

#607948 MYCOBACTERIUM TUBERCULOSIS, SUSCEPTIBILITY TO

OMIM Gene ID	HGNC	UniProtAC
107470	IFNGR1	P15260
147570	IFNG	P01579
155540	MC3R	P41968
158105	CCL2	P13500
600266	SLC11A1	P49279
602441	CISH	Q9NSE2
603028	TLR2	O60603
604457	SP110	Q9HB58
604672	CD209	Q9NNX6
606252	TIRAP	P58753
608212	IRGM	A1A4Y4

Table 1: OMIM - UniProtAC mapping

Legend

- N1: #input proteins associated to the significant GO term
- N2: #proteins associated to the significant GO term
- P-value: Bonferroni-corrected p-value of Fisher's exact test
- *red*: go terms not related to the input proteins
- *blue*: go terms related to the input proteins (enriched uniquely by network-based method)
- *green*: go terms ancestors of terms enriched with the standard method (enriched uniquely by network-based method)

1 Standard enrichment

GO Term	N1	N2	P-value	Description
GO:0051704	8	1558	1.26205e-06	multi-organism process
GO:0009617	5	261	7.01381e-06	response to bacterium
GO:0051707	6	607	7.51645e-06	response to other organism
GO:0006955	7	1414	3.04573e-05	immune response
GO:0032496	5	389	5.13591e-05	response to lipopolysaccharide
GO:0006952	7	1580	6.52997e-05	defense response
GO:0002237	5	414	7.00005e-05	response to molecule of bacterial origin
GO:0043207	6	921	8.92031e-05	response to external biotic stimulus
GO:0044126	3	32	9.38251e-05	regulation of growth of symbiont in host
GO:0044130	3	32	9.38251e-05	negative regulation of growth of symbiont in host
GO:0044144	3	32	9.38251e-05	modulation of growth of symbiont involved in interaction with host
GO:0044146	3	32	9.38251e-05	negative regulation of growth of symbiont involved in interaction with host
GO:0009607	6	964	0.000116799	response to biotic stimulus
GO:0002682	7	1758	0.000135702	regulation of immune system process
GO:0006954	5	483	0.000150432	inflammatory response
GO:0032735	3	43	0.000233039	positive regulation of interleukin-12 production
GO:0071219	4	198	0.000243118	cellular response to molecule of bacterial origin
GO:0034341	4	201	0.000258193	response to interferon-gamma
GO:0071216	4	215	0.000337958	cellular response to biotic stimulus
GO:0042742	4	233	0.000465924	defense response to bacterium
GO:0032760	3	56	0.000522363	positive regulation of tumor necrosis factor production
GO:0001817	5	702	0.0009536	regulation of cytokine production
GO:0032642	3	71	0.00107448	regulation of chemokine production
GO:0002376	7	2446	0.00128546	immune system process
GO:0032655	3	79	0.00148474	regulation of interleukin-12 production
GO:0045088	4	320	0.00164789	regulation of innate immune response
GO:0044419	5	788	0.00168256	interspecies interaction between organisms
GO:0002687	3	84	0.00178758	positive regulation of leukocyte migration
GO:0042108	3	85	0.00185268	positive regulation of cytokine biosynthetic process
GO:0050896	11	11721	0.00266492	response to stimulus
GO:0001819	4	374	0.00305842	positive regulation of cytokine production
GO:0051701	3	104	0.00340551	interaction with host
GO:0032680	3	115	0.00460926	regulation of tumor necrosis factor production
GO:0002685	3	119	0.00510845	regulation of leukocyte migration
GO:0032700	2	12	0.00525127	negative regulation of interleukin-17 production
GO:0071220	2	12	0.00525127	cellular response to bacterial lipoprotein
GO:0071221	2	12	0.00525127	cellular response to bacterial lipopeptide
GO:0098542	4	431	0.00535983	defense response to other organism
GO:0032675	3	126	0.00606586	regulation of interleukin-6 production
GO:0034123	2	14	0.00723809	positive regulation of toll-like receptor signaling pathway
GO:0051770	2	14	0.00723809	positive regulation of nitric-oxide synthase biosynthetic process
GO:0070391	2	14	0.00723809	response to lipoteichoic acid
GO:0071223	2	14	0.00723809	cellular response to lipoteichoic acid
GO:0009605	6	1995	0.00819743	response to external stimulus
GO:0002684	5	1093	0.00831989	positive regulation of immune system process
GO:0042035	3	143	0.00886867	regulation of cytokine biosynthetic process
GO:0045410	2	16	0.0095417	positive regulation of interleukin-6 biosynthetic process
GO:0070339	2	16	0.0095417	response to bacterial lipopeptide
GO:0033993	5	1142	0.0102953	response to lipid
GO:0051249	4	513	0.0106502	regulation of lymphocyte activation
GO:0043901	3	154	0.0110741	negative regulation of multi-organism process
GO:0050776	5	1167	0.011436	regulation of immune response
GO:0032493	2	18	0.0121618	response to bacterial lipoprotein
GO:0051769	2	18	0.0121618	regulation of nitric-oxide synthase biosynthetic process
GO:0009891	6	2208	0.014701	positive regulation of biosynthetic process
GO:0002263	3	170	0.0148865	cell activation involved in immune response
GO:0002366	3	170	0.0148865	leukocyte activation involved in immune response
GO:0071346	3	173	0.015686	cellular response to interferon-gamma
GO:0010562	5	1255	0.0162637	positive regulation of phosphorus metabolic process
GO:0045937	5	1255	0.0162637	positive regulation of phosphate metabolic process

Table 2: Overrepresented GO terms with the standard enrichment

GO Term	N1	N2	P-value	Description
GO:0032757	2	21	0.0166847	positive regulation of interleukin-8 production
GO:0002694	4	584	0.0177234	regulation of leukocyte activation
GO:0032660	2	23	0.0200947	regulation of interleukin-17 production
GO:0007165	9	7592	0.0204644	signal transduction
GO:0071222	3	191	0.0210836	cellular response to lipopolysaccharide
GO:0050865	4	624	0.0229782	regulation of cell activation
GO:0060334	2	25	0.0238201	regulation of interferon-gamma-mediated signaling pathway
GO:0042832	2	26	0.025801	defense response to protozoan
GO:0060330	2	26	0.025801	regulation of response to interferon-gamma
GO:0065008	7	3888	0.0286354	regulation of biological quality
GO:0045408	2	28	0.0299991	regulation of interleukin-6 biosynthetic process
GO:0001818	3	215	0.0300099	negative regulation of cytokine production
GO:0019079	2	29	0.032216	viral genome replication
GO:0043903	3	223	0.0334603	regulation of symbiosis, encompassing mutualism through parasitism
GO:0001562	2	30	0.0345117	response to protozoan
GO:0043489	2	31	0.0368861	RNA stabilization
GO:0048255	2	31	0.0368861	mRNA stabilization
GO:0031347	4	706	0.0372344	regulation of defense response
GO:0050670	3	238	0.0406144	regulation of lymphocyte proliferation
GO:0051247	5	1526	0.0417231	positive regulation of protein metabolic process
GO:0071622	2	33	0.0418701	regulation of granulocyte chemotaxis
GO:0032944	3	241	0.0421561	regulation of mononuclear cell proliferation
GO:0006950	7	4134	0.0429229	response to stress
GO:0032103	3	245	0.044271	positive regulation of response to external stimulus
GO:0070663	3	248	0.0459022	regulation of leukocyte proliferation
GO:0000060	2	36	0.0499349	protein import into nucleus, translocation

Table 3: Overrepresented GO terms with the standard enrichment

2 Network-based enrichment

GO Term	N1	N2	P-value	Description
GO:0001816	4	232	0.00105677	cytokine production
GO:0034097	7	2017	0.00113914	response to cytokine
GO:0002440	3	61	0.00138473	production of molecular mediator of immune response
GO:0002274	4	290	0.00256822	myeloid leukocyte activation
GO:0042116	3	78	0.0029181	macrophage activation
GO:0002252	6	1396	0.00299662	immune effector process
GO:0042592	8	3571	0.00307329	homeostatic process
GO:0051092	4	312	0.00343308	positive regulation of NF-kappaB transcription factor activity
GO:0050778	6	1484	0.00427672	positive regulation of immune response
GO:0006935	5	841	0.00598896	chemotaxis
GO:0042330	5	841	0.00598896	taxis
GO:0007259	3	100	0.00617787	JAK-STAT cascade
GO:0051251	5	874	0.00722659	positive regulation of lymphocyte activation
GO:0043123	4	400	0.00917674	positive regulation of I-kappaB kinase/NF-kappaB signaling
GO:0045428	3	117	0.00990804	regulation of nitric oxide biosynthetic process
GO:0002696	5	941	0.0103568	positive regulation of leukocyte activation
GO:0010759	2	13	0.0112028	positive regulation of macrophage chemotaxis
GO:0050766	3	122	0.0112352	positive regulation of phagocytosis
GO:0050867	5	996	0.0136511	positive regulation of cell activation
GO:0045087	6	1935	0.019832	innate immune response
GO:0045080	2	18	0.021955	positive regulation of chemokine biosynthetic process
GO:0030888	3	153	0.0221481	regulation of B cell proliferation
GO:0019221	5	1123	0.0244228	cytokine-mediated signaling pathway
GO:0002460	3	160	0.0253193	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin s
GO:0002690	3	164	0.027259	positive regulation of leukocyte chemotaxis
GO:0050830	3	173	0.0319764	defense response to Gram-positive bacterium
GO:0050764	3	179	0.0354025	regulation of phagocytosis
GO:0050871	3	179	0.0354025	positive regulation of B cell activation
GO:0010758	2	23	0.036272	regulation of macrophage chemotaxis
GO:0006897	5	1228	0.0376011	endocytosis
GO:0055065	5	1233	0.0383446	metal ion homeostasis
GO:0071675	2	24	0.0395622	regulation of mononuclear cell migration

Table 4: Overrepresented terms with the network-based enrichment. Only terms not detected with the standard method.