

S6 Table. *Mycobacterium leprae* specific proteins. The unique proteins present in the genome of *M. leprae* mapped for their GO functions, subcellular and transmembrane localization, gene expression profiles from a GEO dataset (under-expressed in green, over-expressed in red), essentiality (flux balance based predictions), virulence and presence of human orthologs.

Entry	Gene names	Length	Human Homologues	Gene Expression	Gene ontology (GO)	Transmembrane
Q9CBI3	ML1928	45	No	-2.07	integral component of membrane [GO:0016021]	Yes
Q9CCI8	ML0777	64	No	-0.49	integral component of membrane [GO:0016021]	Yes
Q9CBV9	ML1523	96	No	0.08	integral component of membrane [GO:0016021]	Yes
Q9CDF0	ML0009	63	No	-0.14	integral component of membrane [GO:0016021]	Yes
Q7AQ76	ML1292	80	No	0.00	integral component of membrane [GO:0016021]	Yes
Q7APW0	ML2347	336	No	0.28	integral component of membrane [GO:0016021]	Yes
Q9CCC6	ML0958	143	No	-0.68	integral component of membrane [GO:0016021]	Yes
Q9CCZ1	ML2651	105	No	-0.46	integral component of membrane [GO:0016021]	Yes

Q9CBG6	ML1990	80	No	-1.27	integral component of membrane [GO:0016021]	Yes
Q7AQ91	ML1148	51	No	-0.19		
Q9CC35	ML1344	86	No	-0.91	DNA binding [GO:0003677]	
Q9CBR2	ML1717	97	No	-0.04		
Q9CBD1	ML2177	317	No	0.13	cytoplasm [GO:0005737]; uridine phosphorylase activity [GO:0004850]; nucleoside metabolic process [GO:0009116]; nucleotide catabolic process [GO:0009166]	
Q07297	sra ML0411 MLCL383.14	408	No	0.18		
Q9CDF1	ML0008	124	No	-0.73		
Q9CDE2	ML0024	83	No	-0.06		
Q9CDE1	ML0025	96	No	-0.68		
Q9CDC8	ML0070	87	No	0.11		
Q9CD77	ML0141	84	No	-0.50		
Q9CD73	ML0152	62	No	-0.85		
Q7AQN3	ML0162	92	No	-0.28		
Q9CD59	ML0217	81	No	-0.29		
Q7AQL5	ML0218	128	No	0.02		
Q7AQK1	ML0291	130	No	-0.36		
Q9CCX2	ML0292	79	No	-1.78		
Q9CCX1	ML0293	69	No	1.49		
Q7AQJ8	ML0308	234	No	0.06		

Q9CCU2	ML0447	158	No	0.00	heme binding [GO:0020037]; iron ion binding [GO:0005506]; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen [GO:0016705]
Q7AQJ2	ML0448	90	No	0.34	
Q9CCT8	ML0464	95	No	-0.75	
Q7AQI7	ML0470	96	No	-0.71	
Q9CCR6	ML0527	84	No	0.09	
Q9CCN7	ML0568	197	No	-0.91	
Q7AQI4	ML0574	105	No	-0.21	
Q7AQI3	ML0576	76	No	-0.76	
Q7AQH1	ML0656	93	No	-0.13	
Q7AQH0	ML0659	108	No	-0.19	
Q9CCM5	ML0664	87	No	-0.15	
Q9CCM3	ML0679	75	No	0.00	
Q9CCK3	ML0757	230	No	-0.43	
Q9CCG0	ML0837	127	No	-0.68	
Q7AQE5	ML0863	104	No	-0.46	
Q9CCD5	ML0928	94	No	-0.65	
Q9CCD4	ML0938	98	No	-0.50	
Q9CCD3	ML0939	80	No	-0.13	
Q9CCD0	ML0950	66	No	-0.13	
Q9CCC7	ML0957	124	No	0.17	
Q9CCC5	ML0959	117	No	-0.21	
Q9CCC4	ML0963	154	No	-0.04	
Q9CCC3	ML0964	85	No	-0.04	
Q9CCB7	ML1010	80	No	0.00	
Q9CCB6	ML1011	140	No	0.30	
Q9CCB3	ML1018	71	No	0.15	
Q7AQA0	ML1057	117	No	-0.84	
Q9CC71	ML1186	100	No	0.37	
Q9CC60	ML1243	153	No	1.66	
Q9CC51	ML1275	78	No	-0.51	

Q9CC28	ML1384	112	No	-0.59		
Q9CC03	ML1445	74	No	-0.76		
Q9CBU8	ML1575	97	No	0.21		
Q7AQ39	ML1601	121	No	0.15	catalytic activity [GO:0003824]; biosynthetic process [GO:0009058]	
Q9CBT9	ML1602	106	No	-0.19		
Q9CBT8	ML1603	86	No	-0.77		
Q9CBT7	ML1604	129	No	-0.33		
Q9CBT6	ML1605	66	No	-0.46		
Q7AQ24	ML1788	154	No	0.07		
Q9CBJ3	ML1915	114	No	-0.06		
Q9CBH4	ML1976	115	No	0.34		
Q9CBH3	ML1979	135	No	0.31		
Q9CBG7	ML1989	116	No	-0.16		
Q9CBF6	ML2035	87	No	0.06		
Q9CBF4	ML2044	73	No	-0.67		
Q9CBD4	ML2172	118	No	0.12		
Q9CBD2	ML2176	85	No	-1.33		
Q9CBC5	ML2201	79	No	-1.00		
Q9CBC0	ML2244	113	No	-0.27		
Q9CBB9	ML2249	105	No	-0.21		
Q7APX0	ML2252	78	No	-0.37		
Q9CBA2	ML2283	104	No	1.04		
Q9CBA1	ML2284	119	No	-0.18		
Q49942	ML2346	301	No	0.14		
Q9CB35	ML2468	126	No	-1.19		
Q9CD23	ML2562	96	No	-0.37		
Q9CD21	ML2567	159	No	0.00		
Q9CCY7	ML2666	84	No	-0.56		
Q49769	ML0638 B1937_F3_110	100	No	-0.45	extracellular region [GO:0005576]	