

Cluster 1	ID	Name	p-value	q-value Bo	q-value FD
ACAN	GO:00507	positive regulation of immune response	8.66E-08	0.000125	0.000108
ANK3	GO:00027	immune response-activating signal transduction	1.49E-07	0.000216	0.000108
SYTL2	GO:00027	immune response-regulating signaling pathway	2.44E-07	0.000353	0.000118
STARD5	GO:00022	activation of immune response	3.3E-07	0.000478	0.000119
C15orf5	GO:00069	immune response	4.16E-07	0.000601	0.00012
RPL21P44	GO:00507	regulation of immune response	8.12E-07	0.001174	0.000196
SAMD9	GO:00326	regulation of interferon-alpha production	1.15E-06	0.001669	0.000238
IFIH1	GO:00326	interferon-alpha production	1.33E-06	0.001918	0.00024
SMC6	GO:00026	positive regulation of immune system process	1.51E-06	0.002186	0.000243
CDH6	GO:00018	positive regulation of cytokine production	1.82E-06	0.002634	0.000263
FKBP11	GO:00313	positive regulation of defense response	2.06E-06	0.002981	0.000271
PAG1	GO:00069	inflammatory response	2.53E-06	0.003656	0.000305
CLDN1	GO:00326	regulation of interleukin-6 production	5E-06	0.007225	0.000556
FCGR1A	GO:00326	interleukin-6 production	6.05E-06	0.008743	0.000625
LY86	GO:00069	defense response	7.68E-06	0.0111	0.000721
TLR7	GO:00450	innate immune response	7.98E-06	0.01154	0.000721
TLR1	GO:00321	positive regulation of response to external stimuli	1.17E-05	0.01687	0.000992
CD300A	GO:00341	toll-like receptor 7 signaling pathway	1.32E-05	0.01909	0.001061
HAVCR2	GO:00341	regulation of homotypic cell-cell adhesion	1.55E-05	0.02245	0.001165
CLEC5A	GO:00022	pattern recognition receptor signaling pathway	1.61E-05	0.0233	0.001165
IL1B	GO:00507	regulation of cytokine secretion	1.9E-05	0.02746	0.00121
	GO:00018	regulation of cytokine production	1.94E-05	0.02799	0.00121
	GO:00986	cell-cell adhesion	2.09E-05	0.03017	0.00121
	GO:00432	response to external biotic stimulus	2.17E-05	0.03139	0.00121
	GO:00517	response to other organism	2.17E-05	0.03139	0.00121
	GO:00712	cellular response to molecule of bacterial origin	2.18E-05	0.03145	0.00121
	GO:00327	positive regulation of chemokine production	2.38E-05	0.03445	0.001221
	GO:00603	regulation of cellular localization	0.000024	0.0347	0.001221
	GO:00022	myeloid leukocyte activation	2.48E-05	0.03585	0.001221
	GO:00027	regulation of leukocyte mediated immunity	2.53E-05	0.03662	0.001221
	GO:00096	response to biotic stimulus	2.83E-05	0.04087	0.001293
	GO:00421	macrophage activation	2.9E-05	0.04198	0.001293
	GO:00341	homotypic cell-cell adhesion	3.11E-05	0.04491	0.001293
	GO:00506	cytokine secretion	3.12E-05	0.04506	0.001293
	GO:00454	positive regulation of interleukin-6 biosynthetic process	3.16E-05	0.04575	0.001293
	GO:00510	regulation of transport	3.32E-05	0.04796	0.001293
	GO:00712	cellular response to biotic stimulus	3.38E-05	0.0488	0.001293
	GO:00018	cytokine production	3.48E-05	0.0503	0.001293
	GO:00510	positive regulation of transport	3.49E-05	0.05043	0.001293
	GO:00421	positive regulation of cytokine biosynthetic process	3.65E-05	0.05283	0.001321
	GO:00026	regulation of immune system process	3.76E-05	0.05434	0.001325
	GO:00071	cell adhesion	4.21E-05	0.06093	0.001441
	GO:00224	regulation of cell-cell adhesion	4.29E-05	0.06196	0.001441
	GO:00226	biological adhesion	4.46E-05	0.06447	0.001465
	GO:19035	regulation of secretion by cell	4.9E-05	0.07081	0.001541
	GO:00327	positive regulation of interferon-gamma production	4.9E-05	0.07088	0.001541
	GO:00327	positive regulation of interleukin-6 production	5.3E-05	0.07669	0.001632
	GO:00326	regulation of chemokine production	6.4E-05	0.09256	0.001928
	GO:00510	regulation of secretion	7.34E-05	0.1062	0.002134
	GO:00507	regulation of phagocytosis	7.38E-05	0.1067	0.002134
	GO:00326	chemokine production	7.9E-05	0.1143	0.002214
	GO:00027	innate immune response-activating signal transduction	8.11E-05	0.1173	0.002214
	GO:00512	regulation of protein transport	8.14E-05	0.1177	0.002214
	GO:00106	positive regulation of cell communication	8.4E-05	0.1215	0.002214
	GO:00313	regulation of defense response	8.42E-05	0.1218	0.002214
	GO:00453	leukocyte activation	8.89E-05	0.1285	0.002254
	GO:00022	activation of innate immune response	9.17E-05	0.1326	0.002254

GO:190514	regulation of membrane invagination	9.2E-05	0.133	0.002254
GO:006009	regulation of phagocytosis, engulfment	9.2E-05	0.133	0.002254
GO:005122	positive regulation of protein transport	9.37E-05	0.1354	0.002257
GO:000224	immune effector process	0.000104	0.1496	0.002453
GO:004546	regulation of interleukin-6 biosynthetic process	0.000119	0.172	0.002733
GO:005086	negative regulation of T cell activation	0.000119	0.1722	0.002733
GO:003272	positive regulation of interferon-alpha production	0.000134	0.1934	0.003003
GO:007020	regulation of establishment of protein localization	0.000135	0.1952	0.003003
GO:004202	regulation of cytokine biosynthetic process	0.000145	0.2101	0.003183
GO:004222	interleukin-6 biosynthetic process	0.000149	0.2161	0.003225
GO:190302	negative regulation of leukocyte cell-cell adhesion	0.000153	0.2218	0.003262
GO:190492	positive regulation of establishment of protein localization	0.000156	0.2254	0.003266
GO:003416	toll-like receptor 9 signaling pathway	0.000166	0.2399	0.003383
GO:003264	regulation of interferon-gamma production	0.000166	0.2402	0.003383
GO:005071	positive regulation of cytokine secretion	0.00018	0.2595	0.003503
GO:004508	positive regulation of innate immune response	0.00018	0.2604	0.003503
GO:000177	microglial cell activation	0.000183	0.265	0.003503
GO:003411	negative regulation of homotypic cell-cell adhesion	0.000184	0.2662	0.003503
GO:003242	regulation of type I interferon production	0.000184	0.2662	0.003503
GO:000961	response to bacterium	0.000191	0.2759	0.003583
GO:003260	type I interferon production	0.000194	0.2799	0.003588
GO:004208	cytokine biosynthetic process	0.000198	0.2869	0.003631
GO:004210	cytokine metabolic process	0.000208	0.3012	0.003765
GO:000222	toll-like receptor signaling pathway	0.000219	0.316	0.003899
GO:009852	defense response to other organism	0.000221	0.3199	0.003899
GO:003260	interferon-gamma production	0.000224	0.3236	0.003899
GO:005086	regulation of T cell activation	0.000235	0.3399	0.004046
GO:000177	cell activation	0.000252	0.3647	0.004291
GO:000282	regulation of adaptive immune response based on antigen	0.000257	0.3715	0.004317
GO:000270	regulation of lymphocyte mediated immunity	0.000263	0.3799	0.004317
GO:005072	positive regulation of inflammatory response	0.000263	0.3799	0.004317
GO:190302	regulation of leukocyte cell-cell adhesion	0.000276	0.3989	0.004482
GO:005122	negative regulation of lymphocyte activation	0.000287	0.4148	0.004609
GO:000996	positive regulation of signal transduction	0.000297	0.4291	0.004716
GO:000242	leukocyte mediated immunity	0.000325	0.4699	0.005107
GO:000222	response to molecule of bacterial origin	0.000332	0.48	0.005114
GO:000282	regulation of adaptive immune response	0.000332	0.4807	0.005114
GO:003288	regulation of protein localization	0.000339	0.49	0.005158
GO:004322	negative regulation of ion transport	0.000346	0.5007	0.005216
GO:004508	regulation of innate immune response	0.000396	0.5724	0.005901
GO:003292	secretion by cell	0.0004	0.5785	0.005903
GO:003272	positive regulation of interferon-beta production	0.00043	0.6221	0.006255
GO:003014	regulation of cell adhesion	0.000433	0.6255	0.006255
GO:002240	negative regulation of cell-cell adhesion	0.000437	0.632	0.006257
GO:000269	negative regulation of leukocyte activation	0.000454	0.6558	0.00643
GO:005122	positive regulation of multicellular organismal process	0.000482	0.6974	0.006757
GO:000272	MyD88-dependent toll-like receptor signaling pathway	0.000486	0.7028	0.006757
GO:000222	adaptive immune response	0.000515	0.7445	0.007028
GO:000269	positive regulation of acute inflammatory response	0.000515	0.7449	0.007028
GO:007122	cellular response to lipopolysaccharide	0.000551	0.7972	0.007451
GO:002302	positive regulation of signaling	0.000586	0.8469	0.007842
GO:190122	positive regulation of NIK/NF-kappaB signaling	0.000608	0.8786	0.008061
GO:005086	negative regulation of cell activation	0.000641	0.9264	0.008422
GO:000269	positive regulation of immune effector process	0.000705	1	0.009186
GO:190302	positive regulation of response to wounding	0.000739	1	0.009433
GO:190372	negative regulation of anion transport	0.000743	1	0.009433
GO:005070	regulation of protein secretion	0.000748	1	0.009433
GO:005122	regulation of lymphocyte activation	0.000754	1	0.009433

GO:004690	secretion	0.000757	1	0.009433
GO:003248	negative regulation of type I interferon production	0.000778	1	0.009619
GO:005104	positive regulation of secretion	0.000786	1	0.009637
GO:003274	positive regulation of interleukin-8 production	0.000891	1	0.01031
GO:000269	regulation of immune effector process	0.000896	1	0.01031
GO:003411	toll-like receptor 1 signaling pathway	0.000967	1	0.01031
GO:007164	negative regulation of granulocyte colony-stimulating factor production	0.000967	1	0.01031
GO:000283	negative regulation of immune response to tumor	0.000967	1	0.01031
GO:007144	cellular response to methotrexate	0.000967	1	0.01031
GO:000283	negative regulation of natural killer cell mediated cytotoxicity	0.000967	1	0.01031
GO:190082	positive regulation of membrane depolarization during action potential	0.000967	1	0.01031
GO:005111	negative regulation of NK T cell activation	0.000967	1	0.01031
GO:003550	regulation of myosin light chain kinase activity	0.000967	1	0.01031
GO:003550	positive regulation of myosin light chain kinase activity	0.000967	1	0.01031
GO:000254	serotonin secretion by mast cell	0.000967	1	0.01031
GO:003271	negative regulation of interleukin-3 production	0.000967	1	0.01031
GO:000283	negative regulation of response to tumor cell	0.000967	1	0.01031
GO:000283	negative regulation of natural killer cell mediated cytotoxicity	0.000967	1	0.01031
GO:190124	negative regulation of macrophage colony-stimulating factor production	0.000967	1	0.01031
GO:003264	regulation of interferon-beta production	0.000969	1	0.01031
GO:000283	positive regulation of response to biotic stimulus	0.000969	1	0.01031
GO:003260	interferon-beta production	0.001052	1	0.01102
GO:000288	regulation of myeloid leukocyte mediated immunity	0.001052	1	0.01102
GO:005067	regulation of lymphocyte proliferation	0.001179	1	0.0122
GO:190122	regulation of NIK/NF-kappaB signaling	0.001181	1	0.0122
GO:003294	regulation of mononuclear cell proliferation	0.00121	1	0.01231
GO:007048	T cell aggregation	0.001217	1	0.01231
GO:004211	T cell activation	0.001217	1	0.01231
GO:007159	lymphocyte aggregation	0.001226	1	0.01231
GO:006062	regulation of vesicle-mediated transport	0.001235	1	0.01232
GO:000269	regulation of leukocyte activation	0.001253	1	0.01237
GO:003010	regulation of endocytosis	0.001258	1	0.01237
GO:000270	negative regulation of leukocyte mediated immunity	0.001271	1	0.01242
GO:007048	leukocyte aggregation	0.00129	1	0.01252
GO:003260	regulation of interleukin-2 production	0.001317	1	0.01253
GO:000691	phagocytosis, engulfment	0.001317	1	0.01253
GO:003160	lipopolysaccharide-mediated signaling pathway	0.001317	1	0.01253
GO:007060	regulation of leukocyte proliferation	0.001373	1	0.01298
GO:000243	inflammatory response to antigenic stimulus	0.001413	1	0.01326
GO:003411	positive regulation of homotypic cell-cell adhesion	0.001424	1	0.01329
GO:005070	positive regulation of phagocytosis	0.001461	1	0.01354
GO:001502	protein transport	0.001521	1	0.01401
GO:000930	protein secretion	0.001569	1	0.01436
GO:003264	regulation of interleukin-8 production	0.001612	1	0.01466
GO:000714	leukocyte cell-cell adhesion	0.001634	1	0.01476
GO:005080	regulation of cell activation	0.001656	1	0.01485
GO:003260	interleukin-2 production	0.001664	1	0.01485
GO:000710	negative regulation of cell adhesion	0.00168	1	0.01491
GO:190253	positive regulation of intracellular signal transduction	0.001742	1	0.01521
GO:005071	positive regulation of protein secretion	0.001778	1	0.01521
GO:000690	phagocytosis	0.001778	1	0.01521
GO:001032	membrane invagination	0.001825	1	0.01521
GO:001974	pentacyclic triterpenoid metabolic process	0.001932	1	0.01521
GO:006010	negative regulation of phagocytosis, engulfment	0.001932	1	0.01521
GO:190250	negative regulation of eosinophil activation	0.001932	1	0.01521
GO:200041	negative regulation of eosinophil migration	0.001932	1	0.01521
GO:000251	natural killer cell tolerance induction	0.001932	1	0.01521
GO:000178	antibody-dependent cellular cytotoxicity	0.001932	1	0.01521

GO:00362	response to diuretic	0.001932	1	0.01521
GO:00106	positive regulation of cell communication by elec	0.001932	1	0.01521
GO:00726	maintenance of protein location in membrane	0.001932	1	0.01521
GO:00726	maintenance of protein location in plasma memb	0.001932	1	0.01521
GO:20005	negative regulation of immunological synapse fo	0.001932	1	0.01521
GO:00424	detection of triacyl bacterial lipopeptide	0.001932	1	0.01521
GO:00026	regulation of tolerance induction dependent upon	0.001932	1	0.01521
GO:19025	negative regulation of activation of Janus kinase	0.001932	1	0.01521
GO:19051	negative regulation of membrane invagination	0.001932	1	0.01521
GO:00067	triterpenoid metabolic process	0.001932	1	0.01521
GO:00326	interleukin-8 production	0.001935	1	0.01521
GO:00903	positive regulation of intracellular protein transp	0.002093	1	0.01636
GO:00024	lymphocyte mediated immunity	0.002115	1	0.01644
GO:00427	defense response to bacterium	0.002137	1	0.01653
GO:00327	positive regulation of tumor necrosis factor produ	0.002167	1	0.01658
GO:00324	positive regulation of type I interferon production	0.002167	1	0.01658
GO:00024	adaptive immune response based on somatic recc	0.002205	1	0.01678
GO:00224	positive regulation of cell-cell adhesion	0.002228	1	0.01686
GO:00321	regulation of response to external stimulus	0.002239	1	0.01686
GO:19035	positive regulation of tumor necrosis factor super	0.002287	1	0.01714
GO:00506	negative regulation of lymphocyte proliferation	0.002473	1	0.01834
GO:00329	negative regulation of mononuclear cell prolifera	0.002473	1	0.01834
GO:00022	myeloid cell activation involved in immune resp	0.002667	1	0.01878
GO:00326	interleukin-1 production	0.002667	1	0.01878
GO:00434	negative regulation of MAP kinase activity	0.002667	1	0.01878
GO:00801	regulation of response to stress	0.002798	1	0.01878
GO:00706	negative regulation of leukocyte proliferation	0.002799	1	0.01878
GO:00466	lymphocyte proliferation	0.002849	1	0.01878
GO:00026	regulation of acute inflammatory response	0.002867	1	0.01878
GO:00027	positive regulation of lymphocyte mediated imm	0.002867	1	0.01878
GO:00712	cellular response to mechanical stimulus	0.002867	1	0.01878
GO:00362	response to statin	0.002897	1	0.01878
GO:20005	regulation of immunological synapse formation	0.002897	1	0.01878
GO:00703	detection of bacterial lipopeptide	0.002897	1	0.01878
GO:19025	negative regulation of neutrophil activation	0.002897	1	0.01878
GO:20011	negative regulation of T cell activation via T cell	0.002897	1	0.01878
GO:00717	response to triacyl bacterial lipopeptide	0.002897	1	0.01878
GO:00716	granulocyte colony-stimulating factor production	0.002897	1	0.01878
GO:00717	cellular response to triacyl bacterial lipopeptide	0.002897	1	0.01878
GO:00343	type III interferon production	0.002897	1	0.01878
GO:00605	positive regulation of vitamin D biosynthetic pro	0.002897	1	0.01878
GO:00381	toll-like receptor TLR1:TLR2 signaling pathway	0.002897	1	0.01878
GO:20001	negative regulation of branching morphogenesis	0.002897	1	0.01878
GO:00605	positive regulation of calcidiol 1-monooxygenase	0.002897	1	0.01878
GO:00461	positive regulation of vitamin metabolic process	0.002897	1	0.01878
GO:00326	regulation of interleukin-3 production	0.002897	1	0.01878
GO:00716	regulation of granulocyte colony-stimulating fact	0.002897	1	0.01878
GO:00343	regulation of type III interferon production	0.002897	1	0.01878
GO:19004	negative regulation of defense response to bacter	0.002897	1	0.01878
GO:00024	tolerance induction dependent upon immune resp	0.002897	1	0.01878
GO:00329	mononuclear cell proliferation	0.00293	1	0.01892
GO:00028	positive regulation of adaptive immune response	0.003004	1	0.01931
GO:00321	activation of protein kinase activity	0.003269	1	0.02091
GO:19035	regulation of protein targeting	0.003327	1	0.02119
GO:00706	leukocyte proliferation	0.003387	1	0.02148
GO:00323	regulation of intracellular transport	0.003414	1	0.02156
GO:00024	myeloid leukocyte mediated immunity	0.003508	1	0.02172
GO:00028	positive regulation of adaptive immune response	0.003508	1	0.02172

GO:000242	immune response-activating cell surface receptor	0.003756	1	0.02172
GO:007016	negative regulation of adiponectin secretion	0.003861	1	0.02172
GO:004249	detection of bacterial lipoprotein	0.003861	1	0.02172
GO:000244	type II hypersensitivity	0.003861	1	0.02172
GO:190256	regulation of eosinophil activation	0.003861	1	0.02172
GO:000186	type III hypersensitivity	0.003861	1	0.02172
GO:003268	negative regulation of interferon-alpha production	0.003861	1	0.02172
GO:003261	interleukin-3 production	0.003861	1	0.02172
GO:190124	regulation of macrophage colony-stimulating factor production	0.003861	1	0.02172
GO:007111	resolution of recombination intermediates	0.003861	1	0.02172
GO:000234	serotonin production involved in inflammatory response	0.003861	1	0.02172
GO:190082	regulation of membrane depolarization during cardiac action potential	0.003861	1	0.02172
GO:001486	smooth muscle adaptation	0.003861	1	0.02172
GO:004534	positive regulation of interferon-alpha biosynthesis	0.003861	1	0.02172
GO:000179	type IIa hypersensitivity	0.003861	1	0.02172
GO:000289	regulation of type II hypersensitivity	0.003861	1	0.02172
GO:003636	macrophage colony-stimulating factor production	0.003861	1	0.02172
GO:000244	serotonin secretion involved in inflammatory response	0.003861	1	0.02172
GO:190446	positive regulation of tumor necrosis factor secretion	0.003861	1	0.02172
GO:003309	positive regulation of immature T cell proliferation	0.003861	1	0.02172
GO:000179	positive regulation of type IIa hypersensitivity	0.003861	1	0.02172
GO:003088	negative regulation of myeloid dendritic cell activation	0.003861	1	0.02172
GO:000289	positive regulation of type II hypersensitivity	0.003861	1	0.02172
GO:000186	positive regulation of type III hypersensitivity	0.003861	1	0.02172
GO:000186	regulation of type III hypersensitivity	0.003861	1	0.02172
GO:000179	regulation of type IIa hypersensitivity	0.003861	1	0.02172
GO:004409	negative regulation of molecular function	0.003979	1	0.0223
GO:005072	regulation of inflammatory response	0.004049	1	0.0226
GO:003249	response to lipopolysaccharide	0.004082	1	0.0227
GO:004664	lymphocyte activation	0.00416	1	0.02305
GO:000196	leukocyte mediated cytotoxicity	0.004375	1	0.02414
GO:004236	positive regulation of protein import into nucleus	0.004627	1	0.02534
GO:000276	positive regulation of leukocyte mediated immunity	0.004627	1	0.02534
GO:004216	positive regulation of T cell proliferation	0.004712	1	0.02546
GO:001922	regulation of phosphate metabolic process	0.004776	1	0.02546
GO:005084	negative regulation of B cell receptor signaling pathway	0.004824	1	0.02546
GO:007172	cellular response to diacyl bacterial lipopeptide	0.004824	1	0.02546
GO:000244	chronic inflammatory response to antigenic stimulus	0.004824	1	0.02546
GO:003309	positive regulation of immature T cell proliferation	0.004824	1	0.02546
GO:009896	regulation of membrane depolarization during action potential	0.004824	1	0.02546
GO:200118	regulation of T cell activation via T cell receptor	0.004824	1	0.02546
GO:007048	monocyte aggregation	0.004824	1	0.02546
GO:007172	response to diacyl bacterial lipopeptide	0.004824	1	0.02546
GO:190459	positive regulation of protein import	0.004885	1	0.02569
GO:000276	immune response-regulating cell surface receptor	0.004934	1	0.02585
GO:005111	regulation of phosphorus metabolic process	0.004955	1	0.02587
GO:001819	peptidyl-amino acid modification	0.005374	1	0.02783
GO:000602	glycosaminoglycan biosynthetic process	0.005422	1	0.02783
GO:000602	aminoglycan biosynthetic process	0.005514	1	0.02783
GO:000269	negative regulation of immune effector process	0.005514	1	0.02783
GO:190382	positive regulation of cellular protein localization	0.005598	1	0.02783
GO:190351	mucopolysaccharide metabolic process	0.0057	1	0.02783
GO:007122	cellular response to bacterial lipoprotein	0.005786	1	0.02783
GO:003562	response to stilbenoid	0.005786	1	0.02783
GO:190256	regulation of neutrophil activation	0.005786	1	0.02783
GO:007016	adiponectin secretion	0.005786	1	0.02783
GO:003142	response to methotrexate	0.005786	1	0.02783
GO:001406	negative regulation of serotonin secretion	0.005786	1	0.02783

GO:007122	cellular response to bacterial lipopeptide	0.005786	1	0.02783
GO:007032	response to bacterial lipopeptide	0.005786	1	0.02783
GO:200011	regulation of branching morphogenesis of a nerv	0.005786	1	0.02783
GO:200041	regulation of eosinophil migration	0.005786	1	0.02783
GO:006034	positive regulation of cell adhesion molecule pro	0.005786	1	0.02783
GO:004534	regulation of interferon-alpha biosynthetic proce	0.005786	1	0.02783
GO:004534	interferon-alpha biosynthetic process	0.005786	1	0.02783
GO:000959	detection of virus	0.005786	1	0.02783
GO:007010	regulation of adiponectin secretion	0.005786	1	0.02783
GO:003806	NIK/NF-kappaB signaling	0.005794	1	0.02783
GO:003474	cellular hormone metabolic process	0.005794	1	0.02783
GO:003150	protein-containing complex localization	0.005794	1	0.02783
GO:004671	viral entry into host cell	0.005889	1	0.0282
GO:003139	regulation of protein modification process	0.006036	1	0.02863
GO:003238	positive regulation of intracellular transport	0.006141	1	0.02863
GO:005212	movement in host environment	0.006178	1	0.02863
GO:004440	entry into host	0.006178	1	0.02863
GO:005182	entry into other organism involved in symbiotic i	0.006178	1	0.02863
GO:009752	granulocyte migration	0.006178	1	0.02863
GO:003268	regulation of tumor necrosis factor production	0.006178	1	0.02863
GO:003020	entry into host cell	0.006178	1	0.02863
GO:005180	entry into cell of other organism involved in sym	0.006178	1	0.02863
GO:005219	movement in environment of other organism invc	0.006178	1	0.02863
GO:003264	tumor necrosis factor production	0.006275	1	0.02899
GO:003314	regulation of intracellular protein transport	0.006446	1	0.02968
GO:190354	regulation of tumor necrosis factor superfamily c	0.006473	1	0.02971
GO:004682	positive regulation of nucleocytoplasmic transpo	0.006673	1	0.03002
GO:004330	negative regulation of mast cell degranulation	0.006747	1	0.03002
GO:003359	response to L-ascorbic acid	0.006747	1	0.03002
GO:000282	negative regulation of T-helper 1 type immune re	0.006747	1	0.03002
GO:001019	response to ozone	0.006747	1	0.03002
GO:004534	positive regulation of interferon-beta biosynthesi	0.006747	1	0.03002
GO:003249	response to bacterial lipoprotein	0.006747	1	0.03002
GO:190440	regulation of tumor necrosis factor secretion	0.006747	1	0.03002
GO:006059	regulation of caldiol 1-monooxygenase activity	0.006747	1	0.03002
GO:007122	cellular response to magnesium ion	0.006747	1	0.03002
GO:007170	tumor necrosis factor superfamily cytokine produ	0.006774	1	0.03005
GO:190355	positive regulation of secretion by cell	0.007083	1	0.03132
GO:000268	negative regulation of immune system process	0.007224	1	0.03185
GO:004580	positive regulation of endocytosis	0.007291	1	0.03195
GO:000190	cell killing	0.007291	1	0.03195
GO:004578	positive regulation of cell adhesion	0.007463	1	0.03244
GO:007190	negative regulation of protein serine/threonine ki	0.007503	1	0.03244
GO:001820	peptidyl-lysine modification	0.007511	1	0.03244
GO:001092	regulation of phosphatase activity	0.007609	1	0.03244
GO:003160	positive regulation of lipopolysaccharide-mediat	0.007708	1	0.03244
GO:199077	tumor necrosis factor secretion	0.007708	1	0.03244
GO:000229	T cell activation via T cell receptor contact with	0.007708	1	0.03244
GO:003088	regulation of myeloid dendritic cell activation	0.007708	1	0.03244
GO:004541	positive regulation of interleukin-8 biosynthetic p	0.007708	1	0.03244
GO:000288	positive regulation of hypersensitivity	0.007708	1	0.03244
GO:004330	eosinophil activation	0.007708	1	0.03244
GO:006034	regulation of cell adhesion molecule production	0.007708	1	0.03244
GO:003300	negative regulation of mast cell activation involv	0.007708	1	0.03244
GO:190018	positive regulation of protein localization to nucl	0.007717	1	0.03244
GO:001692	protein sumoylation	0.007934	1	0.03316
GO:005077	negative regulation of immune response	0.007934	1	0.03316
GO:005067	positive regulation of lymphocyte proliferation	0.008044	1	0.03352

GO:00329	positive regulation of mononuclear cell proliferation	0.008265	1	0.03434
GO:19033	regulation of regulated secretory pathway	0.008376	1	0.03471
GO:00306	polyketide metabolic process	0.008667	1	0.03511
GO:00511	regulation of NK T cell activation	0.008667	1	0.03511
GO:00028	positive regulation of acute inflammatory response	0.008667	1	0.03511
GO:00328	negative regulation of natural killer cell activation	0.008667	1	0.03511
GO:00395	MDA-5 signaling pathway	0.008667	1	0.03511
GO:00140	negative regulation of glutamate secretion	0.008667	1	0.03511
GO:00352	ectopic germ cell programmed cell death	0.008667	1	0.03511
GO:00605	regulation of vitamin D biosynthetic process	0.008667	1	0.03511
GO:00706	positive regulation of leukocyte proliferation	0.008945	1	0.03613
GO:00019	regulation of protein phosphorylation	0.009035	1	0.03639
GO:00028	regulation of natural killer cell mediated immune response	0.009626	1	0.03682
GO:00105	regulation of activation of Janus kinase activity	0.009626	1	0.03682
GO:00330	regulation of immature T cell proliferation in thymus	0.009626	1	0.03682
GO:00702	positive regulation of mucus secretion	0.009626	1	0.03682
GO:19004	positive regulation of defense response to bacterium	0.009626	1	0.03682
GO:00341	positive regulation of heterotypic cell-cell adhesion	0.009626	1	0.03682
GO:00603	cell adhesion molecule production	0.009626	1	0.03682
GO:00453	regulation of interferon-beta biosynthetic process	0.009626	1	0.03682
GO:00453	interferon-beta biosynthetic process	0.009626	1	0.03682
GO:00140	regulation of serotonin secretion	0.009626	1	0.03682
GO:19038	negative regulation of voltage-gated potassium channel activity	0.009626	1	0.03682
GO:00716	positive regulation of monocyte chemotactic protein production	0.009626	1	0.03682
GO:00331	positive regulation of histone phosphorylation	0.009626	1	0.03682
GO:00028	regulation of natural killer cell mediated cytotoxicity	0.009626	1	0.03682
GO:00024	natural killer cell mediated immune response to tumor	0.009626	1	0.03682
GO:00024	natural killer cell mediated cytotoxicity directed at tumor	0.009626	1	0.03682
GO:19022	negative regulation of delayed rectifier potassium channel activity	0.009626	1	0.03682
GO:00028	negative regulation of myeloid leukocyte mediated cytotoxicity	0.009626	1	0.03682
GO:00450	positive regulation of chemokine biosynthetic process	0.009626	1	0.03682
GO:19030	regulation of response to wounding	0.009944	1	0.03794
GO:00025	acute inflammatory response	0.01013	1	0.03856
GO:00353	regulation of protein dephosphorylation	0.01038	1	0.03939
GO:00080	cell recognition	0.0105	1	0.03944
GO:00330	negative regulation of mast cell activation	0.01058	1	0.03944
GO:00330	immature T cell proliferation in thymus	0.01058	1	0.03944
GO:00487	branching morphogenesis of a nerve	0.01058	1	0.03944
GO:00028	regulation of hypersensitivity	0.01058	1	0.03944
GO:00316	positive regulation of fever generation	0.01058	1	0.03944
GO:00070	cytoskeletal anchoring at plasma membrane	0.01058	1	0.03944
GO:00434	negative regulation of MAPK cascade	0.011	1	0.0408
GO:00440	regulation of anion transport	0.011	1	0.0408
GO:00302	glycosaminoglycan metabolic process	0.01113	1	0.0409
GO:00353	regulation of dephosphorylation	0.01113	1	0.0409
GO:00439	positive regulation of multi-organism process	0.01126	1	0.0409
GO:00458	positive regulation of protein kinase activity	0.01138	1	0.0409
GO:19051	positive regulation of membrane invagination	0.01154	1	0.0409
GO:00022	macrophage activation involved in immune response	0.01154	1	0.0409
GO:00028	positive regulation of inflammatory response to antigen	0.01154	1	0.0409
GO:00487	positive regulation of astrocyte differentiation	0.01154	1	0.0409
GO:19031	regulation of establishment of endothelial barrier	0.01154	1	0.0409
GO:00330	regulation of immature T cell proliferation	0.01154	1	0.0409
GO:00423	vitamin D biosynthetic process	0.01154	1	0.0409
GO:00423	keratan sulfate catabolic process	0.01154	1	0.0409
GO:00601	positive regulation of phagocytosis, engulfment	0.01154	1	0.0409
GO:00454	regulation of interleukin-8 biosynthetic process	0.01154	1	0.0409
GO:00316	regulation of fever generation	0.01154	1	0.0409

GO:19015	regulation of endothelial cell development	0.01154	1	0.0409
GO:00324	detection of molecule of bacterial origin	0.01154	1	0.0409
GO:00433	negative regulation of leukocyte degranulation	0.01154	1	0.0409
GO:00066	steroid biosynthetic process	0.01164	1	0.04117
GO:00517	interaction with host	0.01177	1	0.04153
GO:00421	regulation of T cell proliferation	0.01191	1	0.04183
GO:00019	positive regulation of protein phosphorylation	0.01198	1	0.04183
GO:00975	myeloid leukocyte migration	0.01204	1	0.04183
GO:00508	T cell receptor signaling pathway	0.01217	1	0.04183
GO:00423	regulation of phosphorylation	0.0122	1	0.04183
GO:00026	regulation of leukocyte migration	0.0123	1	0.04183
GO:00060	aminoglycan metabolic process	0.0123	1	0.04183
GO:00161	vesicle-mediated transport	0.01233	1	0.04183
GO:00719	regulation of protein serine/threonine kinase acti	0.01246	1	0.04183
GO:19041	positive regulation of membrane depolarization	0.0125	1	0.04183
GO:00330	immature T cell proliferation	0.0125	1	0.04183
GO:00422	interleukin-8 biosynthetic process	0.0125	1	0.04183
GO:00702	regulation of mucus secretion	0.0125	1	0.04183
GO:00450	regulation of chemokine biosynthetic process	0.0125	1	0.04183
GO:00109	magnesium ion homeostasis	0.0125	1	0.04183
GO:00425	positive regulation of tumor necrosis factor biosy	0.0125	1	0.04183
GO:00801	response to phenylpropanoid	0.0125	1	0.04183
GO:00025	hypersensitivity	0.0125	1	0.04183
GO:00327	positive regulation of granulocyte macrophage cc	0.0125	1	0.04183
GO:00106	regulation of cell communication by electrical co	0.0125	1	0.04183
GO:00306	regulation of vitamin metabolic process	0.0125	1	0.04183
GO:00323	positive regulation of prostaglandin secretion	0.0125	1	0.04183
GO:00431	positive regulation of I-kappaB kinase/NF-kappa	0.01298	1	0.04333
GO:00510	negative regulation of transport	0.01326	1	0.04371
GO:00316	positive regulation of heat generation	0.01345	1	0.04371
GO:00330	positive regulation of T cell differentiation in thy	0.01345	1	0.04371
GO:00511	NK T cell activation	0.01345	1	0.04371
GO:00420	chemokine biosynthetic process	0.01345	1	0.04371
GO:00323	regulation of prostaglandin secretion	0.01345	1	0.04371
GO:20004	positive regulation of thymocyte aggregation	0.01345	1	0.04371
GO:00450	positive regulation of interferon-gamma biosynth	0.01345	1	0.04371
GO:00017	immunological synapse formation	0.01345	1	0.04371
GO:00458	positive regulation of membrane potential	0.01345	1	0.04371
GO:00450	positive regulation of interleukin-2 biosynthetic p	0.01345	1	0.04371
GO:19004	regulation of defense response to bacterium	0.01345	1	0.04371
GO:00336	positive regulation of kinase activity	0.0136	1	0.0441
GO:00423	regulation of protein import into nucleus	0.01395	1	0.04499
GO:00423	positive regulation of phosphorylation	0.01396	1	0.04499
GO:00703	positive regulation of ERK1 and ERK2 cascade	0.01423	1	0.04499
GO:00302	hyaluronan biosynthetic process	0.01441	1	0.04499
GO:00519	negative regulation of amino acid transport	0.01441	1	0.04499
GO:00510	positive regulation of membrane protein ectodon	0.01441	1	0.04499
GO:00307	sequestering of triglyceride	0.01441	1	0.04499
GO:00326	regulation of granulocyte macrophage colony-sti	0.01441	1	0.04499
GO:00072	I-kappaB phosphorylation	0.01441	1	0.04499
GO:00507	chemokine metabolic process	0.01441	1	0.04499
GO:00453	type I interferon biosynthetic process	0.01441	1	0.04499
GO:00016	fever generation	0.01441	1	0.04499
GO:00457	positive regulation of action potential	0.01441	1	0.04499
GO:00028	regulation of acute inflammatory response to anti	0.01441	1	0.04499
GO:20006	positive regulation of sodium ion transmembrane	0.01441	1	0.04499
GO:00326	granulocyte macrophage colony-stimulating fact	0.01441	1	0.04499
GO:00331	regulation of histone phosphorylation	0.01441	1	0.04499

	GO:19045	regulation of protein import	0.01451	1	0.04523
	GO:00429	activation of Janus kinase activity	0.01536	1	0.04686
	GO:00028	regulation of response to tumor cell	0.01536	1	0.04686
	GO:00507	negative regulation of phagocytosis	0.01536	1	0.04686
	GO:00430	positive regulation of macrophage activation	0.01536	1	0.04686
	GO:00028	regulation of immune response to tumor cell	0.01536	1	0.04686
	GO:00018	serotonin secretion	0.01536	1	0.04686
	GO:00316	regulation of heat generation	0.01536	1	0.04686
	GO:00508	regulation of B cell receptor signaling pathway	0.01536	1	0.04686
	GO:00423	fat-soluble vitamin biosynthetic process	0.01536	1	0.04686
	GO:00726	eosinophil migration	0.01536	1	0.04686
	GO:00512	positive regulation of protein metabolic process	0.01587	1	0.0483
	GO:00716	monocyte chemotactic protein-1 production	0.01631	1	0.04894
	GO:00323	prostaglandin secretion	0.01631	1	0.04894
	GO:00702	mucus secretion	0.01631	1	0.04894
	GO:00308	negative regulation of B cell proliferation	0.01631	1	0.04894
	GO:00459	negative regulation of natural killer cell mediated	0.01631	1	0.04894
	GO:00716	regulation of monocyte chemotactic protein-1 pr	0.01631	1	0.04894
	GO:00325	positive regulation of phosphoprotein phosphatas	0.01631	1	0.04894
	GO:00171	regulation of exocytosis	0.01643	1	0.04919
	GO:00713	cellular response to lipid	0.01668	1	0.04983
	GO:19035	negative regulation of secretion by cell	0.01673	1	0.04989
Cluster 2	ID	Name	p-value	q-value Bo	q-value FD
	RGS1	GO:00453 leukocyte activation	6.22E-13	5.5E-10	5.5E-10
	CD69	GO:00017 cell activation	8.1E-12	7.16E-09	3.58E-09
	GPR183	GO:00704 T cell aggregation	7.22E-10	6.38E-07	1.24E-07
	CD3G	GO:00421 T cell activation	7.22E-10	6.38E-07	1.24E-07
	GZMK	GO:00715 lymphocyte aggregation	7.35E-10	6.5E-07	1.24E-07
	IL2RA	GO:00704 leukocyte aggregation	8.4E-10	7.42E-07	1.24E-07
	AMICA1	GO:00466 lymphocyte activation	1.03E-09	9.14E-07	1.31E-07
	FYB	GO:00071 leukocyte cell-cell adhesion	1.56E-09	1.38E-06	1.72E-07
	PIK3CG	GO:00069 immune response	3.84E-08	3.4E-05	3.77E-06
	DOCK2	GO:00022 myeloid leukocyte activation	1.62E-07	0.000143	1.43E-05
	DOCK8	GO:00986 cell-cell adhesion	3.82E-07	0.000338	3.07E-05
	SNX10	GO:00430 regulation of GTPase activity	2.88E-06	0.002548	0.000199
	ST8SIA4	GO:00466 lymphocyte proliferation	2.97E-06	0.002629	0.000199
	IQGAP2	GO:00329 mononuclear cell proliferation	3.15E-06	0.002784	0.000199
	APBB1IP	GO:00706 leukocyte proliferation	4.23E-06	0.00374	0.000249
	ARHGAP2	GO:00025 leukocyte differentiation	6.12E-06	0.005412	0.000338
	CASP1	GO:00300 lymphocyte differentiation	7.8E-06	0.006891	0.000405
	NPL	GO:00420 T cell proliferation	1.06E-05	0.009342	0.000519
	MOP-1	GO:00022 immune effector process	1.38E-05	0.01218	0.000641
	CLEC7A	GO:00023 leukocyte activation involved in immune respons	1.62E-05	0.01436	0.000712
	TLR8	GO:00022 cell activation involved in immune response	1.69E-05	0.01496	0.000712
	P2RY13	GO:00381 interleukin-2-mediated signaling pathway	1.87E-05	0.01653	0.000722
	C14orf106	GO:00435 positive regulation of GTPase activity	1.88E-05	0.0166	0.000722
	MS4A14	GO:00302 T cell differentiation	1.99E-05	0.01755	0.000731
	CD3E	GO:00071 cell adhesion	2.12E-05	0.01875	0.00075
	IL2RG	GO:00226 biological adhesion	2.27E-05	0.02008	0.000772
	KCNA3	GO:00513 positive regulation of hydrolase activity	2.6E-05	0.02299	0.000852
	KLRG1	GO:00713 cellular response to interleukin-2	2.8E-05	0.02477	0.000885
	RHOH	GO:00026 positive regulation of immune system process	3.71E-05	0.03277	0.00113
	TMEM154	GO:00512 positive regulation of lymphocyte activation	6.2E-05	0.05482	0.001827
		GO:00513 regulation of hydrolase activity	6.41E-05	0.05666	0.001828
		GO:00706 response to interleukin-2	6.71E-05	0.05929	0.001853
		GO:00026 positive regulation of leukocyte activation	9.58E-05	0.0847	0.002567
		GO:00508 positive regulation of cell activation	0.000114	0.101	0.00297
		GO:00455 mast cell activation	0.000119	0.1053	0.003007

GO:003009	hemopoiesis	0.000124	0.11	0.003036
GO:000268	regulation of immune system process	0.000127	0.1123	0.003036
GO:004506	negative thymic T cell selection	0.000169	0.1492	0.003731
GO:000177	immunological synapse formation	0.000169	0.1492	0.003731
GO:000266	regulation of T cell tolerance induction	0.000169	0.1492	0.003731
GO:004853	hematopoietic or lymphoid organ development	0.000174	0.1537	0.003748
GO:004308	positive regulation of catalytic activity	0.000191	0.1687	0.00391
GO:004338	negative T cell selection	0.000195	0.172	0.00391
GO:000251	T cell tolerance induction	0.000195	0.172	0.00391
GO:003410	homotypic cell-cell adhesion	0.000207	0.1829	0.004063
GO:007022	lymphocyte apoptotic process	0.000229	0.2024	0.004363
GO:007159	thymocyte aggregation	0.000237	0.2094	0.004363
GO:003307	T cell differentiation in thymus	0.000237	0.2094	0.004363
GO:000252	immune system development	0.000245	0.2161	0.004411
GO:004578	positive regulation of cell adhesion	0.000268	0.2366	0.004732
GO:005087	positive regulation of T cell activation	0.000278	0.246	0.004823
GO:003411	positive regulation of homotypic cell-cell adhesion	0.000302	0.2668	0.005132
GO:190303	positive regulation of leukocyte cell-cell adhesion	0.000322	0.2844	0.005367
GO:005124	regulation of lymphocyte activation	0.000331	0.2925	0.005417
GO:003014	regulation of cell adhesion	0.000344	0.3041	0.005528
GO:000693	inflammatory response	0.000363	0.3206	0.005725
GO:000264	regulation of tolerance induction	0.000387	0.3423	0.005902
GO:000177	microglial cell activation	0.000387	0.3423	0.005902
GO:000271	immune response-activating signal transduction	0.000413	0.365	0.006187
GO:002240	positive regulation of cell-cell adhesion	0.000546	0.4824	0.007989
GO:004506	thymic T cell selection	0.000551	0.4873	0.007989
GO:000276	immune response-regulating signaling pathway	0.000574	0.5076	0.008187
GO:007188	leukocyte apoptotic process	0.000609	0.5382	0.008521
GO:000269	regulation of leukocyte activation	0.000617	0.5453	0.008521
GO:003633	dendritic cell migration	0.000644	0.5692	0.008757
GO:000224	activation of immune response	0.000703	0.6218	0.00939
GO:004409	positive regulation of molecular function	0.000712	0.6291	0.00939
GO:003134	regulation of defense response	0.000773	0.6829	0.01004
GO:000250	tolerance induction	0.000796	0.7036	0.0102
GO:005086	regulation of cell activation	0.000868	0.767	0.0109
GO:004663	alpha-beta T cell activation	0.000876	0.7742	0.0109
GO:005067	positive regulation of lymphocyte proliferation	0.000972	0.8595	0.01194
GO:003294	positive regulation of mononuclear cell proliferation	0.001013	0.8952	0.01226
GO:005086	regulation of T cell activation	0.001028	0.9088	0.01228
GO:000242	immune response-activating cell surface receptor	0.001088	0.9614	0.01282
GO:007060	positive regulation of leukocyte proliferation	0.00114	1	0.01326
GO:000726	small GTPase mediated signal transduction	0.00117	1	0.01343
GO:190303	regulation of leukocyte cell-cell adhesion	0.001201	1	0.01361
GO:005077	regulation of immune response	0.001247	1	0.01396
GO:004663	alpha-beta T cell proliferation	0.001278	1	0.01412
GO:003411	regulation of homotypic cell-cell adhesion	0.001294	1	0.01412
GO:006148	memory T cell proliferation	0.001398	1	0.01489
GO:003414	toll-like receptor 8 signaling pathway	0.001398	1	0.01489
GO:000803	cell recognition	0.00145	1	0.01526
GO:000276	immune response-regulating cell surface receptor	0.001558	1	0.0162
GO:003426	negative regulation of GTPase activity	0.00171	1	0.01758
GO:005087	T cell receptor signaling pathway	0.001809	1	0.01838
GO:000689	endocytosis	0.002016	1	0.02025
GO:005077	positive regulation of immune response	0.002097	1	0.02079
GO:004506	T cell selection	0.002117	1	0.02079
GO:003811	interleukin-7-mediated signaling pathway	0.00279	1	0.02634
GO:009876	response to interleukin-7	0.00279	1	0.02634
GO:009876	cellular response to interleukin-7	0.00279	1	0.02634

GO:002240	regulation of cell-cell adhesion	0.002801	1	0.02634
GO:007023	T cell apoptotic process	0.003156	1	0.02937
GO:004211	macrophage activation	0.003474	1	0.03161
GO:004666	positive regulation of alpha-beta T cell activation	0.003474	1	0.03161
GO:005067	regulation of lymphocyte proliferation	0.003504	1	0.03161
GO:003294	regulation of mononuclear cell proliferation	0.003594	1	0.03209
GO:000998	cell-cell recognition	0.003919	1	0.03465
GO:004210	positive regulation of cytokine biosynthetic process	0.004035	1	0.03488
GO:007060	regulation of leukocyte proliferation	0.004064	1	0.03488
GO:005084	antigen receptor-mediated signaling pathway	0.004064	1	0.03488
GO:005071	positive regulation of interleukin-1 alpha secretion	0.004183	1	0.03488
GO:007122	cellular response to molecule of fungal origin	0.004183	1	0.03488
GO:004601	regulation of T cell homeostatic proliferation	0.004183	1	0.03488
GO:007022	regulation of lymphocyte apoptotic process	0.00427	1	0.03528
GO:003274	positive regulation of interferon-gamma production	0.004886	1	0.03999
GO:000690	phagocytosis	0.005227	1	0.04038
GO:000227	myeloid cell activation involved in immune response	0.00554	1	0.04038
GO:001920	N-acetylneuraminic acid catabolic process	0.005573	1	0.04038
GO:003502	positive regulation of Rac protein signal transduction	0.005573	1	0.04038
GO:000170	membrane raft polarization	0.005573	1	0.04038
GO:003282	positive regulation of CD4-positive, CD25-positive, alpha-beta T cell activation	0.005573	1	0.04038
GO:001089	negative regulation of triglyceride catabolic process	0.005573	1	0.04038
GO:004534	positive regulation of interferon-alpha biosynthesis	0.005573	1	0.04038
GO:000260	positive regulation of T cell anergy	0.005573	1	0.04038
GO:003158	membrane raft distribution	0.005573	1	0.04038
GO:000291	positive regulation of lymphocyte anergy	0.005573	1	0.04038
GO:000227	myeloid dendritic cell activation involved in immune response	0.005573	1	0.04038
GO:005511	negative regulation of cardiac muscle contraction	0.005573	1	0.04038
GO:000170	T cell homeostatic proliferation	0.005573	1	0.04038
GO:003129	T cell costimulation	0.005812	1	0.04177
GO:003129	lymphocyte costimulation	0.00595	1	0.04208
GO:007120	cellular response to mechanical stimulus	0.00595	1	0.04208
GO:000724	I-kappaB kinase/NF-kappaB signaling	0.006186	1	0.04312
GO:000690	defense response	0.006195	1	0.04312
GO:004666	regulation of alpha-beta T cell activation	0.006375	1	0.04402
GO:004558	positive regulation of T cell differentiation	0.006519	1	0.04467
GO:005070	regulation of interleukin-1 alpha secretion	0.006962	1	0.04593
GO:003224	secretory granule localization	0.006962	1	0.04593
GO:003577	interleukin-4-mediated signaling pathway	0.006962	1	0.04593
GO:005160	membrane raft localization	0.006962	1	0.04593
GO:003282	regulation of CD4-positive, CD25-positive, alpha-beta T cell activation	0.006962	1	0.04593
GO:005087	positive regulation of B cell activation	0.007417	1	0.04857
GO:000718	G protein-coupled receptor signaling pathway	0.007672	1	0.04987

Cluster 3	ID	Name	p-value	q-value Bo	q-value FD
CCDC80	GO:003033	regulation of cell migration	3.36E-06	0.003581	0.00139
HLA-DPB1	GO:000714	cell adhesion	4.09E-06	0.004363	0.00139
LAPTM5	GO:002261	biological adhesion	4.36E-06	0.004655	0.00139
CD74	GO:200014	regulation of cell motility	5.21E-06	0.005561	0.00139
COL1A1	GO:000690	defense response	7.68E-06	0.008193	0.001418
PCOLCE	GO:005127	regulation of cellular component movement	8.89E-06	0.009486	0.001418
TGFBI	GO:004001	regulation of locomotion	9.31E-06	0.009928	0.001418
F2R	GO:000150	blood vessel development	2.31E-05	0.02465	0.002273
DOCK10	GO:000170	cell activation	2.39E-05	0.02554	0.002273
GOLGA8E	GO:005167	localization of cell	2.55E-05	0.02723	0.002273
LOC100511	GO:004887	cell motility	2.55E-05	0.02723	0.002273
CD53	GO:005090	leukocyte migration	2.56E-05	0.02728	0.002273
LYZ	GO:000194	vasculature development	2.88E-05	0.03075	0.002365
CX3CR1	GO:003059	leukocyte chemotaxis	3.51E-05	0.03746	0.002572

CXCR4	GO:000694 inflammatory response	3.8E-05	0.04051	0.002572
CD163	GO:007134 cellular response to cytokine stimulus	3.86E-05	0.04116	0.002572
C3AR1	GO:000152 angiogenesis	6.16E-05	0.06568	0.003863
SLCO2B1	GO:003409 response to cytokine	8.71E-05	0.09295	0.005072
FCGR3A	GO:006032 cell chemotaxis	9.03E-05	0.09638	0.005072
IFI30	GO:001988 antigen processing and presentation of exogenous antigenic peptide	9.62E-05	0.1026	0.005132
	GO:004001 locomotion	0.000104	0.1109	0.005282
	GO:000249 antigen processing and presentation of peptide antigen via MHC class II	0.000112	0.1197	0.005363
	GO:000250 antigen processing and presentation of peptide antigen via MHC class I	0.000116	0.1234	0.005363
	GO:004864 anatomical structure formation involved in morphogenesis	0.000127	0.1354	0.005442
	GO:001647 cell migration	0.000128	0.136	0.005442
	GO:004851 blood vessel morphogenesis	0.000139	0.1478	0.005569
	GO:001922 cytokine-mediated signaling pathway	0.000141	0.1504	0.005569
	GO:004664 lymphocyte proliferation	0.000171	0.1826	0.006522
	GO:003294 mononuclear cell proliferation	0.000178	0.1897	0.006542
	GO:000692 movement of cell or subcellular component	0.000185	0.1973	0.006578
	GO:007060 leukocyte proliferation	0.000216	0.2309	0.007448
	GO:009860 cell-cell adhesion	0.000225	0.2398	0.007492
	GO:009002 positive regulation of neutrophil chemotaxis	0.000283	0.3018	0.009146
	GO:007234 cardiovascular system development	0.000341	0.3634	0.01038
	GO:007235 circulatory system development	0.000341	0.3634	0.01038
	GO:007162 positive regulation of granulocyte chemotaxis	0.000353	0.3764	0.01045
	GO:009003 regulation of neutrophil chemotaxis	0.000404	0.4306	0.01154
	GO:000694 immune response	0.000417	0.4444	0.01154
	GO:190262 positive regulation of neutrophil migration	0.00043	0.459	0.01154
	GO:003014 regulation of cell adhesion	0.000433	0.4616	0.01154
	GO:005124 positive regulation of multicellular organismal process	0.000482	0.5146	0.01235
	GO:004824 macrophage chemotaxis	0.000486	0.5186	0.01235
	GO:000249 antigen processing and presentation of exogenous antigenic peptide	0.000514	0.5488	0.01276
	GO:001988 antigen processing and presentation of exogenous antigenic peptide	0.00058	0.619	0.01383
	GO:009752 myeloid leukocyte migration	0.00059	0.6295	0.01383
	GO:000181 positive regulation of cytokine production	0.000596	0.6363	0.01383
	GO:190262 regulation of neutrophil migration	0.00064	0.683	0.01453
	GO:004800 antigen processing and presentation of peptide antigen via MHC class II	0.000705	0.7524	0.01567
	GO:003032 positive regulation of cell migration	0.000754	0.8048	0.01642
	GO:200014 positive regulation of cell motility	0.00084	0.8963	0.0171
	GO:007162 regulation of granulocyte chemotaxis	0.000852	0.9094	0.0171
	GO:005092 regulation of chemotaxis	0.000871	0.9296	0.0171
	GO:003296 collagen biosynthetic process	0.000891	0.9502	0.0171
	GO:004532 leukocyte activation	0.000906	0.967	0.0171
	GO:005125 positive regulation of cellular component movement	0.000925	0.9871	0.0171
	GO:007171 sodium-independent icosanoid transport	0.000967	1	0.0171
	GO:000288 negative regulation of chronic inflammatory response	0.000967	1	0.0171
	GO:190012 negative regulation of renin secretion into blood	0.000967	1	0.0171
	GO:000246 tolerance induction to nonself antigen	0.000967	1	0.0171
	GO:190261 cellular response to fluoride	0.000967	1	0.0171
	GO:004001 positive regulation of locomotion	0.000978	1	0.0171
	GO:005192 regulation of sensory perception	0.00101	1	0.01711
	GO:005193 regulation of sensory perception of pain	0.00101	1	0.01711
	GO:004209 T cell proliferation	0.001089	1	0.01816
	GO:005109 positive regulation of developmental process	0.001121	1	0.0184
	GO:007048 T cell aggregation	0.001217	1	0.01924
	GO:004211 T cell activation	0.001217	1	0.01924
	GO:007159 lymphocyte aggregation	0.001226	1	0.01924
	GO:007048 leukocyte aggregation	0.00129	1	0.01995
	GO:005077 regulation of immune response	0.001312	1	0.02
	GO:001988 antigen processing and presentation	0.001356	1	0.02038
	GO:000828 positive regulation of cell proliferation	0.001483	1	0.02198

GO:000714 leukocyte cell-cell adhesion	0.001634	1	0.02359
GO:009028 positive regulation of calcium ion import	0.001664	1	0.02359
GO:004211 macrophage activation	0.001664	1	0.02359
GO:000716 negative regulation of cell adhesion	0.00168	1	0.02359
GO:004559 positive regulation of cell differentiation	0.001807	1	0.02455
GO:000288 regulation of chronic inflammatory response to n	0.001932	1	0.02455
GO:190027 negative regulation of long-term synaptic potenti	0.001932	1	0.02455
GO:003569 macrophage migration inhibitory factor signaling	0.001932	1	0.02455
GO:000254 chronic inflammatory response to non-antigenic s	0.001932	1	0.02455
GO:002202 telencephalon cell migration	0.001935	1	0.02455
GO:000692 chemotaxis	0.001949	1	0.02455
GO:004231 taxis	0.001974	1	0.02455
GO:004320 response to external biotic stimulus	0.001979	1	0.02455
GO:005170 response to other organism	0.001979	1	0.02455
GO:006144 connective tissue development	0.002006	1	0.0246
GO:002188 forebrain cell migration	0.002108	1	0.02556
GO:000961 response to bacterium	0.002141	1	0.02567
GO:003210 regulation of response to external stimulus	0.002239	1	0.02654
GO:000720 positive regulation of cytosolic calcium ion conc	0.002321	1	0.02722
GO:000960 response to biotic stimulus	0.002368	1	0.02746
GO:007009 chemokine-mediated signaling pathway	0.002667	1	0.03059
GO:000181 regulation of cytokine production	0.002734	1	0.03104
GO:007130 cellular response to vitamin E	0.002897	1	0.03122
GO:004469 tooth eruption	0.002897	1	0.03122
GO:000228 microglial cell activation involved in immune res	0.002897	1	0.03122
GO:000752 establishment of synaptic specificity at neuromus	0.002897	1	0.03122
GO:000240 tolerance induction dependent upon immune resp	0.002897	1	0.03122
GO:005148 regulation of cytosolic calcium ion concentration	0.002985	1	0.03173
GO:006033 interferon-gamma-mediated signaling pathway	0.003004	1	0.03173
GO:003164 regulation of neurological system process	0.003074	1	0.03184
GO:000269 positive regulation of leukocyte chemotaxis	0.003074	1	0.03184
GO:003214 activation of protein kinase activity	0.003269	1	0.03353
GO:005077 positive regulation of immune response	0.003414	1	0.03469
GO:003059 neutrophil chemotaxis	0.003508	1	0.03531
GO:004212 regulation of cell proliferation	0.00367	1	0.0366
GO:000243 immune response-activating cell surface receptor	0.003756	1	0.03711
GO:190261 response to fluoride	0.003861	1	0.03779
GO:000180 cytokine production	0.003974	1	0.03855
GO:003249 response to lipopolysaccharide	0.004082	1	0.03924
GO:004664 lymphocyte activation	0.00416	1	0.03964
GO:004814 regulation of fibroblast proliferation	0.004211	1	0.03976
GO:199026 neutrophil migration	0.004375	1	0.04095
GO:004814 fibroblast proliferation	0.004458	1	0.04118
GO:003019 extracellular matrix organization	0.004496	1	0.04118
GO:004300 extracellular structure organization	0.004531	1	0.04118
GO:004340 regulation of MAP kinase activity	0.004567	1	0.04118
GO:000223 response to molecule of bacterial origin	0.004639	1	0.04118
GO:000268 regulation of leukocyte chemotaxis	0.004712	1	0.04118
GO:000290 negative regulation of mature B cell apoptotic pr	0.004824	1	0.04118
GO:000290 regulation of mature B cell apoptotic process	0.004824	1	0.04118
GO:000243 complement receptor mediated signaling pathway	0.004824	1	0.04118
GO:190011 regulation of renin secretion into blood stream	0.004824	1	0.04118
GO:000290 mature B cell apoptotic process	0.004824	1	0.04118
GO:000270 immune response-regulating cell surface receptor	0.004934	1	0.04178
GO:007162 granulocyte chemotaxis	0.004973	1	0.04178
GO:009770 connective tissue replacement	0.005786	1	0.04573
GO:003570 hematopoietic stem cell migration	0.005786	1	0.04573
GO:007212 positive regulation of glomerular mesangial cell j	0.005786	1	0.04573

	GO:000194	intramembranous ossification	0.005786	1	0.04573
	GO:000224	connective tissue replacement involved in inflam	0.005786	1	0.04573
	GO:000267	negative regulation of chronic inflammatory resp	0.005786	1	0.04573
	GO:003607	direct ossification	0.005786	1	0.04573
	GO:000310	(negative regulation of glomerular filtration	0.005786	1	0.04573
	GO:009027	regulation of calcium ion import	0.005984	1	0.04695
	GO:005192	positive regulation of calcium ion transport	0.006081	1	0.04702
	GO:003290	collagen metabolic process	0.006081	1	0.04702
	GO:009755	granulocyte migration	0.006178	1	0.04742
	GO:004480	(multi-organism membrane fusion	0.006747	1	0.0494
	GO:003960	membrane fusion involved in viral entry into hos	0.006747	1	0.0494
	GO:000260	(positive regulation of dendritic cell antigen proce	0.006747	1	0.0494
	GO:000200	renin secretion into blood stream	0.006747	1	0.0494
	GO:001900	(fusion of virus membrane with host plasma mem	0.006747	1	0.0494
	GO:200034	positive regulation of chemokine (C-X-C motif)	0.006747	1	0.0494
	GO:000268	positive regulation of leukocyte migration	0.006774	1	0.0494
	GO:000687	cellular calcium ion homeostasis	0.006805	1	0.0494
	GO:005092	positive regulation of chemotaxis	0.006876	1	0.04958
Cluster 4	ID	Name	p-value	q-value Bo	q-value FD
CARTPT	GO:004578	positive regulation of cell adhesion	2.01E-06	0.002654	0.002654
PLEK	GO:002240	(positive regulation of cell-cell adhesion	5.04E-06	0.006674	0.003199
EVI2B	GO:003009	hemopoiesis	8.3E-06	0.01098	0.003199
PTPRC	GO:004855	hematopoietic or lymphoid organ development	1.18E-05	0.01561	0.003199
AOAH	GO:004558	positive regulation of gamma-delta T cell differe	1.32E-05	0.01747	0.003199
ADAM28	GO:003362	cell adhesion mediated by integrin	1.63E-05	0.02152	0.003199
ITGA4	GO:000252	immune system development	1.69E-05	0.02239	0.003199
TM6SF1	GO:004664	positive regulation of gamma-delta T cell activat	2.46E-05	0.03257	0.004072
ALOX5	GO:004558	regulation of gamma-delta T cell differentiation	3.16E-05	0.04186	0.004227
FAM49B	GO:003014	regulation of cell adhesion	3.59E-05	0.04752	0.004227
PLXNC1	GO:000714	cell adhesion	4.21E-05	0.05575	0.004227
ARL4C	GO:002240	(regulation of cell-cell adhesion	4.29E-05	0.05669	0.004227
CD4	GO:002261	biological adhesion	4.46E-05	0.05899	0.004227
HLA-DM1	GO:004664	regulation of gamma-delta T cell activation	4.83E-05	0.06387	0.004227
IL10RA	GO:004592	positive regulation of phosphate metabolic proce	5.11E-05	0.06763	0.004227
NCKAP1L	GO:001050	(positive regulation of phosphorus metabolic proc	5.11E-05	0.06763	0.004227
SFRP2	GO:004249	gamma-delta T cell differentiation	5.79E-05	0.07661	0.004506
GPR116	GO:190300	positive regulation of leukocyte cell-cell adhesio	7.14E-05	0.09448	0.005249
GNG2	GO:000722	integrin-mediated signaling pathway	9.93E-05	0.1313	0.006912
ITGA6	GO:000252	leukocyte differentiation	0.000118	0.1554	0.007772
	GO:004664	gamma-delta T cell activation	0.000134	0.177	0.008044
	GO:003362	positive regulation of cell adhesion mediated by i	0.000134	0.177	0.008044
	GO:004210	(positive regulation of T cell proliferation	0.000141	0.187	0.008129
	GO:009860	cell-cell adhesion	0.000225	0.2973	0.01205
	GO:000999	response to extracellular stimulus	0.000244	0.3229	0.01205
	GO:003018	B cell differentiation	0.000246	0.3249	0.01205
	GO:000177	cell activation	0.000252	0.3337	0.01205
	GO:004232	positive regulation of phosphorylation	0.000255	0.3373	0.01205
	GO:003210	(regulation of response to external stimulus	0.000271	0.3579	0.01216
	GO:190300	regulation of leukocyte cell-cell adhesion	0.000276	0.3649	0.01216
	GO:005080	positive regulation of cell activation	0.000318	0.4208	0.01294
	GO:005067	positive regulation of lymphocyte proliferation	0.000319	0.422	0.01294
	GO:003009	lymphocyte differentiation	0.000325	0.4299	0.01294
	GO:003294	positive regulation of mononuclear cell proliferat	0.000332	0.4398	0.01294
	GO:007060	positive regulation of leukocyte proliferation	0.000375	0.4961	0.01388
	GO:004555	regulation of B cell differentiation	0.000378	0.4997	0.01388
	GO:004308	positive regulation of catalytic activity	0.000443	0.5865	0.01585
	GO:003080	cortical actin cytoskeleton organization	0.000458	0.6055	0.01593
	GO:005124	positive regulation of multicellular organismal pi	0.000482	0.6381	0.01636

GO:003410	homotypic cell-cell adhesion	0.000515	0.6811	0.01703
GO:003030	regulation of cell migration	0.000551	0.7283	0.01776
GO:004210	regulation of T cell proliferation	0.00058	0.7676	0.01785
GO:200120	regulation of extrinsic apoptotic signaling pathway	0.00058	0.7676	0.01785
GO:003080	positive regulation of B cell proliferation	0.00064	0.8469	0.01896
GO:004580	regulation of protein kinase activity	0.000671	0.8882	0.01896
GO:003080	cortical cytoskeleton organization	0.000673	0.8909	0.01896
GO:003360	regulation of cell adhesion mediated by integrin	0.000673	0.8909	0.01896
GO:200010	regulation of cell motility	0.000745	0.9859	0.0202
GO:004000	locomotion	0.00076	1	0.0202
GO:003140	positive regulation of protein modification process	0.000763	1	0.0202
GO:001920	regulation of phosphate metabolic process	0.000818	1	0.02046
GO:005110	regulation of phosphorus metabolic process	0.000855	1	0.02046
GO:199070	clathrin-dependent extracellular exosome endocytosis	0.000967	1	0.02046
GO:001090	regulation of inositol-polyphosphate 5-phosphatase activity	0.000967	1	0.02046
GO:003280	positive regulation of epinephrine secretion	0.000967	1	0.02046
GO:000690	induction by virus of host cell-cell fusion	0.000967	1	0.02046
GO:006110	negative regulation of dermatome development	0.000967	1	0.02046
GO:003080	phospholipase C-inhibiting G protein-coupled receptor signaling pathway	0.000967	1	0.02046
GO:004330	positive regulation of CD8-positive, alpha-beta T cell activation	0.000967	1	0.02046
GO:001090	positive regulation of inositol-polyphosphate 5-phosphatase activity	0.000967	1	0.02046
GO:006030	regulation of cell diameter	0.000967	1	0.02046
GO:003410	heterotypic cell-cell adhesion	0.000969	1	0.02046
GO:004350	regulation of kinase activity	0.000978	1	0.02046
GO:000750	response to nutrient	0.001004	1	0.02046
GO:004500	T cell selection	0.00101	1	0.02046
GO:001640	cell migration	0.001022	1	0.02046
GO:003160	cellular response to extracellular stimulus	0.001046	1	0.02046
GO:005070	negative regulation of peptidyl-tyrosine phosphorylation	0.001052	1	0.02046
GO:005120	regulation of cellular component movement	0.001075	1	0.02059
GO:004200	T cell proliferation	0.001089	1	0.02059
GO:004000	regulation of locomotion	0.001109	1	0.02067
GO:004580	positive regulation of protein kinase activity	0.00113	1	0.02077
GO:005060	regulation of lymphocyte proliferation	0.001179	1	0.02137
GO:003290	regulation of mononuclear cell proliferation	0.00121	1	0.02164
GO:004400	positive regulation of molecular function	0.001283	1	0.02264
GO:005080	positive regulation of T cell activation	0.001339	1	0.02329
GO:007060	regulation of leukocyte proliferation	0.001373	1	0.02329
GO:005080	antigen receptor-mediated signaling pathway	0.001373	1	0.02329
GO:003410	positive regulation of homotypic cell-cell adhesion	0.001424	1	0.02385
GO:003360	positive regulation of kinase activity	0.001444	1	0.02387
GO:003080	regulation of B cell proliferation	0.001461	1	0.02387
GO:005070	regulation of peptidyl-tyrosine phosphorylation	0.001495	1	0.02412
GO:003020	T cell differentiation	0.001586	1	0.02454
GO:009000	regulation of anatomical structure size	0.00159	1	0.02454
GO:009710	extrinsic apoptotic signaling pathway	0.001623	1	0.02454
GO:000710	leukocyte cell-cell adhesion	0.001634	1	0.02454
GO:005080	regulation of cell activation	0.001656	1	0.02454
GO:004660	positive regulation of alpha-beta T cell activation	0.001664	1	0.02454
GO:005160	localization of cell	0.00167	1	0.02454
GO:004880	cell motility	0.00167	1	0.02454
GO:000190	positive regulation of protein phosphorylation	0.00175	1	0.02544
GO:005080	B cell receptor signaling pathway	0.00177	1	0.02546
GO:004210	B cell activation	0.001818	1	0.02556
GO:003530	helper T cell enhancement of adaptive immune response	0.001932	1	0.02556
GO:007050	protein secretion by platelet	0.001932	1	0.02556
GO:000330	cell-matrix adhesion involved in amoeboid cell migration	0.001932	1	0.02556
GO:004330	regulation of CD8-positive, alpha-beta T cell differentiation	0.001932	1	0.02556

GO:001092	negative regulation of inositol phosphate biosynt	0.001932	1	0.02556
GO:200047	regulation of hematopoietic stem cell migration	0.001932	1	0.02556
GO:200047	positive regulation of hematopoietic stem cell mi	0.001932	1	0.02556
GO:005133	regulation of transferase activity	0.002162	1	0.02798
GO:003166	response to nutrient levels	0.002168	1	0.02798
GO:190210	regulation of leukocyte differentiation	0.002205	1	0.02798
GO:004232	regulation of phosphorylation	0.002227	1	0.02798
GO:003227	positive regulation of cellular protein metabolic p	0.002242	1	0.02798
GO:004597	negative regulation of phosphate metabolic proce	0.002263	1	0.02798
GO:001056	negative regulation of phosphorus metabolic pro	0.002263	1	0.02798
GO:004858	negative regulation of response to stimulus	0.002288	1	0.02803
GO:007149	cellular response to external stimulus	0.002564	1	0.03112
GO:004667	lymphocyte proliferation	0.002849	1	0.03276
GO:000257	leukotriene production involved in inflammatory	0.002897	1	0.03276
GO:200007	negative regulation of planar cell polarity pathwa	0.002897	1	0.03276
GO:000237	immunoglobulin biosynthetic process	0.002897	1	0.03276
GO:007037	actin polymerization-dependent cell motility	0.002897	1	0.03276
GO:200007	regulation of planar cell polarity pathway involv	0.002897	1	0.03276
GO:190497	regulation of midbrain dopaminergic neuron diff	0.002897	1	0.03276
GO:000867	lipopolysaccharide metabolic process	0.002897	1	0.03276
GO:003297	mononuclear cell proliferation	0.00293	1	0.03285
GO:005087	regulation of calcium-mediated signaling	0.003004	1	0.03312
GO:000287	positive regulation of adaptive immune response	0.003004	1	0.03312
GO:004667	regulation of alpha-beta T cell activation	0.003074	1	0.03355
GO:005127	positive regulation of protein metabolic process	0.003098	1	0.03355
GO:005127	positive regulation of lymphocyte activation	0.003125	1	0.03355
GO:004558	positive regulation of T cell differentiation	0.003144	1	0.03355
GO:003217	activation of protein kinase activity	0.003269	1	0.0346
GO:005137	positive regulation of transferase activity	0.003305	1	0.03471
GO:007067	leukocyte proliferation	0.003387	1	0.03528
GO:000287	positive regulation of adaptive immune response	0.003508	1	0.03626
GO:004210	B cell proliferation	0.003583	1	0.03635
GO:005087	positive regulation of B cell activation	0.003583	1	0.03635
GO:005087	regulation of T cell activation	0.003599	1	0.03635
GO:000247	immune response-activating cell surface receptor	0.003756	1	0.03649
GO:190327	positive regulation of leukocyte tethering or rolli	0.003861	1	0.03649
GO:000257	arachidonic acid metabolite production involved	0.003861	1	0.03649
GO:004267	negative regulation of mesodermal cell fate speci	0.003861	1	0.03649
GO:000697	negative regulation of cell adhesion involved in s	0.003861	1	0.03649
GO:006118	regulation of dermatome development	0.003861	1	0.03649
GO:006107	dermatome development	0.003861	1	0.03649
GO:005090	diapedesis	0.003861	1	0.03649
GO:007007	negative regulation of glucagon secretion	0.003861	1	0.03649
GO:000267	positive regulation of leukocyte activation	0.004049	1	0.03799
GO:004567	positive regulation of lymphocyte differentiation	0.00413	1	0.03822
GO:000647	protein dephosphorylation	0.004149	1	0.03822
GO:004667	lymphocyte activation	0.00416	1	0.03822
GO:003411	regulation of homotypic cell-cell adhesion	0.004286	1	0.0391
GO:003019	extracellular matrix organization	0.004496	1	0.04074
GO:004306	extracellular structure organization	0.004531	1	0.04078
GO:004340	regulation of MAP kinase activity	0.004567	1	0.04082
GO:000197	negative regulation of T cell mediated cytotoxici	0.004824	1	0.04227
GO:006107	sclerotome development	0.004824	1	0.04227
GO:009007	negative regulation of protein homodimerization	0.004824	1	0.04227
GO:000277	immune response-regulating cell surface receptor	0.004934	1	0.04294
GO:190370	regulation of hemopoiesis	0.005086	1	0.04397
GO:200127	negative regulation of extrinsic apoptotic signalin	0.00524	1	0.04502
GO:003257	regulation of cellular component size	0.005358	1	0.04573

	GO:001816	peptidyl-tyrosine phosphorylation	0.00568	1	0.04584
	GO:005090	leukocyte migration	0.005721	1	0.04584
	GO:001821	peptidyl-tyrosine modification	0.005762	1	0.04584
	GO:003362	positive regulation of integrin activation	0.005786	1	0.04584
	GO:000292	positive regulation of humoral immune response	0.005786	1	0.04584
	GO:004855	bone marrow development	0.005786	1	0.04584
	GO:003570	hematopoietic stem cell migration	0.005786	1	0.04584
	GO:001057	positive regulation of platelet activation	0.005786	1	0.04584
	GO:190469	midbrain morphogenesis	0.005786	1	0.04584
	GO:003550	negative regulation of myosin-light-chain-phosph	0.005786	1	0.04584
	GO:200130	lipoxin metabolic process	0.005786	1	0.04584
	GO:190499	positive regulation of leukocyte adhesion to vasc	0.005786	1	0.04584
	GO:003139	regulation of protein modification process	0.006036	1	0.04753
	GO:000170	formation of primary germ layer	0.006178	1	0.04836
	GO:200122	regulation of apoptotic signaling pathway	0.006714	1	0.04902
	GO:000692	movement of cell or subcellular component	0.006726	1	0.04902
	GO:004480	multi-organism membrane fusion	0.006747	1	0.04902
	GO:000340	planar cell polarity pathway involved in axis elor	0.006747	1	0.04902
	GO:003960	membrane fusion involved in viral entry into hos	0.006747	1	0.04902
	GO:190435	regulation of dopaminergic neuron differentiatio	0.006747	1	0.04902
	GO:200000	negative regulation of non-canonical Wnt signali	0.006747	1	0.04902
	GO:001900	fusion of virus membrane with host plasma mem	0.006747	1	0.04902
	GO:004830	positive regulation of isotype switching to IgG is	0.006747	1	0.04902
	GO:200000	regulation of stem cell division	0.006747	1	0.04902
	GO:004260	regulation of mesodermal cell fate specification	0.006747	1	0.04902
	GO:200118	positive regulation of CD8-positive, alpha-beta T	0.006747	1	0.04902
	GO:000268	positive regulation of leukocyte migration	0.006774	1	0.04902
	GO:002300	negative regulation of signaling	0.006781	1	0.04902
Cluster 5	ID	Name	p-value	q-value Bo	q-value FD
OLR1	GO:000232	B cell proliferation involved in immune response	0.003486	0.5159	0.4597
TMEM200	GO:000931	oligosaccharide biosynthetic process	0.00904	1	0.4597
MPHOSPF	GO:003558	G protein-coupled purinergic nucleotide receptor	0.009732	1	0.4597
ZNF107	GO:003559	purinergic nucleotide receptor signaling pathway	0.01525	1	0.4597
CRYGS	GO:003558	G protein-coupled purinergic receptor signaling p	0.01594	1	0.4597
SNRPA1	GO:003558	purinergic receptor signaling pathway	0.02143	1	0.4597
FP6628	GO:001010	response to X-ray	0.0228	1	0.4597
RPS20P27	GO:000178	B cell homeostasis	0.02485	1	0.4597
KIAA1147	GO:000238	immunoglobulin production involved in immuno	0.03638	1	0.5149
B3GALT2	GO:000231	B cell activation involved in immune response	0.04445	1	0.5149
IKBIP	GO:000931	oligosaccharide metabolic process	0.04579	1	0.5149
GPR34	GO:009050	RNA phosphodiester bond hydrolysis, endonucle	0.04646	1	0.5149
RNASE2					
GAPT					
TMTC2					

q-value FDR B&Y

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q-value FDR B&Y

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q-value FDR B&Y

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q-value FDR B&Y

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