsA2 idsB	probable deaminase, riboflavin synthesis aredoxin and mycothiol putative γ-glutamyl transpeptidase γ-glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase geranylgeranyl, similar geranyl transfergeranyl, similar geranyl
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2895 Rv0816c Rv1470 Rv1471 Rv3913 Rv3913 Rv3913 Rv3914 11. Menaqu terpenoids Rv2682c Rv0562 Rv0989c Rv2173 Rv3383c Rv3383c	loxin, gluta ggtA ggtB gorA thiX trxA trxB trxC uinone, PC dxs grcC1 grcC2 idsA idsA2 idsB menA	probable deaminase, riboflavin synthesis aredoxin and mycothiol putative γ-glutamyl transpeptidase γ -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase 4-dihydroxy-2-naphthoate
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1471 Rv3913 Rv3914 11. Menaqu terpenoids Rv2682c Rv0562 Rv0989c Rv3398c Rv2173 Rv3383c Rv2173 Rv3383c Rv0534c Rv0534c	loxin, gluta ggtA ggtB gorA thiX trxB trxC uinone, PC dxs grcC1 grcC2 idsA idsA2 idsB menA mon8	probable daaminase, riboflavin synthesis rredoxin and mycothiol putative y-glutamyl transpeptidase y-glutamyl transpeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl prophosphate synthase transfergeranyl, similar geranyl prophosphate synthase transfergeranyl, similar geranyl prophosphate synthase transfergeranyl, similar geranyl prophosphate synthase transfergeranyl sy
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv3913 Rv3913 Rv3913 Rv3913 Rv3914 11. Menaqu terpenoids Rv2682c Rv0562 Rv0989c Rv3398c Rv2173 Rv3383c Rv0334c Rv0534c Rv0534c	loxin, gluta ggtA ggtB gorA thiX trxA trxB trxC uinone, PC dxs grcC1 grcC2 idsA idsA2 idsB menA menB	probable deaminase, riboflavin synthesis aredoxin and mycothiol putative γ-glutamyl transpeptidase γ -glutamyltranspeptidase γ -glutamyltranspeptidase glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin 2Q, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase - automyltransferase naphthoate synthase
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3913 Rv3913 Rv3914 11. Menaqu terpenoids Rv2682c Rv0562 Rv0989c Rv3383c Rv2173 Rv3383c Rv0534c Rv0553 Rv0554	loxin, gluta ggtA ggtB gorA thiX trxA trxB trxC uinone, PC dxs grcC1 grcC2 idsA idsA2 idsA idsA2 idsB menA menB menD	probable daaminase, riboflavin synthesis aredoxin and mycothiol putative γ-glutamyl transpeptidase γ -glutamyltranspeptidase γ -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase synthase geranylgeranyl pyrophosphate synthase synthase ase asynthase geranylgeranyl pyrophosphate synthase ase aphthoate synthase 2-succinyl-6-hydroxy-2-4-cyclo-
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menaqu terpenoids Rv2682c Rv0562 Rv0989c Rv3398c Rv2173 Rv3383c Rv2173 Rv3383c Rv0548c Rv0548c Rv0555	loxin, gluta ggtA ggtB gorA thiX trxA trxB trxC uinone, PC dxs grcC1 grcC2 idsA idsA2 idsA2 idsB menA menB menC menD	probable deaminase, riboflavin synthesis aredoxin and mycothiol putative γ-glutamyl transpeptidase γ-glutamyltranspeptidase grecursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase Il geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase 4-dihydroxy-2-naphthoate octaprenyltransferase naphthoate synthase 2-succinyl-6-Tydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv3913 Rv3913 Rv3914 11. Menaqu terpenoids Rv2682c Rv0562 Rv0562 Rv0580c Rv3398c Rv2173 Rv3383c Rv0553 Rv0555 Rv0555 Rv0554c	loxin, gluta ggtA ggtB gorA thiX trxB trxC uinone, PC dxs grcC1 grcC2 idsA idsA2 idsA menA menB menC menD menE	probable daaminase, riboflavin synthesis aredoxin and mycothiol putative y-glutamyl transpeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase Neptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase cataprenyl transferase naphthoate synthase -succinylbenzoate-CoA synthase 2-succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3913 Rv3913 Rv3914 11. Menaqu terpenoids Rv2682c Rv0562 Rv0562 Rv0989c Rv2173 Rv3398c Rv2173 Rv3398c Rv0554c Rv0553 Rv0555 Rv0554c Rv05542c Rv05542c	loxin, gluta ggtA ggtB gorA thiX trxA trxB trxC uinone, PC dxs grcC1 grcC2 idsA idsA2 idsB menA menB menC menD menE menG	probable daaminase, riboflavin synthesis vedoxin and mycothiol putative γ-glutamyl transpeptidase γ -glutamyl transpeptidase γ -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3913 Rv3913 Rv3913 Rv3914 11. Menaqu terpenoids Rv2682c Rv0989c Rv3383c Rv0542c Rv0534c Rv0542c Rv0542c Rv0542c Rv0542c Rv0542c Rv0542c Rv0542c	loxin, gluta ggtA ggtB gorA thiX trxA trxB trxC uinone, PC dxs grcC1 grcC2 idsA idsA2 idsA2 idsB menA menB menC menD menE menG	probable daaminase, riboflavin synthesis aredoxin and mycothiol putative γ-glutamyl transpeptidase γ -glutamyltranspeptidase γ -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase synthase ageranylgeranyl pyrophosphate synthase ageranylgeranyl pyrophosphate synthase 2-denetyltransferase naphthoate synthase <i>S</i> -adenosylmethionine: 2-demethylinenaquinone
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menaqu terpenoids Rv0562 Rv0989c Rv3398c Rv2173 Rv3383c Rv0534c Rv0548c Rv0548c Rv0555 Rv0542c Rv0542c Rv3853 Rv3853 Rv387c	loxin, gluta ggtA ggtB ggrA thiX trxB trxC dxs grcC1 dxs grcC2 idsA idsA2 idsB menA menB menC menD menE menG phyA_	probable daaminase, riboflavin synthesis redoxin and mycothiol putative y-glutamyl transpeptidase y-glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II heptagrenyl prophosphate synthase II heptagrenyl prophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase cotaprenyltransferase naphthoate synthase o-succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase o-succinyl-6-nydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase S-adenosylmethionine: 2-demethylmenaquinone phytoene synthase
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv3913 Rv3913 Rv3914 11. Menaqu terpenoids Rv0562 Rv0562 Rv0562 Rv0562 Rv0398c Rv2173 Rv3398c Rv0534c Rv0534c Rv0555 Rv0542c Rv0542c Rv0542c Rv0542c Rv3397c Rv3397c	loxin, gluta ggtA ggtB gorA thiX trxB trxC uinone, PC dxs grcC1 grcC2 idsA idsA2 idsA menA menC menD menC menG phyA pqqE	probable daaminase, riboflavin synthesis aredoxin and mycothiol putative y-glutamyl transpeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase Neptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase octaprenyltransferase naphthoate synthase 2-succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase o-succerybenzoic acid-CoA ligase S-adenosylmethionine: 2-demethylmenaquinone phytoene synthase
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3913 Rv3914 11. Menaqu terpenoids Rv0562 Rv0562 Rv0562 Rv0580 Rv2173 Rv3398c Rv0553 Rv0555 Rv0555 Rv0555 Rv0558 Rv3397c Rv0558	loxin, gluta ggtA ggtB gorA thiX trxA trxB trxC uinone, PC dxs grcC1 grcC2 idsA idsA2 idsA idsA2 idsB menA menC menD menC menG phyA pqqE ubiF	probable daaminase, riboflavin synthesis aredoxin and mycothiol putative y-glutamyl transpeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase sociaprenyltransferase naphthoate synthase o-succinyle-hydroxy-2.4-cyclo- hexadiene-1-carboxylate synthase o-succinylbenzoic acid-CoA signase S-adenosylmethionine: 2-demethylmenaquinone phytoene synthase coenzyme PQQ synthesis protein E ubiguinone/menaguinone biosyn-
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3913 Rv3914 11. Menaqu terpenoids Rv2682c Rv0562 Rv0989c Rv3398c Rv3398c Rv2173 Rv3383c Rv0534c Rv0553 Rv0552 Rv0552 Rv0552 Rv0552 Rv0552 Rv0552 Rv0552 Rv0558	loxin, gluta ggtA ggtB gorA thiX trxA trxB trxC uinone, PC dxs grcC1 grcC2 idsA idsA2 idsA idsA2 idsB menA menB menC menD phyA pqqE ubiE	probable daaminase, riboflavin synthesis aredoxin and mycothiol putative γ-glutamyl transpeptidase γ -glutamyltranspeptidase γ -glutamyltranspeptidase γ -glutamyltranspeptidase glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin 2Q, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase synthase synthase Soctaprenyltransferase naphthoate synthase -succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase -succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase -succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase -succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase -succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase -succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase -succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase -succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase -succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase cosucyme PQQ synthesis protein E ubiquinone/menaquinone biosyn- thesis methyltransferase
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menaqu terpenoids Rv2682c Rv0562 Rv0989c Rv3398c Rv2173 Rv3383c Rv0548c Rv0548c Rv0548c Rv0548c Rv0548c Rv3397c Rv3397c Rv0588	loxin, gluta ggtA ggtB gorA thiX trxA trxB trxC uinone, PC dxs grcC1 grcC2 idsA idsA2 idsA idsA2 idsB menA menB menC menD phyA pqqE ubiE	probable daaminase, riboflavin synthesis aredoxin and mycothiol putative γ-glutamyl transpeptidase γ-glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxins QQ, ubiquinone and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase II geranylgeranyl pyrophosphate synthase transfergeranyl, similar geranyl pyrophosphate synthase -succinylbenzoite-CoA synthase -succinyl-6-hydroxy-2.4-cyclo- hexadiene-1-carboxylate synthase 2-demethylmenaquinone phytoene synthase coenzyme PQQ synthesis protein E ubiquinone/menaquinone biosyn- thesis methyltransferase
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menaqu terpenoids Rv2682c Rv0562 Rv0562 Rv0562 Rv3398c Rv2173 Rv3383c Rv2173 Rv3383c Rv0534c Rv0548c Rv0553 Rv0555 Rv0542c Rv3397c Rv3397c Rv3397c Rv0588 Rv3397c Rv0588 Rv2558 Rv2558	loxin, gluta ggtA ggtB ggrA thiX trxB trxC uinone, PC dxs grcC1 grcC2 idsA idsA2 idsA2 idsB menA menB menC menD menE menG phyA pqqE ubiE	probable daaminase, riboflavin synthesis redoxin and mycothiol putative y-glutamyl transpeptidase y-glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II heptagrenyl prophosphate synthase geranylgeranyl prophosphate synthase transfergeranyl, similar geranyl prophosphate synthase ocaprenyltransferase naphthoate synthase o-succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase o-succinylbenzoic acid-CoA sigase S-adenosylmethionine: 2-demethylmenaquinone phytoene synthase coenzyme PQQ synthesis protein E ubiquinone/menaquinone biosyn- thesis methyltransferase
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv313 Rv3913 Rv3914 11. Menaque terpenoids Rv0562 Rv0562 Rv0989c Rv3398c Rv0533 Rv0553 Rv0553 Rv0553 Rv0553 Rv0558 12. Herme a Rv0559 Rv0556	loxin, gluta ggtA ggtB gorA trxB trxB trxC uinone, PC dxs grcC1 grcC2 idsA idsA2 idsA menA menB menC menD menE menG phyA pqqE ubiE	probable daaminase, riboflavin synthesis redoxin and mycothiol putative y-glutamyl transpeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase Neptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase cataprenyltansferase naphthoate synthase 0-succinylbenzoate-CoA synthase 2-succinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase consucylenyloenzoic acid-CoA ligase S-adenosylmethionine: 2-demethylmenaquinone phytoene synthase coenzyme PQQ synthesis protein E ubiquinone/menaquinone biosyn- thesis methyltransferase
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv1470 Rv3913 Rv3913 Rv3914 11. Menaqu terpenoids Rv2682c Rv0562 Rv0989c Rv3398c Rv2173 Rv3383c Rv3383c Rv0542c Rv0548c Rv0548c Rv0548c Rv0548c Rv0548c Rv0548c Rv0548c Rv0548c Rv0548c Rv0548c Rv0558 12. Heme a Rv0512 No5512	loxin, gluta ggtA ggtB gorA thiX trxA trxB trxC uinone, PC dxs grcC1 grcC2 idsA idsA2 idsA idsA2 idsB menA menB menC phyA pqqE ubiE and porphy hemA hemB	probable daaminase, riboflavin synthesis aredoxin and mycothiol putative γ-glutamyl transpeptidase γ -glutamyltranspeptidase γ -glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin neductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase geranylgeranyl pyrophosphate synthase synth
Rv3300c 10. Thiored Rv0773c Rv2394 Rv2855 Rv0816c Rv1470 Rv1471 Rv3913 Rv3914 11. Menaqu terpenoids Rv2682c Rv0562 Rv0989c Rv3398c Rv2173 Rv3398c Rv2173 Rv3398c Rv0534c Rv0548c Rv0546c Rv0540 Rv054	loxin, gluta ggtA ggtB gorA thiX trxB trxC uinone, PC dxs grcC1 grcC2 idsA idsA2 idsA2 idsB menA menB menC menD menE menG phyA pqqE ubiE	probable daaminase, riboflavin synthesis redoxin and mycothiol putative y-glutamyl transpeptidase y-glutamyltranspeptidase precursor glutathione reductase homologue equivalent to <i>M. leprae</i> ThiX thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin reductase thioredoxin and other 1-deoxy-D-xylulose 5-phosphate synthase heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II heptaprenyl diphosphate synthase II heptagrenyl prophosphate synthase transfergeranyl, similar geranyl prophosphate synthase octaprenyltransferase naphthoate synthase ocsucinyl-6-hydroxy-2,4-cyclo- hexadiene-1-carboxylate synthase o-succinylbenzoic acid-CoA sigase S-adenosylmethionine: 2-demethylmenaquinone phytoene synthase coenzyme PQQ synthesis protein E ubiquinone/menaquinone biosyn- thesis methyltransferase r/rin glutamyl-tRNA reductase o-aminolevulinic acid dehydratase porphobilinogen deaminase

1100324	hemK hemL	protoporphyrinogen oxidase glutamate-1-semialdehyde amino- transforaso
Rv2388c	hemN	oxygen-independent copropor- phyrinogen III oxidase
Rv2677c Rv1485	hemY' hemZ	protoporphyrinogen oxidase ferrochelatase
13. Cobala	min	
Rv2849c Rv2848c	cobA cobB	cob(I)alamin adenosyltransferase cobyrinic acid a,c-diamide synthase
Rv2231c	cobC	aminotransferase
Rv2236c	cobD	cobinamide synthase
Rv2064	cobG	percorrin reductase
RV2065	cobl	Cobl. Cob. I fusion protoin
Rv2070c	cobK	precorrin reductase
Rv2072c	cobl	probable methyltransferase
Rv2071c	cobM	precorrin-3 methylase
Rv2062c	cobN	cobalt insertion
Rv2208	cobS	cobalamin (5'-phosphate)
Rv2207	cobT	nicotinate-nucleotide-dimethyl- benzimidazole transferase
Rv0254c	cobU	cobinamide kinase
Rv0255c	cobQ	cobyric acid synthase
Rv3713	cobQ2	possible cobyric acid synthase
Rv0306	-	similar to BluB cobalamin synthe- sis protein <i>R. capsulatus</i>
14. Iron uti	lization	
Rv1876	bfrA	bacterioferritin
Rv3841	bfrB	bacterioferritin
Rv3215	entC	probable isochorismate synthase
Rv3214	entD	weak similarity to many phospho-
Rv2895c	viuB	similar to proteins involved in
Rv3525c	-	similar to ferripyochelin binding
		protein
H. Lipid bio	osynthesis	
1. Synthes	is of fatty	and mycolic acids
Rv3285	accA3	acetyl/propionyl CoA carboxylase α subunit
Rv0904c	accD3	acetyl/propionyl CoA carboxylase β subunit
Rv3799c	accD4	acetyl/propionyl CoA carboxylase β subunit
Rv3280	accD5	acetyl/propionyl CoA carboxylase
Rv2247	accD6	acetyl/propionyl CoA carboxylase
Rv2244	асрМ	acyl carrier protein (meromycolate
Rv2523c	acpS	CoA:apo-[ACP] pantethienephos- photransferase
		malonyl CoA-[ACP] transacylase
Rv2243	fabD	
Rv2243 Rv0649	fabD fabD2	malonyl CoA-[ACP] transacylase
Rv2243 Rv0649 Rv1483	fabD fabD2 fabG1	malonyl CoA-[ACP] transacylase 3-oxoacyl-[ACP] reductase (aka MabA)
Rv2243 Rv0649 Rv1483 Rv1350	fabD fabD2 fabG1 fabG2	malonyl CoA-[ACP] transacylase 3-oxoacyl-[ACP] reductase (aka MabA) 3-oxoacyl-[ACP] Reductase
Rv2243 Rv0649 Rv1483 Rv1350 Rv2002	fabD fabD2 fabG1 fabG2 fabG3	malonyl CoA-[ACP] transacylase 3-oxoacyl-[ACP] reductase (aka MabA) 3-oxoacyl-[ACP] Reductase 3-oxoacyl-[ACP] reductase
Rv2243 Rv0649 Rv1483 Rv1350 Rv2002 Rv0242c	fabD fabD2 fabG1 fabG2 fabG3 fabG4	Malonyi CoA-[ACP] transacylase 3-oxoacyl-[ACP] reductase (aka MabA) 3-oxoacyl-[ACP] Reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase
Rv2243 Rv0649 Rv1483 Rv1350 Rv2002 Rv0242c Rv2766c	fabD fabD2 fabG1 fabG2 fabG3 fabG4 fabG5	malonyi CoA-[ACP] transacylase 3-oxoacyl-[ACP] reductase (aka MabA) 3-oxoacyl-[ACP] Reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase
Rv2243 Rv0649 Rv1483 Rv1350 Rv2002 Rv0242c Rv0242c Rv2766c Rv0533c	fabD fabD2 fabG1 fabG2 fabG3 fabG4 fabG5 fabH	malonyl Co-[ACP] transacylase 3-oxoacyl-[ACP] reductase (aka MabA) 3-oxoacyl-[ACP] Reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase
Rv2243 Rv0649 Rv1483 Rv1350 Rv2002 Rv0242c Rv0242c Rv0533c Rv2524c	fabD fabD2 fabG1 fabG2 fabG3 fabG4 fabG5 fabH fas	malonyl CoA-[ACP] transacylase analonyl CoA-[ACP] transacylase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-
Rv2243 Rv0649 Rv1483 Rv1350 Rv2002 Rv0242c Rv0242c Rv0533c Rv2524c Rv1484 Pv2245	fabD fabD2 fabG1 fabG2 fabG3 fabG4 fabG5 fabH fas inhA kacA	malonyi CoA-[ACP] transacylase analonyi CoA-[ACP] transacylase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase β-ketoacyl-ACP synthase III fatty acid synthase enoyl-[ACP] reductase 8-ketoacyl-ACP synthase
Rv2243 Rv0649 Rv1483 Rv1350 Rv2002 Rv0242c Rv0233c Rv2566c Rv1484 Rv2245	fabD fabD2 fabG1 fabG2 fabG3 fabG4 fabG5 fabH fas inhA kasA	malonyl CoA-[ACP] transacylase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] Reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase β-ketoacyl-ACP synthase enoyl-[ACP] reductase β-ketoacyl-ACP synthase (meromycolate extension)
Rv2243 Rv0649 Rv1483 Rv1350 Rv2002 Rv0242c Rv0242c Rv0533c Rv254c Rv1484 Rv2245 Rv2246	fabD fabD2 fabG1 fabG2 fabG3 fabG4 fabG5 fabH fas inhA kasA kasB	Matony CoA-[ACP] transacylase analony CoA-[ACP] transacylase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase β-ketoacyl-ACP synthase (meromycolate extension) β-ketoacyl-ACP synthase (meromycolate extension)
Rv2243 Rv0649 Rv1483 Rv1350 Rv2002 Rv0242c Rv0533c Rv2524c Rv1484 Rv2245 Rv2246 Rv2246 Rv2246	fabD fabD2 fabG1 fabG2 fabG3 fabG4 fabG5 fabH fas inhA kasA kasB tesB1	malony CoA-[ACP] transacylase analony CoA-[ACP] transacylase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase β-ketoacyl-ACP synthase III fatty acid synthase enoyl-[ACP] reductase β-ketoacyl-ACP synthase (meromycolate extension) β-ketoacyl-ACP synthase (meromycolate extension) thioesterase II
Rv2243 Rv0649 Rv1483 Rv1350 Rv2002 Rv2766c Rv2524c Rv2524c Rv2524c Rv2545 Rv2245 Rv2246 Rv2246	fabD fabD2 fabG1 fabG2 fabG3 fabG4 fabG5 fabH fas inhA kasA kasB tesB1 tesB1	malonyl CoA-[ACP] transacylase 3-oxoacyl-[ACP] reductase (aka MabA) 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase β-ketoacyl-ACP synthase III fatty acid synthase enoyl-[ACP] reductase β-ketoacyl-ACP synthase (meromycolate extension) β-ketoacyl-ACP synthase (meromycolate extension) thioesterase II thioesterase II
Rv2243 Rv0649 Rv1483 Rv1350 Rv2002 Rv2766C Rv0533C Rv2784 Rv1844 Rv2245 Rv2246 Rv1884 Rv2246 Rv1618 Rv02305	fabD fabD2 fabG1 fabG2 fabG3 fabG4 fabG5 fabH fas inhA kasA kasB tesB1 tesB2 -	malonyl CoA[ACP] transacylase analonyl CoA[ACP] transacylase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase β-ketoacyl-ACP synthase III fatty acid synthase enoyl-[ACP] reductase β-ketoacyl-ACP synthase (meromycolate extension) β-ketoacyl-ACP synthase (meromycolate extension) thioesterase II thioesterase II thioesterase II thioesterase II
Rv2243 Rv0649 Rv1483 Rv1350 Rv2022 Rv0242c Rv2524c Rv2524c Rv2524c Rv2524c Rv2524c Rv2524c Rv2524c Rv2542 Rv2246 Rv2246 Rv2246 Rv1618 Rv2605c Rv0033 Rv1344	fabD fabD2 fabG1 fabG2 fabG3 fabG4 fabG4 fabG5 fabH fas inhA kasA kasB tesB1 tesB2 -	malony CoA-[ACP] transacylase analony CoA-[ACP] transacylase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase β-ketoacyl-ACP synthase III fatty acid synthase enoyl-[ACP] reductase β-ketoacyl-ACP synthase (meromycolate extension) β-ketoacyl-ACP synthase (meromycolate extension) thioesterase II possible acyl carrier protein possible acyl carrier protein
Rv2243 Rv0649 Rv1483 Rv1350 Rv2002 Rv0242C Rv2524C Rv1584 Rv2524C Rv1484 Rv2245 Rv2245 Rv2246 Rv1618 Rv2605C Rv0334 Rv1344 Rv1344 Rv1344	fabD fabD2 fabG1 fabG3 fabG4 fabG4 fabG4 fabG5 fabH fas inhA kasA kasB tesB1 tesB2 - -	malonyl CoA-[ACP] transacylase analonyl CoA-[ACP] transacylase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase β-ketoacyl-ACP synthase III fatty acid synthase enoyl-[ACP] reductase β-ketoacyl-ACP synthase (meromycolate extension) β-ketoacyl-ACP synthase (meromycolate extension) thioesterase II thioesterase II possible acyl carrier protein possible acyl carrier protein possible biotin carboxylase
Rv2243 Rv0649 Rv1483 Rv1350 Rv2002 Rv0242c Rv2524c Rv2524c Rv2524c Rv2524c Rv2524c Rv2524c Rv2524c Rv2246 Rv2246 Rv2246 Rv1618 Rv2605c Rv0033 Rv1344 Rv1722 Rv3221c Rv3222c	fabD fabD2 fabG1 fabG2 fabG3 fabG4 fabG4 fabG4 fabG4 fabG4 fabG5 fabH fas inhA kasA kasB tesB1 tesB2 - -	$\label{eq:constraint} \begin{tabular}{lllllllllllllllllllllllllllllllllll$
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Rv2243 Rv0649 Rv1483 Rv1350 Rv2002 Rv0242C Rv2546 Rv1548 Rv2246 Rv1484 Rv2245 Rv2246 Rv1618 Rv2246 Rv1618 Rv2246 Rv1618 Rv2605c Rv0333 Rv1344 Rv1722 Rv3221c Rv3292c Rv0392c Rv0503c Rv0824c	fabD2 fabG2 fabG1 fabG2 fabG3 fabG4 fabG4 fabG4 fabG4 fabG4 fabG4 fas inhA kasA kasB tesB1 tesB2 - - - - - - - - - - - - - - - - - - -	malonyl CoA-[ACP] transacylase malonyl CoA-[ACP] transacylase 3-oxoacyl-[ACP] reductase (aka MabA) 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase β-ketoacyl-ACP synthase III fatty acid synthase enoyl-[ACP] reductase β-ketoacyl-ACP synthase (meromycolate extension) β-ketoacyl-ACP synthase (meromycolate extension) b-ketoacyl-ACP synthase (meromycolate extension) b-ketoacyl-ACP synthase (meromycolate extension) bioesterase II possible acyl carrier protein possible acyl carrier protein p
Rv2243 Rv2649 Rv1483 Rv1350 Rv2002 Rv2766c Rv0533c Rv2546 Rv1484 Rv2245 Rv2246 Rv1618 Rv2605c Rv0033 Rv1344 Rv1722 Rv3221c Rv3221c Rv3391 Rv3391 Rv3392 Rv3391 Rv3392 Rv3292 Rv329	fabD2 fabG2 fabG1 fabG2 fabG3 fabG4 fabG4 fabG4 fabG4 fabG4 fabH fas kasA kasB tesB1 tesB2 - - - - - - - - - - - - - - - - - - -	malonyl CoA-[ACP] transacylase malonyl CoA-[ACP] transacylase 3-oxoacyl-[ACP] reductase (aka MabA) 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase β-ketoacyl-ACP synthase III fatty acid synthase enoyl-[ACP] reductase β-ketoacyl-ACP synthase (meromycolate extension) β-ketoacyl-ACP synthase (meromycolate extension) β-ketoacyl-ACP synthase (meromycolate extension) β-ketoacyl-ACP synthase (meromycolate extension) b-ketoacyl-ACP synthase (meromycolate extension) thioesterase II possible acyl carrier protein possible acyl carrier protein possible biotin carboxylase resembles biotin carboxylase resembles biotin carboxylase resembles biotin carboxylase resembles acyl carrier protein possible ac
Rv2243 Rv0649 Rv1483 Rv1350 Rv2002 Rv0242c Rv2766c Rv0533c Rv2524c Rv2524c Rv2524c Rv2524c Rv2524c Rv2524c Rv2524c Rv2524c Rv2524c Rv2524c Rv2524c Rv3931 Rv3932c Rv3932c Rv3932c Rv3932c Rv3932c Rv3932c Rv3932c Rv3932c Rv3932c Rv3932c Rv3932c Rv3932c	fabD2 fabG2 fabG1 fabG2 fabG3 fabG4 fabG5 fabH fas inhA kasA kasB tesB1 tesB2 - - - - - - - - - - - - - - - - - - -	malonyl CoA-[ACP] transacylase malonyl CoA-[ACP] transacylase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase B-ketoacyl-ACP synthase (meromycolate extension) β-ketoacyl-ACP synthase (meromycolate extension) β-ketoacyl-ACP synthase (meromycolate extension) β-ketoacyl-ACP synthase (meromycolate extension) bioesterase II possible acyl carrier protein possible acyl carrier protein thosetase 1 cyclopropane mycolic acid synthase 1 cyclopropane mycolic acid syn- thase 2 acyl-[ACP] desaturase acyl-[ACP] desaturase acyl-[ACP] desaturase
Rv2243 Rv0649 Rv1483 Rv1350 Rv2002 Rv0242C Rv2524C Rv1484 Rv2245 Rv2246 Rv1484 Rv2245 Rv2246 Rv1618 Rv2605C Rv0033 Rv1344 Rv1722 2. Modifica Rv3472 2. Modifica Rv3939 Rv3939C Rv0503C	fabD2 fabD2 fabG1 fabG1 fabG2 fabG3 fabG4 fabH fas inhA kasA kasB tesB1 tesB2 - - - - - - - - - - - - - - - - - - -	hindonyi CoA-[ACP] transacylase malonyi CoA-[ACP] transacylase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase β-ketoacyl-ACP synthase (meromycolate extension) β-ketoacyl-ACP synthase (meromycolate extension) β-ketoacyl-ACP synthase (meromycolate extension) β-ketoacyl-ACP synthase (meromycolate extension) thioesterase II thioesterase II possible acyl carrier protein possible acyl carrier protein thioesterase I y and mycolic acids synthase 1 acyl-[ACP] desaturase acyl-[ACP] desaturase acyl-[ACP] desaturase acyl-[ACP] desaturase acyl-[ACP] desaturase methoxymycolic acid synthase 1 methoxymycolic acid synthase 2
Rv2243 Rv0649 Rv1483 Rv1350 Rv2002 Rv0242C Rv2524C Rv2524C Rv2524C Rv2524C Rv2246 Rv1484 Rv2245 Rv2246 Rv1618 Rv2246 Rv1618 Rv1344 Rv1722 Rv3291C Rv3292C Rv0503C Rv0503C Rv0503C Rv0503C Rv0503C Rv0504C Rv1094C Rv1094C Rv0645C Rv0645C Rv0643C	fabD2 fabD2 fabG1 fabG1 fabG2 fabG3 fabG4 fabG4 fabG4 fabH fas inhA kasA kasB tesB1 tesB2 - - - - - - - - - - - - - - - - - - -	malonyl CoA-[ACP] transavylase malonyl CoA-[ACP] transavylase 3-oxoacyl-[ACP] reductase (aka MabA) 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase 3-oxoacyl-[ACP] reductase β-ketoacyl-ACP synthase III fatty acid synthase enoyl-[ACP] reductase β-ketoacyl-ACP synthase (meromycolate extension) β-ketoacyl-ACP synthase (meromycolate extension) β-ketoacyl-ACP synthase (meromycolate extension) bioesterase II possible acyl carrier protein possible acyl-[ACP] desaturase acyl-[ACP] desaturase methoxymycolic acid synthase 1 methoxymycolic acid synthase 3
Rv2243 Rv2649 Rv1483 Rv1350 Rv2002 Rv2766c Rv0533c Rv2546 Rv1484 Rv2245 Rv2246 Rv1618 Rv2605c Rv0033 Rv1344 Rv1722 Rv3221c Rv3221c Rv3391 Rv3391 Rv3391 Rv3392 Rv0503c Rv0503c Rv0503c Rv0503c Rv0504c Rv0246 Rv0642c Rv0642c	fabD2 fabG2 fabG1 fabG2 fabG3 fabG4 fabG5 fabH fas kasA kasB tesB1 tesB2 - - - - - - - - - - - - - - - - - - -	 Indionyl CoA-[ACP] transacylase malonyl CoA-[ACP] transacylase a-oxoacyl-[ACP] reductase b-ketoacyl-ACP synthase III fatty acid synthase (meromycolate extension) b-ketoacyl-ACP synthase (meromycolate extension) b-ketoacyl-ACP synthase (meromycolate extension) thioesterase II possible acyl carrier protein possible acyl a
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Rv0470c	umaA2	unknown mycolic acid methyl- transferase	Rv2931 Rv2932 Rv2933
3. Acyltran	sferases,	mycoloyltransferases and	Rv2934
Rv2289	cdh	CDP-diacylglycerol phosphatidyl-	Rv2928
Bv2881c	cdsA	nyorolase phosphatidate cytidylyltransferase	RV1544
Rv3804c	fbpA	antigen 85A, mycolyltransferase	J. Broad re
Rv1886c	fbpB	antigen 85B, mycolyltransferase	1. Repress
Rv3803c	fbpC1	antigen 85C, mycolyltransferase	Rv1657
Rv0129c	fbpC2	antigen 85C', mycolytransferase	Rv1267c
Rv0564c	gpdA1	glycerol-3-phosphate dehydroge-	
		nase	Rv1909c
Rv2982c	gpdA2	glycerol-3-phosphate dehydroge-	Rv2359
D::0010a		nase	Rv2919c
RV2012C	pgsA	CDP-diacyigiyceroi-giyceroi-3-	RV2711
		foraço	RV2720
Dv1922	nac A 2	CDP diacylalycorol alycorol 2	NV14/9
HV1022	рузяг	phosphate phosphatidyltraps-	Bv3602
		ferase	1100032
Bv2746c	pasA3	CDP-diacylalycerol-alycerol-3-	Bv3164c
	190.10	phosphate phosphatidyltrans-	
		ferase	Rv0212c
Rv1551	plsB1	glycerol-3-phosphate acyltrans-	Rv0117
		ferase	
Rv2482c	plsB2	glycerol-3-phosphate acyltrans-	Rv1379
		ferase	
Rv0437c	psd	putative phosphatidylserine	Rv2788
_		decarboxylase	
Rv0436c	pssA	CDP-diacylglycerol-serine	Rv3082c
D. 0045.		o-phosphatidyltransferase	D. 0010
RV0045C	-	possible dinydrolipoamide acetyi-	RV3219
D::0014a		transferase	Ducocoa
RV0914C	-	nrobable fatty and CoA reductan	RV3260C
By1627c	-	linid carrier protein	Bv3416
Rv1814	-	nossible C-5 sterol desaturase	1100410
Bv1867	-	similar to acetyl CoA	Bv3681c
		synthase/lipid carriers	
Rv2261c	-	apolipoprotein N-acyltrans-	Rv0023
		ferase-a	Rv0043c
Rv2262c		apolipoprotein N-acyltrans-	
		ferase-b	Rv0067c
Rv3523	-	lipid carrier protein	
Rv3720		C-term similar to cyclopropane	Rv0078
		fatty acid synthases	D. 0001
I. Daludvatia		with a second a section south a sis	RV0081
Rv2940c	mae	mycocerosic acid synthese	By0135c
Bv2384	mhtA	mycobactin/exochelin synthesis	Bv0144
		(salicylate-AMP ligase)	Rv0158
Rv2383c	mbtB	mycobactin/exochelin synthesis	
		(serine/threonine ligation)	Rv0165c
Rv2382c	mbtC	mycobactin/exochelin synthesis	
Rv2381c	mbtD	mycobactin/exochelin synthesis	Rv0195
		(polyketide synthase)	
Rv2380c	mbtE	mycobactin/exochelin synthesis	Rv0196
Bu2270a	mhtE	(Iysine ligation)	Bu0000
NV23/90	motr	(lycino ligation)	RV0232
By2378c	mhtG	mycobactin/exochelin synthesis	Bv0238
	more	(lysine hydroxylase)	
Bv2377c	mbtH	mycobactin/exochelin synthesis	Rv0273c
Rv0101	nrp	unknown non-ribosomal peptide	Rv0302
		synthase	
Rv1153c	omt	PKS o-methyltransferase	Rv0324
Rv3824c	papA1	PKS-associated protein, unknown	Rv0328
		function	
Rv3820c	papA2	PKS-associated protein, unknown	Rv0348
D. 1100		function	RV0377
RVI182	рарАЗ	function	DV020C
By1528c	nan44	PKS-associated protein unknown	HV0300
11010200	papria	function	Bv0452
Bv2939	papA5	PKS-associated protein, unknown	Bv0465c
	<i>μμ</i> τ-	function	
Rv2946c	pks1	polyketide synthase	Rv0472c
Rv1660	pks10	polyketide synthase (chalcone	
			Rv0474
Rv1665		synthase-like)	
_	pks11	synthase-like) polyketide synthase (chalcone	
Rv2048c	pks11	synthase-like) polyketide synthase (chalcone synthase-like)	Rv0485
	pks11 pks12	synthase-like) polyketide synthase (chalcone synthase-like) polyketide synthase (erythronolide	Rv0485
D. 0000a	pks11 pks12	synthase-like) polyketide synthase (chalcone synthase-like) polyketide synthase (erythronolide synthase-like)	Rv0485 Rv0494
Rv3800c	pks11 pks12 pks13	synthase-like) polyketide synthase (chalcone synthase-like) polyketide synthase (erythronolide synthase-like) polyketide synthase	Rv0485 Rv0494
Rv3800c Rv1342c	pks11 pks12 pks13 pks14	synthase-like) polyketide synthase (chalcone synthase-like) polyketide synthase (erythronolide synthase-like) polyketide synthase polyketide synthase (chalcone synthase)	Rv0485 Rv0494 Rv0552 Bv0576
Rv3800c Rv1342c	pks11 pks12 pks13 pks14 pks15	synthase-like) polyketide synthase (chalcone synthase-like) polyketide synthase (erythronolide synthase-like) polyketide synthase polyketide synthase (chalcone synthase-like) polyketide synthase	Rv0485 Rv0494 Rv0552 Rv0576 Bv0586
Rv3800c Rv1342c Rv2947c Bv1013	pks11 pks12 pks13 pks14 pks15 pks16	synthase-like) polyketide synthase (chalcone synthase-like) polyketide synthase (erythronolide synthase-like) polyketide synthase polyketide synthase polyketide synthase polyketide synthase	Rv0485 Rv0494 Rv0552 Rv0576 Rv0586
Rv3800c Rv1342c Rv2947c Rv1013 Rv1663	pks11 pks12 pks13 pks14 pks15 pks16 pks17	synthase-like) polyketide synthase (chalcone synthase-like) polyketide synthase (erythronolide synthase-like) polyketide synthase polyketide synthase polyketide synthase polyketide synthase polyketide synthase	Rv0485 Rv0494 Rv0552 Rv0576 Rv0586 Rv0586
Rv3800c Rv1342c Rv2947c Rv1013 Rv1663 Rv1372	pks11 pks12 pks13 pks14 pks15 pks16 pks17 pks18	synthase-like) polyketide synthase (chalcone synthase-like) polyketide synthase (erythronolide synthase-like) polyketide synthase polyketide synthase polyketide synthase polyketide synthase polyketide synthase polyketide synthase	Rv0485 Rv0494 Rv0552 Rv0576 Rv0586 Rv0586
Rv3800c Rv1342c Rv2947c Rv1013 Rv1663 Rv1372 Rv3825c	pks11 pks12 pks13 pks14 pks15 pks16 pks17 pks18 pks2	synthase-like) polyketide synthase (chalcone synthase-like) polyketide synthase (erythronolide synthase-like) polyketide synthase polyketide synthase polyketide synthase polyketide synthase polyketide synthase polyketide synthase polyketide synthase	Rv0485 Rv0494 Rv0552 Rv0576 Rv0586 Rv0650 Rv0653c
Rv3800c Rv1342c Rv2947c Rv1013 Rv1663 Rv1372 Rv3825c Rv1180	pks11 pks12 pks13 pks14 pks15 pks16 pks16 pks17 pks18 pks2 pks3	synthase-like) polyketide synthase (chalcone synthase-like) polyketide synthase (erythronolide synthase-like) polyketide synthase polyketide synthase polyketide synthase polyketide synthase polyketide synthase polyketide synthase	Rv0485 Rv0494 Rv0552 Rv0576 Rv0586 Rv0650 Rv0653c Rv0681
Rv3800c Rv1342c Rv1013 Rv1663 Rv1372 Rv3825c Rv1180 Rv1181	pks11 pks12 pks13 pks14 pks15 pks16 pks16 pks17 pks18 pks2 pks3 pks4	synthase-like) polyketide synthase (chalcone synthase-like) polyketide synthase (erythronolide synthase-like) polyketide synthase polyketide synthase polyketide synthase polyketide synthase polyketide synthase polyketide synthase polyketide synthase polyketide synthase polyketide synthase	Rv0485 Rv0494 Rv0552 Rv0576 Rv0586 Rv0650 Rv0653c Rv0681
Rv3800c Rv1342c Rv1013 Rv1663 Rv1663 Rv1372 Rv3825c Rv1180 Rv1181 Rv1527c	pks11 pks12 pks13 pks14 pks15 pks16 pks17 pks18 pks2 pks3 pks4 pks5	synthase-like) polyketide synthase (chalcone synthase-like) polyketide synthase (erythronolide synthase-like) polyketide synthase polyketide synthase	Rv0485 Rv0494 Rv0552 Rv0576 Rv0586 Rv0650 Rv0653c Rv0681 Rv0691c
Rv3800c Rv1342c Rv1013 Rv1013 Rv1663 Rv1372 Rv3825c Rv1180 Rv1181 Rv1527c Rv0405	pks11 pks12 pks13 pks14 pks16 pks16 pks17 pks18 pks2 pks3 pks2 pks3 pks5 pks6	synthase-like) polyketide synthase (chalcone synthase-like) polyketide synthase (erythronolide synthase-like) polyketide synthase polyketide synthase	Rv0485 Rv0494 Rv0552 Rv0576 Rv0586 Rv0650 Rv0653c Rv0681 Rv0691c
Rv3800c Rv1342c Rv1013 Rv1663 Rv1372 Rv3825c Rv1180 Rv1181 Rv1527c Rv0405 Rv1661	pks11 pks12 pks13 pks14 pks16 pks16 pks17 pks18 pks2 pks3 pks4 pks5 pks6 pks6 pks7	synthase-like) polyketide synthase (chalcone synthase-like) polyketide synthase (erythronolide synthase-like) polyketide synthase polyketide synthase	Rv0485 Rv0494 Rv0552 Rv0556 Rv0586 Rv0650 Rv0653c Rv0681 Rv0691c Rv0737
Rv3800c Rv1342c Rv1013 Rv1663 Rv1372 Rv3825c Rv1180 Rv1181 Rv1527c Rv0405 Rv1661 Rv1662 Dv1664	pks11 pks12 pks13 pks14 pks15 pks16 pks17 pks18 pks2 pks3 pks4 pks5 pks6 pks7 pks8	synthase-like) polyketide synthase (chalcone synthase-like) polyketide synthase (erythronolide synthase-like) polyketide synthase polyketide synthase	Rv0485 Rv0494 Rv0552 Rv0576 Rv0586 Rv0650 Rv0650 Rv0691c Rv0737 Rv0737

1	ppsA	phenolpthiocerol synthesis (pksB)
2	ppsB ppsC	phenolpthiocerol synthesis (<i>pksC</i>) phenolpthiocerol synthesis (<i>pksD</i>)
4	ppsD	phenolpthiocerol synthesis (<i>pksE</i>)
5	ppsE tosA	phenolpthiocerol synthesis (<i>pksF</i>)
5 4	-	probable ketoacyl reductase
dra	aulatory f	unationa
ress	ors/activat	tors
7	argR	arginine repressor
/C	embri	(AfsR/DndI/RedD family)
9c	furA	ferric uptake regulatory protein
9 Pc	turB alnB	terric uptake regulatory protein
1	ideR	iron dependent repressor, IdeR
) a	lexA moxB	LexA, SOS repressor protein
	moxiii	homologue
2	moxR2	transcriptional regulator, MoxR
4c	moxR3	transcriptional regulator, MoxR
2c	nadR	homologue similar to <i>E.coli</i> NadB
7	oxyS	transcriptional regulator (LysR
a	nvr B	family) regulatory protein pyrimidine
	pyiii	biosynthesis
3	sirR	iron-dependent transcriptional
2c	virS	putative virulence regulating
		protein (AraC/XyIS family)
9	whiB1	WhiB transcriptional activator homologue
C	whiB2	WhiB transcriptional activator
6	whiB3	Nomologue WhiB transcriptional activator
		homologue
10	whiB4	WhiB transcriptional activator homologue
3	-	putative transcriptional regulator
3c	-	transcriptional regulator (GntR family)
7c	-	transcriptional regulator
3	-	(TetH/AcrH family) transcriptional regulator
		(TetR/AcrR family)
1	-	transcriptional regulator (ArsR family)
5c	-	putative transcriptional regulator
4 २	-	putative transcriptional regulator
5		(TetR/AcrR family)
5C	-	transcriptional regulator (GntR
5	-	transcriptional regulator
_		(LuxR/UhpA family)
c	-	(TetR/AcrR family)
2	-	transcriptional regulator
3	-	(TetR/AcrR family) transcriptional regulator
		(TetR/AcrR family)
3c	-	putative transcriptional regulator
2	-	(TetR/AcrR family)
4	-	putative transcriptional regulator
5	-	(TetR/AcrR family)
3	-	putative transcriptional regulator
(-	family)
6	-	transcriptional regulator
2	-	(LuxR/UhpA family) putative transcriptional regulator
- 5c	-	transcriptional regulator
20	-	(PbsX/Xre family) transcriptional regulator
		(TetR/AcrR family)
4	-	transcriptional regulator (PbsX/Xre family)
5	-	transcriptional regulator (ROK
4	-	family) transcriptional regulator (GntB
		family)
2	-	putative transcriptional regulator
5	-	transcriptional regulator (GntR
h	_	family)
-		family)
3c 1	-	putative transcriptional regulator
		(TetR/AcrR family)
1c	-	transcriptional regulator
7	-	putative transcriptional regulator
4c	-	putative transcriptional regulator
<u>-</u> U	-	ranscriptional regulator (GITIH

╴┙╧╶╧╧╼╧┙╡╣╡ او چروپ کن کمک نیز میک و از کرنے کے وروز و و و بر انگریں کا والی از اور و مرز از از کرنے کے لیے ان پریریز از کا کمک کے مرز ور از م Ĵ. ڔڔڔڔڔ² و کر و ^مرر کر و ^رادان کر کرک برد کر و و روز و 77/00 11211 11211 ن در بر بر در از بری و طوان و بر از در ایک و ╺╾╴╧╶╷╧╶┊╻┊╶┊╸┊┙┊┙┊┊┊┊┊┊┊┊┊┊┊ *ال الخود حد الله الحرك المحكم الحرك المحال الحرك الحرك المحكم المحكم المحكم المحل الحرك المحلم المحل المحلم المحل المحلم ال* 1 <u>____</u> و المراجع المسلمان كام المراجع المراجع المسلمان المراجع المسلمان المراجع المسلمان المراجع المسلمان المراجع ال 2 ĸ

╵╞╒╶^{┿┿┿}┊╧╡┍╶╶┍╵┙╒╵╡╞╶╻╸┍╸┿┿╧┿┽╸╕╡╵┍╾┍╸ 100 400 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - 200 - $\frac{1}{2} \left(\frac{1}{2} \left(\frac{1}{2} \left(\frac{1}{2} \left(\frac{1}{2} \right) + \frac{1}{2} \left(\frac{1}{2} \right) \right) \right) \left(\frac{1}{2} \left(\frac{1}{2} \right) + \frac{1}{2} \left(\frac{1}{2} \left(\frac{1}{2} \right) + \frac{1}{2} \left(\frac{1}{2} \right) \right) \right) \left(\frac{1}{2} \left(\frac{1}{2} \right) + \frac{1}{2} \left(\frac{1}{2} \right) \right) \left(\frac{1}{2} \left(\frac{1}{2} \right) + \frac{1}{2} \left(\frac{1}{2} \right) \right) \left(\frac{1}{2} \left(\frac{1}{2} \right) + \frac{1}{2} \left(\frac{1}{2} \right) \right) \left(\frac{1}{2} \left(\frac{1}{2} \right) + \frac{1}{2} \left(\frac{1}{2} \right) \right) \left(\frac{1}{2} \left(\frac{1}{2} \right) + \frac{1}{2} \left(\frac{1}{2} \right) \right) \left(\frac{1}{2} \right)$ ݘݲ*ݯݱݾݸݷݸݱݸݾݸݵݬݷݬݯݸݷݸݲݥݛݸݵݷݬݾݖݖݵݯݢݥݖݖݖݸݙݸݷݷݚݵݵݵݖݵݸݙݵݱݸݵݸݷݸݷݬݷݖݖݾݷݷݬݷݣݯݵݵݸݷݵݷݬݥݷݷݬݽݵݵݵݖݥݥݸݷݵݭݥݾݷݷݸݵݥݷݔݥ* ورجوا والمحافي والمحافية والمنافية والمنافية ł $-\frac{1}{2} + \frac{1}{2} + \frac{1$ ب کرو خر خربر کرو کرد کرو کرو کرو کرو کرو کرو کرو کرو کر کرو $\frac{1}{2} \sum_{i=1}^{n} \sum_{j=1}^{n} \sum_{i=1}^{n} \sum_{j=1}^{n} \sum_{j=1}^$ ر^{ای} _{الل} کسک روز کسک و کسک و کر ایک کر ایک میں مکر رائی کس<u>ک میں میں کر ک</u>ر میں میں کر کر کر کر کر کر کر کر کر موال ŀŀ ٥٣) نې روې و ٩٩ مې و ٩٩ مې و ٩٩ مې و ٩٩ مې ⁴⁴ و ⁴⁴ و مې ⁴ ورو ⁴ و ۲. <u>، بې چې چې کې د مورم کې کې د مرکزې کې کې د مورم کې کې د مرکزې کې د مرکزې کې د</u> 10 00 1 و کو چرچی ایک کرکرکرکرکرکا مرجع <u>I</u>..... ł

		family)
Rv0823c	-	transcriptional regulator
		(NifR3/Smm1 family)
Rv0827c	-	transcriptional regulator (ArsR
		family)
Rv0890c	-	transcriptional regulator
		(LuxR/UhpA family)
Rv0891c	-	putative transcriptional regulator
Rv0894	-	putative transcriptional regulator
Rv1019	-	transcriptional regulator
		(TetR/AcrR family)
Rv1049	-	transcriptional regulator (MarR
		family)
Rv1129c	-	transcriptional regulator
		(PbsX/Xre family)
Rv1151c	-	putative transcriptional regulator
Rv1152	-	transcriptional regulator (GntR
		family)
Rv1167c	-	putative transcriptional regulator
Rv1219c	-	putative transcriptional regulator
Rv1255c	-	transcriptional regulator
		(TetR/AcrR family)
Rv1332	-	putative transcriptional regulator
Rv1353c	-	transcriptional regulator
		(TetR/AcrR family)
Rv1358	-	transcriptional regulator
		(LuxR/UhpA family)
Rv1359	-	putative transcriptional regulator
Rv1395	-	transcriptional regulator
		(AraC/XvIS family)
Bv1404	-	transcriptional regulator (MarB
		family)
Rv1423	-	putative transcriptional regulator
Rv1460	-	putative transcriptional regulator
Rv1474c		transcriptional regulator
		(TetB/AcrB family)
Bv1534	-	transcriptional regulator
110100-1		(TetB/AcrB family)
Bv1556	_	putative transcriptional regulator
Bv1674c	_	putative transcriptional regulator
Dv16750	_	putative transcriptional regulator
DV1710	-	
NV1/19	-	
D. 1770		lamily)
RV1773C	-	transcriptional regulator (ICIR
D. 1770a		larrilly)
RV1776C	-	putative transcriptional regulator
RV1816	-	putative transcriptional regulator
Rv1846C	-	putative transcriptional regulator
Rv1931c	-	transcriptional regulator
		(AraC/XVIS tamily)
		(Arao/Ayio farmiy)
Rv1956	-	putative transcriptional regulator
Rv1956 Rv1963c	-	putative transcriptional regulator putative transcriptional regulator
Rv1956 Rv1963c Rv1985c	-	putative transcriptional regulator putative transcriptional regulator transcriptional regulator (LysR
Rv1956 Rv1963c Rv1985c	-	putative transcriptional regulator putative transcriptional regulator transcriptional regulator (LysR family)
Rv1956 Rv1963c Rv1985c Rv1990c	- - -	putative transcriptional regulator putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator
Rv1956 Rv1963c Rv1985c Rv1990c Rv1994c	-	putative transcriptional regulator putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR
Rv1956 Rv1963c Rv1985c Rv1990c Rv1994c	-	putative transcriptional regulator putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family)
Rv1956 Rv1963c Rv1985c Rv1990c Rv1994c Rv2017	-	putative transcriptional regulator putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator
Rv1956 Rv1963c Rv1985c Rv1990c Rv1994c Rv2017	-	(Placky) transcriptional regulator putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (PbsX/Xre family)
Rv1956 Rv1963c Rv1985c Rv1990c Rv1994c Rv2017 Rv2021c	-	putative transcriptional regulator putative transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (PbsXXre family) putative transcriptional regulator
Rv1956 Rv1963c Rv1985c Rv1990c Rv1994c Rv2017 Rv2021c Rv2034	-	(Place Ny) is transcriptional regulator putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (Pbs/X/re family) putative transcriptional regulator transcriptional regulator transcriptional regulator
Rv1956 Rv1963c Rv1985c Rv1990c Rv1994c Rv2017 Rv2021c Rv2034		(Place Algorithm)) putative transcriptional regulator putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator (MerR family) putative transcriptional regulator (PbsXXre family) putative transcriptional regulator transcriptional regulator family)
Rv1956 Rv1963c Rv1985c Rv1990c Rv1994c Rv2017 Rv2021c Rv2034 Rv2175c	- - - - -	(Placky) transcriptional regulator putative transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator transcriptional regulator (PbsX/Xre family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator
Rv1956 Rv1963c Rv1985c Rv1990c Rv1994c Rv2017 Rv2021c Rv2024 Rv2175c Rv2250c		(NaON) transcriptional regulator putative transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator (MeR family) putative transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator
Rv1956 Rv1963c Rv1985c Rv1990c Rv1994c Rv2017 Rv2021c Rv2034 Rv2175c Rv2250c Rv2258c		(NaON) transcriptional regulator putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (PbsXXre family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator
Rv1956 Rv1963c Rv1985c Rv1990c Rv2017 Rv2021c Rv2034 Rv2175c Rv2250c Rv2282c		(NaON)/O tamily) putative transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator transcriptional regulator (PbsX/Xre family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator
Rv1956 Rv1963c Rv1990c Rv1990c Rv2017 Rv2021c Rv2034 Rv2175c Rv2250c Rv2258c Rv2288c		(NaON)/C transcriptional regulator putative transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator (MeR family) putative transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator family)
Rv1956 Rv1985c Rv1990c Rv1990c Rv2017 Rv2017 Rv2021c Rv2034 Rv2175c Rv2250c Rv2258c Rv2282c		(HabAy)G tamis)) putative transcriptional regulator putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator (MerR family) putative transcriptional regulator (PbsX/xre family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator family) putative transcriptional regulator (LysR family)
Rv1956 Rv1985c Rv1990c Rv1990c Rv2017 Rv2021c Rv2034 Rv2175c Rv2250c Rv2250c Rv2250c Rv2282c Rv2282c		(NaXy)'s tamis)) putative transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator (PbsX/Xre family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator transcriptional regulator transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (LysR family)
Rv1956 Rv1985c Rv1985c Rv1990c Rv2017 Rv2017 Rv2021c Rv2034 Rv2250c Rv2250c Rv2282c Rv2282c Rv2308 Rv2324		(http://www.international.com/ putative transcriptional regulator transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator (MerR family) putative transcriptional regulator (Pbs/X/re family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator
Rv1956 Rv1963c Rv1990c Rv1990c Rv2017 Rv2021c Rv2034 Rv2250c Rv2250c Rv2250c Rv2250c Rv22308 Rv2304 Rv2308		(Natory) transcriptional regulator putative transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator (MerR family) putative transcriptional regulator (PbsX/Kr family) putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator transcriptional regulator (Lrp/AsnC family)
Rv1956 Rv1985c Rv1985c Rv1990c Rv2017 Rv2017 Rv2021c Rv2034 Rv2175c Rv2250c Rv2250c Rv2250c Rv2282c Rv2308 Rv2308 Rv2358		(https://stranscriptional regulator putative transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator (PbsX/Xre family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator family) putative transcriptional regulator (Lrg/AsnC family) transcriptional regulator (ArsR family)
Rv1956 Rv1985c Rv1990c Rv1990c Rv2017 Rv2021c Rv2024 Rv2250c Rv2250c Rv2250c Rv2280c Rv2308 Rv2308 Rv2388 Rv2488c		(HadNy)'s transcriptional regulator putative transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator (PbsX/Xre family) putative transcriptional regulator transcriptional regulator (PbsX/Xre family) putative transcriptional regulator putative transcriptional regulator family) putative transcriptional regulator (Lrp/AsnC family) transcriptional regulator (ArsR family) transcriptional regulator (ArsR family) transcriptional regulator (ArsR family)
Rv1956 Rv1963c Rv1990c Rv1990c Rv2904 Rv2017 Rv2016 Rv2250c Rv2250c Rv2258c Rv2258c Rv2258c Rv2282c Rv2282c		(http://www.commissional.commis
Rv1956 Rv1985c Rv1990c Rv1990c Rv2017 Rv2021c Rv2034 Rv2175c Rv2250c Rv2250c Rv2250c Rv2282 Rv2388 Rv2388 Rv2388 Rv2388 Rv2488c Rv2506		(http://www.commission
Rv1956 Rv1985c Rv1985c Rv1990c Rv2017 Rv2017 Rv2021c Rv2034 Rv2175c Rv2250c Rv2250c Rv228c Rv2308 Rv2308 Rv2358 Rv2488c Rv2506		(HadNy/G tamily) putative transcriptional regulator putative transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator (PbsX/Xre family) putative transcriptional regulator transcriptional regulator transcriptional regulator putative transcriptional regulator (LysR family) putative transcriptional regulator (LysR family) transcriptional regulator (ArsR family) transcriptional regulator (LysR/UhpA family) transcriptional regulator (LosR/UhpA family)
Rv1956 Rv1985c Rv1990c Rv2990c Rv2017 Rv2021c Rv2034 Rv2175c Rv2258c Rv2258c Rv2282c Rv2282c Rv2308 Rv2308 Rv2308 Rv2488c Rv2488c Rv2506 Rv2621c		(http://www.international.regulator putative transcriptional regulator transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (PbsX/kc family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator (Lrp/AsnC family) transcriptional regulator (LusR/UpA family) transcriptional regulator (LusR/UpA family) transcriptional regulator (TetR/AcrR family) putative transcriptional regulator
Rv1956 Rv1985c Rv1990c Rv1990c Rv2017 Rv2021c Rv2034 Rv2175c Rv2250c Rv2250c Rv2250c Rv2250c Rv2288 Rv2388 Rv2388 Rv2388 Rv2388 Rv2488c Rv2506 Rv2621c Rv2621c		(HadNyIS tamis)) putative transcriptional regulator putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator family) putative transcriptional regulator (LysR family) putative transcriptional regulator (LysR family) transcriptional regulator (ArsR family) transcriptional regulator (LuxR/UhpA family) transcriptional regulator (TetR/AcrR family) putative transcriptional regulator (TetR/AcrR family)
Rv1956 Rv1985c Rv1985c Rv1990c Rv2017 Rv2017 Rv2021c Rv2024 Rv2175c Rv2250c Rv2250c Rv2282c Rv2308 Rv2308 Rv2308 Rv2358 Rv2488c Rv2506 Rv2506 Rv2621c Rv2640c		(HadNy/G tamily) putative transcriptional regulator putative transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator (PbsX/Xre family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator (LysR family) putative transcriptional regulator (LysR family) transcriptional regulator (ArsR family) transcriptional regulator (LorR/UhpA family) transcriptional regulator (TetR/AcrR family) putative transcriptional regulator transcriptional regulator (TetR/AcrR family)
Rv1956 Rv1985c Rv1990c Rv1990c Rv2017 Rv2021c Rv2034 Rv2175C Rv2250c Rv2250c Rv2250c Rv2250c Rv2282 Rv2388 Rv2388 Rv2388 Rv2488c Rv2488c Rv2488c Rv2506 Rv2640c		(http://www.international.regulator putative transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (PbsX/Ke family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator (Lrp/AsnC family) transcriptional regulator (ArsR family) transcriptional regulator (LusR/UhpA family) transcriptional regulator (TetR/AcrR family) putative transcriptional regulator transcriptional regulator (TetR/AcrR family) putative transcriptional regulator transcriptional regulator (TarsR family) putative transcriptional regulator transcriptional regulator (TetR/AcrR family) putative transcriptional regulator transcriptional regulator (ArsR family)
Rv1956 Rv1985c Rv1985c Rv1990c Rv2017 Rv2017 Rv2021c Rv2034 Rv2175c Rv2250c Rv250c Rv25		(HadNy) transcriptional regulator putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (PbsX/Xre family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator family) putative transcriptional regulator (LysR family) putative transcriptional regulator (LysR family) transcriptional regulator (ArsR family) transcriptional regulator (LuxR/UhpA family) transcriptional regulator (TetR/AcrR family) putative transcriptional regulator transcriptional regulator (TetR/AcrR family) transcriptional regulator (ArsR family)
Rv1956 Rv1963c Rv1990c Rv1990c Rv2017 Rv2017 Rv2021c Rv2250c Rv2250c Rv2250c Rv2250c Rv2250c Rv2250c Rv2250c Rv2250c Rv2250c Rv2250c Rv2250c Rv2250c Rv22640c Rv2640c Rv2642 Rv2649		(HabAyJo tamis)) putative transcriptional regulator putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (PbsX/Kr family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (LyrAsC family) transcriptional regulator (LuxR/UhpA family) putative transcriptional regulator (TetR/AcrR family) putative transcriptional regulator transcriptional regulator (TetR/AcrR family) putative transcriptional regulator transcriptional regulator (TetR/AcrR family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator family) putative transcriptional regulator (ArsR family)
Rv1956 Rv1985c Rv1990c Rv1990c Rv2017 Rv2021c Rv2034 Rv2175c Rv2250c Rv2250c Rv2250c Rv2282c Rv2282c Rv2388 Rv2388 Rv2388 Rv2488c Rv2488c Rv2488c Rv2488c Rv2640c Rv2640c Rv2640c		(HabAy) transcriptional regulator putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (PbsXXre family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator (LysRASC family) putative transcriptional regulator transcriptional regulator (LysRASC family) transcriptional regulator (TetR/AcrR family) putative transcriptional regulator transcriptional regulator (TetR/AcrR family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator transcriptional regulator (ArsR family)
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Rv1956 Rv1985c Rv1985c Rv1985c Rv1990c Rv2017 Rv2017 Rv2017 Rv2017 Rv2017 Rv2017 Rv2017 Rv2017 Rv2017 Rv2038 Rv2388 Rv2388 Rv2488c Rv2640c Rv2640c Rv2640c Rv2640c Rv2641c Rv2642 Rv2887 Rv2912c Rv3050c Rv3050c		(HaGNA)G tamis)) putative transcriptional regulator transcriptional regulator (LysR family) putative transcriptional regulator transcriptional regulator (MerR family) putative transcriptional regulator (PbsX/Xre family) putative transcriptional regulator transcriptional regulator (ArsR family) putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator putative transcriptional regulator family) putative transcriptional regulator putative transcriptional regulator (LysAsnC family) putative transcriptional regulator (LrgAAsnC family) transcriptional regulator (ArsR family) transcriptional regulator (LusR/UhpA family) transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator (LrgAAsnC family) putative transcriptional regulator transcriptional regulator transcriptional regulator (CrgRAcrR family) transcriptional regulator (MarR family) transcriptional regulator (MarR family) transcriptional regulator (IcR family) transcriptional regulator (IcR family) transcriptional regulator (IcR family)
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By3160c	_	putative transcriptional regulator
Dv21670		putative transcriptional regulator
Dv21720	-	transcriptional regulator
HV31730	-	(TotP/AcrD family)
D. 0100		(TetR/AcrR Tarrilly)
RV3183	-	putative transcriptional regulator
Rv3208	-	transcriptional regulator
_		(TetR/AcrR family)
Rv3249c	-	transcriptional regulator
		(TetR/AcrR family)
Rv3291c	-	transcriptional regulator
		(Lrp/AsnC family)
Bv3295	-	transcriptional regulator
		(TetB/AcrB family)
Dv2224		transcriptional regulator (MorP
HV3334	-	fomily)
D. 0405 -		lamily)
RV3405C	-	putative transcriptional regulator
RV3522	-	putative transcriptional regulator
Rv3557c	-	transcriptional regulator
		(TetR/AcrR family)
Rv3574	-	transcriptional regulator
		(TetR/AcrR family)
Rv3575c	-	transcriptional regulator (Lacl
		family)
Rv3583c	-	putative transcriptional regulator
Bv3676	-	transcriptional regulator (Crp/Enr
		family)
Dv26790		transcriptional regulator (LycP
HV3070C	-	
D. 0700		lamily)
RV3736	-	transcriptional regulator
B 07.11		(Arac/XyIS family)
Rv3744	-	transcriptional regulator (ArsR
		family)
Rv3830c	-	transcriptional regulator
		(TetR/AcrR family)
Bv3833	-	transcriptional regulator
		(AraC/Xy/S family)
Dv2040		(Alao/Aylo lamily)
RV3040	-	putative transcriptional regulator
RV3855	-	putative transcriptional regulator
2. Two cor	nponent sy	/stems
Rv1028c	kdpD	sensor histidine kinase
Rv1027c	kdpE	two-component response
		regulator
Bv3246c	mtrA	two-component response
		regulator
Dv22450	mtrB	sonsor histiding kinaso
Dv09440	narl	two component response
NV0644C	TIALL	two-component response
-		regulator
RV0757	phoP	two-component response
		regulator
Rv0758	phoR	regulator sensor histidine kinase
Rv0758 Rv0491	phoR regX3	regulator sensor histidine kinase two-component response
Rv0758 Rv0491	phoR regX3	regulator sensor histidine kinase two-component response regulator
Rv0758 Rv0491 Rv0490	phoR regX3 senX3	regulator sensor histidine kinase two-component response regulator sensor histidine kinase
Rv0758 Rv0491 Rv0490 Rv0602c	phoR regX3 senX3 tcrA	regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response
Rv0758 Rv0491 Rv0490 Rv0602c	phoR regX3 senX3 tcrA	regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator
Rv0758 Rv0491 Rv0490 Rv0602c	phoR regX3 senX3 tcrA	regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator
Rv0758 Rv0491 Rv0490 Rv0602c Rv0260c	phoR regX3 senX3 tcrA -	regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator two-component response regulator
Rv0758 Rv0491 Rv0490 Rv0602c Rv0260c	phoR regX3 senX3 tcrA -	regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator two-component response regulator
Rv0758 Rv0491 Rv0490 Rv0602c Rv0260c Rv0600c	phoR regX3 senX3 tcrA -	regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase
Rv0758 Rv0491 Rv0490 Rv0602c Rv0260c Rv0600c Rv0601c	phoR regX3 senX3 tcrA - -	regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase
Rv0758 Rv0491 Rv0602c Rv0260c Rv0600c Rv0600c Rv0601c Rv0818	phoR regX3 senX3 tcrA - - -	regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase sensor histidine kinase two-component response
Rv0758 Rv0491 Rv0490 Rv0602c Rv0260c Rv0600c Rv0601c Rv0818	phoR regX3 senX3 tcrA - - -	regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase sensor histidine kinase two-component response regulator
Rv0758 Rv0491 Rv0602c Rv0260c Rv0600c Rv0601c Rv0818 Rv0845	phoR regX3 senX3 tcrA - - -	regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase sensor histidine kinase two-component response regulator sensor histidine kinase
Rv0758 Rv0491 Rv0602c Rv0260c Rv0600c Rv0600c Rv0601c Rv0845 Rv0902c	phoR regX3 senX3 tcrA - - - - -	regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator wo-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase sensor histidine kinase
Rv0758 Rv0491 Rv0602c Rv0260c Rv0601c Rv0601c Rv0845 Rv0902c Rv0903c	phoR regX3 senX3 tcrA - - - - - -	regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase sensor histidine kinase
Rv0758 Rv0491 Rv0490 Rv0602c Rv0600c Rv0601c Rv0818 Rv0845 Rv0902c Rv0903c	phoR regX3 senX3 tcrA - - - - - - - - -	regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase
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Rv0758 Rv0491 Rv0602c Rv0600c Rv0600c Rv0600c Rv0600c Rv0845 Rv0902c Rv0903c	phoR regX3 senX3 tcrA - - - - - - - - - -	regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator wo-component response regulator sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase two-component response regulator two-component response regulator
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Rv0758 Rv0491 Rv0490 Rv0490 Rv0602c Rv0602c Rv0845 Rv0802c Rv0802c Rv0803c Rv0803c Rv0903c Rv0982 Rv0982 Rv1032c Rv1032c Rv1032c Rv1626 Rv2027c Rv3133c Rv3133c Rv3220c Rv0315c 3. Serine-1 phosphata Rv0015c Rv0314c Rv0314c Rv0410c Rv143 Rv143 Rv0314c Rv0410c Rv143 Rv143 Rv144 Rv144 Rv144 Rv2041c Rv2041c Rv2041c Rv2041c Rv2041c Rv2041c Rv2041c Rv2041c Rv2041c	phoR regX3 senX3 tcrA - - - - - - - - - - - - - - - - - - -	regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator wo-component response regulator sensor histidine kinase sensor histidine kinase two-component response regulator sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase sensor histidine kinase sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator protein sensor histidine kinase two-component response regulator protein sensor histidine kinase two-component response regulator protein sensor histidine kinase serine-threonine protein kinase
Rv0758 Rv0490 Rv0490 Rv0490 Rv0602c Rv0600c Rv0845 Rv0903c Rv0981 Rv0982 Rv1032c Rv1032c Rv1032c Rv1032c Rv132c Rv3132c Rv3132c Rv3764c Rv0015c Rv04105 Rv0410c Rv1746 Rv0410c Rv247c	phoR regX3 senX3 tcrA - - - - - - - - - - - - - - - - - - -	regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator putative sensory transduction protein sensor histidine kinase two-component response regulator putative sensory transduction protein sensor histidine kinase sensor his
Rv0758 Rv0490 Rv0490 Rv0490 Rv0602c Rv0602c Rv0602c Rv0602c Rv0602c Rv0602c Rv0845 Rv0903c Rv0981 Rv0982 Rv1032c Rv1032c Rv1032c Rv1032c Rv1032c Rv1032c Rv3133c Rv3133c Rv3143 Rv3220c Rv0756c 3. Serine-1 Phosphata Rv015c Rv01742 Rv0314c Rv1743 Rv1266c Rv2088 Rv3080c Rv2080c	phoR regX3 senX3 tcrA - - - - - - - - - - - - - - - - - - -	regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase sensor histidine kinase two-component response regulator two-component response regulator sensor histidine kinase sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator sensor histidine kinase two-component response regulator putative sensory transduction protein serine-thilte kinase sensor histidine kinase serine-threonine protein kinase serine-threonine protein kinase serine-threonine protein kinase serine-threonine protein kinase serine-threonine protein kinase serine-threonine protein kinase

		truppoted
Dv00180	000	nutativo phosphoprotoin phos
11000100	PPP	nhatase
Bv2234	ntnA	low molecular weight protein-tyro-
	papri	sine-phosphatase
Rv0153c	-	putative protein-tyrosine-phos-
		phatase
II. Macrom	olecule m	netabolism
A. Synthes	is and mo	dification of macromolecules
1. Ribosom	nal protein	synthesis and modification
Rv3420c	riml	ribosomal protein S18 acetyl
		transferase
Rv0995	rimJ	acetylation of 30S S5 subunit
RV0641	rpiA	505 ribosomal protein L1
RV0704	rplC	50S ribosomal protein L3
By0702	rnID	50S ribosomal protein L4
Bv0716	rnIF	50S ribosomal protein L5
Rv0719	rpIE	50S ribosomal protein L6
Rv0056	rpll	50S ribosomal protein L9
Rv0651	rpIJ	50S ribosomal protein L10
Rv0640	rplK	50S ribosomal protein L11
Rv0652	rpIL	50S ribosomal protein L7/L12
Rv3443c	rpIM	50S ribosomal protein L13
Rv0714	rpIN	50S ribosomal protein L14
Rv0723	rplO	50S ribosomal protein L15
RV0708	rpiP	50S ribosomal protein L16
RV3456C	rpiQ	505 ribosomal protein L17
By2904c	rolS	50S ribosomal protein L19
Bv1643	rnIT	50S ribosomal protein L20
Bv2442c	rolU	50S ribosomal protein L21
Rv0706	rpIV	50S ribosomal protein L22
Rv0703	rpIW	50S ribosomal protein L23
Rv0715	rpIX	50S ribosomal protein L24
Rv1015c	rpIY	50S ribosomal protein L25
Rv2441c	rpmA	50S ribosomal protein L27
Rv0105c	rpmB	50S ribosomal protein L28
RV2058C	rpmC	505 ribosomal protein L28
By0722	rnmD	50S ribosomal protein L30
Rv1298	rpmE	50S ribosomal protein L31
Rv2057c	rpmG	50S ribosomal protein L33
Rv3924c	rpmH	50S ribosomal protein L34
Rv1642	rpmI	50S ribosomal protein L35
Rv1630	rneA	30S ribosomal protein S1
Rv2890c	rnsB	30S ribosomal protein S2
Rv0707	rpsC	30S ribosomal protein S3
Rv3458c	rpsD	30S ribosomal protein S4
Rv0721	rpsE	30S ribosomal protein S5
Rv0053	rpsF	30S ribosomal protein S6
RV0683	rpsG rpoU	30S ribosomal protein S7
Rv3442c	rnsl	30S ribosomal protein S9
Bv0700	rpsJ	30S ribosomal protein S10
Rv3459c	rpsK	30S ribosomal protein S11
Rv0682	rpsL	30S ribosomal protein S12
Rv3460c	rpsM	30S ribosomal protein S13
Rv0/1/	rpsN	30S ribosomal protein S14
RV2056C	rpsiv2	305 ribosomal protein 514
Bv2909c	rnsP	30S ribosomal protein S16
Rv0710	rpsQ	30S ribosomal protein S17
Rv0055	rpsR	30S ribosomal protein S18
Rv2055c	rpsR2	30S ribosomal protein S18
Rv0705	rpsS	30S ribosomal protein S19
Rv2412	rpsT	30S ribosomal protein S20
RV3241C	-	member of S30AE ribosomal
		protein idiniiy
2. Ribosom	e modifica	ation and maturation
Rv1010	ksgA	16S rRNA dimethyltransferase
Rv2838c	rbfA	ribosome-binding factor A
Rv2907c	rimM	16S rRNA processing protein
3 Aminoco	WI TRNA ~	unthases and their modification
Rv25550	alaS	alanvl-tRNA svnthase
Rv1292	argS	arginyl-tRNA synthase
Rv2572c	aspS	aspartyl-tRNA synthase
Rv3580c	cysS	cysteinyl-tRNA synthase
Rv2130c	cysS2	cysteinyl-tRNA synthase
HV1406 By30110	IMI aatA	memonyi-tRINA formyltransferase
INJUTIC	yain	subunit B
Rv3009c	gatB	glu-tRNA-gln amidotransferase,
	-	subunit A
Rv3012c	gatC	glu-tRNA-gln amidotransferase,
Dv20022	altS	subunit C
Rv2357c	gits alvS	giulangi-inina synthase
Rv2580c	hisS	histidyl-tRNA synthase
Rv1536	ileS	isoleucyl-tRNA synthase
Rv0041	leuS	leucyl-tRNA synthase
Rv3598c	lysS	lysyl-tRNA synthase
Rv1640c	lysX	C-term lysyl-tRNA synthase
HV1007C	metS	metnionyi-tRNA synthase
111049	pileo	prienyialanyi-ιπινΑ synifiase α subunit

By1650	nhoT	nhonylalanyl-tRNA synthese B	Bv:
1101050	prier	eubunit	
Bv2845c	proS	prolyl-tRNA synthese	Bv:
Dv29240	proo	cond tPNA synthase	
By2614c	thrS	throopyl-tRNA synthase	Bv2
Pv20140	trmD	tPNA (quanina N1) mothyltrans	
HV29000	umb	foraso	Bv:
By3336c	trnS	tryptophanyl tBNA synthase	
By1689	tyrS	tyrosyl-tRNA synthase	Rv3
By2448c	valS	valvl-tRNA synthase	Rv
11724400	valo	valyr a nor oynalase	Rv
4 Nucleo	nroteins		
Bv1407	fmu	similar to Emu protein	
Bv3852	hns	HU-histone protein	6. F
Bv2986c	hunB	DNA-binding protein II	Rv
Bv1388	mIHF	integration host factor	Rv
		·····g·····	Rv
5. DNA re	plication.	repair, recombination and restric-	Rv
tion/modi	fication		Rv
By1317c	alkA	DNA-3-methyladenine glycosi-	Rv.
	cano i	dase II	Rv
Bv2836c	dinF	DNA-damage-inducible protein F	Rv
Bv1329c	dinG	probable ATP-dependent helicase	Rv
Bv3056	dinP	DNA-damage-inducible protein	Rv
Bv1537	dinX	probable DNA-damage-inducible	Rv
		protein	Rv
Bv0001	dnaA	chromosomal replication initiator	Rv
		protein	Rv
Bv0058	dnaB	DNA helicase (contains intein)	Rv
Bv1547	dnaE1	DNA polymerase III, α subunit	
Rv3370c	dnaE2	DNA polymerase III α chain	7. F
Rv2343c	dnaG	DNA primase	trar
Rv0002	dnaN	DNA polymerase III. B subunit	Rv
Bv3711c	dnaQ	DNA polymerase III ϵ chain	
By3721c	dnaZX	DNA polymerase III ~ (dnaZ) and	Rv2
11007210	unuen	τ (dnaX)	
By2924c	fna	formamidopyrimidine-DNA glyco-	Rv2
TWEDERO	ipg	svlase	Rv
Bv0006	avrA	DNA gyrase subunit A	Rv
By0005	avrB	DNA gyrase subunit B	
By2092c	helY	probable belicase Ski2 subfamily	Rv
By2101	helZ	probable helicase, Shf2/Bad54	Rv3
1102101	noiz	family	
Bv2756c	hsdM	type I restriction/modification sys-	Rv
	noum	tem DNA methylase	
Bv2755c	hsdS'	type I restriction/modification sys-	Rv ⁻
	neae	tem specificity determinant	
Bv3296	lhr	ATP-dependent helicase	Rv
By3014c	ligA	DNA ligase	Rv
By3062	liaB	DNA ligase	By
1100002	ngo	Divinguoo	
By/3731	liaC	probable DNA ligase	By
Rv3731 Bv1020	ligC mfd	probable DNA ligase transcription-repair coupling factor	Rv Bv
Rv3731 Rv1020 Bv2528c	ligC mfd mrr	probable DNA ligase transcription-repair coupling factor restriction system protein	Rv Rv Rv
Rv3731 Rv1020 Rv2528c Rv2985	ligC mfd mrr mutT1	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue	Rv Rv Rv
Rv3731 Rv1020 Rv2528c Rv2985 Bv1160	ligC mfd mrr mutT1 mutT2	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue	Rv Rv Rv
Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Bv0413	ligC mfd mrr mutT1 mutT2 mutT3	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue	Rv Rv Rv Rv
Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Bv3589	ligC mfd mrr mutT1 mutT2 mutT3 mutY	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue MutT homologue probable DNA divcosvlase	Rv Rv2 Rv2 Rv2 Rv2
Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Bv3297	ligC mfd mrr mutT1 mutT2 mutT3 mutY nei	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease VIII	Rv Rv2 Rv2 Rv2 Rv2 Rv2
Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Rv3297 Rv3674c	ligC mfd mrr mutT1 mutT2 mutT3 mutY nei nth	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease III probable endonuclease III	Rv Rv Rv Rv Rv Rv
Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Rv3297 Rv3674c Rv1316c	ligC mfd mrr mutT1 mutT2 mutT3 mutT3 nutY nei nth oat	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue MutT homologue probable DNA glycosylase probable endonuclease VIII probable endonuclease III methylated.DNA-protein.cysteine	Rv Rv Rv Rv Rv Rv Rv Rv
Rv3731 Rv1020 Rv2528c Rv1160 Rv0413 Rv3589 Rv3297 Rv3674c Rv1316c	ligC mfd mrr mutT1 mutT2 mutT3 mutT3 nei nth ogt	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease VIII probable endonuclease III methylated-DNA-protein-cysteine methyltransferase	Rv Rv Rv Rv Rv Rv Rv Rv
Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Rv3297 Rv3674c Rv1316c Bv1629	ligC mfd mrr mutT1 mutT2 mutT3 mutT3 nei nth ogt polA	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease VIII probable endonuclease VIII methylated-DNA-protein-cysteine methyltransferase DNA oplumerase I	Rv Rv Rv Rv Rv Rv Rv Rv Rv Rv Rv Rv Rv
Rv3731 Rv1020 Rv2528c Rv1160 Rv0413 Rv3589 Rv3674c Rv1316c Rv1629 Rv1629	ligC mfd mrr mutT1 mutT2 mutT3 mutY nei nth ogt polA priA	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue motable DNA glycosylase probable endonuclease VIII probable endonuclease VIII probable endonuclease III methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n'	Rv Rv Rv Rv Rv Rv Rv Rv Rv Rv Rv Rv Rv R
Rv3731 Rv1020 Rv2528c Rv1985 Rv1160 Rv0413 Rv3589 Rv3297 Rv3674c Rv1316c Rv1629 Rv1402	ligC mfd mrr mutT1 mutT2 mutT3 mutY nei nth ogt polA priA	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease VIII probable endonuclease VIII probable endonuclease III methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (renicration factor Y)	Rv Rv Rv Rv Rv Rv Rv Rv Rv Rv Rv Rv Rv R
Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Rv3297 Rv3674c Rv1316c Rv1629 Rv1402	ligC mfd mrr mutT1 mutT2 mutT3 mutY nei nth ogt polA priA radA	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease VIII probable endonuclease VIII methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair Bada homo-	Rv: Rv: Rv: Rv: Rv: Rv: Rv: Rv: Rv: Rv:
Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Rv3297 Rv3674c Rv1316c Rv1629 Rv1402 Rv3585	ligC mfd mrr mutT1 mutT2 mutT3 mutY nei nth ogt polA priA radA	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue motable DNA glycosylase probable endonuclease VIII probable endonuclease VIII methylated-DNA-protein-cysteine methyltransferase I DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- loque	Rv Rv Rv Rv Rv Rv Rv Rv Rv Rv Rv Rv Rv R
Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Rv3297 Rv3674c Rv1316c Rv1629 Rv1629 Rv1402 Rv3585	ligC mfd mrr mutT1 mutT2 mutT3 mutY nei nih ogt polA priA radA	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease VIII probable endonuclease VIII probable endonuclease III methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein)	Rv: Rv: Rv: Rv: Rv: Rv: Rv: Rv: Rv: Rv:
Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Rv3297 Rv3674c Rv1316c Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c	ligC mfd mrr mutT1 mutT2 mutT3 mutY nei nth ogt polA priA radA recA	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease VIII methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exordenovrihonuclease V	Rv Rv Rv Rv Rv Rv Rv Rv Rv Rv Rv Rv Rv R
Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Rv3297 Rv3674c Rv1316c Rv1629 Rv1402 Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0631c	ligC mfd mrr mutT1 mutT2 mutT3 mutY nei nth ogt poIA priA radA recA recC	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue MutT homologue probable DNA glycosylase probable endonuclease VIII probable endonuclease VIII methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein ry (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V	Rv: Rv: Rv: Rv: Rv: Rv: Rv: Rv: Rv: Rv:
Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Rv3297 Rv3674c Rv1316c Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0631c Rv0639c	ligC mfd mrr mutT1 mutT2 mutT2 mutT2 nei nth ogt polA priA radA recB recC recD	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease VIII probable endonuclease VIII probable endonuclease III methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V	RV RV RV RV RV RV RV RV RV RV RV RV RV R
Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Rv3297 Rv3674c Rv1316c Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0630c Rv0631c Rv0629c Rv0003	ligC mfd mrr mutT1 mutT3 mutY nei mutY nei nih ogt polA priA recA recC recC recC recF	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease VIII methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induc-	RV RV RV RV RV RV RV RV RV RV RV RV RV R
Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Rv3297 Rv3674c Rv1316c Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0631c Rv0631c Rv0629c Rv0003	ligC mfd mrr mutT1 mutT2 mutT2 mutT2 mutT2 mutT2 nei nth ogt polA priA recA recC recC recC recC recF	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease VIII probable endonuclease VIII methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine wedeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induc- tion	RV RV RV RV RV RV RV RV RV RV RV RV RV R
Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Rv3297 Rv3674c Rv1316c Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0631c Rv0630c Rv0631c Rv0639 Rv2973c	ligC mfd mrr mutT1 mutT3 mutY nei nith ogt poIA priA recA recB recC recD recF recG	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease VIII probable endonuclease VIII probable endonuclease VIII probable endonuclease III methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induc- tion ATP-debendent DNA helicase	RV RV RV RV RV RV RV RV RV RV RV RV RV R
Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Rv3297 Rv3674c Rv1316c Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0630c Rv0630c Rv0631c Rv0629c Rv0003 Rv2973c Rv1696	ligC mfd mrr mutT1 mutT3 mutY nei mutY nei nei polA priA recA recC recC recC recC recF recG	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease VIII methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induc- tion ATP-dependent DNA helicase recombination and DNA repair	RV RV RV RV RV RV RV RV RV RV RV RV RV R
Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Rv3297 Rv3674c Rv1316c Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0631c Rv0631c Rv0631c Rv0631c Rv0631c Rv0631c Rv0631c Rv0631c Rv0631c Rv0631c Rv0631c Rv0631c Rv0631c Rv073c Rv1696 Rv3715c	ligC mfd mrr mutT1 mutT2	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease VIII probable endonuclease III methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induc- tion ATP-dependent DNA helicase recombination and DNA helicase	Rvize Rviz Rvize Rvize Rvize Rviz Rviz Rviz Rviz Rviz Rviz Rviz Rviz
Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Rv3297 Rv3674c Rv1316c Rv1629 Rv1402 Rv3585 Rv2737c Rv0631c Rv0631c Rv0631c Rv0631c Rv0033 Rv2973c Rv1696 Rv3715c	ligC mfd mrr mutT1 mutT3 mutY nei nith ogt poIA priA recA recB recC recD recF recC recR recR	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease VIII probable endonuclease VIII probable endonuclease VIII probable endonuclease III methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V 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	Rvi Rvi Rvi Rvi Rvi Rvi Rvi Rvi Rvi Rvi
Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Rv3297 Rv3674c Rv1316c Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0630c Rv0631c Rv0629c Rv0003 Rv0029 Rv0003 Rv2973c Rv1696 Rv3715c	ligC mfd mrr mutT1 mutT3 mutY nei mutY nei nei polA priA recA recD recC recD recC recR recR recR recR	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease III methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V 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	Rviz Rviz Rviz Rviz Rviz Rviz Rviz Rviz
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Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Rv3297 Rv3674c Rv1316c Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0631c Rv0631c Rv0630 Rv2737c Rv0033 Rv2973c Rv3715c Rv2736c Rv2736c Rv2593c	ligC mfd mrr mutT1 mutT3 mutY nei nih ogt poIA priA recA recB recC recC recC recF recF recG recR recR recR recR recR	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease VIII probable endonuclease VIII probable endonuclease III methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein rotein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V 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 Holiiday junction binding protein, DNA helicase	Rvz Rvz Rvz Rvz Rvz Rvz Rvz Rvz Rvz Rvz
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Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Rv3297 Rv3674c Rv1316c Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0630c Rv0631c Rv0630c Rv0631c Rv0629c Rv0003 Rv2973c Rv1696 Rv3715c Rv2736c Rv2593c Rv2592c Rv2594c Rv0054	ligC mfd mrr mutT1 mutT3 mutY nei mutY nei mutY nei polA priA radA radA radA racA racC racD racC racC racC racC racR racR racR racX ruvX ruvX ssb	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease III methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V HNA replication and DNA repair RecBC-Independent process of DNA repair regulatory protein for RecA Holliday junction binding protein, Holliday junction binding protein Holliday junction resolvase, endo- deoxyribonuclease	Rvz Rvz Rvz Rvz Rvz Rvz Rvz Rvz Rvz Rvz
Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Rv1316c Rv13297 Rv3674c Rv1316c Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0630c Rv0630c Rv0629c Rv0003 Rv2737c Rv0629c Rv0003 Rv2737c Rv0629c Rv0003 Rv2737c Rv2629c Rv2736c Rv2592c Rv2592c Rv054 Rv0054 Rv1210	ligC mfd mrr mutT1 mutT2 mutT3 mutT2 mutT3	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease VIII probable endonuclease VIII probable endonuclease III methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V 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 binding protein Holliday junction binding protein Holliday junction binding protein DNA -samethyladenine glycosi-	Rvizer Rvzzer Rvzzer Rvzzer Rvzzer Rvze Rvzer Rvzer Rvzer Rvz Rvz Rvzer Rvzer Rvze Rvz Rvz Rvz Rvz Rvz
Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Rv3297 Rv3674c Rv1316c Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0631c Rv0631c Rv0631 Rv2973c Rv2736c Rv2736c Rv2593c Rv2592c Rv2594c Rv0054 Rv1210	ligC mfd mrr mutT1 mutT3 mutY nei nih ogt poIA priA radA recB recC recC recC recC recC recC recC recR recR recR recR recR recR recR recR	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease VIII probable endonuclease VIII probable endonuclease VIII probable endonuclease III methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein rotein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V 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 protein Holliday junction protein Holliday junction protein Holliday junction protein Holliday junction protein Holliday junction protein DNA-3-methyladenine glycosi- dase I	RVI RVI RVI RVI RVI RVI RVI RVI RVI RVI
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Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Rv1316c Rv137c Rv3674c Rv1316c Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0630c Rv0630c Rv0630c Rv0629c Rv0003 Rv2737c Rv0629c Rv0003 Rv2737c Rv2620c Rv0033 Rv2736c Rv2592cc Rv054 Rv1210 Rv3646c Rv2976c	ligC mfd mrr mutT1 mutT2 mutT3	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease VIII probable endonuclease VIII probable endonuclease VIII methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V 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 binding protein Holliday junction binding protein Holliday junction binding protein Holliday junction binding protein DNA -sparetyladenine glycosi- dase I DNA topoisomerase uracil-DNA glycosylase	RV2 RV2 RV2 RV2 RV2 RV2 RV2 RV2 RV2 RV2
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Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Rv3297 Rv3674c Rv1316c Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0630c Rv0630c Rv0630c Rv0630c Rv0630c Rv0630c Rv0630c Rv1696 Rv3715c Rv2736c Rv2593c Rv2594c Rv054 Rv1210 Rv3646c Rv2976c Rv1633 Rv1420 Rv1633 Rv1420 Rv0949	ligC mfd mrr mutT1 mutT3 mutY nei nin nei nei polA priA radA radA radA radA radA racB recC recD recC recR recR recR recR recR recR recR recR	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease III methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinates (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and DNA repair ReeBC-Independent process of DNA repair ReeBC-Independent process of DNA repair Multiday junction binding protein, DNA helicase Holliday junction binding protein Holliday junction binding protein Holliday junction binding protein DNA-s-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	Rvize Rvize Rvize
Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Rv1316c Rv1629 Rv1316c Rv1629 Rv1316c Rv13297 Rv3674c Rv1316c Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0003 Rv2973c Rv2592c Rv054 Rv12592c Rv054 Rv12592c Rv054 Rv1250 Rv2592c Rv054 Rv1250 Rv2592c Rv054 Rv120 Rv054 Rv120 Rv054 Rv1633 Rv1638 Rv1638 Rv1638 Rv1638 Rv1639 Rv3198c	ligC mfd mrr mutT1 mutT2 mutT3 mutY nei nith ogt polA priA radA recB recC recD recF recC recC recC recR recR recR recR recC recR recR recC recC recP recC recD recF recC recD recF recC recD recD recC recD recC recD recC recD recC recD recC recD recC recD recC recD recC recD recC recD recD recC recD recD recD recD recD recD recD recD	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease VIII probable endonuclease VIII probable endonuclease VIII probable endonuclease VIII probable endonuclease III methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V 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 Holliday junction binding protein Holliday junction binding protein Holliday junction binding protein DNA-s-methyladenine glycosi- dase I DNA topoisomerase uracit-DNA glycosylase excinuclease ABC subunit A excinuclease ABC subunit K excinuclease ABC subunit C DNA-dependent ATPase I and helicase II putative UvrD	Rvizik Rv
Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv3589 Rv3589 Rv1316c Rv1629 Rv1316c Rv1629 Rv1627 Rv3674c Rv1316c Rv1629 Rv1627 Rv0630c Rv0631c Rv2593c Rv2592c Rv2592c Rv0054 Rv1210 Rv3646c Rv1633 Rv1420 Rv0949 Rv3198c Rv0427c	ligC mfd mrr mutT1 mutT2 mutT3 mutY nei nth ogt poIA priA radA radA radA radA racB recC recC recC recC recR recR recR recR recR recR recR recR	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease VIII probable endonuclease VIII probable endonuclease VIII probable endonuclease III methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA replication and SOS induc- tion ATP-dependent DNA helicase recombination binding protein, DNA repair regulatory protein for RecA Holliday junction binding protein, DNA helicase Holliday junction binding protein Holliday junction binding protein DNA-3-methyladenine glycosi- dase I DNA topoisomerase uracii-DNA glycosylase excinuclease ABC subunit A excinuclease ABC subunit K excinuclease ABC subunit C DNA-dependent ATPase I and helicase II putative UvrD exodeoxyribonuclease III	Rvizik Rv
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Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv3589 Rv3674c Rv1316c Rv1629 Rv1610 Rv1629 Rv1627 Rv3674c Rv1316c Rv1629 Rv1620 Rv3685 Rv2737c Rv0630c Rv0630c Rv0630c Rv0630c Rv0631c Rv0632c Rv0633c Rv2592c Rv2592c Rv054 Rv1210 Rv3646c Rv1633 Rv1420 Rv3198c Rv0427c Rv0071 Rv0841	ligC mfd mrr mutT1 mutT3 mutY nei nth ogt poIA priA radA radA radA radA racB recC recC recC recC recR recR recR recR recR recR recR recR	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease VIII probable endonuclease VIII probable endonuclease VIII probable endonuclease III methylated-DNA-protein-cysteine methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V 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 binding protein DNA-3-methyladenine glycosi- dase I DNA topoisomerase uracii-DNA glycosylase excinuclease ABC subunit A excinuclease ABC subunit K 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	Rvizik Rvizik
Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Rv3297 Rv3674c Rv1316c Rv1629 Rv1402 Rv3585 Rv2737c Rv0630c Rv0630c Rv0630c Rv0630c Rv0630c Rv0630c Rv0630c Rv0630c Rv1696 Rv3715c Rv2736c Rv2593c Rv2594c Rv2594c Rv054 Rv1633 Rv1200 Rv1633 Rv1420 Rv3646c Rv1633 Rv1420 Rv3198c Rv04276 Rv0071 Rv3198c Rv0424 Rv0544 Rv0294	ligC mfd mrr mutT1 mutT3 mutY nei nin ogt polA priA radA racA recB recC recD recF recR recR recR recR recR recR recR recR	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease III methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein-cysteine methylated-DNA-protein cysteine probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V DNA repair ReeBC-Independent process of DNA repair ReeBC-Independent process of DNA repair ReeBC-Independent protein, DNA helicase Holliday junction binding protein Holliday junction binding protein Holliday junction binding protein DNA-s-methyladenine glycosi- dase I DNA topoisomerase uracil-DNA glycosylase 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 possible formamidopyrimidine- DNA glycosylase	Rvize Rvize
Rv3731 Rv1020 Rv2528c Rv2985 Rv1160 Rv0413 Rv3589 Rv1316c Rv1629 Rv1316c Rv1629 Rv13207 Rv3585 Rv2737c Rv0630c Rv0031 Rv2737c Rv0630c Rv0031 Rv2737c Rv0630c Rv0031 Rv2737c Rv0630c Rv0731c Rv2736c Rv2592c Rv0544 Rv1250 Rv2592c Rv054 Rv1638 Rv1638 Rv1638 Rv1638 Rv0427c Rv0949 Rv3198c Rv04427c Rv0944 Rv1688	ligC mfd mrr mutT1 mutT2 mutT3 mutY nei nih ogt polA priA radA radA racB recC recD recF recD recF recR recR recR recR recR recR recR recR	probable DNA ligase transcription-repair coupling factor restriction system protein MutT homologue MutT homologue probable DNA glycosylase probable endonuclease VIII probable endonuclease VIII probable endonuclease VIII probable endonuclease VIII probable endonuclease VIII probable endonuclease III methyltransferase DNA polymerase I putative primosomal protein n' (replication factor Y) probable DNA repair RadA homo- logue recombinase (contains intein) exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V exodeoxyribonuclease V 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 Holliday junction binding protein Holliday junction binding protein DNA helicase Holliday junction protein DNA topoisomerase uracit-DNA glycosylase excinuclease ABC subunit A excinuclease ABC subunit A 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 helicose possible formamidopyrimidine- DNA glycosylase probable JMA helicase	Rvizik Rv

2090	-	partially similar to DNA poly-	2. DNA
.0101		merase I	Rv0670
2191	-	proteins	Rv1108 Rv1107
2464c	-	endonuclease VIII	3. Prote
3201c	-	helicase	Rv3305 Rv3306
32020	-	probable DNA methylase	Rv2461
3644c	-	similar in N-term to DNA poly- merase III	Rv2460
Protein t	ranslation	and modification	Rv2457
0429c 2534c	def efp	polypeptide deformylase elongation factor P	Rv2667
2882c	frr	ribosome recycling factor	D-0410
0684 0120c	lusA fusA2	elongation factor G	Rv3419 Rv2725
1080c	greA	transcription elongation factor G	Rv1223
3462c	infA	initiation factor IF-1	Rv2861
2839c	infB infC	initiation factor IF-2	Rv0734
0009	nniA	peptidyl-prolyl <i>cis-trans</i> isomerase	Bv0319
2582	ppiB	peptidyl-prolyl <i>cis-trans</i> isomerase	Rv0125
1299	prfA	peptide chain release factor 1	Rv2213
3105c	prfB	peptide chain release factor 2	Rv0800
2889C	IST tuf	elongation factor EF-Is	RV2467
			Rv2535
RNA syr	nthesis, Ri n dee D	ATD dependent DNA	Rv2782
1253	deaD	AI P-dependent DNA/RNA	Rv2109
2783c	apsl	pppGpp synthase and polyribo-	Rv0782
	31	nucleotide phosphorylase	Rv0781
2841c	nusA	transcription termination factor	Rv0724
2533c	nusB	N-utilization substance protein B	D. 0100
0639	nusG	transcription antitermination	RV0198
3907c	pcnA	polynucleotide polymerase	Rv0840
3232c	pvdS	alternative sigma factor for	Rv0983
		siderophore production	Rv1977
3211	rhIE	probable ATP-dependent	Rv3668
1207	rho	RNA nelicase	HV3671
1297	IIIO	factor rho	Rv3886
3457c	rpoA	α subunit of RNA polymerase	
0667	rpoB	β subunit of RNA polymerase	4. Polys
0668	rpoC	β' subunit of RNA polymerase	lipids
1364c	rsbU	SigB regulation protein	Rv0062
3287C	rsDVV sig A	anti-sigma B factor BNA polymerase sigma factor	RV3915 Rv0315
2703	SigA	(aka MysA, RpoV)	Rv1090
2710	sigB	RNA polymerase sigma factor (aka MvsB)	Rv1327
2069	sigC	ECF subfamily sigma subunit	
3414c	sigD	ECF subfamily sigma subunit	Rv1333
1221	sigE	ECF subfamily sigma subunit	Rv3463
01920	sigr ciaC	ECF subtamily sigma subunit	RV3/1/
3223c	siga siaH	ECF subfamily sigma subunit	
1189	sigl	ECF family sigma factor	5. Ester
3328c	sigJ	similar to SigI, ECF family	Rv0220
0445c	sigK	ECF-type sigma factor	Rv1923
/0/35 /2011	sigL sigM	sigma-/0 factors ECF subfamily	RV3//5
3911	Sigivi	SigF	Rv0646
3366	spoU	probable rRNA methylase	Rv1399
3455c	truA	probable pseudouridylate syn-	Rv1400
0700-	4	thase	Rv1900
1644	truB tenP	THINA pseudouridine 55 synthase	Rv1407
1044	131111	ferase	Rv2284
3649	-	ATP-dependent DNA/RNA heli-	Rv2970
		case	Rv1426
	,		Rv2463
Polysaco	charides (o	tytoplasmic)	Rv2485
1328	alaP	probable glycogen phosphory-	Rv3176
15640	alaX	lase probable glycogen debranching	Rv2045
15630	alaY	enzyme nutative α-amylase	Rv3203
1562c	glgZ	maltooligosyltrehalose trehalohy- drolase	Rv2351 Bv2350
0126	-	probable glycosyl hydrolase	Rv2349
1781c	-	probable 4-α-glucanotransferase	Rv1755
2471	-	probable maltase α -glucosidase	Rv1104 Rv1105
<i>Degrada</i> RNA	ation of ma	acromolecules	6. Arom
1014c	pth rpc	peptidyl-tRNA hydrolase	Rv3469
2925C	rne	similar at C-term to ribo-	Rv0316
2902c	rnhB rnnA	ribonuclease HII ribonuclease R protein compo-	Rv0771
50206	הקווי	nent	Rv0939
1340	rphA	ribonuclease PH	Rv1723

NA		(and a set of the set
108c	end xseA	exonuclease IV (apurinase)
107c	xseB	exonuclease VII small subunit
Proteins	nentides	and alvcopentides
305c	amiA	probable aminohydrolase
3306c	amiB	probable aminohydrolase
3596c	clpC clpD	ATP-dependent Clp protease
24010	cipP	teolytic subunit
2460c	clpP2	ATP-dependent Clp protease pro-
		teolytic subunit
2457c	clpX	ATP-dependent Clp protease
2667	clpX'	similar to ClpC from <i>M. leprae</i> but
	- 1	shorter
3419c	gcp	glycoprotease
2/250	hflX htrA	GTP-binding protein
223 2861c	man	methionine aminopentidase
0734	map'	probable methionine aminopepti-
		dase
0319	pcp	pyrrolidone-carboxylate peptidase
213	pepA pepB	aminopentidase A/I
0800	pepC	aminopeptidase I
2467	pepD	probable aminopeptidase
2089c	pepE	cytoplasmic peptidase
25350	pepQ	cytoplasmic peptidase
1020	рерп	(insulinase)
2109c	prcA	proteasome α-type subunit 1
2110c	prcB	proteasome β -type subunit 2
0782	ptrBa	protease II, α subunit
)724	ригыр snnA	protease IV signal pentide penti-
// 24	oppri	dase
)198c	-	probable zinc metalloprotease
)457c	-	probable peptidase
0840C	-	probable proline iminopeptidase
977	-	probable zinc metallopeptidase
8668c	-	probable alkaline serine protease
3671c	-	probable serine protease
8883c	-	probable secreted protease
00886	-	protease
olysacc	harides, li	popolysaccharides and phospho-
ls		
062	celA	cellulase/endoglucanase
)315	-	probable 6-1.3-qlucanase
090	-	probable inactivated
		cellulase/endoglucanase
327c	-	probable glycosyl hydrolase, α-
333	_	amylase family probable bydrolase
3463	-	probable neuraminidase
3717	-	possible N-acetylmuramoyl-L-ala-
		nine amidase
sterase	s and lipa	ses
)220	lipC .	probable esterase
923	lipD	probable esterase
3//5	lipE	probable hydrolase
)646c	lipG	probable esterase
399c	lipH	probable lipase
400c	lipl	probable lipase
900C	iipJ linK	probable acetyl-bydrolase
497	lipL	esterase
2284	lipМ	probable esterase
2970c	lipN	probable lipase/esterase
426c	lipO lipP	probable esterase
2403 2485c	lipQ	probable carboxivesterase
8084	lipR	probable acetyl-hydrolase
3176c	lipS	probable esterase/lipase
2045c	lipT	probable carboxylesterase
203	lipU lipV	probable esterase
)200)217c	lipW	probable esterase
2351c	plcA	phospholipase C precursor
2350c	plcB	phospholipase C precursor
2349c	plcC	phospholipase C precursor
104	- -	probable esterase pseudogene
105	-	probable esterase pseudogene
romet	buchen '	2020
vromatic 3469c	nydrocart mhnF	probable 4-hydroxy-2-oxovalerate
		aldolase
0316	-	probable muconolactone iso-
)771	_	merase
,,,,,	-	tone decarboxylase
939	-	probable dehydrase
723	-	6-aminohexanoate-dimer hydro-

Rv2715	-	2-hydroxymuconic semialdehyde
Dv25200		nydrolase
Dv25240	-	4 bydroxy 2 oxovalorate aldolase
Rv3536c	-	aromatic hydrocarbon degrada-
11000000	-	tion
C. Cell env	velope	
1. Lipoprot	eins (IppA	- <i>lpr0</i>) 65
2. Surface	polysacch	arides, lipopolysaccharides, pro-
teins and a	antigens	
Rv0806c	cpsY	probable UDP-glucose-4-
		epimerase
Rv3811	csp	secreted protein
Rv1677	dsbF	highly similar to C-term Mpt53
Rv3794	embA	involved in arabinogalactan syn-
		thesis
Rv3795	embB	involved in arabinogalactan syn-
D. 0700		thesis
RV3793	embC	Involved in arabinogalactan syn-
Dv2075	agate	Inesis
Dv0112	esalo	probable CDP manpage deby
HVUTIZ	yca	dratase
Bv0113	amh∆	nhosphohentose isomerase
By2965c	kdtR	linopolysaccharide core biosyn-
11023030	KULD	thesis protein
Bv2878c	mnt53	secreted protein Mpt53
Rv1980c	mpt64	secreted immunogenic protein
		Mpb64/Mpt64
Rv2875	mpt70	major secreted immunogenic pro-
		tein Mpt70 precursor
Rv2873	mpt83	surface lipoprotein Mpt83
Rv0899	ompA	member of OmpA family
Rv3810	, pirĠ	cell surface protein precursor (Erp
		protein)
Rv3782	rfbE	similar to rhamnosyl transferase
Rv1302	rfe	undecaprenyl-phosphate α-N-
		acetylglucosaminyltransferase
Rv2145c	wag31	antigen 84 (aka wag31)
Rv0431	-	tuberculin related peptide (AT103)
Rv0954	-	cell envelope antigen
Rv1514c	-	involved in polysaccharide syn-
D. 4540		thesis
HV1518	-	Involved in exopolysaccharide
D. 1750		synthesis
RV1/30	-	partial culliase
RV1910C	-	woak similarity to pollon antigons
Rv1984c		probable secreted protein
Rv1987		probable secreted protein
D 0000	_	probable exported protease
By2223C		
Rv2223c Rv2224c	-	propable exported protease
Rv2223c Rv2224c Rv2301	-	probable exported protease probable cutinase
Rv2223c Rv2224c Rv2301 Rv2345	-	probable exported protease probable cutinase precursor of probable membrane
Rv2223c Rv2224c Rv2301 Rv2345	-	probable exported protease probable cutinase precursor of probable membrane protein
Rv2223c Rv2224c Rv2301 Rv2345 Rv2672	-	probable exported protease probable cutinase precursor of probable membrane protein putative exported protease
Rv2223c Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c	-	probable exported protease probable cutinase precursor of probable membrane protein putative exported protease similar to Esat6
Rv2223c 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
Rv2223c 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 pro-
Rv2223c 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 pro- tease
Rv2223c Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c Rv3449 Rv3451		probable cutinase probable cutinase precursor of probable membrane protein putative exported protease similar to Esat6 probable secreted protein probable precursor of serine pro- tease probable cutinase
Rv22223c Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c Rv3449 Rv3449 Rv3451 Rv3452		probable extinase procursor of probable membrane protein putative exported protease similar to Esat6 probable secreted protein probable precursor of serine pro- tease probable cutinase probable cutinase precursor
Rv2223c Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c Rv3449 Rv3451 Rv3452 Rv3724		probable cutinase probable cutinase protable cutinase protable cutinase protable exported protease similar to Esat6 probable secreted protein probable secreted protein probable precursor of serine pro- tease probable cutinase precursor probable cutinase precursor probable cutinase precursor
Rv22223c Rv2224c Rv2301 Rv2345 Rv3019c Rv3019c Rv3019c Rv3019c Rv3451 Rv3452 Rv3451 Rv3452 Rv3724		probable cutinase probable cutinase protable cutinase protable cutinase protative exported protease similar to Esat6 probable secreted protein probable precursor of serine pro- tease probable cutinase probable cutinase precursor probable cutinase precursor
HV2223c Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c Rv3449 Rv3451 Rv3452 Rv3724 3. Murein s	- - - - - - - - - - - -	probable exported protease probable cutinase protein putative exported protease similar to Esat6 probable secreted protein probable secreted protein probable precursor of serine pro- tease probable cutinase probable cutinase precursor probable cutinase precursor nd peptidoglycan
HV2223c Rv2224c Rv2301 Rv2345 Rv2672 Rv3019c Rv3036c Rv3449 Rv3451 Rv3452 Rv3724 3. Murein s Rv2911 Bv29912	- - - - - - - - - - - - - - - - - - -	probable exported protease probable cutinase protection putative exported protease similar to Esat6 probable secreted protein probable secreted protein probable precursor of serine pro- tease probable cutinase precursor probable cutinase precursor probable cutinase precursor nd peptidoglycan penicillin binding protein pealenine_Destance to proce
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HV2223c RV2224c RV22301 RV2242c RV2301 RV2245 RV3036C RV3036C RV3036C RV3449 RV3449 RV3451 RV3036C RV3449 RV3451 RV3452 RV3911 RV29811 RV3809c RV1018c RV3809c RV1018c RV3832c RV1100 RV1315 RV0482 Rv2155c Rv2155c Rv2155c Rv2157c Rv3332 Rv0016c Rv382c Rv00516c Rv382	- - - - - - - - - - - - - - - - - - -	probable cutinase probable cutinase probable cutinase protative exported protease similar to Esat6 probable secreted protein probable precursor of serine pro- tease probable cutinase precursor probable cutinase precursor probable cutinase precursor probable cutinase precursor probable cutinase precursor probable cutinase precursor probable cutinase precursor D-alanine-D-alanine ligase A UDP-sacetylglucosamine pyrophosphorylase LytB protein homologue very similar to LytB UDP-N-acetylglucosamine-1-car- boxyvinyltransferase UDP-N-acetylenolpyruvoylglu- cosamine reductase UDP-N-acetylenolpyruvoylglu- cosamine reductase UDP-N-acetyl-muramate-alanine ligase UDP-N-acetyl-muramoylalanine-D- glutamate ligase meso-diaminopimelate-adding enzyme D-alanine:D-alanine-adding enzyme transferase in peptidoglycan syn- thesis glutamate racemase phospho-N-acetylmuramoyl- petapeptide transferase N-acetylglucosamine-6-P- deacetylase penicillin-binding protein penicillin-binding protein class A neglitine protein 2 penicillin-binding protein 2 penicillin-binding protein 2 penicillin-binding protein
HV2223c RV2234C RV2231 RV22341 RV22345 RV22342 RV3036C RV3036C RV3036C RV3036C RV3036C RV3036C RV3036C RV3036C RV3036C RV3036C RV2057 RV2057 RV2057 RV2157 R	- - - - - - - - - - - - - - - - - - -	probable cutinase probable cutinase protexile cutinase protexile cutinase protexile cutinase probable secreted protein probable precursor of serine pro- tease probable cutinase precursor probable cutinase precursor UDP-N-acety/glucosamine-1-car- boxyvinyltransferase UDP-N-acety/glucosamine-1-car- boxyvinyltransferase UDP-N-acety/glucosamine-D- glutamate ligase meso-diaminopimelate-adding enzyme D-alanine:D-alanine-adding enzyme D-alanine:D-alanine-adding enzyme phospho-N-acety/glucosamine-6-P- deacetylase penicillin-binding protein penicillin-binding protein class A penicillin binding protein
HV2223c RV2234C RV2231 RV2234 RV2231 RV2234 RV2345 RV2345 RV3036C RV3449 RV3452 RV3452 RV3452 RV3452 RV3452 RV2911 RV2981C RV2981C RV2981C RV2981C RV2981C RV2981C RV2155C RV2055C RV2	- - - - - - - - - - - - - - - - - - -	probable cutinase probable cutinase protable cutinase protable secreted protease similar to Esat6 probable secreted protein probable precursor of serine pro- tease probable cutinase precursor probable cutinase precursor probable cutinase precursor probable cutinase precursor probable cutinase precursor probable cutinase precursor probable cutinase precursor D-alanine-D-alanine ligase A UDP-glatcopyranose mutase UDP-vacetylglucosamine pyrophosphorylase LytB protein homologue very similar to LytB UDP-N-acetylglucosamine-1-car- boxyvinyltransferase UDP-N-acetylglucosamine-1-car- boxyvinyltransferase UDP-N-acetylglucosamine-1-car- boxyvinyltransferase UDP-N-acetylglucosamine-D- glutamate ligase <i>meso</i> -diaminopimelate-adding enzyme transferase in peptidoglycan syn- thesis glutamate racemase phospho-N-acetylmuramoyl- petapetide transferase N-acetylglucosamine-6-P- deacetylase pencillin-binding protein pencillin-binding protein class A penicillin binding protein ftsW/RodA/SpovE family probable penicillin binding protein

Rv1367c	-	probable penicillin binding protein	Rv10
Rv1730c Rv1922	-	probable penicillin binding protein probable penicillin binding protein	Rv10
Rv2864c Rv3330	-	probable penicillin binding protein probable penicillin binding protein	Rv32
Rv3627c	-	probable penicillin binding protein	Bv28
4. Conserv	ed membr	ane proteins	By18
By0507	mmpl 2	protein	By03
Du0000	mmal 0	protein	
NV02000	ninpL3	protein	Rv09
RV0450C	mmpL4	protein	Rv26
Rv0676c	mmpL5	conserved large membrane protein	Rv26
Rv1557	mmpL6	conserved large membrane protein	Rv22
Rv2942	mmpL7	conserved large membrane protein	Rv27
Rv3823c	mmpL8	conserved large membrane protein	Rv31 Rv32
Rv2339	mmpL9	conserved large membrane protein	Rv37
Rv1183	mmpL10	conserved large membrane	
Rv0202c	mmpL11	conserved large membrane	3. Ca
Rv1522c	mmpL12	conserved large membrane	Rv34
Rv0403c	mmpS1	conserved small membrane	Rv19 Rv12
Rv0506	mmpS2	conserved small membrane	Rv12
Rv2198c	mmpS3	protein conserved small membrane	Rv12
Rv0451c	mmpS4	protein conserved small membrane	Rv33 Rv28
Rv0677c	mmpS5	protein conserved small membrane	Rv28
		protein	Rv28
5. Other me	embrane p	proteins 211	Bv28
III. Cell pro	cesses	proteins	Bv23
1. Amino a	cids	protonio	Rv23
Rv2127	ansP	L-asparagine permease	Rv23
Rv0346c	aroP2	probable aromatic amino acid	Rv12
		permease	Rv20
Rv0917 Rv1704c	betP cycA	glycine betaine transport transport of D-alanine, D-serine	Rv20 Rv20
Rv3666c	dppA	and glycine probable peptide transport system	Rv20
Bv3665c	dooB	permease probable peptide transport system	4. An Rv26
Bv3664c	dnnC	permease probable pentide transport system	Rv26 Bv35
By3663c	dnnD	permease probable ABC-transporter	Rv26
Rv0522	gabP	probable 4-amino butyrate trans-	Dv22
Rv0411c	gInH	putative glutamine binding protein	D. 00
RV2504	ginQ	protein	RV23
Rv1280c	оррА	probable oligopeptide transport protein	Rv18 Rv18
Rv1283c Rv1282c	оррВ оррС	oligopeptide transport protein oligopeptide transport system per-	Rv18
Rv1281c	oppD	mease probable peptide transport protein	Rv18
Rv2320c Rv3253c	rocE -	arginine/ornithine transporter probable cationic amino acid	Rv23
Rv3454	-	transport possible proline permease	Rv17 Rv02
2. Cations			Rv02
Rv2920c	amt	putative ammonium transporter	Rv09
Rv1607	chaA	putative calcium/proton antiporter	
Rv1239c	corA	probable magnesium and cobalt transport protein	Rv09
Rv0092 Rv0103c	ctpA ctpB	cation-transporting ATPase cation transport ATPase	Rv08
Rv3270 Rv1469	ctpC ctpD	cation transport ATPase probable cadmium-transporting	Rv33
By0908	ctnF	ATPase probable cation transport ATPase	Rv08
Rv1997	ctpF	probable cation transport ATPase	Rv05
Rv0425c	ctpH	C-terminal region putative cation-	Rv22
B 0/07	ata l	transporting ATPase probable magnesium transport	Hv09
Rv010/c	cipi	ATD	-
Rv0107c Rv0969	ctpV	ATPase cation transport ATPase	Rv09
Rv0107c Rv0969 Rv3044 Rv0265c	ctpV fecB fecB2	ATPase cation transport ATPase putative FeIII-dicitrate transporter iron transport protein FeIII dici-	Rv09 Rv09
Rv0969 Rv3044 Rv0265c trate Rv1029	ctpV fecB fecB2 kdpA	ATPase cation transport ATPase putative FellI-dicitrate transporter iron transport protein FellI dici- transporter potassium-transporting ATPase A	Rv09 Rv09 Rv09

030	kdpB	potassium-transporting ATPase B
031	kdpC	potassium-transporting ATPase C
236c	kefB	probable glutathione-regulated
377c	merT	possible mercury resistance
311	mgtC	probable magnesium transport
362	mgtE	putative magnesium ion
356 924c	nicT nramp	probable nickel transport protein transmembrane protein belonging
691	trkA	probable potassium uptake pro-
692	trkB	probable potassium uptake pro-
287 723	yjcE -	probable Na+/H+ exchanger probable membrane protein, tellurium resistance
162c 237c		probable membrane protein possible potassium channel protein
743c	-	probable cation-transporting
arboby	drates or	ranic acids and alcohols
143	dctA	C4-dicarboxylate transport protein
176c	kgtP	sugar transport protein
902c	nanT	probable sialic acid transporter
236	sugA	membrane protein probably involved in sugar transport
237 238	sugB sugC	sugar transport protein ABC transporter component of
	U	sugar uptake system
331	sugl	probable sugar transport protein
335c	ugpA	<i>sn</i> -glycerol-3-phosphate permease
333c	ugpB	sn-glycerol-3-phosphate-binding periplasmic lipoprotein
332c	ugpC	sn-glycerol-3-phosphate transport ATP-binding protein
334c	ugpE	sn-glycerol-3-phosphate transport system protein
316	uspA	sugar transport protein
318	uspC	sugar transport protein
317	uspE	sugar transport protein
138c		probable ABC sugar transporter
)39c	-	probable sugar transporter
040c	-	probable sugar transporter
041c	-	probable sugar transporter
nions		
584	arsA	probable arsenical pump
585	arsB	probable arsenical pump
5/8 5/3	ars62	probable arsenical pump
397c	cysA	sulphate transport ATP-binding
399c	cysT	sulphate transport system perme-
398c	cysW	sulphate transport system perme-
357	modA	molybdate binding protein
358	modB	transport system permease, molybdate uptake
359	modC	molybdate uptake ABC- transporter
360	modD	precursor of Apa (45/47 kD secreted protein)
329c	narK1	probable nitrite extrusion protein
737c	narK2	nitrite extrusion protein
261C 267	narK3 narLl	nitrite extrusion protein 1
934	phoS1	protein 2 PstS component of phosphate
928	phoS2	uptake PstS component of phosphate
320	phoT	uptake phosphate transport system ABC
301c	phoY1	phosphate transport system
321c	phoY2	phosphate transport system
545c	pitA	low-affinity inorganic phosphate transporter
281 930	pitB pstA1	phosphate permease PstA component of phosphate
936	pstA2	uptake PstA component of phosphate
933	pstB	uptake ABC transport component of
935	pstC	phosphate uptake PstC component of phosphate
929	pstC2	uptake membrane-bound component of

Rv0932c	pstS	phosphate transport system PstS component of phosphate	Rv1821	secA2	unit SecA, preprotein translocase sub-	Rv3500c Rv3501c	-	part of mce4 opero part of mce4 opero	on on
D::0400a		uptake	D::0507-		unit	Rv3896c	-	putative p60 homo	logue
Rv2400c Rv0143c	subl -	sulphate binding precursor probable chloride channel	RV2587C Rv0638	secD secE	protein-export membrane protein SecE preprotein translocase	RV3922C	-	possible nemolysir	1
Rv1707	-	probable sulphate permease	Rv2586c	secF	protein-export membrane protein	B. IS elem	ents, Repe	eated sequences, a	nd Phage
Rv1739c	-	possible sulphate transporter	Rv1440	secG	protein-export membrane protein	1. IS eleme	ents	10	
Rv3679 Rv3680	-	possible anion transporter	Bv0732	secY	SecG SecY subunit of preprotein translo-	IS6110 IS1081		16 copies 6 copies	
					case	Others		37 copies	
5. Fatty aci	id transpoi	rt 	Rv2462c	tig	chaperone protein, similar to	2 DED 120	=12 family	Z copies	
Rv3540c	ltp2	non-specific lipid transport protein	Rv2813	-	probable general secretion path-	2.1111 701		7 copies	
C E#1					way protein	3. Phage-r	elated fund	ctions	
 Efflux pr Bv2936 	drrA	similar daunorubicin resistance	E. Adapta	tions and a	atypical conditions	Rv2894c Rv1701	xerC xerD	integrase/recombinintegrase	nase
		ABC-transporter	Rv1901	cinA	competence damage protein	Rv1054	-	integrase-a	
Rv2937	drrB	similar daunorubicin resistance	Rv3648c	cspA	cold shock protein, transcriptional	Rv1055	-	integrase-b	tod protoin
Rv2938	drrC	similar daunorubicin resistance	Rv0871	cspB	probable cold shock protein	Rv1573	-	phiRV1 phage rela	ted protein
		transmembrane protein	Rv3063	cstA	starvation-induced stress	Rv1575	-	phiRV1 phage rela	ted protein
Rv2846c Rv3065	etpA emrF	putative efflux protein resistance to ethidium bromide	Bv3490	otsA	response protein probable α α-trebalose-phosphate	Rv15760 Rv1577c	-	phiRV1 phage rela	ted protein
Rv0783c	-	multidrug resistance protein		01071	synthase	Rv1578c	-	phiRV1 phage rela	ted protein
Rv0849	-	possible quinolone efflux pump	Rv2006	otsB	trehalose-6-phosphate phos-	Rv1579c	-	phiRV1 phage rela	ted protein
Rv1145	-	probable drug transporter	Rv3372	otsB2	trehalose-6-phosphate phos-	Rv15800	1	phiRV1 phage rela	ted protein
Rv1250	-	probable drug efflux protein	D 0750	.,	phatase	Rv1582c	- 0	phiRV1 phage rela	ted protein
Rv1258c	-	probable multidrug resistance	Rv3758c Bv3757c	proV proW	osmoprotection ABC transporter	Rv1583c Bv1584c		phiRV1 phage rela	ted protein
Rv1410c	-	probable drug efflux protein	Rv3759c	proX	similar to osmoprotection proteins	Rv1585c	-	phiRV1 phage rela	ted protein
Rv1634	-	probable drug efflux protein	Rv3756c	proZ	transport system permease	Rv1586c	-	phiRV1 integrase	
110100		pump	1101020		lase	Rv2310	-	excisionase	
Rv2136c	-	putative bacitracin resistance pro-	E Data il			Rv2646	-	phiRV2 integrase	te da seteta
Bv2209	-	tein probable drug efflux protein	F. Detoxitio Rv2428	cation ahpC	alkyl hydroperoxide reductase	Rv2647 Rv2650c	-	phiRV2 phage rela	ited protein
Rv2333c	-	probable tetracenomycin C resis-	Rv2429	ahpD	member of AhpC/TSA family	Rv2651c	-	phiRV2 prohead pi	rotease
Dv2004		tance protein	Rv2238c	ahpE bon	member of AhpC/TSA family	Rv2652c	-	phiRV2 phage rela	ted protein
1112334	-	protein	Rv1608c	bcp bcpB	probable bacterioferritin comigra-	Rv2654c	-	phiRV2 phage rela	ited protein
Rv1877	-	probable drug efflux protein	D 0/70		tory protein	Rv2655c	-	phiRV2 phage rela	ted protein
Rv2459	-	probable drug efflux protein	Rv3473c	броА	probable non-heme bromoperoxi-	Rv2656C Rv2657c	-	similar to gp36 of r	ited protein
B. Chapero	ones/Heat	shock	Rv1123c	bpoB	probable non-heme bromoperoxi-			phage L5	
Rv0384c	clpB dpa l	heat shock protein	Dv0554	hnoC	dase probable non home bromenerovi	Rv2658c	-	phiRV2 phage rela	ted protein
1100002	unaj	ATPase	HV0554	bpoc	dase	Rv2830c	-	similar to phage P	1 <i>phd</i> gene
Rv2373c	dnaJ2	DnaJ homologue	Rv3617	ephA	probable epoxide hydrolase	Rv3750c	-	excisionase	
Rv0350	dnaK	70 kD heat shock protein, chromo- some replication	Rv1938 Rv1124	ephB enhC	probable epoxide hydrolase	Rv3/51	-	putative integrase	
Rv3417c	groEL1	60 kD chaperonin 1	Rv2214c	ephD	probable epoxide hydrolase	C. PE and	PPE famil	lies	
Rv0440	groEL2	60 kD chaperonin 2	Rv3670	ephE ophE	probable epoxide hydrolase	1. PE fami	ly	29 mombors	
Rv0351	grpE	stimulates DnaK ATPase activity	Rv3171c	hpx	probable epoxide nydrolase probable non-heme haloperoxi-	PE_PGRS	subfamily	61 members	
Rv2374c	hrcA	heat-inducible transcription	B (000		dase				
Bv0251c	hsp	repressor possible heat shock protein	Rv1908c Rv3846	katG sodA	catalase-peroxidase superoxide dismutase	2. PPE fan	nily	68 members	
Rv0353	hspR	heat shock regulator	Rv0432	sodC	superoxide dismutase precursor -	D. Antibiot	ic producti	on and resistance	
Rv2031c	hspX	14kD antigen, heat shock protein	By1032	tov	(Cu-Zn)	Rv2068c	blaC lat	class A β-lactamas	Se sforaso
Rv2299c	htpG	heat shock protein Hsp90 family	Rv0634c	-	putative glyoxylase II	Rv2043c	pncA	pyrazinamide resis	stance/sensitivity
Rv0563	htpX	probable (transmembrane) heat	Rv2581c	-	putative glyoxylase II	Rv0133	-	possible puromycir	n N-acetyltrans-
Rv2701c	suhB	putative extragenic suppressor	RV3177	-	dase	Rv0262c	-	aminoglycoside 2'-	N-acetvltrans-
		protein						ferase	
Rv3269		probable heat shock protein	IV. Other	~ <u>~</u>		Rv0802c Bv1082	-	acetyltransferase	ensis ImhF
C. Cell divi	ision		Rv0169	mce1	cell invasion protein	Rv1170	-	similar to S. lincoln	nensis ImbE
Rv3641c	fic	possible cell division protein	Rv0589	mce2	cell invasion protein	Rv1347c	-	possible aminogly	coside 6'-N-
Rv361020	nse ftsH	inner membrane protein.	Rv3499c	mce4	cell invasion protein	Rv2036	-	similar to lincomvc	in production
_		chaperone	Rv3100c	smpB	probable small protein b	_		genes	
Rv2748c Bv2151c	ftsK ftsQ	chromosome partitioning	Rv1694 Rv0024	tlyA -	cytotoxin/hemolysin homologue	Rv2303c	-	similar to S. griseu resistance protein	s macrotetrolide
Rv2154c	ftsW	membrane protein (shape determi-	Rv0167	-	part of mce1 operon	Rv3225c	-	probable aminogly	coside 3'-phos-
By31010	fts¥	nation)	Rv0168	-	part of <i>mce1</i> operon	By27000	_	photransferases	referaçe
Rv2921c	ftsY	cell division protein FtsY	Rv0171	-	part of mce1 operon	Rv3817	-	probable aminogly	coside 3'-phos-
Rv2150c	ftsZ	circumferential ring, GTPase	Rv0172	-	part of mce1 operon			photransferase	
Rv3919c Rv3625c	gia mesJ	probable cell cycle protein	Rv0174 Rv0587	-	part of <i>mce1</i> operon part of <i>mce2</i> operon	E. Bacterio	ocin-like pr	oteins	3
Rv3917c	parA	chromosome partitioning; DNA -	Rv0588	-	part of <i>mce2</i> operon		_		
Bv3918c	parR	binding possibly involved in chromosome	Rv0590 Rv0591	-	part of mce2 operon	F. Cytochro	ome P450	enzymes	22
	puid	partitioning	Rv0592	-	part of mce2 operon	G. Coenzy	me F420-	dependent	
Rv2922c	smc	member of Smc1/Cut3/Cut14	Rv0594	-	part of mce2 operon	enzyme	es -		3
Rv0012	-	possible cell division protein	Rv1477	-	putative exported p60 protein	H. Miscella	aneous tra	nsferases	61
Rv0435c	-	ATPase of AAA-family	Dud (TC		homologue	1 11-1-1		anhatar I	
HV21150 Rv3213c	-	AI Pase of AAA-tamily	HV1478	-	putative exported p60 protein homologue	i. Miscellar	neous pho lases	spnatases, lyases,	18
		regation	Rv1566c	-	putative exported p60 protein				-
Rv1708	-	possible role in chromosome parti-	Bv1064		homologue	J. Cyclase	s		6
		lioning	Rv1965	-	part of mce3 operon	K. Chelata	ses		2
D. Protein	and peptic	le secretion	Rv1967	-	part of mce3 operon	VC	ad here - 1	ationla	010
Rv29160 Rv2903c	lin lepB	signal recognition particle protein signal peptidase I	Rv1968	-	part of <i>mce3</i> operon part of <i>mce3</i> operon	v. Conserv	eu nypoth	eucais	912
Rv1614	lgt	prolipoprotein diacylglyceryl trans-	Rv1971	-	part of mce3 operon	VI. Unknow	vns		606
Bv1530	lsn4	terase linoprotein signal pentidase	Rv2190c	-	putative p60 homologue	τοται			3924
Rv0379	sec	probable transport protein	Rv3496c	-	part of mce4 operon	. U IAL			30L-1
_		SecE/Sec61- γ family	Rv3497c	-	part of mce4 operon				
Bv32400	SACA	Seca preprotein transicease cub	BUSICIAN						