TableS3. KEGG of Venn in Figure7 E

GelMA_HA_No Trend Only	Description	Qvalue
ko04657	IL-17 signaling pathway	5.92E-07
ko03030	DNA replication	8.26E-07
ko04979	Cholesterol metabolism	3.81E-05
ko03420	Nucleotide excision repair	4.05E-04
ko04110	Cell cycle	5.14E-04
ko03010	Ribosome	5.24E-04
ko04625	C-type lectin receptor signaling pathwa	9.12E-04
ko05166	HTLV-I infection	2.06E-03
ko03460	Fanconi anemia pathway	2.87E-03
ko05323	Rheumatoid arthritis	3.18E-03
ko03430	Mismatch repair	4.25E-03
ko01523	Antifolate resistance	4.84E-03
ko04659	Th17 cell differentiation	8.32E-03
ko04658	Th1 and Th2 cell differentiation	9.45E-03
ko04612	Antigen processing and presentation	1.18E-02
ko04620	Toll-like receptor signaling pathway	1.41E-02
ko05134	Legionellosis	1.52E-02
ko00511	Other glycan degradation	1.57E-02
ko00520	Amino sugar and nucleotide sugar met	1.81E-02
ko05133	Pertussis	2.74E-02
ko04210	Apoptosis	3.28E-02
ko05203	Viral carcinogenesis	3.51E-02
ko05221	Acute myeloid leukemia	4.07E-02
ko00240	Pyrimidine metabolism	4.62E-02
Medium_No Trend Only		
ko05200	Pathways in cancer	5.96E-05
ko04510	Focal adhesion	1.70E-03
ko05222	Small cell lung cancer	3.77E-03
ko04611	Platelet activation	4.21E-03
ko04610	Complement and coagulation cascades	8.52E-03
ko04640	Hematopoietic cell lineage	1.04E-02
ko05165	Human papillomavirus infection	4.19E-02
GelMA_HA_No Trend Common		
ko04142	Lysosome	1.67E-11
ko04061	Viral protein interaction with cytokine	1.57E-09
ko04380	Osteoclast differentiation	2.02E-08
ko04668	TNF signaling pathway	2.71E-05
ko05332	Graft-versus-host disease	5.89E-05
ko05321	Inflammatiory bowel disease (IBD)	2.36E-04
ko04062	Chemokine signaling pathway	5.14E-04
ko04940	Type I diabetes mellitus	4.02E-03
ko05144	Malaria	8.32E-03
ko05145	Toxoplasmosis	8.32E-03
ko04933	AGE-RAGE signaling pathway in diab	2.32E-02
Medium_No Trend Common		
ko04061	Viral protein interaction with cytokine	1.08E-15
ko04142	Lysosome	5.86E-05
ko04062	Chemokine signaling pathway	7.62E-05
ko04380	Osteoclast differentiation	6.20E-04
ko04933	AGE-RAGE signaling pathway in diab	6.66E-04
ko04668	TNF signaling pathway	7.49E-04
ko05332	Graft-versus-host disease	1.11E-03
ko05145	Toxoplasmosis	1.56E-02
ko04940	Type I diabetes mellitus	2.04E-02
ko05144	Malaria	2.17E-02
ko05321	Inflammatiory bowel disease (IBD)	2.88E-02
GelMA_HA_Trend Only		

ko04726	Serotonergic synapse	6.58E-04
ko04270	Vascular smooth muscle contraction	6.58E-04
ko00260	Glycine, serine and threonine metaboli	1.63E-03
ko04010	MAPK signaling pathway	3.48E-03
ko04929	GnRH secretion	3.72E-03
ko04540	Gap junction	4.14E-03
ko04721	Synaptic vesicle cycle	4.14E-03
ko04972	Pancreatic secretion	8.09E-03
ko04927	Cortisol synthesis and secretion	1.13E-02
ko02010	ABC transporters	1.38E-02
ko04750	Inflammatory mediator regulation of T	1.50E-02
ko04310	Wnt signaling pathway	2.00E-02
ko04014	Ras signaling pathway	2.05E-02
ko04728	Dopaminergic synapse	2.55E-02
ko04730	Long-term depression	2.62E-02
ko04072	Phospholipase D signaling pathway	4.15E-02
ko04350	TGF-beta signaling pathway	4.73E-02
Medium_ Trend Only		
ko05031	Amphetamine addiction	8.95E-04
GelMA_HA_Trend Common		
ko04020	Calcium signaling pathway	1.89E-13
ko05033	Nicotine addiction	1.74E-10
ko04727	GABAergic synapse	6.26E-09
ko04022	cGMP - PKG signaling pathway	1.45E-07
ko04724	Glutamatergic synapse	5.81E-07
ko04713	Circadian entrainment	1.60E-06
ko05032	Morphine addiction	1.71E-06
ko04911	Insulin secretion	8.75E-06
ko04742	Taste transduction	3.44E-05
ko04024	cAMP signaling pathway	5.13E-05
ko05412	Arrhythmogenic right ventricular cardi	9.33E-05
ko04261	Adrenergic signaling in cardiomyocyte	2.26E-04
ko05410	Hypertrophic cardiomyopathy (HCM)	3.10E-04
ko04360	Axon guidance	5.83E-04
ko04921	Oxytocin signaling pathway	6.58E-04
ko04971	Gastric acid secretion	1.33E-03
ko04723	Retrograde endocannabinoid signaling	1.45E-03
ko04924	Renin secretion	1.45E-03
ko05168	Herpes simplex infection	1.45E-03
ko05414	Dilated cardiomyopathy (DCM)	1.58E-03
ko04260	Cardiac muscle contraction	2.57E-03
ko04970	Salivary secretion	4.14E-03
ko04725	Cholinergic synapse	9.86E-03
ko04925	Aldosterone synthesis and secretion	1.09E-02
ko05030	Cocaine addiction	1.74E-02
ko00250	Alanine, aspartate and glutamate metal	4.04E-02
Medium_ Trend Common		
ko04020	Calcium signaling pathway	8.45E-09
ko04727	GABAergic synapse	1.21E-06
ko05168	Herpes simplex infection	1.62E-06
ko05033	Nicotine addiction	2.92E-06
ko05032	Morphine addiction	2.50E-04
ko04911	Insulin secretion	2.50E-04
ko04713	Circadian entrainment	2.97E-04
ko04024	cAMP signaling pathway	4.00E-04
ko04723	Retrograde endocannabinoid signaling	3.77E-03
ko04261	Adrenergic signaling in cardiomyocyte	6.31E-03
ko04724	Glutamatergic synapse	6.46E-03
ko04725	Cholinergic synapse	8.70E-03
ko04925	Aldosterone synthesis and secretion	8.70E-03
ko04742	Taste transduction	9.86E-03
ko04921	Oxytocin signaling pathway	9.86E-03
ko00250	Alanine, aspartate and glutamate metal	9.86E-03
ko04971	Gastric acid secretion	1.35E-02
ko05414	Dilated cardiomyopathy (DCM)	1.67E-02
ko04924	Renin secretion	1.84E-02
ko05412	Arrhythmogenic right ventricular cardi	2.07E-02
ko04970	Salivary secretion	2.07E-02
ko05410	Hypertrophic cardiomyopathy (HCM)	2.07E-02
ko04260	Cardiac muscle contraction	2.42E-02
ko05030	Cocaine addiction	3.36E-02
ko04022	cGMP - PKG signaling pathway	4.17E-02

ko04360	Axon guidance	4.17E-02

Table S4. GO of Venn in Figure 7 F

GelMA_HA_No Trend Only	Description	Qvalue
GO:0044427	chromosomal part	1.70E-21
GO:0005694	chromosome	1.70E-21
GO:1903047	mitotic cell cycle process	3.12E-13
GO:0043228	non-membrane-bounded organelle	1.20E-12
GO:0043232	intracellular non-membrane-bounded organelle	1.79E-12
GO:0007049	cell cycle	2.32E-12
GO:0000278	mitotic cell cycle	2.77E-12
GO:0098687	chromosomal region	3.87E-12
GO:0007051	spindle organization	1.34E-11
GO:0022402	cell cycle process	1.39E-11
GO:0007052	mitotic spindle organization	1.52E-11
GO:1902850	microtubule cytoskeleton organization involved in mitosis	1.76E-11
GO:0000777	condensed chromosome kinetochore	2.38E-11
GO:0031974	membrane-enclosed lumen	3.81E-11
GO:0043233	organelle lumen	3.81E-11
GO:0070013	intracellular organelle lumen	3.81E-11
GO:0051301	cell division	9.02E-11
GO:0000776	kinetochore	1.23E-10
GO:0044446	intracellular organelle part	6.73E-10
GO:0000785	chromatin	9.19E-10
GO:0140014	mitotic nuclear division	2.75E-09
GO:0071103	DNA conformation change	2.92E-08
GO:0006259	DNA metabolic process	3.64E-08
GO:1901360	organic cyclic compound metabolic process	5.79E-08
GO:0006974	cellular response to DNA damage stimulus	7.13E-08
GO:0000075	cell cycle checkpoint	1.21E-07
GO:0044422	organelle part	1.46E-07
GO:0005654	nucleoplasm	1.55E-07
GO:0051276	chromosome organization	2.06E-07
GO:0006323	DNA packaging	2.08E-07
GO:0043227	membrane-bounded organelle	4.48E-07
GO:0032993	protein-DNA complex	5.62E-07
GO:0031981	nuclear lumen	6.10E-07
GO:0044424	intracellular part	8.38E-07
GO:0033554	cellular response to stress	8.53E-07
GO:0005622	intracellular	8.54E-07
GO:0044815	DNA packaging complex	9.06E-07
GO:0051726	regulation of cell cycle	1.44E-06
GO:0006725	cellular aromatic compound metabolic process	1.62E-06
GO:0034641	cellular nitrogen compound metabolic process	1.62E-06
GO:0046483	heterocycle metabolic process	2.75E-06
GO:0044428	nuclear part	3.55E-06
GO:0044419	interspecies interaction between organisms	4.08E-06
GO:0006139	nucleobase-containing compound metabolic process	5.49E-06
GO:0048285	organelle fission	5.87E-06
GO:0009892	negative regulation of metabolic process	5.89E-06
GO:0043229	intracellular organelle	6.00E-06
GO:0007093	mitotic cell cycle checkpoint	7.97E-06
GO:0006260	DNA replication	8.88E-06
GO:0044403	symbiont process	9.36E-06
GO:0030261	chromosome condensation	1.02E-05
GO:0010629	negative regulation of gene expression	1.11E-05
GO:0006281	DNA repair	1.19E-05
GO:0044237	cellular metabolic process	1.21E-05
GO:0005657	replication fork	1.21E-05
GO:0016032	viral process	1.26E-05
GO:0009058	biosynthetic process	1.35E-05
GO:0006334	nucleosome assembly	1.36E-05
GO:0007346	regulation of mitotic cell cycle	1.64E-05
GO:0044770	cell cycle phase transition	1.67E-05
GO:0005774	vacuolar membrane	1.77E-05
GO:0000228	nuclear chromosome	1.77E-05
GO:0031497	chromatin assembly	1.97E-05
GO:0008152	metabolic process	2.38E-05
GO:0034508	centromere complex assembly	2.84E-05
GO:0044786	cell cycle DNA replication	3.53E-05
GO:0034080	CENP-A containing nucleosome assembly	3.53E-05
GO:0061641	CENP-A containing chromatin organization	3.53E-05
GO:0044772	mitotic cell cycle phase transition	3.59E-05
GO:0044249	cellular biosynthetic process	3.64E-05

GO:0006310	DNA recombination	3.68E-05
GO:0045787	positive regulation of cell cycle	4.43E-05
GO:0005737	cytoplasm	5.50E-05
GO:0043231	intracellular membrane-bounded organelle	5.72E-05
GO:0045786	negative regulation of cell cycle	6.37E-05
GO:0090304	nucleic acid metabolic process	6.56E-05
GO:0042611	MHC protein complex	6.59E-05
GO:0009890	negative regulation of biosynthetic process	7.25E-05
GO:0009411	response to UV	7.81E-05
GO:0042613	MHC class II protein complex	7.88E-05
GO:0045892	negative regulation of transcription, DNA-templated	7.93E-05
GO:0005634	nucleus	8.03E-05
GO:0044444	cytoplasmic part	8.39E-05
GO:1903507	negative regulation of nucleic acid-templated transcription	8.94E-05
GO:1902679	negative regulation of RNA biosynthetic process	9.92E-05
GO:0010564	regulation of cell cycle process	9.93E-05
GO:0019222	regulation of metabolic process	0.0001
GO:0009891	positive regulation of biosynthetic process	0.0001
GO:0031323	regulation of cellular metabolic process	0.0001
GO:0010605	negative regulation of macromolecule metabolic process	0.00011
GO:0031055	chromatin remodeling at centromere	0.00012
GO:0043226	organelle	0.00012
GO:0000786	nucleosome	0.00012
GO:0042627	chylomicron	0.00012
GO:0002396	MHC protein complex assembly	0.00012
GO:0045935	positive regulation of nucleobase-containing compound me	0.00012
GO:1901576	organic substance biosynthetic process	0.00013
GO:0044271	cellular nitrogen compound biosynthetic process	0.00014
GO:0035578	azurophil granule lumen	0.00014
GO:0051052	regulation of DNA metabolic process	0.00015
GO:0031327	negative regulation of cellular biosynthetic process	0.00015
GO:0005819	spindle	0.00017
GO:0071404	cellular response to low-density lipoprotein particle stimulu	0.00021
GO:0031328	positive regulation of cellular biosynthetic process	0.00021
GO:0051233	spindle midzone	0.00023
GO:0048002	antigen processing and presentation of peptide antigen	0.00023
GO:0045934	negative regulation of nucleobase-containing compound me	0.00024
GO:0006807	nitrogen compound metabolic process	0.00024
GO:0031324	negative regulation of cellular metabolic process	0.00024
GO:0009059	macromolecule biosynthetic process	0.00025
GO:0071704	organic substance metabolic process	0.00025
GO:0019882	antigen processing and presentation	0.00028
GO:0033260	nuclear DNA replication	0.00029
GO:0019083	viral transcription	0.00029
GO:0051253	negative regulation of RNA metabolic process	0.00029
GO:0032133	chromosome passenger complex	0.00031
GO:0000796	condensin complex	0.00034
GO:0030894	replisome	0.00035
GO:0031570	DNA integrity checkpoint	0.00036
GO:1901987	regulation of cell cycle phase transition	0.00037
GO:1901990	regulation of mitotic cell cycle phase transition	0.00037
GO:0006336	DNA replication-independent nucleosome assembly	0.00038
GO:0036297	interstrand cross-link repair	0.00042
GO:0042359	vitamin D metabolic process	0.00042
GO:0042770	signal transduction in response to DNA damage	0.00046
GO:1901362	organic cyclic compound biosynthetic process	0.00046
GO:0003735	structural constituent of ribosome	0.0005
GO:0034724	DNA replication-independent nucleosome organization	0.00052
GO:0007088	regulation of mitotic nuclear division	0.00053
GO:0044391	ribosomal subunit	0.00054
GO:0000922	spindle pole	0.00054
GO:0006333	chromatin assembly or disassembly	0.00055
GO:0034645	cellular macromolecule biosynthetic process	0.00057
GO:0002501	peptide antigen assembly with MHC protein complex	0.00057
GO:0051172	negative regulation of nitrogen compound metabolic proces	0.00058
GO:0022626	cytosolic ribosome	0.00058
GO:0002221	pattern recognition receptor signaling pathway	0.00058
GO:2000113	negative regulation of cellular macromolecule biosynthetic	0.00059
GO:0034654	nucleobase-containing compound biosynthetic process	0.00062
GO:0051256	mitotic spindle midzone assembly	0.00062
GO:0015949	nucleobase-containing small molecule interconversion	0.00065
GO:0034375	high-density lipoprotein particle remodeling	0.00065

GO:0043691	reverse cholesterol transport	0.00065
GO:0009110	vitamin biosynthetic process	0.00068
GO:0010558	negative regulation of macromolecule biosynthetic process	0.00073
GO:0043170	macromolecule metabolic process	0.00074
GO:0018130	heterocycle biosynthetic process	0.00075
GO:0055092	sterol homeostasis	0.00075
GO:1901988	negative regulation of cell cycle phase transition	0.00076
GO:0007076	mitotic chromosome condensation	0.00078
GO:0006342	chromatin silencing	0.0008
GO:0051171	regulation of nitrogen compound metabolic process	0.0008
GO:0019438	aromatic compound biosynthetic process	0.00084
GO:0034470	ncRNA processing	0.00084
GO:0045637	regulation of myeloid cell differentiation	0.00084
GO:0060255	regulation of macromolecule metabolic process	0.00087
GO:0044238	primary metabolic process	0.00088
GO:0065004	protein-DNA complex assembly	0.00088
GO:0044260	cellular macromolecule metabolic process	0.00089
GO:0045814	negative regulation of gene expression, epigenetic	0.00089
GO:0051235	maintenance of location	0.00092
GO:0072395	signal transduction involved in cell cycle checkpoint	0.00094
GO:0005515	protein binding	0.00094
GO:0002495	antigen processing and presentation of peptide antigen via	0.00097
GO:0006270	DNA replication initiation	0.00097
GO:0090305	nucleic acid phosphodiester bond hydrolysis	0.00097
GO:1990023	mitotic spindle midzone	0.00101
GO:0010948	negative regulation of cell cycle process	0.00102
GO:0010885	regulation of cholesterol storage	0.00102
GO:0032201	telomere maintenance via semi-conservative replication	0.00108
GO:0010557	positive regulation of macromolecule biosynthetic process	0.00108
GO:0055088	lipid homeostasis	0.0011
GO:0006271	DNA strand elongation involved in DNA replication	0.0011
GO:0005730	nucleolus	0.00115
GO:0090068	positive regulation of cell cycle process	0.00115
GO:0080135	regulation of cellular response to stress	0.00117
GO:0045893	positive regulation of transcription, DNA-templated	0.00118
GO:1903508	positive regulation of nucleic acid-templated transcription	0.00118
GO:1902680	positive regulation of RNA biosynthetic process	0.00124
GO:0034728	nucleosome organization	0.00133
GO:0042632	cholesterol homeostasis	0.00141
GO:0019058	viral life cycle	0.00145
GO:0044283	small molecule biosynthetic process	0.00149
GO:0002478	antigen processing and presentation of exogenous peptide a	0.00149
GO:0005840	ribosome	0.0015
GO:0080090	regulation of primary metabolic process	0.00151
GO:0008608	attachment of spindle microtubules to kinetochore	0.00152
GO:0005658	alpha DNA polymerase:primase complex	0.00153
GO:0034363	intermediate-density lipoprotein particle	0.00153
GO:0002504	antigen processing and presentation of peptide or polysacch	0.00165
GO:0034384	high-density lipoprotein particle clearance	0.00166
GO:0051988	regulation of attachment of spindle microtubules to kinetoc	0.00166
GO:0043154	negative regulation of cysteine-type endopeptidase activity	0.00177
GO:1901991	negative regulation of mitotic cell cycle phase transition	0.00178
GO:0006297	nucleotide-excision repair, DNA gap filling	0.00178
GO:0000022	mitotic spindle elongation	0.00179
GO:0002291	T cell activation via T cell receptor contact with antigen bo	0.00179
GO:0034371	chylomicron remodeling	0.00179
GO:0051231	spindle elongation	0.00179
GO:1902749	regulation of cell cycle G2/M phase transition	0.0018
GO:0006614	SRP-dependent cotranslational protein targeting to membra	0.00181
GO:0034361	very-low-density lipoprotein particle	0.0019
GO:0034385	triglyceride-rich plasma lipoprotein particle	0.0019
GO:0045598	regulation of fat cell differentiation	0.00195
GO:0006766	vitamin metabolic process	0.00196
GO:0002218	activation of innate immune response	0.00207
GO:0044281	small molecule metabolic process	0.00214
GO:0044839	cell cycle G2/M phase transition	0.00217
GO:0019886	antigen processing and presentation of exogenous peptide a	0.00217
GO:0042802	identical protein binding	0.00217
GO:0051701	interaction with host	0.00222
GO:0043596	nuclear replication fork	0.00222
GO:0002758	innate immune response-activating signal transduction	0.00224
GO:0000018	regulation of DNA recombination	0.00227

GO:0050810	regulation of steroid biosynthetic process	0.00227
GO:0006269	DNA replication, synthesis of RNA primer	0.00234
GO:1904044	response to aldosterone	0.00234
GO:0045944	positive regulation of transcription by RNA polymerase II	0.00238
GO:2001188	regulation of T cell activation via T cell receptor contact wi	0.00238
GO:0046885	regulation of hormone biosynthetic process	0.00241
GO:0006613	cotranslational protein targeting to membrane	0.00244
GO:0000083	regulation of transcription involved in G1/S transition of m	0.00253
GO:0071156	regulation of cell cycle arrest	0.00256
GO:0009163	nucleoside biosynthetic process	0.00256
GO:0000082	G1/S transition of mitotic cell cycle	0.0026
GO:0015934	large ribosomal subunit	0.00263
GO:0071556	integral component of lumenal side of endoplasmic reticulu	0.00263
GO:0098553	lumenal side of endoplasmic reticulum membrane	0.00263
GO:0034154	toll-like receptor 7 signaling pathway	0.00267
GO:0051255	spindle midzone assembly	0.00267
GO:0045930	negative regulation of mitotic cell cycle	0.00267
GO:0051985	negative regulation of chromosome segregation	0.0027
GO:1901659	glycosyl compound biosynthetic process	0.0027
GO:0044454	nuclear chromosome part	0.0027
GO:0072401	signal transduction involved in DNA integrity checkpoint	0.00273
GO:0072422	signal transduction involved in DNA damage checkpoint	0.00273
GO:0072686	mitotic spindle	0.00276
GO:1904813	ficolin-1-rich granule lumen	0.00277
GO:0043601	nuclear replisome	0.00297
GO:0046700	heterocycle catabolic process	0.00309
GO:0051254	positive regulation of RNA metabolic process	0.00314
GO:0002544	chronic inflammatory response	0.00315
GO:0051382	kinetochore assembly	0.00315
GO:0045911	positive regulation of DNA recombination	0.00339
GO:0002181	cytoplasmic translation	0.00339
GO:0006302	double-strand break repair	0.00347
GO:0000226	microtubule cytoskeleton organization	0.00352
GO:0060968	regulation of gene silencing	0.00352
GO:0045670	regulation of osteoclast differentiation	0.00353
GO:2000117	negative regulation of cysteine-type endopeptidase activity	0.00358
GO:0006364	rRNA processing	0.00371
GO:0009889	regulation of biosynthetic process	0.00373
GO:1901361	organic cyclic compound catabolic process	0.00374
GO:0097193	intrinsic apoptotic signaling pathway	0.00376
GO:0019439	aromatic compound catabolic process	0.00383
GO:0019884	antigen processing and presentation of exogenous antigen	0.00387
GO:0044843	cell cycle G1/S phase transition	0.00404
GO:0016070	RNA metabolic process	0.00408
GO:0045454	cell redox homeostasis	0.00412
GO:0003676	nucleic acid binding	0.00413
GO:0007050	cell cycle arrest	0.0043
GO:0006775	fat-soluble vitamin metabolic process	0.00432
GO:0030330	DNA damage response, signal transduction by p53 class me	0.00432
GO:0003677	DNA binding	0.00442
GO:0002763	positive regulation of myeloid leukocyte differentiation	0.00446
GO:0044270	cellular nitrogen compound catabolic process	0.00455
GO:0045066	regulatory T cell differentiation	0.00471
GO:0022625	cytosolic large ribosomal subunit	0.00473
GO:0034404	nucleobase-containing small molecule biosynthetic process	0.00473
GO:0000077	DNA damage checkpoint	0.00489
GO:2001251	negative regulation of chromosome organization	0.00489
GO:0006284	base-excision repair	0.0049
GO:0006261	DNA-dependent DNA replication	0.00491
GO:0022616	DNA strand elongation	0.00496
GO:0042474	middle ear morphogenesis	0.00502
GO:0033700	phospholipid efflux	0.00506
GO:0034122	negative regulation of toll-like receptor signaling pathway	0.00506
GO:0048246	macrophage chemotaxis	0.00506
GO:0044445	cytosolic part	0.0052
GO:1902969	mitotic DNA replication	0.00525
GO:0007569	cell aging	0.00534
GO:0040029	regulation of gene expression, epigenetic	0.00543
GO:0010628	positive regulation of gene expression	0.00546
GO:0071824	protein-DNA complex subunit organization	0.00547
GO:0000122	negative regulation of transcription by RNA polymerase II	0.00553
GO:0009954	proximal/distal pattern formation	0.00564

GO:0032633	interleukin-4 production	0.00564
GO:0032673	regulation of interleukin-4 production	0.00564
GO:0034368	protein-lipid complex remodeling	0.00564
GO:0034369	plasma lipoprotein particle remodeling	0.00564
GO:0016051	carbohydrate biosynthetic process	0.00606
GO:0032392	DNA geometric change	0.0062
GO:0006296	nucleotide-excision repair, DNA incision, 5'-to lesion	0.00624
GO:0071478	cellular response to radiation	0.00626
GO:0051054	positive regulation of DNA metabolic process	0.00628
GO:0005767	secondary lysosome	0.00631
GO:0002361	CD4-positive, CD25-positive, alpha-beta regulatory T cell c	0.00634
GO:0010369	chromocenter	0.00655
GO:0034362	low-density lipoprotein particle	0.00655
GO:0051304	chromosome separation	0.00655
GO:0032200	telomere organization	0.00658
GO:0035821	modification of morphology or physiology of other organis	0.0067
GO:0032010	phagolysosome	0.00672
GO:0002363	alpha-beta T cell lineage commitment	0.00679
GO:0000723	telomere maintenance	0.00681
GO:0006996	organelle organization	0.00681
GO:0045940	positive regulation of steroid metabolic process	0.00681
GO:0051302	regulation of cell division	0.00694
GO:0032508	DNA duplex unwinding	0.00714
GO:0044774	mitotic DNA integrity checkpoint	0.00714
GO:0009314	response to radiation	0.00724
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-me	0.00754
GO:0046983	protein dimerization activity	0.00757
GO:0009112	nucleobase metabolic process	0.00767
GO:0031326	regulation of cellular biosynthetic process	0.00767
GO:0031262	Ndc80 complex	0.00772
GO:0033256	I-kappaB/NF-kappaB complex	0.00772
GO:0035976	transcription factor AP-1 complex	0.00772
GO:0010984	regulation of lipoprotein particle clearance	0.00773
GO:0045444	fat cell differentiation	0.00809
GO:0016572	histone phosphorylation	0.00825
GO:0034655	nucleobase-containing compound catabolic process	0.00826
GO:1901617	organic hydroxy compound biosynthetic process	0.00827
GO:1902563	regulation of neutrophil activation	0.00835
GO:2001198	regulation of dendritic cell differentiation	0.00835
GO:0032693	negative regulation of interleukin-10 production	0.00853
GO:1901363	heterocyclic compound binding	0.00862
GO:0097159	organic cyclic compound binding	0.00873
GO:0042771	intrinsic apoptotic signaling pathway in response to DNA d	0.00876
GO:0018158	protein oxidation	0.00885
GO:0010032	meiotic chromosome condensation	0.00893
GO:0015889	cobalamin transport	0.00893
GO:0019262	N-acetylneuraminate catabolic process	0.00893
GO:1903232	melanosome assembly	0.00893
GO:0042605	peptide antigen binding	0.00946
GO:0045047	protein targeting to ER	0.00957
GO:0000086	G2/M transition of mitotic cell cycle	0.00992
GO:0006287	base-excision repair, gap-filling	0.01027
GO:0034367	protein-containing complex remodeling	0.01027
GO:0009142	nucleoside triphosphate biosynthetic process	0.01027
GO:0002399	MHC class II protein complex assembly	0.0103
GO:0002503	peptide antigen assembly with MHC class II protein comple	0.0103
GO:0034164	negative regulation of toll-like receptor 9 signaling pathwa	0.0103
GO:1902564	negative regulation of neutrophil activation	0.0103
GO:1990637	response to prolactin	0.0103
GO:0005829	cytosol	0.01052
GO:0033683	nucleotide-excision repair, DNA incision	0.01072
GO:0042769	DNA damage response, detection of DNA damage	0.01072
GO:0071482	cellular response to light stimulus	0.01072
GO:0019080	viral gene expression	0.01078
GO:0070268	cornification	0.01094
GO:0009395	phospholipid catabolic process	0.01094
GO:0030890	positive regulation of B cell proliferation	0.01094
GO:0072539	T-helper 17 cell differentiation	0.01141
GO:1904666	regulation of ubiquitin protein ligase activity	0.01141
GO:0010389	regulation of G2/M transition of mitotic cell cycle	0.01143
GO:0002577	regulation of antigen processing and presentation	0.01144
GO:0042276	error-prone translesion synthesis	0.01144

GO:0006641	triglyceride metabolic process	0.01181
GO:0032465	regulation of cytokinesis	0.01192
GO:0071840	cellular component organization or biogenesis	0.01246
GO:0000079	regulation of cyclin-dependent protein serine/threonine kina	0.01299
GO:0031334	positive regulation of protein complex assembly	0.0133
GO:0002755	MyD88-dependent toll-like receptor signaling pathway	0.0134
GO:0090322	regulation of superoxide metabolic process	0.0134
GO:0008202	steroid metabolic process	0.01347
GO:0030670	phagocytic vesicle membrane	0.01363
GO:0090734	site of DNA damage	0.01363
GO:0034144	negative regulation of toll-like receptor 4 signaling pathway	0.01371
GO:0060346	bone trabecula formation	0.01371
GO:0032735	positive regulation of interleukin-12 production	0.01373
GO:0046461	neutral lipid catabolic process	0.01374
GO:0046464	acylglycerol catabolic process	0.01374
GO:0034162	toll-like receptor 9 signaling pathway	0.01375
GO:0042451	purine nucleoside biosynthetic process	0.01375
GO:0046129	purine ribonucleoside biosynthetic process	0.01375
GO:0000725	recombinational repair	0.01395
GO:0005815	microtubule organizing center	0.01439
GO:0005876	spindle microtubule	0.01451
GO:0002070	epithelial cell maturation	0.01451
GO:1902166	negative regulation of intrinsic apoptotic signaling pathway	0.01451
GO:1901264	carbohydrate derivative transport	0.01496
GO:0046598	positive regulation of viral entry into host cell	0.01505
GO:2000508	regulation of dendritic cell chemotaxis	0.01505
GO:0003682	chromatin binding	0.01514
GO:0072413	signal transduction involved in mitotic cell cycle checkpoin	0.01543
GO:0002507	tolerance induction	0.01557
GO:0046503	glycerolipid catabolic process	0.01564
GO:0070542	response to fatty acid	0.01624
GO:0051225	spindle assembly	0.01638
GO:0072599	establishment of protein localization to endoplasmic reticul	0.01638
GO:1990748	cellular detoxification	0.01638
GO:0045596	negative regulation of cell differentiation	0.01653
GO:0002449	lymphocyte mediated immunity	0.01653
GO:1903707	negative regulation of hemopoiesis	0.0166
GO:0019219	regulation of nucleobase-containing compound metabolic p	0.01661
GO:0060575	intestinal epithelial cell differentiation	0.01665
GO:0045589	regulation of regulatory T cell differentiation	0.01667
GO:0010467	gene expression	0.01675
GO:0044242	cellular lipid catabolic process	0.01677
GO:1901615	organic hydroxy compound metabolic process	0.01693
GO:0034358	plasma lipoprotein particle	0.01696
GO:1990777	lipoprotein particle	0.01696
GO:0045667	regulation of osteoblast differentiation	0.01705
GO:0042455	ribonucleoside biosynthetic process	0.01724
GO:0140097	catalytic activity, acting on DNA	0.01732
GO:0030669	clathrin-coated endocytic vesicle membrane	0.01733
GO:0060333	interferon-gamma-mediated signaling pathway	0.01739
GO:0032350	regulation of hormone metabolic process	0.01744
GO:0042254	ribosome biogenesis	0.01759
GO:0120115	Lsm2-8 complex	0.01762
GO:0016052	carbohydrate catabolic process	0.01835
GO:2001020	regulation of response to DNA damage stimulus	0.01835
GO:0006165	nucleoside diphosphate phosphorylation	0.01885
GO:0032753	positive regulation of interleukin-4 production	0.01914
GO:0045672	positive regulation of osteoclast differentiation	0.01914
GO:0000724	double-strand break repair via homologous recombination	0.01939
GO:0009148	pyrimidine nucleoside triphosphate biosynthetic process	0.01972
GO:0043486	histone exchange	0.01972
GO:2001141	regulation of RNA biosynthetic process	0.02018
GO:0015918	sterol transport	0.0203
GO:0032774	RNA biosynthetic process	0.02039
GO:0000731	DNA synthesis involved in DNA repair	0.02039
GO:0021602	cranial nerve morphogenesis	0.02084
GO:0006639	acylglycerol metabolic process	0.02128
GO:0051129	negative regulation of cellular component organization	0.02131
GO:0010468	regulation of gene expression	0.02159
GO:0045668	negative regulation of osteoblast differentiation	0.02182
GO:0050869	negative regulation of B cell activation	0.02182
GO:0000791	euchromatin	0.02187

GO:0019985	translesion synthesis	0.02212
GO:0031099	regeneration	0.02212
GO:0002676	regulation of chronic inflammatory response	0.02212
GO:0002924	negative regulation of humoral immune response mediated	0.02212
GO:0006689	ganglioside catabolic process	0.02212
GO:0010886	positive regulation of cholesterol storage	0.02212
GO:0010989	negative regulation of low-density lipoprotein particle clear	0.02212
GO:0032466	negative regulation of cytokinesis	0.02212
GO:0046836	glycolipid transport	0.02212
GO:0016072	rRNA metabolic process	0.02238
GO:0005813	centrosome	0.02249
GO:0006206	pyrimidine nucleobase metabolic process	0.02254
GO:0051044	positive regulation of membrane protein ectodomain proteo	0.02254
GO:0055091	phospholipid homeostasis	0.02254
GO:0016042	lipid catabolic process	0.02254
GO:0019218	regulation of steroid metabolic process	0.02257
GO:1904029	regulation of cyclin-dependent protein kinase activity	0.02257
GO:0002253	activation of immune response	0.0226
GO:0000781	chromosome, telomeric region	0.02266
GO:0098754	detoxification	0.02291
GO:0010894	negative regulation of steroid biosynthetic process	0.02316
GO:0032682	negative regulation of chemokine production	0.02316
GO:0001836	release of cytochrome c from mitochondria	0.0232
GO:1902402	signal transduction involved in mitotic DNA damage check	0.0232
GO:1902403	signal transduction involved in mitotic DNA integrity chec	0.0232
GO:0006638	neutral lipid metabolic process	0.02338
GO:0046939	nucleotide phosphorylation	0.02338
GO:0002764	immune response-regulating signaling pathway	0.02432
GO:0048704	embryonic skeletal system morphogenesis	0.02456
GO:0071813	lipoprotein particle binding	0.02485
GO:0071814	protein-lipid complex binding	0.02485
GO:0002923	regulation of humoral immune response mediated by circul	0.02492
GO:0043922	negative regulation by host of viral transcription	0.02492
GO:0150079	negative regulation of neuroinflammatory response	0.02492
GO:1904667	negative regulation of ubiquitin protein ligase activity	0.02492
GO:2000779	regulation of double-strand break repair	0.02503
GO:0035404	histone-serine phosphorylation	0.02559
GO:0035747	natural killer cell chemotaxis	0.02559
GO:2000510	positive regulation of dendritic cell chemotaxis	0.02559
GO:0006355	regulation of transcription, DNA-templated	0.02573
GO:0072331	signal transduction by p53 class mediator	0.02687
GO:1903506	regulation of nucleic acid-templated transcription	0.0269
GO:0019900	kinase binding	0.02708
GO:0050691	regulation of defense response to virus by host	0.02723
GO:0000183	chromatin silencing at rDNA	0.02765
GO:0032371	regulation of sterol transport	0.02774
GO:0032374	regulation of cholesterol transport	0.02774
GO:0002523	leukocyte migration involved in inflammatory response	0.02795
GO:0045655	regulation of monocyte differentiation	0.02795
GO:0019217	regulation of fatty acid metabolic process	0.02798
GO:0015630	microtubule cytoskeleton	0.02811
GO:0000444	MIS12/MIND type complex	0.02818
GO:1990726	Lsm1-7-Pat1 complex	0.02818
GO:0002757	immune response-activating signal transduction	0.02843
GO:0006412	translation	0.02844
GO:0033044	regulation of chromosome organization	0.02844
GO:1901654	response to ketone	0.02848
GO:0032088	negative regulation of NF-kappaB transcription factor activ	0.02863
GO:0042446	hormone biosynthetic process	0.02863
GO:0070192	chromosome organization involved in meiotic cell cycle	0.02865
GO:0045639	positive regulation of myeloid cell differentiation	0.02915
GO:0098869	cellular oxidant detoxification	0.02915
GO:0070972	protein localization to endoplasmic reticulum	0.02947
GO:0045132	meiotic chromosome segregation	0.03036
GO:0006301	postreplication repair	0.03074
GO:0045600	positive regulation of fat cell differentiation	0.03074
GO:0009147	pyrimidine nucleoside triphosphate metabolic process	0.03158
GO:0045120	pronucleus	0.03225
GO:0010997	anaphase-promoting complex binding	0.03256
GO:0043603	cellular amide metabolic process	0.03339
GO:0010224	response to UV-B	0.03339
GO:0060192	negative regulation of lipase activity	0.03339

GO:0090713	immunological memory process	0.03339
GO:1902165	regulation of intrinsic apoptotic signaling pathway in respo	0.03339
GO:0044450	microtubule organizing center part	0.03359
GO:0009987	cellular process	0.03365
GO:0007143	female meiotic nuclear division	0.03382
GO:0010957	negative regulation of vitamin D biosynthetic process	0.03382
GO:0032829	regulation of CD4-positive, CD25-positive, alpha-beta regu	0.03382
GO:0032831	positive regulation of CD4-positive, CD25-positive, alpha-b	0.03382
GO:0060023	soft palate development	0.03382
GO:0060266	negative regulation of respiratory burst involved in inflamm	0.03382
GO:0060268	negative regulation of respiratory burst	0.03382
GO:0061757	leukocyte adhesion to arterial endothelial cell	0.03382
GO:1905333	regulation of gastric motility	0.03382
GO:0030204	chondroitin sulfate metabolic process	0.03427
GO:0030866	cortical actin cytoskeleton organization	0.03427
GO:2000134	negative regulation of G1/S transition of mitotic cell cycle	0.03438
GO:0032994	protein-lipid complex	0.03451
GO:0000737	DNA catabolic process, endonucleolytic	0.03458
GO:0072538	T-helper 17 type immune response	0.03458
GO:0006977	DNA damage response, signal transduction by p53 class me	0.0348
GO:0046434	organophosphate catabolic process	0.03483
GO:0071158	positive regulation of cell cycle arrest	0.03569
GO:0042180	cellular ketone metabolic process	0.0358
GO:0034364	high-density lipoprotein particle	0.03605
GO:0031571	mitotic G1 DNA damage checkpoint	0.03608
GO:0090307	mitotic spindle assembly	0.03608
GO:0001823	mesonephros development	0.03608
GO:0046165	alcohol biosynthetic process	0.03617
GO:0005688	U6 snRNP	0.03665
GO:0072528	pyrimidine-containing compound biosynthetic process	0.03695
GO:0009201	ribonucleoside triphosphate biosynthetic process	0.03742
GO:0031391	Elg1 RFC-like complex	0.03756
GO:0033181	plasma membrane proton-transporting V-type ATPase comp	0.03756
GO:0035985	senescence-associated heterochromatin focus	0.03756
GO:0097149	centralspindlin complex	0.03756
GO:0006351	transcription, DNA-templated	0.03804
GO:0032488	Cdc42 protein signal transduction	0.03865
GO:0034370	triglyceride-rich lipoprotein particle remodeling	0.03865
GO:0046348	amino sugar catabolic process	0.03865
GO:1905168	positive regulation of double-strand break repair via homolo	0.03865
GO:0032479	regulation of type I interferon production	0.03865
GO:0032606	type I interferon production	0.03865
GO:1902254	negative regulation of intrinsic apoptotic signaling pathway	0.03865
GO:0031668	cellular response to extracellular stimulus	0.0392
GO:0034502	protein localization to chromosome	0.0392
GO:0097659	nucleic acid-templated transcription	0.03924
GO:0051817	modification of morphology or physiology of other organism	0.03946
GO:0022627	cytosolic small ribosomal subunit	0.03954
GO:0045931	positive regulation of mitotic cell cycle	0.04052
GO:0060964	regulation of gene silencing by miRNA	0.04072
GO:0006694	steroid biosynthetic process	0.04072
GO:0060249	anatomical structure homeostasis	0.04122
GO:0072431	signal transduction involved in mitotic G1 DNA damage ch	0.04122
GO:1902400	intracellular signal transduction involved in G1 DNA damag	0.04122
GO:0023026	MHC class II protein complex binding	0.04145
GO:0055102	lipase inhibitor activity	0.04145
GO:0005488	binding	0.04145
GO:0031726	CCR1 chemokine receptor binding	0.04145
GO:0072345	NAADP-sensitive calcium-release channel activity	0.04145
GO:0006309	apoptotic DNA fragmentation	0.04189
GO:0010884	positive regulation of lipid storage	0.04189
GO:0045939	negative regulation of steroid metabolic process	0.04189
GO:0071459	protein localization to chromosome, centromeric region	0.04189
GO:0044783	G1 DNA damage checkpoint	0.042
GO:0044819	mitotic G1/S transition checkpoint	0.042
GO:0046006	regulation of activated T cell proliferation	0.04203
GO:1901293	nucleoside phosphate biosynthetic process	0.04221
GO:0006054	N-acetylneuraminate metabolic process	0.04227
GO:0034378	chylomicron assembly	0.04227
GO:0045657	positive regulation of monocyte differentiation	0.04227
GO:0062012	regulation of small molecule metabolic process	0.04251
GO:0009165	nucleotide biosynthetic process	0.04251

GO:0002158	osteoclast proliferation	0.04251
GO:0034382	chylomicron remnant clearance	0.04251
GO:0071830	triglyceride-rich lipoprotein particle clearance	0.04251
GO:1901724	positive regulation of cell proliferation involved in kidney c	0.04251
GO:2000501	regulation of natural killer cell chemotaxis	0.04251
GO:0060969	negative regulation of gene silencing	0.04251
GO:0097421	liver regeneration	0.04251
GO:0000303	response to superoxide	0.04258
GO:0006294	nucleotide-excision repair, preincision complex assembly	0.04258
GO:0046134	pyrimidine nucleoside biosynthetic process	0.04258
GO:0002230	positive regulation of defense response to virus by host	0.04272
GO:0002712	regulation of B cell mediated immunity	0.04272
GO:0002889	regulation of immunoglobulin mediated immune response	0.04272
GO:0019216	regulation of lipid metabolic process	0.04272
GO:0062013	positive regulation of small molecule metabolic process	0.04272
GO:0001807	regulation of type IV hypersensitivity	0.04272
GO:0002266	follicular dendritic cell activation	0.04272
GO:0002277	myeloid dendritic cell activation involved in immune respo	0.04272
GO:0002397	MHC class I protein complex assembly	0.04272
GO:0002774	Fc receptor mediated inhibitory signaling pathway	0.04272
GO:0007057	spindle assembly involved in female meiosis I	0.04272
GO:0010956	negative regulation of calcidiol 1-monooxygenase activity	0.04272
GO:0021569	rhombomere 3 development	0.04272
GO:0030910	olfactory placode formation	0.04272
GO:0032875	regulation of DNA endoreduplication	0.04272
GO:0035283	central nervous system segmentation	0.04272
GO:0035284	brain segmentation	0.04272
GO:0035986	senescence-associated heterochromatin focus assembly	0.04272
GO:0048852	diencephalon morphogenesis	0.04272
GO:0055095	lipoprotein particle mediated signaling	0.04272
GO:0055096	low-density lipoprotein particle mediated signaling	0.04272
GO:0060557	positive regulation of vitamin D biosynthetic process	0.04272
GO:0060559	positive regulation of calcidiol 1-monooxygenase activity	0.04272
GO:0071698	olfactory placode development	0.04272
GO:0071699	olfactory placode morphogenesis	0.04272
GO:0090402	oncogene-induced cell senescence	0.04272
GO:1905463	negative regulation of DNA duplex unwinding	0.04272
GO:2000520	regulation of immunological synapse formation	0.04272
GO:2001190	positive regulation of T cell activation via T cell receptor c	0.04272
GO:0005975	carbohydrate metabolic process	0.04388
GO:0034660	ncRNA metabolic process	0.04413
GO:0002377	immunoglobulin production	0.04432
GO:0010556	regulation of macromolecule biosynthetic process	0.0445
GO:0002639	positive regulation of immunoglobulin production	0.04477
GO:0031936	negative regulation of chromatin silencing	0.04515
GO:0046112	nucleobase biosynthetic process	0.04515
GO:1903978	regulation of microglial cell activation	0.04515
GO:0047655	allyl-alcohol dehydrogenase activity	0.04539
GO:0044773	mitotic DNA damage checkpoint	0.04554
GO:0072332	intrinsic apoptotic signaling pathway by p53 class mediator	0.04627
GO:1902652	secondary alcohol metabolic process	0.04638
GO:0045861	negative regulation of proteolysis	0.04672
GO:0006275	regulation of DNA replication	0.04672
GO:1902807	negative regulation of cell cycle G1/S phase transition	0.04672
GO:0006518	peptide metabolic process	0.04771
GO:0046364	monosaccharide biosynthetic process	0.04831
GO:0060147	regulation of posttranscriptional gene silencing	0.04849
GO:0060966	regulation of gene silencing by RNA	0.04849
GO:0009988	cell-cell recognition	0.04851
GO:0043043	peptide biosynthetic process	0.04896
GO:1901135	carbohydrate derivative metabolic process	0.04898
GO:0051180	vitamin transport	0.04924
GO:1990000	amyloid fibril formation	0.04965
GO:0071825	protein-lipid complex subunit organization	0.04965
GO:0007017	microtubule-based process	0.04965
GO:1901575	organic substance catabolic process	0.04965
GO:0002637	regulation of immunoglobulin production	0.04965
GO:0010875	positive regulation of cholesterol efflux	0.04965
GO:0051004	regulation of lipoprotein lipase activity	0.04965
GO:0070987	error-free translesion synthesis	0.04965
Medium_No Trend Only		
GO:0001667	ameboidal-type cell migration	3.05E-12

GO:0030199	collagen fibril organization	3.92E-12
GO:0002040	sprouting angiogenesis	2.00E-09
GO:0007599	hemostasis	4.67E-09
GO:0050817	coagulation	5.63E-09
GO:0007596	blood coagulation	9.07E-09
GO:0005788	endoplasmic reticulum lumen	1.49E-08
GO:0001936	regulation of endothelial cell proliferation	1.03E-07
GO:0001935	endothelial cell proliferation	2.42E-07
GO:0030168	platelet activation	3.94E-07
GO:0043534	blood vessel endothelial cell migration	5.11E-07
GO:0048871	multicellular organismal homeostasis	5.66E-07
GO:0003158	endothelium development	1.23E-06
GO:0034103	regulation of tissue remodeling	1.31E-06
GO:0061041	regulation of wound healing	1.38E-06
GO:0010594	regulation of endothelial cell migration	1.40E-06
GO:0005518	collagen binding	2.05E-06
GO:0098644	complex of collagen trimers	2.39E-06
GO:0001503	ossification	3.25E-06
GO:0030020	extracellular matrix structural constituent conferring tensil	3.99E-06
GO:0009719	response to endogenous stimulus	5.82E-06
GO:0033628	regulation of cell adhesion mediated by integrin	8.25E-06
GO:0022617	extracellular matrix disassembly	8.59E-06
GO:0045121	membrane raft	1.15E-05
GO:0098857	membrane microdomain	1.15E-05
GO:0050679	positive regulation of epithelial cell proliferation	1.50E-05
GO:0050777	negative regulation of immune response	1.78E-05
GO:0050818	regulation of coagulation	2.04E-05
GO:0002042	cell migration involved in sprouting angiogenesis	3.54E-05
GO:0042832	defense response to protozoan	3.55E-05
GO:0045446	endothelial cell differentiation	3.71E-05
GO:0048729	tissue morphogenesis	3.95E-05
GO:0001938	positive regulation of endothelial cell proliferation	5.21E-05
GO:0007369	gastrulation	5.33E-05
GO:0043535	regulation of blood vessel endothelial cell migration	5.70E-05
GO:1900046	regulation of hemostasis	6.24E-05
GO:0044706	multi-multicellular organism process	6.38E-05
GO:0098589	membrane region	6.88E-05
GO:0001562	response to protozoan	7.53E-05
GO:0035924	cellular response to vascular endothelial growth factor stim	7.65E-05
GO:0006869	lipid transport	9.21E-05
GO:0030193	regulation of blood coagulation	9.25E-05
GO:0060055	angiogenesis involved in wound healing	0.0001
GO:0010634	positive regulation of epithelial cell migration	0.00011
GO:0045576	mast cell activation	0.00011
GO:0038084	vascular endothelial growth factor signaling pathway	0.00011
GO:0010876	lipid localization	0.00012
GO:0005583	fibrillar collagen trimer	0.00014
GO:0098643	banded collagen fibril	0.00014
GO:0001776	leukocyte homeostasis	0.00015
GO:0010243	response to organonitrogen compound	0.00015
GO:0002720	positive regulation of cytokine production involved in imm	0.00016
GO:0032835	glomerulus development	0.00017
GO:0071495	cellular response to endogenous stimulus	0.00018
GO:0010712	regulation of collagen metabolic process	0.00018
GO:0002675	positive regulation of acute inflammatory response	0.00019
GO:0048608	reproductive structure development	0.00024
GO:0050819	negative regulation of coagulation	0.00024
GO:0098657	import into cell	0.00027
GO:0090184	positive regulation of kidney development	0.00027
GO:0002532	production of molecular mediator involved in inflammatory	0.00028
GO:0031214	biomineral tissue development	0.00029
GO:0070161	anchoring junction	0.00032
GO:0061458	reproductive system development	0.00033
GO:0002448	mast cell mediated immunity	0.0004
GO:1903727	positive regulation of phospholipid metabolic process	0.0004
GO:0070304	positive regulation of stress-activated protein kinase signali	0.00042
GO:0033003	regulation of mast cell activation	0.00042
GO:0007264	small GTPase mediated signal transduction	0.00044
GO:0023057	negative regulation of signaling	0.00047
GO:0048872	homeostasis of number of cells	0.00047
GO:0014068	positive regulation of phosphatidylinositol 3-kinase signali	0.00048
GO:0007229	integrin-mediated signaling pathway	0.00048

GO:0010648	negative regulation of cell communication	0.00051
GO:0071229	cellular response to acid chemical	0.00052
GO:0030282	bone mineralization	0.00052
GO:0046660	female sex differentiation	0.00052
GO:0032147	activation of protein kinase activity	0.00053
GO:0034446	substrate adhesion-dependent cell spreading	0.00054
GO:0071363	cellular response to growth factor stimulus	0.00054
GO:0009968	negative regulation of signal transduction	0.00055
GO:0004222	metalloendopeptidase activity	0.00056
GO:0001894	tissue homeostasis	0.00057
GO:0010595	positive regulation of endothelial cell migration	0.0006
GO:1901698	response to nitrogen compound	0.00061
GO:0030183	B cell differentiation	0.00061
GO:0046777	protein autophosphorylation	0.00064
GO:1900047	negative regulation of hemostasis	0.00075
GO:0005912	adherens junction	0.00075
GO:0002009	morphogenesis of an epithelium	0.00083
GO:0061134	peptidase regulator activity	0.00089
GO:0070848	response to growth factor	0.0009
GO:0002062	chondrocyte differentiation	0.00095
GO:0007565	female pregnancy	0.00098
GO:0043406	positive regulation of MAP kinase activity	0.00102
GO:0002710	negative regulation of T cell mediated immunity	0.00106
GO:0072012	glomerulus vasculature development	0.00106
GO:0032874	positive regulation of stress-activated MAPK cascade	0.00108
GO:0070141	response to UV-A	0.00113
GO:0030036	actin cytoskeleton organization	0.00113
GO:0061042	vascular wound healing	0.00123
GO:0098543	detection of other organism	0.00123
GO:0002064	epithelial cell development	0.00126
GO:0006897	endocytosis	0.00128
GO:0001569	branching involved in blood vessel morphogenesis	0.00139
GO:0045601	regulation of endothelial cell differentiation	0.00142
GO:0022612	gland morphogenesis	0.00147
GO:0004953	icosanoid receptor activity	0.0015
GO:1903670	regulation of sprouting angiogenesis	0.00154
GO:0030195	negative regulation of blood coagulation	0.00155
GO:0014812	muscle cell migration	0.00158
GO:0005902	microvillus	0.00159
GO:0012505	endomembrane system	0.0016
GO:0042267	natural killer cell mediated cytotoxicity	0.0016
GO:0070167	regulation of biomineral tissue development	0.00176
GO:0043303	mast cell degranulation	0.00177
GO:0002719	negative regulation of cytokine production involved in imm	0.0018
GO:2000241	regulation of reproductive process	0.0018
GO:0071902	positive regulation of protein serine/threonine kinase activi	0.00184
GO:0048565	digestive tract development	0.00187
GO:0045124	regulation of bone resorption	0.00187
GO:0003006	developmental process involved in reproduction	0.00188
GO:0014909	smooth muscle cell migration	0.00195
GO:0048333	mesodermal cell differentiation	0.00206
GO:0048407	platelet-derived growth factor binding	0.00207
GO:0003151	outflow tract morphogenesis	0.00218
GO:0001656	metanephros development	0.00221
GO:0034109	homotypic cell-cell adhesion	0.00221
GO:0046850	regulation of bone remodeling	0.00225
GO:0006022	aminoglycan metabolic process	0.00243
GO:0061135	endopeptidase regulator activity	0.00244
GO:0002279	mast cell activation involved in immune response	0.00244
GO:0038065	collagen-activated signaling pathway	0.00245
GO:0046545	development of primary female sexual characteristics	0.00257
GO:0048483	autonomic nervous system development	0.00262
GO:0034330	cell junction organization	0.00268
GO:0110110	positive regulation of animal organ morphogenesis	0.00277
GO:0016702	oxidoreductase activity, acting on single donors with incorp	0.00284
GO:0060191	regulation of lipase activity	0.00293
GO:0061437	renal system vasculature development	0.00294
GO:0061440	kidney vasculature development	0.00294
GO:0070527	platelet aggregation	0.00301
GO:0002701	negative regulation of production of molecular mediator of	0.00304
GO:0032965	regulation of collagen biosynthetic process	0.00304
GO:0090049	regulation of cell migration involved in sprouting angiogen	0.00304

GO:0007178	transmembrane receptor protein serine/threonine kinase sig	0.00324
GO:0010950	positive regulation of endopeptidase activity	0.00329
GO:0051055	negative regulation of lipid biosynthetic process	0.0033
GO:0090136	epithelial cell-cell adhesion	0.0033
GO:0060393	regulation of pathway-restricted SMAD protein phosphoryl	0.00331
GO:0051090	regulation of DNA-binding transcription factor activity	0.00338
GO:1901681	sulfur compound binding	0.00347
GO:0014910	regulation of smooth muscle cell migration	0.00347
GO:0006810	transport	0.00361
GO:0061005	cell differentiation involved in kidney development	0.00365
GO:2001056	positive regulation of cysteine-type endopeptidase activity	0.00388
GO:0035023	regulation of Rho protein signal transduction	0.00388
GO:0060389	pathway-restricted SMAD protein phosphorylation	0.00389
GO:0090050	positive regulation of cell migration involved in sprouting	0.00396
GO:0016701	oxidoreductase activity, acting on single donors with incorp	0.00423
GO:0032526	response to retinoic acid	0.0043
GO:0030858	positive regulation of epithelial cell differentiation	0.00434
GO:0060135	maternal process involved in female pregnancy	0.00434
GO:0051057	positive regulation of small GTPase mediated signal transd	0.0044
GO:0098581	detection of external biotic stimulus	0.00441
GO:0001912	positive regulation of leukocyte mediated cytotoxicity	0.00445
GO:0007219	Notch signaling pathway	0.00445
GO:0045453	bone resorption	0.00446
GO:0010952	positive regulation of peptidase activity	0.00449
GO:0001787	natural killer cell proliferation	0.0045
GO:0010543	regulation of platelet activation	0.00451
GO:0007584	response to nutrient	0.00452
GO:1904894	positive regulation of STAT cascade	0.00454
GO:0001945	lymph vessel development	0.00459
GO:0098751	bone cell development	0.00462
GO:0043394	proteoglycan binding	0.00479
GO:0005614	interstitial matrix	0.00495
GO:0005925	focal adhesion	0.00502
GO:0014066	regulation of phosphatidylinositol 3-kinase signaling	0.00506
GO:0060840	artery development	0.00517
GO:0033691	sialic acid binding	0.0052
GO:0007266	Rho protein signal transduction	0.00541
GO:0046683	response to organophosphorus	0.00541
GO:1901699	cellular response to nitrogen compound	0.00555
GO:0003206	cardiac chamber morphogenesis	0.00555
GO:0007015	actin filament organization	0.00563
GO:1903672	positive regulation of sprouting angiogenesis	0.00563
GO:2000826	regulation of heart morphogenesis	0.00563
GO:1905563	negative regulation of vascular endothelial cell proliferatio	0.00566
GO:0002370	natural killer cell cytokine production	0.00567
GO:0002727	regulation of natural killer cell cytokine production	0.00567
GO:0050839	cell adhesion molecule binding	0.00575
GO:0002886	regulation of myeloid leukocyte mediated immunity	0.00579
GO:0043536	positive regulation of blood vessel endothelial cell migratio	0.00579
GO:0010544	negative regulation of platelet activation	0.00579
GO:0005924	cell-substrate adherens junction	0.00604
GO:0004866	endopeptidase inhibitor activity	0.00611
GO:0090092	regulation of transmembrane receptor protein serine/threon	0.00613
GO:0030500	regulation of bone mineralization	0.00624
GO:0030055	cell-substrate junction	0.00633
GO:0016043	cellular component organization	0.00635
GO:0031622	positive regulation of fever generation	0.0065
GO:0044691	tooth eruption	0.0065
GO:0032740	positive regulation of interleukin-17 production	0.0065
GO:0010810	regulation of cell-substrate adhesion	0.00651
GO:0043009	chordate embryonic development	0.00664
GO:0034105	positive regulation of tissue remodeling	0.00666
GO:0071417	cellular response to organonitrogen compound	0.00672
GO:0033089	positive regulation of T cell differentiation in thymus	0.00682
GO:0097035	regulation of membrane lipid distribution	0.00682
GO:0048566	embryonic digestive tract development	0.00685
GO:0070169	positive regulation of biomineral tissue development	0.00694
GO:1901652	response to peptide	0.00728
GO:0001570	vasculogenesis	0.00743
GO:0008237	metallopeptidase activity	0.00752
GO:0005178	integrin binding	0.00755
GO:0005161	platelet-derived growth factor receptor binding	0.00766

GO:0046579	positive regulation of Ras protein signal transduction	0.00774
GO:0001701	in utero embryonic development	0.00778
GO:0032623	interleukin-2 production	0.00782
GO:0032663	regulation of interleukin-2 production	0.00782
GO:0006687	glycosphingolipid metabolic process	0.00782
GO:0030414	peptidase inhibitor activity	0.00787
GO:0051056	regulation of small GTPase mediated signal transduction	0.00793
GO:0035590	purinergic nucleotide receptor signaling pathway	0.00815
GO:0045995	regulation of embryonic development	0.00823
GO:0046330	positive regulation of JNK cascade	0.00823
GO:1901222	regulation of NIK/NF-kappaB signaling	0.00833
GO:1903510	mucopolysaccharide metabolic process	0.00833
GO:0001946	lymphangiogenesis	0.00841
GO:0016045	detection of bacterium	0.00841
GO:0034134	toll-like receptor 2 signaling pathway	0.00841
GO:0048844	artery morphogenesis	0.00871
GO:0045137	development of primary sexual characteristics	0.00889
GO:0045833	negative regulation of lipid metabolic process	0.00898
GO:0007498	mesoderm development	0.0091
GO:0035850	epithelial cell differentiation involved in kidney developme	0.0091
GO:0055123	digestive system development	0.0095
GO:0099515	actin filament-based transport	0.0095
GO:0034135	regulation of toll-like receptor 2 signaling pathway	0.0095
GO:0070493	thrombin-activated receptor signaling pathway	0.0095
GO:0060021	roof of mouth development	0.00959
GO:0032970	regulation of actin filament-based process	0.00967
GO:0061515	myeloid cell development	0.00967
GO:0071300	cellular response to retinoic acid	0.00967
GO:0048546	digestive tract morphogenesis	0.00997
GO:0060443	mammary gland morphogenesis	0.00997
GO:0034204	lipid translocation	0.01005
GO:0071260	cellular response to mechanical stimulus	0.01012
GO:0046427	positive regulation of JAK-STAT cascade	0.01012
GO:0009792	embryo development ending in birth or egg hatching	0.01012
GO:0003205	cardiac chamber development	0.01028
GO:0035587	purinergic receptor signaling pathway	0.01066
GO:0030234	enzyme regulator activity	0.01084
GO:0070302	regulation of stress-activated protein kinase signaling casca	0.01095
GO:0014074	response to purine-containing compound	0.01151
GO:0001990	regulation of systemic arterial blood pressure by hormone	0.01177
GO:0008047	enzyme activator activity	0.01197
GO:0002260	lymphocyte homeostasis	0.01227
GO:0009128	purine nucleoside monophosphate catabolic process	0.01228
GO:0072109	glomerular mesangium development	0.01228
GO:0051130	positive regulation of cellular component organization	0.01232
GO:0032814	regulation of natural killer cell activation	0.01267
GO:0030246	carbohydrate binding	0.01302
GO:0004954	prostanoid receptor activity	0.01302
GO:0097493	structural molecule activity conferring elasticity	0.01302
GO:1903845	negative regulation of cellular response to transforming gro	0.01305
GO:0031915	positive regulation of synaptic plasticity	0.01305
GO:0046643	regulation of gamma-delta T cell activation	0.01305
GO:0008064	regulation of actin polymerization or depolymerization	0.01319
GO:0043552	positive regulation of phosphatidylinositol 3-kinase activity	0.01353
GO:0006968	cellular defense response	0.01361
GO:0097366	response to bronchodilator	0.01361
GO:0008289	lipid binding	0.01394
GO:0046629	gamma-delta T cell activation	0.014
GO:0007548	sex differentiation	0.0141
GO:0001773	myeloid dendritic cell activation	0.01424
GO:0038111	interleukin-7-mediated signaling pathway	0.01424
GO:0043304	regulation of mast cell degranulation	0.01424
GO:0061311	cell surface receptor signaling pathway involved in heart de	0.01424
GO:0046636	negative regulation of alpha-beta T cell activation	0.01429
GO:0043168	anion binding	0.01431
GO:0032355	response to estradiol	0.01454
GO:0003272	endocardial cushion formation	0.01473
GO:0009595	detection of biotic stimulus	0.01473
GO:0034123	positive regulation of toll-like receptor signaling pathway	0.01473
GO:0090025	regulation of monocyte chemotaxis	0.01473
GO:0030832	regulation of actin filament length	0.01474
GO:0008585	female gonad development	0.01496

GO:0045332	phospholipid translocation	0.01496
GO:0043525	positive regulation of neuron apoptotic process	0.01524
GO:0014031	mesenchymal cell development	0.01548
GO:0008154	actin polymerization or depolymerization	0.01548
GO:0071559	response to transforming growth factor beta	0.01548
GO:0001974	blood vessel remodeling	0.01548
GO:0014911	positive regulation of smooth muscle cell migration	0.01548
GO:0045777	positive regulation of blood pressure	0.01548
GO:0090287	regulation of cellular response to growth factor stimulus	0.01556
GO:0016174	NAD(P)H oxidase activity	0.01601
GO:0030023	extracellular matrix constituent conferring elasticity	0.01601
GO:0090101	negative regulation of transmembrane receptor protein seri	0.01639
GO:0060411	cardiac septum morphogenesis	0.01639
GO:0009725	response to hormone	0.01691
GO:0006027	glycosaminoglycan catabolic process	0.01691
GO:0033273	response to vitamin	0.01691
GO:0048010	vascular endothelial growth factor receptor signaling pathw	0.01691
GO:0002729	positive regulation of natural killer cell cytokine productio	0.01719
GO:0071493	cellular response to UV-B	0.01719
GO:0006909	phagocytosis	0.01739
GO:0015914	phospholipid transport	0.01757
GO:0048332	mesoderm morphogenesis	0.01757
GO:0002551	mast cell chemotaxis	0.01757
GO:0032372	negative regulation of sterol transport	0.01757
GO:0032375	negative regulation of cholesterol transport	0.01757
GO:0033079	immature T cell proliferation	0.01757
GO:0070243	regulation of thymocyte apoptotic process	0.01757
GO:0010811	positive regulation of cell-substrate adhesion	0.01777
GO:0043028	cysteine-type endopeptidase regulator activity involved in a	0.0178
GO:0005021	vascular endothelial growth factor-activated receptor activi	0.0178
GO:0030041	actin filament polymerization	0.01833
GO:0009268	response to pH	0.0184
GO:0032872	regulation of stress-activated MAPK cascade	0.01852
GO:0061008	hepaticobiliary system development	0.01883
GO:0071772	response to BMP	0.01883
GO:0071773	cellular response to BMP stimulus	0.01883
GO:0031098	stress-activated protein kinase signaling cascade	0.01883
GO:0031638	zymogen activation	0.01883
GO:1904705	regulation of vascular smooth muscle cell proliferation	0.01883
GO:1990874	vascular smooth muscle cell proliferation	0.01883
GO:0000146	microfilament motor activity	0.01884
GO:0061028	establishment of endothelial barrier	0.01891
GO:0006919	activation of cysteine-type endopeptidase activity involved	0.01901
GO:0014033	neural crest cell differentiation	0.01901
GO:0071560	cellular response to transforming growth factor beta stimul	0.01919
GO:0015748	organophosphate ester transport	0.01934
GO:0033006	regulation of mast cell activation involved in immune resp	0.01938
GO:1903319	positive regulation of protein maturation	0.01938
GO:0032956	regulation of actin cytoskeleton organization	0.01959
GO:0036035	osteoclast development	0.02031
GO:0070431	nucleotide-binding oligomerization domain containing 2 si	0.02031
GO:0072044	collecting duct development	0.02031
GO:0001784	phosphotyrosine residue binding	0.02034
GO:0006196	AMP catabolic process	0.02057
GO:0014805	smooth muscle adaptation	0.02057
GO:0014900	muscle hyperplasia	0.02057
GO:0019322	pentose biosynthetic process	0.02057
GO:0051754	meiotic sister chromatid cohesion, centromeric	0.02057
GO:0061591	calcium activated galactosylceramide scrambling	0.02057
GO:0071603	endothelial cell-cell adhesion	0.02057
GO:0032911	negative regulation of transforming growth factor beta1 pro	0.02065
GO:0034136	negative regulation of toll-like receptor 2 signaling pathwa	0.02065
GO:0035234	ectopic germ cell programmed cell death	0.02065
GO:0035744	T-helper 1 cell cytokine production	0.02065
GO:0072008	glomerular mesangial cell differentiation	0.02065
GO:1900748	positive regulation of vascular endothelial growth factor si	0.02065
GO:2000554	regulation of T-helper 1 cell cytokine production	0.02065
GO:2000556	positive regulation of T-helper 1 cell cytokine production	0.02065
GO:0030833	regulation of actin filament polymerization	0.02065
GO:0090288	negative regulation of cellular response to growth factor sti	0.02065
GO:0001889	liver development	0.02077
GO:0001755	neural crest cell migration	0.02077

GO:0003081	regulation of systemic arterial blood pressure by renin-angi	0.02109
GO:0050995	negative regulation of lipid catabolic process	0.02109
GO:0006024	glycosaminoglycan biosynthetic process	0.02109
GO:0030728	ovulation	0.02116
GO:0032717	negative regulation of interleukin-8 production	0.02116
GO:0032930	positive regulation of superoxide anion generation	0.02116
GO:0048745	smooth muscle tissue development	0.02116
GO:0046677	response to antibiotic	0.02139
GO:0002320	lymphoid progenitor cell differentiation	0.02142
GO:0051403	stress-activated MAPK cascade	0.02158
GO:0045622	regulation of T-helper cell differentiation	0.02167
GO:0060412	ventricular septum morphogenesis	0.02167
GO:2000177	regulation of neural precursor cell proliferation	0.02182
GO:0042445	hormone metabolic process	0.02226
GO:0003231	cardiac ventricle development	0.0225
GO:0014032	neural crest cell development	0.02297
GO:0002715	regulation of natural killer cell mediated immunity	0.02297
GO:0003197	endocardial cushion development	0.02297
GO:1903053	regulation of extracellular matrix organization	0.02297
GO:0042542	response to hydrogen peroxide	0.0232
GO:0001707	mesoderm formation	0.02328
GO:0001885	endothelial cell development	0.02328
GO:0042698	ovulation cycle	0.02328
GO:0045834	positive regulation of lipid metabolic process	0.02329
GO:0032620	interleukin-17 production	0.02364
GO:0032660	regulation of interleukin-17 production	0.02364
GO:0048048	embryonic eye morphogenesis	0.02364
GO:1904707	positive regulation of vascular smooth muscle cell prolifera	0.02364
GO:1901888	regulation of cell junction assembly	0.02367
GO:0016459	myosin complex	0.02379
GO:0001772	immunological synapse	0.02379
GO:0003779	actin binding	0.02429
GO:0005044	scavenger receptor activity	0.02429
GO:0032757	positive regulation of interleukin-8 production	0.02436
GO:0001660	fever generation	0.02436
GO:0031652	positive regulation of heat generation	0.02436
GO:0033080	immature T cell proliferation in thymus	0.02436
GO:0043589	skin morphogenesis	0.02436
GO:0060907	positive regulation of macrophage cytokine production	0.02436
GO:0061043	regulation of vascular wound healing	0.02436
GO:0072205	metanephric collecting duct development	0.02436
GO:2001204	regulation of osteoclast development	0.02436
GO:0043551	regulation of phosphatidylinositol 3-kinase activity	0.02526
GO:0072577	endothelial cell apoptotic process	0.02526
GO:0060627	regulation of vesicle-mediated transport	0.02533
GO:0019835	cytolysis	0.02533
GO:0071711	basement membrane organization	0.02533
GO:0030898	actin-dependent ATPase activity	0.02568
GO:0005520	insulin-like growth factor binding	0.02568
GO:0006026	aminoglycan catabolic process	0.02597
GO:0110053	regulation of actin filament organization	0.0261
GO:0050830	defense response to Gram-positive bacterium	0.02656
GO:0030512	negative regulation of transforming growth factor beta rece	0.0267
GO:0048705	skeletal system morphogenesis	0.02681
GO:0005588	collagen type V trimer	0.02728
GO:0010954	positive regulation of protein processing	0.02736
GO:0021879	forebrain neuron differentiation	0.02742
GO:0001649	osteoblast differentiation	0.02769
GO:0048864	stem cell development	0.02776
GO:0016798	hydrolase activity, acting on glycosyl bonds	0.02806
GO:0072132	mesenchyme morphogenesis	0.02851
GO:0070482	response to oxygen levels	0.02851
GO:0044853	plasma membrane raft	0.02871
GO:0001771	immunological synapse formation	0.02875
GO:0003376	sphingosine-1-phosphate receptor signaling pathway	0.02875
GO:0009169	purine ribonucleoside monophosphate catabolic process	0.02875
GO:0031650	regulation of heat generation	0.02875
GO:0060841	venous blood vessel development	0.02875
GO:0097531	mast cell migration	0.02875
GO:0150078	positive regulation of neuroinflammatory response	0.02875
GO:0032703	negative regulation of interleukin-2 production	0.02901
GO:0045606	positive regulation of epidermal cell differentiation	0.02901

GO:0051384	response to glucocorticoid	0.02912
GO:0009125	nucleoside monophosphate catabolic process	0.03043
GO:0032928	regulation of superoxide anion generation	0.03043
GO:0035988	chondrocyte proliferation	0.03043
GO:0060444	branching involved in mammary gland duct morphogenesis	0.03043
GO:0072574	hepatocyte proliferation	0.03043
GO:0072575	epithelial cell proliferation involved in liver morphogenesis	0.03043
GO:1902547	regulation of cellular response to vascular endothelial grow	0.03043
GO:0003203	endocardial cushion morphogenesis	0.03066
GO:0070232	regulation of T cell apoptotic process	0.03066
GO:0045603	positive regulation of endothelial cell differentiation	0.03075
GO:0060973	cell migration involved in heart development	0.03075
GO:0033005	positive regulation of mast cell activation	0.03101
GO:0045780	positive regulation of bone resorption	0.03101
GO:0046852	positive regulation of bone remodeling	0.03101
GO:0060231	mesenchymal to epithelial transition	0.03101
GO:0072091	regulation of stem cell proliferation	0.03104
GO:0008593	regulation of Notch signaling pathway	0.03104
GO:0001659	temperature homeostasis	0.0313
GO:0006953	acute-phase response	0.03178
GO:0002686	negative regulation of leukocyte migration	0.03178
GO:0098760	response to interleukin-7	0.03178
GO:0098761	cellular response to interleukin-7	0.03178
GO:1905332	positive regulation of morphogenesis of an epithelium	0.03178
GO:0006023	aminoglycan biosynthetic process	0.03183
GO:0051091	positive regulation of DNA-binding transcription factor acti	0.03188
GO:2000243	positive regulation of reproductive process	0.03265
GO:0036293	response to decreased oxygen levels	0.03323
GO:0004955	prostaglandin receptor activity	0.03337
GO:0016803	ether hydrolase activity	0.03337
GO:0060251	regulation of glial cell proliferation	0.03359
GO:0007265	Ras protein signal transduction	0.03401
GO:0002765	immune response-inhibiting signal transduction	0.03425
GO:0010887	negative regulation of cholesterol storage	0.03425
GO:0031620	regulation of fever generation	0.03425
GO:0032817	regulation of natural killer cell proliferation	0.03425
GO:0045586	regulation of gamma-delta T cell differentiation	0.03425
GO:1901201	regulation of extracellular matrix assembly	0.03425
GO:1904238	pericyte cell differentiation	0.03425
GO:1905522	negative regulation of macrophage migration	0.03425
GO:2001187	positive regulation of CD8-positive, alpha-beta T cell activa	0.03425
GO:0003170	heart valve development	0.03505
GO:0050854	regulation of antigen receptor-mediated signaling pathway	0.03505
GO:0072210	metanephric nephron development	0.03534
GO:0008406	gonad development	0.0356
GO:0045236	CXCR chemokine receptor binding	0.03583
GO:0002020	protease binding	0.03599
GO:0002360	T cell lineage commitment	0.03637
GO:0045577	regulation of B cell differentiation	0.03637
GO:0048147	negative regulation of fibroblast proliferation	0.03637
GO:0050858	negative regulation of antigen receptor-mediated signaling	0.03637
GO:0090303	positive regulation of wound healing	0.03696
GO:0050922	negative regulation of chemotaxis	0.03733
GO:0001666	response to hypoxia	0.03921
GO:2000351	regulation of endothelial cell apoptotic process	0.03928
GO:0090218	positive regulation of lipid kinase activity	0.03944
GO:0001958	endochondral ossification	0.03944
GO:0010714	positive regulation of collagen metabolic process	0.03944
GO:0036075	replacement ossification	0.03944
GO:0043032	positive regulation of macrophage activation	0.03944
GO:0060706	cell differentiation involved in embryonic placenta develop	0.03944
GO:0015629	actin cytoskeleton	0.03948
GO:0001709	cell fate determination	0.03984
GO:0021983	pituitary gland development	0.03984
GO:0032924	activin receptor signaling pathway	0.03984
GO:1901658	glycosyl compound catabolic process	0.03984
GO:0048609	multicellular organismal reproductive process	0.0403
GO:0004857	enzyme inhibitor activity	0.04046
GO:0072009	nephron epithelium development	0.04113
GO:0002430	complement receptor mediated signaling pathway	0.04175
GO:0002863	positive regulation of inflammatory response to antigenic st	0.04175
GO:0014831	gastro-intestinal system smooth muscle contraction	0.04175

GO:0032490	detection of molecule of bacterial origin	0.04175
GO:0032966	negative regulation of collagen biosynthetic process	0.04175
GO:0033083	regulation of immature T cell proliferation	0.04175
GO:0033629	negative regulation of cell adhesion mediated by integrin	0.04175
GO:0038063	collagen-activated tyrosine kinase receptor signaling pathw	0.04175
GO:0043383	negative T cell selection	0.04175
GO:0071635	negative regulation of transforming growth factor beta prod	0.04175
GO:1902337	regulation of apoptotic process involved in morphogenesis	0.04175
GO:1904748	regulation of apoptotic process involved in development	0.04175
GO:2001279	regulation of unsaturated fatty acid biosynthetic process	0.04175
GO:0003179	heart valve morphogenesis	0.04175
GO:0060350	endochondral bone morphogenesis	0.04175
GO:0045992	negative regulation of embryonic development	0.04175
GO:0051043	regulation of membrane protein ectodomain proteolysis	0.04175
GO:0071425	hematopoietic stem cell proliferation	0.04175
GO:0072576	liver morphogenesis	0.04175
GO:0032732	positive regulation of interleukin-1 production	0.04358
GO:0061180	mammary gland epithelium development	0.04358
GO:0038036	sphingosine-1-phosphate receptor activity	0.0436
GO:0002534	cytokine production involved in inflammatory response	0.04371
GO:1900015	regulation of cytokine production involved in inflammatory	0.04371
GO:0033630	positive regulation of cell adhesion mediated by integrin	0.04407
GO:1900746	regulation of vascular endothelial growth factor signaling p	0.04407
GO:0042269	regulation of natural killer cell mediated cytotoxicity	0.04425
GO:0050856	regulation of T cell receptor signaling pathway	0.04425
GO:1904407	positive regulation of nitric oxide metabolic process	0.04425
GO:1905314	semi-lunar valve development	0.04425
GO:0060349	bone morphogenesis	0.04453
GO:1903725	regulation of phospholipid metabolic process	0.04453
GO:0010934	macrophage cytokine production	0.04467
GO:0010935	regulation of macrophage cytokine production	0.04467
GO:0042574	retinal metabolic process	0.04467
GO:0045717	negative regulation of fatty acid biosynthetic process	0.04467
GO:0060099	regulation of phagocytosis, engulfment	0.04467
GO:0004867	serine-type endopeptidase inhibitor activity	0.04473
GO:0009158	ribonucleoside monophosphate catabolic process	0.04483
GO:0031649	heat generation	0.04483
GO:0035743	CD4-positive, alpha-beta T cell cytokine production	0.04483
GO:0070242	thymocyte apoptotic process	0.04483
GO:1904892	regulation of STAT cascade	0.04505
GO:0003279	cardiac septum development	0.04511
GO:0032535	regulation of cellular component size	0.04539
GO:0046328	regulation of JNK cascade	0.04543
GO:0035270	endocrine system development	0.04575
GO:0060759	regulation of response to cytokine stimulus	0.04611
GO:0001542	ovulation from ovarian follicle	0.04658
GO:0001866	NK T cell proliferation	0.04658
GO:0002606	positive regulation of dendritic cell antigen processing and	0.04658
GO:0014827	intestine smooth muscle contraction	0.04658
GO:0034354	'de novo' NAD biosynthetic process from tryptophan	0.04658
GO:0035989	tendon development	0.04658
GO:0038001	paracrine signaling	0.04658
GO:0043376	regulation of CD8-positive, alpha-beta T cell differentiatior	0.04658
GO:0060369	positive regulation of Fc receptor mediated stimulatory sigr	0.04658
GO:0072007	mesangial cell differentiation	0.04658
GO:0010574	regulation of vascular endothelial growth factor production	0.04678
GO:0060395	SMAD protein signal transduction	0.04696
GO:0098651	basement membrane collagen trimer	0.04836
GO:1902742	apoptotic process involved in development	0.04886
GelMA_HA_No Trend Common		
GO:0002376	immune system process	1.92E-27
GO:0002366	leukocyte activation involved in immune response	3.25E-23
GO:0002263	cell activation involved in immune response	5.17E-23
GO:0045321	leukocyte activation	1.56E-21
GO:0001775	cell activation	6.56E-21
GO:0006955	immune response	1.75E-20
GO:0002274	myeloid leukocyte activation	2.40E-20
GO:0036230	granulocyte activation	2.56E-20
GO:0002446	neutrophil mediated immunity	7.80E-20
GO:0042119	neutrophil activation	7.80E-20
GO:0043312	neutrophil degranulation	1.77E-19
GO:0043299	leukocyte degranulation	1.85E-19

GO:0002283	neutrophil activation involved in immune response	1.85E-19
GO:0002275	myeloid cell activation involved in immune response	2.18E-19
GO:0002444	myeloid leukocyte mediated immunity	6.26E-19
GO:0002443	leukocyte mediated immunity	2.17E-15
GO:0006950	response to stress	3.27E-14
GO:0008283	cell proliferation	6.51E-14
GO:0002252	immune effector process	8.74E-14
GO:0042127	regulation of cell proliferation	1.30E-13
GO:0032496	response to lipopolysaccharide	7.98E-13
GO:0002237	response to molecule of bacterial origin	1.06E-12
GO:0000779	condensed chromosome, centromeric region	1.16E-12
GO:0000323	lytic vacuole	1.16E-12
GO:0005764	lysosome	1.16E-12
GO:0002520	immune system development	1.57E-12
GO:0050900	leukocyte migration	2.25E-12
GO:0034097	response to cytokine	4.95E-12
GO:0002682	regulation of immune system process	5.71E-12
GO:0002521	leukocyte differentiation	6.35E-12
GO:0030595	leukocyte chemotaxis	7.67E-12
GO:0048534	hematopoietic or lymphoid organ development	8.52E-12
GO:0071222	cellular response to lipopolysaccharide	1.52E-11
GO:0071345	cellular response to cytokine stimulus	1.52E-11
GO:0000775	chromosome, centromeric region	1.62E-11
GO:0007059	chromosome segregation	1.68E-11
GO:0007159	leukocyte cell-cell adhesion	1.76E-11
GO:0030141	secretory granule	3.81E-11
GO:0097529	myeloid leukocyte migration	4.01E-11
GO:0060326	cell chemotaxis	4.64E-11
GO:0071219	cellular response to molecule of bacterial origin	6.18E-11
GO:0000793	condensed chromosome	7.46E-11
GO:0034341	response to interferon-gamma	1.32E-10
GO:1903037	regulation of leukocyte cell-cell adhesion	1.56E-10
GO:0042110	T cell activation	1.65E-10
GO:0030097	hemopoiesis	2.34E-10
GO:0045055	regulated exocytosis	2.38E-10
GO:0070062	extracellular exosome	2.44E-10
GO:0032944	regulation of mononuclear cell proliferation	2.82E-10
GO:0022407	regulation of cell-cell adhesion	2.96E-10
GO:1903561	extracellular vesicle	3.27E-10
GO:0070663	regulation of leukocyte proliferation	3.30E-10
GO:0005773	vacuole	3.33E-10
GO:0043230	extracellular organelle	3.42E-10
GO:0050670	regulation of lymphocyte proliferation	4.56E-10
GO:0006954	inflammatory response	5.32E-10
GO:0071216	cellular response to biotic stimulus	5.71E-10
GO:0002685	regulation of leukocyte migration	5.75E-10
GO:0000070	mitotic sister chromatid segregation	6.81E-10
GO:0008284	positive regulation of cell proliferation	7.83E-10
GO:1903039	positive regulation of leukocyte cell-cell adhesion	8.55E-10
GO:0000819	sister chromatid segregation	9.23E-10
GO:0044421	extracellular region part	1.06E-09
GO:0005615	extracellular space	1.18E-09
GO:0050863	regulation of T cell activation	1.19E-09
GO:0019221	cytokine-mediated signaling pathway	1.25E-09
GO:0031982	vesicle	2.11E-09
GO:0002684	positive regulation of immune system process	2.56E-09
GO:0022409	positive regulation of cell-cell adhesion	2.75E-09
GO:0046649	lymphocyte activation	5.29E-09
GO:0071346	cellular response to interferon-gamma	5.37E-09
GO:0050865	regulation of cell activation	6.17E-09
GO:0044437	vacuolar part	6.61E-09
GO:0006952	defense response	6.87E-09
GO:0048522	positive regulation of cellular process	8.82E-09
GO:0097530	granulocyte migration	9.36E-09
GO:0098813	nuclear chromosome segregation	1.27E-08
GO:0006887	exocytosis	1.29E-08
GO:0001817	regulation of cytokine production	1.33E-08
GO:0001816	cytokine production	1.33E-08
GO:0070661	leukocyte proliferation	1.41E-08
GO:0048518	positive regulation of biological process	1.41E-08
GO:0050870	positive regulation of T cell activation	1.57E-08
GO:0070820	tertiary granule	1.76E-08

GO:1990266	neutrophil migration	2.31E-08
GO:0002573	myeloid leukocyte differentiation	3.18E-08
GO:0032943	mononuclear cell proliferation	3.26E-08
GO:0045087	innate immune response	3.64E-08
GO:0005775	vacuolar lumen	3.76E-08
GO:0042129	regulation of T cell proliferation	3.79E-08
GO:0030593	neutrophil chemotaxis	4.19E-08
GO:0002694	regulation of leukocyte activation	4.47E-08
GO:0002687	positive regulation of leukocyte migration	5.54E-08
GO:0031325	positive regulation of cellular metabolic process	7.51E-08
GO:0046651	lymphocyte proliferation	8.83E-08
GO:0030667	secretory granule membrane	1.01E-07
GO:0040017	positive regulation of locomotion	1.01E-07
GO:0070887	cellular response to chemical stimulus	1.20E-07
GO:0051272	positive regulation of cellular component movement	1.21E-07
GO:2000147	positive regulation of cell motility	1.40E-07
GO:0044433	cytoplasmic vesicle part	1.46E-07
GO:0030155	regulation of cell adhesion	1.51E-07
GO:0071621	granulocyte chemotaxis	1.69E-07
GO:0051173	positive regulation of nitrogen compound metabolic proces	1.75E-07
GO:0071674	mononuclear cell migration	2.06E-07
GO:0000280	nuclear division	2.14E-07
GO:0008219	cell death	2.21E-07
GO:0009893	positive regulation of metabolic process	2.39E-07
GO:0030099	myeloid cell differentiation	2.40E-07
GO:0042098	T cell proliferation	2.42E-07
GO:0033993	response to lipid	3.95E-07
GO:0002819	regulation of adaptive immune response	3.98E-07
GO:0012501	programmed cell death	4.35E-07
GO:0072676	lymphocyte migration	4.38E-07
GO:0043202	lysosomal lumen	4.48E-07
GO:0099503	secretory vesicle	4.85E-07
GO:0051249	regulation of lymphocyte activation	6.07E-07
GO:0080134	regulation of response to stress	6.51E-07
GO:0051704	multi-organism process	6.84E-07
GO:0030335	positive regulation of cell migration	7.84E-07
GO:0101002	ficolin-1-rich granule	8.26E-07
GO:1902105	regulation of leukocyte differentiation	8.80E-07
GO:0009617	response to bacterium	9.04E-07
GO:0048519	negative regulation of biological process	1.02E-06
GO:0032946	positive regulation of mononuclear cell proliferation	1.14E-06
GO:0060205	cytoplasmic vesicle lumen	1.19E-06
GO:0031983	vesicle lumen	1.36E-06
GO:0010604	positive regulation of macromolecule metabolic process	1.41E-06
GO:0045785	positive regulation of cell adhesion	1.44E-06
GO:0050866	negative regulation of cell activation	1.69E-06
GO:1902107	positive regulation of leukocyte differentiation	1.69E-06
GO:0002688	regulation of leukocyte chemotaxis	1.75E-06
GO:0048523	negative regulation of cellular process	1.85E-06
GO:0009607	response to biotic stimulus	1.85E-06
GO:0097708	intracellular vesicle	1.91E-06
GO:0031410	cytoplasmic vesicle	1.94E-06
GO:0051707	response to other organism	1.99E-06
GO:0032103	positive regulation of response to external stimulus	2.02E-06
GO:0030217	T cell differentiation	2.02E-06
GO:0043207	response to external biotic stimulus	2.12E-06
GO:0034774	secretory granule lumen	2.14E-06
GO:0050671	positive regulation of lymphocyte proliferation	2.29E-06
GO:0050867	positive regulation of cell activation	2.63E-06
GO:0002822	regulation of adaptive immune response based on somatic r	3.45E-06
GO:0071396	cellular response to lipid	3.56E-06
GO:0042581	specific granule	3.93E-06
GO:0002695	negative regulation of leukocyte activation	4.12E-06
GO:0001819	positive regulation of cytokine production	4.76E-06
GO:0002285	lymphocyte activation involved in immune response	5.51E-06
GO:0070665	positive regulation of leukocyte proliferation	5.70E-06
GO:0070098	chemokine-mediated signaling pathway	5.80E-06
GO:0030098	lymphocyte differentiation	6.21E-06
GO:0005765	lysosomal membrane	6.45E-06
GO:0098852	lytic vacuole membrane	6.45E-06
GO:0042362	fat-soluble vitamin biosynthetic process	6.55E-06
GO:0002690	positive regulation of leukocyte chemotaxis	6.55E-06

GO:0031349	positive regulation of defense response	6.55E-06
GO:0048584	positive regulation of response to stimulus	6.85E-06
GO:0010941	regulation of cell death	7.39E-06
GO:0050764	regulation of phagocytosis	8.72E-06
GO:0042981	regulation of apoptotic process	9.76E-06
GO:0010033	response to organic substance	9.79E-06
GO:0002696	positive regulation of leukocyte activation	9.79E-06
GO:0005766	primary lysosome	9.79E-06
GO:0042582	azurophil granule	9.79E-06
GO:0002548	monocyte chemotaxis	1.02E-05
GO:0000940	condensed chromosome outer kinetochore	1.02E-05
GO:1901701	cellular response to oxygen-containing compound	1.08E-05
GO:0030316	osteoclast differentiation	1.10E-05
GO:1990868	response to chemokine	1.10E-05
GO:1990869	cellular response to chemokine	1.10E-05
GO:0042102	positive regulation of T cell proliferation	1.14E-05
GO:0072677	eosinophil migration	1.16E-05
GO:0042592	homeostatic process	1.28E-05
GO:0034381	plasma lipoprotein particle clearance	1.36E-05
GO:0006915	apoptotic process	1.43E-05
GO:0051251	positive regulation of lymphocyte activation	1.46E-05
GO:0002224	toll-like receptor signaling pathway	1.47E-05
GO:1903706	regulation of hemopoiesis	1.47E-05
GO:0070371	ERK1 and ERK2 cascade	1.62E-05
GO:0002699	positive regulation of immune effector process	1.72E-05
GO:0002706	regulation of lymphocyte mediated immunity	1.79E-05
GO:0002703	regulation of leukocyte mediated immunity	1.79E-05
GO:0050921	positive regulation of chemotaxis	2.02E-05
GO:0070664	negative regulation of leukocyte proliferation	2.21E-05
GO:0043067	regulation of programmed cell death	2.27E-05
GO:0072678	T cell migration	2.30E-05
GO:0046903	secretion	2.31E-05
GO:1901700	response to oxygen-containing compound	2.34E-05
GO:0032615	interleukin-12 production	2.35E-05
GO:0032655	regulation of interleukin-12 production	2.35E-05
GO:0045621	positive regulation of lymphocyte differentiation	2.35E-05
GO:0001906	cell killing	2.98E-05
GO:0042368	vitamin D biosynthetic process	3.14E-05
GO:0071310	cellular response to organic substance	3.16E-05
GO:0045582	positive regulation of T cell differentiation	3.68E-05
GO:0045088	regulation of innate immune response	3.81E-05
GO:1903708	positive regulation of hemopoiesis	3.92E-05
GO:0032635	interleukin-6 production	3.92E-05
GO:0032675	regulation of interleukin-6 production	3.92E-05
GO:0046631	alpha-beta T cell activation	3.95E-05
GO:0008009	chemokine activity	4.30E-05
GO:0050776	regulation of immune response	4.51E-05
GO:0050766	positive regulation of phagocytosis	5.38E-05
GO:0032640	tumor necrosis factor production	5.86E-05
GO:0032680	regulation of tumor necrosis factor production	5.86E-05
GO:0032940	secretion by cell	5.86E-05
GO:0031347	regulation of defense response	5.86E-05
GO:0051250	negative regulation of lymphocyte activation	6.18E-05
GO:0071706	tumor necrosis factor superfamily cytokine production	6.56E-05
GO:1903555	regulation of tumor necrosis factor superfamily cytokine pr	6.56E-05
GO:0050920	regulation of chemotaxis	6.82E-05
GO:0070372	regulation of ERK1 and ERK2 cascade	7.40E-05
GO:0051383	kinetochore organization	7.53E-05
GO:0032642	regulation of chemokine production	7.77E-05
GO:0043281	regulation of cysteine-type endopeptidase activity involved	7.95E-05
GO:0048247	lymphocyte chemotaxis	9.07E-05
GO:0032609	interferon-gamma production	9.41E-05
GO:0007010	cytoskeleton organization	9.52E-05
GO:0051983	regulation of chromosome segregation	9.58E-05
GO:0032602	chemokine production	9.92E-05
GO:0001818	negative regulation of cytokine production	9.93E-05
GO:0007568	aging	9.93E-05
GO:0043085	positive regulation of catalytic activity	0.00012
GO:0060558	regulation of calcidiol 1-monooxygenase activity	0.00012
GO:0042116	macrophage activation	0.00012
GO:0150077	regulation of neuroinflammatory response	0.00013
GO:0022408	negative regulation of cell-cell adhesion	0.00013

GO:0046632	alpha-beta T cell differentiation	0.00014
GO:0060556	regulation of vitamin D biosynthetic process	0.00015
GO:0043367	CD4-positive, alpha-beta T cell differentiation	0.00015
GO:0101003	ficolin-1-rich granule membrane	0.00016
GO:0097237	cellular response to toxic substance	0.00017
GO:0070821	tertiary granule membrane	0.00018
GO:0032649	regulation of interferon-gamma production	0.00018
GO:0045335	phagocytic vesicle	0.00018
GO:1901136	carbohydrate derivative catabolic process	0.00018
GO:0045089	positive regulation of innate immune response	0.00019
GO:0050672	negative regulation of lymphocyte proliferation	0.0002
GO:0032270	positive regulation of cellular protein metabolic process	0.0002
GO:0008285	negative regulation of cell proliferation	0.00021
GO:0046635	positive regulation of alpha-beta T cell activation	0.00022
GO:0071402	cellular response to lipoprotein particle stimulus	0.00023
GO:0032613	interleukin-10 production	0.00023
GO:0032653	regulation of interleukin-10 production	0.00023
GO:1905517	macrophage migration	0.00023
GO:0002456	T cell mediated immunity	0.00024
GO:0019915	lipid storage	0.00025
GO:0034644	cellular response to UV	0.00025
GO:0032945	negative regulation of mononuclear cell proliferation	0.00025
GO:0035710	CD4-positive, alpha-beta T cell activation	0.00029
GO:0045730	respiratory burst	0.00031
GO:0050790	regulation of catalytic activity	0.00032
GO:2000116	regulation of cysteine-type endopeptidase activity	0.00032
GO:0000778	condensed nuclear chromosome kinetochore	0.00034
GO:0000780	condensed nuclear chromosome, centromeric region	0.00034
GO:2000816	negative regulation of mitotic sister chromatid separation	0.00034
GO:0032695	negative regulation of interleukin-12 production	0.00034
GO:0007162	negative regulation of cell adhesion	0.00038
GO:0055094	response to lipoprotein particle	0.00039
GO:0045619	regulation of lymphocyte differentiation	0.00039
GO:0051338	regulation of transferase activity	0.00041
GO:0001909	leukocyte mediated cytotoxicity	0.00041
GO:0001932	regulation of protein phosphorylation	0.00042
GO:0031663	lipopolysaccharide-mediated signaling pathway	0.00042
GO:0043410	positive regulation of MAPK cascade	0.00042
GO:0009636	response to toxic substance	0.00046
GO:0030139	endocytic vesicle	0.00047
GO:0051306	mitotic sister chromatid separation	0.00047
GO:1903038	negative regulation of leukocyte cell-cell adhesion	0.00048
GO:0042325	regulation of phosphorylation	0.00049
GO:0097006	regulation of plasma lipoprotein particle levels	0.0005
GO:0034599	cellular response to oxidative stress	0.00052
GO:0010985	negative regulation of lipoprotein particle clearance	0.00052
GO:0001934	positive regulation of protein phosphorylation	0.00052
GO:0019377	glycolipid catabolic process	0.00056
GO:0070374	positive regulation of ERK1 and ERK2 cascade	0.00056
GO:0045580	regulation of T cell differentiation	0.00057
GO:0051247	positive regulation of protein metabolic process	0.00057
GO:0043066	negative regulation of apoptotic process	0.00057
GO:0050778	positive regulation of immune response	0.00057
GO:0045841	negative regulation of mitotic metaphase/anaphase transitio	0.00057
GO:0060548	negative regulation of cell death	0.0006
GO:0030855	epithelial cell differentiation	0.0006
GO:0002286	T cell activation involved in immune response	0.00062
GO:0051716	cellular response to stimulus	0.00064
GO:0010878	cholesterol storage	0.00065
GO:0043069	negative regulation of programmed cell death	0.00065
GO:0010562	positive regulation of phosphorus metabolic process	0.00065
GO:0045937	positive regulation of phosphate metabolic process	0.00065
GO:0002761	regulation of myeloid leukocyte differentiation	0.00066
GO:0050868	negative regulation of T cell activation	0.00066
GO:1905819	negative regulation of chromosome separation	0.00066
GO:0002824	positive regulation of adaptive immune response based on s	0.00066
GO:2000516	positive regulation of CD4-positive, alpha-beta T cell activa	0.00066
GO:0012506	vesicle membrane	0.00068
GO:0030071	regulation of mitotic metaphase/anaphase transition	0.0007
GO:0031401	positive regulation of protein modification process	0.0007
GO:1902533	positive regulation of intracellular signal transduction	0.0007
GO:0035579	specific granule membrane	0.00071

GO:0052547	regulation of peptidase activity	0.00071
GO:0010965	regulation of mitotic sister chromatid separation	0.00073
GO:0045604	regulation of epidermal cell differentiation	0.00073
GO:0002697	regulation of immune effector process	0.00074
GO:0043408	regulation of MAPK cascade	0.00074
GO:0045859	regulation of protein kinase activity	0.00075
GO:0002821	positive regulation of adaptive immune response	0.00075
GO:0002335	mature B cell differentiation	0.00076
GO:0032963	collagen metabolic process	0.00079
GO:0010883	regulation of lipid storage	0.0008
GO:0046479	glycosphingolipid catabolic process	0.00084
GO:0042327	positive regulation of phosphorylation	0.00084
GO:0050730	regulation of peptidyl-tyrosine phosphorylation	0.00086
GO:0002683	negative regulation of immune system process	0.00086
GO:0043372	positive regulation of CD4-positive, alpha-beta T cell differ	0.00087
GO:0033048	negative regulation of mitotic sister chromatid segregation	0.00089
GO:0030666	endocytic vesicle membrane	0.00089
GO:0007094	mitotic spindle assembly checkpoint	0.00092
GO:0071173	spindle assembly checkpoint	0.00092
GO:0071174	mitotic spindle checkpoint	0.00092
GO:0006801	superoxide metabolic process	0.00094
GO:0051347	positive regulation of transferase activity	0.00097
GO:0031341	regulation of cell killing	0.00097
GO:0046638	positive regulation of alpha-beta T cell differentiation	0.00097
GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	0.00099
GO:0034612	response to tumor necrosis factor	0.00099
GO:1904724	tertiary granule lumen	0.00101
GO:1902100	negative regulation of metaphase/anaphase transition of cel	0.00106
GO:0045682	regulation of epidermis development	0.00108
GO:0048661	positive regulation of smooth muscle cell proliferation	0.00108
GO:0043030	regulation of macrophage activation	0.0011
GO:0048245	eosinophil chemotaxis	0.0011
GO:0007091	metaphase/anaphase transition of mitotic cell cycle	0.00113
GO:0002312	B cell activation involved in immune response	0.00114
GO:0032268	regulation of cellular protein metabolic process	0.00114
GO:0009628	response to abiotic stimulus	0.00117
GO:0031577	spindle checkpoint	0.00128
GO:0042379	chemokine receptor binding	0.0013
GO:0001618	virus receptor activity	0.0013
GO:0104005	hijacked molecular function	0.0013
GO:0030260	entry into host cell	0.00138
GO:0044409	entry into host	0.00138
GO:0051806	entry into cell of other organism involved in symbiotic inte	0.00138
GO:0050729	positive regulation of inflammatory response	0.00139
GO:0052548	regulation of endopeptidase activity	0.00139
GO:0046634	regulation of alpha-beta T cell activation	0.0014
GO:0002250	adaptive immune response	0.00143
GO:1902099	regulation of metaphase/anaphase transition of cell cycle	0.00146
GO:0150076	neuroinflammatory response	0.00148
GO:0046718	viral entry into host cell	0.00149
GO:0006979	response to oxidative stress	0.00152
GO:0010742	macrophage derived foam cell differentiation	0.00152
GO:0090077	foam cell differentiation	0.00152
GO:0036021	endolysosome lumen	0.00153
GO:0051828	entry into other organism involved in symbiotic interaction	0.00157
GO:0033046	negative regulation of sister chromatid segregation	0.00158
GO:0019220	regulation of phosphate metabolic process	0.00158
GO:0051174	regulation of phosphorus metabolic process	0.00158
GO:0032611	interleukin-1 beta production	0.00158
GO:0032651	regulation of interleukin-1 beta production	0.00158
GO:0044877	protein-containing complex binding	0.00173
GO:0001228	DNA-binding transcription activator activity, RNA polyme	0.00173
GO:0005126	cytokine receptor binding	0.00173
GO:0031100	animal organ regeneration	0.00177
GO:0034447	very-low-density lipoprotein particle clearance	0.00179
GO:0032720	negative regulation of tumor necrosis factor production	0.0018
GO:0034113	heterotypic cell-cell adhesion	0.0018
GO:0002294	CD4-positive, alpha-beta T cell differentiation involved in i	0.00182
GO:0071356	cellular response to tumor necrosis factor	0.00184
GO:0051783	regulation of nuclear division	0.00185
GO:0046514	ceramide catabolic process	0.00185
GO:0045807	positive regulation of endocytosis	0.00192

GO:0045766	positive regulation of angiogenesis	0.00208
GO:0051321	meiotic cell cycle	0.0021
GO:0046466	membrane lipid catabolic process	0.00211
GO:2000403	positive regulation of lymphocyte migration	0.00211
GO:0002709	regulation of T cell mediated immunity	0.00214
GO:0050664	oxidoreductase activity, acting on NAD(P)H, oxygen as acc	0.00217
GO:0005125	cytokine activity	0.00221
GO:0034121	regulation of toll-like receptor signaling pathway	0.00225
GO:0002287	alpha-beta T cell activation involved in immune response	0.00227
GO:0002293	alpha-beta T cell differentiation involved in immune respo	0.00227
GO:0044784	metaphase/anaphase transition of cell cycle	0.00228
GO:0016192	vesicle-mediated transport	0.00232
GO:0030659	cytoplasmic vesicle membrane	0.00248
GO:0043549	regulation of kinase activity	0.00258
GO:0072593	reactive oxygen species metabolic process	0.00263
GO:0030656	regulation of vitamin metabolic process	0.00267
GO:0002708	positive regulation of lymphocyte mediated immunity	0.0027
GO:0032612	interleukin-1 production	0.0027
GO:0032652	regulation of interleukin-1 production	0.0027
GO:0010942	positive regulation of cell death	0.0027
GO:0032722	positive regulation of chemokine production	0.0028
GO:1903556	negative regulation of tumor necrosis factor superfamily cy	0.00286
GO:0043373	CD4-positive, alpha-beta T cell lineage commitment	0.003
GO:0010743	regulation of macrophage derived foam cell differentiation	0.003
GO:0034614	cellular response to reactive oxygen species	0.003
GO:1903046	meiotic cell cycle process	0.00312
GO:0002292	T cell differentiation involved in immune response	0.00339
GO:0033047	regulation of mitotic sister chromatid segregation	0.00339
GO:0010035	response to inorganic substance	0.00341
GO:0008630	intrinsic apoptotic signaling pathway in response to DNA d	0.00341
GO:0042130	negative regulation of T cell proliferation	0.00347
GO:1905818	regulation of chromosome separation	0.00347
GO:0071347	cellular response to interleukin-1	0.00349
GO:0051128	regulation of cellular component organization	0.00351
GO:0002313	mature B cell differentiation involved in immune response	0.00352
GO:2000401	regulation of lymphocyte migration	0.00358
GO:0033045	regulation of sister chromatid segregation	0.00358
GO:0071900	regulation of protein serine/threonine kinase activity	0.00363
GO:0045860	positive regulation of protein kinase activity	0.00363
GO:0071214	cellular response to abiotic stimulus	0.0037
GO:0104004	cellular response to environmental stimulus	0.0037
GO:0002705	positive regulation of leukocyte mediated immunity	0.0037
GO:1905952	regulation of lipid localization	0.00381
GO:1902531	regulation of intracellular signal transduction	0.00398
GO:1904018	positive regulation of vasculature development	0.00411
GO:0032715	negative regulation of interleukin-6 production	0.00412
GO:2000404	regulation of T cell migration	0.00412
GO:0030149	sphingolipid catabolic process	0.00416
GO:0036336	dendritic cell migration	0.00416
GO:0097190	apoptotic signaling pathway	0.00417
GO:0046637	regulation of alpha-beta T cell differentiation	0.00432
GO:0033344	cholesterol efflux	0.00442
GO:0045058	T cell selection	0.00442
GO:0071675	regulation of mononuclear cell migration	0.00442
GO:0045839	negative regulation of mitotic nuclear division	0.00447
GO:0022414	reproductive process	0.00483
GO:0048568	embryonic organ development	0.00486
GO:1903557	positive regulation of tumor necrosis factor superfamily cyt	0.00492
GO:0016310	phosphorylation	0.00513
GO:0032760	positive regulation of tumor necrosis factor production	0.00525
GO:0045123	cellular extravasation	0.00526
GO:0050673	epithelial cell proliferation	0.00529
GO:0002460	adaptive immune response based on somatic recombination	0.00529
GO:0010631	epithelial cell migration	0.00531
GO:0000003	reproduction	0.00535
GO:0002269	leukocyte activation involved in inflammatory response	0.00548
GO:0030225	macrophage differentiation	0.00548
GO:0010466	negative regulation of peptidase activity	0.00572
GO:0002407	dendritic cell chemotaxis	0.00581
GO:0044092	negative regulation of molecular function	0.00581
GO:0046209	nitric oxide metabolic process	0.00582
GO:0030856	regulation of epithelial cell differentiation	0.00623

GO:0043086	negative regulation of catalytic activity	0.00625
GO:0060429	epithelium development	0.00645
GO:0050678	regulation of epithelial cell proliferation	0.00645
GO:0001890	placenta development	0.00651
GO:0030888	regulation of B cell proliferation	0.00659
GO:0042093	T-helper cell differentiation	0.00659
GO:1905521	regulation of macrophage migration	0.0066
GO:0090132	epithelium migration	0.00681
GO:0001774	microglial cell activation	0.00681
GO:0035987	endodermal cell differentiation	0.00681
GO:2000406	positive regulation of T cell migration	0.00681
GO:0032755	positive regulation of interleukin-6 production	0.00692
GO:2001057	reactive nitrogen species metabolic process	0.00694
GO:0140013	meiotic nuclear division	0.00729
GO:1901216	positive regulation of neuron death	0.00767
GO:0000942	condensed nuclear chromosome outer kinetochore	0.00772
GO:0048660	regulation of smooth muscle cell proliferation	0.00804
GO:0001704	formation of primary germ layer	0.00822
GO:0030100	regulation of endocytosis	0.00824
GO:0042554	superoxide anion generation	0.00825
GO:0002440	production of molecular mediator of immune response	0.00831
GO:1905954	positive regulation of lipid localization	0.00832
GO:0033674	positive regulation of kinase activity	0.00867
GO:0097028	dendritic cell differentiation	0.00876
GO:0014070	response to organic cyclic compound	0.00876
GO:0071496	cellular response to external stimulus	0.00877
GO:0043370	regulation of CD4-positive, alpha-beta T cell differentiatio	0.00878
GO:0002468	dendritic cell antigen processing and presentation	0.00885
GO:0072540	T-helper 17 cell lineage commitment	0.00885
GO:0035690	cellular response to drug	0.00885
GO:0032637	interleukin-8 production	0.0093
GO:0032677	regulation of interleukin-8 production	0.0093
GO:0048598	embryonic morphogenesis	0.00954
GO:0043369	CD4-positive or CD8-positive, alpha-beta T cell lineage co	0.00991
GO:0002702	positive regulation of production of molecular mediator of	0.01024
GO:0002700	regulation of production of molecular mediator of immune	0.01027
GO:0010915	regulation of very-low-density lipoprotein particle clearanc	0.0103
GO:0010916	negative regulation of very-low-density lipoprotein particle	0.0103
GO:0038156	interleukin-3-mediated signaling pathway	0.0103
GO:0031399	regulation of protein modification process	0.0104
GO:0036019	endolysosome	0.01048
GO:0048020	CCR chemokine receptor binding	0.01061
GO:0032733	positive regulation of interleukin-10 production	0.01072
GO:0042221	response to chemical	0.01072
GO:0090183	regulation of kidney development	0.01076
GO:0010951	negative regulation of endopeptidase activity	0.01078
GO:0030574	collagen catabolic process	0.011
GO:1905953	negative regulation of lipid localization	0.011
GO:0006809	nitric oxide biosynthetic process	0.01102
GO:0032729	positive regulation of interferon-gamma production	0.01102
GO:0090130	tissue migration	0.01105
GO:2000377	regulation of reactive oxygen species metabolic process	0.01123
GO:0048659	smooth muscle cell proliferation	0.01143
GO:0070555	response to interleukin-1	0.01148
GO:0043020	NADPH oxidase complex	0.01167
GO:0030301	cholesterol transport	0.01196
GO:0003338	metanephros morphogenesis	0.01266
GO:0009967	positive regulation of signal transduction	0.01268
GO:0002698	negative regulation of immune effector process	0.01272
GO:0031294	lymphocyte costimulation	0.01278
GO:0009790	embryo development	0.01295
GO:0098636	protein complex involved in cell adhesion	0.0132
GO:0002295	T-helper cell lineage commitment	0.01327
GO:0045591	positive regulation of regulatory T cell differentiation	0.01327
GO:0034383	low-density lipoprotein particle clearance	0.0134
GO:0002711	positive regulation of T cell mediated immunity	0.01363
GO:0048144	fibroblast proliferation	0.01371
GO:0007135	meiosis II	0.01371
GO:0045144	meiotic sister chromatid segregation	0.01371
GO:0051177	meiotic sister chromatid cohesion	0.01371
GO:0061983	meiosis II cell cycle process	0.01371
GO:0043068	positive regulation of programmed cell death	0.01374

GO:0045165	cell fate commitment	0.01375
GO:0070301	cellular response to hydrogen peroxide	0.01379
GO:0033077	T cell differentiation in thymus	0.01461
GO:0051784	negative regulation of nuclear division	0.01464
GO:0051336	regulation of hydrolase activity	0.01566
GO:0006793	phosphorus metabolic process	0.01599
GO:0038024	cargo receptor activity	0.0165
GO:0048146	positive regulation of fibroblast proliferation	0.01714
GO:0043627	response to estrogen	0.01722
GO:0042088	T-helper 1 type immune response	0.0174
GO:0045684	positive regulation of epidermis development	0.01744
GO:2000514	regulation of CD4-positive, alpha-beta T cell activation	0.01751
GO:0051234	establishment of localization	0.01751
GO:0048771	tissue remodeling	0.01754
GO:0043065	positive regulation of apoptotic process	0.01758
GO:0071407	cellular response to organic cyclic compound	0.01775
GO:0001910	regulation of leukocyte mediated cytotoxicity	0.01837
GO:0098805	whole membrane	0.01924
GO:0045428	regulation of nitric oxide biosynthetic process	0.01955
GO:0000302	response to reactive oxygen species	0.02017
GO:0001706	endoderm formation	0.02039
GO:0002820	negative regulation of adaptive immune response	0.02039
GO:0048732	gland development	0.02129
GO:0030857	negative regulation of epithelial cell differentiation	0.02182
GO:0030851	granulocyte differentiation	0.02212
GO:0032689	negative regulation of interferon-gamma production	0.02212
GO:0045616	regulation of keratinocyte differentiation	0.02212
GO:0043368	positive T cell selection	0.02212
GO:0043615	astrocyte cell migration	0.02212
GO:0050878	regulation of body fluid levels	0.02231
GO:0048145	regulation of fibroblast proliferation	0.02323
GO:0002704	negative regulation of leukocyte mediated immunity	0.02449
GO:0010575	positive regulation of vascular endothelial growth factor pr	0.02559
GO:1900745	positive regulation of p38MAPK cascade	0.02559
GO:0035580	specific granule lumen	0.02608
GO:0042060	wound healing	0.02621
GO:0032964	collagen biosynthetic process	0.02662
GO:0051246	regulation of protein metabolic process	0.02663
GO:0071236	cellular response to antibiotic	0.02678
GO:0045862	positive regulation of proteolysis	0.02687
GO:0033627	cell adhesion mediated by integrin	0.02697
GO:2000379	positive regulation of reactive oxygen species metabolic pr	0.02697
GO:0071295	cellular response to vitamin	0.02697
GO:0010573	vascular endothelial growth factor production	0.02765
GO:0046633	alpha-beta T cell proliferation	0.02765
GO:0008305	integrin complex	0.02818
GO:0031960	response to corticosteroid	0.0282
GO:0006796	phosphate-containing compound metabolic process	0.02842
GO:0051216	cartilage development	0.02854
GO:1901214	regulation of neuron death	0.02862
GO:0031343	positive regulation of cell killing	0.02865
GO:1902106	negative regulation of leukocyte differentiation	0.02915
GO:0010632	regulation of epithelial cell migration	0.03028
GO:0018212	peptidyl-tyrosine modification	0.03028
GO:0097435	supramolecular fiber organization	0.03074
GO:0061900	glial cell activation	0.03074
GO:1902930	regulation of alcohol biosynthetic process	0.03074
GO:0000165	MAPK cascade	0.03339
GO:0023014	signal transduction by protein phosphorylation	0.03339
GO:0001101	response to acid chemical	0.03339
GO:2000108	positive regulation of leukocyte apoptotic process	0.03382
GO:0034142	toll-like receptor 4 signaling pathway	0.03427
GO:0046640	regulation of alpha-beta T cell proliferation	0.03472
GO:0043280	positive regulation of cysteine-type endopeptidase activity i	0.03531
GO:0001822	kidney development	0.03538
GO:0030278	regulation of ossification	0.03695
GO:0043405	regulation of MAP kinase activity	0.03804
GO:0007492	endoderm development	0.03865
GO:0010888	negative regulation of lipid storage	0.03865
GO:0046641	positive regulation of alpha-beta T cell proliferation	0.03865
GO:0071887	leukocyte apoptotic process	0.03865
GO:0002823	negative regulation of adaptive immune response based on	0.0388

GO:0002367	cytokine production involved in immune response	0.0392
GO:0002718	regulation of cytokine production involved in immune respo	0.0392
GO:0046849	bone remodeling	0.0392
GO:0031295	T cell costimulation	0.04122
GO:0016175	superoxide-generating NADPH oxidase activity	0.04145
GO:0045824	negative regulation of innate immune response	0.042
GO:0006569	tryptophan catabolic process	0.04227
GO:0042436	indole-containing compound catabolic process	0.04227
GO:0043301	negative regulation of leukocyte degranulation	0.04227
GO:0045060	negative thymic T cell selection	0.04227
GO:0046218	indolalkylamine catabolic process	0.04227
GO:0071492	cellular response to UV-A	0.04227
GO:1902510	regulation of apoptotic DNA fragmentation	0.04227
GO:0002883	regulation of hypersensitivity	0.04251
GO:0002369	T cell cytokine production	0.04251
GO:0002724	regulation of T cell cytokine production	0.04251
GO:0002825	regulation of T-helper 1 type immune response	0.04258
GO:0046890	regulation of lipid biosynthetic process	0.04272
GO:0038187	pattern recognition receptor activity	0.04356
GO:0051345	positive regulation of hydrolase activity	0.04427
GO:0010744	positive regulation of macrophage derived foam cell differe	0.04515
GO:0030050	vesicle transport along actin filament	0.04515
GO:0043031	negative regulation of macrophage activation	0.04515
GO:0045618	positive regulation of keratinocyte differentiation	0.04515
GO:0032731	positive regulation of interleukin-1 beta production	0.04672
GO:0030203	glycosaminoglycan metabolic process	0.04682
GO:0002228	natural killer cell mediated immunity	0.04693
GO:0002707	negative regulation of lymphocyte mediated immunity	0.04706
GO:0043300	regulation of leukocyte degranulation	0.04706
GO:0042113	B cell activation	0.04745
GO:0043542	endothelial cell migration	0.04819
GO:1903426	regulation of reactive oxygen species biosynthetic process	0.04831
GO:1903409	reactive oxygen species biosynthetic process	0.04849
GO:2000106	regulation of leukocyte apoptotic process	0.04851
GO:0001913	T cell mediated cytotoxicity	0.04924
GO:0033002	muscle cell proliferation	0.0493
GO:0070228	regulation of lymphocyte apoptotic process	0.04965
GO:0031670	cellular response to nutrient	0.04965
GO:0002827	positive regulation of T-helper 1 type immune response	0.04965
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GO:0002376	immune system process	3.00E-32
GO:0001775	cell activation	1.66E-31
GO:0006954	inflammatory response	4.18E-28
GO:0045321	leukocyte activation	1.39E-27
GO:0008283	cell proliferation	5.32E-26
GO:0042127	regulation of cell proliferation	8.87E-26
GO:0006955	immune response	3.26E-25
GO:0002274	myeloid leukocyte activation	2.00E-24
GO:0070887	cellular response to chemical stimulus	3.35E-24
GO:0010033	response to organic substance	1.36E-22
GO:0002366	leukocyte activation involved in immune response	5.32E-22
GO:0002263	cell activation involved in immune response	1.15E-21
GO:0034097	response to cytokine	3.43E-21
GO:0030155	regulation of cell adhesion	1.23E-20
GO:0071310	cellular response to organic substance	1.88E-20
GO:0043299	leukocyte degranulation	2.16E-20
GO:0071345	cellular response to cytokine stimulus	6.12E-20
GO:0002444	myeloid leukocyte mediated immunity	7.24E-20
GO:0051716	cellular response to stimulus	1.51E-19
GO:0002275	myeloid cell activation involved in immune response	2.87E-19
GO:0050900	leukocyte migration	3.58E-19
GO:0002682	regulation of immune system process	8.83E-19
GO:0044421	extracellular region part	6.43E-18
GO:0008284	positive regulation of cell proliferation	8.45E-18
GO:0036230	granulocyte activation	1.17E-17
GO:0002446	neutrophil mediated immunity	1.17E-17
GO:0042119	neutrophil activation	1.17E-17
GO:0019221	cytokine-mediated signaling pathway	1.62E-17
GO:0006952	defense response	2.93E-17
GO:0043312	neutrophil degranulation	3.26E-17
GO:0048584	positive regulation of response to stimulus	3.26E-17
GO:0006950	response to stress	6.98E-17

GO:0002521	leukocyte differentiation	8.77E-17
GO:2000147	positive regulation of cell motility	1.06E-16
GO:0002283	neutrophil activation involved in immune response	1.07E-16
GO:0030335	positive regulation of cell migration	1.41E-16
GO:0030595	leukocyte chemotaxis	3.96E-16
GO:0001817	regulation of cytokine production	4.31E-16
GO:0051272	positive regulation of cellular component movement	4.98E-16
GO:0001816	cytokine production	5.25E-16
GO:0002443	leukocyte mediated immunity	5.80E-16
GO:0060326	cell chemotaxis	9.75E-16
GO:0001934	positive regulation of protein phosphorylation	9.75E-16
GO:1901700	response to oxygen-containing compound	2.65E-15
GO:0042221	response to chemical	3.36E-15
GO:0040017	positive regulation of locomotion	3.40E-15
GO:0005615	extracellular space	3.96E-15
GO:0097529	myeloid leukocyte migration	4.54E-15
GO:0050865	regulation of cell activation	6.46E-15
GO:0045785	positive regulation of cell adhesion	1.48E-14
GO:0045055	regulated exocytosis	1.73E-14
GO:0010562	positive regulation of phosphorus metabolic process	2.10E-14
GO:0045937	positive regulation of phosphate metabolic process	2.10E-14
GO:0002252	immune effector process	2.97E-14
GO:0032963	collagen metabolic process	4.27E-14
GO:0042110	T cell activation	4.91E-14
GO:0009967	positive regulation of signal transduction	1.11E-13
GO:0032940	secretion by cell	1.78E-13
GO:0046903	secretion	2.04E-13
GO:0042327	positive regulation of phosphorylation	2.32E-13
GO:0048534	hematopoietic or lymphoid organ development	3.00E-13
GO:0007159	leukocyte cell-cell adhesion	3.13E-13
GO:0043410	positive regulation of MAPK cascade	3.81E-13
GO:1902533	positive regulation of intracellular signal transduction	4.04E-13
GO:0042060	wound healing	4.13E-13
GO:0022407	regulation of cell-cell adhesion	4.29E-13
GO:0042581	specific granule	4.51E-13
GO:0022409	positive regulation of cell-cell adhesion	4.97E-13
GO:0002520	immune system development	5.36E-13
GO:0043085	positive regulation of catalytic activity	1.02E-12
GO:0030097	hemopoiesis	1.20E-12
GO:1903037	regulation of leukocyte cell-cell adhesion	1.37E-12
GO:0031401	positive regulation of protein modification process	1.54E-12
GO:0002694	regulation of leukocyte activation	1.64E-12
GO:0046649	lymphocyte activation	1.79E-12
GO:0030141	secretory granule	2.08E-12
GO:0050866	negative regulation of cell activation	2.13E-12
GO:0001819	positive regulation of cytokine production	2.97E-12
GO:0032270	positive regulation of cellular protein metabolic process	3.78E-12
GO:0006887	exocytosis	4.18E-12
GO:0043542	endothelial cell migration	4.44E-12
GO:0010631	epithelial cell migration	6.80E-12
GO:0002237	response to molecule of bacterial origin	7.41E-12
GO:1901701	cellular response to oxygen-containing compound	7.58E-12
GO:0048518	positive regulation of biological process	7.85E-12
GO:0048522	positive regulation of cellular process	1.30E-11
GO:0090132	epithelium migration	1.47E-11
GO:0001932	regulation of protein phosphorylation	1.55E-11
GO:0072676	lymphocyte migration	1.89E-11
GO:0005125	cytokine activity	1.91E-11
GO:0050790	regulation of catalytic activity	2.10E-11
GO:0070374	positive regulation of ERK1 and ERK2 cascade	2.49E-11
GO:0051247	positive regulation of protein metabolic process	2.50E-11
GO:0090130	tissue migration	2.71E-11
GO:1903039	positive regulation of leukocyte cell-cell adhesion	3.04E-11
GO:0070820	tertiary granule	3.50E-11
GO:0051345	positive regulation of hydrolase activity	7.20E-11
GO:0032496	response to lipopolysaccharide	8.80E-11
GO:0031982	vesicle	1.02E-10
GO:0030098	lymphocyte differentiation	1.03E-10
GO:0050863	regulation of T cell activation	1.06E-10
GO:0042098	T cell proliferation	1.06E-10
GO:0070663	regulation of leukocyte proliferation	1.13E-10
GO:0032944	regulation of mononuclear cell proliferation	1.13E-10

GO:0070661	leukocyte proliferation	1.29E-10
GO:1904018	positive regulation of vasculature development	1.39E-10
GO:0031347	regulation of defense response	1.55E-10
GO:0050670	regulation of lymphocyte proliferation	1.67E-10
GO:0002685	regulation of leukocyte migration	2.38E-10
GO:0042129	regulation of T cell proliferation	3.55E-10
GO:0045766	positive regulation of angiogenesis	3.55E-10
GO:0071219	cellular response to molecule of bacterial origin	3.96E-10
GO:0033993	response to lipid	4.07E-10
GO:0043408	regulation of MAPK cascade	4.41E-10
GO:1902531	regulation of intracellular signal transduction	4.75E-10
GO:0071222	cellular response to lipopolysaccharide	5.30E-10
GO:0050776	regulation of immune response	5.60E-10
GO:0071216	cellular response to biotic stimulus	5.71E-10
GO:0050673	epithelial cell proliferation	7.08E-10
GO:0002695	negative regulation of leukocyte activation	7.68E-10
GO:0050878	regulation of body fluid levels	7.83E-10
GO:0008285	negative regulation of cell proliferation	8.72E-10
GO:0070098	chemokine-mediated signaling pathway	1.15E-09
GO:0002684	positive regulation of immune system process	1.20E-09
GO:0032943	mononuclear cell proliferation	1.21E-09
GO:0097530	granulocyte migration	1.33E-09
GO:0042592	homeostatic process	1.58E-09
GO:0002703	regulation of leukocyte mediated immunity	1.63E-09
GO:0071621	granulocyte chemotaxis	2.00E-09
GO:1990868	response to chemokine	2.12E-09
GO:1990869	cellular response to chemokine	2.12E-09
GO:0042325	regulation of phosphorylation	3.02E-09
GO:0046651	lymphocyte proliferation	3.11E-09
GO:0071674	mononuclear cell migration	3.27E-09
GO:0030593	neutrophil chemotaxis	3.38E-09
GO:0002548	monocyte chemotaxis	3.80E-09
GO:0050870	positive regulation of T cell activation	3.86E-09
GO:0031410	cytoplasmic vesicle	3.99E-09
GO:0097708	intracellular vesicle	3.99E-09
GO:0002819	regulation of adaptive immune response	4.16E-09
GO:0008009	chemokine activity	5.02E-09
GO:0030217	T cell differentiation	5.03E-09
GO:0035579	specific granule membrane	5.17E-09
GO:0002683	negative regulation of immune system process	5.22E-09
GO:0030667	secretory granule membrane	5.44E-09
GO:0030574	collagen catabolic process	6.44E-09
GO:1990266	neutrophil migration	6.71E-09
GO:0070821	tertiary granule membrane	1.36E-08
GO:0099503	secretory vesicle	1.49E-08
GO:0070372	regulation of ERK1 and ERK2 cascade	1.53E-08
GO:0019220	regulation of phosphate metabolic process	1.86E-08
GO:0051174	regulation of phosphorus metabolic process	1.86E-08
GO:0048771	tissue remodeling	2.08E-08
GO:0051336	regulation of hydrolase activity	2.90E-08
GO:0050678	regulation of epithelial cell proliferation	2.92E-08
GO:1902105	regulation of leukocyte differentiation	3.10E-08
GO:0050920	regulation of chemotaxis	5.08E-08
GO:0070371	ERK1 and ERK2 cascade	5.83E-08
GO:0050867	positive regulation of cell activation	8.73E-08
GO:0033627	cell adhesion mediated by integrin	9.62E-08
GO:0080134	regulation of response to stress	1.14E-07
GO:0046631	alpha-beta T cell activation	1.46E-07
GO:0032103	positive regulation of response to external stimulus	1.82E-07
GO:0034341	response to interferon-gamma	1.82E-07
GO:0045621	positive regulation of lymphocyte differentiation	1.98E-07
GO:0044433	cytoplasmic vesicle part	2.12E-07
GO:0002573	myeloid leukocyte differentiation	2.53E-07
GO:0010941	regulation of cell death	2.73E-07
GO:0051249	regulation of lymphocyte activation	2.95E-07
GO:0043068	positive regulation of programmed cell death	3.43E-07
GO:0035987	endodermal cell differentiation	3.46E-07
GO:0000323	lytic vacuole	3.51E-07
GO:0005764	lysosome	3.51E-07
GO:0002367	cytokine production involved in immune response	3.58E-07
GO:0002718	regulation of cytokine production involved in immune respo	3.58E-07
GO:0002822	regulation of adaptive immune response based on somatic r	3.76E-07

GO:0031399	regulation of protein modification process	3.84E-07
GO:0007162	negative regulation of cell adhesion	3.97E-07
GO:0002687	positive regulation of leukocyte migration	4.28E-07
GO:0002696	positive regulation of leukocyte activation	4.44E-07
GO:0010942	positive regulation of cell death	4.61E-07
GO:0051250	negative regulation of lymphocyte activation	5.44E-07
GO:1902107	positive regulation of leukocyte differentiation	5.68E-07
GO:0001818	negative regulation of cytokine production	7.02E-07
GO:0043065	positive regulation of apoptotic process	7.03E-07
GO:0050764	regulation of phagocytosis	7.40E-07
GO:0008219	cell death	7.91E-07
GO:0048523	negative regulation of cellular process	8.15E-07
GO:0072678	T cell migration	8.19E-07
GO:0018212	peptidyl-tyrosine modification	8.25E-07
GO:0002699	positive regulation of immune effector process	8.78E-07
GO:0048519	negative regulation of biological process	9.01E-07
GO:0032946	positive regulation of mononuclear cell proliferation	9.11E-07
GO:0001822	kidney development	9.12E-07
GO:0071396	cellular response to lipid	1.09E-06
GO:0031349	positive regulation of defense response	1.09E-06
GO:0042102	positive regulation of T cell proliferation	1.39E-06
GO:0010632	regulation of epithelial cell migration	1.51E-06
GO:0002688	regulation of leukocyte chemotaxis	1.63E-06
GO:0070664	negative regulation of leukocyte proliferation	1.65E-06
GO:0045619	regulation of lymphocyte differentiation	1.75E-06
GO:0050671	positive regulation of lymphocyte proliferation	1.76E-06
GO:0002706	regulation of lymphocyte mediated immunity	2.22E-06
GO:0071346	cellular response to interferon-gamma	2.23E-06
GO:0002700	regulation of production of molecular mediator of immune	2.24E-06
GO:0032635	interleukin-6 production	2.28E-06
GO:0032675	regulation of interleukin-6 production	2.28E-06
GO:0001704	formation of primary germ layer	2.36E-06
GO:0000165	MAPK cascade	2.59E-06
GO:0023014	signal transduction by protein phosphorylation	2.59E-06
GO:0045860	positive regulation of protein kinase activity	2.60E-06
GO:0070665	positive regulation of leukocyte proliferation	2.76E-06
GO:0001909	leukocyte mediated cytotoxicity	2.82E-06
GO:0048247	lymphocyte chemotaxis	2.86E-06
GO:0050729	positive regulation of inflammatory response	3.09E-06
GO:0030856	regulation of epithelial cell differentiation	3.16E-06
GO:1903708	positive regulation of hemopoiesis	3.42E-06
GO:0043067	regulation of programmed cell death	3.43E-06
GO:0032609	interferon-gamma production	3.82E-06
GO:0050672	negative regulation of lymphocyte proliferation	3.83E-06
GO:0032268	regulation of cellular protein metabolic process	5.45E-06
GO:0002456	T cell mediated immunity	5.46E-06
GO:0032945	negative regulation of mononuclear cell proliferation	5.54E-06
GO:0031325	positive regulation of cellular metabolic process	5.74E-06
GO:0022408	negative regulation of cell-cell adhesion	6.04E-06
GO:0097435	supramolecular fiber organization	6.04E-06
GO:0045859	regulation of protein kinase activity	6.12E-06
GO:0051173	positive regulation of nitrogen compound metabolic proces	6.13E-06
GO:0042981	regulation of apoptotic process	6.16E-06
GO:1901136	carbohydrate derivative catabolic process	6.22E-06
GO:0050766	positive regulation of phagocytosis	6.75E-06
GO:0005773	vacuole	7.25E-06
GO:0032649	regulation of interferon-gamma production	7.57E-06
GO:0009636	response to toxic substance	7.86E-06
GO:0009790	embryo development	8.19E-06
GO:0050868	negative regulation of T cell activation	8.19E-06
GO:0010604	positive regulation of macromolecule metabolic process	8.25E-06
GO:0009893	positive regulation of metabolic process	8.28E-06
GO:0045582	positive regulation of T cell differentiation	9.34E-06
GO:0001706	endoderm formation	9.52E-06
GO:0012501	programmed cell death	9.71E-06
GO:0033674	positive regulation of kinase activity	1.01E-05
GO:1903038	negative regulation of leukocyte cell-cell adhesion	1.01E-05
GO:0031341	regulation of cell killing	1.08E-05
GO:0071706	tumor necrosis factor superfamily cytokine production	1.16E-05
GO:1903555	regulation of tumor necrosis factor superfamily cytokine pr	1.16E-05
GO:0060429	epithelium development	1.37E-05
GO:0042130	negative regulation of T cell proliferation	1.47E-05

GO:0042379	chemokine receptor binding	1.50E-05
GO:0005126	cytokine receptor binding	1.64E-05
GO:0045580	regulation of T cell differentiation	1.70E-05
GO:0002440	production of molecular mediator of immune response	1.72E-05
GO:0051347	positive regulation of transferase activity	1.73E-05
GO:0007492	endoderm development	1.83E-05
GO:0032640	tumor necrosis factor production	1.87E-05
GO:0032680	regulation of tumor necrosis factor production	1.87E-05
GO:0016310	phosphorylation	1.89E-05
GO:0046634	regulation of alpha-beta T cell activation	1.96E-05
GO:0070062	extracellular exosome	2.02E-05
GO:0032964	collagen biosynthetic process	2.04E-05
GO:0030855	epithelial cell differentiation	2.04E-05
GO:0009617	response to bacterium	2.35E-05
GO:0043202	lysosomal lumen	2.41E-05
GO:0043230	extracellular organelle	2.53E-05
GO:0002285	lymphocyte activation involved in immune response	2.55E-05
GO:0002697	regulation of immune effector process	2.58E-05
GO:1903561	extracellular vesicle	2.88E-05
GO:0001906	cell killing	2.93E-05
GO:0032695	negative regulation of interleukin-12 production	3.29E-05
GO:0150076	neuroinflammatory response	3.36E-05
GO:0048598	embryonic morphogenesis	3.54E-05
GO:0043549	regulation of kinase activity	3.54E-05
GO:0051251	positive regulation of lymphocyte activation	3.62E-05
GO:0098636	protein complex involved in cell adhesion	3.74E-05
GO:0042116	macrophage activation	4.29E-05
GO:0050921	positive regulation of chemotaxis	4.43E-05
GO:0006915	apoptotic process	4.60E-05
GO:0008305	integrin complex	4.63E-05
GO:0000003	reproduction	4.64E-05
GO:0022414	reproductive process	5.12E-05
GO:0016192	vesicle-mediated transport	5.25E-05
GO:0002709	regulation of T cell mediated immunity	5.36E-05
GO:0060548	negative regulation of cell death	5.42E-05
GO:0033002	muscle cell proliferation	5.86E-05
GO:0001101	response to acid chemical	6.19E-05
GO:0051216	cartilage development	6.36E-05
GO:0097237	cellular response to toxic substance	6.58E-05
GO:0035690	cellular response to drug	7.07E-05
GO:0150077	regulation of neuroinflammatory response	8.46E-05
GO:0030099	myeloid cell differentiation	8.54E-05
GO:0046632	alpha-beta T cell differentiation	9.21E-05
GO:0051338	regulation of transferase activity	9.25E-05
GO:0002690	positive regulation of leukocyte chemotaxis	9.25E-05
GO:0045087	innate immune response	9.91E-05
GO:0048144	fibroblast proliferation	0.0001
GO:2000106	regulation of leukocyte apoptotic process	0.0001
GO:0046635	positive regulation of alpha-beta T cell activation	0.0001
GO:0045682	regulation of epidermis development	0.00011
GO:0034774	secretory granule lumen	0.00012
GO:0101003	ficolin-1-rich granule membrane	0.00012
GO:0043030	regulation of macrophage activation	0.00012
GO:0002820	negative regulation of adaptive immune response	0.00012
GO:0072593	reactive oxygen species metabolic process	0.00012
GO:0035710	CD4-positive, alpha-beta T cell activation	0.00013
GO:0012506	vesicle membrane	0.00014
GO:0010035	response to inorganic substance	0.00015
GO:0052548	regulation of endopeptidase activity	0.00016
GO:0002705	positive regulation of leukocyte mediated immunity	0.00018
GO:0002704	negative regulation of leukocyte mediated immunity	0.00018
GO:0090183	regulation of kidney development	0.00018
GO:0101002	ficolin-1-rich granule	0.00018
GO:0032755	positive regulation of interleukin-6 production	0.0002
GO:0006793	phosphorus metabolic process	0.0002
GO:0048145	regulation of fibroblast proliferation	0.0002
GO:0014070	response to organic cyclic compound	0.0002
GO:0052547	regulation of peptidase activity	0.0002
GO:0051246	regulation of protein metabolic process	0.00022
GO:0005775	vacuolar lumen	0.00023
GO:1903557	positive regulation of tumor necrosis factor superfamily cyt	0.00024
GO:0002702	positive regulation of production of molecular mediator of i	0.00024

GO:0045730	respiratory burst	0.00024
GO:0034113	heterotypic cell-cell adhesion	0.00024
GO:0006979	response to oxidative stress	0.00025
GO:0006796	phosphate-containing compound metabolic process	0.00025
GO:0002698	negative regulation of immune effector process	0.00026
GO:0006801	superoxide metabolic process	0.00026
GO:0042554	superoxide anion generation	0.00026
GO:1903706	regulation of hemopoiesis	0.00026
GO:0031343	positive regulation of cell killing	0.00028
GO:0060205	cytoplasmic vesicle lumen	0.00028
GO:0045165	cell fate commitment	0.00031
GO:0050730	regulation of peptidyl-tyrosine phosphorylation	0.00031
GO:0031983	vesicle lumen	0.00032
GO:0030100	regulation of endocytosis	0.00032
GO:0045604	regulation of epidermal cell differentiation	0.00032
GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	0.00034
GO:0051128	regulation of cellular component organization	0.00036
GO:0043207	response to external biotic stimulus	0.00036
GO:0009607	response to biotic stimulus	0.00037
GO:0030659	cytoplasmic vesicle membrane	0.00038
GO:0098805	whole membrane	0.00041
GO:0046633	alpha-beta T cell proliferation	0.00041
GO:0046637	regulation of alpha-beta T cell differentiation	0.00042
GO:0042088	T-helper 1 type immune response	0.00042
GO:0051707	response to other organism	0.00046
GO:0032637	interleukin-8 production	0.00046
GO:0032677	regulation of interleukin-8 production	0.00046
GO:0035580	specific granule lumen	0.00047
GO:0002313	mature B cell differentiation involved in immune response	0.00048
GO:0034599	cellular response to oxidative stress	0.00048
GO:0032760	positive regulation of tumor necrosis factor production	0.00048
GO:2000379	positive regulation of reactive oxygen species metabolic pr	0.00048
GO:0030666	endocytic vesicle membrane	0.0005
GO:0071492	cellular response to UV-A	0.00051
GO:0048659	smooth muscle cell proliferation	0.00052
GO:0032613	interleukin-10 production	0.00054
GO:0032653	regulation of interleukin-10 production	0.00054
GO:0001618	virus receptor activity	0.00056
GO:0104005	hijacked molecular function	0.00056
GO:0072677	eosinophil migration	0.00057
GO:0002335	mature B cell differentiation	0.00058
GO:0048660	regulation of smooth muscle cell proliferation	0.00058
GO:0046638	positive regulation of alpha-beta T cell differentiation	0.00059
GO:0043300	regulation of leukocyte degranulation	0.0006
GO:0071356	cellular response to tumor necrosis factor	0.0006
GO:0001910	regulation of leukocyte mediated cytotoxicity	0.0006
GO:0044092	negative regulation of molecular function	0.00062
GO:0048661	positive regulation of smooth muscle cell proliferation	0.00067
GO:0045807	positive regulation of endocytosis	0.00068
GO:0044437	vacuolar part	0.00083
GO:0030203	glycosaminoglycan metabolic process	0.00087
GO:0043281	regulation of cysteine-type endopeptidase activity involved	0.00093
GO:0048568	embryonic organ development	0.00095
GO:0043069	negative regulation of programmed cell death	0.00105
GO:0043367	CD4-positive, alpha-beta T cell differentiation	0.0011
GO:0007568	aging	0.0011
GO:0031960	response to corticosteroid	0.00111
GO:0000940	condensed chromosome outer kinetochore	0.00113
GO:0050664	oxidoreductase activity, acting on NAD(P)H, oxygen as acc	0.00116
GO:0045058	T cell selection	0.0012
GO:0001913	T cell mediated cytotoxicity	0.00139
GO:0070555	response to interleukin-1	0.00139
GO:0034612	response to tumor necrosis factor	0.0014
GO:0051983	regulation of chromosome segregation	0.00145
GO:0002228	natural killer cell mediated immunity	0.00145
GO:0043020	NADPH oxidase complex	0.00149
GO:0043280	positive regulation of cysteine-type endopeptidase activity i	0.00154
GO:0042093	T-helper cell differentiation	0.0016
GO:0002708	positive regulation of lymphocyte mediated immunity	0.00165
GO:0000302	response to reactive oxygen species	0.00167
GO:2000116	regulation of cysteine-type endopeptidase activity	0.00169
GO:0032729	positive regulation of interferon-gamma production	0.00171

GO:2000401	regulation of lymphocyte migration	0.00176
GO:0032642	regulation of chemokine production	0.00176
GO:0031100	animal organ regeneration	0.00176
GO:0002823	negative regulation of adaptive immune response based on	0.00177
GO:0030139	endocytic vesicle	0.00182
GO:0097028	dendritic cell differentiation	0.00187
GO:0032722	positive regulation of chemokine production	0.00187
GO:0032615	interleukin-12 production	0.0019
GO:0032655	regulation of interleukin-12 production	0.0019
GO:2000404	regulation of T cell migration	0.00196
GO:0002821	positive regulation of adaptive immune response	0.00198
GO:0071887	leukocyte apoptotic process	0.00198
GO:0043405	regulation of MAP kinase activity	0.00206
GO:0043066	negative regulation of apoptotic process	0.00215
GO:0032602	chemokine production	0.00217
GO:0046849	bone remodeling	0.00217
GO:1903046	meiotic cell cycle process	0.00233
GO:0032611	interleukin-1 beta production	0.00245
GO:0032651	regulation of interleukin-1 beta production	0.00245
GO:0071900	regulation of protein serine/threonine kinase activity	0.00248
GO:2000377	regulation of reactive oxygen species metabolic process	0.00262
GO:0034614	cellular response to reactive oxygen species	0.00263
GO:0045088	regulation of innate immune response	0.00264
GO:0002294	CD4-positive, alpha-beta T cell differentiation involved in i	0.00271
GO:0002250	adaptive immune response	0.00294
GO:0002407	dendritic cell chemotaxis	0.00294
GO:0034381	plasma lipoprotein particle clearance	0.00304
GO:0002825	regulation of T-helper 1 type immune response	0.00309
GO:0002824	positive regulation of adaptive immune response based on s	0.00313
GO:0036336	dendritic cell migration	0.00314
GO:0007059	chromosome segregation	0.00329
GO:0051234	establishment of localization	0.00347
GO:0002287	alpha-beta T cell activation involved in immune response	0.00347
GO:0002293	alpha-beta T cell differentiation involved in immune respon	0.00347
GO:0000778	condensed nuclear chromosome kinetochore	0.00355
GO:0000780	condensed nuclear chromosome, centromeric region	0.00355
GO:0030225	macrophage differentiation	0.00356
GO:0009628	response to abiotic stimulus	0.00401
GO:0048020	CCR chemokine receptor binding	0.00436
GO:1904724	tertiary granule lumen	0.00437
GO:0046640	regulation of alpha-beta T cell proliferation	0.00451
GO:0048146	positive regulation of fibroblast proliferation	0.00481
GO:0071236	cellular response to antibiotic	0.00487
GO:2000514	regulation of CD4-positive, alpha-beta T cell activation	0.00496
GO:0071347	cellular response to interleukin-1	0.00497
GO:0002224	toll-like receptor signaling pathway	0.00522
GO:0002707	negative regulation of lymphocyte mediated immunity	0.00523
GO:0048732	gland development	0.00553
GO:0010965	regulation of mitotic sister chromatid separation	0.00555
GO:0060556	regulation of vitamin D biosynthetic process	0.00567
GO:0048245	eosinophil chemotaxis	0.00579
GO:0002312	B cell activation involved in immune response	0.00608
GO:0002292	T cell differentiation involved in immune response	0.00624
GO:0036021	endolysosome lumen	0.00626
GO:0140013	meiotic nuclear division	0.00649
GO:0032612	interleukin-1 production	0.00655
GO:0032652	regulation of interleukin-1 production	0.00655
GO:1901216	positive regulation of neuron death	0.00666
GO:0002468	dendritic cell antigen processing and presentation	0.00682
GO:0071402	cellular response to lipoprotein particle stimulus	0.00685
GO:2000108	positive regulation of leukocyte apoptotic process	0.00692
GO:0045862	positive regulation of proteolysis	0.00695
GO:0045089	positive regulation of innate immune response	0.00715
GO:0019915	lipid storage	0.00743
GO:0010466	negative regulation of peptidase activity	0.00774
GO:0007091	metaphase/anaphase transition of mitotic cell cycle	0.00782
GO:1903556	negative regulation of tumor necrosis factor superfamily cy	0.00782
GO:0010951	negative regulation of endopeptidase activity	0.00782
GO:0045123	cellular extravasation	0.00782
GO:0050778	positive regulation of immune response	0.00796
GO:0045684	positive regulation of epidermis development	0.00815
GO:0071675	regulation of mononuclear cell migration	0.0083

GO:0051321	meiotic cell cycle	0.00833
GO:1902106	negative regulation of leukocyte differentiation	0.00834
GO:0046718	viral entry into host cell	0.0085
GO:0034121	regulation of toll-like receptor signaling pathway	0.00858
GO:0051306	mitotic sister chromatid separation	0.00871
GO:0043086	negative regulation of catalytic activity	0.00915
GO:0046514	ceramide catabolic process	0.0095
GO:0042368	vitamin D biosynthetic process	0.0095
GO:0045335	phagocytic vesicle	0.00963
GO:0055094	response to lipoprotein particle	0.01005
GO:0030260	entry into host cell	0.01012
GO:0044409	entry into host	0.01012
GO:0051806	entry into cell of other organism involved in symbiotic inte	0.01012
GO:0070301	cellular response to hydrogen peroxide	0.01012
GO:0010883	regulation of lipid storage	0.01066
GO:0032689	negative regulation of interferon-gamma production	0.01086
GO:0045616	regulation of keratinocyte differentiation	0.01086
GO:2000816	negative regulation of mitotic sister chromatid separation	0.01086
GO:0030071	regulation of mitotic metaphase/anaphase transition	0.01089
GO:0032720	negative regulation of tumor necrosis factor production	0.01089
GO:0032731	positive regulation of interleukin-1 beta production	0.01089
GO:0051828	entry into other organism involved in symbiotic interaction	0.0116
GO:0030278	regulation of ossification	0.01167
GO:0032733	positive regulation of interleukin-10 production	0.01177
GO:1905818	regulation of chromosome separation	0.01194
GO:0019377	glycolipid catabolic process	0.01228
GO:0071407	cellular response to organic cyclic compound	0.01239
GO:0002286	T cell activation involved in immune response	0.01254
GO:0010742	macrophage derived foam cell differentiation	0.01267
GO:0090077	foam cell differentiation	0.01267
GO:0071496	cellular response to external stimulus	0.01284
GO:0016175	superoxide-generating NADPH oxidase activity	0.01302
GO:0010985	negative regulation of lipoprotein particle clearance	0.01305
GO:0002460	adaptive immune response based on somatic recombination	0.01365
GO:0010878	cholesterol storage	0.014
GO:0030050	vesicle transport along actin filament	0.014
GO:0032715	negative regulation of interleukin-6 production	0.01429
GO:0010575	positive regulation of vascular endothelial growth factor pr	0.01473
GO:0046641	positive regulation of alpha-beta T cell proliferation	0.01474
GO:0044784	metaphase/anaphase transition of cell cycle	0.01505
GO:0043370	regulation of CD4-positive, alpha-beta T cell differentiatio	0.01505
GO:1903409	reactive oxygen species biosynthetic process	0.01523
GO:0031663	lipopolysaccharide-mediated signaling pathway	0.01524
GO:0045841	negative regulation of mitotic metaphase/anaphase transitio	0.01548
GO:0000779	condensed chromosome, centromeric region	0.01635
GO:1905953	negative regulation of lipid localization	0.01676
GO:0046466	membrane lipid catabolic process	0.01691
GO:2000403	positive regulation of lymphocyte migration	0.01691
GO:2000516	positive regulation of CD4-positive, alpha-beta T cell activa	0.01691
GO:0002883	regulation of hypersensitivity	0.01719
GO:0046479	glycosphingolipid catabolic process	0.01757
GO:0033045	regulation of sister chromatid segregation	0.01834
GO:1905819	negative regulation of chromosome separation	0.0184
GO:0001890	placenta development	0.0187
GO:0031295	T cell costimulation	0.01883
GO:0051704	multi-organism process	0.01903
GO:0044877	protein-containing complex binding	0.01926
GO:0000819	sister chromatid segregation	0.01932
GO:0010743	regulation of macrophage derived foam cell differentiation	0.01938
GO:1905521	regulation of macrophage migration	0.02027
GO:1902099	regulation of metaphase/anaphase transition of cell cycle	0.02057
GO:0010915	regulation of very-low-density lipoprotein particle clearanc	0.02057
GO:0010916	negative regulation of very-low-density lipoprotein particle	0.02057
GO:0038156	interleukin-3-mediated signaling pathway	0.02057
GO:0045839	negative regulation of mitotic nuclear division	0.02077
GO:0070228	regulation of lymphocyte apoptotic process	0.02077
GO:0002827	positive regulation of T-helper 1 type immune response	0.02142
GO:0007094	mitotic spindle assembly checkpoint	0.02167
GO:0071173	spindle assembly checkpoint	0.02167
GO:0071174	mitotic spindle checkpoint	0.02167
GO:0046209	nitric oxide metabolic process	0.02178
GO:1901214	regulation of neuron death	0.02178

GO:0000793	condensed chromosome	0.02229
GO:0001774	microglial cell activation	0.02297
GO:0033048	negative regulation of mitotic sister chromatid segregation	0.02297
GO:0061900	glial cell activation	0.0232
GO:0010573	vascular endothelial growth factor production	0.02364
GO:0008630	intrinsic apoptotic signaling pathway in response to DNA d	0.02367
GO:0006569	tryptophan catabolic process	0.02436
GO:0042436	indole-containing compound catabolic process	0.02436
GO:0043301	negative regulation of leukocyte degranulation	0.02436
GO:0045060	negative thymic T cell selection	0.02436
GO:0046218	indolalkylamine catabolic process	0.02436
GO:1902510	regulation of apoptotic DNA fragmentation	0.02436
GO:0033047	regulation of mitotic sister chromatid segregation	0.02437
GO:0097006	regulation of plasma lipoprotein particle levels	0.02446
GO:0042113	B cell activation	0.02522
GO:0030851	granulocyte differentiation	0.02522
GO:1902100	negative regulation of metaphase/anaphase transition of cel	0.02522
GO:0003338	metanephros morphogenesis	0.02533
GO:0030149	sphingolipid catabolic process	0.02533
GO:0033077	T cell differentiation in thymus	0.02554
GO:2001057	reactive nitrogen species metabolic process	0.02554
GO:1905952	regulation of lipid localization	0.0256
GO:0001228	DNA-binding transcription activator activity, RNA polymer	0.02568
GO:0038024	cargo receptor activity	0.02593
GO:0030316	osteoclast differentiation	0.02595
GO:0098813	nuclear chromosome segregation	0.02627
GO:1905954	positive regulation of lipid localization	0.02656
GO:0000942	condensed nuclear chromosome outer kinetochore	0.02728
GO:0031294	lymphocyte costimulation	0.02742
GO:0031577	spindle checkpoint	0.02786
GO:0036019	endolysosome	0.02796
GO:0034644	cellular response to UV	0.02875
GO:0030857	negative regulation of epithelial cell differentiation	0.02875
GO:0072540	T-helper 17 cell lineage commitment	0.02875
GO:0043627	response to estrogen	0.03043
GO:0051383	kinetochore organization	0.03043
GO:0034383	low-density lipoprotein particle clearance	0.03066
GO:0046890	regulation of lipid biosynthetic process	0.03103
GO:0007010	cytoskeleton organization	0.03255
GO:0006809	nitric oxide biosynthetic process	0.03265
GO:0007135	meiosis II	0.03425
GO:0034447	very-low-density lipoprotein particle clearance	0.03425
GO:0045144	meiotic sister chromatid segregation	0.03425
GO:0051177	meiotic sister chromatid cohesion	0.03425
GO:0061983	meiosis II cell cycle process	0.03425
GO:0030301	cholesterol transport	0.03449
GO:0030888	regulation of B cell proliferation	0.03505
GO:0051784	negative regulation of nuclear division	0.03505
GO:0034142	toll-like receptor 4 signaling pathway	0.03534
GO:0033046	negative regulation of sister chromatid segregation	0.03555
GO:2000406	positive regulation of T cell migration	0.03637
GO:0045428	regulation of nitric oxide biosynthetic process	0.03733
GO:0038187	pattern recognition receptor activity	0.03821
GO:0051783	regulation of nuclear division	0.03889
GO:0031670	cellular response to nutrient	0.03889
GO:0033344	cholesterol efflux	0.03928
GO:1903426	regulation of reactive oxygen species biosynthetic process	0.03933
GO:0002369	T cell cytokine production	0.03944
GO:0002724	regulation of T cell cytokine production	0.03944
GO:1900745	positive regulation of p38MAPK cascade	0.03944
GO:0000775	chromosome, centromeric region	0.0405
GO:0002761	regulation of myeloid leukocyte differentiation	0.0416
GO:0000070	mitotic sister chromatid segregation	0.04163
GO:0097190	apoptotic signaling pathway	0.04175
GO:0030656	regulation of vitamin metabolic process	0.04175
GO:1905517	macrophage migration	0.04175
GO:0043369	CD4-positive or CD8-positive, alpha-beta T cell lineage co	0.04175
GO:0002269	leukocyte activation involved in inflammatory response	0.04371
GO:0010888	negative regulation of lipid storage	0.04407
GO:0043373	CD4-positive, alpha-beta T cell lineage commitment	0.04407
GO:0042362	fat-soluble vitamin biosynthetic process	0.04467
GO:0002295	T-helper cell lineage commitment	0.04483

GO:0010744	positive regulation of macrophage derived foam cell differe	0.04483
GO:0043031	negative regulation of macrophage activation	0.04483
GO:0045591	positive regulation of regulatory T cell differentiation	0.04483
GO:0045618	positive regulation of keratinocyte differentiation	0.04483
GO:0005766	primary lysosome	0.04524
GO:0042582	azurophil granule	0.04524
GO:0005765	lysosomal membrane	0.04524
GO:0098852	lytic vacuole membrane	0.04524
GO:0000280	nuclear division	0.04652
GO:0002711	positive regulation of T cell mediated immunity	0.04658
GO:1902930	regulation of alcohol biosynthetic process	0.04658
GO:0043615	astrocyte cell migration	0.04658
GO:0060558	regulation of calcidiol 1-monooxygenase activity	0.04658
GO:0043372	positive regulation of CD4-positive, alpha-beta T cell differ	0.04678
GO:0071295	cellular response to vitamin	0.04678
GO:0071214	cellular response to abiotic stimulus	0.04782
GO:0104004	cellular response to environmental stimulus	0.04782
GO:0045824	negative regulation of innate immune response	0.04859
GO:0043368	positive T cell selection	0.04886
GelMA_HA_Trend Only		
GO:0007186	G protein-coupled receptor signaling pathway	4.83E-07
GO:0014046	dopamine secretion	3.11E-06
GO:0014059	regulation of dopamine secretion	3.11E-06
GO:0043169	cation binding	1.82E-05
GO:0031256	leading edge membrane	2.00E-05
GO:1903818	positive regulation of voltage-gated potassium channel acti	4.28E-05
GO:0005251	delayed rectifier potassium channel activity	4.39E-05
GO:0019229	regulation of vasoconstriction	0.00011
GO:0046872	metal ion binding	0.00011
GO:0015696	ammonium transport	0.00012
GO:2001023	regulation of response to drug	0.00013
GO:0009925	basal plasma membrane	0.00013
GO:0015459	potassium channel regulator activity	0.00015
GO:0005922	connexin complex	0.00021
GO:0043167	ion binding	0.00023
GO:0060041	retina development in camera-type eye	0.00028
GO:0022804	active transmembrane transporter activity	0.00028
GO:0031279	regulation of cyclase activity	0.0003
GO:0045178	basal part of cell	0.00035
GO:0097731	9+0 non-motile cilium	0.00036
GO:0003351	epithelial cilium movement	0.00045
GO:0051954	positive regulation of amine transport	0.00045
GO:0015291	secondary active transmembrane transporter activity	0.00046
GO:0060359	response to ammonium ion	0.00047
GO:0098688	parallel fiber to Purkinje cell synapse	0.00054
GO:0005921	gap junction	0.00058
GO:0007274	neuromuscular synaptic transmission	0.00071
GO:0005243	gap junction channel activity	0.00072
GO:0060074	synapse maturation	0.00089
GO:0010107	potassium ion import	0.00096
GO:0032591	dendritic spine membrane	0.00102
GO:0002862	negative regulation of inflammatory response to antigenic s	0.00127
GO:0021799	cerebral cortex radially oriented cell migration	0.00139
GO:0008306	associative learning	0.00144
GO:0097733	photoreceptor cell cilium	0.00155
GO:0015293	symporter activity	0.00158
GO:0008331	high voltage-gated calcium channel activity	0.0016
GO:0022829	wide pore channel activity	0.00162
GO:0048168	regulation of neuronal synaptic plasticity	0.00165
GO:0140115	export across plasma membrane	0.00165
GO:0051928	positive regulation of calcium ion transport	0.0019
GO:0001964	startle response	0.00198
GO:0050951	sensory perception of temperature stimulus	0.00198
GO:0048265	response to pain	0.0022
GO:0005326	neurotransmitter transporter activity	0.0023
GO:0031032	actomyosin structure organization	0.00234
GO:0005342	organic acid transmembrane transporter activity	0.0024
GO:0097091	synaptic vesicle clustering	0.00243
GO:0060042	retina morphogenesis in camera-type eye	0.00253
GO:0021537	telencephalon development	0.00268
GO:1903539	protein localization to postsynaptic membrane	0.00274
GO:0051955	regulation of amino acid transport	0.0028

GO:0043177	organic acid binding	0.00293
GO:0008514	organic anion transmembrane transporter activity	0.00297
GO:0043271	negative regulation of ion transport	0.00301
GO:0007196	adenylate cyclase-inhibiting G protein-coupled glutamate r	0.00301
GO:1990504	dense core granule exocytosis	0.00301
GO:0003333	amino acid transmembrane transport	0.00301
GO:0034776	response to histamine	0.00308
GO:0060452	positive regulation of cardiac muscle contraction	0.00308
GO:0005283	amino acid:sodium symporter activity	0.00314
GO:0005883	neurofilament	0.00325
GO:0046943	carboxylic acid transmembrane transporter activity	0.00329
GO:0046068	cGMP metabolic process	0.00345
GO:0060004	reflex	0.00345
GO:0002790	peptide secretion	0.00354
GO:0015238	drug transmembrane transporter activity	0.00369
GO:0001640	adenylate cyclase inhibiting G protein-coupled glutamate r	0.00369
GO:0098988	G protein-coupled glutamate receptor activity	0.00369
GO:0030551	cyclic nucleotide binding	0.00369
GO:0019897	extrinsic component of plasma membrane	0.0037
GO:1904861	excitatory synapse assembly	0.00403
GO:0050795	regulation of behavior	0.00404
GO:0071875	adrenergic receptor signaling pathway	0.00432
GO:0043083	synaptic cleft	0.00433
GO:0045761	regulation of adenylate cyclase activity	0.00453
GO:0086019	cell-cell signaling involved in cardiac conduction	0.00453
GO:0045776	negative regulation of blood pressure	0.00467
GO:0044060	regulation of endocrine process	0.00472
GO:1901385	regulation of voltage-gated calcium channel activity	0.00472
GO:1903531	negative regulation of secretion by cell	0.00472
GO:0044305	calyx of Held	0.00506
GO:0089717	spanning component of membrane	0.00506
GO:0097449	astrocyte projection	0.00506
GO:0098992	neuronal dense core vesicle	0.0052
GO:1902259	regulation of delayed rectifier potassium channel activity	0.00549
GO:0051592	response to calcium ion	0.00663
GO:0042135	neurotransmitter catabolic process	0.00699
GO:0051339	regulation of lyase activity	0.00712
GO:1904862	inhibitory synapse assembly	0.00728
GO:0045926	negative regulation of growth	0.00744
GO:0007263	nitric oxide mediated signal transduction	0.00744
GO:0009065	glutamine family amino acid catabolic process	0.00744
GO:1901018	positive regulation of potassium ion transmembrane transp	0.00744
GO:0030286	dynein complex	0.00749
GO:0042551	neuron maturation	0.0076
GO:0051953	negative regulation of amine transport	0.00781
GO:0098664	G protein-coupled serotonin receptor signaling pathway	0.00781
GO:0030324	lung development	0.0081
GO:1903523	negative regulation of blood circulation	0.0082
GO:0035633	maintenance of permeability of blood-brain barrier	0.00821
GO:0098810	neurotransmitter reuptake	0.00821
GO:0006940	regulation of smooth muscle contraction	0.00834
GO:0072347	response to anesthetic	0.00941
GO:0051051	negative regulation of transport	0.00946
GO:0008191	metalloendopeptidase inhibitor activity	0.00964
GO:0004993	G protein-coupled serotonin receptor activity	0.01072
GO:0005184	neuropeptide hormone activity	0.01072
GO:0099589	serotonin receptor activity	0.01072
GO:0002526	acute inflammatory response	0.01095
GO:0086067	AV node cell to bundle of His cell communication	0.01127
GO:0030323	respiratory tube development	0.01127
GO:0036157	outer dynein arm	0.01163
GO:0044327	dendritic spine head	0.01163
GO:1990454	L-type voltage-gated calcium channel complex	0.01163
GO:0008569	ATP-dependent microtubule motor activity, minus-end-dire	0.01201
GO:0098796	membrane protein complex	0.01206
GO:0035929	steroid hormone secretion	0.01207
GO:0045933	positive regulation of muscle contraction	0.0121
GO:0046717	acid secretion	0.0121
GO:0015807	L-amino acid transport	0.01257
GO:2001222	regulation of neuron migration	0.01257
GO:0015701	bicarbonate transport	0.01308
GO:0016048	detection of temperature stimulus	0.01359

GO:0021801	cerebral cortex radial glia guided migration	0.01359
GO:0022030	telencephalon glial cell migration	0.01359
GO:0071880	adenylate cyclase-activating adrenergic receptor signaling	0.01359
GO:1903859	regulation of dendrite extension	0.01359
GO:0007340	acrosome reaction	0.01373
GO:0042417	dopamine metabolic process	0.01373
GO:0003002	regionalization	0.01395
GO:0097484	dendrite extension	0.01399
GO:0099622	cardiac muscle cell membrane repolarization	0.01399
GO:0007210	serotonin receptor signaling pathway	0.01411
GO:0014072	response to isoquinoline alkaloid	0.01411
GO:0043278	response to morphine	0.01411
GO:0060541	respiratory system development	0.01413
GO:0003407	neural retina development	0.01413
GO:0046888	negative regulation of hormone secretion	0.01413
GO:0015370	solute:sodium symporter activity	0.01419
GO:0015171	amino acid transmembrane transporter activity	0.01421
GO:0009799	specification of symmetry	0.01533
GO:0009410	response to xenobiotic stimulus	0.01545
GO:0072178	nephric duct morphogenesis	0.0156
GO:0050708	regulation of protein secretion	0.01638
GO:1903825	organic acid transmembrane transport	0.0166
GO:0007368	determination of left/right symmetry	0.0166
GO:0008227	G protein-coupled amine receptor activity	0.01723
GO:0070696	transmembrane receptor protein serine/threonine kinase bin	0.0173
GO:0002138	retinoic acid biosynthetic process	0.01745
GO:0010496	intercellular transport	0.01745
GO:0071286	cellular response to magnesium ion	0.01745
GO:0099026	anchored component of presynaptic membrane	0.01754
GO:0035855	megakaryocyte development	0.01755
GO:0055003	cardiac myofibril assembly	0.01755
GO:0005892	acetylcholine-gated channel complex	0.01763
GO:0048593	camera-type eye morphogenesis	0.01788
GO:0005343	organic acid:sodium symporter activity	0.01891
GO:0005328	neurotransmitter:sodium symporter activity	0.01891
GO:0042043	neurexin family protein binding	0.01891
GO:0033612	receptor serine/threonine kinase binding	0.01891
GO:0099072	regulation of postsynaptic membrane neurotransmitter rece	0.01938
GO:0019911	structural constituent of myelin sheath	0.01959
GO:0071242	cellular response to ammonium ion	0.01969
GO:0086014	atrial cardiac muscle cell action potential	0.01984
GO:0086026	atrial cardiac muscle cell to AV node cell signaling	0.01984
GO:0086066	atrial cardiac muscle cell to AV node cell communication	0.01984
GO:0097386	glial cell projection	0.02005
GO:0009855	determination of bilateral symmetry	0.02016
GO:0007212	dopamine receptor signaling pathway	0.02034
GO:0009187	cyclic nucleotide metabolic process	0.02034
GO:0001941	postsynaptic membrane organization	0.02105
GO:0030501	positive regulation of bone mineralization	0.02105
GO:0033165	interphotoreceptor matrix	0.02116
GO:0044300	cerebellar mossy fiber	0.02116
GO:0014047	glutamate secretion	0.0213
GO:0086012	membrane depolarization during cardiac muscle cell action	0.0213
GO:0005004	GPI-linked ephrin receptor activity	0.02153
GO:1903763	gap junction channel activity involved in cell communicati	0.02153
GO:0010765	positive regulation of sodium ion transport	0.02251
GO:0016338	calcium-independent cell-cell adhesion via plasma membra	0.02251
GO:0060384	innervation	0.02251
GO:0010459	negative regulation of heart rate	0.02251
GO:0016188	synaptic vesicle maturation	0.02251
GO:0038003	opioid receptor signaling pathway	0.02251
GO:0048791	calcium ion-regulated exocytosis of neurotransmitter	0.02251
GO:0071947	protein deubiquitination involved in ubiquitin-dependent pr	0.02251
GO:0046887	positive regulation of hormone secretion	0.02259
GO:0043267	negative regulation of potassium ion transport	0.02282
GO:0046339	diacylglycerol metabolic process	0.02301
GO:0051350	negative regulation of lyase activity	0.02301
GO:0070633	transepithelial transport	0.02327
GO:0099590	neurotransmitter receptor internalization	0.02327
GO:0006855	drug transmembrane transport	0.02372
GO:0003774	motor activity	0.0238
GO:0008081	phosphoric diester hydrolase activity	0.02494

GO:0005003	ephrin receptor activity	0.02542
GO:0005416	amino acid:cation symporter activity	0.02542
GO:1990939	ATP-dependent microtubule motor activity	0.02542
GO:0060996	dendritic spine development	0.02567
GO:0060986	endocrine hormone secretion	0.02567
GO:0071277	cellular response to calcium ion	0.0267
GO:0030133	transport vesicle	0.02673
GO:1905039	carboxylic acid transmembrane transport	0.02783
GO:0015812	gamma-aminobutyric acid transport	0.02834
GO:0033605	positive regulation of catecholamine secretion	0.02834
GO:0072578	neurotransmitter-gated ion channel clustering	0.02834
GO:0090128	regulation of synapse maturation	0.02834
GO:1900452	regulation of long-term synaptic depression	0.02834
GO:0003777	microtubule motor activity	0.02944
GO:0071855	neuropeptide receptor binding	0.03028
GO:0017075	syntaxin-1 binding	0.03046
GO:0035255	ionotropic glutamate receptor binding	0.03046
GO:0006584	catecholamine metabolic process	0.03065
GO:0009712	catechol-containing compound metabolic process	0.03065
GO:0044214	spanning component of plasma membrane	0.03089
GO:0002673	regulation of acute inflammatory response	0.0312
GO:0009306	protein secretion	0.03126
GO:0001540	amyloid-beta binding	0.0318
GO:0051931	regulation of sensory perception	0.0319
GO:0044070	regulation of anion transport	0.03201
GO:0007216	G protein-coupled glutamate receptor signaling pathway	0.0327
GO:0034331	cell junction maintenance	0.0327
GO:0043116	negative regulation of vascular permeability	0.0327
GO:0045989	positive regulation of striated muscle contraction	0.0327
GO:0060572	morphogenesis of an epithelial bud	0.0327
GO:0042428	serotonin metabolic process	0.03273
GO:0070782	phosphatidylserine exposure on apoptotic cell surface	0.03273
GO:0097119	postsynaptic density protein 95 clustering	0.03273
GO:0031234	extrinsic component of cytoplasmic side of plasma membra	0.03383
GO:0015294	solute:cation symporter activity	0.03491
GO:0005313	L-glutamate transmembrane transporter activity	0.03554
GO:1901338	catecholamine binding	0.03554
GO:0034587	piRNA metabolic process	0.03584
GO:0071435	potassium ion export	0.03584
GO:0097623	potassium ion export across plasma membrane	0.03584
GO:0042908	xenobiotic transport	0.03586
GO:0060306	regulation of membrane repolarization	0.03586
GO:0042461	photoreceptor cell development	0.03664
GO:0043090	amino acid import	0.03664
GO:1905144	response to acetylcholine	0.03697
GO:1905145	cellular response to acetylcholine	0.03697
GO:0007194	negative regulation of adenylate cyclase activity	0.03781
GO:0019098	reproductive behavior	0.03803
GO:0095500	acetylcholine receptor signaling pathway	0.03803
GO:1903831	signal transduction involved in cellular response to ammoni	0.03803
GO:0015740	C4-dicarboxylate transport	0.0385
GO:0010676	positive regulation of cellular carbohydrate metabolic proce	0.0385
GO:0061098	positive regulation of protein tyrosine kinase activity	0.0385
GO:0090280	positive regulation of calcium ion import	0.0385
GO:0043279	response to alkaloid	0.0385
GO:0010460	positive regulation of heart rate	0.03855
GO:0086011	membrane repolarization during action potential	0.03855
GO:0097205	renal filtration	0.03855
GO:0099623	regulation of cardiac muscle cell membrane repolarization	0.03855
GO:0099625	ventricular cardiac muscle cell membrane repolarization	0.03855
GO:0045822	negative regulation of heart contraction	0.03855
GO:0060571	morphogenesis of an epithelial fold	0.03855
GO:0007185	transmembrane receptor protein tyrosine phosphatase signa	0.03855
GO:0009448	gamma-aminobutyric acid metabolic process	0.03855
GO:0010754	negative regulation of cGMP-mediated signaling	0.03855
GO:0046958	nonassociative learning	0.03855
GO:0086029	Purkinje myocyte to ventricular cardiac muscle cell signalii	0.03855
GO:0086068	Purkinje myocyte to ventricular cardiac muscle cell commu	0.03855
GO:0097151	positive regulation of inhibitory postsynaptic potential	0.03855
GO:0098828	modulation of inhibitory postsynaptic potential	0.03855
GO:1990349	gap junction-mediated intercellular transport	0.03855
GO:0090533	cation-transporting ATPase complex	0.03896

GO:0099516	ion antiporter activity	0.0399
GO:0005127	ciliary neurotrophic factor receptor binding	0.04105
GO:0005229	intracellular calcium activated chloride channel activity	0.04117
GO:0022841	potassium ion leak channel activity	0.04117
GO:0061778	intracellular chloride channel activity	0.04117
GO:0043954	cellular component maintenance	0.04136
GO:0051279	regulation of release of sequestered calcium ion into cytoso	0.0419
GO:0005938	cell cortex	0.04192
GO:0009898	cytoplasmic side of plasma membrane	0.04192
GO:0030902	hindbrain development	0.0428
GO:0044291	cell-cell contact zone	0.04297
GO:0060287	epithelial cilium movement involved in determination of le	0.04412
GO:0086070	SA node cell to atrial cardiac muscle cell communication	0.04412
GO:0099550	trans-synaptic signaling, modulating synaptic transmission	0.04412
GO:0099566	regulation of postsynaptic cytosolic calcium ion concentrati	0.04412
GO:0005310	dicarboxylic acid transmembrane transporter activity	0.04436
GO:0046847	filopodium assembly	0.04441
GO:0030863	cortical cytoskeleton	0.04503
GO:0016328	lateral plasma membrane	0.04503
GO:0060998	regulation of dendritic spine development	0.04517
GO:0051590	positive regulation of neurotransmitter transport	0.04806
GO:0051930	regulation of sensory perception of pain	0.04806
GO:0086091	regulation of heart rate by cardiac conduction	0.04806
GO:0061333	renal tubule morphogenesis	0.04891
GO:0072028	nephron morphogenesis	0.04891
GO:0015272	ATP-activated inward rectifier potassium channel activity	0.04934
GO:Medium_ Trend Only		
GO:0000978	RNA polymerase II proximal promoter sequence-specific D	0.00058
GO:0070050	neuron cellular homeostasis	0.00071
GO:0000987	proximal promoter sequence-specific DNA binding	0.00126
GO:0022010	central nervous system myelination	0.00138
GO:0032291	axon ensheathment in central nervous system	0.00138
GO:0044458	motile cilium assembly	0.00151
GO:0044782	cilium organization	0.00156
GO:0040007	growth	0.00174
GO:0099509	regulation of presynaptic cytosolic calcium ion concentratic	0.00235
GO:0035107	appendage morphogenesis	0.00257
GO:0035108	limb morphogenesis	0.00257
GO:0032421	stereocilium bundle	0.00334
GO:0060271	cilium assembly	0.00344
GO:2000969	positive regulation of AMPA receptor activity	0.00368
GO:0021782	glial cell development	0.00401
GO:0044212	transcription regulatory region DNA binding	0.00461
GO:0001067	regulatory region nucleic acid binding	0.00528
GO:0000976	transcription regulatory region sequence-specific DNA binc	0.0056
GO:1990837	sequence-specific double-stranded DNA binding	0.00785
GO:0008038	neuron recognition	0.00929
GO:0043565	sequence-specific DNA binding	0.01008
GO:0008092	cytoskeletal protein binding	0.01008
GO:0010739	positive regulation of protein kinase A signaling	0.01033
GO:0010880	regulation of release of sequestered calcium ion into cytoso	0.01056
GO:0048747	muscle fiber development	0.01122
GO:0048736	appendage development	0.01186
GO:0060173	limb development	0.01186
GO:0030031	cell projection assembly	0.01191
GO:0035641	locomotory exploration behavior	0.01205
GO:0099150	regulation of postsynaptic specialization assembly	0.01205
GO:0150052	regulation of postsynapse assembly	0.01205
GO:0120031	plasma membrane bounded cell projection assembly	0.01264
GO:0001539	cilium or flagellum-dependent cell motility	0.01275
GO:0060285	cilium-dependent cell motility	0.01275
GO:1900451	positive regulation of glutamate receptor signaling pathway	0.01301
GO:0071625	vocalization behavior	0.01318
GO:2000257	regulation of protein activation cascade	0.01356
GO:1903514	release of sequestered calcium ion into cytosol by endoplasi	0.01423
GO:0017080	sodium channel regulator activity	0.01629
GO:0014003	oligodendrocyte development	0.01791
GO:0007628	adult walking behavior	0.01793
GO:0086064	cell communication by electrical coupling involved in cardi	0.01976
GO:0048787	presynaptic active zone membrane	0.02111
GO:0030326	embryonic limb morphogenesis	0.02117
GO:0035113	embryonic appendage morphogenesis	0.02117

GO:0010738	regulation of protein kinase A signaling	0.02163
GO:1905383	protein localization to presynapse	0.02388
GO:0097440	apical dendrite	0.02464
GO:0014044	Schwann cell development	0.02576
GO:0014808	release of sequestered calcium ion into cytosol by sarcoplas	0.02576
GO:0070296	sarcoplasmic reticulum calcium ion transport	0.02658
GO:0099151	regulation of postsynaptic density assembly	0.02658
GO:0048670	regulation of collateral sprouting	0.02658
GO:0007519	skeletal muscle tissue development	0.02683
GO:0060538	skeletal muscle organ development	0.0271
GO:0021987	cerebral cortex development	0.0273
GO:1905874	regulation of postsynaptic density organization	0.02732
GO:0060080	inhibitory postsynaptic potential	0.02742
GO:0090659	walking behavior	0.02816
GO:0061387	regulation of extent of cell growth	0.0285
GO:0003009	skeletal muscle contraction	0.02859
GO:0030517	negative regulation of axon extension	0.02859
GO:0008228	opsonization	0.03222
GO:0005954	calcium- and calmodulin-dependent protein kinase complex	0.03401
GO:0098862	cluster of actin-based cell projections	0.03882
GO:0043501	skeletal muscle adaptation	0.04007
GO:0030449	regulation of complement activation	0.04091
GO:0036064	ciliary basal body	0.04412
GO:0032098	regulation of appetite	0.0447
GO:0043034	costamere	0.04473
GO:0030426	growth cone	0.04724
GO:0060077	inhibitory synapse	0.0483
GO:0048788	cytoskeleton of presynaptic active zone	0.0498

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GO:0097458	neuron part	4.46E-52
GO:0042995	cell projection	1.79E-48
GO:0099537	trans-synaptic signaling	2.04E-48
GO:0007268	chemical synaptic transmission	2.04E-48
GO:0098916	anterograde trans-synaptic signaling	2.04E-48
GO:0099536	synaptic signaling	6.79E-47
GO:0120025	plasma membrane bounded cell projection	1.92E-45
GO:0043005	neuron projection	1.07E-44
GO:0045202	synapse	2.48E-43
GO:0044456	synapse part	6.47E-37
GO:1902495	transmembrane transporter complex	2.19E-35
GO:0097060	synaptic membrane	2.19E-35
GO:0034702	ion channel complex	1.11E-34
GO:0044463	cell projection part	8.11E-33
GO:0120038	plasma membrane bounded cell projection part	8.11E-33
GO:1990351	transporter complex	1.80E-32
GO:0022839	ion gated channel activity	1.14E-31
GO:0007399	nervous system development	5.46E-31
GO:0036477	somatodendritic compartment	6.24E-31
GO:0050804	modulation of chemical synaptic transmission	2.47E-29
GO:0099177	regulation of trans-synaptic signaling	3.60E-29
GO:0045211	postsynaptic membrane	3.94E-29
GO:0098794	postsynapse	1.24E-26
GO:0046873	metal ion transmembrane transporter activity	4.68E-25
GO:0034703	cation channel complex	1.26E-24
GO:0097447	dendritic tree	2.06E-24
GO:0022008	neurogenesis	4.94E-24
GO:0030425	dendrite	5.01E-24
GO:0034765	regulation of ion transmembrane transport	1.07E-23
GO:0098655	cation transmembrane transport	3.42E-23
GO:0034762	regulation of transmembrane transport	5.63E-23
GO:0044057	regulation of system process	2.40E-22
GO:0042391	regulation of membrane potential	2.62E-22
GO:0098793	presynapse	3.92E-22
GO:0006813	potassium ion transport	5.56E-22
GO:0048699	generation of neurons	6.41E-22
GO:0071804	cellular potassium ion transport	1.41E-20
GO:0071805	potassium ion transmembrane transport	1.41E-20
GO:0008324	cation transmembrane transporter activity	5.26E-20
GO:0022890	inorganic cation transmembrane transporter activity	5.26E-20
GO:0099240	intrinsic component of synaptic membrane	1.16E-19
GO:0022832	voltage-gated channel activity	1.20E-19
GO:0006836	neurotransmitter transport	1.69E-19

GO:0043025	neuronal cell body	2.06E-19
GO:0005244	voltage-gated ion channel activity	2.18E-19
GO:0030424	axon	3.22E-19
GO:0044297	cell body	3.24E-19
GO:0060078	regulation of postsynaptic membrane potential	6.09E-19
GO:0048666	neuron development	6.81E-19
GO:0007610	behavior	6.81E-19
GO:0030182	neuron differentiation	8.00E-19
GO:0099699	integral component of synaptic membrane	8.40E-19
GO:0022843	voltage-gated cation channel activity	1.10E-18
GO:0003008	system process	2.05E-18
GO:0098984	neuron to neuron synapse	5.99E-18
GO:0015079	potassium ion transmembrane transporter activity	8.76E-18
GO:0035637	multicellular organismal signaling	2.00E-17
GO:0098662	inorganic cation transmembrane transport	3.14E-17
GO:0015672	monovalent inorganic cation transport	3.51E-17
GO:0099572	postsynaptic specialization	4.62E-17
GO:0048812	neuron projection morphogenesis	7.02E-17
GO:0099055	integral component of postsynaptic membrane	1.28E-16
GO:0051960	regulation of nervous system development	1.85E-16
GO:0031175	neuron projection development	3.25E-16
GO:0048858	cell projection morphogenesis	4.56E-16
GO:0120039	plasma membrane bounded cell projection morphogenesis	5.33E-16
GO:0050808	synapse organization	5.99E-16
GO:0005267	potassium channel activity	6.87E-16
GO:0099634	postsynaptic specialization membrane	7.98E-16
GO:0042734	presynaptic membrane	1.02E-15
GO:0098936	intrinsic component of postsynaptic membrane	1.06E-15
GO:1903522	regulation of blood circulation	2.06E-15
GO:0030030	cell projection organization	2.08E-15
GO:0032279	asymmetric synapse	2.85E-15
GO:0098978	glutamatergic synapse	3.33E-15
GO:0120036	plasma membrane bounded cell projection organization	3.71E-15
GO:0032989	cellular component morphogenesis	4.41E-15
GO:1904062	regulation of cation transmembrane transport	5.63E-15
GO:0034705	potassium channel complex	5.66E-15
GO:0014069	postsynaptic density	7.98E-15
GO:0032990	cell part morphogenesis	1.34E-14
GO:0048667	cell morphogenesis involved in neuron differentiation	3.90E-14
GO:0008076	voltage-gated potassium channel complex	1.51E-13
GO:0001505	regulation of neurotransmitter levels	1.82E-13
GO:0023061	signal release	2.52E-13
GO:0015077	monovalent inorganic cation transmembrane transporter act	2.71E-13
GO:2001257	regulation of cation channel activity	2.81E-13
GO:0008016	regulation of heart contraction	2.84E-13
GO:0005249	voltage-gated potassium channel activity	3.43E-13
GO:0007218	neuropeptide signaling pathway	9.43E-13
GO:0000904	cell morphogenesis involved in differentiation	1.42E-12
GO:0050806	positive regulation of synaptic transmission	1.59E-12
GO:0007193	adenylate cyclase-inhibiting G protein-coupled receptor sig	1.86E-12
GO:0061337	cardiac conduction	1.94E-12
GO:0030594	neurotransmitter receptor activity	2.61E-12
GO:0060047	heart contraction	3.52E-12
GO:0010959	regulation of metal ion transport	3.95E-12
GO:0022898	regulation of transmembrane transporter activity	4.11E-12
GO:0007215	glutamate receptor signaling pathway	4.45E-12
GO:0003015	heart process	6.03E-12
GO:0048167	regulation of synaptic plasticity	7.17E-12
GO:0007417	central nervous system development	7.76E-12
GO:0032412	regulation of ion transmembrane transporter activity	8.52E-12
GO:0008528	G protein-coupled peptide receptor activity	9.27E-12
GO:0001653	peptide receptor activity	9.38E-12
GO:0050767	regulation of neurogenesis	1.40E-11
GO:0007409	axonogenesis	1.58E-11
GO:0099565	chemical synaptic transmission, postsynaptic	1.95E-11
GO:0001508	action potential	2.00E-11
GO:0032409	regulation of transporter activity	2.14E-11
GO:0099643	signal release from synapse	2.43E-11
GO:0099060	integral component of postsynaptic specialization membran	2.46E-11
GO:0015837	amine transport	2.76E-11
GO:0098839	postsynaptic density membrane	2.86E-11
GO:0035249	synaptic transmission, glutamatergic	3.31E-11

GO:0061564	axon development	3.32E-11
GO:0007269	neurotransmitter secretion	4.23E-11
GO:0015276	ligand-gated ion channel activity	4.78E-11
GO:0022834	ligand-gated channel activity	4.78E-11
GO:0060079	excitatory postsynaptic potential	5.81E-11
GO:0051952	regulation of amine transport	7.34E-11
GO:0031344	regulation of cell projection organization	1.16E-10
GO:0098948	intrinsic component of postsynaptic specialization membra	1.98E-10
GO:0043204	perikaryon	2.84E-10
GO:0060076	excitatory synapse	2.84E-10
GO:0007611	learning or memory	3.72E-10
GO:0120035	regulation of plasma membrane bounded cell projection org	3.72E-10
GO:0098889	intrinsic component of presynaptic membrane	4.49E-10
GO:0043197	dendritic spine	5.04E-10
GO:0032590	dendrite membrane	5.17E-10
GO:0098960	postsynaptic neurotransmitter receptor activity	5.62E-10
GO:0022824	transmitter-gated ion channel activity	5.62E-10
GO:0022835	transmitter-gated channel activity	5.62E-10
GO:0051962	positive regulation of nervous system development	5.75E-10
GO:1902476	chloride transmembrane transport	6.13E-10
GO:0031644	regulation of neurological system process	7.16E-10
GO:0044309	neuron spine	7.48E-10
GO:0010975	regulation of neuron projection development	8.18E-10
GO:0044306	neuron projection terminus	8.93E-10
GO:1900449	regulation of glutamate receptor signaling pathway	9.64E-10
GO:0006814	sodium ion transport	9.64E-10
GO:0043266	regulation of potassium ion transport	1.23E-09
GO:0007416	synapse assembly	1.23E-09
GO:0005230	extracellular ligand-gated ion channel activity	1.23E-09
GO:0051588	regulation of neurotransmitter transport	1.27E-09
GO:0033267	axon part	1.54E-09
GO:0032589	neuron projection membrane	2.01E-09
GO:0045664	regulation of neuron differentiation	2.23E-09
GO:0015893	drug transport	2.42E-09
GO:0099601	regulation of neurotransmitter receptor activity	2.61E-09
GO:0099529	neurotransmitter receptor activity involved in regulation of	2.64E-09
GO:0030672	synaptic vesicle membrane	2.71E-09
GO:0099501	exocytic vesicle membrane	2.71E-09
GO:0051966	regulation of synaptic transmission, glutamatergic	2.91E-09
GO:0050954	sensory perception of mechanical stimulus	3.57E-09
GO:0099504	synaptic vesicle cycle	3.97E-09
GO:0098982	GABA-ergic synapse	5.80E-09
GO:0043679	axon terminus	8.81E-09
GO:0044441	ciliary part	8.83E-09
GO:0050890	cognition	1.33E-08
GO:0015081	sodium ion transmembrane transporter activity	2.17E-08
GO:1904064	positive regulation of cation transmembrane transport	2.57E-08
GO:0098656	anion transmembrane transport	2.72E-08
GO:1904315	transmitter-gated ion channel activity involved in regulatio	2.95E-08
GO:0005929	cilium	3.53E-08
GO:0044304	main axon	3.98E-08
GO:0050877	nervous system process	4.07E-08
GO:0050433	regulation of catecholamine secretion	4.17E-08
GO:0099056	integral component of presynaptic membrane	4.40E-08
GO:0098661	inorganic anion transmembrane transport	5.93E-08
GO:0097479	synaptic vesicle localization	6.22E-08
GO:0097485	neuron projection guidance	6.46E-08
GO:0031646	positive regulation of neurological system process	7.13E-08
GO:0017158	regulation of calcium ion-dependent exocytosis	7.13E-08
GO:1901379	regulation of potassium ion transmembrane transport	7.13E-08
GO:0016079	synaptic vesicle exocytosis	7.13E-08
GO:0033555	multicellular organismal response to stress	7.35E-08
GO:0007612	learning	7.51E-08
GO:0050953	sensory perception of light stimulus	8.07E-08
GO:0007411	axon guidance	9.22E-08
GO:0008188	neuropeptide receptor activity	9.51E-08
GO:0015844	monoamine transport	9.55E-08
GO:0009582	detection of abiotic stimulus	1.12E-07
GO:0050803	regulation of synapse structure or activity	1.13E-07
GO:0017156	calcium ion regulated exocytosis	1.16E-07
GO:0006821	chloride transport	1.22E-07
GO:0007601	visual perception	1.31E-07

GO:0034767	positive regulation of ion transmembrane transport	1.40E-07
GO:0150034	distal axon	1.41E-07
GO:0007605	sensory perception of sound	1.57E-07
GO:0034764	positive regulation of transmembrane transport	1.77E-07
GO:0009581	detection of external stimulus	1.91E-07
GO:0046928	regulation of neurotransmitter secretion	2.11E-07
GO:0008509	anion transmembrane transporter activity	2.29E-07
GO:0006941	striated muscle contraction	2.29E-07
GO:0050432	catecholamine secretion	2.32E-07
GO:0030534	adult behavior	2.43E-07
GO:0051937	catecholamine transport	2.53E-07
GO:0051965	positive regulation of synapse assembly	2.66E-07
GO:0031253	cell projection membrane	2.68E-07
GO:0070382	exocytic vesicle	2.75E-07
GO:0009914	hormone transport	2.80E-07
GO:2000463	positive regulation of excitatory postsynaptic potential	4.70E-07
GO:0035725	sodium ion transmembrane transport	6.14E-07
GO:0098878	neurotransmitter receptor complex	6.57E-07
GO:0051963	regulation of synapse assembly	6.57E-07
GO:0046879	hormone secretion	6.64E-07
GO:0099003	vesicle-mediated transport in synapse	7.54E-07
GO:0097014	ciliary plasm	8.03E-07
GO:0005930	axoneme	8.33E-07
GO:0015698	inorganic anion transport	8.99E-07
GO:0031225	anchored component of membrane	9.26E-07
GO:0099095	ligand-gated anion channel activity	9.40E-07
GO:1902710	GABA receptor complex	1.02E-06
GO:0050807	regulation of synapse organization	1.10E-06
GO:0008021	synaptic vesicle	1.16E-06
GO:0015108	chloride transmembrane transporter activity	1.28E-06
GO:0007613	memory	1.49E-06
GO:0070588	calcium ion transmembrane transport	1.57E-06
GO:0098815	modulation of excitatory postsynaptic potential	1.58E-06
GO:0008328	ionotropic glutamate receptor complex	1.83E-06
GO:0016323	basolateral plasma membrane	1.83E-06
GO:0046883	regulation of hormone secretion	2.22E-06
GO:0005516	calmodulin binding	2.29E-06
GO:0099061	integral component of postsynaptic density membrane	2.42E-06
GO:1902711	GABA-A receptor complex	2.49E-06
GO:0044298	cell body membrane	2.68E-06
GO:0015872	dopamine transport	2.79E-06
GO:0048489	synaptic vesicle transport	2.85E-06
GO:0097480	establishment of synaptic vesicle localization	2.85E-06
GO:0015103	inorganic anion transmembrane transporter activity	2.96E-06
GO:0019226	transmission of nerve impulse	3.11E-06
GO:0043268	positive regulation of potassium ion transport	3.11E-06
GO:0099094	ligand-gated cation channel activity	3.32E-06
GO:0060291	long-term synaptic potentiation	3.54E-06
GO:0031674	I band	3.54E-06
GO:0005253	anion channel activity	3.71E-06
GO:0032809	neuronal cell body membrane	3.81E-06
GO:0098693	regulation of synaptic vesicle cycle	4.77E-06
GO:0019228	neuronal action potential	4.84E-06
GO:0050769	positive regulation of neurogenesis	4.89E-06
GO:1901381	positive regulation of potassium ion transmembrane transpo	4.92E-06
GO:0035418	protein localization to synapse	5.45E-06
GO:0005254	chloride channel activity	5.87E-06
GO:0016324	apical plasma membrane	5.95E-06
GO:0050805	negative regulation of synaptic transmission	5.99E-06
GO:1903779	regulation of cardiac conduction	5.99E-06
GO:0044447	axoneme part	8.06E-06
GO:0042383	sarcolemma	8.06E-06
GO:0034707	chloride channel complex	8.90E-06
GO:0007420	brain development	9.75E-06
GO:0007626	locomotory behavior	9.80E-06
GO:0004890	GABA-A receptor activity	1.00E-05
GO:0016917	GABA receptor activity	1.02E-05
GO:0007214	gamma-aminobutyric acid signaling pathway	1.04E-05
GO:2000311	regulation of AMPA receptor activity	1.04E-05
GO:2000300	regulation of synaptic vesicle exocytosis	1.11E-05
GO:2000310	regulation of NMDA receptor activity	1.11E-05
GO:1902803	regulation of synaptic vesicle transport	1.11E-05

GO:0099146	intrinsic component of postsynaptic density membrane	1.12E-05
GO:0050982	detection of mechanical stimulus	1.32E-05
GO:0005891	voltage-gated calcium channel complex	1.38E-05
GO:0050974	detection of mechanical stimulus involved in sensory perce	1.43E-05
GO:0005237	inhibitory extracellular ligand-gated ion channel activity	1.58E-05
GO:0006937	regulation of muscle contraction	1.86E-05
GO:0060292	long-term synaptic depression	2.27E-05
GO:0042063	gliogenesis	2.37E-05
GO:1903305	regulation of regulated secretory pathway	2.46E-05
GO:0022604	regulation of cell morphogenesis	3.01E-05
GO:0001764	neuron migration	3.24E-05
GO:0045666	positive regulation of neuron differentiation	3.29E-05
GO:0048640	negative regulation of developmental growth	3.31E-05
GO:0043194	axon initial segment	3.77E-05
GO:0070252	actin-mediated cell contraction	3.86E-05
GO:0048786	presynaptic active zone	3.95E-05
GO:0015085	calcium ion transmembrane transporter activity	4.26E-05
GO:0051932	synaptic transmission, GABAergic	4.43E-05
GO:0060322	head development	4.75E-05
GO:0099054	presynapse assembly	4.75E-05
GO:0007389	pattern specification process	4.81E-05
GO:0097730	non-motile cilium	5.00E-05
GO:0034706	sodium channel complex	6.14E-05
GO:0042596	fear response	6.29E-05
GO:0010720	positive regulation of cell development	6.34E-05
GO:0099568	cytoplasmic region	6.39E-05
GO:0030072	peptide hormone secretion	7.17E-05
GO:0099560	synaptic membrane adhesion	7.57E-05
GO:0060048	cardiac muscle contraction	8.15E-05
GO:0003341	cilium movement	9.05E-05
GO:0016247	channel regulator activity	9.25E-05
GO:0099172	presynapse organization	9.77E-05
GO:0030048	actin filament-based movement	0.00011
GO:0022851	GABA-gated chloride ion channel activity	0.00011
GO:0008066	glutamate receptor activity	0.00011
GO:1903169	regulation of calcium ion transmembrane transport	0.00011
GO:0030018	Z disc	0.00013
GO:0030315	T-tubule	0.00013
GO:0030017	sarcomere	0.00014
GO:0005262	calcium channel activity	0.00015
GO:0051924	regulation of calcium ion transport	0.00016
GO:0043292	contractile fiber	0.00016
GO:0048638	regulation of developmental growth	0.00017
GO:0086001	cardiac muscle cell action potential	0.00017
GO:0017157	regulation of exocytosis	0.00017
GO:0044449	contractile fiber part	0.00018
GO:0001504	neurotransmitter uptake	0.00018
GO:0086010	membrane depolarization during action potential	0.00018
GO:0001518	voltage-gated sodium channel complex	0.00019
GO:0001662	behavioral fear response	0.00021
GO:0048839	inner ear development	0.00022
GO:0006835	dicarboxylic acid transport	0.00022
GO:0030016	myofibril	0.00022
GO:0002027	regulation of heart rate	0.00023
GO:0005245	voltage-gated calcium channel activity	0.00023
GO:0090276	regulation of peptide hormone secretion	0.00027
GO:0005858	axonemal dynein complex	0.00028
GO:0090596	sensory organ morphogenesis	0.00031
GO:0086002	cardiac muscle cell action potential involved in contraction	0.00032
GO:0015800	acidic amino acid transport	0.00033
GO:0016358	dendrite development	0.00035
GO:0098685	Schaffer collateral - CA1 synapse	0.00037
GO:0005231	excitatory extracellular ligand-gated ion channel activity	0.00037
GO:0042562	hormone binding	0.00038
GO:0032414	positive regulation of ion transmembrane transporter activi	0.00038
GO:0031045	dense core granule	0.00041
GO:0032838	plasma membrane bounded cell projection cytoplasm	0.00041
GO:0002209	behavioral defense response	0.00045
GO:1903524	positive regulation of blood circulation	0.00045
GO:2001259	positive regulation of cation channel activity	0.00045
GO:0090257	regulation of muscle system process	0.00046
GO:0010469	regulation of signaling receptor activity	0.00046

GO:0010001	glial cell differentiation	0.00046
GO:0019233	sensory perception of pain	0.00046
GO:0017046	peptide hormone binding	0.00046
GO:0021885	forebrain cell migration	0.0005
GO:0098739	import across plasma membrane	0.0005
GO:0031346	positive regulation of cell projection organization	0.00051
GO:0051961	negative regulation of nervous system development	0.00057
GO:0043583	ear development	0.00059
GO:0010752	regulation of cGMP-mediated signaling	0.0006
GO:0019934	cGMP-mediated signaling	0.00062
GO:0050770	regulation of axonogenesis	0.00069
GO:0099174	regulation of presynapse organization	0.0007
GO:1905606	regulation of presynapse assembly	0.0007
GO:0004181	metallocarboxypeptidase activity	0.00072
GO:0005272	sodium channel activity	0.00074
GO:0086003	cardiac muscle cell contraction	0.00079
GO:0042472	inner ear morphogenesis	0.00081
GO:0032411	positive regulation of transporter activity	0.00085
GO:0022029	telencephalon cell migration	0.00085
GO:0008277	regulation of G protein-coupled receptor signaling pathway	0.00088
GO:0035082	axoneme assembly	0.00089
GO:0030239	myofibril assembly	0.00089
GO:0045823	positive regulation of heart contraction	0.00091
GO:0030073	insulin secretion	0.00092
GO:0099106	ion channel regulator activity	0.00095
GO:0043949	regulation of cAMP-mediated signaling	0.00096
GO:0098659	inorganic cation import across plasma membrane	0.00096
GO:0099587	inorganic ion import across plasma membrane	0.00096
GO:0010721	negative regulation of cell development	0.00097
GO:0046658	anchored component of plasma membrane	0.001
GO:0030658	transport vesicle membrane	0.00101
GO:0010769	regulation of cell morphogenesis involved in differentiatio	0.00104
GO:0001750	photoreceptor outer segment	0.0011
GO:0050910	detection of mechanical stimulus involved in sensory perce	0.0011
GO:0030285	integral component of synaptic vesicle membrane	0.00116
GO:0098686	hippocampal mossy fiber to CA3 synapse	0.00116
GO:0010771	negative regulation of cell morphogenesis involved in diffe	0.00119
GO:0042923	neuropeptide binding	0.0012
GO:0051899	membrane depolarization	0.00121
GO:0051968	positive regulation of synaptic transmission, glutamatergic	0.00129
GO:0097106	postsynaptic density organization	0.00139
GO:1901016	regulation of potassium ion transmembrane transporter acti	0.00139
GO:0005540	hyaluronic acid binding	0.00144
GO:0050905	neuromuscular process	0.00145
GO:0099084	postsynaptic specialization organization	0.00147
GO:0010976	positive regulation of neuron projection development	0.00155
GO:0050773	regulation of dendrite development	0.00174
GO:0002028	regulation of sodium ion transport	0.00176
GO:0005248	voltage-gated sodium channel activity	0.00194
GO:0034704	calcium channel complex	0.00198
GO:0051705	multi-organism behavior	0.00208
GO:0099528	G protein-coupled neurotransmitter receptor activity	0.00208
GO:0003700	DNA-binding transcription factor activity	0.00208
GO:0050796	regulation of insulin secretion	0.0022
GO:0033017	sarcoplasmic reticulum membrane	0.00225
GO:0060560	developmental growth involved in morphogenesis	0.00226
GO:0097120	receptor localization to synapse	0.00244
GO:0070509	calcium ion import	0.0025
GO:0031345	negative regulation of cell projection organization	0.00253
GO:0099173	postsynapse organization	0.0026
GO:0021795	cerebral cortex cell migration	0.00273
GO:0050771	negative regulation of axonogenesis	0.0028
GO:0007422	peripheral nervous system development	0.00301
GO:0050768	negative regulation of neurogenesis	0.00301
GO:0007631	feeding behavior	0.00334
GO:1902475	L-alpha-amino acid transmembrane transport	0.00338
GO:0007158	neuron cell-cell adhesion	0.00345
GO:0060402	calcium ion transport into cytosol	0.00348
GO:0045956	positive regulation of calcium ion-dependent exocytosis	0.00366
GO:0098563	intrinsic component of synaptic vesicle membrane	0.00368
GO:0086065	cell communication involved in cardiac conduction	0.0037
GO:0042165	neurotransmitter binding	0.00381

GO:0008307	structural constituent of muscle	0.00381
GO:0043198	dendritic shaft	0.00406
GO:0098858	actin-based cell projection	0.00433
GO:0016082	synaptic vesicle priming	0.00453
GO:1990573	potassium ion import across plasma membrane	0.00472
GO:0008344	adult locomotory behavior	0.00513
GO:1904427	positive regulation of calcium ion transmembrane transport	0.0055
GO:0048588	developmental cell growth	0.00556
GO:0001917	photoreceptor inner segment	0.00586
GO:1905114	cell surface receptor signaling pathway involved in cell-cell	0.00587
GO:0055001	muscle cell development	0.00632
GO:0031280	negative regulation of cyclase activity	0.00632
GO:0098698	postsynaptic specialization assembly	0.00632
GO:0000981	DNA-binding transcription factor activity, RNA polymerase	0.00643
GO:0032281	AMPA glutamate receptor complex	0.00661
GO:0060401	cytosolic calcium ion transport	0.00667
GO:0035176	social behavior	0.00689
GO:0051703	intraspecies interaction between organisms	0.00689
GO:1901019	regulation of calcium ion transmembrane transporter activit	0.00707
GO:0033268	node of Ranvier	0.00713
GO:0086009	membrane repolarization	0.0076
GO:0045745	positive regulation of G protein-coupled receptor signaling	0.00808
GO:0042471	ear morphogenesis	0.0081
GO:0010644	cell communication by electrical coupling	0.00821
GO:0004983	neuropeptide Y receptor activity	0.00915
GO:0008503	benzodiazepine receptor activity	0.00915
GO:0097553	calcium ion transmembrane import into cytosol	0.00975
GO:0097107	postsynaptic density assembly	0.01079
GO:0044325	ion channel binding	0.01089
GO:0098814	spontaneous synaptic transmission	0.01127
GO:0014704	intercalated disc	0.01188
GO:0042692	muscle cell differentiation	0.01224
GO:0021953	central nervous system neuron differentiation	0.01316
GO:0001578	microtubule bundle formation	0.01339
GO:0016529	sarcoplasmic reticulum	0.01462
GO:0016528	sarcoplasm	0.01462
GO:0010977	negative regulation of neuron projection development	0.01543
GO:0055002	striated muscle cell development	0.01543
GO:0061669	spontaneous neurotransmitter secretion	0.01745
GO:0099569	presynaptic cytoskeleton	0.01754
GO:0048589	developmental growth	0.01779
GO:0031594	neuromuscular junction	0.0184
GO:0060170	ciliary membrane	0.01861
GO:0007272	ensheathment of neurons	0.0187
GO:0008366	axon ensheathment	0.0187
GO:1901606	alpha-amino acid catabolic process	0.01938
GO:0042552	myelination	0.02016
GO:0048709	oligodendrocyte differentiation	0.02047
GO:0050879	multicellular organismal movement	0.02051
GO:0050881	musculoskeletal movement	0.02051
GO:0007618	mating	0.02105
GO:0022848	acetylcholine-gated cation-selective channel activity	0.02269
GO:0032228	regulation of synaptic transmission, GABAergic	0.02282
GO:0022011	myelination in peripheral nervous system	0.02327
GO:0032292	peripheral nervous system axon ensheathment	0.02327
GO:0051146	striated muscle cell differentiation	0.02388
GO:0004970	ionotropic glutamate receptor activity	0.02542
GO:0010522	regulation of calcium ion transport into cytosol	0.02567
GO:0007528	neuromuscular junction development	0.02567
GO:0006942	regulation of striated muscle contraction	0.02753
GO:0000977	RNA polymerase II regulatory region sequence-specific DN	0.03046
GO:0001012	RNA polymerase II regulatory region DNA binding	0.03046
GO:0072562	blood microparticle	0.03186
GO:0045214	sarcomere organization	0.0319
GO:0099175	regulation of postsynapse organization	0.03263
GO:0031630	regulation of synaptic vesicle fusion to presynaptic active z	0.03273
GO:0007018	microtubule-based movement	0.03333
GO:0060997	dendritic spine morphogenesis	0.03401
GO:0043195	terminal bouton	0.03404
GO:0048639	positive regulation of developmental growth	0.03616
GO:0045665	negative regulation of neuron differentiation	0.03664
GO:0099068	postsynapse assembly	0.03697

GO:0048813	dendrite morphogenesis	0.03832
GO:0055117	regulation of cardiac muscle contraction	0.03844
GO:0043950	positive regulation of cAMP-mediated signaling	0.0385
GO:0035235	ionotropic glutamate receptor signaling pathway	0.03855
GO:0009063	cellular amino acid catabolic process	0.0419
GO:1990138	neuron projection extension	0.04564
GO:0010927	cellular component assembly involved in morphogenesis	0.04897
Medium_ Trend Common		
GO:0097458	neuron part	1.02E-45
GO:0099537	trans-synaptic signaling	1.57E-37
GO:0007268	chemical synaptic transmission	1.57E-37
GO:0098916	anterograde trans-synaptic signaling	1.57E-37
GO:0099536	synaptic signaling	3.17E-37
GO:0043005	neuron projection	1.90E-36
GO:0045202	synapse	1.90E-36
GO:0042995	cell projection	8.27E-35
GO:0044456	synapse part	9.38E-34
GO:0120025	plasma membrane bounded cell projection	9.38E-34
GO:0097060	synaptic membrane	1.48E-32
GO:1902495	transmembrane transporter complex	7.78E-29
GO:1990351	transporter complex	2.21E-28
GO:0098794	postsynapse	2.26E-27
GO:0034702	ion channel complex	2.89E-27
GO:0007399	nervous system development	9.98E-27
GO:0045211	postsynaptic membrane	1.31E-26
GO:0036477	somatodendritic compartment	3.02E-24
GO:0050804	modulation of chemical synaptic transmission	3.30E-23
GO:0099177	regulation of trans-synaptic signaling	4.46E-23
GO:0042391	regulation of membrane potential	5.04E-23
GO:0044463	cell projection part	5.93E-23
GO:0120038	plasma membrane bounded cell projection part	5.93E-23
GO:0034703	cation channel complex	2.24E-20
GO:0044297	cell body	4.58E-20
GO:0022839	ion gated channel activity	5.42E-20
GO:0060078	regulation of postsynaptic membrane potential	1.69E-19
GO:0048666	neuron development	1.83E-19
GO:0022008	neurogenesis	2.34E-19
GO:0099240	intrinsic component of synaptic membrane	8.21E-19
GO:0043025	neuronal cell body	1.24E-18
GO:0098984	neuron to neuron synapse	3.07E-18
GO:0098793	presynapse	3.09E-18
GO:0048699	generation of neurons	3.99E-18
GO:0099634	postsynaptic specialization membrane	4.50E-18
GO:0034765	regulation of ion transmembrane transport	7.42E-18
GO:0030182	neuron differentiation	7.55E-18
GO:0099572	postsynaptic specialization	1.36E-17
GO:0099699	integral component of synaptic membrane	1.81E-17
GO:0098655	cation transmembrane transport	2.05E-17
GO:0030030	cell projection organization	2.07E-17
GO:0030424	axon	4.16E-17
GO:0097447	dendritic tree	8.40E-17
GO:0030425	dendrite	1.96E-16
GO:0120036	plasma membrane bounded cell projection organization	2.34E-16
GO:0044057	regulation of system process	2.35E-16
GO:0098978	glutamatergic synapse	2.54E-16
GO:0032279	asymmetric synapse	3.13E-16
GO:0014069	postsynaptic density	4.88E-16
GO:0098936	intrinsic component of postsynaptic membrane	5.00E-16
GO:0099055	integral component of postsynaptic membrane	2.36E-15
GO:0031175	neuron projection development	4.82E-15
GO:0007610	behavior	5.77E-15
GO:0034762	regulation of transmembrane transport	5.77E-15
GO:0006836	neurotransmitter transport	5.77E-15
GO:0048812	neuron projection morphogenesis	8.13E-15
GO:0048858	cell projection morphogenesis	1.39E-14
GO:0050808	synapse organization	2.52E-14
GO:0035637	multicellular organismal signaling	2.55E-14
GO:0120039	plasma membrane bounded cell projection morphogenesis	3.33E-14
GO:1904062	regulation of cation transmembrane transport	4.15E-14
GO:0098839	postsynaptic density membrane	5.47E-14
GO:0042734	presynaptic membrane	6.94E-14
GO:0048667	cell morphogenesis involved in neuron differentiation	1.02E-13

GO:0032990	cell part morphogenesis	1.08E-13
GO:0099565	chemical synaptic transmission, postsynaptic	1.37E-13
GO:0099060	integral component of postsynaptic specialization membran	1.46E-13
GO:0098948	intrinsic component of postsynaptic specialization membran	1.81E-13
GO:0046873	metal ion transmembrane transporter activity	7.21E-13
GO:0030594	neurotransmitter receptor activity	1.30E-12
GO:2001257	regulation of cation channel activity	1.92E-12
GO:0098662	inorganic cation transmembrane transport	2.04E-12
GO:0022898	regulation of transmembrane transporter activity	2.91E-12
GO:0060079	excitatory postsynaptic potential	3.12E-12
GO:0032412	regulation of ion transmembrane transporter activity	4.19E-12
GO:0032409	regulation of transporter activity	9.58E-12
GO:0006813	potassium ion transport	1.21E-11
GO:1903522	regulation of blood circulation	1.22E-11
GO:0008016	regulation of heart contraction	1.23E-11
GO:1900449	regulation of glutamate receptor signaling pathway	2.29E-11
GO:0015276	ligand-gated ion channel activity	4.24E-11
GO:0022834	ligand-gated channel activity	4.24E-11
GO:0031644	regulation of neurological system process	5.25E-11
GO:0043204	perikaryon	5.27E-11
GO:0034705	potassium channel complex	5.63E-11
GO:0007269	neurotransmitter secretion	6.10E-11
GO:0033267	axon part	6.61E-11
GO:0005230	extracellular ligand-gated ion channel activity	1.01E-10
GO:0099643	signal release from synapse	1.02E-10
GO:0051960	regulation of nervous system development	1.03E-10
GO:0022824	transmitter-gated ion channel activity	1.14E-10
GO:0022835	transmitter-gated channel activity	1.14E-10
GO:0022890	inorganic cation transmembrane transporter activity	1.27E-10
GO:0032989	cellular component morphogenesis	1.51E-10
GO:0051588	regulation of neurotransmitter transport	1.73E-10
GO:0001505	regulation of neurotransmitter levels	1.74E-10
GO:0071804	cellular potassium ion transport	1.74E-10
GO:0071805	potassium ion transmembrane transport	1.74E-10
GO:0007215	glutamate receptor signaling pathway	1.78E-10
GO:0099529	neurotransmitter receptor activity involved in regulation of	2.13E-10
GO:0098960	postsynaptic neurotransmitter receptor activity	2.70E-10
GO:0008324	cation transmembrane transporter activity	3.00E-10
GO:0050806	positive regulation of synaptic transmission	4.66E-10
GO:0008076	voltage-gated potassium channel complex	6.12E-10
GO:0060047	heart contraction	6.28E-10
GO:0099601	regulation of neurotransmitter receptor activity	7.41E-10
GO:0007416	synapse assembly	1.13E-09
GO:0005244	voltage-gated ion channel activity	1.20E-09
GO:0098889	intrinsic component of presynaptic membrane	1.67E-09
GO:0022832	voltage-gated channel activity	1.74E-09
GO:0098982	GABA-ergic synapse	1.80E-09
GO:0023061	signal release	2.13E-09
GO:0061337	cardiac conduction	2.53E-09
GO:0007218	neuropeptide signaling pathway	2.75E-09
GO:0061564	axon development	2.78E-09
GO:0015672	monovalent inorganic cation transport	2.88E-09
GO:1904315	transmitter-gated ion channel activity involved in regulation	2.98E-09
GO:0003015	heart process	3.11E-09
GO:0007409	axonogenesis	5.81E-09
GO:0099061	integral component of postsynaptic density membrane	7.03E-09
GO:0098878	neurotransmitter receptor complex	7.53E-09
GO:0099146	intrinsic component of postsynaptic density membrane	7.91E-09
GO:0048167	regulation of synaptic plasticity	1.08E-08
GO:0001508	action potential	1.08E-08
GO:0005929	cilium	1.27E-08
GO:0003008	system process	1.45E-08
GO:0000904	cell morphogenesis involved in differentiation	1.58E-08
GO:0031646	positive regulation of neurological system process	1.64E-08
GO:0099056	integral component of presynaptic membrane	1.75E-08
GO:0010959	regulation of metal ion transport	1.99E-08
GO:0015079	potassium ion transmembrane transporter activity	2.01E-08
GO:0043197	dendritic spine	2.19E-08
GO:0044306	neuron projection terminus	2.52E-08
GO:0044309	neuron spine	2.64E-08
GO:0031344	regulation of cell projection organization	2.92E-08
GO:0008328	ionotropic glutamate receptor complex	3.23E-08

GO:0010975	regulation of neuron projection development	3.44E-08
GO:0022843	voltage-gated cation channel activity	3.85E-08
GO:0016079	synaptic vesicle exocytosis	4.11E-08
GO:0030534	adult behavior	4.20E-08
GO:0050767	regulation of neurogenesis	4.96E-08
GO:0044304	main axon	7.52E-08
GO:0046928	regulation of neurotransmitter secretion	8.00E-08
GO:0044441	ciliary part	8.83E-08
GO:1902803	regulation of synaptic vesicle transport	1.03E-07
GO:0098685	Schaffer collateral - CA1 synapse	1.46E-07
GO:0120035	regulation of plasma membrane bounded cell projection org	1.70E-07
GO:0099504	synaptic vesicle cycle	1.78E-07
GO:0150034	distal axon	2.27E-07
GO:0098815	modulation of excitatory postsynaptic potential	2.99E-07
GO:0005267	potassium channel activity	3.69E-07
GO:0007611	learning or memory	4.01E-07
GO:0097479	synaptic vesicle localization	4.24E-07
GO:0099003	vesicle-mediated transport in synapse	5.22E-07
GO:0035249	synaptic transmission, glutamatergic	6.39E-07
GO:0006941	striated muscle contraction	7.22E-07
GO:0097014	ciliary plasm	7.34E-07
GO:0045664	regulation of neuron differentiation	7.48E-07
GO:0005930	axoneme	8.43E-07
GO:0032838	plasma membrane bounded cell projection cytoplasm	9.43E-07
GO:0031674	I band	9.72E-07
GO:0003700	DNA-binding transcription factor activity	1.25E-06
GO:0017156	calcium ion regulated exocytosis	1.29E-06
GO:0097485	neuron projection guidance	1.42E-06
GO:0017158	regulation of calcium ion-dependent exocytosis	1.45E-06
GO:0043679	axon terminus	1.64E-06
GO:2000300	regulation of synaptic vesicle exocytosis	1.80E-06
GO:0007411	axon guidance	2.09E-06
GO:0048489	synaptic vesicle transport	2.10E-06
GO:0097480	establishment of synaptic vesicle localization	2.10E-06
GO:0015077	monovalent inorganic cation transmembrane transporter act	2.25E-06
GO:0051962	positive regulation of nervous system development	2.72E-06
GO:0032589	neuron projection membrane	2.90E-06
GO:0070588	calcium ion transmembrane transport	2.95E-06
GO:0000981	DNA-binding transcription factor activity, RNA polymeras	3.21E-06
GO:0099095	ligand-gated anion channel activity	3.24E-06
GO:2000463	positive regulation of excitatory postsynaptic potential	3.35E-06
GO:0015081	sodium ion transmembrane transporter activity	3.92E-06
GO:0099094	ligand-gated cation channel activity	4.37E-06
GO:0007417	central nervous system development	4.49E-06
GO:0016247	channel regulator activity	4.66E-06
GO:0050890	cognition	4.68E-06
GO:0001653	peptide receptor activity	4.84E-06
GO:0008021	synaptic vesicle	5.01E-06
GO:0043266	regulation of potassium ion transport	5.71E-06
GO:0042383	sarcolemma	5.72E-06
GO:0030018	Z disc	5.93E-06
GO:0035082	axoneme assembly	6.27E-06
GO:0008528	G protein-coupled peptide receptor activity	6.44E-06
GO:0019226	transmission of nerve impulse	7.07E-06
GO:0099560	synaptic membrane adhesion	7.93E-06
GO:2000311	regulation of AMPA receptor activity	7.93E-06
GO:0070382	exocytic vesicle	8.48E-06
GO:0098693	regulation of synaptic vesicle cycle	8.76E-06
GO:1904064	positive regulation of cation transmembrane transport	1.02E-05
GO:0016917	GABA receptor activity	1.13E-05
GO:0048589	developmental growth	1.29E-05
GO:0030672	synaptic vesicle membrane	1.36E-05
GO:0099501	exocytic vesicle membrane	1.36E-05
GO:0050877	nervous system process	1.37E-05
GO:0006814	sodium ion transport	1.41E-05
GO:0007193	adenylate cyclase-inhibiting G protein-coupled receptor sig	1.41E-05
GO:0016324	apical plasma membrane	1.71E-05
GO:0060076	excitatory synapse	1.71E-05
GO:0010001	glial cell differentiation	1.81E-05
GO:1902710	GABA receptor complex	1.82E-05
GO:0032590	dendrite membrane	1.99E-05
GO:0035725	sodium ion transmembrane transport	2.16E-05

GO:0005249	voltage-gated potassium channel activity	2.86E-05
GO:0044449	contractile fiber part	3.51E-05
GO:0050805	negative regulation of synaptic transmission	3.51E-05
GO:0000977	RNA polymerase II regulatory region sequence-specific DN	3.69E-05
GO:0001012	RNA polymerase II regulatory region DNA binding	3.69E-05
GO:0034706	sodium channel complex	3.71E-05
GO:0006821	chloride transport	3.95E-05
GO:0008188	neuropeptide receptor activity	3.95E-05
GO:1902711	GABA-A receptor complex	4.75E-05
GO:0007612	learning	5.64E-05
GO:0042063	gliogenesis	5.88E-05
GO:0015893	drug transport	6.01E-05
GO:0034707	chloride channel complex	6.44E-05
GO:0005237	inhibitory extracellular ligand-gated ion channel activity	6.61E-05
GO:1901379	regulation of potassium ion transmembrane transport	6.74E-05
GO:0099568	cytoplasmic region	7.12E-05
GO:0005254	chloride channel activity	7.40E-05
GO:2000310	regulation of NMDA receptor activity	7.67E-05
GO:0034767	positive regulation of ion transmembrane transport	8.49E-05
GO:0007420	brain development	9.01E-05
GO:0099173	postsynapse organization	9.63E-05
GO:1903779	regulation of cardiac conduction	0.00011
GO:0070252	actin-mediated cell contraction	0.00011
GO:0007626	locomotory behavior	0.00011
GO:0051932	synaptic transmission, GABAergic	0.00012
GO:0043292	contractile fiber	0.00012
GO:0072562	blood microparticle	0.00013
GO:1903169	regulation of calcium ion transmembrane transport	0.00014
GO:0030017	sarcomere	0.00014
GO:0098656	anion transmembrane transport	0.00014
GO:0001578	microtubule bundle formation	0.00015
GO:0035418	protein localization to synapse	0.00015
GO:0005253	anion channel activity	0.00015
GO:0050954	sensory perception of mechanical stimulus	0.00016
GO:0015108	chloride transmembrane transporter activity	0.00017
GO:0031346	positive regulation of cell projection organization	0.00017
GO:0005231	excitatory extracellular ligand-gated ion channel activity	0.00018
GO:0004890	GABA-A receptor activity	0.00019
GO:0010469	regulation of signaling receptor activity	0.00022
GO:0032281	AMPA glutamate receptor complex	0.00022
GO:0033268	node of Ranvier	0.00022
GO:0015698	inorganic anion transport	0.00025
GO:0044447	axoneme part	0.00025
GO:0002027	regulation of heart rate	0.00025
GO:0060048	cardiac muscle contraction	0.00025
GO:0003341	cilium movement	0.00025
GO:0048786	presynaptic active zone	0.00028
GO:0016529	sarcoplasmic reticulum	0.00029
GO:0007214	gamma-aminobutyric acid signaling pathway	0.00034
GO:0099054	presynapse assembly	0.00038
GO:0048638	regulation of developmental growth	0.00042
GO:0034704	calcium channel complex	0.00043
GO:1902476	chloride transmembrane transport	0.00051
GO:0022851	GABA-gated chloride ion channel activity	0.00052
GO:0016358	dendrite development	0.00052
GO:0005891	voltage-gated calcium channel complex	0.00053
GO:0055001	muscle cell development	0.00053
GO:0030315	T-tubule	0.00054
GO:0007605	sensory perception of sound	0.00054
GO:0050769	positive regulation of neurogenesis	0.00055
GO:0010976	positive regulation of neuron projection development	0.00056
GO:0099172	presynapse organization	0.00057
GO:0015103	inorganic anion transmembrane transporter activity	0.00058
GO:0051963	regulation of synapse assembly	0.00058
GO:0008344	adult locomotory behavior	0.00058
GO:0086003	cardiac muscle cell contraction	0.00058
GO:0033017	sarcoplasmic reticulum membrane	0.00058
GO:0016528	sarcoplasm	0.00059
GO:0030016	myofibril	0.00061
GO:0005272	sodium channel activity	0.00061
GO:0099084	postsynaptic specialization organization	0.00068
GO:0007613	memory	0.00072

GO:0099068	postsynapse assembly	0.00073
GO:0043194	axon initial segment	0.00076
GO:0086001	cardiac muscle cell action potential	0.00077
GO:0048709	oligodendrocyte differentiation	0.0008
GO:0048813	dendrite morphogenesis	0.00083
GO:0060291	long-term synaptic potentiation	0.00086
GO:0007018	microtubule-based movement	0.00086
GO:0060322	head development	0.00086
GO:0051952	regulation of amine transport	0.00089
GO:0099106	ion channel regulator activity	0.0009
GO:0051924	regulation of calcium ion transport	0.00096
GO:0044298	cell body membrane	0.00097
GO:0033555	multicellular organismal response to stress	0.00098
GO:0046883	regulation of hormone secretion	0.00105
GO:0009582	detection of abiotic stimulus	0.00105
GO:0015837	amine transport	0.00109
GO:0001764	neuron migration	0.00111
GO:0043195	terminal bouton	0.00117
GO:0034764	positive regulation of transmembrane transport	0.00121
GO:0050803	regulation of synapse structure or activity	0.00123
GO:0001662	behavioral fear response	0.00123
GO:1901606	alpha-amino acid catabolic process	0.00127
GO:0055002	striated muscle cell development	0.00127
GO:0051966	regulation of synaptic transmission, glutamatergic	0.00127
GO:0015844	monoamine transport	0.00129
GO:0048588	developmental cell growth	0.00129
GO:0045666	positive regulation of neuron differentiation	0.00136
GO:0009914	hormone transport	0.00138
GO:0019228	neuronal action potential	0.00138
GO:0099175	regulation of postsynapse organization	0.00143
GO:0060292	long-term synaptic depression	0.00144
GO:0098698	postsynaptic specialization assembly	0.00147
GO:0004970	ionotropic glutamate receptor activity	0.00149
GO:2001259	positive regulation of cation channel activity	0.00157
GO:0048640	negative regulation of developmental growth	0.00165
GO:0051965	positive regulation of synapse assembly	0.00165
GO:0097730	non-motile cilium	0.00168
GO:0009581	detection of external stimulus	0.00172
GO:0010752	regulation of cGMP-mediated signaling	0.00181
GO:0006937	regulation of muscle contraction	0.00186
GO:0050807	regulation of synapse organization	0.00188
GO:0019233	sensory perception of pain	0.00189
GO:0010721	negative regulation of cell development	0.00192
GO:0001917	photoreceptor inner segment	0.00199
GO:0044325	ion channel binding	0.00205
GO:0008277	regulation of G protein-coupled receptor signaling pathway	0.00207
GO:0010769	regulation of cell morphogenesis involved in differentiation	0.00207
GO:0002209	behavioral defense response	0.00208
GO:0032809	neuronal cell body membrane	0.00216
GO:0098563	intrinsic component of synaptic vesicle membrane	0.00235
GO:0050910	detection of mechanical stimulus involved in sensory percep	0.00235
GO:0098739	import across plasma membrane	0.00236
GO:0030239	myofibril assembly	0.00245
GO:0097106	postsynaptic density organization	0.00246
GO:0008509	anion transmembrane transporter activity	0.00246
GO:0032414	positive regulation of ion transmembrane transporter activit	0.00247
GO:0030048	actin filament-based movement	0.00247
GO:0051937	catecholamine transport	0.00253
GO:0009063	cellular amino acid catabolic process	0.00254
GO:0042552	myelination	0.0027
GO:1901019	regulation of calcium ion transmembrane transporter activit	0.00285
GO:0098659	inorganic cation import across plasma membrane	0.00286
GO:0099587	inorganic ion import across plasma membrane	0.00286
GO:0031225	anchored component of membrane	0.00296
GO:0035235	ionotropic glutamate receptor signaling pathway	0.00305
GO:0042596	fear response	0.00311
GO:0045823	positive regulation of heart contraction	0.00311
GO:0007422	peripheral nervous system development	0.00319
GO:0097553	calcium ion transmembrane import into cytosol	0.00324
GO:0043268	positive regulation of potassium ion transport	0.00334
GO:0050770	regulation of axonogenesis	0.00344
GO:0046879	hormone secretion	0.00344

GO:0032411	positive regulation of transporter activity	0.00344
GO:0060402	calcium ion transport into cytosol	0.00367
GO:0004983	neuropeptide Y receptor activity	0.00379
GO:0042472	inner ear morphogenesis	0.00379
GO:0042562	hormone binding	0.004
GO:0060560	developmental growth involved in morphogenesis	0.00401
GO:0016323	basolateral plasma membrane	0.00406
GO:0042923	neuropeptide binding	0.00411
GO:0010644	cell communication by electrical coupling	0.00423
GO:0007272	ensheathment of neurons	0.00426
GO:0008366	axon ensheathment	0.00426
GO:0070509	calcium ion import	0.00441
GO:0060401	cytosolic calcium ion transport	0.00452
GO:0099174	regulation of presynapse organization	0.00461
GO:1905606	regulation of presynapse assembly	0.00461
GO:0035176	social behavior	0.00464
GO:0051703	intraspecies interaction between organisms	0.00464
GO:0050771	negative regulation of axonogenesis	0.00464
GO:0010927	cellular component assembly involved in morphogenesis	0.00486
GO:0051899	membrane depolarization	0.00506
GO:0030285	integral component of synaptic vesicle membrane	0.00516
GO:0022011	myelination in peripheral nervous system	0.00539
GO:0032292	peripheral nervous system axon ensheathment	0.00539
GO:0010771	negative regulation of cell morphogenesis involved in diffe	0.00578
GO:0098661	inorganic anion transmembrane transport	0.00591
GO:0051961	negative regulation of nervous system development	0.00596
GO:0007601	visual perception	0.00629
GO:0007389	pattern specification process	0.00633
GO:0050768	negative regulation of neurogenesis	0.00633
GO:0050953	sensory perception of light stimulus	0.00656
GO:0043583	ear development	0.00688
GO:0099569	presynaptic cytoskeleton	0.00735
GO:0017157	regulation of exocytosis	0.00749
GO:0010720	positive regulation of cell development	0.00781
GO:0015800	acidic amino acid transport	0.00781
GO:1903524	positive regulation of blood circulation	0.00781
GO:0022604	regulation of cell morphogenesis	0.00782
GO:0050974	detection of mechanical stimulus involved in sensory perce	0.00786
GO:0008066	glutamate receptor activity	0.00804
GO:1901016	regulation of potassium ion transmembrane transporter acti	0.00837
GO:0042165	neurotransmitter binding	0.00888
GO:0050796	regulation of insulin secretion	0.009
GO:0090276	regulation of peptide hormone secretion	0.00929
GO:0031345	negative regulation of cell projection organization	0.00942
GO:1903305	regulation of regulated secretory pathway	0.00955
GO:0042471	ear morphogenesis	0.00955
GO:0099528	G protein-coupled neurotransmitter receptor activity	0.01006
GO:0061669	spontaneous neurotransmitter secretion	0.01025
GO:0048839	inner ear development	0.01034
GO:0008307	structural constituent of muscle	0.01112
GO:1990138	neuron projection extension	0.01131
GO:0045956	positive regulation of calcium ion-dependent exocytosis	0.01149
GO:0015085	calcium ion transmembrane transporter activity	0.01153
GO:0031594	neuromuscular junction	0.01158
GO:0006942	regulation of striated muscle contraction	0.01177
GO:0086002	cardiac muscle cell action potential involved in contraction	0.01186
GO:0001518	voltage-gated sodium channel complex	0.01204
GO:0021885	forebrain cell migration	0.01205
GO:0045665	negative regulation of neuron differentiation	0.0126
GO:0043950	positive regulation of cAMP-mediated signaling	0.01275
GO:0097107	postsynaptic density assembly	0.01318
GO:0021795	cerebral cortex cell migration	0.0134
GO:0002028	regulation of sodium ion transport	0.01356
GO:0043198	dendritic shaft	0.01384
GO:0030072	peptide hormone secretion	0.01402
GO:0048639	positive regulation of developmental growth	0.01424
GO:0051146	striated muscle cell differentiation	0.01424
GO:0031045	dense core granule	0.0146
GO:0045214	sarcomere organization	0.01552
GO:0010522	regulation of calcium ion transport into cytosol	0.01587
GO:0098686	hippocampal mossy fiber to CA3 synapse	0.01587
GO:0019934	cGMP-mediated signaling	0.01599

GO:0050982	detection of mechanical stimulus	0.0169
GO:0030073	insulin secretion	0.01802
GO:0005858	axonemal dynein complex	0.01845
GO:0031630	regulation of synaptic vesicle fusion to presynaptic active z	0.01846
GO:0060997	dendritic spine morphogenesis	0.01846
GO:1901381	positive regulation of potassium ion transmembrane transpo	0.01846
GO:0015872	dopamine transport	0.01949
GO:0005262	calcium channel activity	0.01991
GO:1905114	cell surface receptor signaling pathway involved in cell-cell	0.02163
GO:0022029	telencephalon cell migration	0.02163
GO:0051705	multi-organism behavior	0.02163
GO:0090257	regulation of muscle system process	0.02163
GO:0007528	neuromuscular junction development	0.02234
GO:0031280	negative regulation of cyclase activity	0.02368
GO:0043949	regulation of cAMP-mediated signaling	0.02386
GO:0090596	sensory organ morphogenesis	0.02456
GO:0050432	catecholamine secretion	0.02462
GO:0086065	cell communication involved in cardiac conduction	0.02462
GO:0005516	calmodulin binding	0.02464
GO:0046658	anchored component of plasma membrane	0.02497
GO:0051968	positive regulation of synaptic transmission, glutamatergic	0.02576
GO:0004181	metallocarboxypeptidase activity	0.02578
GO:0031253	cell projection membrane	0.02637
GO:0007618	mating	0.02658
GO:0098814	spontaneous synaptic transmission	0.02658
GO:0016082	synaptic vesicle priming	0.02658
GO:0050773	regulation of dendrite development	0.02683
GO:0007158	neuron cell-cell adhesion	0.02732
GO:0055117	regulation of cardiac muscle contraction	0.02749
GO:0001504	neurotransmitter uptake	0.02757
GO:0050433	regulation of catecholamine secretion	0.02757
GO:0050879	multicellular organismal movement	0.02757
GO:0050881	musculoskeletal movement	0.02757
GO:0010977	negative regulation of neuron projection development	0.02987
GO:1904427	positive regulation of calcium ion transmembrane transport	0.03158
GO:1990573	potassium ion import across plasma membrane	0.03328
GO:0008503	benzodiazepine receptor activity	0.03331
GO:0005248	voltage-gated sodium channel activity	0.03368
GO:0086010	membrane depolarization during action potential	0.03412
GO:0014704	intercalated disc	0.0345
GO:0050905	neuromuscular process	0.03511
GO:0098858	actin-based cell projection	0.03793
GO:0006835	dicarboxylic acid transport	0.03805
GO:0097120	receptor localization to synapse	0.03805
GO:1902475	L-alpha-amino acid transmembrane transport	0.03805
GO:0005245	voltage-gated calcium channel activity	0.03905
GO:0022848	acetylcholine-gated cation-selective channel activity	0.03905
GO:0032228	regulation of synaptic transmission, GABAergic	0.03924
GO:0021953	central nervous system neuron differentiation	0.04108
GO:0086009	membrane repolarization	0.04162
GO:0017046	peptide hormone binding	0.04166
GO:0045745	positive regulation of G protein-coupled receptor signaling	0.04518
GO:0042692	muscle cell differentiation	0.04562
GO:0030658	transport vesicle membrane	0.04563
GO:0007631	feeding behavior	0.0467
GO:0001750	photoreceptor outer segment	0.04724
GO:0060170	ciliary membrane	0.04724
GO:0005540	hyaluronic acid binding	0.04758