

Supplementary Table 5

10 day old NOD vs. NOD.B10 islets: GO terms associated with differentially changed genes (FDR q-value < 0.05)

10 day old NOD islets: GO terms associated with genes upregulated by ≥3-fold

GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)*
GO:0031045	dense core granule	2.41E-06	1.56E-03	14.00 (15592,17,393,6)
GO:0030425	dendrite	2.23E-06	2.16E-03	2.58 (15592,462,393,30)
GO:0044297	cell body	9.46E-06	3.66E-03	2.21 (15592,627,393,35)
GO:0043005	neuron projection	1.93E-06	3.74E-03	1.96 (15592,1075,393,53)
GO:0120025	plasma membrane bounded cell projection	8.17E-06	3.95E-03	1.72 (15592,1524,393,66)
GO:0097458	neuron part	1.31E-05	4.24E-03	1.65 (15592,1704,393,71)
GO:0045202	synapse	2.78E-05	7.68E-03	1.89 (15592,943,393,45)
GO:0032940	secretion by cell	7.14E-06	1.54E-02	2.77 (15592,344,393,24)
GO:0046887	positive regulation of hormone secretion	6.44E-06	1.62E-02	3.94 (15592,151,393,15)
GO:0044463	cell projection part	7.53E-05	1.62E-02	1.68 (15592,1319,393,56)
GO:0023061	signal release	1.08E-06	1.63E-02	4.54 (15592,131,393,15)
GO:0032024	positive regulation of insulin secretion	5.65E-06	1.71E-02	5.39 (15592,81,393,11)
GO:0090277	positive regulation of peptide hormone secretion	3.56E-06	1.79E-02	4.73 (15592,109,393,13)
GO:0051648	vesicle localization	9.47E-06	1.79E-02	4.33 (15592,119,393,13)
GO:0120038	plasma membrane bounded cell projection part	7.53E-05	1.82E-02	1.68 (15592,1319,393,56)
GO:0010817	regulation of hormone levels	5.01E-06	1.89E-02	2.47 (15592,481,393,30)
GO:0009914	hormone transport	1.14E-05	1.91E-02	5.02 (15592,87,393,11)
GO:0051650	establishment of vesicle localization	2.59E-06	1.96E-02	4.87 (15592,106,393,13)
GO:0090276	regulation of peptide hormone secretion	1.57E-05	1.97E-02	3.32 (15592,203,393,17)
GO:0030072	peptide hormone secretion	1.54E-05	2.12E-02	6.05 (15592,59,393,9)
GO:0046883	regulation of hormone secretion	1.85E-05	2.16E-02	2.93 (15592,271,393,20)
GO:0051179	localization	1.54E-05	2.32E-02	1.41 (15592,3393,393,121)
GO:0050796	regulation of insulin secretion	2.17E-05	2.34E-02	3.56 (15592,167,393,15)
GO:0042995	cell projection	1.24E-04	2.40E-02	1.55 (15592,1794,393,70)
GO:0034448	EGO complex	1.53E-04	2.69E-02	23.80 (15592,5,393,3)
GO:0042026	protein refolding	2.91E-05	2.93E-02	9.52 (15592,25,393,6)
GO:0046879	hormone secretion	3.52E-05	3.13E-02	4.90 (15592,81,393,10)
GO:0006810	transport	3.37E-05	3.18E-02	1.45 (15592,2821,393,103)
GO:0051234	establishment of localization	4.28E-05	3.60E-02	1.43 (15592,2941,393,106)
GO:0030073	insulin secretion	5.57E-05	3.83E-02	6.94 (15592,40,393,7)
GO:0010970	transport along microtubule	5.40E-05	3.89E-02	3.68 (15592,140,393,13)
GO:0099111	microtubule-based transport	5.40E-05	4.08E-02	3.68 (15592,140,393,13)
GO:0046903	secretion	5.18E-05	4.12E-02	2.35 (15592,439,393,26)
GO:0099523	presynaptic cytosol	2.84E-04	4.58E-02	8.27 (15592,24,393,5)
GO:0043025	neuronal cell body	3.10E-04	4.62E-02	2.03 (15592,546,393,28)

10 day old NOD islets: GO terms associated with genes upregulated by ≥3-fold

GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)*
GO:0031012	extracellular matrix	2.78E-29	5.39E-26	8.03 (15592,415,220,47)
GO:0062023	collagen-containing extracellular matrix	2.34E-26	2.26E-23	8.75 (15592,324,220,40)
GO:0005201	extracellular matrix structural constituent	5.22E-22	2.30E-18	14.17 (15592,125,220,25)
GO:0044421	extracellular region part	1.90E-20	1.23E-17	3.43 (15592,1407,220,68)
GO:0005576	extracellular region	6.81E-20	3.29E-17	3.59 (15592,1243,220,63)
GO:0005615	extracellular space	3.02E-18	1.17E-15	3.59 (15592,1144,220,58)
GO:0009653	anatomical structure morphogenesis	8.80E-20	1.33E-15	3.52 (15592,1288,220,64)
GO:0007155	cell adhesion	8.50E-15	6.42E-11	4.31 (15592,642,220,39)
GO:0022610	biological adhesion	1.34E-14	6.74E-11	4.25 (15592,651,220,39)
GO:0050793	regulation of developmental process	1.88E-14	7.09E-11	2.39 (15592,2314,220,78)
GO:0048869	cellular developmental process	6.70E-14	1.45E-10	2.30 (15592,2470,220,80)
GO:0051239	regulation of multicellular organismal process	6.01E-14	1.51E-10	2.21 (15592,2724,220,85)
GO:0045595	regulation of cell differentiation	5.85E-14	1.77E-10	2.71 (15592,1645,220,63)
GO:0030198	extracellular matrix organization	1.15E-13	2.17E-10	7.68 (15592,203,220,22)
GO:0032502	developmental process	1.31E-13	2.19E-10	1.89 (15592,4054,220,108)
GO:0048856	anatomical structure development	2.33E-13	3.53E-10	2.14 (15592,2842,220,86)
GO:2000026	regulation of multicellular organismal development	3.77E-13	5.18E-10	2.52 (15592,1854,220,66)
GO:0048729	tissue morphogenesis	5.46E-13	6.88E-10	5.29 (15592,375,220,28)
GO:0048513	animal organ development	6.18E-13	7.18E-10	3.10 (15592,1119,220,49)
GO:0045596	negative regulation of cell differentiation	1.04E-12	1.12E-09	3.88 (15592,675,220,37)
GO:0043062	extracellular structure organization	1.62E-12	1.63E-09	6.75 (15592,231,220,22)
GO:0051093	negative regulation of developmental process	1.97E-12	1.86E-09	3.34 (15592,913,220,43)
GO:0030154	cell differentiation	8.61E-12	7.65E-09	2.45 (15592,1791,220,62)
GO:0007166	cell surface receptor signaling pathway	1.00E-11	8.43E-09	2.79 (15592,1294,220,51)
GO:0051241	negative regulation of multicellular organismal process	1.97E-11	1.57E-08	2.91 (15592,1145,220,47)
GO:0009887	animal organ morphogenesis	3.45E-11	2.60E-08	4.30 (15592,478,220,29)
GO:0030199	collagen fibril organization	3.83E-11	2.76E-08	16.59 (15592,47,220,11)
GO:0005198	structural molecule activity	1.49E-11	3.29E-08	4.17 (15592,527,220,31)
GO:0005581	collagen trimer	2.39E-10	7.71E-08	12.15 (15592,70,220,12)
GO:0090287	regulation of cellular response to growth factor stimulus	2.64E-10	1.81E-07	5.81 (15592,244,220,20)
GO:0060411	cardiac septum morphogenesis	2.84E-10	1.87E-07	11.98 (15592,71,220,12)
GO:0048646	anatomical structure formation involved in morphogenesis	4.38E-10	2.76E-07	3.45 (15592,677,220,33)
GO:0044420	extracellular matrix component	1.04E-09	2.89E-07	14.77 (15592,48,220,10)
GO:0009986	cell surface	2.50E-09	6.04E-07	3.58 (15592,574,220,29)
GO:0009888	tissue development	1.67E-09	9.72E-07	3.64 (15592,564,220,29)
GO:0060412	ventricular septum morphogenesis	1.66E-09	1.00E-06	17.24 (15592,37,220,9)
GO:0030510	regulation of BMP signaling pathway	2.82E-09	1.58E-06	9.89 (15592,86,220,12)
GO:0005604	basement membrane	1.15E-08	2.46E-06	8.77 (15592,97,220,12)
GO:0060415	muscle tissue morphogenesis	4.88E-09	2.64E-06	10.83 (15592,72,220,11)
GO:0090092	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	5.94E-09	3.09E-06	5.82 (15592,207,220,17)
GO:0032501	multicellular organismal process	6.26E-09	3.15E-06	1.83 (15592,3142,220,81)
GO:0019838	growth factor binding	7.63E-09	8.41E-06	7.30 (15592,136,220,14)
GO:0048598	embryonic morphogenesis	2.21E-08	1.08E-05	4.10 (15592,380,220,22)
GO:0005539	glycosaminoglycan binding	7.45E-09	1.09E-05	6.16 (15592,184,220,16)
GO:0010810	regulation of cell-substrate adhesion	2.45E-08	1.16E-05	5.67 (15592,200,220,16)
GO:0042127	regulation of cell proliferation	2.63E-08	1.21E-05	2.34 (15592,1426,220,47)

GO:0030020	extracellular matrix structural constituent conferring tensile strength	1.83E-08	1.35E-05	16.68 (15592,34,220,8)
GO:0048583	regulation of response to stimulus	3.10E-08	1.38E-05	1.78 (15592,3193,220,80)
GO:0005509	calcium ion binding	1.82E-08	1.60E-05	3.58 (15592,515,220,26)
GO:0007275	multicellular organism development	5.11E-08	2.09E-05	2.51 (15592,1128,220,40)
GO:0035295	tube development	4.92E-08	2.12E-05	5.81 (15592,183,220,15)
GO:0007167	enzyme linked receptor protein signaling pathway	5.11E-08	2.14E-05	3.76 (15592,433,220,23)
GO:0022603	regulation of anatomical structure morphogenesis	5.88E-08	2.34E-05	2.67 (15592,955,220,36)
GO:0009966	regulation of signal transduction	7.59E-08	2.94E-05	1.91 (15592,2409,220,65)
GO:0005102	signaling receptor binding	5.88E-08	3.70E-05	2.36 (15592,1320,220,44)
GO:2000145	regulation of cell motility	1.06E-07	3.99E-05	2.76 (15592,847,220,33)
GO:0006357	regulation of transcription by RNA polymerase II	1.35E-07	4.86E-05	2.12 (15592,1705,220,51)
GO:0030334	regulation of cell migration	1.34E-07	4.95E-05	2.79 (15592,813,220,32)
GO:0035239	tube morphogenesis	1.52E-07	5.33E-05	4.41 (15592,289,220,18)
GO:0060429	epithelium development	1.63E-07	5.60E-05	5.74 (15592,173,220,14)
GO:0090101	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	1.80E-07	6.03E-05	7.72 (15592,101,220,11)
GO:0048523	negative regulation of cellular process	2.02E-07	6.65E-05	1.62 (15592,3992,220,91)
GO:0051270	regulation of cellular component movement	2.25E-07	7.09E-05	2.62 (15592,919,220,34)
GO:0055008	cardiac muscle tissue morphogenesis	2.30E-07	7.10E-05	10.12 (15592,63,220,9)
GO:0040012	regulation of locomotion	2.25E-07	7.24E-05	2.62 (15592,919,220,34)
GO:0010646	regulation of cell communication	2.51E-07	7.59E-05	1.79 (15592,2767,220,70)
GO:0060284	regulation of cell development	2.59E-07	7.67E-05	2.56 (15592,969,220,35)
GO:2000027	regulation of animal organ morphogenesis	2.66E-07	7.74E-05	5.51 (15592,180,220,14)
GO:0090288	negative regulation of cellular response to growth factor stimulus	2.83E-07	8.07E-05	6.59 (15592,129,220,12)
GO:0023051	regulation of signaling	3.10E-07	8.69E-05	1.78 (15592,2782,220,70)
GO:1903707	negative regulation of hemopoiesis	4.64E-07	1.28E-04	6.30 (15592,135,220,12)
GO:0030155	regulation of cell adhesion	5.94E-07	1.60E-04	3.00 (15592,615,220,26)
GO:1902106	negative regulation of leukocyte differentiation	6.05E-07	1.60E-04	7.79 (15592,91,220,10)
GO:0001503	ossification	6.77E-07	1.76E-04	6.78 (15592,115,220,11)
GO:0048731	system development	8.26E-07	2.12E-04	2.87 (15592,667,220,27)
GO:0030021	extracellular matrix structural constituent conferring compression resistance	3.90E-07	2.15E-04	29.53 (15592,12,220,5)
GO:0010628	positive regulation of gene expression	9.97E-07	2.51E-04	2.02 (15592,1715,220,49)
GO:0005912	adherens junction	1.47E-06	2.85E-04	4.20 (15592,270,220,16)
GO:0010717	regulation of epithelial to mesenchymal transition	1.18E-06	2.88E-04	8.39 (15592,76,220,9)
GO:0051094	positive regulation of developmental process	1.17E-06	2.89E-04	2.20 (15592,1320,220,41)
GO:0032989	cellular component morphogenesis	1.25E-06	2.99E-04	3.25 (15592,480,220,22)
GO:0003179	heart valve morphogenesis	1.27E-06	3.00E-04	12.40 (15592,40,220,7)
GO:0048519	negative regulation of biological process	1.32E-06	3.06E-04	1.53 (15592,4404,220,95)
GO:0003184	pulmonary valve morphogenesis	1.43E-06	3.28E-04	23.62 (15592,15,220,5)
GO:0010468	regulation of gene expression	1.55E-06	3.49E-04	1.66 (15592,3194,220,75)
GO:1905330	regulation of morphogenesis of an epithelium	1.60E-06	3.55E-04	7.02 (15592,101,220,10)
GO:0097435	supramolecular fiber organization	1.66E-06	3.63E-04	3.58 (15592,376,220,19)
GO:0070161	anchoring junction	2.15E-06	3.79E-04	4.08 (15592,278,220,16)
GO:0008284	positive regulation of cell proliferation	1.84E-06	3.92E-04	2.57 (15592,826,220,30)
GO:0048704	embryonic skeletal system morphogenesis	1.83E-06	3.95E-04	7.97 (15592,80,220,9)
GO:0010721	negative regulation of cell development	2.00E-06	4.21E-04	3.70 (15592,345,220,18)
GO:0003180	aortic valve morphogenesis	2.06E-06	4.26E-04	22.15 (15592,16,220,5)
GO:0036075	replacement ossification	2.67E-06	5.38E-04	14.66 (15592,29,220,6)
GO:0001958	endochondral ossification	2.67E-06	5.45E-04	14.66 (15592,29,220,6)
GO:0007162	negative regulation of cell adhesion	3.14E-06	6.24E-04	4.20 (15592,253,220,15)
GO:0030324	lung development	3.38E-06	6.63E-04	7.42 (15592,86,220,9)
GO:0030178	negative regulation of Wnt signaling pathway	3.57E-06	6.93E-04	5.73 (15592,136,220,11)
GO:0007389	pattern specification process	4.08E-06	7.71E-04	3.68 (15592,327,220,17)
GO:0048585	negative regulation of response to stimulus	4.14E-06	7.72E-04	2.09 (15592,1388,220,41)
GO:0016339	calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules	4.04E-06	7.73E-04	13.72 (15592,31,220,6)
GO:0030514	negative regulation of BMP signaling pathway	4.56E-06	8.01E-04	10.34 (15592,48,220,7)
GO:0048518	positive regulation of biological process	4.45E-06	8.10E-04	1.45 (15592,5036,220,103)
GO:0008283	cell proliferation	4.56E-06	8.10E-04	3.10 (15592,480,220,21)
GO:0072073	kidney epithelium development	4.41E-06	8.13E-04	8.46 (15592,67,220,8)
GO:0009719	response to endogenous stimulus	4.54E-06	8.17E-04	2.62 (15592,730,220,27)
GO:0009893	positive regulation of metabolic process	4.75E-06	8.25E-04	1.65 (15592,3050,220,71)
GO:0048705	skeletal system morphogenesis	4.83E-06	8.29E-04	6.22 (15592,114,220,10)
GO:0050839	cell adhesion molecule binding	1.71E-06	8.39E-04	4.72 (15592,210,220,14)
GO:0045665	negative regulation of neuron differentiation	5.22E-06	8.87E-04	4.30 (15592,231,220,14)
GO:0031328	positive regulation of cellular biosynthetic process	5.58E-06	9.37E-04	1.96 (15592,1663,220,46)
GO:0001656	metanephros development	5.94E-06	9.86E-04	12.89 (15592,33,220,6)
GO:0030279	negative regulation of ossification	6.16E-06	1.01E-03	8.10 (15592,70,220,8)
GO:0030335	positive regulation of cell migration	6.88E-06	1.12E-03	3.02 (15592,493,220,21)
GO:0048562	embryonic organ morphogenesis	7.10E-06	1.14E-03	5.96 (15592,119,220,10)
GO:0040017	positive regulation of locomotion	7.20E-06	1.15E-03	2.91 (15592,535,220,22)
GO:0006355	regulation of transcription, DNA-templated	7.50E-06	1.17E-03	1.75 (15592,2393,220,59)
GO:0016477	cell migration	7.47E-06	1.18E-03	2.61 (15592,706,220,26)
GO:0051240	positive regulation of multicellular organismal process	8.24E-06	1.26E-03	1.95 (15592,1635,220,45)
GO:1903506	regulation of nucleic acid-templated transcription	8.21E-06	1.27E-03	1.74 (15592,2400,220,59)
GO:0048522	positive regulation of cellular process	8.42E-06	1.27E-03	1.47 (15592,4519,220,94)
GO:0051173	positive regulation of nitrogen compound metabolic process	8.84E-06	1.32E-03	1.68 (15592,2692,220,64)
GO:0003181	atrioventricular valve morphogenesis	9.04E-06	1.33E-03	16.87 (15592,21,220,5)
GO:2001141	regulation of RNA biosynthetic process	9.23E-06	1.33E-03	1.74 (15592,2409,220,59)
GO:0031325	positive regulation of cellular metabolic process	9.36E-06	1.33E-03	1.66 (15592,2813,220,66)
GO:0010604	positive regulation of macromolecule metabolic process	9.03E-06	1.34E-03	1.66 (15592,2810,220,66)
GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	9.20E-06	1.34E-03	5.20 (15592,150,220,11)
GO:0009891	positive regulation of biosynthetic process	9.51E-06	1.34E-03	1.92 (15592,1697,220,46)
GO:0045893	positive regulation of transcription, DNA-templated	9.96E-06	1.38E-03	2.07 (15592,1337,220,39)
GO:2000147	positive regulation of cell motility	9.92E-06	1.39E-03	2.95 (15592,505,220,21)
GO:1903508	positive regulation of nucleic acid-templated transcription	1.05E-05	1.44E-03	2.06 (15592,1340,220,39)
GO:1902680	positive regulation of RNA biosynthetic process	1.07E-05	1.45E-03	2.06 (15592,1341,220,39)
GO:0072300	positive regulation of metanephric glomerulus development	1.10E-05	1.48E-03	53.15 (15592,4,220,3)
GO:0019222	regulation of metabolic process	1.11E-05	1.48E-03	1.43 (15592,5000,220,101)
GO:0019220	regulation of phosphate metabolic process	1.16E-05	1.54E-03	1.98 (15592,1500,220,42)
GO:0051174	regulation of phosphorus metabolic process	1.18E-05	1.56E-03	1.98 (15592,1501,220,42)
GO:0001932	regulation of protein phosphorylation	1.20E-05	1.56E-03	2.10 (15592,1247,220,37)
GO:0008201	heparin binding	3.84E-06	1.69E-03	5.69 (15592,137,220,11)
GO:0033627	cell adhesion mediated by integrin	1.46E-05	1.89E-03	15.41 (15592,23,220,5)
GO:0005583	fibrillar collagen trimer	1.18E-05	1.90E-03	25.77 (15592,11,220,4)

GO:0051272	positive regulation of cellular component movement	1.54E-05	1.97E-03	2.86 (15592,520,220,21)
GO:0008285	negative regulation of cell proliferation	1.62E-05	2.05E-03	2.69 (15592,606,220,23)
GO:0045581	negative regulation of T cell differentiation	1.63E-05	2.05E-03	10.90 (15592,39,220,6)
GO:0031345	negative regulation of cell projection organization	1.65E-05	2.06E-03	4.48 (15592,190,220,12)
GO:0060255	regulation of macromolecule metabolic process	1.68E-05	2.08E-03	1.45 (15592,4590,220,94)
GO:0090179	planar cell polarity pathway involved in neural tube closure	1.75E-05	2.13E-03	23.62 (15592,12,220,4)
GO:0030278	regulation of ossification	1.74E-05	2.14E-03	4.45 (15592,191,220,12)
GO:0010977	negative regulation of neuron projection development	1.80E-05	2.17E-03	4.84 (15592,161,220,11)
GO:0060071	Wnt signaling pathway, planar cell polarity pathway	1.83E-05	2.19E-03	14.77 (15592,24,220,5)
GO:0030512	negative regulation of transforming growth factor beta receptor signaling pathway	1.85E-05	2.20E-03	8.41 (15592,59,220,7)
GO:0043393	regulation of protein binding	1.90E-05	2.24E-03	4.09 (15592,225,220,13)
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	1.98E-05	2.32E-03	3.60 (15592,295,220,15)
GO:0048754	branching morphogenesis of an epithelial tube	2.16E-05	2.51E-03	5.25 (15592,135,220,10)
GO:0051960	regulation of nervous system development	2.19E-05	2.53E-03	2.27 (15592,937,220,30)
GO:0050789	regulation of biological process	2.23E-05	2.55E-03	1.25 (15592,8652,220,152)
GO:0030111	regulation of Wnt signaling pathway	2.27E-05	2.58E-03	3.77 (15592,263,220,14)
GO:1903845	negative regulation of cellular response to transforming growth factor beta stimulus	2.31E-05	2.61E-03	8.13 (15592,61,220,7)
GO:0009968	negative regulation of signal transduction	2.40E-05	2.69E-03	2.18 (15592,1038,220,32)
GO:0016342	catenin complex	1.83E-05	2.72E-03	14.77 (15592,24,220,5)
GO:0050767	regulation of neurogenesis	2.61E-05	2.87E-03	2.33 (15592,851,220,28)
GO:0030545	receptor regulator activity	7.16E-06	2.87E-03	3.37 (15592,378,220,18)
GO:0017147	Wnt-protein binding	8.50E-06	2.88E-03	12.15 (15592,35,220,6)
GO:0050768	negative regulation of neurogenesis	2.60E-05	2.89E-03	3.52 (15592,302,220,15)
GO:0003700	DNA-binding transcription factor activity	7.86E-06	2.89E-03	2.49 (15592,797,220,28)
GO:0072298	regulation of metanephric glomerulus development	2.71E-05	2.97E-03	42.52 (15592,5,220,3)
GO:0003002	regionalization	2.74E-05	2.98E-03	3.95 (15592,233,220,13)
GO:0000902	cell morphogenesis	2.87E-05	3.09E-03	3.94 (15592,234,220,13)
GO:0045668	negative regulation of osteoblast differentiation	2.91E-05	3.11E-03	9.89 (15592,43,220,6)
GO:0045995	regulation of embryonic development	3.16E-05	3.36E-03	5.64 (15592,113,220,9)
GO:0001657	ureteric bud development	3.32E-05	3.51E-03	9.66 (15592,44,220,6)
GO:0048018	receptor ligand activity	1.12E-05	3.53E-03	3.41 (15592,353,220,17)
GO:0045667	regulation of osteoblast differentiation	3.38E-05	3.55E-03	5.60 (15592,114,220,9)
GO:0042325	regulation of phosphorylation	3.44E-05	3.58E-03	1.98 (15592,1360,220,38)
GO:0090178	regulation of establishment of planar polarity involved in neural tube closure	3.46E-05	3.58E-03	20.25 (15592,14,220,4)
GO:0050730	regulation of peptidyl-tyrosine phosphorylation	3.57E-05	3.65E-03	3.86 (15592,239,220,13)
GO:0010557	positive regulation of macromolecule biosynthetic process	3.56E-05	3.66E-03	1.89 (15592,1572,220,42)
GO:0045165	cell fate commitment	3.77E-05	3.83E-03	4.92 (15592,144,220,10)
GO:0048870	cell motility	4.17E-05	4.20E-03	2.36 (15592,780,220,26)
GO:0045620	negative regulation of lymphocyte differentiation	4.31E-05	4.28E-03	9.24 (15592,46,220,6)
GO:0051254	positive regulation of RNA metabolic process	4.29E-05	4.29E-03	1.94 (15592,1426,220,39)
GO:0045664	regulation of neuron differentiation	4.41E-05	4.35E-03	2.46 (15592,691,220,24)
GO:0032963	collagen metabolic process	4.88E-05	4.79E-03	9.05 (15592,47,220,6)
GO:0045937	positive regulation of phosphate metabolic process	5.05E-05	4.90E-03	2.17 (15592,980,220,30)
GO:0010562	positive regulation of phosphorus metabolic process	5.05E-05	4.93E-03	2.17 (15592,980,220,30)
GO:0048407	platelet-derived growth factor binding	1.75E-05	5.13E-03	23.62 (15592,12,220,4)
GO:0032808	lacrimal gland development	5.37E-05	5.17E-03	35.44 (15592,6,220,3)
GO:0010811	positive regulation of cell-substrate adhesion	5.42E-05	5.18E-03	5.27 (15592,121,220,9)
GO:0072164	mesonephric tubule development	5.51E-05	5.24E-03	8.86 (15592,48,220,6)
GO:0098609	cell-cell adhesion	5.63E-05	5.25E-03	3.29 (15592,323,220,15)
GO:0016055	Wnt signaling pathway	5.57E-05	5.26E-03	3.96 (15592,215,220,12)
GO:0048468	cell development	5.63E-05	5.28E-03	2.55 (15592,612,220,22)
GO:0034329	cell junction assembly	5.78E-05	5.36E-03	5.23 (15592,122,220,9)
GO:0045935	positive regulation of nucleobase-containing compound metabolic process	5.84E-05	5.39E-03	1.85 (15592,1606,220,42)
GO:0061138	morphogenesis of a branching epithelium	5.98E-05	5.44E-03	4.66 (15592,152,220,11)
GO:0010648	negative regulation of cell communication	5.96E-05	5.46E-03	2.06 (15592,1138,220,33)
GO:0051961	negative regulation of nervous system development	6.04E-05	5.47E-03	3.27 (15592,325,220,15)
GO:0072163	mesonephric epithelium development	6.21E-05	5.59E-03	8.68 (15592,49,220,6)
GO:0017015	regulation of transforming growth factor beta receptor signaling pathway	6.32E-05	5.65E-03	5.91 (15592,96,220,8)
GO:0023057	negative regulation of signaling	6.49E-05	5.77E-03	2.05 (15592,1143,220,33)
GO:0060070	canonical Wnt signaling pathway	6.85E-05	6.02E-03	6.89 (15592,72,220,7)
GO:0040011	locomotion	6.83E-05	6.04E-03	2.25 (15592,851,220,27)
GO:0001822	kidney development	6.98E-05	6.10E-03	5.10 (15592,125,220,9)
GO:1905114	cell surface receptor signaling pathway involved in cell-cell signaling	7.27E-05	6.27E-03	3.85 (15592,221,220,12)
GO:0006928	movement of cell or subcellular component	7.23E-05	6.28E-03	2.06 (15592,1099,220,32)
GO:1903844	regulation of cellular response to transforming growth factor beta stimulus	7.32E-05	6.29E-03	5.79 (15592,98,220,8)
GO:0002009	morphogenesis of an epithelium	7.37E-05	6.29E-03	3.39 (15592,293,220,14)
GO:0051098	regulation of binding	7.43E-05	6.31E-03	3.06 (15592,370,220,16)
GO:0045944	positive regulation of transcription by RNA polymerase II	7.49E-05	6.32E-03	2.09 (15592,1051,220,31)
GO:0048701	embryonic cranial skeleton morphogenesis	7.89E-05	6.55E-03	11.07 (15592,32,220,5)
GO:0003151	outflow tract morphogenesis	7.81E-05	6.56E-03	8.34 (15592,51,220,6)
GO:0060351	cartilage development involved in endochondral bone morphogenesis	7.95E-05	6.56E-03	16.68 (15592,17,220,4)
GO:0048514	blood vessel morphogenesis	7.87E-05	6.57E-03	5.73 (15592,99,220,8)
GO:0065009	regulation of molecular function	8.07E-05	6.62E-03	1.69 (15592,2185,220,52)
GO:0007417	central nervous system development	8.90E-05	7.27E-03	6.61 (15592,75,220,7)
GO:0001763	morphogenesis of a branching structure	9.19E-05	7.47E-03	4.43 (15592,160,220,10)
GO:0001934	positive regulation of protein phosphorylation	9.52E-05	7.69E-03	2.20 (15592,868,220,27)
GO:0007219	Notch signaling pathway	9.72E-05	7.82E-03	5.56 (15592,102,220,8)
GO:0045597	positive regulation of cell differentiation	9.79E-05	7.83E-03	2.13 (15592,967,220,29)
GO:0051171	regulation of nitrogen compound metabolic process	1.01E-04	8.01E-03	1.42 (15592,4401,220,88)
GO:1905276	regulation of epithelial tube formation	1.01E-04	8.04E-03	15.75 (15592,18,220,4)
GO:0031323	regulation of cellular metabolic process	1.05E-04	8.27E-03	1.40 (15592,4664,220,92)
GO:0035567	non-canonical Wnt signaling pathway	1.07E-04	8.34E-03	10.42 (15592,34,220,5)
GO:0042733	embryonic digit morphogenesis	1.08E-04	8.43E-03	7.87 (15592,54,220,6)
GO:1901342	regulation of vasculature development	1.13E-04	8.74E-03	3.25 (15592,305,220,14)
GO:0051252	regulation of RNA metabolic process	1.16E-04	8.88E-03	1.59 (15592,2623,220,59)
GO:0007507	heart development	1.15E-04	8.89E-03	3.67 (15592,232,220,12)
GO:0031401	positive regulation of protein modification process	1.17E-04	8.93E-03	2.04 (15592,1077,220,31)
GO:0090090	negative regulation of canonical Wnt signaling pathway	1.27E-04	9.54E-03	5.35 (15592,106,220,8)
GO:0010629	negative regulation of gene expression	1.27E-04	9.55E-03	1.88 (15592,1393,220,37)
GO:0072215	regulation of metanephros development	1.27E-04	9.56E-03	14.92 (15592,19,220,4)
GO:0070208	protein heterotrimerization	1.27E-04	9.61E-03	14.92 (15592,19,220,4)
GO:0060828	regulation of canonical Wnt signaling pathway	1.30E-04	9.65E-03	3.90 (15592,200,220,11)
GO:0030241	skeletal muscle myosin thick filament assembly	1.47E-04	1.08E-02	26.58 (15592,8,220,3)

GO:0048539	bone marrow development	1.47E-04	1.08E-02	26.58 (15592.8,220.3)
GO:0010812	negative regulation of cell-substrate adhesion	1.47E-04	1.09E-02	7.46 (15592.57,220.6)
GO:0071688	striated muscle myosin thick filament assembly	1.47E-04	1.09E-02	26.58 (15592.8,220.3)
GO:0097485	neuron projection guidance	1.52E-04	1.10E-02	4.17 (15592.170,220.10)
GO:0065007	biological regulation	1.53E-04	1.11E-02	1.20 (15592.9126,220.155)
GO:1903706	regulation of hemopoiesis	1.56E-04	1.12E-02	3.00 (15592.354,220.15)
GO:0044331	cell-cell adhesion mediated by cadherin	1.56E-04	1.12E-02	14.17 (15592.20,220.4)
GO:0031399	regulation of protein modification process	1.59E-04	1.13E-02	1.81 (15592.1570,220.40)
GO:0090175	regulation of establishment of planar polarity	1.61E-04	1.14E-02	9.58 (15592.37,220.5)
GO:0008083	growth factor activity	4.16E-05	1.15E-02	5.45 (15592.117,220.9)
GO:0019219	regulation of nucleobase-containing compound metabolic process	1.71E-04	1.21E-02	1.54 (15592.2899,220.63)
GO:0071495	cellular response to endogenous stimulus	1.77E-04	1.24E-02	2.56 (15592.527,220.19)
GO:2000112	regulation of cellular macromolecule biosynthetic process	1.82E-04	1.27E-02	1.55 (15592.2785,220.61)
GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	1.84E-04	1.27E-02	4.07 (15592.174,220.10)
GO:0045892	negative regulation of transcription, DNA-templated	1.84E-04	1.27E-02	2.05 (15592.1003,220.29)
GO:0007267	cell-cell signaling	1.83E-04	1.28E-02	3.28 (15592.281,220.13)
GO:0008347	glial cell migration	1.91E-04	1.31E-02	13.50 (15592.21,220.4)
GO:0046639	negative regulation of alpha-beta T cell differentiation	1.91E-04	1.31E-02	13.50 (15592.21,220.4)
GO:0051216	cartilage development	1.97E-04	1.33E-02	5.84 (15592.85,220.7)
GO:1903507	negative regulation of nucleic acid-templated transcription	1.96E-04	1.34E-02	2.04 (15592.1007,220.29)
GO:0097156	fasciculation of motor neuron axon	1.98E-04	1.34E-02	70.87 (15592.2,220.2)
GO:1902679	negative regulation of RNA biosynthetic process	2.00E-04	1.34E-02	2.04 (15592.1008,220.29)
GO:0002683	negative regulation of immune system process	2.05E-04	1.37E-02	2.81 (15592.404,220.16)
GO:0070051	fibrinogen binding	5.37E-05	1.39E-02	35.44 (15592.6,220.3)
GO:0031033	myosin filament organization	2.19E-04	1.42E-02	23.62 (15592.9,220.3)
GO:0060348	bone development	2.14E-04	1.43E-02	6.97 (15592.61,220.6)
GO:0001817	regulation of cytokine production	2.15E-04	1.43E-02	2.44 (15592.580,220.20)
GO:0040008	regulation of growth	2.17E-04	1.43E-02	2.38 (15592.626,220.21)
GO:0045785	positive regulation of cell adhesion	2.18E-04	1.43E-02	2.91 (15592.365,220.15)
GO:0031034	myosin filament assembly	2.19E-04	1.43E-02	23.62 (15592.9,220.3)
GO:1901681	sulfur compound binding	5.83E-05	1.43E-02	3.94 (15592.216,220.12)
GO:0010556	regulation of macromolecule biosynthetic process	2.26E-04	1.47E-02	1.53 (15592.2867,220.62)
GO:0007165	signal transduction	2.31E-04	1.49E-02	1.50 (15592.3112,220.66)
GO:0042327	positive regulation of phosphorylation	2.33E-04	1.50E-02	2.09 (15592.917,220.27)
GO:0046872	metal ion binding	6.48E-05	1.50E-02	1.56 (15592.3045,220.67)
GO:0007156	homophilic cell adhesion via plasma membrane adhesion molecules	2.44E-04	1.56E-02	5.64 (15592.88,220.7)
GO:0023052	signaling	2.55E-04	1.63E-02	3.01 (15592.330,220.14)
GO:0034332	adherens junction organization	2.56E-04	1.63E-02	6.75 (15592.63,220.6)
GO:0043169	cation binding	7.39E-05	1.63E-02	1.55 (15592.3118,220.68)
GO:0031326	regulation of cellular biosynthetic process	2.64E-04	1.67E-02	1.51 (15592.3004,220.64)
GO:0048568	embryonic organ development	2.66E-04	1.68E-02	4.28 (15592.149,220.9)
GO:0033002	muscle cell proliferation	2.77E-04	1.73E-02	12.33 (15592.23,220.4)
GO:0071230	cellular response to amino acid stimulus	2.79E-04	1.74E-02	6.64 (15592.64,220.6)
GO:0010975	regulation of neuron projection development	2.83E-04	1.76E-02	2.46 (15592.547,220.19)
GO:0080090	regulation of primary metabolic process	2.89E-04	1.79E-02	1.38 (15592.4526,220.88)
GO:0004714	transmembrane receptor protein tyrosine kinase activity	8.73E-05	1.83E-02	8.18 (15592.52,220.6)
GO:0060742	epithelial cell differentiation involved in prostate gland development	3.09E-04	1.87E-02	21.26 (15592.10,220.3)
GO:0010605	negative regulation of macromolecule metabolic process	3.04E-04	1.88E-02	1.63 (15592.2128,220.49)
GO:0003149	membranous septum morphogenesis	3.09E-04	1.88E-02	21.26 (15592.10,220.3)
GO:0072216	positive regulation of metanephros development	3.09E-04	1.88E-02	21.26 (15592.10,220.3)
GO:0010838	positive regulation of keratinocyte proliferation	3.09E-04	1.89E-02	21.26 (15592.10,220.3)
GO:0009952	anterior/posterior pattern specification	3.09E-04	1.90E-02	4.20 (15592.152,220.9)
GO:0010771	negative regulation of cell morphogenesis involved in differentiation	3.21E-04	1.93E-02	5.39 (15592.92,220.7)
GO:0051781	positive regulation of cell division	3.31E-04	1.98E-02	6.44 (15592.66,220.6)
GO:0035108	limb morphogenesis	3.43E-04	2.04E-02	5.33 (15592.93,220.7)
GO:0035107	appendage morphogenesis	3.43E-04	2.05E-02	5.33 (15592.93,220.7)
GO:0055006	cardiac cell development	3.71E-04	2.20E-02	8.05 (15592.44,220.5)
GO:0000122	negative regulation of transcription by RNA polymerase II	3.87E-04	2.28E-02	2.18 (15592.749,220.23)
GO:0120163	negative regulation of cold-induced thermogenesis	4.12E-04	2.42E-02	7.87 (15592.45,220.5)
GO:0090193	positive regulation of glomerulus development	4.21E-04	2.45E-02	19.33 (15592.11,220.3)
GO:0097094	craniofacial suture morphogenesis	4.21E-04	2.46E-02	19.33 (15592.11,220.3)
GO:0120161	regulation of cold-induced thermogenesis	4.40E-04	2.56E-02	4.46 (15592.127,220.8)
GO:0000981	DNA-binding transcription factor activity, RNA polymerase II-specific	1.39E-04	2.79E-02	2.46 (15592.606,220.21)
GO:0009889	regulation of biosynthetic process	4.83E-04	2.80E-02	1.48 (15592.3069,220.64)
GO:0022408	negative regulation of cell-cell adhesion	4.93E-04	2.84E-02	3.94 (15592.162,220.9)
GO:0048638	regulation of developmental growth	5.03E-04	2.89E-02	2.81 (15592.353,220.14)
GO:0010769	regulation of cell morphogenesis involved in differentiation	5.17E-04	2.96E-02	2.94 (15592.313,220.13)
GO:0048762	mesenchymal cell differentiation	5.30E-04	3.01E-02	5.91 (15592.72,220.6)
GO:0045765	regulation of angiogenesis	5.30E-04	3.02E-02	3.10 (15592.274,220.12)
GO:0001501	skeletal system development	5.41E-04	3.06E-02	4.33 (15592.131,220.8)
GO:0051128	regulation of cellular component organization	5.48E-04	3.09E-02	1.57 (15592.2300,220.51)
GO:0030240	skeletal muscle thin filament assembly	5.55E-04	3.12E-02	17.72 (15592.12,220.3)
GO:0032879	regulation of localization	5.61E-04	3.14E-02	1.54 (15592.2480,220.54)
GO:0072091	regulation of stem cell proliferation	5.71E-04	3.18E-02	5.83 (15592.73,220.6)
GO:0060672	epithelial cell morphogenesis involved in placental branching	5.89E-04	3.23E-02	47.25 (15592.3,220.2)
GO:0097155	fasciculation of sensory neuron axon	5.89E-04	3.24E-02	47.25 (15592.3,220.2)
GO:0061144	alveolar secondary septum development	5.89E-04	3.25E-02	47.25 (15592.3,220.2)
GO:0003219	cardiac right ventricle formation	5.89E-04	3.26E-02	47.25 (15592.3,220.2)
GO:0034330	cell junction organization	5.88E-04	3.27E-02	3.84 (15592.166,220.9)
GO:0030856	regulation of epithelial cell differentiation	5.99E-04	3.27E-02	4.26 (15592.133,220.8)
GO:0003208	cardiac ventricle morphogenesis	6.05E-04	3.29E-02	10.12 (15592.28,220.4)
GO:0050794	regulation of cellular process	6.08E-04	3.30E-02	1.21 (15592.8140,220.139)
GO:0048584	positive regulation of response to stimulus	6.14E-04	3.30E-02	1.66 (15592.1790,220.42)
GO:0007411	axon guidance	6.14E-04	3.31E-02	3.82 (15592.167,220.9)
GO:0051129	negative regulation of cellular component organization	6.48E-04	3.47E-02	2.19 (15592.680,220.21)
GO:0005518	collagen binding	2.14E-04	3.63E-02	6.97 (15592.61,220.6)
GO:0051253	negative regulation of RNA metabolic process	6.97E-04	3.71E-02	1.89 (15592.1088,220.29)
GO:0090171	chondrocyte morphogenesis	7.14E-04	3.71E-02	16.36 (15592.13,220.3)
GO:0051172	negative regulation of nitrogen compound metabolic process	6.96E-04	3.72E-02	1.62 (15592.1973,220.45)
GO:0003429	growth plate cartilage chondrocyte morphogenesis	7.14E-04	3.72E-02	16.36 (15592.13,220.3)
GO:0005178	integrin binding	2.11E-04	3.72E-02	4.97 (15592.114,220.8)
GO:0003422	growth plate cartilage morphogenesis	7.14E-04	3.73E-02	16.36 (15592.13,220.3)
GO:0043200	response to amino acid	7.08E-04	3.75E-02	5.60 (15592.76,220.6)

GO:0003414	chondrocyte morphogenesis involved in endochondral bone morphogenesis	7.14E-04	3.75E-02	16.36 (15592,13,220,3)
GO:0061418	regulation of transcription from RNA polymerase II promoter in response to hypoxia	7.14E-04	3.76E-02	16.36 (15592,13,220,3)
GO:0005515	protein binding	2.05E-04	3.76E-02	1.25 (15592,7551,220,133)
GO:2000647	negative regulation of stem cell proliferation	7.14E-04	3.77E-02	16.36 (15592,13,220,3)
GO:0051302	regulation of cell division	7.28E-04	3.77E-02	4.14 (15592,137,220,8)
GO:0030617	transforming growth factor beta receptor, inhibitory cytoplasmic mediator activity	1.98E-04	3.80E-02	70.87 (15592,2,220,2)
GO:0090183	regulation of kidney development	7.40E-04	3.82E-02	6.95 (15592,51,220,5)
GO:0018108	peptidyl-tyrosine phosphorylation	8.13E-04	4.16E-02	5.45 (15592,78,220,6)
GO:0001525	angiogenesis	8.11E-04	4.17E-02	3.14 (15592,248,220,11)
GO:0005911	cell-cell junction	3.24E-04	4.18E-02	2.69 (15592,421,220,16)
GO:0032270	positive regulation of cellular protein metabolic process	8.31E-04	4.24E-02	1.76 (15592,1369,220,34)
GO:0001527	microfibril	3.09E-04	4.27E-02	21.26 (15592,10,220,3)
GO:0010558	negative regulation of macromolecule biosynthetic process	8.71E-04	4.43E-02	1.82 (15592,1210,220,31)
GO:0000904	cell morphogenesis involved in differentiation	8.79E-04	4.46E-02	4.02 (15592,141,220,8)
GO:0008045	motor neuron axon guidance	9.00E-04	4.52E-02	9.14 (15592,31,220,4)
GO:1902692	regulation of neuroblast proliferation	9.00E-04	4.53E-02	9.14 (15592,31,220,4)
GO:0048739	cardiac muscle fiber development	8.99E-04	4.54E-02	15.19 (15592,14,220,3)
GO:0120035	regulation of plasma membrane bounded cell projection organization	9.20E-04	4.61E-02	2.13 (15592,699,220,21)
GO:0007043	cell-cell junction assembly	9.29E-04	4.62E-02	5.32 (15592,80,220,6)
GO:0014910	regulation of smooth muscle cell migration	9.29E-04	4.63E-02	5.32 (15592,80,220,6)
GO:0009892	negative regulation of metabolic process	9.55E-04	4.73E-02	1.53 (15592,2356,220,51)
GO:0001837	epithelial to mesenchymal transition	9.63E-04	4.74E-02	6.56 (15592,54,220,5)
GO:0050679	positive regulation of epithelial cell proliferation	9.68E-04	4.75E-02	3.58 (15592,178,220,9)
GO:0051147	regulation of muscle cell differentiation	9.63E-04	4.76E-02	3.96 (15592,143,220,8)
GO:0018212	peptidyl-tyrosine modification	9.92E-04	4.85E-02	5.25 (15592,81,220,6)

4 week old NOD vs. NOD.B10 islets: GO terms associated with differentially changed genes (FDR q-value < 0.05)

*No GO terms associated with genes downregulated by ≥3-fold

4 week old NOD islets: GO terms associated with genes upregulated by ≥3-fold

GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)*
GO:0007186	G protein-coupled receptor signaling pathway	4.32E-12	3.26E-08	3.77 (15592,780,191,36)
GO:0050877	nervous system process	7.35E-12	3.70E-08	3.37 (15592,968,191,40)
GO:0003008	system process	3.75E-12	5.67E-08	2.97 (15592,1320,191,48)
GO:0004984	olfactory receptor activity	8.14E-10	3.59E-06	5.44 (15592,300,191,20)
GO:0007600	sensory perception	2.05E-09	7.73E-06	3.70 (15592,617,191,28)
GO:0007608	sensory perception of smell	2.78E-09	8.40E-06	5.07 (15592,322,191,20)
GO:0004888	transmembrane signaling receptor activity	4.77E-09	1.05E-05	3.12 (15592,863,191,33)
GO:0031224	intrinsic component of membrane	1.51E-08	2.92E-05	1.73 (15592,3958,191,84)
GO:0007606	sensory perception of chemical stimulus	1.33E-08	3.34E-05	4.63 (15592,353,191,20)
GO:0016021	integral component of membrane	3.49E-08	3.38E-05	1.73 (15592,3818,191,81)
GO:0038023	signaling receptor activity	1.59E-07	2.33E-04	2.70 (15592,999,191,33)
GO:0060089	molecular transducer activity	4.35E-07	4.79E-04	2.58 (15592,1044,191,33)
GO:1902475	L-alpha-amino acid transmembrane transport	5.86E-07	1.27E-03	18.84 (15592,26,191,6)
GO:0089718	amino acid import across plasma membrane	7.12E-07	1.34E-03	27.21 (15592,15,191,5)
GO:0043090	amino acid import	1.02E-06	1.55E-03	25.51 (15592,16,191,5)
GO:0032501	multicellular organismal process	9.70E-07	1.63E-03	1.74 (15592,3142,191,67)
GO:0044425	membrane part	6.33E-06	4.08E-03	1.47 (15592,5108,191,92)
GO:0098739	import across plasma membrane	4.05E-06	5.57E-03	8.59 (15592,76,191,8)
GO:0005044	scavenger receptor activity	7.28E-06	6.42E-03	12.56 (15592,39,191,6)
GO:0015807	L-amino acid transport	1.50E-05	1.74E-02	11.13 (15592,44,191,6)
GO:0007610	behavior	1.41E-05	1.77E-02	2.97 (15592,550,191,20)
GO:0038024	cargo receptor activity	3.64E-05	2.68E-02	7.62 (15592,75,191,7)
GO:0015813	L-glutamate transmembrane transport	2.68E-05	2.89E-02	21.77 (15592,15,191,4)
GO:0006855	drug transmembrane transport	3.17E-05	3.19E-02	9.80 (15592,50,191,6)
GO:1905039	carboxylic acid transmembrane transport	5.11E-05	4.29E-02	7.23 (15592,79,191,7)
GO:0044297	cell body	8.89E-05	4.30E-02	2.60 (15592,627,191,20)
GO:0005576	extracellular region	1.11E-04	4.30E-02	2.04 (15592,1243,191,31)
GO:1903825	organic acid transmembrane transport	5.11E-05	4.54E-02	7.23 (15592,79,191,7)
GO:1901607	alpha-amino acid biosynthetic process	4.95E-05	4.67E-02	9.07 (15592,54,191,6)
GO:0003333	amino acid transmembrane transport	6.10E-05	4.85E-02	8.75 (15592,56,191,6)

12 week old NOD vs. NOD.B10 islets: GO terms associated with differentially changed genes (FDR q-value < 0.05)

12 week old NOD islets: GO terms associated with genes upregulated by ≥3-fold

GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)*
GO:0002376	immune system process	2.36E-75	3.56E-71	3.76 (15592,1185,794,227)
GO:0002682	regulation of immune system process	2.98E-52	2.26E-48	3.31 (15592,1114,794,188)
GO:0006955	immune response	2.81E-46	1.42E-42	4.08 (15592,635,794,132)
GO:0002684	positive regulation of immune system process	7.80E-46	2.95E-42	3.81 (15592,726,794,141)
GO:0045321	leukocyte activation	1.41E-44	4.27E-41	5.02 (15592,403,794,103)
GO:0002250	adaptive immune response	2.22E-41	5.59E-38	7.38 (15592,181,794,68)
GO:0050776	regulation of immune response	2.91E-41	6.28E-38	3.93 (15592,614,794,123)
GO:0001775	cell activation	1.34E-39	2.54E-36	4.46 (15592,453,794,103)
GO:0002694	regulation of leukocyte activation	6.69E-39	1.12E-35	4.43 (15592,452,794,102)
GO:0050865	regulation of cell activation	8.37E-38	1.27E-34	4.20 (15592,491,794,105)
GO:0051249	regulation of lymphocyte activation	3.58E-37	4.92E-34	4.79 (15592,369,794,90)
GO:0046649	lymphocyte activation	5.32E-36	6.71E-33	5.03 (15592,324,794,83)
GO:0050778	positive regulation of immune response	1.36E-35	1.58E-32	4.36 (15592,428,794,95)
GO:0050870	positive regulation of T cell activation	5.74E-29	6.19E-26	6.42 (15592,162,794,53)
GO:0051251	positive regulation of lymphocyte activation	2.13E-28	2.15E-25	5.29 (15592,230,794,62)
GO:0050863	regulation of T cell activation	3.50E-28	3.31E-25	4.93 (15592,263,794,66)
GO:0002429	immune response-activating cell surface receptor signaling pathway	3.77E-28	3.35E-25	7.97 (15592,106,794,43)
GO:0050851	antigen receptor-mediated signaling pathway	6.59E-28	5.25E-25	8.63 (15592,91,794,40)
GO:1903039	positive regulation of leukocyte cell-cell adhesion	6.41E-28	5.38E-25	6.03 (15592,176,794,54)
GO:0002768	immune response-regulating cell surface receptor signaling pathway	1.67E-27	1.27E-24	7.51 (15592,115,794,44)
GO:0002696	positive regulation of leukocyte activation	5.75E-27	4.14E-24	4.71 (15592,275,794,66)
GO:0050867	positive regulation of cell activation	2.02E-26	1.39E-23	4.55 (15592,289,794,67)
GO:0002253	activation of immune response	3.09E-26	2.03E-23	5.30 (15592,211,794,57)
GO:0050670	regulation of lymphocyte proliferation	3.24E-26	2.04E-23	5.61 (15592,189,794,54)
GO:0002521	leukocyte differentiation	3.63E-26	2.19E-23	4.64 (15592,275,794,65)

GO:0032944	regulation of mononuclear cell proliferation	5.73E-26	3.33E-23	5.55 (15592,191,794,54)
GO:0098552	side of membrane	1.76E-26	3.41E-23	4.07 (15592,367,794,76)
GO:0070663	regulation of leukocyte proliferation	9.02E-26	5.05E-23	5.40 (15592,200,794,55)
GO:1903037	regulation of leukocyte cell-cell adhesion	1.04E-25	5.43E-23	4.85 (15592,247,794,61)
GO:0022409	positive regulation of cell-cell adhesion	1.03E-25	5.57E-23	5.29 (15592,208,794,56)
GO:0009897	external side of plasma membrane	2.50E-25	2.42E-22	4.37 (15592,301,794,67)
GO:0002764	immune response-regulating signaling pathway	2.48E-24	1.25E-21	5.73 (15592,168,794,49)
GO:0050864	regulation of B cell activation	5.61E-24	2.73E-21	6.88 (15592,117,794,41)
GO:0048584	positive regulation of response to stimulus	7.64E-24	3.61E-21	2.07 (15592,1790,794,189)
GO:0002757	immune response-activating signal transduction	8.56E-24	3.92E-21	5.84 (15592,158,794,47)
GO:0006952	defense response	1.33E-23	5.89E-21	2.79 (15592,781,794,111)
GO:0050896	response to stimulus	3.01E-23	1.30E-20	1.62 (15592,3912,794,323)
GO:0048583	regulation of response to stimulus	1.04E-22	4.35E-20	1.71 (15592,3193,794,278)
GO:0042110	T cell activation	1.15E-22	4.57E-20	5.08 (15592,197,794,51)
GO:0030098	lymphocyte differentiation	1.15E-22	4.70E-20	5.08 (15592,197,794,51)
GO:0050671	positive regulation of lymphocyte proliferation	1.37E-22	5.32E-20	6.78 (15592,113,794,39)
GO:0070665	positive regulation of leukocyte proliferation	1.73E-22	6.54E-20	6.55 (15592,120,794,40)
GO:0032946	positive regulation of mononuclear cell proliferation	2.87E-22	1.06E-19	6.66 (15592,115,794,39)
GO:0002252	immune effector process	1.28E-21	4.59E-19	3.74 (15592,357,794,68)
GO:0022407	regulation of cell-cell adhesion	3.44E-21	1.21E-18	3.77 (15592,344,794,66)
GO:0002697	regulation of immune effector process	7.23E-21	2.48E-18	3.77 (15592,339,794,65)
GO:0042102	positive regulation of T cell proliferation	7.65E-21	2.57E-18	7.76 (15592,81,794,32)
GO:0001817	regulation of cytokine production	4.03E-20	1.32E-17	2.95 (15592,580,794,87)
GO:0050853	B cell receptor signaling pathway	1.08E-19	3.46E-17	12.50 (15592,33,794,21)
GO:0001819	positive regulation of cytokine production	3.11E-19	9.79E-17	3.47 (15592,373,794,66)
GO:0045785	positive regulation of cell adhesion	4.16E-19	1.28E-16	3.50 (15592,365,794,65)
GO:0042129	regulation of T cell proliferation	7.83E-19	2.37E-16	5.47 (15592,140,794,39)
GO:1902105	regulation of leukocyte differentiation	1.14E-18	3.39E-16	4.05 (15592,257,794,53)
GO:0002703	regulation of leukocyte mediated immunity	1.32E-18	3.84E-16	4.59 (15592,197,794,46)
GO:0002699	positive regulation of immune effector process	4.03E-17	1.15E-14	4.31 (15592,205,794,45)
GO:0045619	regulation of lymphocyte differentiation	6.00E-17	1.68E-14	4.88 (15592,157,794,39)
GO:0043207	response to external biotic stimulus	8.39E-17	2.30E-14	2.62 (15592,653,794,87)
GO:0009607	response to biotic stimulus	2.33E-16	6.29E-14	2.56 (15592,676,794,88)
GO:0002819	regulation of adaptive immune response	2.98E-16	7.90E-14	4.67 (15592,164,794,39)
GO:1903706	regulation of hemopoiesis	4.70E-16	1.20E-13	3.27 (15592,354,794,59)
GO:0050852	T cell receptor signaling pathway	4.68E-16	1.22E-13	7.44 (15592,66,794,25)
GO:0030155	regulation of cell adhesion	6.69E-16	1.68E-13	2.62 (15592,615,794,82)
GO:0042113	B cell activation	1.46E-15	3.62E-13	5.10 (15592,131,794,34)
GO:0002706	regulation of lymphocyte mediated immunity	1.56E-15	3.80E-13	4.81 (15592,147,794,36)
GO:0030217	T cell differentiation	1.96E-15	4.70E-13	5.37 (15592,117,794,32)
GO:0031347	regulation of defense response	3.05E-15	7.19E-13	2.71 (15592,536,794,74)
GO:0030888	regulation of B cell proliferation	3.35E-15	7.80E-13	7.66 (15592,59,794,23)
GO:0007166	cell surface receptor signaling pathway	7.79E-15	1.78E-12	1.99 (15592,1294,794,131)
GO:0048518	positive regulation of biological process	8.07E-15	1.82E-12	1.40 (15592,5036,794,358)
GO:0006950	response to stress	1.01E-14	2.25E-12	1.69 (15592,2261,794,195)
GO:0046651	lymphocyte proliferation	1.06E-14	2.32E-12	6.63 (15592,74,794,25)
GO:0032943	mononuclear cell proliferation	1.51E-14	3.27E-12	6.55 (15592,75,794,25)
GO:0002822	regulation of adaptive immune response based on somatic recombination of immune receptors	1.88E-14	3.96E-12	4.58 (15592,150,794,35)
GO:0046634	regulation of alpha-beta T cell activation	1.88E-14	4.01E-12	5.96 (15592,89,794,27)
GO:1902107	positive regulation of leukocyte differentiation	1.97E-14	4.09E-12	4.70 (15592,142,794,34)
GO:0002366	leukocyte activation involved in immune response	4.95E-14	1.01E-11	4.99 (15592,122,794,31)
GO:0045087	innate immune response	5.68E-14	1.15E-11	3.17 (15592,328,794,53)
GO:0070661	leukocyte proliferation	6.31E-14	1.24E-11	5.94 (15592,86,794,26)
GO:0032649	regulation of interferon-gamma production	6.31E-14	1.25E-11	5.94 (15592,86,794,26)
GO:0045058	T cell selection	6.43E-14	1.25E-11	10.83 (15592,29,794,16)
GO:0002478	antigen processing and presentation of exogenous peptide antigen	7.16E-14	1.37E-11	11.78 (15592,25,794,15)
GO:0046635	positive regulation of alpha-beta T cell activation	8.99E-14	1.70E-11	7.08 (15592,61,794,22)
GO:0051707	response to other organism	1.11E-13	2.07E-11	2.66 (15592,502,794,68)
GO:0002263	cell activation involved in immune response	1.28E-13	2.36E-11	4.83 (15592,126,794,31)
GO:0050789	regulation of biological process	1.72E-13	3.12E-11	1.22 (15592,8652,794,539)
GO:0002821	positive regulation of adaptive immune response	1.93E-13	3.47E-11	5.08 (15592,112,794,29)
GO:0002683	negative regulation of immune system process	1.98E-13	3.53E-11	2.87 (15592,404,794,59)
GO:0002824	positive regulation of adaptive immune response based on somatic recombination of immune receptors	2.27E-13	3.98E-11	5.24 (15592,105,794,28)
GO:0045580	regulation of T cell differentiation	2.54E-13	4.41E-11	4.72 (15592,129,794,31)
GO:0019882	antigen processing and presentation	4.82E-13	8.28E-11	6.27 (15592,72,794,23)
GO:0042127	regulation of cell proliferation	4.98E-13	8.46E-11	1.86 (15592,1426,794,135)
GO:0032729	positive regulation of interferon-gamma production	6.55E-13	1.10E-10	6.87 (15592,60,794,21)
GO:0045582	positive regulation of T cell differentiation	7.07E-13	1.17E-10	5.89 (15592,80,794,24)
GO:0002708	positive regulation of lymphocyte mediated immunity	7.39E-13	1.21E-10	5.20 (15592,102,794,27)
GO:1903708	positive regulation of hemopoiesis	9.70E-13	1.58E-10	3.95 (15592,179,794,36)
GO:0002695	negative regulation of leukocyte activation	1.13E-12	1.81E-10	4.24 (15592,153,794,33)
GO:0002460	adaptive immune response based on somatic recomb. of immune receptors built from Ig superfamily domains	1.62E-12	2.58E-10	6.26 (15592,69,794,22)
GO:0019886	antigen processing and presentation of exogenous peptide antigen via MHC class II	1.77E-12	2.78E-10	15.43 (15592,14,794,11)
GO:0080134	regulation of response to stress	2.21E-12	3.44E-10	1.94 (15592,1163,794,115)
GO:0019884	antigen processing and presentation of exogenous antigen	2.67E-12	4.12E-10	9.82 (15592,30,794,15)
GO:0045621	positive regulation of lymphocyte differentiation	2.77E-12	4.23E-10	5.34 (15592,92,794,25)
GO:0002705	positive regulation of leukocyte mediated immunity	2.91E-12	4.40E-10	4.46 (15592,132,794,30)
GO:0050900	leukocyte migration	4.18E-12	6.26E-10	4.05 (15592,160,794,33)
GO:0045061	thymic T cell selection	4.57E-12	6.77E-10	11.60 (15592,22,794,13)
GO:0044459	plasma membrane part	1.15E-12	7.41E-10	1.66 (15592,2133,794,180)
GO:0050871	positive regulation of B cell activation	5.82E-12	8.54E-10	5.92 (15592,73,794,22)
GO:0005515	protein binding	2.37E-13	1.05E-09	1.26 (15592,7551,794,484)
GO:0042613	MHC class II protein complex	2.21E-12	1.07E-09	19.64 (15592,9,794,9)
GO:0050866	negative regulation of cell activation	9.75E-12	1.42E-09	3.84 (15592,174,794,34)
GO:0009605	response to external stimulus	1.12E-11	1.61E-09	1.94 (15592,1106,794,109)
GO:0032101	regulation of response to external stimulus	1.49E-11	2.13E-09	2.25 (15592,672,794,77)
GO:0007049	cell cycle	1.85E-11	2.61E-09	2.23 (15592,688,794,78)
GO:0002495	antigen processing and presentation of peptide antigen via MHC class II	1.93E-11	2.67E-09	13.50 (15592,16,794,11)
GO:0002504	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	1.93E-11	2.70E-09	13.50 (15592,16,794,11)
GO:0009986	cell surface	7.74E-12	3.00E-09	2.39 (15592,574,794,70)
GO:0008284	positive regulation of cell proliferation	2.49E-11	3.42E-09	2.09 (15592,826,794,88)
GO:0048002	antigen processing and presentation of peptide antigen	2.53E-11	3.44E-09	7.42 (15592,45,794,17)
GO:0022402	cell cycle process	3.08E-11	4.16E-09	2.22 (15592,682,794,77)

GO:0009617	response to bacterium	3.98E-11	5.33E-09	2.99 (15592,296,794,45)
GO:0002274	myeloid leukocyte activation	4.16E-11	5.52E-09	4.77 (15592,103,794,25)
GO:0045577	regulation of B cell differentiation	4.78E-11	6.29E-09	9.16 (15592,30,794,14)
GO:0051250	negative regulation of lymphocyte activation	6.06E-11	7.90E-09	4.23 (15592,130,794,28)
GO:0002449	lymphocyte mediated immunity	8.56E-11	1.11E-08	6.12 (15592,61,794,19)
GO:0002443	leukocyte mediated immunity	1.10E-10	1.41E-08	5.43 (15592,76,794,21)
GO:0065007	biological regulation	1.58E-10	2.00E-08	1.18 (15592,9126,794,549)
GO:0042330	taxis	1.66E-10	2.09E-08	3.09 (15592,254,794,40)
GO:0048522	positive regulation of cellular process	2.67E-10	3.33E-08	1.35 (15592,4519,794,310)
GO:0031343	positive regulation of cell killing	2.93E-10	3.63E-08	5.74 (15592,65,794,19)
GO:1903047	mitotic cell cycle process	3.37E-10	4.14E-08	2.54 (15592,409,794,53)
GO:0050794	regulation of cellular process	3.54E-10	4.31E-08	1.20 (15592,8140,794,499)
GO:0002260	lymphocyte homeostasis	3.59E-10	4.34E-08	6.42 (15592,52,794,17)
GO:0006935	chemotaxis	4.23E-10	5.08E-08	3.05 (15592,251,794,39)
GO:0001776	leukocyte homeostasis	5.21E-10	6.11E-08	5.57 (15592,67,794,19)
GO:0030183	B cell differentiation	5.18E-10	6.12E-08	5.03 (15592,82,794,21)
GO:0051240	positive regulation of multicellular organismal process	5.15E-10	6.13E-08	1.67 (15592,1635,794,139)
GO:0031341	regulation of cell killing	8.35E-10	9.71E-08	4.70 (15592,92,794,22)
GO:0004715	non-membrane spanning protein tyrosine kinase activity	5.48E-11	1.21E-07	7.66 (15592,41,794,16)
GO:0018108	peptidyl-tyrosine phosphorylation	1.31E-09	1.51E-07	5.04 (15592,78,794,20)
GO:0060326	cell chemotaxis	1.37E-09	1.56E-07	3.53 (15592,167,794,30)
GO:0042611	MHC protein complex	6.14E-10	1.98E-07	10.80 (15592,20,794,11)
GO:0050869	negative regulation of B cell activation	1.98E-09	2.25E-07	7.98 (15592,32,794,13)
GO:0007159	leukocyte cell-cell adhesion	2.03E-09	2.29E-07	6.69 (15592,44,794,15)
GO:0018212	peptidyl-tyrosine modification	2.68E-09	3.00E-07	4.85 (15592,81,794,20)
GO:0002685	regulation of leukocyte migration	3.21E-09	3.57E-07	3.33 (15592,183,794,31)
GO:0050715	positive regulation of cytokine secretion	3.30E-09	3.61E-07	3.93 (15592,125,794,25)
GO:0002700	regulation of production of molecular mediator of immune response	3.30E-09	3.64E-07	3.93 (15592,125,794,25)
GO:0043368	positive T cell selection	3.50E-09	3.78E-07	12.62 (15592,14,794,9)
GO:0043383	negative T cell selection	3.50E-09	3.81E-07	12.62 (15592,14,794,9)
GO:0007165	signal transduction	3.80E-09	4.04E-07	1.42 (15592,3112,794,225)
GO:0098542	defense response to other organism	3.79E-09	4.06E-07	2.63 (15592,328,794,44)
GO:0050727	regulation of inflammatory response	3.93E-09	4.15E-07	2.70 (15592,305,794,42)
GO:0050790	regulation of catalytic activity	4.11E-09	4.32E-07	1.64 (15592,1608,794,134)
GO:1901987	regulation of cell cycle phase transition	4.15E-09	4.32E-07	2.87 (15592,260,794,38)
GO:0023023	MHC protein complex binding	3.76E-10	5.52E-07	17.46 (15592,9,794,8)
GO:0050764	regulation of phagocytosis	6.14E-09	6.35E-07	4.43 (15592,93,794,21)
GO:0051239	regulation of multicellular organismal process	7.45E-09	7.66E-07	1.45 (15592,2724,794,201)
GO:0032103	positive regulation of response to external stimulus	7.58E-09	7.69E-07	2.76 (15592,277,794,39)
GO:0031295	T cell costimulation	7.57E-09	7.73E-07	9.00 (15592,24,794,11)
GO:0048872	homeostasis of number of cells	1.01E-08	1.02E-06	3.51 (15592,151,794,27)
GO:0030890	positive regulation of B cell proliferation	1.09E-08	1.09E-06	7.09 (15592,36,794,13)
GO:0050854	regulation of antigen receptor-mediated signaling pathway	1.09E-08	1.09E-06	6.01 (15592,49,794,15)
GO:0031349	positive regulation of defense response	1.19E-08	1.18E-06	2.76 (15592,270,794,38)
GO:0046641	positive regulation of alpha-beta T cell proliferation	1.29E-08	1.26E-06	9.82 (15592,20,794,10)
GO:0031294	lymphocyte costimulation	1.29E-08	1.26E-06	8.64 (15592,25,794,11)
GO:1901990	regulation of mitotic cell cycle phase transition	1.30E-08	1.26E-06	2.90 (15592,237,794,35)
GO:0008283	cell proliferation	1.40E-08	1.35E-06	2.25 (15592,480,794,55)
GO:0051301	cell division	1.62E-08	1.55E-06	2.40 (15592,393,794,48)
GO:0002285	lymphocyte activation involved in immune response	1.89E-08	1.79E-06	4.36 (15592,90,794,20)
GO:0050707	regulation of cytokine secretion	1.96E-08	1.85E-06	3.24 (15592,176,794,29)
GO:0000775	chromosome, centromeric region	7.11E-09	1.97E-06	3.67 (15592,139,794,26)
GO:0030101	natural killer cell activation	2.69E-08	2.52E-06	6.11 (15592,45,794,14)
GO:0001910	regulation of leukocyte mediated cytotoxicity	2.70E-08	2.52E-06	4.71 (15592,75,794,18)
GO:0032675	regulation of interleukin-6 production	3.00E-08	2.78E-06	3.65 (15592,129,794,24)
GO:0002715	regulation of natural killer cell mediated immunity	3.33E-08	3.07E-06	6.55 (15592,39,794,13)
GO:0065009	regulation of molecular function	3.35E-08	3.07E-06	1.49 (15592,2185,794,166)
GO:0007059	chromosome segregation	3.43E-08	3.08E-06	3.89 (15592,111,794,22)
GO:0048869	cellular developmental process	3.41E-08	3.09E-06	1.45 (15592,2470,794,183)
GO:0042035	regulation of cytokine biosynthetic process	3.40E-08	3.10E-06	4.22 (15592,93,794,20)
GO:0046640	regulation of alpha-beta T cell proliferation	3.69E-08	3.30E-06	7.14 (15592,33,794,12)
GO:0045060	negative thymic T cell selection	4.48E-08	3.98E-06	12.08 (15592,13,794,8)
GO:0006954	inflammatory response	4.85E-08	4.26E-06	2.55 (15592,308,794,40)
GO:0045088	regulation of innate immune response	4.84E-08	4.28E-06	2.81 (15592,238,794,34)
GO:0050830	defense response to Gram-positive bacterium	5.19E-08	4.54E-06	4.53 (15592,78,794,18)
GO:0097028	dendritic cell differentiation	5.39E-08	4.69E-06	7.71 (15592,28,794,11)
GO:0001912	positive regulation of leukocyte mediated cytotoxicity	6.20E-08	5.36E-06	5.36 (15592,55,794,15)
GO:0005886	plasma membrane	2.29E-08	5.54E-06	1.38 (15592,3333,794,234)
GO:0032715	negative regulation of interleukin-6 production	6.56E-08	5.64E-06	6.23 (15592,41,794,13)
GO:0030595	leukocyte chemotaxis	7.06E-08	5.99E-06	3.89 (15592,106,794,21)
GO:0034341	response to interferon-gamma	7.06E-08	6.03E-06	3.89 (15592,106,794,21)
GO:0032663	regulation of interleukin-2 production	8.98E-08	7.59E-06	5.61 (15592,49,794,14)
GO:0032680	regulation of tumor necrosis factor production	9.85E-08	8.27E-06	3.34 (15592,147,794,25)
GO:0010564	regulation of cell cycle process	1.01E-07	8.45E-06	2.11 (15592,522,794,56)
GO:0051276	chromosome organization	1.08E-07	8.99E-06	2.59 (15592,281,794,37)
GO:0005488	binding	8.21E-09	9.05E-06	1.13 (15592,10693,794,615)
GO:0045954	positive regulation of natural killer cell mediated cytotoxicity	1.13E-07	9.31E-06	8.18 (15592,24,794,10)
GO:0002717	positive regulation of natural killer cell mediated immunity	1.13E-07	9.36E-06	8.18 (15592,24,794,10)
GO:0048519	negative regulation of biological process	1.25E-07	1.02E-05	1.29 (15592,4404,794,290)
GO:1903555	regulation of tumor necrosis factor superfamily cytokine production	1.29E-07	1.05E-05	3.29 (15592,149,794,25)
GO:0002237	response to molecule of bacterial origin	1.48E-07	1.19E-05	2.78 (15592,226,794,32)
GO:0051704	multi-organism process	1.50E-07	1.21E-05	1.87 (15592,766,794,73)
GO:0050777	negative regulation of immune response	1.52E-07	1.21E-05	3.47 (15592,130,794,23)
GO:0051726	regulation of cell cycle	1.56E-07	1.24E-05	1.82 (15592,854,794,79)
GO:0042742	defense response to bacterium	1.69E-07	1.33E-05	3.08 (15592,172,794,27)
GO:0030154	cell differentiation	1.70E-07	1.34E-05	1.52 (15592,1791,794,139)
GO:1901988	negative regulation of cell cycle phase transition	1.75E-07	1.37E-05	3.45 (15592,131,794,23)
GO:1902531	regulation of intracellular signal transduction	1.77E-07	1.38E-05	1.59 (15592,1486,794,120)
GO:0038083	peptidyl-tyrosine autophosphorylation	1.85E-07	1.43E-05	6.97 (15592,31,794,11)
GO:0023026	MHC class II protein complex binding	1.71E-08	1.51E-05	19.64 (15592,6,794,6)
GO:0001772	immunological synapse	7.90E-08	1.70E-05	6.73 (15592,35,794,12)
GO:0042098	T cell proliferation	2.22E-07	1.71E-05	6.20 (15592,38,794,12)
GO:0042269	regulation of natural killer cell mediated cytotoxicity	2.22E-07	1.71E-05	6.20 (15592,38,794,12)

GO:0045059	positive thymic T cell selection	2.39E-07	1.82E-05	12.50 (15592,11,794,7)
GO:0007229	integrin-mediated signaling pathway	2.66E-07	1.99E-05	4.55 (15592,69,794,16)
GO:0050672	negative regulation of lymphocyte proliferation	2.66E-07	2.00E-05	4.55 (15592,69,794,16)
GO:0046631	alpha-beta T cell activation	2.64E-07	2.01E-05	5.19 (15592,53,794,14)
GO:0032945	negative regulation of mononuclear cell proliferation	2.66E-07	2.01E-05	4.55 (15592,69,794,16)
GO:0019724	B cell mediated immunity	2.80E-07	2.08E-05	7.55 (15592,26,794,10)
GO:0001818	negative regulation of cytokine production	2.85E-07	2.11E-05	2.75 (15592,221,794,31)
GO:0007346	regulation of mitotic cell cycle	2.98E-07	2.18E-05	2.16 (15592,445,794,49)
GO:0009966	regulation of signal transduction	2.97E-07	2.19E-05	1.43 (15592,2409,794,175)
GO:0007051	spindle organization	3.02E-07	2.21E-05	3.59 (15592,115,794,21)
GO:0002702	positive regulation of production of molecular mediator of immune response	3.05E-07	2.22E-05	4.06 (15592,87,794,18)
GO:0051336	regulation of hydrolase activity	3.16E-07	2.28E-05	1.79 (15592,854,794,78)
GO:0002827	positive regulation of T-helper 1 type immune response	3.72E-07	2.66E-05	8.42 (15592,21,794,9)
GO:0016064	immunoglobulin mediated immune response	3.72E-07	2.68E-05	8.42 (15592,21,794,9)
GO:0006911	phagocytosis, engulfment	3.85E-07	2.74E-05	6.55 (15592,33,794,11)
GO:0051282	regulation of sequestering of calcium ion	3.90E-07	2.77E-05	3.67 (15592,107,794,20)
GO:0002825	regulation of T-helper 1 type immune response	4.24E-07	2.99E-05	7.27 (15592,27,794,10)
GO:0042108	positive regulation of cytokine biosynthetic process	4.35E-07	3.06E-05	4.68 (15592,63,794,15)
GO:0042101	T cell receptor complex	2.04E-07	3.59E-05	10.47 (15592,15,794,8)
GO:0032655	regulation of interleukin-12 production	5.16E-07	3.61E-05	5.32 (15592,48,794,13)
GO:0030099	myeloid cell differentiation	5.38E-07	3.75E-05	2.99 (15592,171,794,26)
GO:0006959	humoral immune response	5.48E-07	3.80E-05	3.47 (15592,119,794,21)
GO:0046637	regulation of alpha-beta T cell differentiation	5.54E-07	3.82E-05	4.91 (15592,56,794,14)
GO:0005819	spindle	2.00E-07	3.87E-05	3.32 (15592,142,794,24)
GO:0070664	negative regulation of leukocyte proliferation	6.06E-07	4.16E-05	4.30 (15592,73,794,16)
GO:0090022	regulation of neutrophil chemotaxis	6.29E-07	4.30E-05	7.01 (15592,28,794,10)
GO:0046632	alpha-beta T cell differentiation	7.52E-07	5.08E-05	5.61 (15592,42,794,12)
GO:0046638	positive regulation of alpha-beta T cell differentiation	7.52E-07	5.10E-05	5.61 (15592,42,794,12)
GO:0099024	plasma membrane invagination	7.52E-07	5.12E-05	5.61 (15592,42,794,12)
GO:0032879	regulation of localization	8.16E-07	5.48E-05	1.40 (15592,2480,794,177)
GO:0046777	protein autophosphorylation	8.38E-07	5.61E-05	2.85 (15592,186,794,27)
GO:0001782	B cell homeostasis	9.17E-07	6.10E-05	6.77 (15592,29,794,10)
GO:0002761	regulation of myeloid leukocyte differentiation	9.68E-07	6.39E-05	3.48 (15592,113,794,20)
GO:0050921	positive regulation of chemotaxis	9.65E-07	6.40E-05	3.35 (15592,123,794,21)
GO:0005694	chromosome	4.01E-07	6.47E-05	2.18 (15592,423,794,47)
GO:0090068	positive regulation of cell cycle process	9.92E-07	6.52E-05	2.65 (15592,222,794,30)
GO:0098687	chromosomal region	4.43E-07	6.60E-05	2.65 (15592,237,794,32)
GO:0002275	myeloid cell activation involved in immune response	1.04E-06	6.76E-05	6.00 (15592,36,794,11)
GO:0034097	response to cytokine	1.03E-06	6.77E-05	2.02 (15592,505,794,52)
GO:0048523	negative regulation of cellular process	1.07E-06	6.93E-05	1.29 (15592,3992,794,262)
GO:0014066	regulation of phosphatidylinositol 3-kinase signaling	1.07E-06	6.94E-05	3.93 (15592,85,794,17)
GO:2000401	regulation of lymphocyte migration	1.11E-06	7.11E-05	5.01 (15592,51,794,13)
GO:0030889	negative regulation of B cell proliferation	1.21E-06	7.75E-05	8.73 (15592,18,794,8)
GO:0050766	positive regulation of phagocytosis	1.24E-06	7.94E-05	4.33 (15592,68,794,15)
GO:1902715	positive regulation of interferon-gamma secretion	1.26E-06	8.00E-05	13.09 (15592,9,794,6)
GO:0042100	B cell proliferation	1.31E-06	8.30E-05	6.55 (15592,30,794,10)
GO:0051094	positive regulation of developmental process	1.34E-06	8.47E-05	1.58 (15592,1320,794,106)
GO:0098802	plasma membrane receptor complex	6.43E-07	8.89E-05	3.12 (15592,151,794,24)
GO:0045639	positive regulation of myeloid cell differentiation	1.51E-06	9.48E-05	3.84 (15592,87,794,17)
GO:0009967	positive regulation of signal transduction	1.66E-06	1.03E-04	1.57 (15592,1310,794,105)
GO:0002637	regulation of immunoglobulin production	1.69E-06	1.05E-04	4.51 (15592,61,794,14)
GO:1901991	negative regulation of mitotic cell cycle phase transition	1.71E-06	1.05E-04	3.36 (15592,117,794,20)
GO:0000278	mitotic cell cycle	1.71E-06	1.06E-04	3.36 (15592,117,794,20)
GO:2000514	regulation of CD4-positive, alpha-beta T cell activation	1.78E-06	1.09E-04	4.82 (15592,53,794,13)
GO:0002886	regulation of myeloid leukocyte mediated immunity	1.78E-06	1.09E-04	4.82 (15592,53,794,13)
GO:0030695	GTPase regulator activity	1.73E-07	1.09E-04	2.71 (15592,239,794,33)
GO:2000516	positive regulation of CD4-positive, alpha-beta T cell activation	1.85E-06	1.13E-04	6.33 (15592,31,794,10)
GO:0098797	plasma membrane protein complex	8.76E-07	1.13E-04	2.10 (15592,448,794,48)
GO:0045588	positive regulation of gamma-delta T cell differentiation	1.94E-06	1.18E-04	16.36 (15592,6,794,5)
GO:0046645	positive regulation of gamma-delta T cell activation	1.94E-06	1.18E-04	16.36 (15592,6,794,5)
GO:0004896	cytokine receptor activity	1.61E-07	1.18E-04	4.45 (15592,75,794,17)
GO:0051345	positive regulation of hydrolase activity	1.98E-06	1.19E-04	2.04 (15592,461,794,48)
GO:1902533	positive regulation of intracellular signal transduction	2.00E-06	1.20E-04	1.73 (15592,865,794,76)
GO:0001773	myeloid dendritic cell activation	2.15E-06	1.28E-04	7.07 (15592,25,794,9)
GO:0006909	phagocytosis	2.23E-06	1.32E-04	4.15 (15592,71,794,15)
GO:0002709	regulation of T cell mediated immunity	2.23E-06	1.32E-04	4.15 (15592,71,794,15)
GO:0002688	regulation of leukocyte chemotaxis	2.24E-06	1.32E-04	3.57 (15592,99,794,18)
GO:1902622	regulation of neutrophil migration	2.52E-06	1.48E-04	5.54 (15592,39,794,11)
GO:0032735	positive regulation of interleukin-12 production	2.57E-06	1.50E-04	6.14 (15592,32,794,10)
GO:0005096	GTPase activator activity	3.16E-07	1.55E-04	2.74 (15592,222,794,31)
GO:0032496	response to lipopolysaccharide	2.69E-06	1.57E-04	2.63 (15592,209,794,28)
GO:0098772	molecular function regulator	2.89E-07	1.59E-04	1.59 (15592,1436,794,116)
GO:0045637	regulation of myeloid cell differentiation	2.75E-06	1.60E-04	2.74 (15592,186,794,26)
GO:0045937	positive regulation of phosphate metabolic process	2.84E-06	1.64E-04	1.66 (15592,980,794,83)
GO:0010562	positive regulation of phosphorus metabolic process	2.84E-06	1.65E-04	1.66 (15592,980,794,83)
GO:0050920	regulation of chemotaxis	3.04E-06	1.75E-04	2.73 (15592,187,794,26)
GO:0032743	positive regulation of interleukin-2 production	3.14E-06	1.78E-04	6.80 (15592,26,794,9)
GO:2000106	regulation of leukocyte apoptotic process	3.12E-06	1.79E-04	3.83 (15592,82,794,16)
GO:0002724	regulation of T cell cytokine production	3.14E-06	1.79E-04	6.80 (15592,26,794,9)
GO:0004713	protein tyrosine kinase activity	4.08E-07	1.80E-04	3.52 (15592,117,794,21)
GO:0035556	intracellular signal transduction	3.48E-06	1.97E-04	1.58 (15592,1204,794,97)
GO:0002889	regulation of immunoglobulin mediated immune response	3.57E-06	2.00E-04	4.91 (15592,48,794,12)
GO:0002712	regulation of B cell mediated immunity	3.57E-06	2.01E-04	4.91 (15592,48,794,12)
GO:0010324	membrane invagination	3.57E-06	2.02E-04	4.91 (15592,48,794,12)
GO:0002864	regulation of acute inflammatory response to antigenic stimulus	3.89E-06	2.17E-04	9.16 (15592,15,794,7)
GO:0030234	enzyme regulator activity	5.43E-07	2.18E-04	1.79 (15592,836,794,76)
GO:0002704	negative regulation of leukocyte mediated immunity	4.52E-06	2.51E-04	4.81 (15592,49,794,12)
GO:0048585	negative regulation of response to stimulus	4.56E-06	2.53E-04	1.53 (15592,1388,794,108)
GO:0050730	regulation of peptidyl-tyrosine phosphorylation	4.63E-06	2.55E-04	2.46 (15592,239,794,30)
GO:0006956	complement activation	4.76E-06	2.62E-04	5.78 (15592,34,794,10)
GO:0031399	regulation of protein modification process	4.99E-06	2.73E-04	1.49 (15592,1570,794,119)
GO:0023051	regulation of signaling	5.54E-06	3.02E-04	1.34 (15592,2782,794,190)
GO:0043370	regulation of CD4-positive, alpha-beta T cell differentiation	5.58E-06	3.04E-04	5.14 (15592,42,794,11)

GO:0098636	protein complex involved in cell adhesion	2.57E-06	3.11E-04	6.14 (15592,32,794,10)
GO:0010646	regulation of cell communication	5.87E-06	3.18E-04	1.34 (15592,2767,794,189)
GO:0001771	immunological synapse formation	6.34E-06	3.42E-04	10.71 (15592,11,794,6)
GO:0051383	kinetochore organization	6.60E-06	3.54E-04	8.59 (15592,16,794,7)
GO:0045579	positive regulation of B cell differentiation	6.60E-06	3.55E-04	8.59 (15592,16,794,7)
GO:0071593	lymphocyte aggregation	6.68E-06	3.57E-04	19.64 (15592,4,794,4)
GO:0019221	cytokine-mediated signaling pathway	6.72E-06	3.58E-04	2.56 (15592,207,794,27)
GO:0001816	cytokine production	6.98E-06	3.70E-04	3.61 (15592,87,794,16)
GO:0019220	regulation of phosphate metabolic process	7.20E-06	3.80E-04	1.49 (15592,1500,794,114)
GO:0090023	positive regulation of neutrophil chemotaxis	7.37E-06	3.88E-04	7.14 (15592,22,794,8)
GO:0051174	regulation of phosphorus metabolic process	7.42E-06	3.90E-04	1.49 (15592,1501,794,114)
GO:0051246	regulation of protein metabolic process	7.85E-06	4.11E-04	1.37 (15592,2362,794,165)
GO:0002687	positive regulation of leukocyte migration	8.01E-06	4.17E-04	3.04 (15592,129,794,20)
GO:0002861	regulation of inflammatory response to antigenic stimulus	8.77E-06	4.52E-04	6.09 (15592,29,794,9)
GO:1902100	negative regulation of metaphase/anaphase transition of cell cycle	8.77E-06	4.54E-04	6.09 (15592,29,794,9)
GO:0001562	response to protozoan	8.77E-06	4.55E-04	6.09 (15592,29,794,9)
GO:0042325	regulation of phosphorylation	8.86E-06	4.56E-04	1.52 (15592,1360,794,105)
GO:0071622	regulation of granulocyte chemotaxis	9.11E-06	4.67E-04	4.91 (15592,44,794,11)
GO:0051338	regulation of transferase activity	9.25E-06	4.72E-04	1.72 (15592,765,794,67)
GO:0032760	positive regulation of tumor necrosis factor production	9.46E-06	4.81E-04	3.53 (15592,89,794,16)
GO:0050868	negative regulation of T cell activation	9.50E-06	4.82E-04	3.37 (15592,99,794,17)
GO:0016477	cell migration	9.62E-06	4.86E-04	1.75 (15592,706,794,63)
GO:0045089	positive regulation of innate immune response	1.00E-05	5.04E-04	2.82 (15592,153,794,22)
GO:0050855	regulation of B cell receptor signaling pathway	1.07E-05	5.39E-04	8.09 (15592,17,794,7)
GO:0071624	positive regulation of granulocyte chemotaxis	1.08E-05	5.41E-04	6.83 (15592,23,794,8)
GO:1903557	positive regulation of tumor necrosis factor superfamily cytokine production	1.10E-05	5.47E-04	3.49 (15592,90,794,16)
GO:0043235	receptor complex	4.86E-06	5.54E-04	2.22 (15592,328,794,37)
GO:0010389	regulation of G2/M transition of mitotic cell cycle	1.13E-05	5.61E-04	3.87 (15592,71,794,14)
GO:0022610	biological adhesion	1.17E-05	5.79E-04	1.78 (15592,651,794,59)
GO:1905819	negative regulation of chromosome separation	1.20E-05	5.89E-04	5.89 (15592,30,794,9)
GO:1902751	positive regulation of cell cycle G2/M phase transition	1.20E-05	5.91E-04	5.89 (15592,30,794,9)
GO:0002883	regulation of hypersensitivity	1.21E-05	5.94E-04	9.82 (15592,12,794,6)
GO:1902713	regulation of interferon-gamma secretion	1.21E-05	5.96E-04	9.82 (15592,12,794,6)
GO:0043549	regulation of kinase activity	1.29E-05	6.30E-04	1.76 (15592,668,794,60)
GO:0044427	chromosomal part	5.95E-06	6.40E-04	1.71 (15592,815,794,71)
GO:0043085	positive regulation of catalytic activity	1.38E-05	6.70E-04	1.62 (15592,959,794,79)
GO:0006468	protein phosphorylation	1.44E-05	6.96E-04	1.79 (15592,626,794,57)
GO:0002698	negative regulation of immune effector process	1.54E-05	7.43E-04	3.13 (15592,113,794,18)
GO:0032673	regulation of interleukin-4 production	1.55E-05	7.43E-04	6.55 (15592,24,794,8)
GO:0006958	complement activation, classical pathway	1.55E-05	7.45E-04	6.55 (15592,24,794,8)
GO:0002763	positive regulation of myeloid leukocyte differentiation	1.62E-05	7.75E-04	4.28 (15592,55,794,12)
GO:0042327	positive regulation of phosphorylation	1.64E-05	7.84E-04	1.63 (15592,917,794,76)
GO:0002726	positive regulation of T cell cytokine production	1.68E-05	7.98E-04	7.64 (15592,18,794,7)
GO:0051783	regulation of nuclear division	1.75E-05	8.31E-04	2.66 (15592,170,794,23)
GO:0051784	negative regulation of nuclear division	1.80E-05	8.42E-04	4.60 (15592,47,794,11)
GO:0002833	positive regulation of response to biotic stimulus	1.80E-05	8.44E-04	4.60 (15592,47,794,11)
GO:0072676	lymphocyte migration	1.80E-05	8.47E-04	4.60 (15592,47,794,11)
GO:0051247	positive regulation of protein metabolic process	1.82E-05	8.47E-04	1.47 (15592,1465,794,110)
GO:0070887	cellular response to chemical stimulus	1.80E-05	8.49E-04	1.49 (15592,1399,794,106)
GO:0002820	negative regulation of adaptive immune response	1.83E-05	8.51E-04	5.04 (15592,39,794,10)
GO:0000776	kinetochore	8.69E-06	8.85E-04	3.14 (15592,119,794,19)
GO:0051983	regulation of chromosome segregation	1.94E-05	8.98E-04	3.34 (15592,94,794,16)
GO:1902749	regulation of cell cycle G2/M phase transition	1.94E-05	8.98E-04	3.51 (15592,84,794,15)
GO:0048534	hematopoietic or lymphoid organ development	1.97E-05	9.08E-04	2.52 (15592,195,794,25)
GO:0048302	regulation of isotype switching to IgG isotypes	2.16E-05	9.91E-04	9.06 (15592,13,794,6)
GO:2000404	regulation of T cell migration	2.33E-05	1.07E-03	4.91 (15592,40,794,10)
GO:0051049	regulation of transport	2.40E-05	1.09E-03	1.43 (15592,1674,794,122)
GO:0040017	positive regulation of locomotion	2.46E-05	1.12E-03	1.84 (15592,535,794,50)
GO:0045807	positive regulation of endocytosis	2.50E-05	1.14E-03	2.67 (15592,162,794,22)
GO:0002831	regulation of response to biotic stimulus	2.52E-05	1.14E-03	2.91 (15592,128,794,19)
GO:0032753	positive regulation of interleukin-4 production	2.54E-05	1.14E-03	7.23 (15592,19,794,7)
GO:0002690	positive regulation of leukocyte chemotaxis	2.54E-05	1.14E-03	3.62 (15592,76,794,14)
GO:0033045	regulation of sister chromatid segregation	2.54E-05	1.14E-03	3.62 (15592,76,794,14)
GO:0002577	regulation of antigen processing and presentation	2.54E-05	1.15E-03	7.23 (15592,19,794,7)
GO:0005164	tumor necrosis factor receptor binding	3.14E-06	1.15E-03	6.80 (15592,26,794,9)
GO:0016020	membrane	1.21E-05	1.17E-03	1.18 (15592,6327,794,380)
GO:0051716	cellular response to stimulus	2.76E-05	1.23E-03	1.35 (15592,2328,794,160)
GO:0072686	mitotic spindle	1.34E-05	1.23E-03	3.82 (15592,72,794,14)
GO:0033003	regulation of mast cell activation	2.94E-05	1.30E-03	4.79 (15592,41,794,10)
GO:0002707	negative regulation of lymphocyte mediated immunity	2.94E-05	1.31E-03	4.79 (15592,41,794,10)
GO:0007155	cell adhesion	2.97E-05	1.31E-03	1.74 (15592,642,794,57)
GO:0043372	positive regulation of CD4-positive, alpha-beta T cell differentiation	3.00E-05	1.32E-03	6.04 (15592,26,794,8)
GO:0032660	regulation of interleukin-17 production	3.00E-05	1.32E-03	6.04 (15592,26,794,8)
GO:0031401	positive regulation of protein modification process	3.15E-05	1.38E-03	1.55 (15592,1077,794,85)
GO:0044425	membrane part	1.57E-05	1.38E-03	1.21 (15592,5108,794,315)
GO:2000026	regulation of multicellular organismal development	3.24E-05	1.42E-03	1.40 (15592,1854,794,132)
GO:0007093	mitotic cell cycle checkpoint	3.31E-05	1.44E-03	3.21 (15592,98,794,16)
GO:0002711	positive regulation of T cell mediated immunity	3.36E-05	1.46E-03	4.32 (15592,50,794,11)
GO:1901989	positive regulation of cell cycle phase transition	3.44E-05	1.49E-03	3.35 (15592,88,794,15)
GO:0000075	cell cycle checkpoint	3.55E-05	1.53E-03	2.95 (15592,120,794,18)
GO:2001187	positive regulation of CD8-positive, alpha-beta T cell activation	3.59E-05	1.54E-03	10.91 (15592,9,794,5)
GO:0046643	regulation of gamma-delta T cell activation	3.59E-05	1.54E-03	10.91 (15592,9,794,5)
GO:0045586	regulation of gamma-delta T cell differentiation	3.59E-05	1.55E-03	10.91 (15592,9,794,5)
GO:0044093	positive regulation of molecular function	3.70E-05	1.56E-03	1.49 (15592,1292,794,98)
GO:0010948	negative regulation of cell cycle process	3.67E-05	1.57E-03	2.48 (15592,190,794,24)
GO:0098813	nuclear chromosome segregation	3.69E-05	1.57E-03	4.68 (15592,42,794,10)
GO:0072376	protein activation cascade	3.69E-05	1.57E-03	4.68 (15592,42,794,10)
GO:0050708	regulation of protein secretion	3.78E-05	1.60E-03	1.92 (15592,429,794,42)
GO:0006897	endocytosis	3.82E-05	1.61E-03	2.04 (15592,346,794,36)
GO:1903038	negative regulation of leukocyte cell-cell adhesion	3.93E-05	1.65E-03	3.03 (15592,110,794,17)
GO:0060589	nucleoside-triphosphatase regulator activity	4.94E-06	1.67E-03	2.34 (15592,277,794,33)
GO:0006310	DNA recombination	4.02E-05	1.68E-03	2.59 (15592,167,794,22)
GO:0046456	icosanoid biosynthetic process	4.08E-05	1.69E-03	5.82 (15592,27,794,8)

GO:0010971	positive regulation of G2/M transition of mitotic cell cycle	4.08E-05	1.70E-03	5.82 (15592,27,794,8)
GO:0042832	defense response to protozoan	4.08E-05	1.70E-03	5.82 (15592,27,794,8)
GO:0001932	regulation of protein phosphorylation	4.16E-05	1.72E-03	1.50 (15592,1247,794,95)
GO:0010647	positive regulation of cell communication	4.26E-05	1.76E-03	1.45 (15592,1478,794,109)
GO:0043550	regulation of lipid kinase activity	4.59E-05	1.88E-03	4.57 (15592,43,794,10)
GO:0051209	release of sequestered calcium ion into cytosol	4.59E-05	1.88E-03	4.57 (15592,43,794,10)
GO:0002791	regulation of peptide secretion	4.58E-05	1.89E-03	1.87 (15592,461,794,44)
GO:0051985	negative regulation of chromosome segregation	4.69E-05	1.92E-03	5.05 (15592,35,794,9)
GO:0010033	response to organic substance	4.84E-05	1.97E-03	1.40 (15592,1751,794,125)
GO:0030097	hemopoiesis	4.84E-05	1.97E-03	3.11 (15592,101,794,16)
GO:1905818	regulation of chromosome separation	4.86E-05	1.97E-03	3.86 (15592,61,794,12)
GO:0051272	positive regulation of cellular component movement	4.87E-05	1.97E-03	1.81 (15592,520,794,48)
GO:0010522	regulation of calcium ion transport into cytosol	5.16E-05	2.08E-03	3.24 (15592,91,794,15)
GO:0001891	phagocytic cup	2.54E-05	2.14E-03	7.23 (15592,19,794,7)
GO:0045589	regulation of regulatory T cell differentiation	5.36E-05	2.16E-03	6.55 (15592,21,794,7)
GO:0030335	positive regulation of cell migration	5.38E-05	2.16E-03	1.83 (15592,493,794,46)
GO:0045787	positive regulation of cell cycle	5.41E-05	2.16E-03	2.08 (15592,311,794,33)
GO:0045841	negative regulation of mitotic metaphase/anaphase transition	5.46E-05	2.18E-03	5.61 (15592,28,794,8)
GO:0051270	regulation of cellular component movement	5.54E-05	2.20E-03	1.58 (15592,919,794,74)
GO:0035639	purine ribonucleoside triphosphate binding	7.03E-06	2.21E-03	1.49 (15592,1532,794,116)
GO:0045597	positive regulation of cell differentiation	5.65E-05	2.24E-03	1.56 (15592,967,794,77)
GO:0045576	mast cell activation	5.76E-05	2.28E-03	7.85 (15592,15,794,6)
GO:1902850	microtubule cytoskeleton organization involved in mitosis	5.88E-05	2.32E-03	3.20 (15592,92,794,15)
GO:0002573	myeloid leukocyte differentiation	5.88E-05	2.32E-03	3.20 (15592,92,794,15)
GO:0002823	negative regulation of adaptive immune response based on somatic recombination of immune receptors	5.98E-05	2.32E-03	4.91 (15592,36,794,9)
GO:1902099	regulation of metaphase/anaphase transition of cell cycle	5.96E-05	2.33E-03	4.08 (15592,53,794,11)
GO:0002714	positive regulation of B cell mediated immunity	5.98E-05	2.33E-03	4.91 (15592,36,794,9)
GO:0002891	positive regulation of immunoglobulin mediated immune response	5.98E-05	2.33E-03	4.91 (15592,36,794,9)
GO:0002673	regulation of acute inflammatory response	5.96E-05	2.34E-03	4.08 (15592,53,794,11)
GO:0045930	negative regulation of mitotic cell cycle	6.08E-05	2.36E-03	2.40 (15592,196,794,24)
GO:0002718	regulation of cytokine production involved in immune response	6.12E-05	2.36E-03	3.55 (15592,72,794,13)
GO:0030334	regulation of cell migration	6.31E-05	2.43E-03	1.62 (15592,813,794,67)
GO:0007204	positive regulation of cytosolic calcium ion concentration	6.64E-05	2.55E-03	2.26 (15592,235,794,27)
GO:0042105	alpha-beta T cell receptor complex	3.20E-05	2.58E-03	15.71 (15592,5,794,4)
GO:0007088	regulation of mitotic nuclear division	6.82E-05	2.62E-03	2.64 (15592,149,794,20)
GO:0032060	bleb assembly	6.88E-05	2.63E-03	9.82 (15592,10,794,5)
GO:0051283	negative regulation of sequestering of calcium ion	6.96E-05	2.66E-03	4.36 (15592,45,794,10)
GO:2000145	regulation of cell motility	6.99E-05	2.66E-03	1.60 (15592,847,794,69)
GO:0031234	extrinsic component of cytoplasmic side of plasma membrane	3.43E-05	2.66E-03	3.99 (15592,59,794,12)
GO:0071346	cellular response to interferon-gamma	7.03E-05	2.67E-03	3.31 (15592,83,794,14)
GO:0043029	T cell homeostasis	7.20E-05	2.72E-03	5.42 (15592,29,794,8)
GO:2000816	negative regulation of mitotic sister chromatid separation	7.20E-05	2.73E-03	5.42 (15592,29,794,8)
GO:0032268	regulation of cellular protein metabolic process	7.32E-05	2.76E-03	1.34 (15592,2197,794,150)
GO:0031325	positive regulation of cellular metabolic process	7.40E-05	2.78E-03	1.29 (15592,2813,794,185)
GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	7.54E-05	2.81E-03	2.48 (15592,174,794,22)
GO:0050858	negative regulation of antigen receptor-mediated signaling pathway	7.52E-05	2.82E-03	6.25 (15592,22,794,7)
GO:0043087	regulation of GTPase activity	7.53E-05	2.82E-03	2.13 (15592,276,794,30)
GO:0009987	cellular process	7.80E-05	2.90E-03	1.09 (15592,10789,794,597)
GO:0040011	locomotion	8.07E-05	3.00E-03	1.59 (15592,851,794,69)
GO:0097367	carbohydrate derivative binding	1.02E-05	3.01E-03	1.42 (15592,1861,794,135)
GO:0009893	positive regulation of metabolic process	8.15E-05	3.02E-03	1.27 (15592,3050,794,198)
GO:0071310	cellular response to organic substance	8.20E-05	3.03E-03	1.50 (15592,1139,794,87)
GO:0023056	positive regulation of signaling	8.39E-05	3.09E-03	1.43 (15592,1486,794,108)
GO:0001934	positive regulation of protein phosphorylation	8.45E-05	3.11E-03	1.58 (15592,868,794,70)
GO:2000107	negative regulation of leukocyte apoptotic process	8.49E-05	3.11E-03	4.27 (15592,46,794,10)
GO:0050714	positive regulation of protein secretion	8.75E-05	3.20E-03	2.15 (15592,265,794,29)
GO:0043299	leukocyte degranulation	8.82E-05	3.20E-03	7.36 (15592,16,794,6)
GO:0045076	regulation of interleukin-2 biosynthetic process	8.82E-05	3.21E-03	7.36 (15592,16,794,6)
GO:0001779	natural killer cell differentiation	8.82E-05	3.21E-03	7.36 (15592,16,794,6)
GO:0006691	leukotriene metabolic process	8.82E-05	3.22E-03	7.36 (15592,16,794,6)
GO:0071216	cellular response to biotic stimulus	9.07E-05	3.28E-03	2.51 (15592,164,794,21)
GO:0050798	activated T cell proliferation	9.22E-05	3.32E-03	13.09 (15592,6,794,4)
GO:0032609	interferon-gamma production	9.22E-05	3.33E-03	13.09 (15592,6,794,4)
GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	9.32E-05	3.34E-03	3.63 (15592,65,794,12)
GO:0002701	negative regulation of production of molecular mediator of immune response	9.39E-05	3.34E-03	5.24 (15592,30,794,8)
GO:0007052	mitotic spindle organization	9.32E-05	3.35E-03	3.63 (15592,65,794,12)
GO:0050728	negative regulation of inflammatory response	9.36E-05	3.35E-03	2.74 (15592,129,794,18)
GO:0043304	regulation of mast cell degranulation	9.39E-05	3.35E-03	5.24 (15592,30,794,8)
GO:0031348	negative regulation of defense response	9.46E-05	3.36E-03	2.39 (15592,189,794,23)
GO:2000147	positive regulation of cell motility	9.56E-05	3.39E-03	1.79 (15592,505,794,46)
GO:0010965	regulation of mitotic sister chromatid separation	1.01E-04	3.57E-03	3.86 (15592,56,794,11)
GO:0010959	regulation of metal ion transport	1.03E-04	3.62E-03	1.95 (15592,363,794,36)
GO:0002720	positive regulation of cytokine production involved in immune response	1.03E-04	3.63E-03	4.18 (15592,47,794,10)
GO:0051128	regulation of cellular component organization	1.04E-04	3.64E-03	1.32 (15592,2300,794,155)
GO:0071219	cellular response to molecule of bacterial origin	1.07E-04	3.75E-03	2.63 (15592,142,794,19)
GO:0045786	negative regulation of cell cycle	1.09E-04	3.80E-03	1.94 (15592,364,794,36)
GO:0051173	positive regulation of nitrogen compound metabolic process	1.13E-04	3.95E-03	1.29 (15592,2692,794,177)
GO:0071345	cellular response to cytokine stimulus	1.14E-04	3.96E-03	1.90 (15592,393,794,38)
GO:0000777	condensed chromosome kinetochore	5.36E-05	3.99E-03	6.55 (15592,21,794,7)
GO:1902532	negative regulation of intracellular signal transduction	1.17E-04	4.06E-03	1.80 (15592,480,794,44)
GO:0032555	purine ribonucleotide binding	1.47E-05	4.06E-03	1.46 (15592,1590,794,118)
GO:0033006	regulation of mast cell activation involved in immune response	1.21E-04	4.10E-03	5.07 (15592,31,794,8)
GO:1902624	positive regulation of neutrophil migration	1.21E-04	4.11E-03	5.07 (15592,31,794,8)
GO:0051382	kinetochore assembly	1.21E-04	4.12E-03	8.93 (15592,11,794,5)
GO:0000819	sister chromatid segregation	1.21E-04	4.12E-03	5.07 (15592,31,794,8)
GO:0043405	regulation of MAP kinase activity	1.22E-04	4.12E-03	2.11 (15592,270,794,29)
GO:0048304	positive regulation of isotype switching to IgG isotypes	1.21E-04	4.13E-03	8.93 (15592,11,794,5)
GO:0000940	condensed chromosome outer kinetochore	5.76E-05	4.13E-03	7.85 (15592,15,794,6)
GO:0030593	neutrophil chemotaxis	1.20E-04	4.14E-03	3.79 (15592,57,794,11)
GO:0032502	developmental process	1.20E-04	4.14E-03	1.22 (15592,4054,794,252)
GO:0019370	leukotriene biosynthetic process	1.21E-04	4.14E-03	8.93 (15592,11,794,5)
GO:0045086	positive regulation of interleukin-2 biosynthetic process	1.21E-04	4.15E-03	8.93 (15592,11,794,5)
GO:0006968	cellular defense response	1.21E-04	4.16E-03	8.93 (15592,11,794,5)

GO:0002244	hematopoietic progenitor cell differentiation	1.24E-04	4.17E-03	3.01 (15592,98,794,15)
GO:0042531	positive regulation of tyrosine phosphorylation of STAT protein	1.24E-04	4.18E-03	4.09 (15592,48,794,10)
GO:0046427	positive regulation of JAK-STAT cascade	1.26E-04	4.24E-03	3.52 (15592,67,794,12)
GO:0042609	CD4 receptor binding	1.67E-05	4.32E-03	12.27 (15592,8,794,5)
GO:0035984	cellular response to trichostatin A	1.32E-04	4.34E-03	19.64 (15592,3,794,3)
GO:0002834	regulation of response to tumor cell	1.31E-04	4.35E-03	6.93 (15592,17,794,6)
GO:0035983	response to trichostatin A	1.32E-04	4.35E-03	19.64 (15592,3,794,3)
GO:0002837	regulation of immune response to tumor cell	1.31E-04	4.36E-03	6.93 (15592,17,794,6)
GO:0032270	positive regulation of cellular protein metabolic process	1.31E-04	4.36E-03	1.43 (15592,1369,794,100)
GO:0071663	positive regulation of granzyme B production	1.32E-04	4.36E-03	19.64 (15592,3,794,3)
GO:0030852	regulation of granulocyte differentiation	1.31E-04	4.37E-03	6.93 (15592,17,794,6)
GO:0071661	regulation of granzyme B production	1.32E-04	4.37E-03	19.64 (15592,3,794,3)
GO:1903046	meiotic cell cycle process	1.33E-04	4.39E-03	2.76 (15592,121,794,17)
GO:0048469	cell maturation	1.38E-04	4.53E-03	2.86 (15592,110,794,16)
GO:0007094	mitotic spindle assembly checkpoint	1.40E-04	4.57E-03	5.73 (15592,24,794,7)
GO:0050793	regulation of developmental process	1.40E-04	4.57E-03	1.32 (15592,2314,794,155)
GO:0017076	purine nucleotide binding	2.07E-05	4.57E-03	1.45 (15592,1602,794,118)
GO:0071173	spindle assembly checkpoint	1.40E-04	4.58E-03	5.73 (15592,24,794,7)
GO:0010604	positive regulation of macromolecule metabolic process	1.41E-04	4.60E-03	1.28 (15592,2810,794,183)
GO:0032653	regulation of interleukin-10 production	1.45E-04	4.70E-03	4.42 (15592,40,794,9)
GO:0008047	enzyme activator activity	2.05E-05	4.76E-03	1.97 (15592,418,794,42)
GO:0000778	condensed nuclear chromosome kinetochore	6.88E-05	4.76E-03	9.82 (15592,10,794,5)
GO:0032553	ribonucleotide binding	2.02E-05	4.94E-03	1.45 (15592,1601,794,118)
GO:0033048	negative regulation of mitotic sister chromatid segregation	1.54E-04	5.00E-03	4.91 (15592,32,794,8)
GO:0008285	negative regulation of cell proliferation	1.57E-04	5.10E-03	1.69 (15592,606,794,52)
GO:0040012	regulation of locomotion	1.63E-04	5.26E-03	1.54 (15592,919,794,72)
GO:0051130	positive regulation of cellular component organization	1.63E-04	5.26E-03	1.47 (15592,1162,794,87)
GO:0051924	regulation of calcium ion transport	1.67E-04	5.38E-03	2.17 (15592,235,794,26)
GO:0042221	response to chemical	1.68E-04	5.38E-03	1.32 (15592,2165,794,146)
GO:0006928	movement of cell or subcellular component	1.75E-04	5.61E-03	1.48 (15592,1099,794,83)
GO:0045839	negative regulation of mitotic nuclear division	1.77E-04	5.64E-03	4.31 (15592,41,794,9)
GO:0043300	regulation of leukocyte degranulation	1.77E-04	5.65E-03	4.31 (15592,41,794,9)
GO:0000281	mitotic cytokinesis	1.78E-04	5.66E-03	3.93 (15592,50,794,10)
GO:0002793	positive regulation of peptide secretion	1.83E-04	5.82E-03	2.03 (15592,290,794,30)
GO:0048870	cell motility	1.84E-04	5.83E-03	1.59 (15592,780,794,63)
GO:0050901	leukocyte tethering or rolling	1.87E-04	5.90E-03	6.55 (15592,18,794,6)
GO:0061756	leukocyte adhesion to vascular endothelial cell	1.87E-04	5.91E-03	6.55 (15592,18,794,6)
GO:0043011	myeloid dendritic cell differentiation	1.87E-04	5.92E-03	6.55 (15592,18,794,6)
GO:0033046	negative regulation of sister chromatid segregation	1.94E-04	6.07E-03	4.76 (15592,33,794,8)
GO:1902106	negative regulation of leukocyte differentiation	1.95E-04	6.07E-03	3.02 (15592,91,794,14)
GO:0060402	calcium ion transport into cytosol	1.93E-04	6.08E-03	3.60 (15592,60,794,11)
GO:0016310	phosphorylation	1.94E-04	6.08E-03	1.57 (15592,813,794,65)
GO:0050856	regulation of T cell receptor signaling pathway	1.94E-04	6.08E-03	4.76 (15592,33,794,8)
GO:0043408	regulation of MAPK cascade	1.96E-04	6.10E-03	1.65 (15592,642,794,54)
GO:0002836	positive regulation of response to tumor cell	1.98E-04	6.14E-03	8.18 (15592,12,794,5)
GO:0002839	positive regulation of immune response to tumor cell	1.98E-04	6.16E-03	8.18 (15592,12,794,5)
GO:0050859	negative regulation of B cell receptor signaling pathway	2.06E-04	6.38E-03	11.22 (15592,7,794,4)
GO:0031641	regulation of myelination	2.11E-04	6.51E-03	3.85 (15592,51,794,10)
GO:0030071	regulation of mitotic metaphase/anaphase transition	2.11E-04	6.52E-03	3.85 (15592,51,794,10)
GO:1904894	positive regulation of STAT cascade	2.24E-04	6.88E-03	3.32 (15592,71,794,12)
GO:0043547	positive regulation of GTPase activity	2.39E-04	7.32E-03	2.25 (15592,201,794,23)
GO:0019955	cytokine binding	3.49E-05	7.32E-03	3.06 (15592,109,794,17)
GO:2000403	positive regulation of lymphocyte migration	2.43E-04	7.37E-03	4.62 (15592,34,794,8)
GO:0005524	ATP binding	3.68E-05	7.38E-03	1.50 (15592,1243,794,95)
GO:0043551	regulation of phosphatidylinositol 3-kinase activity	2.43E-04	7.39E-03	4.62 (15592,34,794,8)
GO:0031577	spindle checkpoint	2.43E-04	7.40E-03	5.29 (15592,26,794,7)
GO:0071174	mitotic spindle checkpoint	2.43E-04	7.41E-03	5.29 (15592,26,794,7)
GO:0043552	positive regulation of phosphatidylinositol 3-kinase activity	2.43E-04	7.43E-03	5.29 (15592,26,794,7)
GO:0097553	calcium ion transmembrane import into cytosol	2.50E-04	7.57E-03	3.78 (15592,52,794,10)
GO:0002312	B cell activation involved in immune response	2.60E-04	7.86E-03	4.11 (15592,43,794,9)
GO:0010863	positive regulation of phospholipase C activity	2.62E-04	7.91E-03	6.20 (15592,19,794,6)
GO:0001894	tissue homeostasis	2.66E-04	8.01E-03	2.61 (15592,128,794,17)
GO:0097529	myeloid leukocyte migration	2.76E-04	8.29E-03	2.92 (15592,94,794,14)
GO:1903169	regulation of calcium ion transmembrane transport	2.93E-04	8.78E-03	2.51 (15592,141,794,18)
GO:0007010	cytoskeleton organization	3.13E-04	9.37E-03	1.58 (15592,748,794,60)
GO:0043067	regulation of programmed cell death	3.16E-04	9.45E-03	1.41 (15592,1369,794,98)
GO:0030100	regulation of endocytosis	3.22E-04	9.59E-03	2.02 (15592,272,794,28)
GO:0032970	regulation of actin filament-based process	3.23E-04	9.60E-03	1.88 (15592,356,794,34)
GO:0045859	regulation of protein kinase activity	3.26E-04	9.67E-03	1.64 (15592,609,794,51)
GO:0006259	DNA metabolic process	3.30E-04	9.78E-03	1.65 (15592,594,794,50)
GO:0051347	positive regulation of transferase activity	3.44E-04	1.02E-02	1.71 (15592,504,794,44)
GO:0000724	double-strand break repair via homologous recombination	3.46E-04	1.02E-02	3.00 (15592,85,794,13)
GO:0000725	recombinational repair	3.46E-04	1.02E-02	3.00 (15592,85,794,13)
GO:0043407	negative regulation of MAP kinase activity	3.49E-04	1.02E-02	3.38 (15592,64,794,11)
GO:0071621	granulocyte chemotaxis	3.49E-04	1.03E-02	3.38 (15592,64,794,11)
GO:0032956	regulation of actin cytoskeleton organization	3.69E-04	1.08E-02	1.93 (15592,316,794,31)
GO:0098657	import into cell	3.82E-04	1.12E-02	1.77 (15592,432,794,39)
GO:0045084	positive regulation of interleukin-12 biosynthetic process	3.96E-04	1.15E-02	9.82 (15592,8,794,4)
GO:0032817	regulation of natural killer cell proliferation	3.96E-04	1.15E-02	9.82 (15592,8,794,4)
GO:0002858	regulation of natural killer cell mediated cytotoxicity directed against tumor cell target	3.96E-04	1.15E-02	9.82 (15592,8,794,4)
GO:0002855	regulation of natural killer cell mediated immune response to tumor cell	3.96E-04	1.15E-02	9.82 (15592,8,794,4)
GO:0000070	mitotic sister chromatid segregation	4.00E-04	1.15E-02	4.91 (15592,28,794,7)
GO:0033047	regulation of mitotic sister chromatid segregation	4.01E-04	1.15E-02	3.32 (15592,65,794,11)
GO:2000508	regulation of dendritic cell chemotaxis	3.96E-04	1.16E-02	9.82 (15592,8,794,4)
GO:0002920	regulation of humoral immune response	4.00E-04	1.16E-02	4.91 (15592,28,794,7)
GO:0000226	microtubule cytoskeleton organization	4.08E-04	1.17E-02	1.89 (15592,332,794,32)
GO:0051241	negative regulation of multicellular organismal process	4.08E-04	1.17E-02	1.44 (15592,1145,794,84)
GO:0071222	cellular response to lipopolysaccharide	4.21E-04	1.20E-02	2.51 (15592,133,794,17)
GO:0008092	cytoskeletal protein binding	7.15E-05	1.21E-02	1.59 (15592,879,794,71)
GO:0043168	anion binding	6.80E-05	1.25E-02	1.33 (15592,2368,794,160)
GO:0004672	protein kinase activity	7.11E-05	1.25E-02	1.79 (15592,528,794,48)
GO:0032732	positive regulation of interleukin-1 production	4.43E-04	1.26E-02	3.84 (15592,46,794,9)
GO:0032559	adenyl ribonucleotide binding	6.58E-05	1.26E-02	1.47 (15592,1295,794,97)

GO:0045620	negative regulation of lymphocyte differentiation	4.43E-04	1.27E-02	3.84 (15592,46,794,9)
GO:0033043	regulation of organelle organization	4.50E-04	1.28E-02	1.44 (15592,1132,794,83)
GO:0032814	regulation of natural killer cell activation	4.51E-04	1.28E-02	4.25 (15592,37,794,8)
GO:1990266	neutrophil migration	4.59E-04	1.30E-02	3.27 (15592,66,794,11)
GO:0032740	positive regulation of interleukin-17 production	4.61E-04	1.30E-02	7.01 (15592,14,794,5)
GO:0044770	cell cycle phase transition	4.61E-04	1.30E-02	2.58 (15592,122,794,16)
GO:0042130	negative regulation of T cell proliferation	4.68E-04	1.32E-02	3.51 (15592,56,794,10)
GO:0071900	regulation of protein serine/threonine kinase activity	4.83E-04	1.36E-02	1.80 (15592,393,794,36)
GO:0032652	regulation of interleukin-1 production	4.86E-04	1.37E-02	3.06 (15592,77,794,12)
GO:0032813	tumor necrosis factor receptor superfamily binding	9.44E-05	1.39E-02	4.65 (15592,38,794,9)
GO:0002865	negative regulation of acute inflammatory response to antigenic stimulus	5.06E-04	1.40E-02	14.73 (15592,4,794,3)
GO:0016043	cellular component organization	5.03E-04	1.41E-02	1.19 (15592,4143,794,252)
GO:0002431	Fc receptor mediated stimulatory signaling pathway	5.06E-04	1.41E-02	14.73 (15592,4,794,3)
GO:0002636	positive regulation of germinal center formation	5.06E-04	1.41E-02	14.73 (15592,4,794,3)
GO:0045578	negative regulation of B cell differentiation	5.06E-04	1.41E-02	14.73 (15592,4,794,3)
GO:2000410	regulation of thymocyte migration	5.06E-04	1.41E-02	14.73 (15592,4,794,3)
GO:2000566	positive regulation of CD8-positive, alpha-beta T cell proliferation	5.06E-04	1.42E-02	14.73 (15592,4,794,3)
GO:0043548	phosphatidylinositol 3-kinase binding	9.44E-05	1.44E-02	4.65 (15592,38,794,9)
GO:0045595	regulation of cell differentiation	5.23E-04	1.45E-02	1.35 (15592,1645,794,113)
GO:0044877	protein-containing complex binding	9.34E-05	1.47E-02	1.50 (15592,1127,794,86)
GO:0030554	adenyl nucleotide binding	9.04E-05	1.48E-02	1.46 (15592,1306,794,97)
GO:0002200	somatic diversification of immune receptors	5.46E-04	1.51E-02	4.13 (15592,38,794,8)
GO:1901992	positive regulation of mitotic cell cycle phase transition	5.48E-04	1.51E-02	3.02 (15592,78,794,12)
GO:0021700	developmental maturation	5.50E-04	1.51E-02	2.32 (15592,161,794,19)
GO:0050729	positive regulation of inflammatory response	5.53E-04	1.52E-02	2.53 (15592,124,794,16)
GO:0009615	response to virus	5.63E-04	1.54E-02	2.21 (15592,187,794,21)
GO:0051050	positive regulation of transport	5.85E-04	1.60E-02	1.48 (15592,944,794,71)
GO:0022408	negative regulation of cell-cell adhesion	5.94E-04	1.62E-02	2.30 (15592,162,794,19)
GO:0045121	membrane raft	2.50E-04	1.67E-02	1.95 (15592,323,794,32)
GO:2000406	positive regulation of T cell migration	6.29E-04	1.71E-02	4.58 (15592,30,794,7)
GO:0090218	positive regulation of lipid kinase activity	6.29E-04	1.71E-02	4.58 (15592,30,794,7)
GO:0042104	positive regulation of activated T cell proliferation	6.32E-04	1.71E-02	5.36 (15592,22,794,6)
GO:0098857	membrane microdomain	2.65E-04	1.71E-02	1.94 (15592,324,794,32)
GO:0002456	T cell mediated immunity	6.29E-04	1.72E-02	4.58 (15592,30,794,7)
GO:0045408	regulation of interleukin-6 biosynthetic process	6.32E-04	1.72E-02	5.36 (15592,22,794,6)
GO:1901570	fatty acid derivative biosynthetic process	6.57E-04	1.78E-02	4.03 (15592,39,794,8)
GO:0006260	DNA replication	6.61E-04	1.78E-02	2.49 (15592,126,794,16)
GO:0007076	mitotic chromosome condensation	6.62E-04	1.78E-02	6.55 (15592,15,794,5)
GO:0042981	regulation of apoptotic process	6.79E-04	1.82E-02	1.38 (15592,1349,794,95)
GO:0033004	negative regulation of mast cell activation	6.84E-04	1.82E-02	8.73 (15592,9,794,4)
GO:0002885	positive regulation of hypersensitivity	6.84E-04	1.82E-02	8.73 (15592,9,794,4)
GO:0051223	regulation of protein transport	6.85E-04	1.82E-02	1.59 (15592,629,794,51)
GO:0045835	negative regulation of meiotic nuclear division	6.84E-04	1.83E-02	8.73 (15592,9,794,4)
GO:0036037	CD8-positive, alpha-beta T cell activation	6.84E-04	1.83E-02	8.73 (15592,9,794,4)
GO:0042590	antigen processing and presentation of exogenous peptide antigen via MHC class I	6.84E-04	1.83E-02	8.73 (15592,9,794,4)
GO:0002634	regulation of germinal center formation	6.84E-04	1.84E-02	8.73 (15592,9,794,4)
GO:0071840	cellular component organization or biogenesis	7.01E-04	1.86E-02	1.19 (15592,4221,794,255)
GO:0033674	positive regulation of kinase activity	7.41E-04	1.96E-02	1.73 (15592,432,794,38)
GO:0000779	condensed chromosome, centromeric region	3.58E-04	1.98E-02	5.89 (15592,20,794,6)
GO:0090087	regulation of peptide transport	7.51E-04	1.99E-02	1.57 (15592,663,794,53)
GO:0044421	extracellular region part	3.53E-04	2.01E-02	1.40 (15592,1407,794,100)
GO:0060401	cytosolic calcium ion transport	7.69E-04	2.02E-02	3.09 (15592,70,794,11)
GO:0051279	regulation of release of sequestered calcium ion into cytosol	7.69E-04	2.03E-02	3.09 (15592,70,794,11)
GO:0005764	lysosome	3.51E-04	2.06E-02	1.85 (15592,372,794,35)
GO:0051480	regulation of cytosolic calcium ion concentration	8.03E-04	2.11E-02	1.94 (15592,274,794,27)
GO:0032703	negative regulation of interleukin-2 production	8.19E-04	2.13E-02	5.12 (15592,23,794,6)
GO:0003779	actin binding	1.50E-04	2.13E-02	1.89 (15592,384,794,37)
GO:0000323	lytic vacuole	3.51E-04	2.13E-02	1.85 (15592,372,794,35)
GO:0009968	negative regulation of signal transduction	8.17E-04	2.14E-02	1.44 (15592,1038,794,76)
GO:1900274	regulation of phospholipase C activity	8.19E-04	2.14E-02	5.12 (15592,23,794,6)
GO:0002335	mature B cell differentiation	8.19E-04	2.14E-02	5.12 (15592,23,794,6)
GO:0034113	heterotypic cell-cell adhesion	8.19E-04	2.14E-02	5.12 (15592,23,794,6)
GO:1901700	response to oxygen-containing compound	8.29E-04	2.16E-02	1.45 (15592,989,794,73)
GO:0005884	actin filament	3.46E-04	2.16E-02	3.00 (15592,85,794,13)
GO:0098589	membrane region	4.08E-04	2.19E-02	1.89 (15592,332,794,32)
GO:0000910	cytokinesis	8.69E-04	2.26E-02	3.04 (15592,71,794,11)
GO:0043410	positive regulation of MAPK cascade	8.79E-04	2.28E-02	1.70 (15592,451,794,39)
GO:0010941	regulation of cell death	9.12E-04	2.36E-02	1.35 (15592,1498,794,103)
GO:0045410	positive regulation of interleukin-6 biosynthetic process	9.23E-04	2.38E-02	6.14 (15592,16,794,5)
GO:2001185	regulation of CD8-positive, alpha-beta T cell activation	9.23E-04	2.38E-02	6.14 (15592,16,794,5)
GO:0002863	positive regulation of inflammatory response to antigenic stimulus	9.23E-04	2.38E-02	6.14 (15592,16,794,5)
GO:0002639	positive regulation of immunoglobulin production	9.33E-04	2.40E-02	3.83 (15592,41,794,8)
GO:0044430	cytoskeletal part	4.59E-04	2.40E-02	1.40 (15592,1350,794,96)
GO:0042592	homeostatic process	9.91E-04	2.54E-02	1.38 (15592,1280,794,90)
GO:0060627	regulation of vesicle-mediated transport	9.95E-04	2.55E-02	1.64 (15592,515,794,43)
GO:0008305	integrin complex	5.04E-04	2.57E-02	4.74 (15592,29,794,7)
GO:0098562	cytoplasmic side of membrane	5.25E-04	2.60E-02	3.22 (15592,67,794,11)
GO:0061134	peptidase regulator activity	1.95E-04	2.68E-02	2.38 (15592,173,794,21)
GO:0019899	enzyme binding	2.01E-04	2.68E-02	1.32 (15592,2121,794,143)
GO:0004866	endopeptidase inhibitor activity	2.24E-04	2.90E-02	2.56 (15592,138,794,18)
GO:0005126	cytokine receptor binding	2.34E-04	2.95E-02	2.13 (15592,240,794,26)
GO:0005102	signaling receptor binding	3.28E-04	4.01E-02	1.41 (15592,1320,794,95)
GO:0061135	endopeptidase regulator activity	3.80E-04	4.41E-02	2.45 (15592,144,794,18)
GO:0000166	nucleotide binding	4.14E-04	4.45E-02	1.34 (15592,1807,794,123)
GO:0042287	MHC protein binding	4.00E-04	4.52E-02	4.91 (15592,28,794,7)
GO:0030414	peptidase inhibitor activity	3.80E-04	4.53E-02	2.45 (15592,144,794,18)
GO:1901265	nucleoside phosphate binding	4.14E-04	4.56E-02	1.34 (15592,1807,794,123)
GO:0000922	spindle pole	9.53E-04	4.61E-02	2.59 (15592,106,794,14)
GO:0016773	phosphotransferase activity, alcohol group as acceptor	4.76E-04	4.99E-02	1.62 (15592,619,794,51)

12 week old NOD islets: GO terms associated with genes upregulated by ≥3-fold

GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)*
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GO:0051707	response to other organism	5.36E-12	2.70E-08	3.36 (15592,502,388,42)
GO:0009607	response to biotic stimulus	4.42E-12	3.34E-08	2.97 (15592,676,388,50)
GO:0009617	response to bacterium	1.38E-11	5.22E-08	4.21 (15592,296,388,31)
GO:0005615	extracellular space	3.28E-11	6.34E-08	2.35 (15592,1144,388,67)
GO:0043207	response to external biotic stimulus	4.40E-12	6.65E-08	3.02 (15592,653,388,49)
GO:0009605	response to external stimulus	5.88E-11	1.78E-07	2.36 (15592,1106,388,65)
GO:0044421	extracellular region part	3.86E-10	3.73E-07	2.11 (15592,1407,388,74)
GO:0019730	antimicrobial humoral response	1.04E-09	2.63E-06	9.17 (15592,57,388,13)
GO:0006955	immune response	2.44E-09	5.27E-06	2.72 (15592,635,388,43)
GO:0061844	antimicrobial humoral immune response mediated by antimicrobial peptide	9.34E-09	1.77E-05	9.82 (15592,45,388,11)
GO:0005576	extracellular region	4.02E-08	2.60E-05	2.04 (15592,1243,388,63)
GO:0006952	defense response	1.79E-08	3.00E-05	2.42 (15592,781,388,47)
GO:0051704	multi-organism process	2.74E-08	4.14E-05	2.41 (15592,766,388,46)
GO:0042742	defense response to bacterium	5.79E-08	7.29E-05	4.44 (15592,172,388,19)
GO:0098542	defense response to other organism	5.53E-08	7.60E-05	3.31 (15592,328,388,27)
GO:0002251	organ or tissue specific immune response	1.44E-07	1.68E-04	12.36 (15592,26,388,8)
GO:0051673	membrane disruption in other organism	1.86E-07	2.01E-04	20.09 (15592,12,388,6)
GO:0032879	regulation of localization	3.06E-07	3.09E-04	1.62 (15592,2480,388,100)
GO:0042221	response to chemical	3.93E-07	3.12E-04	1.67 (15592,2165,388,90)
GO:0048519	negative regulation of biological process	3.36E-07	3.17E-04	1.41 (15592,4404,388,155)
GO:0010033	response to organic substance	3.90E-07	3.27E-04	1.77 (15592,1751,388,77)
GO:0051239	regulation of multicellular organismal process	3.73E-07	3.32E-04	1.58 (15592,2724,388,107)
GO:0071219	cellular response to molecule of bacterial origin	4.96E-07	3.57E-04	4.53 (15592,142,388,16)
GO:0030545	receptor regulator activity	8.17E-08	3.60E-04	3.08 (15592,378,388,29)
GO:0002376	immune system process	4.87E-07	3.68E-04	1.97 (15592,1185,388,58)
GO:0080134	regulation of response to stress	5.94E-07	3.90E-04	1.97 (15592,1163,388,57)
GO:0031347	regulation of defense response	5.84E-07	4.01E-04	2.55 (15592,536,388,34)
GO:0071216	cellular response to biotic stimulus	7.21E-07	4.54E-04	4.17 (15592,164,388,17)
GO:0048018	receptor ligand activity	2.46E-07	5.43E-04	3.07 (15592,353,388,27)
GO:0002237	response to molecule of bacterial origin	9.79E-07	5.92E-04	3.56 (15592,226,388,20)
GO:0071222	cellular response to lipopolysaccharide	1.12E-06	6.24E-04	4.53 (15592,133,388,15)
GO:1902531	regulation of intracellular signal transduction	1.10E-06	6.37E-04	1.81 (15592,1486,388,67)
GO:0032496	response to lipopolysaccharide	1.22E-06	6.59E-04	3.65 (15592,209,388,19)
GO:0002385	mucosal immune response	1.34E-06	7.00E-04	11.72 (15592,24,388,7)
GO:0048583	regulation of response to stimulus	1.83E-06	9.24E-04	1.49 (15592,3193,388,118)
GO:0040012	regulation of locomotion	2.06E-06	1.00E-03	2.06 (15592,919,388,47)
GO:0005102	signaling receptor binding	7.63E-07	1.12E-03	1.89 (15592,1320,388,62)
GO:0048523	negative regulation of cellular process	2.42E-06	1.14E-03	1.41 (15592,3992,388,140)
GO:0048518	positive regulation of biological process	2.86E-06	1.31E-03	1.34 (15592,5036,388,168)
GO:0019731	antibacterial humoral response	3.23E-06	1.44E-03	10.42 (15592,27,388,7)
GO:0005125	cytokine activity	1.48E-06	1.64E-03	4.18 (15592,154,388,16)
GO:0043408	regulation of MAPK cascade	4.76E-06	2.05E-03	2.25 (15592,642,388,36)
GO:0005126	cytokine receptor binding	2.50E-06	2.20E-03	3.35 (15592,240,388,20)
GO:0050896	response to stimulus	6.09E-06	2.56E-03	1.40 (15592,3912,388,136)
GO:1901700	response to oxygen-containing compound	6.66E-06	2.65E-03	1.95 (15592,989,388,48)
GO:0042044	fluid transport	6.59E-06	2.69E-03	12.06 (15592,20,388,6)
GO:2000145	regulation of cell motility	6.99E-06	2.71E-03	2.04 (15592,847,388,43)
GO:0051240	positive regulation of multicellular organismal process	7.51E-06	2.84E-03	1.70 (15592,1635,388,69)
GO:0045087	innate immune response	8.29E-06	2.91E-03	2.82 (15592,328,388,23)
GO:0006959	humoral immune response	8.26E-06	2.97E-03	4.39 (15592,119,388,13)
GO:0010646	regulation of cell communication	8.21E-06	3.03E-03	1.50 (15592,2767,388,103)
GO:0002227	innate immune response in mucosa	9.03E-06	3.10E-03	11.48 (15592,21,388,6)
GO:0051046	regulation of secretion	9.28E-06	3.12E-03	2.08 (15592,772,388,40)
GO:0023051	regulation of signaling	1.04E-05	3.42E-03	1.49 (15592,2782,388,103)
GO:0009966	regulation of signal transduction	1.08E-05	3.48E-03	1.53 (15592,2409,388,92)
GO:0050829	defense response to Gram-negative bacterium	1.21E-05	3.80E-03	6.24 (15592,58,388,9)
GO:0048522	positive regulation of cellular process	1.32E-05	4.08E-03	1.34 (15592,4519,388,151)
GO:0030334	regulation of cell migration	1.36E-05	4.10E-03	2.03 (15592,813,388,41)
GO:0042325	regulation of phosphorylation	1.72E-05	5.00E-03	1.74 (15592,1360,388,59)
GO:0033993	response to lipid	1.71E-05	5.07E-03	2.36 (15592,493,388,29)
GO:0051270	regulation of cellular component movement	2.32E-05	6.62E-03	1.92 (15592,919,388,44)
GO:1903524	positive regulation of blood circulation	2.53E-05	6.71E-03	5.09 (15592,79,388,10)
GO:1903530	regulation of secretion by cell	2.59E-05	6.76E-03	2.06 (15592,722,388,37)
GO:0051047	positive regulation of secretion	2.47E-05	6.78E-03	2.41 (15592,451,388,27)
GO:0045604	regulation of epidermal cell differentiation	2.53E-05	6.82E-03	6.56 (15592,49,388,8)
GO:0042045	epithelial fluid transport	2.44E-05	6.83E-03	20.09 (15592,8,388,4)
GO:0016324	apical plasma membrane	1.46E-05	7.07E-03	2.98 (15592,270,388,20)
GO:0051241	negative regulation of multicellular organismal process	3.48E-05	8.76E-03	1.79 (15592,1145,388,51)
GO:0003018	vascular process in circulatory system	3.47E-05	8.90E-03	3.42 (15592,176,388,15)
GO:0065007	biological regulation	3.80E-05	9.41E-03	1.17 (15592,9126,388,265)
GO:0019220	regulation of phosphate metabolic process	4.41E-05	1.07E-02	1.66 (15592,1500,388,62)
GO:0051174	regulation of phosphorus metabolic process	4.49E-05	1.08E-02	1.66 (15592,1501,388,62)
GO:0071396	cellular response to lipid	4.71E-05	1.11E-02	2.74 (15592,293,388,20)
GO:0001817	regulation of cytokine production	5.52E-05	1.28E-02	2.15 (15592,580,388,31)
GO:0080090	regulation of primary metabolic process	5.72E-05	1.29E-02	1.31 (15592,4526,388,148)
GO:0045682	regulation of epidermis development	5.67E-05	1.30E-02	5.17 (15592,70,388,9)
GO:1903532	positive regulation of secretion by cell	5.85E-05	1.30E-02	2.38 (15592,422,388,25)
GO:0010648	negative regulation of cell communication	5.92E-05	1.30E-02	1.77 (15592,1138,388,50)
GO:0009725	response to hormone	6.48E-05	1.40E-02	2.42 (15592,399,388,24)
GO:0023057	negative regulation of signaling	6.62E-05	1.41E-02	1.76 (15592,1143,388,50)
GO:0022600	digestive system process	6.84E-05	1.44E-02	5.74 (15592,56,388,8)
GO:0019222	regulation of metabolic process	7.49E-05	1.55E-02	1.29 (15592,5000,388,160)
GO:0050708	regulation of protein secretion	7.62E-05	1.56E-02	2.34 (15592,429,388,25)
GO:0050789	regulation of biological process	7.87E-05	1.59E-02	1.17 (15592,8652,388,252)
GO:0001932	regulation of protein phosphorylation	8.33E-05	1.66E-02	1.71 (15592,1247,388,53)
GO:0008610	lipid biosynthetic process	8.81E-05	1.73E-02	2.48 (15592,356,388,22)
GO:0035821	modification of morphology or physiology of other organism	1.00E-04	1.92E-02	3.98 (15592,111,388,11)
GO:0045088	regulation of innate immune response	9.98E-05	1.93E-02	2.87 (15592,238,388,17)
GO:1902533	positive regulation of intracellular signal transduction	1.18E-04	2.23E-02	1.86 (15592,865,388,40)
GO:0065008	regulation of biological quality	1.26E-04	2.35E-02	1.39 (15592,3095,388,107)
GO:0050830	defense response to Gram-positive bacterium	1.34E-04	2.46E-02	4.64 (15592,78,388,9)
GO:0050878	regulation of body fluid levels	1.35E-04	2.46E-02	2.80 (15592,244,388,17)
GO:0008083	growth factor activity	3.47E-05	2.55E-02	4.12 (15592,117,388,12)

GO:0042536	negative regulation of tumor necrosis factor biosynthetic process	1.47E-04	2.65E-02	24.11 (15592,5,388,3)
GO:0050794	regulation of cellular process	1.51E-04	2.65E-02	1.17 (15592,8140,388,238)
GO:0031349	positive regulation of defense response	1.51E-04	2.68E-02	2.68 (15592,270,388,18)
GO:0051248	negative regulation of protein metabolic process	1.57E-04	2.70E-02	1.80 (15592,937,388,42)
GO:0003013	circulatory system process	1.57E-04	2.73E-02	3.00 (15592,201,388,15)
GO:0009893	positive regulation of metabolic process	1.77E-04	3.00E-02	1.38 (15592,3050,388,105)
GO:0070851	growth factor receptor binding	5.26E-05	3.31E-02	3.95 (15592,122,388,12)
GO:0031325	positive regulation of cellular metabolic process	2.05E-04	3.44E-02	1.40 (15592,2813,388,98)
GO:0071347	cellular response to interleukin-1	2.22E-04	3.69E-02	5.63 (15592,50,388,7)
GO:0002791	regulation of peptide secretion	2.34E-04	3.84E-02	2.18 (15592,461,388,25)
GO:0016126	sterol biosynthetic process	2.36E-04	3.84E-02	6.70 (15592,36,388,6)
GO:0048871	multicellular organismal homeostasis	2.44E-04	3.93E-02	3.90 (15592,103,388,10)
GO:0009986	cell surface	1.09E-04	4.21E-02	2.10 (15592,574,388,30)
GO:0006954	inflammatory response	2.70E-04	4.25E-02	2.48 (15592,308,388,19)
GO:0031323	regulation of cellular metabolic process	2.70E-04	4.29E-02	1.28 (15592,4664,388,148)
GO:0006925	inflammatory cell apoptotic process	2.89E-04	4.46E-02	20.09 (15592,6,388,3)
GO:0050793	regulation of developmental process	2.89E-04	4.50E-02	1.44 (15592,2314,388,83)
GO:0035296	regulation of tube diameter	3.31E-04	4.77E-02	3.26 (15592,148,388,12)
GO:0044057	regulation of system process	3.37E-04	4.81E-02	2.09 (15592,500,388,26)
GO:0097746	regulation of blood vessel diameter	3.31E-04	4.82E-02	3.26 (15592,148,388,12)
GO:0050880	regulation of blood vessel size	3.31E-04	4.86E-02	3.26 (15592,148,388,12)
GO:0042036	negative regulation of cytokine biosynthetic process	3.28E-04	4.90E-02	8.04 (15592,25,388,5)
GO:0120161	regulation of cold-induced thermogenesis	3.31E-04	4.90E-02	3.48 (15592,127,388,11)
GO:0045823	positive regulation of heart contraction	3.21E-04	4.91E-02	6.35 (15592,38,388,6)
GO:0051246	regulation of protein metabolic process	3.47E-04	4.91E-02	1.43 (15592,2362,388,84)
GO:0035150	regulation of tube size	3.53E-04	4.93E-02	3.24 (15592,149,388,12)
GO:0010460	positive regulation of heart rate	3.28E-04	4.95E-02	8.04 (15592,25,388,5)
GO:0051093	negative regulation of developmental process	3.60E-04	4.95E-02	1.76 (15592,913,388,40)
GO:0048869	cellular developmental process	3.64E-04	4.96E-02	1.42 (15592,2470,388,87)
GO:0050714	positive regulation of protein secretion	3.58E-04	4.97E-02	2.58 (15592,265,388,17)
GO:0031325	positive regulation of cellular metabolic process	9.36E-06	1.33E-03	1.66 (15592,2813,220,66)
GO:0010604	positive regulation of macromolecule metabolic process	9.03E-06	1.34E-03	1.66 (15592,2810,220,66)
GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	9.20E-06	1.34E-03	5.20 (15592,150,220,11)
GO:0009891	positive regulation of biosynthetic process	9.51E-06	1.34E-03	1.92 (15592,1697,220,46)
GO:0045893	positive regulation of transcription, DNA-templated	9.96E-06	1.38E-03	2.07 (15592,1337,220,39)
GO:2000147	positive regulation of cell motility	9.92E-06	1.39E-03	2.95 (15592,505,220,21)
GO:1903508	positive regulation of nucleic acid-templated transcription	1.05E-05	1.44E-03	2.06 (15592,1340,220,39)
GO:1902680	positive regulation of RNA biosynthetic process	1.07E-05	1.45E-03	2.06 (15592,1341,220,39)
GO:0072300	positive regulation of metanephric glomerulus development	1.10E-05	1.48E-03	53.15 (15592,4,220,3)
GO:0019222	regulation of metabolic process	1.11E-05	1.48E-03	1.43 (15592,5000,220,101)
GO:0019220	regulation of phosphate metabolic process	1.16E-05	1.54E-03	1.98 (15592,1500,220,42)
GO:0051174	regulation of phosphorus metabolic process	1.18E-05	1.56E-03	1.98 (15592,1501,220,42)
GO:0001932	regulation of protein phosphorylation	1.20E-05	1.56E-03	2.10 (15592,1247,220,37)
GO:0008201	heparin binding	3.84E-06	1.69E-03	5.69 (15592,137,220,11)
GO:0033627	cell adhesion mediated by integrin	1.46E-05	1.89E-03	15.41 (15592,23,220,5)
GO:0005583	fibrillar collagen trimer	1.18E-05	1.90E-03	25.77 (15592,11,220,4)
GO:0051272	positive regulation of cellular component movement	1.54E-05	1.97E-03	2.86 (15592,520,220,21)
GO:0008285	negative regulation of cell proliferation	1.62E-05	2.05E-03	2.69 (15592,606,220,23)
GO:0045581	negative regulation of T cell differentiation	1.63E-05	2.05E-03	10.90 (15592,39,220,6)
GO:0031345	negative regulation of cell projection organization	1.65E-05	2.06E-03	4.48 (15592,190,220,12)
GO:0060255	regulation of macromolecule metabolic process	1.68E-05	2.08E-03	1.45 (15592,4590,220,94)
GO:0090179	planar cell polarity pathway involved in neural tube closure	1.75E-05	2.13E-03	23.62 (15592,12,220,4)
GO:0030278	regulation of ossification	1.74E-05	2.14E-03	4.45 (15592,191,220,12)
GO:0010977	negative regulation of neuron projection development	1.80E-05	2.17E-03	4.84 (15592,161,220,11)
GO:0060071	Wnt signaling pathway, planar cell polarity pathway	1.83E-05	2.19E-03	14.77 (15592,24,220,5)
GO:0030512	negative regulation of transforming growth factor beta receptor signaling pathway	1.85E-05	2.20E-03	8.41 (15592,59,220,7)
GO:0043393	regulation of protein binding	1.90E-05	2.24E-03	4.09 (15592,225,220,13)
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	1.98E-05	2.32E-03	3.60 (15592,295,220,15)
GO:0048754	branching morphogenesis of an epithelial tube	2.16E-05	2.51E-03	5.25 (15592,135,220,10)
GO:0051960	regulation of nervous system development	2.19E-05	2.53E-03	2.27 (15592,937,220,30)
GO:0050789	regulation of biological process	2.23E-05	2.55E-03	1.25 (15592,8652,220,152)
GO:0030111	regulation of Wnt signaling pathway	2.27E-05	2.58E-03	3.77 (15592,263,220,14)
GO:1903845	negative regulation of cellular response to transforming growth factor beta stimulus	2.31E-05	2.61E-03	8.13 (15592,61,220,7)
GO:0009968	negative regulation of signal transduction	2.40E-05	2.69E-03	2.18 (15592,1038,220,32)
GO:0016342	catenin complex	1.83E-05	2.72E-03	14.77 (15592,24,220,5)
GO:0050767	regulation of neurogenesis	2.61E-05	2.87E-03	2.33 (15592,851,220,28)
GO:0030545	receptor regulator activity	7.16E-06	2.87E-03	3.37 (15592,378,220,18)
GO:0017147	Wnt-protein binding	8.50E-06	2.88E-03	12.15 (15592,35,220,6)
GO:0050768	negative regulation of neurogenesis	2.60E-05	2.89E-03	3.52 (15592,302,220,15)
GO:0003700	DNA-binding transcription factor activity	7.86E-06	2.89E-03	2.49 (15592,797,220,28)
GO:0072298	regulation of metanephric glomerulus development	2.71E-05	2.97E-03	42.52 (15592,5,220,3)
GO:0003002	regionalization	2.74E-05	2.98E-03	3.95 (15592,233,220,13)
GO:0000902	cell morphogenesis	2.87E-05	3.09E-03	3.94 (15592,234,220,13)
GO:0045668	negative regulation of osteoblast differentiation	2.91E-05	3.11E-03	9.89 (15592,43,220,6)
GO:0045995	regulation of embryonic development	3.16E-05	3.36E-03	5.64 (15592,113,220,9)
GO:0001657	ureteric bud development	3.32E-05	3.51E-03	9.66 (15592,44,220,6)
GO:0048018	receptor ligand activity	1.12E-05	3.53E-03	3.41 (15592,353,220,17)
GO:0045667	regulation of osteoblast differentiation	3.38E-05	3.55E-03	5.60 (15592,114,220,9)
GO:0042325	regulation of phosphorylation	3.44E-05	3.58E-03	1.98 (15592,1360,220,38)
GO:0090178	regulation of establishment of planar polarity involved in neural tube closure	3.46E-05	3.58E-03	20.25 (15592,14,220,4)
GO:0050730	regulation of peptidyl-tyrosine phosphorylation	3.57E-05	3.65E-03	3.86 (15592,239,220,13)
GO:0010557	positive regulation of macromolecule biosynthetic process	3.56E-05	3.66E-03	1.89 (15592,1572,220,42)
GO:0045165	cell fate commitment	3.77E-05	3.83E-03	4.92 (15592,144,220,10)
GO:0048870	cell motility	4.17E-05	4.20E-03	2.36 (15592,780,220,26)
GO:0045620	negative regulation of lymphocyte differentiation	4.31E-05	4.28E-03	9.24 (15592,46,220,6)
GO:0051254	positive regulation of RNA metabolic process	4.29E-05	4.29E-03	1.94 (15592,1426,220,39)
GO:0045664	regulation of neuron differentiation	4.41E-05	4.35E-03	2.46 (15592,691,220,24)
GO:0032963	collagen metabolic process	4.88E-05	4.79E-03	9.05 (15592,47,220,6)
GO:0045937	positive regulation of phosphate metabolic process	5.05E-05	4.90E-03	2.17 (15592,980,220,30)
GO:0010562	positive regulation of phosphorus metabolic process	5.05E-05	4.93E-03	2.17 (15592,980,220,30)
GO:0048407	platelet-derived growth factor binding	1.75E-05	5.13E-03	23.62 (15592,12,220,4)
GO:0032808	lacrimal gland development	5.37E-05	5.17E-03	35.44 (15592,6,220,3)
GO:0010811	positive regulation of cell-substrate adhesion	5.42E-05	5.18E-03	5.27 (15592,121,220,9)

GO:0072164	mesonephric tubule development	5.51E-05	5.24E-03	8.86 (15592,48,220,6)
GO:0098609	cell-cell adhesion	5.63E-05	5.25E-03	3.29 (15592,323,220,15)
GO:0016055	Wnt signaling pathway	5.57E-05	5.26E-03	3.96 (15592,215,220,12)
GO:0048468	cell development	5.63E-05	5.28E-03	2.55 (15592,612,220,22)
GO:0034329	cell junction assembly	5.78E-05	5.36E-03	5.23 (15592,122,220,9)
GO:0045935	positive regulation of nucleobase-containing compound metabolic process	5.84E-05	5.39E-03	1.85 (15592,1606,220,42)
GO:0061138	morphogenesis of a branching epithelium	5.98E-05	5.44E-03	4.66 (15592,152,220,10)
GO:0010648	negative regulation of cell communication	5.96E-05	5.46E-03	2.06 (15592,1138,220,33)
GO:0051961	negative regulation of nervous system development	6.04E-05	5.47E-03	3.27 (15592,325,220,15)
GO:0072163	mesonephric epithelium development	6.21E-05	5.59E-03	8.68 (15592,49,220,6)
GO:0017015	regulation of transforming growth factor beta receptor signaling pathway	6.32E-05	5.65E-03	5.91 (15592,96,220,8)
GO:0023057	negative regulation of signaling	6.49E-05	5.77E-03	2.05 (15592,1143,220,33)
GO:0060070	canonical Wnt signaling pathway	6.85E-05	6.02E-03	6.89 (15592,72,220,7)
GO:0040011	locomotion	6.83E-05	6.04E-03	2.25 (15592,851,220,27)
GO:0001822	kidney development	6.98E-05	6.10E-03	5.10 (15592,125,220,9)
GO:1905114	cell surface receptor signaling pathway involved in cell-cell signaling	7.27E-05	6.27E-03	3.85 (15592,221,220,12)
GO:0006928	movement of cell or subcellular component	7.23E-05	6.28E-03	2.06 (15592,1099,220,32)
GO:1903844	regulation of cellular response to transforming growth factor beta stimulus	7.32E-05	6.29E-03	5.79 (15592,98,220,8)
GO:0002009	morphogenesis of an epithelium	7.37E-05	6.29E-03	3.39 (15592,293,220,14)
GO:0051098	regulation of binding	7.43E-05	6.31E-03	3.06 (15592,370,220,16)
GO:0045944	positive regulation of transcription by RNA polymerase II	7.49E-05	6.32E-03	2.09 (15592,1051,220,31)
GO:0048701	embryonic cranial skeleton morphogenesis	7.89E-05	6.55E-03	11.07 (15592,32,220,5)
GO:0003151	outflow tract morphogenesis	7.81E-05	6.56E-03	8.34 (15592,51,220,6)
GO:0060351	cartilage development involved in endochondral bone morphogenesis	7.95E-05	6.56E-03	16.68 (15592,17,220,4)
GO:0048514	blood vessel morphogenesis	7.87E-05	6.57E-03	5.73 (15592,99,220,8)
GO:0065009	regulation of molecular function	8.07E-05	6.62E-03	1.69 (15592,2185,220,52)
GO:0007417	central nervous system development	8.90E-05	7.27E-03	6.61 (15592,75,220,7)
GO:0001763	morphogenesis of a branching structure	9.19E-05	7.47E-03	4.43 (15592,160,220,10)
GO:0001934	positive regulation of protein phosphorylation	9.52E-05	7.69E-03	2.20 (15592,868,220,27)
GO:0007219	Notch signaling pathway	9.72E-05	7.82E-03	5.56 (15592,102,220,8)
GO:0045597	positive regulation of cell differentiation	9.79E-05	7.83E-03	2.13 (15592,967,220,29)
GO:0051171	regulation of nitrogen compound metabolic process	1.01E-04	8.01E-03	1.42 (15592,4401,220,88)
GO:1905276	regulation of epithelial tube formation	1.01E-04	8.04E-03	15.75 (15592,18,220,4)
GO:0031323	regulation of cellular metabolic process	1.05E-04	8.27E-03	1.40 (15592,4664,220,92)
GO:0035567	non-canonical Wnt signaling pathway	1.07E-04	8.34E-03	10.42 (15592,34,220,5)
GO:0042733	embryonic digit morphogenesis	1.08E-04	8.43E-03	7.87 (15592,54,220,6)
GO:1901342	regulation of vasculature development	1.13E-04	8.74E-03	3.25 (15592,305,220,14)
GO:0051252	regulation of RNA metabolic process	1.16E-04	8.88E-03	1.59 (15592,2623,220,59)
GO:0007507	heart development	1.15E-04	8.89E-03	3.67 (15592,232,220,12)
GO:0031401	positive regulation of protein modification process	1.17E-04	8.93E-03	2.04 (15592,1077,220,31)
GO:0090090	negative regulation of canonical Wnt signaling pathway	1.27E-04	9.54E-03	5.35 (15592,106,220,8)
GO:0010629	negative regulation of gene expression	1.27E-04	9.55E-03	1.88 (15592,1393,220,37)
GO:0072215	regulation of metanephros development	1.27E-04	9.56E-03	14.92 (15592,19,220,4)
GO:0070208	protein heterotrimerization	1.27E-04	9.61E-03	14.92 (15592,19,220,4)
GO:0060828	regulation of canonical Wnt signaling pathway	1.30E-04	9.65E-03	3.90 (15592,200,220,11)
GO:0030241	skeletal muscle myosin thick filament assembly	1.47E-04	1.08E-02	26.58 (15592,8,220,3)
GO:0048539	bone marrow development	1.47E-04	1.08E-02	26.58 (15592,8,220,3)
GO:0010812	negative regulation of cell-substrate adhesion	1.47E-04	1.09E-02	7.46 (15592,57,220,6)
GO:0071688	striated muscle myosin thick filament assembly	1.47E-04	1.09E-02	26.58 (15592,8,220,3)
GO:0097485	neuron projection guidance	1.52E-04	1.10E-02	4.17 (15592,170,220,10)
GO:0065007	biological regulation	1.53E-04	1.11E-02	1.20 (15592,9126,220,155)
GO:1903706	regulation of hemopoiesis	1.56E-04	1.12E-02	3.00 (15592,354,220,15)
GO:0044331	cell-cell adhesion mediated by cadherin	1.56E-04	1.12E-02	14.17 (15592,20,220,4)
GO:0031399	regulation of protein modification process	1.59E-04	1.13E-02	1.81 (15592,1570,220,40)
GO:0090175	regulation of establishment of planar polarity	1.61E-04	1.14E-02	9.58 (15592,37,220,5)
GO:0008083	growth factor activity	4.16E-05	1.15E-02	5.45 (15592,117,220,9)
GO:0019219	regulation of nucleobase-containing compound metabolic process	1.71E-04	1.21E-02	1.54 (15592,2899,220,63)
GO:0071495	cellular response to endogenous stimulus	1.77E-04	1.24E-02	2.56 (15592,527,220,19)
GO:2000112	regulation of cellular macromolecule biosynthetic process	1.82E-04	1.27E-02	1.55 (15592,2785,220,61)
GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	1.84E-04	1.27E-02	4.07 (15592,174,220,10)
GO:0045892	negative regulation of transcription, DNA-templated	1.84E-04	1.27E-02	2.05 (15592,1003,220,29)
GO:0007267	cell-cell signaling	1.83E-04	1.28E-02	3.28 (15592,281,220,13)
GO:0008347	glial cell migration	1.91E-04	1.31E-02	13.50 (15592,21,220,4)
GO:0046639	negative regulation of alpha-beta T cell differentiation	1.91E-04	1.31E-02	13.50 (15592,21,220,4)
GO:0051216	cartilage development	1.97E-04	1.33E-02	5.84 (15592,85,220,7)
GO:1903507	negative regulation of nucleic acid-templated transcription	1.96E-04	1.34E-02	2.04 (15592,1007,220,29)
GO:0097156	fasciculation of motor neuron axon	1.98E-04	1.34E-02	70.87 (15592,2,220,2)
GO:1902679	negative regulation of RNA biosynthetic process	2.00E-04	1.34E-02	2.04 (15592,1008,220,29)
GO:0002683	negative regulation of immune system process	2.05E-04	1.37E-02	2.81 (15592,404,220,16)
GO:0070051	fibrinogen binding	5.37E-05	1.39E-02	35.44 (15592,6,220,3)
GO:0031033	myosin filament organization	2.19E-04	1.42E-02	23.62 (15592,9,220,3)
GO:0060348	bone development	2.14E-04	1.43E-02	6.97 (15592,61,220,6)
GO:0001817	regulation of cytokine production	2.15E-04	1.43E-02	2.44 (15592,580,220,20)
GO:0040008	regulation of growth	2.17E-04	1.43E-02	2.38 (15592,626,220,21)
GO:0045785	positive regulation of cell adhesion	2.18E-04	1.43E-02	2.91 (15592,365,220,15)
GO:0031034	myosin filament assembly	2.19E-04	1.43E-02	23.62 (15592,9,220,3)
GO:1901681	sulfur compound binding	5.83E-05	1.43E-02	3.94 (15592,216,220,12)
GO:0010556	regulation of macromolecule biosynthetic process	2.26E-04	1.47E-02	1.53 (15592,2867,220,62)
GO:0007165	signal transduction	2.31E-04	1.49E-02	1.50 (15592,3112,220,66)
GO:0042327	positive regulation of phosphorylation	2.33E-04	1.50E-02	2.09 (15592,917,220,27)
GO:0046872	metal ion binding	6.48E-05	1.50E-02	1.56 (15592,3045,220,67)
GO:0007156	homophilic cell adhesion via plasma membrane adhesion molecules	2.44E-04	1.56E-02	5.64 (15592,88,220,7)
GO:0023052	signaling	2.55E-04	1.63E-02	3.01 (15592,330,220,14)
GO:0034332	adherens junction organization	2.56E-04	1.63E-02	6.75 (15592,63,220,6)
GO:0043169	cation binding	7.39E-05	1.63E-02	1.55 (15592,3118,220,68)
GO:0031326	regulation of cellular biosynthetic process	2.64E-04	1.67E-02	1.51 (15592,3004,220,64)
GO:0048568	embryonic organ development	2.66E-04	1.68E-02	4.28 (15592,149,220,9)
GO:0033002	muscle cell proliferation	2.77E-04	1.73E-02	12.33 (15592,23,220,4)
GO:0071230	cellular response to amino acid stimulus	2.79E-04	1.74E-02	6.64 (15592,64,220,6)
GO:0010975	regulation of neuron projection development	2.83E-04	1.76E-02	2.46 (15592,547,220,19)
GO:0080090	regulation of primary metabolic process	2.89E-04	1.79E-02	1.38 (15592,4526,220,88)
GO:0004714	transmembrane receptor protein tyrosine kinase activity	8.73E-05	1.83E-02	8.18 (15592,52,220,6)
GO:0060742	epithelial cell differentiation involved in prostate gland development	3.09E-04	1.87E-02	21.26 (15592,10,220,3)

GO:0010605	negative regulation of macromolecule metabolic process	3.04E-04	1.88E-02	1.63 (15592,2128,220,49)
GO:0003149	membranous septum morphogenesis	3.09E-04	1.88E-02	21.26 (15592,10,220,3)
GO:0072216	positive regulation of metanephros development	3.09E-04	1.88E-02	21.26 (15592,10,220,3)
GO:0010838	positive regulation of keratinocyte proliferation	3.09E-04	1.89E-02	21.26 (15592,10,220,3)
GO:0009952	anterior/posterior pattern specification	3.09E-04	1.90E-02	4.20 (15592,152,220,9)
GO:0010771	negative regulation of cell morphogenesis involved in differentiation	3.21E-04	1.93E-02	5.39 (15592,92,220,7)
GO:0051781	positive regulation of cell division	3.31E-04	1.98E-02	6.44 (15592,66,220,6)
GO:0035108	limb morphogenesis	3.43E-04	2.04E-02	5.33 (15592,93,220,7)
GO:0035107	appendage morphogenesis	3.43E-04	2.05E-02	5.33 (15592,93,220,7)
GO:0055006	cardiac cell development	3.71E-04	2.20E-02	8.05 (15592,44,220,5)
GO:0000122	negative regulation of transcription by RNA polymerase II	3.87E-04	2.28E-02	2.18 (15592,749,220,23)
GO:0120163	negative regulation of cold-induced thermogenesis	4.12E-04	2.42E-02	7.87 (15592,45,220,5)
GO:0090193	positive regulation of glomerulus development	4.21E-04	2.45E-02	19.33 (15592,11,220,3)
GO:0097094	craniofacial suture morphogenesis	4.21E-04	2.46E-02	19.33 (15592,11,220,3)
GO:0120161	regulation of cold-induced thermogenesis	4.40E-04	2.56E-02	4.46 (15592,127,220,8)
GO:0000981	DNA-binding transcription factor activity, RNA polymerase II-specific	1.39E-04	2.79E-02	2.46 (15592,606,220,21)
GO:0009889	regulation of biosynthetic process	4.83E-04	2.80E-02	1.48 (15592,3069,220,64)
GO:0022408	negative regulation of cell-cell adhesion	4.93E-04	2.84E-02	3.94 (15592,162,220,9)
GO:0048638	regulation of developmental growth	5.03E-04	2.89E-02	2.81 (15592,353,220,14)
GO:0010769	regulation of cell morphogenesis involved in differentiation	5.17E-04	2.96E-02	2.94 (15592,313,220,13)
GO:0048762	mesenchymal cell differentiation	5.30E-04	3.01E-02	5.91 (15592,72,220,6)
GO:0045765	regulation of angiogenesis	5.30E-04	3.02E-02	3.10 (15592,274,220,12)
GO:0001501	skeletal system development	5.41E-04	3.06E-02	4.33 (15592,131,220,8)
GO:0051128	regulation of cellular component organization	5.48E-04	3.09E-02	1.57 (15592,2300,220,51)
GO:0030240	skeletal muscle thin filament assembly	5.55E-04	3.12E-02	17.72 (15592,12,220,3)
GO:0032879	regulation of localization	5.61E-04	3.14E-02	1.54 (15592,2480,220,54)
GO:0072091	regulation of stem cell proliferation	5.71E-04	3.18E-02	5.83 (15592,73,220,6)
GO:0060672	epithelial cell morphogenesis involved in placental branching	5.89E-04	3.23E-02	47.25 (15592,3,220,2)
GO:0097155	fasciculation of sensory neuron axon	5.89E-04	3.24E-02	47.25 (15592,3,220,2)
GO:0061144	alveolar secondary septum development	5.89E-04	3.25E-02	47.25 (15592,3,220,2)
GO:0003219	cardiac right ventricle formation	5.89E-04	3.26E-02	47.25 (15592,3,220,2)
GO:0034330	cell junction organization	5.88E-04	3.27E-02	3.84 (15592,166,220,9)
GO:0030856	regulation of epithelial cell differentiation	5.99E-04	3.27E-02	4.26 (15592,133,220,8)
GO:0003208	cardiac ventricle morphogenesis	6.05E-04	3.29E-02	10.12 (15592,28,220,4)
GO:0050794	regulation of cellular process	6.08E-04	3.30E-02	1.21 (15592,8140,220,139)
GO:0048584	positive regulation of response to stimulus	6.14E-04	3.30E-02	1.66 (15592,1790,220,42)
GO:0007411	axon guidance	6.14E-04	3.31E-02	3.82 (15592,167,220,9)
GO:0051129	negative regulation of cellular component organization	6.48E-04	3.47E-02	2.19 (15592,680,220,21)
GO:0005518	collagen binding	2.14E-04	3.63E-02	6.97 (15592,61,220,6)
GO:0051253	negative regulation of RNA metabolic process	6.97E-04	3.71E-02	1.89 (15592,1088,220,29)
GO:0090171	chondrocyte morphogenesis	7.14E-04	3.71E-02	16.36 (15592,13,220,3)
GO:0051172	negative regulation of nitrogen compound metabolic process	6.96E-04	3.72E-02	1.62 (15592,1973,220,45)
GO:0003429	growth plate cartilage chondrocyte morphogenesis	7.14E-04	3.72E-02	16.36 (15592,13,220,3)
GO:0005178	integrin binding	2.11E-04	3.72E-02	4.97 (15592,114,220,8)
GO:0003422	growth plate cartilage morphogenesis	7.14E-04	3.73E-02	16.36 (15592,13,220,3)
GO:0043200	response to amino acid	7.08E-04	3.75E-02	5.60 (15592,76,220,6)
GO:0003414	chondrocyte morphogenesis involved in endochondral bone morphogenesis	7.14E-04	3.75E-02	16.36 (15592,13,220,3)
GO:0061418	regulation of transcription from RNA polymerase II promoter in response to hypoxia	7.14E-04	3.76E-02	16.36 (15592,13,220,3)
GO:0005515	protein binding	2.05E-04	3.76E-02	1.25 (15592,7551,220,133)
GO:2000647	negative regulation of stem cell proliferation	7.14E-04	3.77E-02	16.36 (15592,13,220,3)
GO:0051302	regulation of cell division	7.28E-04	3.77E-02	4.14 (15592,137,220,8)
GO:0030617	transforming growth factor beta receptor, inhibitory cytoplasmic mediator activity	1.98E-04	3.80E-02	70.87 (15592,2,220,2)
GO:0090183	regulation of kidney development	7.40E-04	3.82E-02	6.95 (15592,51,220,5)
GO:0018108	peptidyl-tyrosine phosphorylation	8.13E-04	4.16E-02	5.45 (15592,78,220,6)
GO:0001525	angiogenesis	8.11E-04	4.17E-02	3.14 (15592,248,220,11)
GO:0005911	cell-cell junction	3.24E-04	4.18E-02	2.69 (15592,421,220,16)
GO:0032270	positive regulation of cellular protein metabolic process	8.31E-04	4.24E-02	1.76 (15592,1369,220,34)
GO:0001527	microfibril	3.09E-04	4.27E-02	21.26 (15592,10,220,3)
GO:0010558	negative regulation of macromolecule biosynthetic process	8.71E-04	4.43E-02	1.82 (15592,1210,220,31)
GO:0000904	cell morphogenesis involved in differentiation	8.79E-04	4.46E-02	4.02 (15592,141,220,8)
GO:0008045	motor neuron axon guidance	9.00E-04	4.52E-02	9.14 (15592,31,220,4)
GO:1902692	regulation of neuroblast proliferation	9.00E-04	4.53E-02	9.14 (15592,31,220,4)
GO:0048739	cardiac muscle fiber development	8.99E-04	4.54E-02	15.19 (15592,14,220,3)
GO:0120035	regulation of plasma membrane bounded cell projection organization	9.20E-04	4.61E-02	2.13 (15592,699,220,21)
GO:0007043	cell-cell junction assembly	9.29E-04	4.62E-02	5.32 (15592,80,220,6)
GO:0014910	regulation of smooth muscle cell migration	9.29E-04	4.63E-02	5.32 (15592,80,220,6)
GO:0009892	negative regulation of metabolic process	9.55E-04	4.73E-02	1.53 (15592,2356,220,51)
GO:0001837	epithelial to mesenchymal transition	9.63E-04	4.74E-02	6.56 (15592,54,220,5)
GO:0050679	positive regulation of epithelial cell proliferation	9.68E-04	4.75E-02	3.58 (15592,178,220,9)
GO:0051147	regulation of muscle cell differentiation	9.63E-04	4.76E-02	3.96 (15592,143,220,8)
GO:0018212	peptidyl-tyrosine modification	9.92E-04	4.85E-02	5.25 (15592,81,220,6)

*Enrichment (N, B, n, b) is defined as follows:

N - is the total number of genes

B - is the total number of genes associated with a specific GO term

n - is the number of genes upregulated or downregulated by ≥ 3 -fold

b - is the number of upregulated or downregulated genes (≥ 3 -fold) in the specific GO term

Enrichment = (b/n) / (B/N)