

Table 6: Genes repressed in *Mycobacterium tuberculosis* H37Rv sigE mutant strain after 90m of 0.05% SDS stress. The following microarray data are for individual interpretation. All genes in this table may not be reproducibly repressed. In addition, the table should not be seen as a complete list of all possibly repressed genes. Description of the data table details and analysis methods are described in the data analysis section.

Spot	Name	Gene	Corrected intensity		Average			Gene product	PCR	Square		Individual array ratios (CH2/CH1)						
			Average		CH1/CH2	StD	SEM			F	root N	N	Biol. Set 1		Biol. Set 2		Biol. Set 3	
			CH1	CH2									mi1031	mi537	mi1014	mi1019	mi1025	mi60
4901	Rv0001	dnaA	7067	4288	1.6	0.6	0.3	chromosomal_replication_initiator_protein	1.1	2	6	0.9	1.0	0.4	0.7	0.4	0.4	
1035	Rv0014c	pknB	8989	6182	1.6	0.7	0.3	serine-threonine_protein_kinase	1.1	2	6	0.9	1.0	0.5	0.5	0.5	0.4	
314	Rv0015c	pknA	7809	5258	1.5	0.3	0.1	serine-threonine_protein_kinase	1.1	2	6	0.8	0.8	0.5	0.7	0.5	0.6	
5103	Rv0024	-	5413	2257	2.4	1.1	0.4	putative_p60_homologue	1.1	2	6	0.5	0.7	0.3	0.3	0.3	0.4	
4384	Rv0029	-	4424	2636	1.6	0.4	0.2		1.1	2	6	0.7	0.7	0.4	0.8	0.7	0.5	
1500	Rv0037c	-	6739	4385	1.6	0.2	0.1	probable_membrane_protein	1.1	2	6	0.7	0.7	0.6	0.6	0.6	0.6	
3122	Rv0039c	-	2622	1722	1.5	0.1	0.1		1.1	2	5	0.6	0.7	0.6	nd	0.7	0.6	
3710	Rv0049	-	3934	2552	1.6	0.3	0.1		1.1	2	6	0.6	0.6	0.5	0.7	0.7	0.8	
1038	Rv0050	ponA	7402	4332	1.7	0.3	0.1	penicillin-bonding_protein	1.1	2	6	0.7	0.7	0.5	0.6	0.5	0.5	
2989	Rv0050	ponA	6476	4463	1.5	0.2	0.1	penicillin-bonding_protein	1.1	2	6	0.7	0.8	0.6	0.7	0.6	0.6	
4902	Rv0058	dnaB	6450	2291	2.7	0.7	0.3	DNA_helicase_(contains_intein)	1.1	2	6	0.5	0.4	0.2	0.5	0.4	0.2	
5624	Rv0058	dnaB	10413	4172	2.6	1.4	0.6	DNA_helicase_(contains_intein)	1.1	2	6	0.7	0.5	0.2	0.3	0.3	0.2	
105	Rv0058	dnaB	13557	8062	1.7	0.3	0.1	DNA_helicase_(contains_intein)	1.1	2	6	0.8	0.6	0.5	0.5	0.5	0.6	
4903	Rv0059	-	4630	2827	1.6	0.4	0.2		1.1	2	6	0.8	0.7	0.5	0.7	0.7	0.4	
4904	Rv0072	-	6656	4221	1.5	0.3	0.1	ABC-transporter_transmembrane_subunit	1.1	2	6	0.5	0.6	0.6	0.9	0.7	0.7	
5626	Rv0073	-	6798	3948	1.6	0.3	0.1	ABC-transporter_ATP-binding_subunit	1.1	2	6	0.5	0.5	0.6	0.8	0.7	0.6	
4906	Rv0076c	-	4447	2853	1.5	0.1	0.1	possible_membrane_spanning_protein	1.2	2	6	0.7	0.7	0.6	0.7	0.6	0.6	
1039	Rv0079	-	5959	2235	2.6	0.3	0.1		1.1	2	6	0.4	0.4	0.5	0.4	0.3	0.4	
5629	Rv0079	-	4565	2137	2.0	0.3	0.1		1.2	2	6	0.5	0.4	0.5	0.6	0.6	0.4	
4908	Rv0080	-	2805	1592	1.6	0.4	0.2		1.1	2	6	0.7	0.7	0.5	0.8	0.5	0.4	
4909	Rv0082	-	2940	1787	1.5	0.4	0.1	probable_oxidoreductase_subunit	1.1	2	6	0.4	0.7	0.6	0.9	0.6	0.6	
3176	Rv0084	hycD	3396	2081	1.5	0.3	0.1	formate_hydrogenlyase_subunit_4	1.1	2	6	0.5	0.6	0.6	0.9	0.7	0.6	
1348	Rv0097	-	4970	2904	1.7	0.4	0.2		1.1	2	6	0.8	0.8	0.5	0.6	0.5	0.5	
627	Rv0107c	ctpl	3729	2173	1.7	0.2	0.1	probable_magnesium_transport_ATPase	1.1	2	6	0.5	0.6	0.7	0.7	0.6	0.5	
1349	Rv0107c	ctpl	3247	2166	1.5	0.2	0.1	probable_magnesium_transport_ATPase	1.1	2	6	0.7	0.6	0.6	0.8	0.7	0.7	
2763	Rv0108c	-	10873	4219	2.6	0.3	0.1		1.2	2	6	0.5	0.4	0.3	0.4	0.4	0.4	
2764	Rv0110	-	3196	1862	1.7	0.3	0.1	transmembrane_protein	1.1	2	6	0.6	0.5	0.4	0.6	0.6	0.6	
5586	Rv0143c	-	4839	3045	1.6	0.1	0.0	probable_chloride_channel	1.1	2	6	0.7	0.6	0.6	0.7	0.6	0.6	
2703	Rv0153c	-	3477	2234	1.5	0.2	0.1	putative_protein-tyrosine-phosphatase	1.1	2	6	0.6	0.6	0.8	0.7	0.7	0.6	
1982	Rv0154c	fadE2	5331	3092	1.6	0.3	0.1	acyl-CoA_dehydrogenase_	1.1	2	6	0.5	0.5	0.7	0.8	0.7	0.6	
1983	Rv0156	pntAB	5814	2403	2.4	0.3	0.1	pyridine_transhydrogenase_subunit_a2	1.1	2	6	0.3	0.4	0.4	0.4	0.5	0.4	
2705	Rv0157	pntB	4918	2859	1.6	0.6	0.3	pyridine_transhydrogenase_subunit_b	1.1	2	6	0.5	0.4	0.6	0.9	0.9	0.5	

5079Rv0163	-	3088	1773	1.7	0.2	0.1	probable_dehydrogenase	1.1	2	6	0.5	0.6	0.6	0.7	0.6	0.6
4358Rv0164	-	14513	9608	1.5	0.3	0.1		1.1	2	6	0.6	0.5	0.6	0.8	0.8	0.8
4359Rv0166	fadD5	4895	1854	2.5	0.9	0.4	acyl-CoA_synthase	1.1	2	6	0.5	0.5	0.2	0.6	0.4	0.3
5081Rv0167	-	8755	2770	3.2	0.8	0.3	part_of_mce1_operon	1.2	2	6	0.4	0.3	0.2	0.3	0.3	0.3
990Rv0168	-	8427	2535	3.2	0.7	0.3	part_of_mce1_operon	1.1	2	6	0.4	0.4	0.3	0.3	0.3	0.2
4360Rv0168	-	8386	3237	2.7	0.9	0.4	part_of_mce1_operon	1.1	2	6	0.5	0.5	0.2	0.4	0.3	0.3
5082Rv0169	mce1	12955	3635	3.7	1.4	0.6	cell_invasion_protein	1.1	2	6	0.4	0.4	0.2	0.2	0.2	0.2
4361Rv0170	-	17073	5416	3.1	1.8	0.7	part_of_mce1_operon	1.1	2	6	0.6	0.5	0.2	0.3	0.2	0.2
5083Rv0171	-	12168	3921	3.0	1.7	0.7	part_of_mce1_operon	1.1	2	6	0.6	0.6	0.2	0.2	0.2	0.2
269Rv0171	-	22442	7258	2.9	2.2	0.9	part_of_mce1_operon	1.1	2	6	0.8	0.5	0.2	0.2	0.2	0.2
991Rv0172	-	18075	6050	2.9	2.0	0.8	part_of_mce1_operon	1.1	2	6	0.7	0.6	0.2	0.2	0.2	0.2
4362Rv0172	-	14088	6892	2.0	1.3	0.5	part_of_mce1_operon	1.1	2	6	0.9	1.0	0.3	0.2	0.3	0.4
270Rv0173	lprK	19850	5770	3.2	2.4	1.0	part_of_mce1_operon	1.1	2	6	0.7	0.5	0.1	0.2	0.2	0.1
1475Rv0174	-	23538	9665	2.3	1.4	0.6	part_of_mce1_operon	1.1	2	6	0.8	0.8	0.2	0.2	0.4	0.2
2197Rv0175	-	10355	4609	2.2	0.3	0.1		1.1	2	6	0.5	0.5	0.4	0.5	0.4	0.4
1476Rv0176	-	8759	4656	1.8	0.3	0.1		1.1	2	6	0.6	0.5	0.4	0.6	0.6	0.5
2198Rv0177	-	7938	4300	1.8	0.2	0.1		1.1	2	6	0.6	0.6	0.6	0.5	0.5	0.4
1477Rv0178	-	15341	7209	2.2	0.5	0.2		1.1	2	6	0.6	0.5	0.4	0.4	0.5	0.4
232Rv0193c	-	4519	2883	1.6	0.2	0.1		1.1	2	6	0.6	0.5	0.7	0.7	0.7	0.7
963Rv0199	-	4461	2744	1.6	0.3	0.1		1.1	2	6	0.5	0.5	0.7	0.8	0.7	0.6
242Rv0200	-	4470	2591	1.7	0.2	0.1	probable_membrane_protein	1.1	2	6	0.7	0.5	0.5	0.7	0.5	0.5
243Rv0202c	mmpL11	3504	2243	1.5	0.4	0.2	conserved_large_membrane_protein	1.1	2	6	0.5	0.4	0.7	0.9	0.8	0.6
1618Rv0220	lipC	15614	7000	2.2	0.4	0.2	probable_esterase	1.1	2	6	0.5	0.4	0.4	0.5	0.6	0.4
5224Rv0225	-	3449	2171	1.6	0.2	0.1	possible_involved_in_LPS_synthesis	1.1	2	6	0.7	0.6	0.6	0.7	0.6	0.5
5225Rv0227c	-	16255	7349	2.3	0.4	0.2	possible_membrane_protein	1.1	2	6	0.4	0.3	0.6	0.4	0.5	0.4
5227Rv0230c	-	6632	3336	1.9	0.3	0.1		1.1	2	6	0.6	0.5	0.4	0.7	0.5	0.4
4506Rv0231	fadE4	6885	3267	2.1	0.2	0.1	acyl-CoA_dehydrogenase_	1.1	2	6	0.5	0.4	0.4	0.6	0.5	0.5
967Rv0236c	-	5046	2173	2.2	0.4	0.2	possible_membrane_protein	1.1	2	6	0.4	0.4	0.5	0.6	0.4	0.4
246Rv0236c	-	2862	1856	1.5	0.2	0.1	possible_membrane_protein	1.1	2	6	0.6	0.5	0.6	0.9	0.7	0.7
968Rv0237	lpqI	3133	1758	1.6	0.5	0.2	beta-hexosaminidase_precursor	1.1	2	6	0.6	0.3	0.8	0.8	0.6	0.7
3855Rv0247c	-	10602	5555	1.9	0.9	0.3	probable_iron-sulphur_protein	1.1	2	6	0.8	0.9	0.2	0.5	0.4	0.4
247Rv0250c	-	10832	6711	1.6	0.6	0.2	unlikely_orf	1.1	2	6	0.9	0.8	0.5	0.5	0.5	0.5
2828Rv0257c	-	9833	5380	1.8	0.3	0.1	very_unlikely_orf	1.1	2	6	0.7	0.6	0.5	0.5	0.5	0.4
976Rv0292	-	7423	5001	1.5	0.2	0.1	unknown_possible_membrane_protein	2.5	2	6	0.8	0.8	0.6	0.8	0.6	0.5
256Rv0295c	-	3947	1967	1.9	0.5	0.2		1.1	2	6	0.5	0.4	0.5	0.8	0.5	0.5
4850Rv0312	-	3706	2365	1.5	0.3	0.1		1.1	2	6	0.6	0.6	0.7	0.9	0.6	0.6
4851Rv0314c	-	7273	3776	1.9	0.2	0.1	unknown_hydrophobic_protein	1.1	2	6	0.6	0.5	0.4	0.6	0.5	0.5
5573Rv0315	-	11577	2628	4.5	1.5	0.6	probable_b-1,3-glucanase	1.2	2	6	0.3	0.3	0.1	0.2	0.2	0.2
4852Rv0316	-	3106	2022	1.5	0.2	0.1	probable_muconolactone_isomerase	1.1	2	6	0.6	0.7	0.6	0.8	0.7	0.6
5123Rv0350	dnaK	7056	3439	2.0	0.9	0.3	70_kD_heat_shock_protein,_chromosome_replication	1.1	2	6	0.8	0.8	0.3	0.4	0.4	0.4

1855Rv0357c	purA	3702	2457	1.5	0.3	0.1	adenylosuccinate_synthase	1.1	2	6	0.6	0.6	0.8	0.6	0.6	0.9
2578Rv0360c	-	3095	1632	1.8	0.5	0.2		1.1	2	6	0.6	0.5	0.4	0.8	0.5	0.5
1857Rv0361	-	6420	3982	1.5	0.2	0.1	possible_membrane_protein	1.1	2	6	0.5	0.5	0.8	0.7	0.7	0.6
2580Rv0364	-	4250	2488	1.6	0.3	0.1		1.1	2	6	0.5	0.5	0.6	0.8	0.6	0.6
1046Rv0379	sec	7588	2957	2.5	0.5	0.2	probable_transport_protein_SecE/Sec61-_g_family	1.1	2	6	0.4	0.3	0.5	0.3	0.5	0.3
3844Rv0404	fadD30	3051	1973	1.5	0.4	0.2	acyl-CoA_synthase	1.1	2	6	0.7	1.0	0.6	0.7	0.5	0.5
3643Rv0407	-	3662	2004	1.8	0.3	0.1	probable_coenzyme_F420-dependent_enzyme	1.2	2	6	0.4	0.6	0.6	0.5	0.7	0.6
3008Rv0409	ackA	5629	3855	1.5	0.2	0.1	acetate_kinase	1.1	2	6	0.7	0.8	0.6	0.6	0.7	0.6
4068Rv0424c	-	3335	2053	1.6	0.3	0.1		1.1	2	6	0.7	0.8	0.5	0.6	0.5	0.6
3932Rv0429c	def	3626	2169	1.7	0.3	0.1	polypeptide_deformylase	1.1	2	5	0.5	0.5	0.7	nd	0.7	0.6
3175Rv0435c	-	3276	2100	1.5	0.3	0.1	ATPase_of_AAA-family	1.1	2	6	0.6	0.6	0.5	0.9	0.7	0.6
3869Rv0443	-	4500	2365	1.8	0.4	0.2		1.1	2	6	0.4	0.5	0.6	0.7	0.7	0.5
3870Rv0445c	sigK	3187	1574	2.0	0.4	0.2	ECF-type_sigma_factor	1.1	2	6	0.5	0.7	0.4	0.5	0.5	0.5
1539Rv0479c	-	10263	5702	1.8	0.2	0.1	unknown_hydrophobic_protein	1.1	2	6	0.6	0.5	0.6	0.6	0.5	0.5
2600Rv0496	-	6567	4319	1.5	0.2	0.1		1.1	2	6	0.6	0.5	0.7	0.7	0.7	0.8
1879Rv0497	-	4766	2757	1.7	0.4	0.1	probable_membrane_protein	1.1	2	6	0.4	0.5	0.8	0.6	0.7	0.7
3649Rv0503c	cmaA2	6535	3562	1.8	0.3	0.1	cyclopropane_mycolic_acid_synthase_2	1.1	2	6	0.7	0.7	0.5	0.6	0.5	0.4
2604Rv0504c	-	4346	2658	1.6	0.2	0.1		1.1	2	6	0.6	0.7	0.6	0.5	0.7	0.5
663Rv0517	-	3036	1963	1.5	0.3	0.1	possible_acyltransferase	1.1	2	6	0.5	0.5	0.8	0.7	0.8	0.7
1385Rv0518	-	2832	1778	1.5	0.3	0.1		1.1	2	6	0.9	0.5	0.6	0.6	0.7	0.6
664Rv0519c	-	3417	1847	1.7	0.4	0.2		1.1	2	6	0.4	0.5	0.8	0.7	0.6	0.5
4621Rv0523c	-	2223	1440	1.6	0.4	0.2		1.2	2	4	0.6	nd	0.8	nd	0.6	0.4
4623Rv0527	ccsA	6605	4404	1.5	0.2	0.1	cytochrome_c-type_biogenesis_protein	1.1	2	6	0.7	0.7	0.5	0.8	0.7	0.6
4624Rv0529	ccsB	3514	2130	1.6	0.3	0.1	cytochrome_c-type_biogenesis_protein	1.1	2	6	0.7	0.7	0.5	0.8	0.7	0.4
4625Rv0531	-	4036	2648	1.5	0.2	0.1	unknown,_membrane_protein.	1.1	2	6	0.6	0.6	0.7	0.8	0.8	0.7
1740Rv0537c	-	4622	2463	1.8	0.3	0.1	unknown,_possible_membrane_protein,	1.1	2	6	0.5	0.5	0.6	0.7	0.6	0.5
2466Rv0546c	-	2646	1663	1.6	0.1	0.0		1.1	2	6	0.7	0.6	0.6	0.6	0.6	0.6
4627Rv0547c	-	4866	2807	1.7	0.4	0.2	putative_oxidoreductase	1.1	2	6	0.5	0.5	0.5	0.8	0.7	0.5
5349Rv0548c	menB	6033	3201	1.8	0.3	0.1	naphthoate_synthase	1.1	2	6	0.5	0.5	0.6	0.6	0.7	0.5
5352Rv0554	bpoC	6039	3854	1.6	0.2	0.1	probable_non-heme_bromoperoxidase	1.1	2	6	0.6	0.6	0.6	0.7	0.8	0.6
4631Rv0555	menD	3346	1888	1.7	0.2	0.1	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate_synthase	1.1	2	6	0.6	0.5	0.5	0.7	0.6	0.6
608Rv0566c	-	5312	2518	2.0	0.3	0.1		1.4	2	6	0.5	0.4	0.6	0.5	0.5	0.5
1331Rv0569	-	5652	2915	1.9	0.6	0.2		1.1	2	6	0.8	0.7	0.4	0.5	0.4	0.4
1049Rv0569	-	3542	2333	1.5	0.2	0.1		1.1	2	6	0.8	0.8	0.6	0.7	0.5	0.6
328Rv0572c	-	5197	2976	1.7	0.1	0.1		1.1	2	6	0.6	0.6	0.5	0.7	0.6	0.6
611Rv0572c	-	3446	2202	1.6	0.2	0.1		2.6	2	6	0.7	0.6	0.8	0.6	0.6	0.6
4061Rv0588	-	10113	4367	2.3	0.6	0.3	part_of_mce2_operon	1.1	2	6	0.6	0.6	0.3	0.4	0.4	0.4
1052Rv0613c	-	5776	3253	1.7	0.4	0.1		1.1	2	6	0.5	0.5	0.8	0.7	0.6	0.6
3650Rv0643c	mmaA3	6423	4229	1.5	0.2	0.1	methoxymycolic_acid_synthase_3	1.1	2	6	0.6	0.6	0.8	0.7	0.7	0.6
672Rv0652	rplL	9194	5288	1.7	0.3	0.1	50S_ribosomal_protein_L7/L12	1.1	2	6	0.5	0.5	0.5	0.6	0.7	0.6

1055Rv0652	rplL	6695	4083	1.6	0.2	0.1	50S_ribosomal_protein_L7/L12	1.1	2	6	0.5	0.6	0.6	0.7	0.8	0.6
1490Rv0666	-	4163	2293	1.8	0.4	0.2		1.1	2	6	0.6	0.7	0.5	0.7	0.5	0.4
1488Rv0669c	-	6677	2882	2.3	0.4	0.2		1.1	2	6	0.4	0.4	0.4	0.5	0.5	0.4
335Rv0672	fadE8	4902	3239	1.5	0.2	0.1	acyl-CoA_dehydrogenase_(aka_aidB)	1.1	2	6	0.7	0.6	0.7	0.8	0.7	0.6
5710Rv0673	-	4060	2419	1.7	0.2	0.1	enoyl-CoA_hydratase/isomerase_superfamily_	1.1	2	6	0.6	0.7	0.5	0.6	0.6	0.5
4374Rv0674	-	3342	2218	1.5	0.4	0.2		1.4	2	6	0.7	0.7	0.5	1.0	0.6	0.5
5493Rv0692	-	10009	4265	2.3	0.3	0.1		1.1	2	6	0.4	0.4	0.4	0.4	0.5	0.4
1884Rv0693	pqqE	5447	1920	2.5	0.8	0.3	coenzyme_PQQ_synthesis_protein_E	1.1	2	6	0.3	0.2	0.6	0.5	0.4	0.4
2606Rv0694	lldD1	8099	2570	2.9	0.7	0.3	L-lactate_dehydrogenase_(cytochrome)_	1.1	2	6	0.3	0.3	0.3	0.5	0.4	0.3
1885Rv0695	-	3210	2003	1.6	0.1	0.1		1.1	2	6	0.6	0.7	0.7	0.6	0.5	0.6
2607Rv0696	-	3678	1600	2.3	0.4	0.2	glycosyltransferase	1.1	2	6	0.5	0.4	0.4	0.5	0.5	0.4
1397Rv0710	rpsQ	8744	5773	1.5	0.3	0.1	30S_ribosomal_protein_S17	1.4	2	6	0.8	0.7	0.7	0.6	0.7	0.5
2612Rv0716	rplE	6448	3351	1.9	0.4	0.2	50S_ribosomal_protein_L5	1.1	2	6	0.4	0.4	0.5	0.6	0.7	0.6
1891Rv0717	rpsN	7487	4546	1.6	0.2	0.1	30S_ribosomal_protein_S14	1.1	2	6	0.5	0.6	0.7	0.6	0.7	0.7
2613Rv0718	rpsH	10459	5720	1.8	0.3	0.1	30S_ribosomal_protein_S8	1.1	2	6	0.5	0.5	0.7	0.7	0.6	0.6
1892Rv0719	rplF	7270	3814	1.8	0.2	0.1	50S_ribosomal_protein_L6	1.1	2	6	0.5	0.5	0.6	0.7	0.5	0.5
2614Rv0720	rplR	4645	2541	1.8	0.4	0.1	50S_ribosomal_protein_L18	1.1	2	6	0.5	0.6	0.4	0.8	0.6	0.5
1893Rv0721	rpsE	6066	2921	2.0	0.3	0.1	30S_ribosomal_protein_S5	1.1	2	6	0.5	0.5	0.4	0.7	0.5	0.5
2615Rv0722	rpmD	8734	4714	1.9	0.2	0.1	50S_ribosomal_protein_L30	1.1	2	6	0.7	0.5	0.5	0.5	0.6	0.5
1894Rv0723	rplO	10071	4993	2.1	0.4	0.2	50S_ribosomal_protein_L15	1.1	2	6	0.6	0.6	0.4	0.5	0.4	0.4
1340Rv0730	-	6819	3858	1.7	0.3	0.1		1.1	2	6	0.5	0.5	0.6	0.7	0.6	0.6
676Rv0732	secY	7306	4528	1.6	0.3	0.1	SecY_subunit_of_preprotein_translocase	1.1	2	6	0.5	0.5	0.7	0.7	0.8	0.7
1398Rv0733	adk	11590	5346	2.1	0.3	0.1	probable_adenylate_kinase	1.1	2	6	0.5	0.4	0.5	0.6	0.5	0.4
3502Rv0733	adk	8809	4580	1.9	0.1	0.0	probable_adenylate_kinase	1.2	2	6	0.5	0.5	0.5	0.5	0.5	0.5
3562Rv0734	map'	4574	1858	2.3	0.5	0.2	probable_methionine_aminopeptidase	1.1	2	6	0.3	0.4	0.5	0.6	0.4	0.4
4224Rv0734	map'	5331	3537	1.7	0.7	0.3	probable_methionine_aminopeptidase	1.1	2	6	0.5	0.5	0.5	1.1	0.5	0.4
4471Rv0760c	-	16075	7674	2.3	0.7	0.3		1.2	2	6	0.6	0.4	0.2	0.4	0.4	0.6
5193Rv0761c	adhB	14132	5060	2.7	0.5	0.2	zinc-containing_alcohol_dehydrogenase	1.1	2	6	0.3	0.3	0.3	0.4	0.4	0.4
4472Rv0762c	-	3620	2279	1.6	0.2	0.1		1.3	2	6	0.7	0.6	0.5	0.7	0.7	0.5
2648Rv0773c	ggtA	3616	2116	1.7	0.5	0.2	putative_g-glutamyl_transpeptidase	1.1	2	6	0.5	0.5	0.3	0.8	0.7	0.7
680Rv0774c	-	4768	2529	1.9	0.2	0.1		1.1	2	6	0.5	0.4	0.6	0.5	0.6	0.6
1927Rv0774c	-	3394	1974	1.6	0.3	0.1		1.2	2	6	0.4	0.6	0.7	0.8	0.6	0.6
633Rv0777	purB	6028	3754	1.5	0.3	0.1	adenylosuccinate_lyase	1.1	2	6	0.5	0.5	0.8	0.7	0.6	0.7
5440Rv0797	IS1547	3702	1925	1.9	0.3	0.1		1.2	2	6	0.5	0.6	0.4	0.6	0.7	0.5
4718Rv0798c	-	10701	4273	2.6	1.0	0.4	similar_to_bacteriocins	1.1	2	6	0.5	0.6	0.1	0.4	0.3	0.4
4153Rv0799c	-	3137	2116	1.5	0.3	0.1		1.1	2	6	0.7	0.8	0.5	0.6	0.8	0.5
2557Rv0799c	-	5870	3929	1.5	0.2	0.1		1.1	2	6	0.8	0.7	0.6	0.6	0.7	0.6
4642Rv0832	PE_PGRS	4602	2712	1.6	0.2	0.1		1.1	2	6	0.5	0.5	0.6	0.7	0.7	0.6
1698Rv0866	moaE2	2899	1859	1.6	0.3	0.1	molybdopterin-converting_factor_subunit_2	1.1	2	6	0.7	0.7	0.4	0.7	0.7	0.5
2420Rv0867c	-	3537	1569	2.1	0.4	0.2	probable_exported_protein	2.5	2	6	0.4	0.4	0.6	0.6	0.5	0.4

1699Rv0868c	moaD2	2951	1440	2.0	0.3	0.1	molybdopterin_converting_factor_subunit_1	1.1	2	6	0.5	0.5	0.4	0.6	0.6	0.4
862Rv0879c	-	3166	1976	1.5	0.4	0.1		1.1	2	6	0.6	0.5	0.7	1.0	0.6	0.7
143Rv0883c	-	13359	7992	1.7	0.2	0.1		1.1	2	6	0.7	0.6	0.5	0.6	0.6	0.6
865Rv0884c	serC	7722	5022	1.5	0.3	0.1	phosphoserine_aminotransferase	1.1	2	6	0.5	0.5	0.7	0.9	0.7	0.8
3027Rv0888	-	14319	6594	2.2	0.5	0.2	possible_membrane_protein	1.2	2	6	0.6	0.5	0.3	0.4	0.4	0.5
1206Rv0904c	accD3	7540	4728	1.5	0.3	0.1	acetyl/propionyl_CoA_carboxylase_b_subunit	2.5	2	6	0.6	0.5	0.7	0.9	0.8	0.7
3556Rv0907	-	3275	1969	1.6	0.2	0.1	probable_penicillin_binding_protein	1.1	2	6	0.6	0.6	0.7	0.8	0.5	0.5
4278Rv0908	ctpE	3313	1892	1.8	0.3	0.1	probable_cation_transport_ATPase	1.1	2	6	0.7	0.7	0.4	0.6	0.5	0.5
4279Rv0910	-	6159	3942	1.6	0.1	0.1		1.1	2	6	0.6	0.6	0.7	0.6	0.7	0.6
1733Rv0919	-	4688	3174	1.5	0.2	0.1		1.2	2	6	0.8	0.7	0.5	0.7	0.7	0.6
1736Rv0925c	-	6588	4389	1.5	0.2	0.1		1.1	2	6	0.6	0.6	0.7	0.8	0.8	0.7
1738Rv0929	pstC2	4685	3294	1.5	0.3	0.1	membrane-bound_component_of_phosphate_transport_system	1.1	2	6	0.8	0.9	0.6	0.7	0.6	0.5
2345Rv0933	pstB	3206	1899	1.6	0.4	0.1	ABC_transport_component_of_phosphate_uptake	1.1	2	6	0.6	0.6	0.9	0.6	0.5	0.6
1623Rv0934	phoS1	19462	4242	4.4	1.1	0.5	PstS_component_of_phosphate_uptake	1.4	2	6	0.3	0.3	0.2	0.3	0.2	0.2
1001Rv0935	pstC	11086	2797	3.9	0.6	0.3	PstC_component_of_phosphate_uptake	1.1	2	6	0.3	0.3	0.3	0.3	0.2	0.2
1622Rv0936	pstA2	5793	3233	1.8	0.3	0.1	PstA_component_of_phosphate_uptake	1.4	2	6	0.6	0.6	0.5	0.7	0.6	0.4
4026Rv0950c	-	8832	2934	3.0	0.8	0.3		1.1	2	6	0.5	0.4	0.2	0.3	0.3	0.3
419Rv0957	purH	5834	2703	2.1	0.3	0.1	phosphoribosylaminoimidazolecarboxamide_formyltransferase_	1.1	2	6	0.5	0.4	0.5	0.6	0.4	0.4
417Rv0961	-	6700	3794	1.8	0.3	0.1		1.2	2	6	0.7	0.6	0.6	0.5	0.4	0.5
4024Rv0966c	-	2482	1509	1.7	0.2	0.1		1.1	2	5	0.7	0.5	0.5	nd	0.7	0.5
406Rv0988	-	7884	5069	1.6	0.6	0.3		1.1	2	6	1.0	0.9	0.5	0.6	0.4	0.4
4017Rv1002c	-	3541	2135	1.7	0.5	0.2	probable_membrane_protein	1.1	2	6	0.8	0.7	0.3	0.7	0.6	0.5
267Rv1010	ksgA	3419	1500	2.1	0.5	0.2	16S_rRNA_dimethyltransferase	1.1	2	6	0.4	0.5	0.4	0.7	0.5	0.3
2193Rv1010	ksgA	4066	2218	1.7	0.4	0.2	16S_rRNA_dimethyltransferase	1.1	2	6	0.6	0.4	0.8	0.5	0.6	0.6
1150Rv1025	-	4065	2394	1.7	0.3	0.1		1.1	2	6	0.7	0.6	0.5	0.7	0.6	0.5
3574Rv1068c	PE_PGRS	9240	5942	1.5	0.2	0.1		2.1	2	6	0.7	0.6	0.6	0.8	0.6	0.6
4552Rv1069c	-	5552	2810	1.9	0.3	0.1		1.1	2	6	0.5	0.6	0.4	0.7	0.5	0.4
5274Rv1070c	echA8	13543	6015	2.3	0.4	0.2	enoyl-CoA_hydratase/isomerase_superfamily_	1.1	2	6	0.5	0.4	0.3	0.5	0.5	0.5
4553Rv1071c	echA9	7443	4220	1.7	0.4	0.1	enoyl-CoA_hydratase/isomerase_superfamily_	1.1	2	6	0.5	0.4	0.5	0.7	0.8	0.6
4557Rv1092c	coaA	10511	4738	2.2	0.3	0.1	pantothenate_kinase	1.4	2	6	0.4	0.5	0.4	0.6	0.5	0.4
5279Rv1093	glyA	5328	3087	1.7	0.3	0.1	serine_hydroxymethyltransferase	1.1	2	6	0.5	0.5	0.6	0.7	0.7	0.6
5280Rv1095	phoH2	6299	3470	1.9	0.4	0.1	PhoH-like_protein	1.1	2	6	0.6	0.6	0.4	0.4	0.6	0.5
5281Rv1097c	-	9585	4599	2.1	0.4	0.2	probable_membrane_spanning_protein	1.1	2	6	0.7	0.5	0.4	0.5	0.4	0.4
4560Rv1098c	fum	11188	6270	1.7	0.2	0.1	fumarase	1.1	2	6	0.6	0.5	0.5	0.7	0.6	0.6
5282Rv1099c	-	6546	3550	1.8	0.3	0.1		1.1	2	6	0.4	0.4	0.6	0.6	0.6	0.6
2398Rv1107c	xseB	4270	2351	1.8	0.2	0.1	exonuclease_VII_small_subunit	1.1	2	6	0.7	0.6	0.5	0.6	0.5	0.5
1186Rv1113	-	6376	4062	1.6	0.2	0.1		1.1	2	6	0.6	0.5	0.6	0.6	0.7	0.7
1191Rv1123c	bpoB	4991	3288	1.5	0.2	0.1	probable_non-heme_bromoperoxidase	1.1	2	6	0.7	0.6	0.6	0.7	0.8	0.6
4078Rv1133c	metE	7924	4647	1.6	0.3	0.1	5-methyltetrahydropteroyltriglutamate-homocysteine	1.1	2	6	0.6	0.4	0.6	0.7	0.7	0.6
693Rv1140	-	6947	3937	1.7	0.3	0.1		1.1	2	6	0.6	0.5	0.5	0.7	0.6	0.5

5451Rv1155	-	7200	4901	1.5	0.2	0.1		1.1	2	6	0.6	0.6	0.7	0.7	0.8	0.7
2568Rv1165	-	4313	3052	1.5	0.2	0.1		1.1	2	6	0.7	0.8	0.6	0.6	0.8	0.6
1287Rv1173	-	8432	4244	1.9	0.3	0.1		1.1	2	6	0.5	0.4	0.5	0.6	0.7	0.5
1484Rv1201c	-	10985	4692	2.2	0.3	0.1		1.1	2	6	0.4	0.4	0.4	0.6	0.4	0.4
1486Rv1205	-	9132	5580	1.6	0.1	0.0		1.1	2	6	0.7	0.6	0.6	0.7	0.6	0.6
3154Rv1206	fadD6	4605	2091	2.1	0.3	0.1	acyl-CoA_synthase	1.4	2	6	0.4	0.5	0.5	0.6	0.4	0.4
3582Rv1220c	-	4622	2423	1.8	0.3	0.1	probable_methyltransferase	1.1	2	6	0.5	0.5	0.6	0.7	0.5	0.4
5445Rv1227c	-	3096	1874	1.6	0.3	0.1	probable_transmembrane_protein	1.1	2	6	0.5	0.7	0.6	0.7	0.8	0.6
2477Rv1229c	mrp	4800	3184	1.5	0.2	0.1	similar_to_MRP/NBP35_ATP-binding_proteins	1.1	2	6	0.7	0.7	0.6	0.6	0.6	0.7
4248Rv1230c	-	2966	1767	1.6	0.4	0.1	possible_membrane_protein	1.1	2	6	0.6	0.8	0.4	0.8	0.6	0.5
569Rv1231c	-	4277	2642	1.6	0.1	0.0		1.1	2	6	0.6	0.6	0.6	0.7	0.6	0.6
677Rv1231c	-	3705	2456	1.5	0.1	0.0		1.1	2	6	0.7	0.6	0.7	0.7	0.7	0.6
1399Rv1233c	-	20626	12443	1.6	0.4	0.2	hydrophobic_protein	1.4	2	6	0.8	0.5	0.7	0.6	0.8	0.4
1292Rv1234	-	8224	5042	1.6	0.2	0.1		1.1	2	6	0.5	0.5	0.6	0.7	0.7	0.6
3454Rv1237	sugB	3608	2274	1.6	0.2	0.1	sugar_transport_protein	1.1	2	6	0.5	0.7	0.8	0.6	0.6	0.6
4177Rv1240	mdh	8824	3577	2.4	0.4	0.2	malate_dehydrogenase	1.1	2	6	0.3	0.5	0.3	0.5	0.5	0.4
3456Rv1241	-	4204	1665	2.4	0.4	0.2		1.1	2	6	0.4	0.4	0.5	0.5	0.3	0.4
4179Rv1244	lpqZ	3133	2054	1.5	0.3	0.1	lipoprotein	1.1	2	6	0.7	0.6	0.4	0.8	0.8	0.7
4181Rv1248c	sucA	3754	2625	1.5	0.3	0.1	2-oxoglutarate_dehydrogenase	1.1	2	6	0.7	0.9	0.7	0.5	0.7	0.6
573Rv1251c	-	3648	2526	1.5	0.1	0.1	some_similarity_to_GTP-binding_proteins	1.1	2	6	0.8	0.6	0.7	0.6	0.7	0.7
5569Rv1252c	lprE	6522	4086	1.6	0.2	0.1	lipoprotein	1.1	2	6	0.8	0.7	0.6	0.6	0.6	0.6
4244Rv1252c	lprE	4880	3052	1.6	0.3	0.1	lipoprotein	1.1	2	6	0.7	0.8	0.5	0.6	0.6	0.6
5568Rv1254	-	3150	2140	1.5	0.3	0.1	acyltransferase	1.1	2	6	0.8	0.8	0.6	0.8	0.6	0.5
4841Rv1279	-	8276	4938	1.6	0.6	0.2	probable_choline_dehydrogenase	2.1	2	6	0.9	0.9	0.4	0.6	0.5	0.4
2658Rv1297	rho	14852	9216	1.6	0.5	0.2	transcription_termination_factor_rho	1.1	2	6	1.0	0.7	0.5	0.5	0.6	0.5
5542Rv1301	-	4678	3251	1.5	0.2	0.1		1.1	2	6	0.8	0.7	0.6	0.6	0.7	0.6
4821Rv1302	rfe	2939	1948	1.5	0.2	0.1	undecaprenyl-phosphate_a-N-acetylglucosaminyltransferase	1.1	2	6	0.5	0.7	0.7	0.7	0.8	0.6
4824Rv1308	atpA	13818	9539	1.5	0.5	0.2	ATP_synthase_a_chain	1.1	2	6	0.9	1.0	0.5	0.6	0.5	0.6
1504Rv1322	-	5489	2940	1.8	0.4	0.2		1.1	2	6	0.6	0.5	0.4	0.7	0.6	0.5
4387Rv1324	-	4125	2606	1.6	0.2	0.1	some_similarity_to_thioredoxins	1.1	2	5	0.5	nd	0.7	0.7	0.6	0.6
3566Rv1333	-	2507	1495	1.6	0.4	0.1	probable_hydrolase	1.1	2	6	0.5	0.9	0.6	0.7	0.6	0.5
1505Rv1336	cysM	7877	4297	1.9	0.4	0.2	cysteine_synthase_B	1.1	2	6	0.7	0.7	0.5	0.5	0.5	0.5
5459Rv1337	-	4578	2965	1.6	0.4	0.2		1.1	2	6	0.8	0.8	0.4	0.5	0.7	0.5
1506Rv1338	murl	4290	2572	1.7	0.2	0.1	glutamate_racemase	1.1	2	6	0.6	0.6	0.5	0.6	0.6	0.5
49Rv1346	fadE14	4711	3166	1.5	0.1	0.1	acyl-CoA_dehydrogenase_	1.1	2	6	0.7	0.6	0.6	0.8	0.7	0.7
856Rv1368	lprF	5987	3590	1.6	0.2	0.1	lipoprotein	1.1	2	6	0.5	0.5	0.6	0.7	0.6	0.7
859Rv1374c	-	8575	5483	1.5	0.3	0.1		1.1	2	6	0.6	0.5	0.7	0.8	0.7	0.8
2620Rv1400c	lipI	3482	2090	1.6	0.3	0.1	probable_lipase	1.1	2	6	0.6	0.5	0.6	0.8	0.7	0.6
3571Rv1422	-	2662	1612	1.7	0.2	0.1		1.1	2	5	0.5	0.6	nd	0.7	0.6	0.5
4498Rv1427c	fadD12	5497	2693	2.0	0.4	0.1	acyl-CoA_synthase	1.1	2	6	0.5	0.6	0.4	0.7	0.5	0.4

5219Rv1428c	-	4574	2927	1.5	0.2	0.1		1.4	2	6	0.6	0.6	0.6	0.8	0.7	0.7
4294Rv1440	secG	4462	2588	1.7	0.2	0.1	protein-export_membrane_protein_SecG	1.1	2	6	0.6	0.6	0.5	0.5	0.7	0.6
2331Rv1440	secG	4060	2554	1.6	0.1	0.1	protein-export_membrane_protein_SecG	1.1	2	6	0.6	0.7	0.6	0.7	0.6	0.6
1607Rv1445c	devB	5711	3209	1.8	0.2	0.1	glucose-6-phosphate_1-dehydrogenase	1.1	2	6	0.6	0.6	0.5	0.5	0.6	0.5
5216Rv1446c	opcA	3918	2378	1.7	0.3	0.1	unknown_function,_may_aid_G6PDH	1.1	2	5	0.7	0.7	0.5	nd	0.5	0.5
4494Rv1447c	zwf2	9801	6795	1.5	0.3	0.1	glucose-6-phosphate_1-dehydrogenase	1.1	2	6	0.9	0.8	0.5	0.7	0.6	0.6
5215Rv1448c	tal	7067	4653	1.5	0.2	0.1	transaldolase	1.1	2	6	0.8	0.7	0.6	0.6	0.6	0.6
1295Rv1454c	qor	7474	4870	1.5	0.2	0.1	Probable_quinone_oxidoreductase	1.1	2	6	0.6	0.5	0.7	0.8	0.8	0.7
1296Rv1456c	-	2635	1641	1.5	0.3	0.1	probable_membrane_protein	1.1	2	6	0.5	0.7	0.6	0.8	0.7	0.5
575Rv1457c	-	4401	3091	1.6	0.1	0.1	probable_membrane_protein	1.1	2	5	0.6	0.6	0.6	0.7	0.6	nd
3463Rv1469	ctpD	5049	3404	1.7	0.2	0.1	probable_cadmium-transporting_ATPase	1.1	2	5	0.5	0.6	0.7	0.7	0.5	nd
4186Rv1472	echA12	5967	2841	2.1	0.4	0.1	enoyl-CoA_hydratase/isomerase_superfamily	1.1	2	6	0.4	0.4	0.5	0.5	0.5	0.6
3465Rv1473	-	6433	4793	1.6	0.3	0.1	ABC_transporter,_possible_in_EF-3_subfamily	1.1	2	4	0.5	nd	0.6	0.7	0.7	nd
1638Rv1477	-	9150	4585	2.0	0.4	0.2	putative_exported_p60_protein_homologue	1.1	2	6	0.6	0.6	0.4	0.5	0.5	0.4
1753Rv1480	-	6812	2277	3.1	1.2	0.5		1.1	2	6	0.5	0.4	0.2	0.3	0.3	0.2
5527Rv1481	-	8117	5103	1.6	0.4	0.2	possible_membrane_protein	1.1	2	6	0.8	0.8	0.5	0.5	0.7	0.5
1748Rv1484	inhA	6683	4071	1.5	0.4	0.1	enoyl-[ACP]_reductase	1.1	2	6	0.5	0.5	0.8	0.8	0.8	0.7
4809Rv1504c	-	3888	2534	1.5	0.3	0.1		1.1	2	6	0.7	0.8	0.5	0.7	0.6	0.6
843Rv1515c	-	9234	4963	1.8	0.1	0.1		1.1	2	6	0.6	0.5	0.5	0.6	0.5	0.6
4299Rv1538c	ansA	2399	1538	1.5	0.3	0.1	L-asparaginase	1.4	2	6	0.5	0.9	0.6	0.8	0.7	0.6
5202Rv1541c	lprI	2946	1936	1.5	0.4	0.2	lipoprotein	1.1	2	6	0.8	0.8	0.4	0.8	0.7	0.5
4479Rv1544	-	7740	3996	1.9	0.6	0.2	probable_ketoacyl_reductase	1.1	2	6	0.5	0.4	0.3	0.8	0.5	0.6
4478Rv1546	-	5036	3209	1.5	0.3	0.1		1.1	2	6	0.5	0.6	0.7	0.9	0.6	0.7
5199Rv1547	dnaE1	11328	5474	2.1	0.5	0.2	DNA_polymerase_III,_a_subunit	1.4	2	6	0.6	0.6	0.3	0.5	0.4	0.5
4101Rv1566c	-	5322	3277	1.6	0.2	0.1	putative_exported_p60_protein_homologue	1.1	2	6	0.6	0.7	0.5	0.7	0.7	0.6
1708Rv1608c	bcpB	6416	3582	1.7	0.2	0.1	probable_bacterioferritin_comigratory_protein	1.1	2	6	0.5	0.6	0.7	0.6	0.6	0.5
4730Rv1611	trpC	10523	4676	2.2	0.3	0.1	indole-3-glycerol_phosphate_synthase	1.1	2	6	0.4	0.5	0.5	0.5	0.5	0.4
5452Rv1612	trpB	7948	2842	2.8	0.5	0.2	tryptophan_synthase_b_chain	1.2	2	6	0.4	0.4	0.2	0.4	0.4	0.3
4731Rv1613	trpA	11519	3800	3.0	0.5	0.2	tryptophan_synthase_a_chain	1.1	2	6	0.4	0.4	0.3	0.4	0.3	0.3
5453Rv1614	lgt	13503	4958	2.8	0.8	0.3	prolipoprotein_diacylglyceryl_transferase	1.1	2	6	0.5	0.4	0.2	0.4	0.3	0.3
4733Rv1617	pykA	7664	4277	1.7	0.5	0.2	pyruvate_kinase	1.1	2	6	0.4	0.3	0.7	0.7	0.7	0.7
3156Rv1617	pykA	7082	3872	1.7	0.5	0.2	pyruvate_kinase	1.1	2	6	0.4	0.4	0.6	0.7	0.7	0.7
5455Rv1618	tesB1	8937	4129	2.1	0.5	0.2	thioesterase_II	1.1	2	6	0.5	0.4	0.3	0.6	0.6	0.5
2952Rv1639c	-	9330	3759	2.5	0.3	0.1		1.1	2	6	0.4	0.4	0.3	0.4	0.5	0.4
3163Rv1648	-	3875	1889	2.0	0.3	0.1	possible_membrane_protein	1.1	2	6	0.5	0.5	0.5	0.6	0.5	0.4
791Rv1649	pheS	5291	3429	1.5	0.2	0.1	phenylalanyl-tRNA_synthase_a_subunit	1.1	2	6	0.7	0.6	0.6	0.6	0.8	0.5
70Rv1650	pheT	4403	2519	1.8	0.1	0.0	phenylalanyl-tRNA_synthase_b_subunit	1.1	2	6	0.6	0.6	0.5	0.6	0.6	0.5
4591Rv1666c	-	4132	2005	1.9	0.5	0.2	Probable_cytochrome_p450	1.1	2	6	0.5	0.5	0.4	0.7	0.6	0.4
4592Rv1668c	-	4248	2510	1.7	0.4	0.1	probable_ABC_transporter	1.1	2	6	0.6	0.6	0.4	0.8	0.6	0.5
5317Rv1676	-	10640	6513	1.6	0.3	0.1	possible_cytochrome_P450	1.1	2	6	0.6	0.8	0.5	0.7	0.6	0.6

4596Rv1677	dsbF	8006	5272	1.5	0.3	0.1	highly_similar_to_C-term_Mpt53	1.1	2	6	0.7	0.7	0.5	0.8	0.6	0.6
5318Rv1678	-	5541	3262	1.7	0.2	0.1	probably_integral_membrane_protein	1.1	2	6	0.7	0.6	0.5	0.6	0.6	0.5
399Rv1689	tyrS	7350	3707	1.9	0.3	0.1	tyrosyl-tRNA_synthase	1.1	2	6	0.4	0.4	0.6	0.6	0.6	0.5
1122Rv1692	-	3819	2515	1.5	0.2	0.1	probable_hydrolase	1.1	2	6	0.8	0.6	0.7	0.6	0.7	0.7
402Rv1695	-	6370	3578	1.7	0.2	0.1		1.1	2	6	0.5	0.5	0.6	0.7	0.6	0.5
403Rv1697	-	12634	6997	1.8	0.2	0.1		1.1	2	6	0.6	0.6	0.5	0.5	0.6	0.5
1125Rv1698	-	7645	4989	1.6	0.3	0.1		1.1	2	6	0.8	0.8	0.5	0.6	0.6	0.5
3288Rv1703c	-	5082	2528	1.9	0.4	0.1	putative_methyltransferase	1.1	2	6	0.5	0.4	0.7	0.6	0.5	0.5
4010Rv1704c	cycA	4571	2425	1.9	0.1	0.0	transport_of_D-alanine,_D-serine_and_glycine	1.1	2	6	0.5	0.5	0.6	0.5	0.6	0.5
404Rv1711	-	4385	2745	1.6	0.2	0.1		1.1	2	6	0.6	0.6	0.7	0.8	0.6	0.6
405Rv1713	-	3579	2361	1.5	0.2	0.1	probable_GTP-binding_protein_YPHC_BACSU	1.1	2	6	0.7	0.7	0.7	0.7	0.6	0.5
389Rv1722	-	3578	2252	1.5	0.3	0.1	possible_biotin_carboxylase	1.1	2	6	0.6	0.6	0.7	0.9	0.6	0.6
3279Rv1738	-	10084	2858	3.4	1.9	0.8		1.1	2	6	0.6	0.4	0.2	0.2	0.2	0.2
3012Rv1745c	-	2675	1807	1.5	0.3	0.1		1.1	2	6	0.7	0.9	0.6	0.6	0.7	0.5
394Rv1745c	-	4608	3156	1.5	0.3	0.1		1.1	2	6	0.7	0.8	0.6	0.8	0.5	0.6
1116Rv1746	pknF	5087	2476	2.0	0.4	0.1	serine-threonine_protein_kinase	1.2	2	6	0.7	0.5	0.4	0.5	0.5	0.4
3013Rv1747	-	5100	2646	1.9	0.4	0.2	ABC_transporter	1.1	2	6	0.5	0.6	0.4	0.7	0.6	0.4
395Rv1747	-	7353	4388	1.7	0.2	0.1	ABC_transporter	1.1	2	6	0.7	0.6	0.5	0.6	0.5	0.6
397Rv1751	-	9597	3759	2.6	0.5	0.2	possible_hydroxylase	1.1	2	6	0.5	0.4	0.4	0.4	0.3	0.3
127Rv1751	-	11205	6815	1.6	0.2	0.1	possible_hydroxylase	1.1	2	6	0.6	0.5	0.7	0.7	0.6	0.6
850Rv1754c	-	6103	3710	1.7	0.3	0.1		1.1	2	6	0.8	0.6	0.4	0.7	0.5	0.6
3741Rv1769	-	3193	2095	1.5	0.2	0.1		1.1	2	6	0.6	0.7	0.7	0.9	0.7	0.5
4938Rv1796	-	6912	4268	1.6	0.4	0.2	probable_protease	1.1	2	6	0.8	0.8	0.4	0.7	0.6	0.5
5660Rv1797	-	4766	2441	1.9	0.6	0.2		1.1	2	6	0.6	0.8	0.4	0.4	0.5	0.4
1528Rv1815	-	9171	4954	1.8	0.5	0.2		1.1	2	6	0.4	0.4	0.7	0.7	0.6	0.6
1526Rv1819c	-	5969	4019	1.5	0.2	0.1	probable_multidrug_resistance_pump	1.1	2	6	0.6	0.8	0.6	0.7	0.8	0.6
2246Rv1822	pgsA2	3186	1985	1.6	0.3	0.1	CDP-diacylglycerol-glycerol-3-phosphate_phosphatidyltransferase	1.1	2	6	0.5	0.7	0.9	0.6	0.6	0.6
1524Rv1823	-	4648	2526	1.8	0.4	0.1		1.1	2	6	0.5	0.7	0.4	0.5	0.6	0.5
1523Rv1825	-	5949	2589	2.3	0.4	0.2		1.1	2	6	0.5	0.5	0.4	0.5	0.4	0.3
3941Rv1826	gcvH	4960	2882	1.7	0.3	0.1	glycine_cleavage_system_H_protein	1.1	2	6	0.7	0.7	0.5	0.6	0.6	0.5
5132Rv1826	gcvH	10490	6652	1.6	0.2	0.1	glycine_cleavage_system_H_protein	1.1	2	6	0.7	0.8	0.6	0.6	0.6	0.6
5127Rv1836c	-	4836	2922	1.6	0.1	0.0		1.1	2	6	0.6	0.6	0.6	0.6	0.6	0.6
4469Rv1850	ureC	3985	2180	1.8	0.5	0.2	urease_a_subunit	1.1	2	6	0.6	0.6	0.3	0.8	0.6	0.4
3942Rv1860	modD	7261	4893	1.5	0.2	0.1	precursor_of_Apa_(45/47_kD_secreted_protein)	1.4	2	6	0.8	0.8	0.6	0.7	0.7	0.6
1580Rv1864c	-	4573	2580	1.7	0.3	0.1		1.4	2	6	0.6	0.6	0.6	0.6	0.7	0.4
816Rv1885c	-	15297	10062	1.5	0.2	0.1		1.1	2	6	0.7	0.6	0.6	0.6	0.8	0.6
2933Rv1908c	katG	9179	5894	1.6	0.2	0.1	catalase-peroxidase_	1.1	2	6	0.8	0.6	0.5	0.7	0.6	0.6
2779Rv1918c	PPE	6903	3707	1.8	0.5	0.2		1.2	2	6	0.8	0.8	0.4	0.5	0.5	0.4
4940Rv1919c	-	10532	6058	1.7	0.3	0.1	weak_similarity_to_pollen_antigens	1.1	2	6	0.4	0.5	0.6	0.7	0.7	0.6
5602Rv1923	lipD	8520	5876	1.5	0.2	0.1	probable_esterase	1.1	2	6	0.7	0.8	0.5	0.6	0.7	0.7

1994Rv1932	tpx	5681	3014	1.8	0.3	0.1	thiol_peroxidase	1.1	2	6	0.4	0.4	0.6	0.6	0.6	0.6
4879Rv1938	ephB	2126	1470	1.5	0.3	0.1	probable_epoxide_hydrolase	1.1	2	5	0.7	0.9	0.6	nd	0.7	0.6
2709Rv1957	-	4532	2721	1.7	0.2	0.1		1.1	2	6	0.7	0.7	0.6	0.6	0.6	0.5
2808Rv1976c	-	3791	2152	1.7	0.3	0.1		1.1	2	6	0.5	0.5	0.7	0.6	0.7	0.5
4832Rv1984c	-	9484	6188	1.6	0.4	0.2	probable_secreted_protein	2.6	2	6	0.4	0.5	0.6	0.7	0.8	0.8
3945Rv1987	-	10587	6258	1.7	0.8	0.3	probable_secreted_protein	1.1	2	6	0.9	1.0	0.4	0.3	0.5	0.4
1944Rv1996	-	4227	2433	1.7	0.2	0.1		1.2	2	6	0.7	0.6	0.7	0.5	0.5	0.5
4564Rv2021c	-	4349	2681	1.6	0.3	0.1	putative_transcriptional_regulator	1.1	2	6	0.5	0.8	0.5	0.7	0.7	0.5
5287Rv2024c	-	2546	1464	1.7	0.3	0.1		1.1	2	6	0.5	0.6	0.4	0.8	0.6	0.6
1681Rv2031c	hspX	6372	1766	2.9	1.4	0.6	14kD_antigen,_heat_shock_protein_Hsp20_family	1.1	2	6	0.4	0.6	0.2	0.4	0.3	0.2
2403Rv2032	-	2812	1582	1.8	0.6	0.3		1.1	2	5	nd	0.8	0.7	0.5	0.4	0.4
4569Rv2043c	pncA	9505	6340	1.5	0.2	0.1	pyrazinamide_resistance/sensitivity	1.1	2	6	0.6	0.6	0.7	0.8	0.7	0.7
4570Rv2045c	lipT	5479	3009	1.7	0.3	0.1	probable_carboxylesterase	1.1	2	6	0.5	0.6	0.5	0.7	0.7	0.5
5292Rv2046	lppI	4031	2038	2.0	0.3	0.1	probable_lipoprotein	1.1	2	6	0.5	0.6	0.5	0.6	0.5	0.4
5293Rv2048c	pks12	7593	3657	2.1	0.5	0.2	polyketide_synthase_(erythronolide_synthase-like)	1.1	2	6	0.5	0.6	0.3	0.6	0.5	0.4
4857Rv2055c	rpsR2	4653	2724	1.7	0.3	0.1	30S_ribosomal_protein_S18	1.1	2	6	0.6	0.6	0.4	0.7	0.6	0.6
2745Rv2061c	-	3866	2329	1.6	0.3	0.1		1.1	2	6	0.5	0.5	0.7	0.6	0.7	0.7
2936Rv2069	sigC	11084	6142	1.7	0.3	0.1	ECF_subfamily_sigma_subunit	1.1	2	6	0.5	0.4	0.6	0.7	0.7	0.6
4483Rv2074	-	15274	6700	2.3	0.5	0.2		1.1	2	6	0.6	0.5	0.4	0.4	0.4	0.4
4486Rv2080	lppJ	10615	6909	1.5	0.2	0.1	lipoprotein	1.1	2	6	0.8	0.6	0.6	0.7	0.6	0.6
5208Rv2081c	-	10165	5134	1.9	0.4	0.2		1.1	2	6	0.6	0.6	0.4	0.5	0.5	0.4
2481Rv2081c	-	5960	3086	1.9	0.2	0.1		1.1	2	6	0.6	0.6	0.5	0.6	0.5	0.4
5209Rv2083	-	3819	2138	1.8	0.3	0.1		1.1	2	6	0.6	0.6	0.4	0.6	0.6	0.5
4488Rv2084	-	3669	2439	1.5	0.3	0.1		1.1	2	6	0.8	0.8	0.5	0.8	0.7	0.5
4635Rv2101	helZ	5265	2394	2.1	0.6	0.3	probable_helicase,_Snf2/Rad54_family	1.1	2	6	0.5	0.4	0.2	0.6	0.6	0.4
2746Rv2102	-	5833	3955	1.5	0.3	0.1		1.1	2	6	0.8	0.9	0.5	0.6	0.6	0.6
5158Rv2108	PPE	5784	3530	1.6	0.4	0.2		1.1	2	6	0.7	0.9	0.6	0.7	0.5	0.5
4442Rv2128	-	5925	3490	1.7	0.4	0.2	unknown_hydrophobic_protein	1.1	2	6	0.8	0.7	0.5	0.6	0.5	0.5
4443Rv2130c	cysS2	3883	2450	1.5	0.2	0.1	cysteinyl-tRNA_synthase	1.1	2	6	0.6	0.6	0.6	0.8	0.6	0.6
5514Rv2137c	-	11540	7038	1.6	0.1	0.1		1.1	2	6	0.6	0.5	0.7	0.6	0.7	0.6
5513Rv2139	pyrD	3599	2192	1.6	0.2	0.1	dihydroorotate_dehydrogenase	1.1	2	6	0.6	0.6	0.5	0.7	0.6	0.6
4791Rv2140c	-	6904	3182	2.1	0.3	0.1		1.1	2	6	0.5	0.4	0.4	0.6	0.4	0.5
5512Rv2141c	dapE2	5850	3639	1.6	0.1	0.0	ArgE/DapE/Acy1/Cpg2/yscS_family	1.1	2	6	0.6	0.6	0.6	0.7	0.7	0.6
4452Rv2156c	murX	7665	4316	1.8	0.3	0.1	phospho-N-acetylmuramoyl-pentapeptide_transferase	1.1	2	6	0.6	0.6	0.4	0.7	0.6	0.6
4450Rv2160c	-	5766	3669	1.6	0.5	0.2	Function:_unknown,_improbable	1.1	2	6	0.9	0.8	0.4	0.7	0.6	0.5
4647Rv2174	-	3195	2061	1.5	0.3	0.1	_probable_membrane_protein	1.1	2	6	0.7	0.7	0.5	0.8	0.8	0.5
3705Rv2190c	-	8222	3851	2.2	1.0	0.4	putative_p60_homologue	1.1	2	6	0.7	0.7	0.3	0.3	0.3	0.3
438Rv2201	asnB	7025	3892	1.8	0.2	0.1	asparagine_synthase_B	1.1	2	6	0.6	0.5	0.5	0.6	0.5	0.6
1229Rv2223c	-	5987	2865	2.1	0.2	0.1	probable_exported_protease	1.1	2	6	0.5	0.5	0.4	0.5	0.5	0.5
1232Rv2230c	-	3550	2340	1.5	0.2	0.1		1.1	2	6	0.7	0.6	0.6	0.7	0.9	0.7

636Rv2232	-	5342	3238	1.6	0.2	0.1		1.1	2	6	0.5	0.5	0.7	0.7	0.7	0.6
4118Rv2238c	ahpE	6949	3676	1.9	0.3	0.1	member_of_AhpC/TSA_family	1.1	2	6	0.6	0.6	0.4	0.4	0.6	0.5
3397Rv2239c	-	7838	5263	1.5	0.1	0.0		1.1	2	6	0.7	0.6	0.7	0.8	0.7	0.6
5370Rv2241	aceE	5620	2994	1.9	0.2	0.1	pyruvate_dehydrogenase_E1_component	1.1	2	6	0.6	0.6	0.5	0.6	0.6	0.5
5638Rv2257c	-	2872	1505	1.9	0.3	0.1		1.1	2	6	0.5	0.5	0.5	0.7	0.6	0.5
4917Rv2258c	-	7426	2983	2.4	0.3	0.1	putative_transcriptional_regulator	1.1	2	6	0.4	0.4	0.4	0.5	0.4	0.4
5639Rv2259	adhE2	3521	1989	1.8	0.4	0.2	putative_alcohol_dehydrogenase_(Zn_dependent)	1.1	2	5	0.4	0.5	0.6	nd	0.7	0.6
4918Rv2260	-	3750	2408	1.5	0.2	0.1		1.1	2	6	0.6	0.6	0.7	0.8	0.7	0.6
2287Rv2271	-	11394	7554	1.5	0.3	0.1		1.1	2	6	0.6	0.6	0.5	0.7	0.9	0.7
4115Rv2273	-	2462	1671	1.5	0.1	0.1		1.1	2	6	0.7	0.8	0.6	0.7	0.7	0.6
3392Rv2276	-	5077	2965	1.6	0.2	0.1	Probable_cytochrome_P-450	1.1	2	5	0.6	0.5	0.6	0.7	0.6	nd
504Rv2288	-	10773	4945	2.2	0.4	0.2		1.1	2	6	0.4	0.4	0.5	0.5	0.4	0.6
1225Rv2289	cdh	13150	3925	3.2	0.6	0.2	CDP-diacylglycerol_phosphatidylhydrolase	1.1	2	6	0.3	0.3	0.3	0.4	0.3	0.2
4109Rv2297	-	6694	4695	1.5	0.2	0.1	PS00343_'anchoring'_hexapeptide	1.4	2	6	0.8	0.7	0.7	0.5	0.8	0.6
4108Rv2299c	htpG	7309	4420	1.7	0.3	0.1	heat_shock_protein_Hsp90_family	1.1	2	6	0.5	0.6	0.4	0.6	0.7	0.7
3385Rv2301	-	2697	1692	1.5	0.3	0.1	probable_cutinase	1.1	2	6	0.5	0.7	0.9	0.6	0.6	0.6
4106Rv2302	-	6954	3666	1.9	0.2	0.1	61.8%_identity_in_76aa	1.1	2	6	0.5	0.5	0.5	0.4	0.5	0.6
161Rv2329c	narK1	5572	2982	1.8	0.1	0.1	probable_nitrite_extrusion_protein	1.1	2	6	0.6	0.5	0.5	0.6	0.5	0.5
5372Rv2335	cysE	3840	2552	1.5	0.3	0.1	serine_acetyltransferase	1.1	2	6	0.6	0.4	0.7	0.7	0.8	0.8
4509Rv2336	-	5214	3369	1.5	0.5	0.2		1.1	2	6	0.9	0.9	0.4	0.7	0.5	0.5
5231Rv2337c	-	3022	1964	1.5	0.3	0.1		1.1	2	6	0.8	0.8	0.6	0.6	0.6	0.5
5232Rv2339	mmpL9	3394	1740	1.9	0.6	0.2	conserved_large_membrane_protein	1.1	2	6	0.7	0.6	0.3	0.6	0.5	0.4
638Rv2344c	dgt	3755	2094	1.8	0.2	0.1	probable_deoxyguanosine_triphosphate_hydrolase	1.1	2	6	0.6	0.5	0.5	0.7	0.6	0.6
2350Rv2352c	PPE	7358	4957	1.5	0.2	0.1		1.1	2	6	0.6	0.6	0.8	0.8	0.6	0.7
5355Rv2357c	glyS	8534	5468	1.5	0.3	0.1	glycyl-tRNA_synthase	1.1	2	6	0.8	0.8	0.7	0.6	0.6	0.5
1563Rv2360c	-	3608	2111	1.8	0.3	0.1		1.1	2	6	0.7	0.7	0.5	0.5	0.6	0.4
5166Rv2375	-	8808	4801	1.8	0.4	0.2		1.1	2	6	0.7	0.6	0.3	0.7	0.5	0.5
769Rv2376c	-	9513	5285	1.7	0.4	0.2		1.1	2	5	0.5	nd	0.5	0.6	0.6	0.8
5151Rv2405	-	2648	1687	1.6	0.2	0.1		1.1	2	5	0.6	0.7	0.5	0.7	0.6	nd
4429Rv2406c	-	5994	3254	1.9	0.3	0.1		1.4	2	6	0.6	0.6	0.4	0.6	0.6	0.5
2267Rv2409c	-	2823	1789	1.5	0.3	0.1		1.1	2	6	0.6	0.7	0.7	0.7	0.4	0.7
1545Rv2410c	-	5036	3191	1.6	0.2	0.1		1.1	2	6	0.7	0.7	0.6	0.7	0.7	0.5
4091Rv2419c	-	2610	1747	1.5	0.1	0.0	putative_phosphoglycerate_mutase	1.1	2	6	0.6	0.7	0.7	0.7	0.6	0.7
4123Rv2427c	proA	3614	2052	1.7	0.2	0.1	g-glutamyl_phosphate_reductase	1.1	2	6	0.5	0.5	0.6	0.7	0.6	0.6
4525Rv2451	-	2906	1846	1.5	0.3	0.1		1.1	2	5	0.5	0.6	0.8	nd	0.6	0.8
4526Rv2453c	-	3411	2071	1.6	0.5	0.2		1.1	2	6	0.7	0.7	0.4	1.0	0.5	0.5
5248Rv2454c	-	7479	4164	1.8	0.2	0.1	oxidoreductase,_beta_subunit	1.1	2	6	0.6	0.7	0.5	0.5	0.5	0.5
5250Rv2458	-	2522	1685	1.5	0.2	0.1	possible_transferase	1.1	2	6	0.7	0.8	0.6	0.8	0.7	0.5
4529Rv2459	-	5648	2693	2.1	0.5	0.2	probable_drug_efflux_protein	1.1	2	6	0.6	0.6	0.3	0.5	0.4	0.4
5251Rv2460c	clpP2	11975	8311	1.5	0.3	0.1	ATP-dependent_Clp_protease_proteolytic_subunit	1.1	2	6	0.8	0.8	0.5	0.7	0.6	0.7

2367Rv2468c	-	5105	3239	1.6	0.1	0.1		1.1	2	6	0.6	0.7	0.7	0.6	0.6	0.6
1646Rv2469c	-	4384	3176	1.8	0.2	0.1		1.1	2	5	0.5	0.6	0.6	nd	0.6	0.5
4531Rv2475c	-	6562	4713	1.5	0.5	0.2		1.1	2	6	0.9	1.0	0.5	0.7	0.5	0.5
5256Rv2482c	plsB2	2659	1528	1.7	0.4	0.2	glycerol-3-phosphate_acyltransferase	1.1	2	6	0.7	0.7	0.5	0.7	0.5	0.4
5257Rv2484c	-	4658	2932	1.6	0.2	0.1		1.1	2	6	0.7	0.8	0.5	0.7	0.7	0.5
4536Rv2485c	lipQ	3439	2020	1.7	0.3	0.1	probable_carboxylesterase	1.1	2	6	0.6	0.7	0.5	0.7	0.6	0.5
1134Rv2507	-	8227	4620	1.8	0.2	0.1	probable_membrane_spanning_protein	1.3	2	6	0.7	0.5	0.5	0.5	0.5	0.5
1135Rv2509	-	9634	5361	1.8	0.2	0.1	putative_oxidoreductase	1.4	2	6	0.6	0.5	0.6	0.5	0.6	0.6
414Rv2510c	-	3123	2012	1.5	0.2	0.1		1.1	2	6	0.7	0.6	0.6	0.8	0.6	0.7
1136Rv2511	-	5335	2919	1.8	0.2	0.1		1.1	2	6	0.5	0.5	0.4	0.5	0.6	0.6
4538Rv2522c	-	3069	2002	1.5	0.2	0.1		1.1	2	6	0.7	0.6	0.6	0.8	0.6	0.7
5260Rv2523c	acpS	4723	2084	2.3	0.6	0.2	CoA:apo-[ACP]_pantethienephosphotransferase	1.1	2	6	0.5	0.6	0.3	0.5	0.5	0.3
4752Rv2535c	pepQ	3720	2381	1.5	0.3	0.1	cytoplasmic_peptidase	1.1	2	6	0.4	0.6	0.7	0.8	0.8	0.7
5473Rv2536	-	4849	3276	1.5	0.1	0.1	potential_membrane_protein	1.1	2	6	0.7	0.7	0.6	0.7	0.8	0.6
1863Rv2550c	-	4205	2472	1.7	0.2	0.1		1.1	2	6	0.7	0.6	0.7	0.5	0.6	0.5
5593Rv2557	-	8293	4826	1.7	0.2	0.1		1.1	2	6	0.7	0.6	0.5	0.6	0.6	0.6
5591Rv2561	-	3116	2029	1.5	0.1	0.0		1.1	2	6	0.7	0.7	0.6	0.7	0.7	0.6
5590Rv2563	-	3112	1808	1.7	0.2	0.1	possible_membrane_protein	1.1	2	6	0.6	0.6	0.5	0.6	0.6	0.6
4868Rv2564	glnQ	8989	3621	2.4	0.4	0.2	probable_ATP-binding_transport_protein	1.1	2	6	0.4	0.4	0.3	0.5	0.4	0.4
2707Rv2565	-	10689	6401	1.7	0.1	0.0		1.4	2	6	0.6	0.6	0.6	0.6	0.6	0.6
2996Rv2582	ppiB	9306	4233	2.2	0.4	0.2	peptidyl-prolyl_cis-trans_isomerase	1.1	2	6	0.5	0.6	0.3	0.5	0.4	0.4
4991Rv2600		8219	2935	2.7	1.1	0.5		1.1	2	6	0.5	0.5	0.2	0.4	0.3	0.2
958Rv2600		6844	3571	2.0	1.1	0.5		1.1	2	6	1.0	0.5	0.3	0.4	0.3	0.3
1177Rv2626c	-	4978	2375	2.0	0.7	0.3		1.1	2	6	0.7	0.8	0.3	0.4	0.5	0.3
1240Rv2633c	-	16638	7016	2.3	0.5	0.2		1.1	2	6	0.5	0.4	0.4	0.3	0.5	0.4
1242Rv2637	dedA	4096	2639	1.5	0.2	0.1	dedA_family	1.1	2	6	0.7	0.6	0.6	0.7	0.7	0.6
4135Rv2672	-	11285	6972	1.6	0.2	0.1	putative_exported_protease	1.1	2	6	0.5	0.5	0.7	0.6	0.7	0.7
3414Rv2673	-	2973	1846	1.6	0.3	0.1	potential_membrane_protein	1.1	2	6	0.5	0.6	0.8	0.7	0.6	0.6
4136Rv2674	-	7898	4775	1.7	0.2	0.1		1.1	2	6	0.6	0.6	0.5	0.6	0.7	0.7
4540Rv2678c	hemE	3391	1927	1.7	0.5	0.2	uroporphyrinogen_decarboxylase	1.1	2	6	0.5	0.6	0.4	1.0	0.6	0.6
4541Rv2680	-	4912	2750	1.7	0.5	0.2		1.1	2	6	0.6	0.5	0.4	0.9	0.6	0.6
5377Rv2680	-	7427	4675	1.6	0.2	0.1		2.6	2	6	0.7	0.7	0.6	0.6	0.7	0.5
4656Rv2697c	dut	6266	4247	1.5	0.2	0.1	deoxyuridine_triphosphatase	1.1	2	6	0.7	0.7	0.5	0.7	0.8	0.6
3666Rv2698	-	3690	2205	1.7	0.2	0.1		1.1	2	6	0.5	0.5	0.6	0.7	0.6	0.7
64Rv2715	-	10392	5997	1.7	0.1	0.1	2-hydroxymuconic_semialdehyde_hydrolase	1.1	2	6	0.6	0.5	0.6	0.6	0.5	0.6
2581Rv2721c	-	6565	3124	2.0	0.3	0.1		1.1	2	6	0.4	0.4	0.5	0.6	0.6	0.5
4742Rv2722	-	4906	3250	1.5	0.1	0.0		1.1	2	6	0.6	0.6	0.7	0.7	0.7	0.7
5465Rv2725c	hflX	4357	2576	1.7	0.2	0.1	GTP-binding_protein	1.1	2	6	0.7	0.5	0.5	0.6	0.7	0.6
4744Rv2726c	dapF	4211	2701	1.5	0.2	0.1	diaminopimelate_epimerase	1.1	2	6	0.6	0.5	0.8	0.7	0.7	0.7
5466Rv2727c	miaA	3211	2001	1.6	0.3	0.1	tRNA_d(2)-isopentenylpyrophosphate_transferase	1.1	2	6	0.7	0.8	0.5	0.6	0.7	0.5

4747Rv2732c	-	3619	2379	1.5	0.2	0.1		2.6	2	6	0.6	0.6	0.7	0.8	0.7	0.7
4885Rv2740	-	2971	1756	1.7	0.2	0.1		1.1	2	6	0.6	0.6	0.5	0.7	0.6	0.6
3087Rv2778c	-	5210	2625	1.9	0.3	0.1		1.1	2	6	0.4	0.5	0.5	0.6	0.6	0.6
2970Rv2798c	-	4381	2848	1.6	0.3	0.1		1.1	2	6	0.5	0.8	0.5	0.7	0.7	0.6
79Rv2816c	-	13927	9377	1.5	0.2	0.1		1.1	2	6	0.8	0.8	0.7	0.6	0.6	0.6
4081Rv2844	-	3732	2060	1.7	0.2	0.1		1.1	2	6	0.5	0.5	0.5	0.7	0.6	0.6
1195Rv2852c	-	5666	3346	1.7	0.1	0.0		1.1	2	6	0.6	0.6	0.6	0.6	0.6	0.5
472Rv2855	gorA	4247	2796	1.5	0.2	0.1	glutathione_reductase_homologue	1.1	2	6	0.8	0.7	0.5	0.7	0.6	0.6
210Rv2858c	aldC	4262	2698	1.5	0.2	0.1	aldehyde_dehydrogenase_phenylacetaldehyde_	1.1	2	6	0.6	0.7	0.6	0.8	0.7	0.6
4805Rv2913c	-	3737	2453	1.5	0.1	0.1	probable_D-amino_acid_aminohydrolase	1.1	2	6	0.6	0.7	0.7	0.8	0.7	0.6
1219Rv2923c	-	4668	2754	1.7	0.4	0.2	YHFA_ECOLI_P24246	1.1	2	6	0.6	0.5	0.4	0.8	0.6	0.7
33Rv2929	-	7630	5331	1.5	0.1	0.1		1.1	2	6	0.7	0.8	0.7	0.6	0.6	0.7
40Rv2945c	lppX	9527	6154	1.7	1.0	0.4	lipoprotein	1.1	2	6	1.1	0.9	0.3	0.4	0.3	0.4
41Rv2947c	pks15	14945	9465	1.7	0.6	0.3	polyketide_synthase_	1.1	2	6	1.0	0.7	0.4	0.4	0.5	0.5
5185Rv2951c	-	7080	3595	1.9	0.4	0.2	putative_oxidoreductase	1.1	2	6	0.4	0.4	0.6	0.7	0.6	0.6
4463Rv2952	-	9125	4010	2.1	0.6	0.2	glycosyltransferase	1.1	2	6	0.4	0.3	0.5	0.7	0.5	0.5
5184Rv2953	-	3307	1863	1.7	0.3	0.1		1.1	2	6	0.7	0.5	0.6	0.7	0.5	0.5
5183Rv2954c	-	5179	2824	1.9	0.4	0.2		1.1	2	6	0.5	0.5	0.3	0.7	0.6	0.6
4462Rv2954c	-	8376	4443	1.8	0.3	0.1		1.1	2	6	0.5	0.5	0.5	0.7	0.6	0.6
4461Rv2955c	-	4273	2706	1.5	0.3	0.1		1.1	2	6	0.5	0.6	0.6	0.8	0.8	0.8
4659Rv2960c	-	5103	3197	1.6	0.1	0.1		1.1	2	6	0.7	0.7	0.6	0.6	0.7	0.5
4454Rv2980	-	2393	1658	1.5	0.3	0.1	unknown_protein_with_hydrophobic_stretch_near_N	1.1	2	5	0.7	0.6	0.6	0.9	nd	0.6
4453Rv2982c	gpdA2	4639	2277	1.9	0.7	0.3	glycerol-3-phosphate_dehydrogenase	1.1	2	6	0.4	0.3	0.4	0.8	0.6	0.6
1570Rv2984	ppk	5304	3322	1.6	0.1	0.0	polyphosphate_kinase	1.1	2	6	0.6	0.6	0.6	0.7	0.7	0.6
1657Rv2992c	gltS	5317	2404	2.1	0.4	0.2	glutamyl-tRNA_synthase	1.1	2	6	0.4	0.4	0.5	0.6	0.5	0.5
2379Rv2993c	-	3731	1973	1.9	0.4	0.1		1.1	2	6	0.5	0.4	0.5	0.6	0.7	0.6
1658Rv2994	-	5593	2923	1.9	0.2	0.1	probable_fluoroquinolone_efflux_protein	1.1	2	6	0.5	0.5	0.5	0.7	0.5	0.5
1659Rv2996c	serA	7564	4901	1.5	0.3	0.1	D-3-phosphoglycerate_dehydrogenase	1.1	2	6	0.5	0.6	0.8	0.8	0.8	0.7
5267Rv3005c	-	5843	2453	2.4	0.2	0.1		1.1	2	6	0.4	0.4	0.4	0.5	0.4	0.4
5270Rv3011c	gatA	2952	1772	1.6	0.3	0.1	glu-tRNA-gln_amidotransferase,_subunit_B	1.1	2	6	0.5	0.6	0.8	0.7	0.6	0.5
5611Rv3030	-	4753	2730	1.7	0.3	0.1		1.1	2	6	0.5	0.5	0.5	0.8	0.6	0.6
5612Rv3032	-	2440	1637	1.5	0.2	0.1		1.1	2	6	0.7	0.7	0.7	0.8	0.6	0.6
2006Rv3039c	echA17	3824	2118	1.8	0.2	0.1	enoyl-CoA_hydratase/isomerase_superfamily	1.1	2	6	0.4	0.5	0.6	0.6	0.6	0.6
2728Rv3040c	-	2769	1834	1.5	0.1	0.0		1.1	2	6	0.7	0.6	0.6	0.7	0.7	0.6
2729Rv3042c	serB2	5448	3437	1.6	0.2	0.1	C-term_similar_to_phosphoserine_phosphatase	1.1	2	6	0.7	0.7	0.5	0.5	0.6	0.7
4896Rv3083	-	4451	1923	2.3	0.4	0.2	probable_monooxygenase	1.1	2	6	0.5	0.5	0.3	0.6	0.5	0.4
5618Rv3084	lipR	2249	1440	1.5	0.3	0.1	probable_acetyl-hydrolase	1.1	2	6	0.7	0.7	0.4	0.8	0.6	0.7
4897Rv3085	-	2498	1471	1.6	0.4	0.1	short_chain_alcohol_dehydrogenase	1.1	2	6	0.7	0.6	0.6	0.9	0.6	0.4
5619Rv3086	adhD	3424	2315	1.5	0.4	0.2	zinc-containing_alcohol_dehydrogenase	2.6	2	6	0.7	1.0	0.5	0.6	0.7	0.5
5477Rv3099c	-	9159	5518	1.7	0.2	0.1		1.1	2	6	0.6	0.5	0.6	0.6	0.6	0.7

1877Rv3119	moaE	6203	3639	1.7	0.2	0.1	molybdopterin-converting_factor_subunit_2	1.1	2	6	0.6	0.7	0.5	0.5	0.5	0.6
2599Rv3120	-	6537	3894	1.7	0.2	0.1	Slight_similarity_to_methyltransferases	1.1	2	6	0.7	0.6	0.5	0.6	0.6	0.6
1776Rv3130c	-	4123	1659	2.3	0.7	0.3		1.1	2	6	0.4	0.6	0.3	0.6	0.4	0.3
3036Rv3130c	-	4245	2177	2.0	0.6	0.3		2.6	2	6	0.5	0.8	0.5	0.4	0.4	0.4
3033Rv3136	PPE	11564	6608	1.7	0.4	0.2		1.1	2	6	0.4	0.4	0.6	0.7	0.6	0.7
225Rv3141	fadB4	6297	3587	1.8	0.2	0.1	3-hydroxyacyl-CoA_dehydrogenase	1.1	2	6	0.7	0.5	0.5	0.6	0.5	0.6
764Rv3141	fadB4	9922	6448	1.5	0.1	0.0	3-hydroxyacyl-CoA_dehydrogenase	1.1	2	6	0.7	0.6	0.7	0.6	0.7	0.7
871Rv3142c	-	9793	5151	1.9	0.4	0.2		1.1	2	6	0.7	0.7	0.5	0.5	0.5	0.4
149Rv3143	-	7414	3628	2.1	0.3	0.1	putative_sensory_transduction_protein	1.1	2	6	0.6	0.5	0.4	0.5	0.4	0.4
2498Rv3144c	PPE	3252	1729	1.8	0.3	0.1		1.1	2	6	0.5	0.7	0.6	0.6	0.5	0.5
870Rv3144c	PPE	3329	2147	1.5	0.2	0.1		2.6	2	6	0.5	0.7	0.7	0.7	0.7	0.6
993Rv3145	nuoA	4833	2783	1.7	0.2	0.1	NADH_dehydrogenase_chain_A	1.1	2	6	0.7	0.6	0.6	0.5	0.5	0.5
869Rv3146	nuoB	9014	4612	2.0	0.5	0.2	NADH_dehydrogenase_chain_B	1.1	2	6	0.7	0.7	0.3	0.5	0.4	0.4
147Rv3147	nuoC	12269	6330	2.1	0.6	0.3	NADH_dehydrogenase_chain_C	1.1	2	6	0.7	0.6	0.3	0.4	0.4	0.5
868Rv3148	nuoD	9695	3901	2.6	1.1	0.4	NADH_dehydrogenase_chain_D	1.1	2	6	0.6	0.6	0.2	0.4	0.3	0.2
146Rv3149	nuoE	9426	6845	1.5	0.3	0.1	NADH_dehydrogenase_chain_E	1.1	2	6	0.8	0.8	0.6	0.7	0.4	0.8
867Rv3150	nuoF	9181	3962	2.3	0.4	0.2	NADH_dehydrogenase_chain_F	1.1	2	6	0.5	0.5	0.3	0.5	0.4	0.4
5559Rv3152	nuoH	10852	4128	2.5	1.4	0.6	NADH_dehydrogenase_chain_H	1.1	2	6	0.7	0.7	0.2	0.3	0.3	0.2
4837Rv3153	nuoI	13085	5362	2.3	1.0	0.4	NADH_dehydrogenase_chain_I	1.1	2	6	0.7	0.7	0.3	0.4	0.3	0.3
4836Rv3155	nuoK	16433	7104	2.1	1.5	0.6	NADH_dehydrogenase_chain_K	1.1	2	6	0.9	0.9	0.3	0.3	0.3	0.2
5557Rv3156	nuoL	9766	5826	1.6	0.5	0.2	NADH_dehydrogenase_chain_L	1.1	2	6	0.8	0.8	0.5	0.6	0.5	0.4
4835Rv3157	nuoM	12981	6579	1.9	0.8	0.3	NADH_dehydrogenase_chain_M	1.1	2	6	0.8	0.8	0.3	0.5	0.4	0.3
3850Rv3158	nuoN	7491	3554	2.0	0.7	0.3	NADH_dehydrogenase_chain_N	1.1	2	6	0.7	0.7	0.4	0.5	0.4	0.3
583Rv3169	-	4817	2135	2.3	0.3	0.1		1.1	2	6	0.4	0.5	0.5	0.5	0.4	0.4
1309Rv3190c	-	3945	2272	1.7	0.2	0.1		1.1	2	6	0.6	0.6	0.5	0.6	0.6	0.5
1311Rv3194c	-	9481	6096	1.6	0.1	0.0		1.2	2	6	0.6	0.6	0.7	0.6	0.6	0.7
4195Rv3198c	uvrD2	2529	1688	1.5	0.2	0.1	putative_UvrD	1.1	2	6	0.7	0.6	0.6	0.8	0.8	0.6
1777Rv3199c	-	5119	2215	2.2	0.3	0.1		1.1	2	6	0.4	0.5	0.4	0.5	0.5	0.4
3474Rv3199c	-	3951	2057	1.9	0.2	0.1		1.1	2	6	0.5	0.6	0.5	0.6	0.5	0.5
4196Rv3200c	-	5482	2909	1.9	0.3	0.1	putative_potassium_channel	1.1	2	6	0.6	0.6	0.4	0.5	0.6	0.5
3427Rv3213c	-	8318	5050	1.6	0.2	0.1	possible_role_in_chromosome_segregation	1.1	2	6	0.5	0.6	0.6	0.7	0.6	0.7
1262Rv3224	-	15062	7881	1.9	0.5	0.2	putative_oxidoreductases	1.1	2	6	0.4	0.4	0.6	0.5	0.8	0.5
3541Rv3229c	desA3	3802	2265	1.7	0.2	0.1	acyl-[ACP]_desaturase	1.1	2	6	0.7	0.6	0.5	0.7	0.6	0.6
4264Rv3232c	pvdS	3830	2034	1.7	0.5	0.2	alternative_sigma_factor_for_siderophore_production	1.1	2	6	0.6	0.6	0.5	0.9	0.5	0.5
3543Rv3233c	-	2848	1455	1.8	0.3	0.1		1.1	2	6	0.5	0.5	0.6	0.6	0.6	0.4
659Rv3241c	-	4725	2757	1.7	0.2	0.1	member_of_S30AE_ribosomal_protein_family	1.1	2	6	0.6	0.7	0.6	0.6	0.6	0.5
1383Rv3246c	mtrA	10321	6501	1.6	0.1	0.0	two-component_response_regulator	1.1	2	6	0.6	0.6	0.6	0.6	0.7	0.7
3545Rv3249c	-	3997	2460	1.5	0.3	0.1	transcriptional_regulator_(TetR/AcrR_family)	1.1	2	6	0.6	0.8	0.6	0.8	0.6	0.5
4267Rv3250c	rubB	5658	2791	1.9	0.3	0.1	rubredoxin_B	1.1	2	6	0.6	0.6	0.5	0.6	0.5	0.4
3546Rv3251c	rubA	3508	2077	1.6	0.3	0.1	rubredoxin_A	1.1	2	6	0.6	0.8	0.6	0.7	0.5	0.5

183Rv3275c	purE	4072	2675	1.5	0.2	0.1	phosphoribosylaminoimidazole_carboxylase	1.1	2	6	0.7	0.5	0.7	0.8	0.7	0.6
905Rv3276c	purK	5280	2994	1.6	0.3	0.1	phosphoribosylaminoimidazole_carboxylase_ATPase_subunit	1.1	2	6	0.6	0.4	0.6	0.8	0.7	0.6
907Rv3280	accD5	18871	12666	1.5	0.3	0.1	acetyl/propionyl_CoA_carboxylase_b_subunit	1.1	2	6	0.5	0.6	0.7	0.7	0.8	0.7
4246Rv3281	-	11383	5552	2.0	0.2	0.1		2.5	2	6	0.5	0.5	0.5	0.5	0.5	0.5
186Rv3281	-	12335	6530	1.9	0.1	0.1		2.4	2	6	0.6	0.5	0.5	0.5	0.5	0.5
3795Rv3292	-	3348	2048	1.6	0.2	0.1		1.1	2	6	0.6	0.7	0.7	0.6	0.6	0.5
189Rv3298c	lpqC	4480	2808	1.5	0.2	0.1		1.1	2	6	0.6	0.5	0.7	0.8	0.6	0.6
5102Rv3301c	phoY1	3980	2525	1.6	0.2	0.1	phosphate_transport_system_regulator	1.1	2	6	0.7	0.8	0.5	0.6	0.6	0.6
1830Rv3302c	glpD2	5816	3029	1.8	0.4	0.2	glycerol-3-phosphate_dehydrogenase	1.1	2	6	0.4	0.5	0.8	0.5	0.6	0.5
591Rv3303c	lpdA	4166	2219	1.8	0.3	0.1	dihydrolipoamide_dehydrogenase	1.1	2	6	0.5	0.4	0.6	0.7	0.5	0.6
1313Rv3304	-	2911	1835	1.5	0.3	0.1		1.1	2	6	0.6	0.5	0.7	0.8	0.7	0.7
1316Rv3310	-	4465	2084	2.1	0.3	0.1	probable_acid_phosphatase	1.1	2	6	0.5	0.5	0.4	0.6	0.5	0.4
3530Rv3311	-	4970	2976	1.6	0.2	0.1		1.1	2	6	0.5	0.5	0.7	0.7	0.7	0.6
595Rv3311	-	9305	6443	1.6	0.2	0.1		1.1	2	5	0.5	0.6	0.7	0.8	0.7	nd
4203Rv3319	sdhB	4230	2673	1.6	0.4	0.2	succinate_dehydrogenase_B	1.1	2	6	0.8	0.8	0.3	0.7	0.7	0.6
1319Rv3327	IS1547	3231	1695	1.9	0.2	0.1		1.1	2	6	0.6	0.4	0.5	0.6	0.6	0.5
1320Rv3329	-	4176	2656	1.5	0.2	0.1	probable_aminotransferase	1.1	2	6	0.6	0.5	0.6	0.7	0.7	0.7
3103Rv3365c	-	3296	1711	1.8	0.4	0.2		1.1	2	6	0.4	0.5	0.6	0.8	0.6	0.6
1280Rv3377c	-	6593	4222	1.7	0.4	0.2	similar_to_many_cyclases_involved_in_steroid_biosynthesis	1.1	2	6	0.8	0.8	0.5	0.5	0.5	0.5
4141Rv3413c	-	5315	3341	1.6	0.1	0.0		1.1	2	6	0.7	0.6	0.6	0.6	0.7	0.6
3658Rv3414c	sigD	7021	4082	1.7	0.1	0.0	ECF_subfamily_sigma_subunit	1.1	2	6	0.6	0.6	0.6	0.6	0.6	0.6
5389Rv3435c	-	3471	2266	1.5	0.2	0.1		1.1	2	6	0.7	0.7	0.6	0.7	0.8	0.5
296Rv3472	-	5720	3577	1.5	0.2	0.1	possible_acyl_carrier_protein	1.1	2	6	0.6	0.6	0.7	0.8	0.7	0.6
1020Rv3477	PE	16434	3055	5.3	0.9	0.4		1.1	2	6	0.2	0.2	0.2	0.2	0.2	0.2
1021Rv3479	-	6875	3285	2.2	0.6	0.3		1.1	2	6	0.7	0.5	0.5	0.5	0.3	0.3
3186Rv3487c	lipF	7071	4046	1.7	0.1	0.0	probable_esterase	1.1	2	6	0.6	0.6	0.6	0.6	0.6	0.5
3907Rv3488	-	3466	2090	1.6	0.3	0.1		1.1	2	6	0.4	0.6	0.8	0.8	0.6	0.6
3188Rv3492c	-	4256	2481	1.7	0.5	0.2		1.1	2	6	0.8	0.8	0.5	0.5	0.5	0.4
2118Rv3493c	-	3076	1964	1.6	0.2	0.1		1.1	2	5	0.6	0.7	nd	0.7	0.5	0.6
3910Rv3493c	-	3341	2198	1.5	0.3	0.1		1.1	2	6	0.7	0.9	0.6	0.9	0.6	0.5
5642Rv3494c	-	2779	1855	1.5	0.4	0.2	part_of_mce4_operon	1.1	2	6	0.8	0.9	0.4	0.7	0.6	0.5
4921Rv3495c	lprN	6644	4154	1.6	0.4	0.2	part_of_mce4_operon	1.1	2	6	0.7	0.9	0.4	0.6	0.6	0.5
5643Rv3496c	-	6288	4035	1.5	0.2	0.1	part_of_mce4_operon	1.1	2	5	nd	0.8	0.7	0.7	0.5	0.6
2034Rv3497c	-	3849	2464	1.5	0.2	0.1	part_of_mce4_operon	1.1	2	6	0.7	0.7	0.7	0.7	0.6	0.5
2756Rv3498c	-	2850	1902	1.5	0.2	0.1	part_of_mce4_operon	1.1	2	6	0.8	0.7	0.6	0.8	0.6	0.6
2035Rv3499c	mce4	6197	3741	1.7	0.2	0.1	cell_invasion_protein	1.1	2	6	0.7	0.6	0.6	0.6	0.5	0.6
2757Rv3500c	-	3227	2134	1.5	0.2	0.1	part_of_mce4_operon	1.1	2	6	0.6	0.7	0.8	0.7	0.6	0.7
4922Rv3509c	livX	4825	3178	1.5	0.3	0.1	probable_acetohydroxyacid_synthase_I_large_subunit	1.1	2	6	0.7	0.7	0.5	0.8	0.7	0.6
173Rv3554	fdxB	5065	2050	2.4	0.5	0.2	ferredoxin	1.1	2	6	0.5	0.4	0.3	0.5	0.4	0.4
900Rv3577	-	3935	2349	1.6	0.3	0.1		1.1	2	6	0.6	0.5	0.7	0.8	0.6	0.7

4254Rv3587c	-	10393	6671	1.6	0.2	0.1		1.1	2	6	0.7	0.6	0.5	0.6	0.6	0.7
3533Rv3588c	-	3821	2051	1.8	0.2	0.1	putative_carbonic_anhydrase	1.1	2	6	0.4	0.6	0.5	0.6	0.6	0.6
4255Rv3589	mutY	2334	1461	1.5	0.3	0.1	probable_DNA_glycosylase	1.1	2	6	0.8	0.7	0.5	0.7	0.6	0.5
2950Rv3592	-	7672	4763	1.6	0.1	0.1		1.1	2	6	0.6	0.6	0.6	0.6	0.7	0.6
4159Rv3598c	lysS	5301	2814	1.9	0.1	0.1	lysyl-tRNA_synthase	1.1	2	6	0.6	0.6	0.5	0.5	0.5	0.5
1270Rv3612c	-	7011	4665	1.5	0.3	0.1		1.1	2	6	0.9	0.8	0.6	0.6	0.7	0.5
309Rv3623	lpqG	4248	2437	1.7	0.3	0.1		1.1	2	6	0.6	0.5	0.6	0.8	0.6	0.5
1030Rv3624c	hpt	5027	3134	1.6	0.1	0.0	probable_hypoxanthine-guanine_phosphoribosyltransferase	1.1	2	6	0.6	0.6	0.6	0.7	0.6	0.6
3915Rv3630	-	2903	1857	1.5	0.2	0.1	unknown_membrane_protein	1.1	2	6	0.6	0.7	0.7	0.8	0.6	0.5
3914Rv3632	-	2439	1650	1.5	0.3	0.1		1.1	2	5	0.6	0.9	0.6	nd	0.7	0.5
3192Rv3633	-	7290	3955	1.8	0.2	0.1		1.1	2	6	0.6	0.5	0.5	0.6	0.6	0.5
303Rv3647c	-	5641	2824	1.9	0.3	0.1		1.2	2	6	0.5	0.5	0.4	0.7	0.5	0.5
5730Rv3648c	cspA	17039	11579	1.5	0.5	0.2	cold_shock_protein,_transcriptional_regulator	1.1	2	6	1.0	0.8	0.5	0.4	0.7	0.6
5732Rv3658c	-	2424	1662	1.5	0.2	0.1	probable_transmembrane_protein	1.1	2	6	0.8	0.7	0.6	0.6	0.7	0.7
5011Rv3662c	-	4669	2111	2.2	0.6	0.2		1.1	2	6	0.6	0.5	0.3	0.5	0.4	0.3
1713Rv3667	acs	7026	4747	1.5	0.1	0.1	acetyl-CoA_synthase	1.1	2	6	0.7	0.6	0.7	0.8	0.7	0.6
5733Rv3668c	-	4330	2838	1.5	0.3	0.1	probable_alkaline_serine_protease	1.1	2	6	0.5	0.7	0.8	0.6	0.8	0.7
4597Rv3671c	-	5831	2462	2.3	0.5	0.2	probable_serine_protease	1.1	2	6	0.4	0.4	0.3	0.6	0.5	0.4
4598Rv3673c	-	6841	3374	2.0	0.3	0.1	protein_disulphide_oxidoreductase	1.1	2	6	0.6	0.5	0.4	0.5	0.5	0.5
5321Rv3676	-	6913	4454	1.5	0.2	0.1	transcriptional_regulator_(Crp/Fnr_family)	1.1	2	6	0.7	0.8	0.5	0.6	0.7	0.6
5322Rv3678c	-	11731	4557	2.6	0.4	0.2	transcriptional_regulator_(LysR_family)	1.1	2	6	0.4	0.3	0.4	0.3	0.5	0.4
2439Rv3688c	-	3471	1908	1.8	0.4	0.2		1.1	2	6	0.4	0.5	0.8	0.6	0.7	0.4
1719Rv3691	-	3215	1997	1.6	0.3	0.1		1.1	2	6	0.6	0.6	0.6	0.8	0.7	0.5
2441Rv3692	moxR2	3915	1928	2.0	0.3	0.1	transcriptional_regulator,_MoxR_homologue	1.1	2	6	0.5	0.6	0.5	0.5	0.4	0.4
1720Rv3693	-	3290	1823	1.7	0.4	0.1		1.1	2	6	0.6	0.5	0.5	0.8	0.7	0.4
5326Rv3698	-	2553	1700	1.5	0.4	0.2		1.1	2	6	0.9	0.7	0.5	0.7	0.6	0.5
4605Rv3699	-	10826	7388	1.5	0.3	0.1	Probable_methyltransferase	1.1	2	6	0.6	0.5	0.7	0.8	0.8	0.8
4607Rv3703c	-	3574	1865	1.8	0.3	0.1		1.1	2	6	0.6	0.5	0.6	0.7	0.5	0.4
2847Rv3705c	-	2162	1535	1.5	0.4	0.2		1.1	2	4	nd	nd	0.5	0.9	0.6	0.7
4608Rv3705c	-	2884	1825	1.5	0.3	0.1		1.1	2	6	0.6	0.9	0.6	0.8	0.8	0.5
1723Rv3711c	dnaQ	4160	2422	1.7	0.2	0.1	DNA_polymerase_III_e_chain	1.1	2	6	0.7	0.6	0.6	0.6	0.5	0.5
1724Rv3713	cobQ2	3229	1487	2.1	0.2	0.1	possible_cobyric_acid_synthase	1.1	2	6	0.4	0.4	0.5	0.5	0.5	0.5
4960Rv3717	-	8000	5111	1.5	0.3	0.1	possible_N-acetylmuramoyl-L-alanine_amidase_	1.1	2	6	0.7	0.7	0.5	0.8	0.6	0.6
4609Rv3720	-	7182	3795	1.9	0.5	0.2	C-term_similar_to_cyclopropane_fatty_acid_synthases	1.1	2	6	0.7	0.7	0.3	0.6	0.5	0.4
5331Rv3721c	dnaZX	3645	2465	1.5	0.2	0.1	DNA_polymerase_III,_g_(dnaZ)_and_t_(dnaX)	1.1	2	6	0.6	0.6	0.6	0.7	0.8	0.8
5333Rv3725	-	8227	3501	2.3	0.4	0.2	putative_oxidoreductase	1.1	2	6	0.5	0.4	0.3	0.5	0.5	0.4
4612Rv3726	-	8171	5073	1.6	0.3	0.1	Putative_alcohol_dehydrogenase,_zinc-type	1.1	2	6	0.7	0.7	0.4	0.7	0.7	0.6
5334Rv3727	-	6454	2172	2.9	0.7	0.3	similar_to_phytoene_dehydrogenase_precursor	1.1	2	6	0.4	0.4	0.2	0.4	0.4	0.3
1729Rv3736	-	4481	2968	1.5	0.2	0.1	transcriptional_regulator_(AraC/XylS_family)	1.1	2	6	0.6	0.7	0.8	0.8	0.6	0.6
2451Rv3737	-	3701	1762	2.0	0.4	0.2	possible_membrane_protein	1.4	2	6	0.5	0.4	0.5	0.7	0.5	0.4

5338Rv3747	-	5899	3539	1.6	0.2	0.1		1.1	2	6	0.6	0.7	0.6	0.6	0.7	0.5
4617Rv3748	-	10337	5574	1.8	0.1	0.1		1.4	2	6	0.5	0.5	0.5	0.6	0.6	0.6
5339Rv3749c	-	5546	3478	1.6	0.4	0.2		1.1	2	6	0.7	0.9	0.4	0.5	0.6	0.6
5341Rv3753c	-	3372	1602	2.1	0.2	0.1		1.1	2	6	0.4	0.6	0.5	0.5	0.5	0.5
4620Rv3754	tyrA	5189	2963	1.8	0.2	0.1	prephenate_dehydrogenase	1.1	2	6	0.5	0.5	0.5	0.7	0.6	0.6
5342Rv3755c	-	7925	5068	1.6	0.1	0.0		1.1	2	6	0.7	0.7	0.6	0.6	0.6	0.7
2795Rv3763	lpqH	9222	3410	2.7	0.3	0.1	19_kD	1.1	2	6	0.4	0.3	0.4	0.4	0.4	0.3
2074Rv3764c	-	5004	2047	2.4	0.4	0.2	sensor_histidine_kinase	1.1	2	6	0.4	0.4	0.4	0.5	0.5	0.4
1011Rv3774	echA21	12997	4462	2.8	0.5	0.2	enoyl-CoA_hydratase/isomerase_superfamily	1.1	2	6	0.3	0.3	0.3	0.5	0.4	0.3
4394Rv3776	-	4502	2314	1.9	0.4	0.2		1.1	2	6	0.5	0.6	0.4	0.7	0.6	0.5
5116Rv3777	-	2914	1655	1.7	0.3	0.1	3-Hydroxyacyl-CoA_Dehydrogenase	1.1	2	6	0.6	0.7	0.6	0.7	0.6	0.4
4395Rv3778c	-	3119	1812	1.7	0.2	0.1	NifS_family_S76601	1.4	2	6	0.6	0.6	0.6	0.7	0.5	0.5
5117Rv3779	-	4113	2176	1.9	0.3	0.1	unknown_membrane_protein	1.1	2	6	0.5	0.7	0.5	0.6	0.5	0.5
4398Rv3784	epiB	7197	3483	1.9	0.4	0.2	probable_UDP-galactose_4-epimerase	1.1	2	6	0.4	0.5	0.4	0.7	0.6	0.5
5120Rv3785	-	3079	1984	1.5	0.2	0.1		1.1	2	6	0.7	0.8	0.6	0.7	0.7	0.5
767Rv3793	embC	6146	3173	1.9	0.4	0.2	involved_in_arabinogalactan_synthesis	1.1	2	6	0.6	0.5	0.4	0.6	0.5	0.5
46Rv3794	embA	8651	2860	3.0	0.6	0.2	involved_in_arabinogalactan_synthesis	1.1	2	6	0.4	0.3	0.3	0.4	0.3	0.3
768Rv3795	embB	4137	2829	1.5	0.3	0.1	involved_in_arabinogalactan_synthesis	1.1	2	6	0.9	0.7	0.6	0.7	0.6	0.5
4963Rv3806c	-	3257	2180	1.5	0.2	0.1	possible_integral_membrane_protein	1.3	2	6	0.7	0.7	0.5	0.8	0.6	0.6
2077Rv3810	pirG	12773	8576	1.5	0.2	0.1	cell_surface_protein_precursor_(Erp_protein)	1.1	2	6	0.7	0.8	0.5	0.7	0.7	0.6
2849Rv3834c	serS	2487	1684	1.5	0.2	0.1	seryl-tRNA_synthase	1.1	2	6	0.7	0.7	0.6	0.5	0.7	0.8
5143Rv3835	-	3199	2055	1.6	0.1	0.0		1.1	2	6	0.6	0.7	0.6	0.7	0.6	0.7
5140Rv3841	bfrB	14326	8314	1.8	0.4	0.2	bacterioferritin	1.1	2	6	0.5	0.4	0.5	0.5	0.7	0.7
2128Rv3842c	glpQ1	3998	2716	1.5	0.2	0.1	glycerophosphoryl_diester_phosphodiesterase	1.1	2	6	0.8	0.7	0.5	0.7	0.6	0.7
289Rv3846	sodA	18968	7905	2.4	0.4	0.2	superoxide_dismutase	1.1	2	6	0.5	0.3	0.4	0.3	0.5	0.4
4965Rv3876	-	9756	5800	1.7	0.5	0.2	Proline_rich	1.1	2	6	0.8	0.8	0.4	0.6	0.5	0.5
653Rv3890c	-	8301	4348	1.9	0.3	0.1		1.1	2	6	0.4	0.4	0.6	0.5	0.6	0.5
1374Rv3891c	-	7692	4273	1.8	0.3	0.1		1.1	2	6	0.5	0.4	0.6	0.6	0.6	0.7
3199Rv3900c	-	5878	3332	1.7	0.2	0.1		1.1	2	6	0.6	0.6	0.6	0.7	0.5	0.5
1034Rv3909	-	4612	2597	1.7	0.3	0.1		1.2	2	6	0.6	0.5	0.7	0.7	0.6	0.5
312Rv3910	-	3213	1896	1.6	0.2	0.1	possible_membrane_protein	1.1	2	6	0.6	0.6	0.6	0.8	0.6	0.5
2733Rv3910	-	8908	5467	1.6	0.1	0.0	possible_membrane_protein	1.1	2	6	0.6	0.6	0.7	0.6	0.7	0.6
2735Rv3914	trxC	12069	4610	2.6	0.3	0.1	thioredoxin	1.1	2	6	0.4	0.3	0.4	0.4	0.4	0.4
5620Rv3920c	-	11769	6352	1.9	0.3	0.1		1.1	2	6	0.7	0.6	0.4	0.5	0.5	0.5
4899Rv3921c	-	13858	6836	2.0	0.2	0.1	unknown_membrane_protein	1.1	2	6	0.5	0.5	0.5	0.5	0.5	0.4
5621Rv3922c	-	8778	5593	1.5	0.2	0.1	possible_hemolysin	1.1	2	6	0.6	0.6	0.7	0.7	0.8	0.6
3478		5720	2360	2.4	0.2	0.1		1.1	2	6	0.4	0.5	0.4	0.5	0.4	0.4