

Supplemental Table 9. The secretory proteins identified in *Mycobacterium tuberculosis*

H37Ra.

Gene ID	Locus tag in <i>M. tuberculosis</i> H37Ra	Gene	Description	Locus tag in <i>M. tuberculosis</i> H37Rv	Gene	Locus tag in <i>M. tuberculosis</i> H37Rv (reference) Culture filter proteins	Locus tag in <i>M. tuberculosis</i> H37Rv (reference) antigens
gi 148662038	MRA_2237	glnA1	glutamine synthetase	Rv2220	glnA1	Rv2220 (1)	Rv2220 (2)
gi 148660661	MRA_0891	serC	phosphoserine aminotransferase	Rv0884c	serC	Rv0884c (3)	
gi 148661098	MRA_1318	atpD	ATP synthase F ₀ F ₁ subunit beta	Rv1310	atpD	Rv1310 (3)	
gi 148659975	MRA_0219	pckA	phosphoenolpyruvate carboxykinase	Rv0211	pckA	Rv0211 (3)	
gi 148663111	MRA_3289	sahH	S-adenosyl-L-homocysteine hydrolase	Rv3248c	sahH	Rv3248c (3)	Rv3248c (4)
gi 148660116	MRA_0359	dnaK	molecular chaperone DnaK	Rv0350	dnaK	Rv0350 (3)	Rv0350 (5)
gi 148660205	MRA_0445	groEL	molecular chaperone GroEL	Rv0440	groEL2	Rv0440 (1)	Rv0440 (6)
gi 148661845	MRA_2046	hspX	antigen Hsp20	Rv2031c	hspX	Rv2031c (7)	Rv2031c (8)
gi 148663282	MRA_3458	groES	co-chaperonin GroES	Rv3418c	groES	Rv3418c (3)	Rv3418c (6)
gi 148660529	MRA_0762	mmsA	MmsA	Rv0753c	mmsA		Rv0753c (4)
gi 148659759	MRA_0002	dnaN	DNA polymerase III subunit beta	Rv0002	dnaN	Rv0002 (3)	
gi 148662881	MRA_3060	fixA	electron transfer flavoprotein subunit beta	Rv3029c	fixA	Rv3029c (9)	
gi 148660009	MRA_0253	fadE5	acyl-CoA dehydrogenase	Rv0244c	fadE5	Rv0244c (3)	
gi 148660036	MRA_0279	fadE6	acyl-CoA dehydrogenase	Rv0271c	fadE6		Rv0271c (10)
gi 148660636	MRA_0867	fadA	acetyl-CoA acetyltransferase	Rv0859	fadA		Rv0859 (10)
gi 148661112	MRA_1331	fadA4	acetyl-CoA acetyltransferase	Rv1323	fadA4	Rv1323 (3)	
gi 148660129	MRA_0372	fba	fructose-bisphosphate aldolase	Rv0363c	fba	Rv0363c (3)	Rv0363c (4)
gi 148661643	MRA_1848	glcB	malate synthase G	Rv1837c	glcB	Rv1837c (3)	Rv1837c (11)
gi 148660007	MRA_0251	fabG	3-ketoacyl-ACP reductase	Rv0242c	fabG	Rv0242c (3)	Rv0242c (4)
gi 148661276	MRA_1493	fabG1	3-oxoacyl-ACP reductase	Rv1483	fabG1		Rv1483 (10)
gi 148660908	MRA_1131	gnd2	6-phosphogluconate dehydrogenase	Rv1122	gnd2	Rv1122 (9)	
gi 148661240	MRA_1457	tal	transaldolase	Rv1448c	tal	Rv1448c (3)	Rv1448c (4)
gi 148663491	MRA_3664	ppa	inorganic pyrophosphatase	Rv3628	ppa	Rv3628 (9)	
gi 148663668	MRA_3840	pks13	polyketide synthase	Rv3800c	pks13		Rv3800c (4)
gi 148660460	MRA_0694	tuf	elongation factor Tu	Rv0685	tuf	Rv0685 (1)	
gi 148660799	MRA_1025	prsA	ribose-phosphate pyrophosphokinase	Rv1017c	prsA	Rv1017c (9)	Rv1017c (10)
gi 148660228	MRA_0468	lpd	dihydrolipoamide dehydrogenase	Rv0462	lpd	Rv0462 (3)	Rv0462 (4)

gi 148662062	MRA_2261	aceE	pyruvate dehydrogenase subunit E1	Rv2241	aceE	Rv2241 (3)	
gi 148660426	MRA_0663	rplL	50S ribosomal protein L7/L12	Rv0652	rplL	Rv0652 (9)	Rv0652 (12)
gi 148660475	MRA_0708	rpsJ	30S ribosomal protein S10	Rv0700	rpsJ		Rv0700 (11)
gi 148662726	MRA_2907	frr	ribosome recycling factor	Rv2882c	frr	Rv2882c (7)	Rv2882c (4)
gi 148662065	MRA_2264	acpP	acyl carrier protein	Rv2244	acpM	Rv2244 (9)	Rv2244 (4)
gi 148659826	MRA_0068	icd2	isocitrate dehydrogenase (NADP) Icd2	Rv0066c	icd2	Rv0066c(9)	Rv0066c (13)
gi 148660884	MRA_1109	fumC	fumarate hydratase	Rv1098c	fumC	Rv1098c (3)	
gi 148660731	MRA_0959	sucD	succinyl-CoA synthetase subunit alpha	Rv0952	sucD	Rv0952 (9)	
gi 148661268	MRA_1485	acn	aconitate hydratase	Rv1475c	can	Rv1475c (3)	Rv1475c (4)
gi 148661113	MRA_1332	-	thioredoxin-related protein	Rv1324	-		Rv1324 (4)
gi 148663109	MRA_3287	mtrA	two component sensory transduction transcriptional regulatory protein MtrA	Rv3246c	mtrA		Rv3246c (14)
gi 148661281	MRA_1497	-	hypothetical protein	Rv1488	-	Rv1488 (9)	
gi 148661431	MRA_1646	-	hypothetical protein	Rv1636	TB15.3	Rv1636 (7)	Rv1636 (15)
gi 148661633	MRA_1839	cfp17	hypothetical protein	Rv1827	cfp17	Rv1827 (3)	Rv1827 (16)
gi 148661955	MRA_2154	-	hypothetical protein	Rv2140c	TB18.6	Rv2140c (3)	Rv2140c (17)
gi 148661961	MRA_2160	wag31	hypothetical protein	Rv2145c	wag31		Rv2145c (18)
gi 148663251	MRA_3428A	-	hypothetical protein	Rv3389c	-	Rv3389c (9)	
gi 148663717	MRA_3889	-	hypothetical protein	Rv3849	-	Rv3849 (3)	

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