Table S1 Gene ontology categories identified by ALIGATOR analysis of the AD GWA data of Harold and colleagues.[1]

The 589 genes identified as having GWAS SNP signals p < 0.001 were used: APOE was included in the gene list. In this analysis one SNP was not allowed to add more than one gene to any gene ontology category. “Study-wide p-value” is the probability of obtaining by chance at least one GO category with a category-specific enrichment p-value at least as significant as that observed.

GO process	Type	total genes in category	#genes on list	p-value	Study-wide corrected p-value	Function
GO:0032488	PROCESS	4	3	<1.00E-05	0.042	Cdc42 protein signal transduction
GO:0033700	PROCESS	8	4	<1.00E-05	0.042	phospholipid efflux
GO:0043691	PROCESS	14	7	<1.00E-05	0.042	reverse cholesterol transport
GO:0030301	PROCESS	34	8	<1.00E-05	0.042	cholesterol transport
GO:0015918	PROCESS	34	8	<1.00E-05	0.042	sterol transport
GO:0034369	PROCESS	18	6	<1.00E-05	0.042	plasma lipoprotein particle remodeling
GO:0034368	PROCESS	18	6	<1.00E-05	0.042	protein-lipid complex remodeling
GO:0034367	PROCESS	18	6	<1.00E-05	0.042	macromolecular complex remodeling
GO:0034375	PROCESS	11	5	<1.00E-05	0.042	high-density lipoprotein particle remodeling
GO:0034382	PROCESS	3	3	<1.00E-05	0.042	chylomicron remnant clearance
GO:0016125	PROCESS	87	11	2.00E-05	0.066	sterol metabolic process
GO:0034364	CELLULAR	20	5	2.00E-05	0.066	high-density lipoprotein particle
GO:0022411	PROCESS	55	8	2.00E-05	0.066	cellular component disassembly
GO:0006958	PROCESS	28	6	2.00E-05	0.066	complement activation, classical pathway
GO:0002455	PROCESS	28	6	2.00E-05	0.066	humoral immune response mediated by circulating immunoglobulin
GO:0042632	PROCESS	33	7	4.00E-05	0.093	cholesterol homeostasis
GO:0055092	PROCESS	33	7	4.00E-05	0.093	sterol homeostasis
GO:0006956	PROCESS	37	6	4.00E-05	0.093	complement activation
GO:0002541	PROCESS	38	6	4.00E-05	0.093	activation of plasma proteins involved in acute inflammatory response
GO:0045087	PROCESS	120	11	6.00E-05	0.113	innate immune response
GO:0008203	PROCESS	78	10	8.00E-05	0.129	cholesterol metabolic process
GO:0034384	PROCESS	5	3	1.00E-04	0.146	high-density lipoprotein particle clearance
GO:0032984	PROCESS	34	6	1.40E-04	0.192	macromolecular complex disassembly
GO:0032376	PROCESS	7	3	1.80E-04	0.226	positive regulation of cholesterol transport
GO:0032373	PROCESS	7	3	1.80E-04	0.226	positive regulation of sterol transport
GO:0010873	PROCESS	6	3	2.00E-04	0.250	positive regulation of cholesterol esterification
GO:0030001	PROCESS	410	36	2.20E-04	0.279	metal ion transport
GO:0034372	PROCESS	6	3	2.20E-04	0.279	very-low-density lipoprotein particle remodeling
GO:0008202	PROCESS	174	15	2.40E-04	0.294	steroid metabolic process
GO:0055088	PROCESS	43	7	2.60E-04	0.316	lipid homeostasis
GO:0006869	PROCESS	131	14	2.80E-04	0.336	lipid transport
GO:0034366	CELLULAR	7	3	2.80E-04	0.336	spherical high-density lipoprotein particle
GO:0034363	CELLULAR	3	2	2.80E-04	0.336	intermediate-density lipoprotein particle
GO:0006812	PROCESS	494	38	3.60E-04	0.404	cation transport
GO:0060228	FUNCTION	4	2	3.60E-04	0.404	phosphatidylcholine-sterol O-acyltransferase activator activity
GO:0032370	PROCESS	9	3	3.60E-04	0.404	positive regulation of lipid transport
GO:0032374	PROCESS	17	4	4.40E-04	0.455	regulation of cholesterol transport
GO:0032371	PROCESS	17	4	4.40E-04	0.455	regulation of sterol transport
GO:0010876	PROCESS	142	14	4.80E-04	0.487	lipid localization
GO:0016485	PROCESS	95	10	4.80E-04	0.487	protein processing
GO:0016064	PROCESS	44	6	4.80E-04	0.487	immunoglobulin mediated immune response
GO:0034370	PROCESS	8	3	5.00E-04	0.505	triglyceride-rich lipoprotein particle remodeling
GO:0019724	PROCESS	46	6	5.80E-04	0.549	B cell mediated immunity
GO:0032395	FUNCTION	8	4	5.80E-04	0.549	MHC class II receptor activity
GO:0043933	PROCESS	512	25	6.00E-04	0.563	macromolecular complex subunit organization
GO:0015672	PROCESS	291	25	6.00E-04	0.563	monovalent inorganic cation transport
GO:0034358	CELLULAR	30	5	6.40E-04	0.580	plasma lipoprotein particle
GO:0032994	CELLULAR	30	5	6.40E-04	0.580	protein-lipid complex
GO:0034381	PROCESS	14	4	6.40E-04	0.580	lipoprotein particle clearance
GO:0070328	PROCESS	6	3	6.40E-04	0.580	triglyceride homeostasis
GO:0051604	PROCESS	104	10	7.20E-04	0.618	protein maturation
GO:0034380	PROCESS	5	3	7.60E-04	0.635	high-density lipoprotein particle assembly
GO:0048584	PROCESS	167	13	8.00E-04	0.648	positive regulation of response to stimulus
GO:0044242	PROCESS	80	8	8.60E-04	0.671	cellular lipid catabolic process
GO:0050746	PROCESS	7	3	8.80E-04	0.675	regulation of lipoprotein metabolic process
GO:0016042	PROCESS	155	12	9.00E-04	0.681	lipid catabolic process
GO:0002526	PROCESS	74	7	9.40E-04	0.700	acute inflammatory response
GO:0004875	FUNCTION	3	2	1.12E-03	0.757	complement receptor activity
GO:0006707	PROCESS	9	3	1.14E-03	0.759	cholesterol catabolic process
GO:0016127	PROCESS	9	3	1.14E-03	0.759	sterol catabolic process
GO:0010872	PROCESS	7	3	1.20E-03	0.772	regulation of cholesterol esterification
GO:0006955	PROCESS	576	25	1.26E-03	0.792	immune response
GO:0006959	PROCESS	68	7	1.30E-03	0.804	humoral immune response
GO:0002253	PROCESS	66	7	1.32E-03	0.809	activation of immune response
GO:0042613	CELLULAR	12	4	1.88E-03	0.912	MHC class II protein complex
GO:0004908	FUNCTION	6	3	1.88E-03	0.912	interleukin-1 receptor activity
GO:0002449	PROCESS	56	6	2.00E-03	0.921	lymphocyte mediated immunity
GO:0008324	FUNCTION	493	35	2.18E-03	0.937	cation transmembrane transporter activity
GO:0002504	PROCESS	15	4	2.32E-03	0.952	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II

GO:0002460	PROCESS	61	6	2.36E-03	0.953	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
GO:0002250	PROCESS	61	6	2.36E-03	0.953	adaptive immune response
GO:0032368	PROCESS	25	4	2.46E-03	0.960	regulation of lipid transport
GO:0006811	PROCESS	690	45	2.48E-03	0.961	ion transport
GO:0001836	PROCESS	16	3	2.58E-03	0.963	release of cytochrome c from mitochondria
GO:0004872	FUNCTION	1518	67	2.74E-03	0.971	receptor activity
GO:0010984	PROCESS	4	2	2.78E-03	0.973	regulation of lipoprotein particle clearance
GO:0051605	PROCESS	65	7	2.82E-03	0.974	protein maturation by peptide bond cleavage
GO:0042592	PROCESS	545	29	3.02E-03	0.980	homeostatic process
GO:0019966	FUNCTION	9	3	3.16E-03	0.981	interleukin-1 binding
GO:0034377	PROCESS	11	3	3.18E-03	0.981	plasma lipoprotein particle assembly
GO:0065005	PROCESS	11	3	3.18E-03	0.981	protein-lipid complex assembly
GO:0010875	PROCESS	6	2	3.54E-03	0.984	positive regulation of cholesterol efflux
GO:0048878	PROCESS	382	23	3.66E-03	0.986	chemical homeostasis
GO:0002376	PROCESS	811	32	3.68E-03	0.986	immune system process
GO:0004871	FUNCTION	1932	83	3.90E-03	0.991	signal transducer activity
GO:0060089	FUNCTION	1932	83	3.90E-03	0.991	molecular transducer activity
GO:0034443	PROCESS	3	2	3.92E-03	0.991	negative regulation of lipoprotein oxidation
GO:0034442	PROCESS	3	2	3.92E-03	0.991	regulation of lipoprotein oxidation
GO:0007266	PROCESS	32	5	3.98E-03	0.991	Rho protein signal transduction
GO:0002443	PROCESS	66	6	4.10E-03	0.991	leukocyte mediated immunity
GO:0031420	FUNCTION	222	20	4.40E-03	0.994	alkali metal ion binding
GO:0042176	PROCESS	59	6	4.48E-03	0.994	regulation of protein catabolic process
GO:0015075	FUNCTION	649	43	4.86E-03	0.996	ion transmembrane transporter activity
GO:0022857	FUNCTION	818	50	4.92E-03	0.996	transmembrane transporter activity
GO:0016126	PROCESS	30	4	5.26E-03	0.996	sterol biosynthetic process
GO:0031402	FUNCTION	113	12	5.34E-03	0.996	sodium ion binding
GO:0004806	FUNCTION	15	3	5.36E-03	0.996	triglyceride lipase activity
GO:0005261	FUNCTION	252	23	5.52E-03	0.997	cation channel activity
GO:0051000	PROCESS	7	2	5.60E-03	0.997	positive regulation of nitric-oxide synthase activity
GO:0051702	PROCESS	7	2	5.72E-03	0.997	interaction with symbiont
GO:0005215	FUNCTION	1074	57	6.40E-03	0.999	transporter activity
GO:0005249	FUNCTION	94	10	6.94E-03	1.000	voltage-gated potassium channel activity
GO:0002684	PROCESS	164	10	7.16E-03	1.000	positive regulation of immune system process
GO:0006706	PROCESS	16	3	7.16E-03	1.000	steroid catabolic process
GO:0006810	PROCESS	2330	96	7.26E-03	1.000	transport
GO:0045940	PROCESS	11	3	7.50E-03	1.000	positive regulation of steroid metabolic process
GO:0008637	PROCESS	24	3	7.56E-03	1.000	apoptotic mitochondrial changes
GO:0000300	CELLULAR	3	2	7.70E-03	1.000	peripheral to membrane of membrane fraction
GO:0008633	PROCESS	21	3	7.80E-03	1.000	activation of pro-apoptotic gene products
GO:0048583	PROCESS	332	17	8.04E-03	1.000	regulation of response to stimulus
GO:0034186	FUNCTION	3	2	8.06E-03	1.000	apolipoprotein A-I binding
GO:0046873	FUNCTION	296	25	8.06E-03	1.000	metal ion transmembrane transporter activity
GO:0006813	PROCESS	146	14	8.10E-03	1.000	potassium ion transport
GO:0051055	PROCESS	10	2	8.12E-03	1.000	negative regulation of lipid biosynthetic process
GO:0010874	PROCESS	7	2	8.18E-03	1.000	regulation of cholesterol efflux
GO:0022836	FUNCTION	284	25	8.20E-03	1.000	gated channel activity
GO:0006814	PROCESS	120	12	8.74E-03	1.000	sodium ion transport
GO:0006694	PROCESS	71	6	8.92E-03	1.000	steroid biosynthetic process
GO:0008076	CELLULAR	80	9	8.92E-03	1.000	voltage-gated potassium channel complex
GO:0034705	CELLULAR	80	9	8.92E-03	1.000	potassium channel complex
GO:0015914	PROCESS	28	6	8.96E-03	1.000	phospholipid transport
GO:0006695	PROCESS	21	3	8.96E-03	1.000	cholesterol biosynthetic process
GO:0009593	PROCESS	29	5	9.18E-03	1.000	detection of chemical stimulus
GO:0002252	PROCESS	95	7	9.42E-03	1.000	immune effector process
GO:0051234	PROCESS	2352	96	9.60E-03	1.000	establishment of localization
GO:0030162	PROCESS	41	4	9.66E-03	1.000	regulation of proteolysis
GO:0046470	PROCESS	16	3	9.66E-03	1.000	phosphatidylcholine metabolic process
GO:0050778	PROCESS	93	7	1.00E-02	1.000	positive regulation of immune response
GO:0042627	CELLULAR	10	2	1.01E-02	1.000	chylomicron
GO:0005267	FUNCTION	124	12	1.01E-02	1.000	potassium channel activity
GO:0009894	PROCESS	91	7	1.03E-02	1.000	regulation of catabolic process
GO:0034703	CELLULAR	123	13	1.04E-02	1.000	cation channel complex
GO:0001772	CELLULAR	7	2	1.07E-02	1.000	immunological synapse
GO:0065003	PROCESS	465	19	1.11E-02	1.000	macromolecular complex assembly
GO:0033017	CELLULAR	13	4	1.18E-02	1.000	sarcoplasmic reticulum membrane
GO:0031232	CELLULAR	4	2	1.23E-02	1.000	extrinsic to external side of plasma membrane
GO:0001848	FUNCTION	8	2	1.26E-02	1.000	complement binding
GO:0034185	FUNCTION	10	3	1.26E-02	1.000	apolipoprotein binding
GO:0009896	PROCESS	44	4	1.33E-02	1.000	positive regulation of catabolic process
GO:0051044	PROCESS	9	2	1.36E-02	1.000	positive regulation of membrane protein ectodomain proteolysis
GO:0017127	FUNCTION	12	3	1.42E-02	1.000	cholesterol transporter activity
GO:0046661	PROCESS	45	4	1.42E-02	1.000	male sex differentiation
GO:0015271	FUNCTION	4	2	1.45E-02	1.000	outward rectifier potassium channel activity
GO:0022843	FUNCTION	134	13	1.47E-02	1.000	voltage-gated cation channel activity
GO:0050748	PROCESS	6	2	1.51E-02	1.000	negative regulation of lipoprotein metabolic process
GO:0022891	FUNCTION	751	44	1.57E-02	1.000	substrate-specific transmembrane transporter activity
GO:0045732	PROCESS	25	3	1.57E-02	1.000	positive regulation of protein catabolic process

GO:0007271	PROCESS	13	2	1.57E-02	1.000	synaptic transmission, cholinergic
GO:0005892	CELLULAR	13	2	1.58E-02	1.000	nicotinic acetylcholine-gated receptor-channel complex
GO:0022892	FUNCTION	880	48	1.61E-02	1.000	substrate-specific transporter activity
GO:0009056	PROCESS	1484	50	1.61E-02	1.000	catabolic process
GO:0034702	CELLULAR	187	16	1.66E-02	1.000	ion channel complex
GO:0015267	FUNCTION	373	28	1.66E-02	1.000	channel activity
GO:0022803	FUNCTION	373	28	1.66E-02	1.000	passive transmembrane transporter activity
GO:0019433	PROCESS	6	2	1.84E-02	1.000	triglyceride catabolic process
GO:0004091	FUNCTION	91	6	1.90E-02	1.000	carboxylesterase activity
GO:0016459	CELLULAR	62	7	1.93E-02	1.000	myosin complex
GO:0060155	PROCESS	4	2	1.94E-02	1.000	platelet dense granule organization
GO:0015248	FUNCTION	14	3	1.98E-02	1.000	sterol transporter activity
GO:0051353	PROCESS	22	3	1.98E-02	1.000	positive regulation of oxidoreductase activity
GO:0032770	PROCESS	11	2	2.00E-02	1.000	positive regulation of monooxygenase activity
GO:0004620	FUNCTION	80	7	2.08E-02	1.000	phospholipase activity
GO:0003950	FUNCTION	25	3	2.12E-02	1.000	NAD+ ADP-ribosyltransferase activity
GO:0012502	PROCESS	228	12	2.20E-02	1.000	induction of programmed cell death
GO:0006874	PROCESS	127	9	2.26E-02	1.000	cellular calcium ion homeostasis
GO:0002682	PROCESS	280	13	2.30E-02	1.000	regulation of immune system process
GO:0004889	FUNCTION	16	2	2.34E-02	1.000	nicotinic acetylcholine-activated cation-selective channel activity
GO:0005216	FUNCTION	355	27	2.34E-02	1.000	ion channel activity
GO:0046464	PROCESS	7	2	2.34E-02	1.000	acylglycerol catabolic process
GO:0044269	PROCESS	7	2	2.34E-02	1.000	glycerol ether catabolic process
GO:0046461	PROCESS	7	2	2.34E-02	1.000	neutral lipid catabolic process
GO:0008238	FUNCTION	72	7	2.39E-02	1.000	exopeptidase activity
GO:0055074	PROCESS	130	9	2.41E-02	1.000	calcium ion homeostasis
GO:0030005	PROCESS	163	10	2.48E-02	1.000	cellular di-, tri-valent inorganic cation homeostasis
GO:0009395	PROCESS	19	3	2.53E-02	1.000	phospholipid catabolic process
GO:0042802	FUNCTION	517	25	2.61E-02	1.000	identical protein binding
GO:0005543	FUNCTION	153	11	2.63E-02	1.000	phospholipid binding
GO:0033344	PROCESS	15	3	2.68E-02	1.000	cholesterol efflux
GO:0004181	FUNCTION	25	4	2.69E-02	1.000	metallocarboxypeptidase activity
GO:0022838	FUNCTION	365	27	2.74E-02	1.000	substrate-specific channel activity
GO:0005184	FUNCTION	19	2	2.77E-02	1.000	neuropeptide hormone activity
GO:0005244	FUNCTION	177	15	2.77E-02	1.000	voltage-gated ion channel activity
GO:0022832	FUNCTION	177	15	2.77E-02	1.000	voltage-gated channel activity
GO:0006629	PROCESS	733	30	2.81E-02	1.000	lipid metabolic process
GO:0007218	PROCESS	81	7	2.85E-02	1.000	neuropeptide signaling pathway
GO:0016763	FUNCTION	45	4	2.91E-02	1.000	transferase activity, transferring pentosyl groups
GO:0016455	FUNCTION	27	3	2.92E-02	1.000	RNA polymerase II transcription mediator activity
GO:0055066	PROCESS	173	10	2.94E-02	1.000	di-, tri-valent inorganic cation homeostasis
GO:0050801	PROCESS	301	17	2.96E-02	1.000	ion homeostasis
GO:0031202	FUNCTION	24	2	2.97E-02	1.000	RNA splicing factor activity, transesterification mechanism
GO:0050776	PROCESS	152	8	2.98E-02	1.000	regulation of immune response
GO:0032312	PROCESS	27	3	3.01E-02	1.000	regulation of ARF GTPase activity
GO:0007159	PROCESS	21	3	3.11E-02	1.000	leukocyte adhesion
GO:0042611	CELLULAR	34	4	3.16E-02	1.000	MHC protein complex
GO:0007548	PROCESS	98	6	3.18E-02	1.000	sex differentiation
GO:0008060	FUNCTION	28	3	3.20E-02	1.000	ARF GTPase activator activity
GO:0001942	PROCESS	26	3	3.21E-02	1.000	hair follicle development
GO:0022405	PROCESS	26	3	3.21E-02	1.000	hair cycle process
GO:0022404	PROCESS	26	3	3.21E-02	1.000	molting cycle process
GO:0052548	PROCESS	68	5	3.28E-02	1.000	regulation of endopeptidase activity
GO:0070325	FUNCTION	15	2	3.30E-02	1.000	lipoprotein receptor binding
GO:0006919	PROCESS	45	4	3.34E-02	1.000	activation of caspase activity
GO:0042633	PROCESS	27	3	3.42E-02	1.000	hair cycle
GO:0042303	PROCESS	27	3	3.42E-02	1.000	molting cycle
GO:0005545	FUNCTION	21	3	3.44E-02	1.000	phosphatidylinositol binding
GO:0006461	PROCESS	325	15	3.51E-02	1.000	protein complex assembly
GO:0070271	PROCESS	325	15	3.51E-02	1.000	protein complex biogenesis
GO:0050999	PROCESS	12	2	3.52E-02	1.000	regulation of nitric-oxide synthase activity
GO:0001530	FUNCTION	11	2	3.59E-02	1.000	lipopolysaccharide binding
GO:0046503	PROCESS	8	2	3.61E-02	1.000	glycerolipid catabolic process
GO:0048806	PROCESS	14	2	3.69E-02	1.000	genitalia development
GO:0048070	PROCESS	8	2	3.73E-02	1.000	regulation of pigmentation during development
GO:0034361	CELLULAR	16	2	3.78E-02	1.000	very-low-density lipoprotein particle
GO:0034385	CELLULAR	16	2	3.78E-02	1.000	triglyceride-rich lipoprotein particle
GO:0033363	PROCESS	7	2	3.80E-02	1.000	secretory granule organization
GO:0008034	FUNCTION	32	5	3.82E-02	1.000	lipoprotein binding
GO:0008305	CELLULAR	28	4	3.87E-02	1.000	integrin complex
GO:0016298	FUNCTION	95	7	3.88E-02	1.000	lipase activity
GO:0006917	PROCESS	227	11	3.89E-02	1.000	induction of apoptosis
GO:0044248	PROCESS	951	30	3.92E-02	1.000	cellular catabolic process
GO:0044255	PROCESS	598	25	3.94E-02	1.000	cellular lipid metabolic process
GO:0052547	PROCESS	72	5	3.94E-02	1.000	regulation of peptidase activity
GO:0042803	FUNCTION	261	15	3.95E-02	1.000	protein homodimerization activity
GO:0051219	FUNCTION	14	2	3.99E-02	1.000	phosphoprotein binding
GO:0051043	PROCESS	12	2	4.05E-02	1.000	regulation of membrane protein ectodomain proteolysis
GO:0005513	PROCESS	9	3	4.05E-02	1.000	detection of calcium ion

GO:0008092	FUNCTION	433	25	4.08E-02	1.000	cytoskeletal protein binding
GO:0004715	FUNCTION	38	4	4.25E-02	1.000	non-membrane spanning protein tyrosine kinase activity
GO:0046466	PROCESS	15	2	4.26E-02	1.000	membrane lipid catabolic process
GO:0030149	PROCESS	15	2	4.26E-02	1.000	sphingolipid catabolic process
GO:0045646	PROCESS	16	2	4.35E-02	1.000	regulation of erythrocyte differentiation
GO:0006508	PROCESS	926	32	4.36E-02	1.000	proteolysis
GO:0042439	PROCESS	26	3	4.42E-02	1.000	ethanolamine and derivative metabolic process
GO:0006873	PROCESS	274	15	4.44E-02	1.000	cellular ion homeostasis
GO:0032012	PROCESS	42	4	4.45E-02	1.000	regulation of ARF protein signal transduction
GO:0032367	PROCESS	4	2	4.47E-02	1.000	intracellular cholesterol transport
GO:0032366	PROCESS	4	2	4.47E-02	1.000	intracellular sterol transport
GO:0030804	PROCESS	9	2	4.49E-02	1.000	positive regulation of cyclic nucleotide biosynthetic process
GO:0030801	PROCESS	9	2	4.49E-02	1.000	positive regulation of cyclic nucleotide metabolic process
GO:0030810	PROCESS	9	2	4.49E-02	1.000	positive regulation of nucleotide biosynthetic process
GO:0045981	PROCESS	9	2	4.49E-02	1.000	positive regulation of nucleotide metabolic process
GO:0050684	PROCESS	15	2	4.50E-02	1.000	regulation of mRNA processing
GO:0030163	PROCESS	936	32	4.61E-02	1.000	protein catabolic process
GO:0043280	PROCESS	51	4	4.73E-02	1.000	positive regulation of caspase activity
GO:0010952	PROCESS	51	4	4.73E-02	1.000	positive regulation of peptidase activity
GO:0045833	PROCESS	19	2	4.77E-02	1.000	negative regulation of lipid metabolic process
GO:0009595	PROCESS	15	2	4.79E-02	1.000	detection of biotic stimulus
GO:0005217	FUNCTION	13	4	4.85E-02	1.000	intracellular ligand-gated ion channel activity
GO:0016021	CELLULAR	4844	168	4.85E-02	1.000	integral to membrane
GO:0033036	PROCESS	946	36	4.86E-02	1.000	macromolecule localization
GO:0006641	PROCESS	31	3	4.86E-02	1.000	triglyceride metabolic process
GO:0042471	PROCESS	50	3	4.86E-02	1.000	ear morphogenesis
GO:0005272	FUNCTION	31	4	4.88E-02	1.000	sodium channel activity
GO:0006954	PROCESS	263	11	4.96E-02	1.000	inflammatory response
GO:0008015	PROCESS	144	9	5.01E-02	1.000	blood circulation
GO:0003013	PROCESS	144	9	5.01E-02	1.000	circulatory system process
GO:0005319	FUNCTION	57	6	5.02E-02	1.000	lipid transporter activity
GO:0055082	PROCESS	280	15	5.04E-02	1.000	cellular chemical homeostasis
GO:0008235	FUNCTION	37	4	5.12E-02	1.000	metalloexopeptidase activity
GO:0015297	FUNCTION	59	6	5.30E-02	1.000	antiporter activity
GO:0045862	PROCESS	20	2	5.34E-02	1.000	positive regulation of proteolysis
GO:0055080	PROCESS	210	12	5.41E-02	1.000	cation homeostasis
GO:0010594	PROCESS	49	4	5.46E-02	1.000	regulation of endothelial cell migration
GO:0046546	PROCESS	39	3	5.49E-02	1.000	development of primary male sexual characteristics
GO:0015020	FUNCTION	28	3	5.52E-02	1.000	glucuronosyltransferase activity
GO:0032365	PROCESS	7	2	5.56E-02	1.000	intracellular lipid transport
GO:0007265	PROCESS	92	6	5.61E-02	1.000	Ras protein signal transduction
GO:0015276	FUNCTION	113	11	5.61E-02	1.000	ligand-gated ion channel activity
GO:0022834	FUNCTION	113	11	5.61E-02	1.000	ligand-gated channel activity
GO:0032844	PROCESS	80	5	5.68E-02	1.000	regulation of homeostatic process
GO:0055091	PROCESS	5	2	5.71E-02	1.000	phospholipid homeostasis
GO:0043167	FUNCTION	3926	138	5.81E-02	1.000	ion binding
GO:0006921	PROCESS	20	2	5.89E-02	1.000	cell structure disassembly during apoptosis
GO:0003006	PROCESS	108	6	5.93E-02	1.000	reproductive developmental process
GO:0043583	PROCESS	68	5	5.93E-02	1.000	ear development
GO:0016192	PROCESS	484	22	5.93E-02	1.000	vesicle-mediated transport
GO:0005769	CELLULAR	64	4	5.93E-02	1.000	early endosome
GO:0051224	PROCESS	34	3	5.98E-02	1.000	negative regulation of protein transport
GO:0030139	CELLULAR	52	5	5.99E-02	1.000	endocytic vesicle
GO:0045834	PROCESS	30	3	6.03E-02	1.000	positive regulation of lipid metabolic process
GO:0007005	PROCESS	104	5	6.11E-02	1.000	mitochondrion organization
GO:0005819	CELLULAR	112	5	6.14E-02	1.000	spindle
GO:0015291	FUNCTION	186	12	6.20E-02	1.000	secondary active transmembrane transporter activity
GO:0051179	PROCESS	2739	106	6.36E-02	1.000	localization
GO:0004180	FUNCTION	36	4	6.37E-02	1.000	carboxypeptidase activity
GO:0006897	PROCESS	181	11	6.38E-02	1.000	endocytosis
GO:0010324	PROCESS	181	11	6.38E-02	1.000	membrane invagination
GO:0006915	PROCESS	446	17	6.38E-02	1.000	apoptosis
GO:0051341	PROCESS	33	3	6.39E-02	1.000	regulation of oxidoreductase activity
GO:0003779	FUNCTION	290	19	6.45E-02	1.000	actin binding
GO:0051336	PROCESS	289	13	6.49E-02	1.000	regulation of hydrolase activity
GO:0030201	PROCESS	13	3	6.50E-02	1.000	heparan sulfate proteoglycan metabolic process
GO:0043279	PROCESS	22	3	6.52E-02	1.000	response to alkaloid
GO:0015464	FUNCTION	18	2	6.55E-02	1.000	acetylcholine receptor activity
GO:0043624	PROCESS	13	2	6.55E-02	1.000	cellular protein complex disassembly
GO:0043241	PROCESS	13	2	6.55E-02	1.000	protein complex disassembly
GO:0042312	PROCESS	14	2	6.71E-02	1.000	regulation of vasodilation
GO:0006875	PROCESS	136	9	6.88E-02	1.000	cellular metal ion homeostasis
GO:0007274	PROCESS	15	2	6.89E-02	1.000	neuromuscular synaptic transmission
GO:0051606	PROCESS	98	7	6.94E-02	1.000	detection of stimulus
GO:0042166	FUNCTION	20	2	7.00E-02	1.000	acetylcholine binding
GO:0009636	PROCESS	36	3	7.01E-02	1.000	response to toxin
GO:0012501	PROCESS	453	17	7.01E-02	1.000	programmed cell death
GO:0051437	PROCESS	63	3	7.03E-02	1.000	positive regulation of ubiquitin-protein ligase activity during mitotic cell cycle

GO:0032409	PROCESS	27	3	7.12E-02	1.000	regulation of transporter activity
GO:0043169	FUNCTION	3876	135	7.13E-02	1.000	cation binding
GO:0046928	PROCESS	12	2	7.30E-02	1.000	regulation of neurotransmitter secretion
GO:0016251	FUNCTION	47	3	7.46E-02	1.000	general RNA polymerase II transcription factor activity
GO:0043535	PROCESS	40	3	7.47E-02	1.000	regulation of blood vessel endothelial cell migration
GO:0015300	FUNCTION	48	5	7.50E-02	1.000	solute:solute antiporter activity
GO:0043285	PROCESS	1074	34	7.50E-02	1.000	biopolymer catabolic process
GO:0051443	PROCESS	65	3	7.51E-02	1.000	positive regulation of ubiquitin-protein ligase activity
GO:0005876	CELLULAR	24	2	7.53E-02	1.000	spindle microtubule
GO:0048518	PROCESS	1531	53	7.59E-02	1.000	positive regulation of biological process
GO:0001816	PROCESS	31	3	7.60E-02	1.000	cytokine production
GO:0016755	FUNCTION	18	2	7.65E-02	1.000	transferase activity, transferring amino-acyl groups
GO:0018210	PROCESS	14	2	7.66E-02	1.000	peptidyl-threonine modification
GO:0009057	PROCESS	1130	35	7.66E-02	1.000	macromolecule catabolic process
GO:0007528	PROCESS	10	2	7.67E-02	1.000	neuromuscular junction development
GO:0051439	PROCESS	66	3	7.68E-02	1.000	regulation of ubiquitin-protein ligase activity during mitotic cell cycle
GO:0030100	PROCESS	50	4	7.71E-02	1.000	regulation of endocytosis
GO:0001950	CELLULAR	5	2	7.75E-02	1.000	plasma membrane enriched fraction
GO:0048286	PROCESS	13	2	7.76E-02	1.000	lung alveolus development
GO:0031331	PROCESS	23	2	7.90E-02	1.000	positive regulation of cellular catabolic process
GO:0030276	FUNCTION	8	2	7.93E-02	1.000	clathrin binding
GO:0019882	PROCESS	54	4	7.99E-02	1.000	antigen processing and presentation
GO:0006639	PROCESS	35	3	8.05E-02	1.000	acylglycerol metabolic process
GO:0006638	PROCESS	35	3	8.05E-02	1.000	neutral lipid metabolic process
GO:0016411	FUNCTION	15	2	8.06E-02	1.000	acylglycerol O-acyltransferase activity
GO:0030003	PROCESS	183	10	8.24E-02	1.000	cellular cation homeostasis
GO:0015385	FUNCTION	7	2	8.29E-02	1.000	sodium:hydrogen antiporter activity
GO:0005451	FUNCTION	7	2	8.29E-02	1.000	monovalent cation:hydrogen antiporter activity
GO:0034374	PROCESS	9	2	8.30E-02	1.000	low-density lipoprotein particle remodeling
GO:0015078	FUNCTION	77	4	8.34E-02	1.000	hydrogen ion transmembrane transporter activity
GO:0005764	CELLULAR	189	8	8.36E-02	1.000	lysosome
GO:0000323	CELLULAR	189	8	8.36E-02	1.000	lytic vacuole
GO:0044403	PROCESS	35	3	8.36E-02	1.000	symbiosis, encompassing mutualism through parasitism
GO:0001540	FUNCTION	12	2	8.37E-02	1.000	beta-amyloid binding
GO:0015629	CELLULAR	224	14	8.37E-02	1.000	actin cytoskeleton
GO:0055065	PROCESS	143	9	8.40E-02	1.000	metal ion homeostasis
GO:0005741	CELLULAR	79	4	8.59E-02	1.000	mitochondrial outer membrane
GO:0031526	CELLULAR	15	2	8.64E-02	1.000	brush border membrane
GO:0015077	FUNCTION	88	5	8.68E-02	1.000	monovalent inorganic cation transmembrane transporter activity
GO:0006805	PROCESS	20	2	8.76E-02	1.000	xenobiotic metabolic process
GO:0006778	PROCESS	25	2	8.82E-02	1.000	porphyrin metabolic process
GO:0033013	PROCESS	25	2	8.82E-02	1.000	tetrapyrrole metabolic process
GO:0006662	PROCESS	37	3	8.84E-02	1.000	glycerol ether metabolic process
GO:0030955	FUNCTION	124	10	8.92E-02	1.000	potassium ion binding
GO:0048741	PROCESS	41	4	8.93E-02	1.000	skeletal muscle fiber development
GO:0006509	PROCESS	13	2	8.94E-02	1.000	membrane protein ectodomain proteolysis
GO:0016363	CELLULAR	48	3	8.99E-02	1.000	nuclear matrix
GO:0051351	PROCESS	68	3	9.00E-02	1.000	positive regulation of ligase activity
GO:0046872	FUNCTION	3842	133	9.03E-02	1.000	metal ion binding
GO:0005231	FUNCTION	46	5	9.10E-02	1.000	excitatory extracellular ligand-gated ion channel activity
GO:0030594	FUNCTION	92	6	9.10E-02	1.000	neurotransmitter receptor activity
GO:0016891	FUNCTION	24	2	9.12E-02	1.000	endoribonuclease activity, producing 5'-phosphomonoesters
GO:0018904	PROCESS	38	3	9.14E-02	1.000	organic ether metabolic process
GO:0030169	FUNCTION	21	4	9.15E-02	1.000	low-density lipoprotein binding
GO:0007165	PROCESS	3016	106	9.18E-02	1.000	signal transduction
GO:0006891	PROCESS	18	2	9.19E-02	1.000	intra-Golgi vesicle-mediated transport
GO:0051049	PROCESS	317	15	9.19E-02	1.000	regulation of transport
GO:0022890	FUNCTION	127	7	9.21E-02	1.000	inorganic cation transmembrane transporter activity
GO:0042165	FUNCTION	93	6	9.21E-02	1.000	neurotransmitter binding
GO:0000041	PROCESS	63	4	9.27E-02	1.000	transition metal ion transport
GO:0047555	FUNCTION	7	2	9.28E-02	1.000	3',5'-cyclic-GMP phosphodiesterase activity
GO:0009986	CELLULAR	248	16	9.34E-02	1.000	cell surface
GO:0043281	PROCESS	65	4	9.36E-02	1.000	regulation of caspase activity
GO:0034623	PROCESS	20	2	9.36E-02	1.000	cellular macromolecular complex disassembly
GO:0044093	PROCESS	481	19	9.41E-02	1.000	positive regulation of molecular function
GO:0015674	PROCESS	141	12	9.43E-02	1.000	di-, tri-valent inorganic cation transport
GO:0043473	PROCESS	37	3	9.51E-02	1.000	pigmentation
GO:0016567	PROCESS	96	5	9.57E-02	1.000	protein ubiquitination
GO:0046578	PROCESS	187	12	9.67E-02	1.000	regulation of Ras protein signal transduction
GO:0006996	PROCESS	1117	35	9.70E-02	1.000	organelle organization
GO:0051438	PROCESS	73	3	9.76E-02	1.000	regulation of ubiquitin-protein ligase activity
GO:0048168	PROCESS	16	2	9.91E-02	1.000	regulation of neuronal synaptic plasticity
GO:0006826	PROCESS	24	2	1.00E-01	1.000	iron ion transport
GO:0042113	PROCESS	53	4	1.00E-01	1.000	B cell activation
GO:0032103	PROCESS	48	4	1.01E-01	1.000	positive regulation of response to external stimulus
GO:0006471	PROCESS	21	2	1.01E-01	1.000	protein amino acid ADP-ribosylation
GO:0022607	PROCESS	639	22	1.02E-01	1.000	cellular component assembly
GO:0004709	FUNCTION	17	2	1.02E-01	1.000	MAP kinase kinase kinase activity
GO:0003008	PROCESS	1267	45	1.02E-01	1.000	system process

GO:0034399	CELLULAR	52	3	1.03E-01	1.000	nuclear periphery
GO:0019835	PROCESS	18	2	1.03E-01	1.000	cytolysis
GO:0015012	PROCESS	10	2	1.04E-01	1.000	heparan sulfate proteoglycan biosynthetic process
GO:0030552	FUNCTION	12	2	1.05E-01	1.000	cAMP binding
GO:0019218	PROCESS	27	3	1.05E-01	1.000	regulation of steroid metabolic process
GO:0060401	PROCESS	15	3	1.06E-01	1.000	cytosolic calcium ion transport
GO:0009410	PROCESS	23	2	1.07E-01	1.000	response to xenobiotic stimulus
GO:0043235	CELLULAR	100	7	1.08E-01	1.000	receptor complex
GO:0005886	CELLULAR	3374	132	1.08E-01	1.000	plasma membrane
GO:0006898	PROCESS	44	4	1.09E-01	1.000	receptor-mediated endocytosis
GO:0030193	PROCESS	25	2	1.10E-01	1.000	regulation of blood coagulation
GO:0032768	PROCESS	21	2	1.10E-01	1.000	regulation of monooxygenase activity
GO:0009611	PROCESS	399	15	1.10E-01	1.000	response to wounding
GO:0005539	FUNCTION	122	7	1.10E-01	1.000	glycosaminoglycan binding
GO:0035091	FUNCTION	92	6	1.11E-01	1.000	phosphoinositide binding
GO:0015380	FUNCTION	17	2	1.12E-01	1.000	anion exchanger activity
GO:0001653	FUNCTION	102	6	1.12E-01	1.000	peptide receptor activity
GO:0003774	FUNCTION	135	9	1.12E-01	1.000	motor activity
GO:0010885	PROCESS	10	2	1.13E-01	1.000	regulation of cholesterol storage
GO:0051340	PROCESS	76	3	1.14E-01	1.000	regulation of ligase activity
GO:0007154	PROCESS	3319	117	1.14E-01	1.000	cell communication
GO:0046983	FUNCTION	420	19	1.14E-01	1.000	protein dimerization activity
GO:0007204	PROCESS	76	5	1.15E-01	1.000	elevation of cytosolic calcium ion concentration
GO:0030425	CELLULAR	77	6	1.16E-01	1.000	dendrite
GO:0000049	FUNCTION	21	2	1.17E-01	1.000	tRNA binding
GO:0000776	CELLULAR	66	3	1.17E-01	1.000	kinetochore
GO:0019838	FUNCTION	89	6	1.17E-01	1.000	growth factor binding
GO:0015485	FUNCTION	15	2	1.18E-01	1.000	cholesterol binding
GO:0019725	PROCESS	356	16	1.18E-01	1.000	cellular homeostasis
GO:0004842	FUNCTION	127	6	1.18E-01	1.000	ubiquitin-protein ligase activity
GO:0000151	CELLULAR	79	4	1.18E-01	1.000	ubiquitin ligase complex
GO:0004114	FUNCTION	24	4	1.19E-01	1.000	3',5'-cyclic-nucleotide phosphodiesterase activity
GO:0015278	FUNCTION	9	3	1.19E-01	1.000	calcium-release channel activity
GO:0004112	FUNCTION	25	4	1.20E-01	1.000	cyclic-nucleotide phosphodiesterase activity
GO:0032446	PROCESS	107	5	1.20E-01	1.000	protein modification by small protein conjugation
GO:0033619	PROCESS	18	2	1.21E-01	1.000	membrane protein proteolysis
GO:0019897	CELLULAR	44	4	1.22E-01	1.000	extrinsic to plasma membrane
GO:0007588	PROCESS	46	4	1.22E-01	1.000	excretion
GO:0043068	PROCESS	305	13	1.23E-01	1.000	positive regulation of programmed cell death
GO:0051588	PROCESS	17	2	1.23E-01	1.000	regulation of neurotransmitter transport
GO:0004888	FUNCTION	1115	41	1.23E-01	1.000	transmembrane receptor activity
GO:0005887	CELLULAR	1099	50	1.24E-01	1.000	integral to plasma membrane
GO:0050818	PROCESS	27	2	1.24E-01	1.000	regulation of coagulation
GO:0048863	PROCESS	22	2	1.25E-01	1.000	stem cell differentiation
GO:0008415	FUNCTION	178	7	1.25E-01	1.000	acyltransferase activity
GO:0016893	FUNCTION	30	2	1.25E-01	1.000	endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters
GO:0051480	PROCESS	80	5	1.25E-01	1.000	cytosolic calcium ion homeostasis
GO:0006066	PROCESS	340	13	1.25E-01	1.000	alcohol metabolic process
GO:0045137	PROCESS	80	4	1.28E-01	1.000	development of primary sexual characteristics
GO:0004702	FUNCTION	57	4	1.28E-01	1.000	receptor signaling protein serine/threonine kinase activity
GO:0048747	PROCESS	47	4	1.29E-01	1.000	muscle fiber development
GO:0010942	PROCESS	308	13	1.29E-01	1.000	positive regulation of cell death
GO:0004623	FUNCTION	25	2	1.29E-01	1.000	phospholipase A2 activity
GO:0051180	PROCESS	21	2	1.30E-01	1.000	vitamin transport
GO:0044459	CELLULAR	1964	89	1.30E-01	1.000	plasma membrane part
GO:0044085	PROCESS	742	23	1.31E-01	1.000	cellular component biogenesis
GO:0046903	PROCESS	216	12	1.31E-01	1.000	secretion
GO:0019935	PROCESS	110	6	1.32E-01	1.000	cyclic-nucleotide-mediated signaling
GO:0019439	PROCESS	17	2	1.33E-01	1.000	aromatic compound catabolic process
GO:0016747	FUNCTION	180	7	1.35E-01	1.000	transferase activity, transferring acyl groups other than amino-acyl groups
GO:0005540	FUNCTION	19	2	1.35E-01	1.000	hyaluronic acid binding
GO:0015301	FUNCTION	19	2	1.35E-01	1.000	anion:anion antiporter activity
GO:0032879	PROCESS	486	21	1.36E-01	1.000	regulation of localization
GO:0016208	FUNCTION	16	2	1.36E-01	1.000	AMP binding
GO:0030247	FUNCTION	130	7	1.36E-01	1.000	polysaccharide binding
GO:0001871	FUNCTION	130	7	1.36E-01	1.000	pattern binding
GO:0016529	CELLULAR	32	4	1.36E-01	1.000	sarcoplasmic reticulum
GO:0030183	PROCESS	33	3	1.37E-01	1.000	B cell differentiation
GO:0015491	FUNCTION	15	3	1.37E-01	1.000	cation:cation antiporter activity
GO:0005792	CELLULAR	174	7	1.39E-01	1.000	microsome
GO:0016050	PROCESS	48	3	1.41E-01	1.000	vesicle organization
GO:0031625	FUNCTION	30	2	1.41E-01	1.000	ubiquitin protein ligase binding
GO:0022403	PROCESS	366	11	1.41E-01	1.000	cell cycle phase
GO:0005219	FUNCTION	5	2	1.41E-01	1.000	ryanodine-sensitive calcium-release channel activity
GO:0005218	FUNCTION	5	2	1.41E-01	1.000	intracellular ligand-gated calcium channel activity
GO:0051345	PROCESS	154	7	1.41E-01	1.000	positive regulation of hydrolase activity
GO:0006644	PROCESS	164	7	1.42E-01	1.000	phospholipid metabolic process

GO:0065008	PROCESS	1109	41	1.42E-01	1.000	regulation of biological quality
GO:0005902	CELLULAR	25	3	1.42E-01	1.000	microvillus
GO:0001664	FUNCTION	82	3	1.43E-01	1.000	G-protein-coupled receptor binding
GO:0005905	CELLULAR	41	3	1.44E-01	1.000	coated pit
GO:0016746	FUNCTION	188	7	1.45E-01	1.000	transferase activity, transferring acyl groups
GO:0034621	PROCESS	302	8	1.45E-01	1.000	cellular macromolecular complex subunit organization
GO:0043122	PROCESS	97	4	1.46E-01	1.000	regulation of I-kappaB kinase/NF-kappaB cascade
GO:0019787	FUNCTION	141	6	1.46E-01	1.000	small conjugating protein ligase activity
GO:0008194	FUNCTION	112	7	1.46E-01	1.000	UDP-glycosyltransferase activity
GO:0016528	CELLULAR	33	4	1.46E-01	1.000	sarcoplasm
GO:0006941	PROCESS	30	3	1.49E-01	1.000	striated muscle contraction
GO:0005777	CELLULAR	97	4	1.49E-01	1.000	peroxisome
GO:0042579	CELLULAR	97	4	1.49E-01	1.000	microbody
GO:0031410	CELLULAR	543	21	1.50E-01	1.000	cytoplasmic vesicle
GO:0000287	FUNCTION	420	19	1.50E-01	1.000	magnesium ion binding
GO:0001525	PROCESS	109	7	1.51E-01	1.000	angiogenesis
GO:0010926	PROCESS	839	29	1.51E-01	1.000	anatomical structure formation
GO:0043623	PROCESS	136	5	1.52E-01	1.000	cellular protein complex assembly
GO:0016023	CELLULAR	459	18	1.52E-01	1.000	cytoplasmic membrane-bounded vesicle
GO:0009066	PROCESS	22	2	1.52E-01	1.000	aspartate family amino acid metabolic process
GO:0005548	FUNCTION	28	4	1.53E-01	1.000	phospholipid transporter activity
GO:0044257	PROCESS	523	15	1.54E-01	1.000	cellular protein catabolic process
GO:0008584	PROCESS	29	2	1.55E-01	1.000	male gonad development
GO:0019637	PROCESS	170	7	1.56E-01	1.000	organophosphate metabolic process
GO:0032991	CELLULAR	2674	73	1.58E-01	1.000	macromolecular complex
GO:0008080	FUNCTION	65	3	1.58E-01	1.000	N-acetyltransferase activity
GO:0008239	FUNCTION	10	2	1.60E-01	1.000	dipeptidyl-peptidase activity
GO:0019229	PROCESS	18	2	1.60E-01	1.000	regulation of vasoconstriction
GO:0042472	PROCESS	41	2	1.60E-01	1.000	inner ear morphogenesis
GO:0043085	PROCESS	432	16	1.61E-01	1.000	positive regulation of catalytic activity
GO:0005251	FUNCTION	12	2	1.61E-01	1.000	delayed rectifier potassium channel activity
GO:0006790	PROCESS	94	6	1.61E-01	1.000	sulfur metabolic process
GO:0031968	CELLULAR	91	4	1.62E-01	1.000	organelle outer membrane
GO:0005615	CELLULAR	585	20	1.62E-01	1.000	extracellular space
GO:0015277	FUNCTION	7	2	1.63E-01	1.000	kainate selective glutamate receptor activity
GO:0031226	CELLULAR	1123	50	1.64E-01	1.000	intrinsic to plasma membrane
GO:0042598	CELLULAR	179	7	1.64E-01	1.000	vesicular fraction
GO:0007519	PROCESS	59	4	1.65E-01	1.000	skeletal muscle tissue development
GO:0060538	PROCESS	59	4	1.65E-01	1.000	skeletal muscle organ development
GO:0031988	CELLULAR	465	18	1.65E-01	1.000	membrane-bounded vesicle
GO:0001948	FUNCTION	20	3	1.66E-01	1.000	glycoprotein binding
GO:0031982	CELLULAR	552	21	1.67E-01	1.000	vesicle
GO:0007157	PROCESS	18	2	1.68E-01	1.000	heterophilic cell adhesion
GO:0005773	CELLULAR	222	8	1.70E-01	1.000	vacuole
GO:0043065	PROCESS	303	12	1.70E-01	1.000	positive regulation of apoptosis
GO:0008610	PROCESS	290	11	1.72E-01	1.000	lipid biosynthetic process
GO:0005024	FUNCTION	16	2	1.72E-01	1.000	transforming growth factor beta receptor activity
GO:0004675	FUNCTION	16	2	1.72E-01	1.000	transmembrane receptor protein serine/threonine kinase activity
GO:0008188	FUNCTION	37	3	1.72E-01	1.000	neuropeptide receptor activity
GO:0046890	PROCESS	30	2	1.72E-01	1.000	regulation of lipid biosynthetic process
GO:0004857	FUNCTION	248	9	1.74E-01	1.000	enzyme inhibitor activity
GO:0044419	PROCESS	265	9	1.75E-01	1.000	interspecies interaction between organisms
GO:0016043	PROCESS	1996	67	1.77E-01	1.000	cellular component organization
GO:0004115	FUNCTION	7	2	1.77E-01	1.000	3',5'-cyclic-AMP phosphodiesterase activity
GO:0042923	FUNCTION	38	3	1.78E-01	1.000	neuropeptide binding
GO:0032318	PROCESS	94	5	1.80E-01	1.000	regulation of Ras GTPase activity
GO:0031091	CELLULAR	53	3	1.80E-01	1.000	platelet alpha granule
GO:0019867	CELLULAR	94	4	1.81E-01	1.000	outer membrane
GO:0043395	FUNCTION	5	2	1.82E-01	1.000	heparan sulfate proteoglycan binding
GO:0015031	PROCESS	679	22	1.82E-01	1.000	protein transport
GO:0010883	PROCESS	19	2	1.83E-01	1.000	regulation of lipid storage
GO:0008643	PROCESS	57	3	1.83E-01	1.000	carbohydrate transport
GO:0009306	PROCESS	20	2	1.86E-01	1.000	protein secretion
GO:0006909	PROCESS	39	3	1.86E-01	1.000	phagocytosis
GO:0007631	PROCESS	44	3	1.87E-01	1.000	feeding behavior
GO:0051099	PROCESS	56	3	1.87E-01	1.000	positive regulation of binding
GO:0032101	PROCESS	114	6	1.88E-01	1.000	regulation of response to external stimulus
GO:0055037	CELLULAR	18	2	1.88E-01	1.000	recycling endosome
GO:0045884	PROCESS	19	2	1.90E-01	1.000	regulation of survival gene product expression
GO:0042102	PROCESS	30	2	1.90E-01	1.000	positive regulation of T cell proliferation
GO:0070011	FUNCTION	514	19	1.90E-01	1.000	peptidase activity, acting on L-amino acid peptides
GO:0032934	FUNCTION	22	2	1.90E-01	1.000	sterol binding
GO:0008284	PROCESS	306	11	1.91E-01	1.000	positive regulation of cell proliferation
GO:0080134	PROCESS	195	7	1.91E-01	1.000	regulation of response to stress
GO:0022804	FUNCTION	319	17	1.91E-01	1.000	active transmembrane transporter activity
GO:0005793	CELLULAR	39	2	1.91E-01	1.000	ER-Golgi intermediate compartment
GO:0019538	PROCESS	2511	74	1.91E-01	1.000	protein metabolic process
GO:0010467	PROCESS	1099	26	1.92E-01	1.000	gene expression
GO:0004521	FUNCTION	43	2	1.92E-01	1.000	endoribonuclease activity

GO:0050808	PROCESS	36	3	1.92E-01	1.000	synapse organization
GO:0007586	PROCESS	79	4	1.93E-01	1.000	digestion
GO:0016573	PROCESS	45	2	1.93E-01	1.000	histone acetylation
GO:0060627	PROCESS	73	4	1.95E-01	1.000	regulation of vesicle-mediated transport
GO:0006816	PROCESS	112	10	1.95E-01	1.000	calcium ion transport
GO:0043565	FUNCTION	524	17	1.95E-01	1.000	sequence-specific DNA binding
GO:0005740	CELLULAR	347	9	1.95E-01	1.000	mitochondrial envelope
GO:0070838	PROCESS	113	10	1.96E-01	1.000	divalent metal ion transport
GO:0045184	PROCESS	685	22	1.97E-01	1.000	establishment of protein localization
GO:0044057	PROCESS	190	11	1.99E-01	1.000	regulation of system process
GO:0008289	FUNCTION	455	20	1.99E-01	1.000	lipid binding
GO:0004402	FUNCTION	36	2	2.00E-01	1.000	histone acetyltransferase activity
GO:0004468	FUNCTION	36	2	2.00E-01	1.000	lysine N-acetyltransferase activity
GO:0007187	PROCESS	100	5	2.01E-01	1.000	G-protein signaling, coupled to cyclic nucleotide second messenger
GO:0016757	FUNCTION	250	11	2.01E-01	1.000	transferase activity, transferring glycosyl groups
GO:0065009	PROCESS	814	27	2.01E-01	1.000	regulation of molecular function
GO:0050877	PROCESS	1010	34	2.01E-01	1.000	neurological system process
GO:0051056	PROCESS	228	13	2.02E-01	1.000	regulation of small GTPase mediated signal transduction
GO:0005179	FUNCTION	102	3	2.02E-01	1.000	hormone activity
GO:0018130	PROCESS	41	2	2.03E-01	1.000	heterocycle biosynthetic process
GO:0051701	PROCESS	27	2	2.03E-01	1.000	interaction with host
GO:0015299	FUNCTION	19	2	2.04E-01	1.000	solute:hydrogen antiporter activity
GO:0070647	PROCESS	132	5	2.04E-01	1.000	protein modification by small protein conjugation or removal
GO:0006473	PROCESS	48	2	2.07E-01	1.000	protein amino acid acetylation
GO:0051246	PROCESS	467	15	2.08E-01	1.000	regulation of protein metabolic process
GO:0016197	PROCESS	47	3	2.08E-01	1.000	endosome transport
GO:0016570	PROCESS	104	4	2.09E-01	1.000	histone modification
GO:0006800	PROCESS	51	3	2.10E-01	1.000	oxygen and reactive oxygen species metabolic process
GO:0035258	FUNCTION	36	2	2.10E-01	1.000	steroid hormone receptor binding
GO:0008233	FUNCTION	530	19	2.10E-01	1.000	peptidase activity
GO:0016758	FUNCTION	170	8	2.10E-01	1.000	transferase activity, transferring hexosyl groups
GO:0031333	PROCESS	29	2	2.11E-01	1.000	negative regulation of protein complex assembly
GO:0031267	FUNCTION	72	5	2.11E-01	1.000	small GTPase binding
GO:0044272	PROCESS	45	3	2.11E-01	1.000	sulfur compound biosynthetic process
GO:0008219	PROCESS	550	19	2.12E-01	1.000	cell death
GO:0007229	PROCESS	55	4	2.12E-01	1.000	integrin-mediated signaling pathway
GO:0008374	FUNCTION	36	2	2.12E-01	1.000	O-acyltransferase activity
GO:0004896	FUNCTION	48	3	2.15E-01	1.000	cytokine receptor activity
GO:0016569	PROCESS	106	4	2.16E-01	1.000	covalent chromatin modification
GO:0004519	FUNCTION	90	3	2.17E-01	1.000	endonuclease activity
GO:0030334	PROCESS	159	8	2.17E-01	1.000	regulation of cell migration
GO:0001726	CELLULAR	56	3	2.17E-01	1.000	ruffle
GO:0015298	FUNCTION	26	3	2.18E-01	1.000	solute:cation antiporter activity
GO:0015293	FUNCTION	121	7	2.18E-01	1.000	symporter activity
GO:0004653	FUNCTION	19	3	2.18E-01	1.000	polypeptide N-acetylgalactosaminyltransferase activity
GO:0016265	PROCESS	554	19	2.19E-01	1.000	death
GO:0042562	FUNCTION	29	3	2.20E-01	1.000	hormone binding
GO:0000279	PROCESS	299	8	2.21E-01	1.000	M phase
GO:0016486	PROCESS	13	2	2.21E-01	1.000	peptide hormone processing
GO:0030516	PROCESS	12	2	2.21E-01	1.000	regulation of axon extension
GO:0030246	FUNCTION	303	12	2.25E-01	1.000	carbohydrate binding
GO:0050927	PROCESS	12	2	2.25E-01	1.000	positive regulation of positive chemotaxis
GO:0050926	PROCESS	12	2	2.25E-01	1.000	regulation of positive chemotaxis
GO:0008528	FUNCTION	97	5	2.26E-01	1.000	peptide receptor activity, G-protein coupled
GO:0030175	CELLULAR	24	2	2.27E-01	1.000	filopodium
GO:0003700	FUNCTION	880	26	2.28E-01	1.000	transcription factor activity
GO:0048514	PROCESS	152	8	2.28E-01	1.000	blood vessel morphogenesis
GO:0008047	FUNCTION	305	15	2.29E-01	1.000	enzyme activator activity
GO:0016407	FUNCTION	78	3	2.29E-01	1.000	acetyltransferase activity
GO:0030141	CELLULAR	139	6	2.30E-01	1.000	secretory granule
GO:0051603	PROCESS	521	14	2.30E-01	1.000	proteolysis involved in cellular protein catabolic process
GO:0007186	PROCESS	950	25	2.30E-01	1.000	G-protein coupled receptor protein signaling pathway
GO:0016814	FUNCTION	30	2	2.30E-01	1.000	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines
GO:0008237	FUNCTION	172	9	2.34E-01	1.000	metallopeptidase activity
GO:0008629	PROCESS	41	2	2.34E-01	1.000	induction of apoptosis by intracellular signals
GO:0005057	FUNCTION	153	8	2.35E-01	1.000	receptor signaling protein activity
GO:0030234	FUNCTION	759	31	2.35E-01	1.000	enzyme regulator activity
GO:0050671	PROCESS	37	2	2.36E-01	1.000	positive regulation of lymphocyte proliferation
GO:0008236	FUNCTION	174	7	2.36E-01	1.000	serine-type peptidase activity
GO:0043087	PROCESS	106	5	2.38E-01	1.000	regulation of GTPase activity
GO:0008081	FUNCTION	81	6	2.39E-01	1.000	phosphoric diester hydrolase activity
GO:0043025	CELLULAR	73	4	2.39E-01	1.000	cell soma
GO:0030228	FUNCTION	14	2	2.40E-01	1.000	lipoprotein receptor activity
GO:0005230	FUNCTION	67	5	2.41E-01	1.000	extracellular ligand-gated ion channel activity
GO:0000777	CELLULAR	48	2	2.41E-01	1.000	condensed chromosome kinetochore
GO:0043394	FUNCTION	7	2	2.42E-01	1.000	proteoglycan binding
GO:0042277	FUNCTION	169	8	2.43E-01	1.000	peptide binding
GO:0017171	FUNCTION	176	7	2.43E-01	1.000	serine hydrolase activity

GO:0005626	CELLULAR	628	26	2.45E-01	1.000	insoluble fraction
GO:0008406	PROCESS	68	3	2.45E-01	1.000	gonad development
GO:0032946	PROCESS	38	2	2.46E-01	1.000	positive regulation of mononuclear cell proliferation
GO:0070665	PROCESS	38	2	2.46E-01	1.000	positive regulation of leukocyte proliferation
GO:0046486	PROCESS	127	5	2.46E-01	1.000	glycerolipid metabolic process
GO:0009190	PROCESS	22	2	2.47E-01	1.000	cyclic nucleotide biosynthetic process
GO:0016787	FUNCTION	2094	66	2.47E-01	1.000	hydrolase activity
GO:0008624	PROCESS	59	3	2.47E-01	1.000	induction of apoptosis by extracellular signals
GO:0060402	PROCESS	14	2	2.47E-01	1.000	calcium ion transport into cytosol
GO:0051128	PROCESS	362	14	2.48E-01	1.000	regulation of cellular component organization
GO:0030335	PROCESS	70	4	2.48E-01	1.000	positive regulation of cell migration
GO:0005938	CELLULAR	104	5	2.49E-01	1.000	cell cortex
GO:0003725	FUNCTION	30	2	2.50E-01	1.000	double-stranded RNA binding
GO:0031329	PROCESS	39	2	2.50E-01	1.000	regulation of cellular catabolic process
GO:0016410	FUNCTION	77	3	2.50E-01	1.000	N-acyltransferase activity
GO:0016765	FUNCTION	47	2	2.50E-01	1.000	transferase activity, transferring alkyl or aryl (other than methyl) groups
GO:0051651	PROCESS	41	2	2.51E-01	1.000	maintenance of location in cell
GO:0044450	CELLULAR	44	2	2.52E-01	1.000	microtubule organizing center part
GO:0007605	PROCESS	80	6	2.53E-01	1.000	sensory perception of sound
GO:0008277	PROCESS	48	3	2.53E-01	1.000	regulation of G-protein coupled receptor protein signaling pathway
GO:0001701	PROCESS	115	5	2.54E-01	1.000	in utero embryonic development
GO:0006952	PROCESS	514	15	2.55E-01	1.000	defense response
GO:0009897	CELLULAR	114	8	2.55E-01	1.000	external side of plasma membrane
GO:0051705	PROCESS	17	2	2.56E-01	1.000	behavioral interaction between organisms
GO:0044448	CELLULAR	60	3	2.56E-01	1.000	cell cortex part
GO:0019898	CELLULAR	461	21	2.57E-01	1.000	extrinsic to membrane
GO:0045471	PROCESS	23	2	2.58E-01	1.000	response to ethanol
GO:0006887	PROCESS	86	5	2.60E-01	1.000	exocytosis
GO:0000775	CELLULAR	106	3	2.61E-01	1.000	chromosome, centromeric region
GO:0030667	CELLULAR	20	2	2.62E-01	1.000	secretory granule membrane
GO:0022402	PROCESS	506	13	2.64E-01	1.000	cell cycle process
GO:0016788	FUNCTION	638	22	2.64E-01	1.000	hydrolase activity, acting on ester bonds
GO:0042129	PROCESS	43	2	2.64E-01	1.000	regulation of T cell proliferation
GO:0019955	FUNCTION	97	4	2.64E-01	1.000	cytokine binding
GO:0031966	CELLULAR	326	8	2.65E-01	1.000	mitochondrial membrane
GO:0015103	FUNCTION	30	2	2.65E-01	1.000	inorganic anion transmembrane transporter activity
GO:0034622	PROCESS	269	6	2.66E-01	1.000	cellular macromolecular complex assembly
GO:0006164	PROCESS	130	6	2.66E-01	1.000	purine nucleotide biosynthetic process
GO:0008270	FUNCTION	2124	60	2.67E-01	1.000	zinc ion binding
GO:0006029	PROCESS	34	3	2.68E-01	1.000	proteoglycan metabolic process
GO:0080135	PROCESS	80	3	2.68E-01	1.000	regulation of cellular response to stress
GO:0008016	PROCESS	60	4	2.69E-01	1.000	regulation of heart contraction
GO:0007268	PROCESS	235	14	2.69E-01	1.000	synaptic transmission
GO:0043543	PROCESS	54	2	2.70E-01	1.000	protein amino acid acylation
GO:0009895	PROCESS	35	2	2.71E-01	1.000	negative regulation of catabolic process
GO:0010743	PROCESS	25	2	2.71E-01	1.000	regulation of macrophage derived foam cell differentiation
GO:0017016	FUNCTION	64	4	2.72E-01	1.000	Ras GTPase binding
GO:0030414	FUNCTION	141	5	2.74E-01	1.000	peptidase inhibitor activity
GO:0016849	FUNCTION	20	2	2.76E-01	1.000	phosphorus-oxygen lyase activity
GO:0007067	PROCESS	201	5	2.77E-01	1.000	mitosis
GO:0000280	PROCESS	201	5	2.77E-01	1.000	nuclear division
GO:0034962	PROCESS	635	16	2.77E-01	1.000	cellular biopolymer catabolic process
GO:0050896	PROCESS	2795	74	2.77E-01	1.000	response to stimulus
GO:0001709	PROCESS	29	2	2.78E-01	1.000	cell fate determination
GO:0001894	PROCESS	33	2	2.78E-01	1.000	tissue homeostasis
GO:0044433	CELLULAR	154	7	2.79E-01	1.000	cytoplasmic vesicle part
GO:0048661	PROCESS	16	2	2.80E-01	1.000	positive regulation of smooth muscle cell proliferation
GO:0051272	PROCESS	75	4	2.80E-01	1.000	positive regulation of cell motion
GO:0043067	PROCESS	616	20	2.81E-01	1.000	regulation of programmed cell death
GO:0043123	PROCESS	89	3	2.81E-01	1.000	positive regulation of I-kappaB kinase/NF-kappaB cascade
GO:0017111	FUNCTION	657	23	2.82E-01	1.000	nucleoside-triphosphatase activity
GO:0000779	CELLULAR	53	2	2.82E-01	1.000	condensed chromosome, centromeric region
GO:0044265	PROCESS	690	17	2.82E-01	1.000	cellular macromolecule catabolic process
GO:0017137	FUNCTION	20	2	2.82E-01	1.000	Rab GTPase binding
GO:0006163	PROCESS	155	7	2.82E-01	1.000	purine nucleotide metabolic process
GO:0006885	PROCESS	26	2	2.82E-01	1.000	regulation of pH
GO:0048871	PROCESS	34	2	2.84E-01	1.000	multicellular organismal homeostasis
GO:0046914	FUNCTION	2560	73	2.84E-01	1.000	transition metal ion binding
GO:0010941	PROCESS	618	20	2.84E-01	1.000	regulation of cell death
GO:0060193	PROCESS	61	3	2.85E-01	1.000	positive regulation of lipase activity
GO:0006979	PROCESS	106	4	2.86E-01	1.000	response to oxidative stress
GO:0005096	FUNCTION	204	11	2.86E-01	1.000	GTPase activator activity
GO:0000087	PROCESS	203	5	2.87E-01	1.000	M phase of mitotic cell cycle
GO:0006916	PROCESS	172	6	2.87E-01	1.000	anti-apoptosis
GO:0007127	PROCESS	36	2	2.89E-01	1.000	meiosis I
GO:0051301	PROCESS	266	7	2.89E-01	1.000	cell division
GO:0009892	PROCESS	618	19	2.91E-01	1.000	negative regulation of metabolic process
GO:0030802	PROCESS	88	5	2.92E-01	1.000	regulation of cyclic nucleotide biosynthetic process
GO:0030808	PROCESS	88	5	2.92E-01	1.000	regulation of nucleotide biosynthetic process

GO:0045177	CELLULAR	107	6	2.92E-01	1.000	apical part of cell
GO:0005903	CELLULAR	31	2	2.94E-01	1.000	brush border
GO:0051248	PROCESS	132	5	2.94E-01	1.000	negative regulation of protein metabolic process
GO:0043234	CELLULAR	2177	63	2.95E-01	1.000	protein complex
GO:0008217	PROCESS	69	3	2.95E-01	1.000	regulation of blood pressure
GO:0016836	FUNCTION	40	2	2.95E-01	1.000	hydro-lyase activity
GO:0051020	FUNCTION	78	5	2.96E-01	1.000	GTPase binding
GO:0048522	PROCESS	1406	44	2.96E-01	1.000	positive regulation of cellular process
GO:0048839	PROCESS	55	3	2.96E-01	1.000	inner ear development
GO:0003702	FUNCTION	216	7	2.97E-01	1.000	RNA polymerase II transcription factor activity
GO:0051704	PROCESS	553	15	2.97E-01	1.000	multi-organism process
GO:0048608	PROCESS	77	3	2.97E-01	1.000	reproductive structure development
GO:0001568	PROCESS	171	8	2.98E-01	1.000	blood vessel development
GO:0009975	FUNCTION	21	2	2.99E-01	1.000	cyclase activity
GO:0007517	PROCESS	176	8	2.99E-01	1.000	muscle organ development
GO:0005275	FUNCTION	66	4	2.99E-01	1.000	amine transmembrane transporter activity
GO:0048285	PROCESS	208	5	3.00E-01	1.000	organelle fission
GO:0000398	PROCESS	140	3	3.04E-01	1.000	nuclear mRNA splicing, via spliceosome
GO:0000377	PROCESS	140	3	3.04E-01	1.000	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
GO:0000375	PROCESS	140	3	3.04E-01	1.000	RNA splicing, via transesterification reactions
GO:0030145	FUNCTION	146	7	3.04E-01	1.000	manganese ion binding
GO:0008064	PROCESS	49	2	3.06E-01	1.000	regulation of actin polymerization or depolymerization
GO:0006518	PROCESS	46	2	3.06E-01	1.000	peptide metabolic process
GO:0040012	PROCESS	174	8	3.07E-01	1.000	regulation of locomotion
GO:0000278	PROCESS	328	8	3.08E-01	1.000	mitotic cell cycle
GO:0051252	PROCESS	1601	40	3.10E-01	1.000	regulation of RNA metabolic process
GO:0003704	FUNCTION	34	2	3.11E-01	1.000	specific RNA polymerase II transcription factor activity
GO:0016044	PROCESS	313	12	3.11E-01	1.000	membrane organization
GO:0031093	CELLULAR	38	2	3.13E-01	1.000	platelet alpha granule lumen
GO:0001944	PROCESS	176	8	3.15E-01	1.000	vasculature development
GO:0007126	PROCESS	82	3	3.16E-01	1.000	meiosis
GO:0051327	PROCESS	82	3	3.16E-01	1.000	M phase of meiotic cell cycle
GO:0050954	PROCESS	84	6	3.17E-01	1.000	sensory perception of mechanical stimulus
GO:0043542	PROCESS	16	2	3.17E-01	1.000	endothelial cell migration
GO:0030799	PROCESS	91	5	3.17E-01	1.000	regulation of cyclic nucleotide metabolic process
GO:0051321	PROCESS	84	3	3.19E-01	1.000	meiotic cell cycle
GO:0006950	PROCESS	1334	36	3.20E-01	1.000	response to stress
GO:0016881	FUNCTION	176	6	3.20E-01	1.000	acid-amino acid ligase activity
GO:0004540	FUNCTION	62	2	3.20E-01	1.000	ribonuclease activity
GO:0005624	CELLULAR	613	24	3.21E-01	1.000	membrane fraction
GO:0050790	PROCESS	712	22	3.21E-01	1.000	regulation of catalytic activity
GO:0000302	PROCESS	42	2	3.22E-01	1.000	response to reactive oxygen species
GO:0015085	FUNCTION	12	2	3.22E-01	1.000	calcium ion transmembrane transporter activity
GO:0051329	PROCESS	81	3	3.22E-01	1.000	interphase of mitotic cell cycle
GO:0060191	PROCESS	70	3	3.23E-01	1.000	regulation of lipase activity
GO:0016209	FUNCTION	44	2	3.24E-01	1.000	antioxidant activity
GO:0030666	CELLULAR	31	2	3.25E-01	1.000	endocytic vesicle membrane
GO:0035023	PROCESS	88	6	3.25E-01	1.000	regulation of Rho protein signal transduction
GO:0019941	PROCESS	517	13	3.26E-01	1.000	modification-dependent protein catabolic process
GO:0043632	PROCESS	517	13	3.26E-01	1.000	modification-dependent macromolecule catabolic process
GO:0006352	PROCESS	73	2	3.27E-01	1.000	transcription initiation
GO:0006140	PROCESS	94	5	3.29E-01	1.000	regulation of nucleotide metabolic process
GO:0000082	PROCESS	46	2	3.29E-01	1.000	G1/S transition of mitotic cell cycle
GO:0050670	PROCESS	52	2	3.30E-01	1.000	regulation of lymphocyte proliferation
GO:0005581	CELLULAR	33	3	3.31E-01	1.000	collagen
GO:0006631	PROCESS	179	6	3.32E-01	1.000	fatty acid metabolic process
GO:0030863	CELLULAR	37	2	3.33E-01	1.000	cortical cytoskeleton
GO:0006281	PROCESS	257	7	3.36E-01	1.000	DNA repair
GO:0051270	PROCESS	175	8	3.37E-01	1.000	regulation of cell motion
GO:0043170	PROCESS	3776	97	3.38E-01	1.000	macromolecule metabolic process
GO:0032268	PROCESS	408	12	3.38E-01	1.000	regulation of cellular protein metabolic process
GO:0008104	PROCESS	773	23	3.38E-01	1.000	protein localization
GO:0046328	PROCESS	53	2	3.38E-01	1.000	regulation of JNK cascade
GO:0043283	PROCESS	3670	95	3.39E-01	1.000	biopolymer metabolic process
GO:0000267	CELLULAR	796	29	3.39E-01	1.000	cell fraction
GO:0016810	FUNCTION	107	4	3.39E-01	1.000	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds
GO:0042060	PROCESS	131	5	3.40E-01	1.000	wound healing
GO:0032944	PROCESS	53	2	3.41E-01	1.000	regulation of mononuclear cell proliferation
GO:0070663	PROCESS	53	2	3.41E-01	1.000	regulation of leukocyte proliferation
GO:0060205	CELLULAR	40	2	3.42E-01	1.000	cytoplasmic membrane-bounded vesicle lumen
GO:0031983	CELLULAR	40	2	3.42E-01	1.000	vesicle lumen
GO:0030166	PROCESS	22	2	3.43E-01	1.000	proteoglycan biosynthetic process
GO:0051235	PROCESS	53	2	3.44E-01	1.000	maintenance of location
GO:0060255	PROCESS	2929	72	3.44E-01	1.000	regulation of macromolecule metabolic process
GO:0032561	FUNCTION	343	10	3.44E-01	1.000	guanyl ribonucleotide binding
GO:0019001	FUNCTION	343	10	3.44E-01	1.000	guanyl nucleotide binding
GO:0033554	PROCESS	442	12	3.44E-01	1.000	cellular response to stress
GO:0009411	PROCESS	49	2	3.45E-01	1.000	response to UV

GO:0051325	PROCESS	84	3	3.45E-01	1.000	interphase
GO:0045121	CELLULAR	82	5	3.45E-01	1.000	membrane raft
GO:0034984	PROCESS	299	8	3.46E-01	1.000	cellular response to DNA damage stimulus
GO:0030551	FUNCTION	20	2	3.46E-01	1.000	cyclic nucleotide binding
GO:0001508	PROCESS	49	3	3.48E-01	1.000	regulation of action potential
GO:0034470	PROCESS	175	4	3.49E-01	1.000	ncRNA processing
GO:0004867	FUNCTION	88	3	3.49E-01	1.000	serine-type endopeptidase inhibitor activity
GO:0000793	CELLULAR	102	3	3.49E-01	1.000	condensed chromosome
GO:0031072	FUNCTION	63	2	3.51E-01	1.000	heat shock protein binding
GO:0042391	PROCESS	89	5	3.52E-01	1.000	regulation of membrane potential
GO:0019226	PROCESS	276	15	3.52E-01	1.000	transmission of nerve impulse
GO:0032940	PROCESS	147	7	3.53E-01	1.000	secretion by cell
GO:0048872	PROCESS	61	2	3.53E-01	1.000	homeostasis of number of cells
GO:0014070	PROCESS	29	2	3.53E-01	1.000	response to organic cyclic substance
GO:0070302	PROCESS	54	2	3.53E-01	1.000	regulation of stress-activated protein kinase signaling pathway
GO:0051046	PROCESS	133	5	3.57E-01	1.000	regulation of secretion
GO:0060341	PROCESS	174	6	3.59E-01	1.000	regulation of cellular localization
GO:0005525	FUNCTION	334	9	3.59E-01	1.000	GTP binding
GO:0051899	PROCESS	19	2	3.59E-01	1.000	membrane depolarization
GO:0008376	FUNCTION	31	3	3.60E-01	1.000	acetylgalactosaminyltransferase activity
GO:0016776	FUNCTION	29	2	3.65E-01	1.000	phosphotransferase activity, phosphate group as acceptor
GO:0008201	FUNCTION	88	4	3.65E-01	1.000	heparin binding
GO:0031253	CELLULAR	40	2	3.65E-01	1.000	cell projection membrane
GO:0002521	PROCESS	88	4	3.65E-01	1.000	leukocyte differentiation
GO:0030324	PROCESS	67	3	3.65E-01	1.000	lung development
GO:0044238	PROCESS	4857	124	3.65E-01	1.000	primary metabolic process
GO:0030054	CELLULAR	461	26	3.65E-01	1.000	cell junction
GO:0005834	CELLULAR	26	2	3.66E-01	1.000	heterotrimeric G-protein complex
GO:0007596	PROCESS	82	3	3.67E-01	1.000	blood coagulation
GO:0050817	PROCESS	82	3	3.67E-01	1.000	coagulation
GO:0048660	PROCESS	25	2	3.68E-01	1.000	regulation of smooth muscle cell proliferation
GO:0016835	FUNCTION	50	2	3.71E-01	1.000	carbon-oxygen lyase activity
GO:0007189	PROCESS	33	2	3.71E-01	1.000	activation of adenylate cyclase activity by G-protein signaling pathway
GO:0010579	PROCESS	33	2	3.71E-01	1.000	positive regulation of adenylate cyclase activity by G-protein signaling pathway
GO:0010578	PROCESS	33	2	3.71E-01	1.000	regulation of adenylate cyclase activity involved in G-protein signaling
GO:0034704	CELLULAR	26	3	3.72E-01	1.000	calcium channel complex
GO:0051592	PROCESS	37	3	3.73E-01	1.000	response to calcium ion
GO:0005768	CELLULAR	260	8	3.76E-01	1.000	endosome
GO:0045165	PROCESS	107	4	3.78E-01	1.000	cell fate commitment
GO:0044421	CELLULAR	842	29	3.78E-01	1.000	extracellular region part
GO:0030832	PROCESS	51	2	3.78E-01	1.000	regulation of actin filament length
GO:0007188	PROCESS	67	3	3.79E-01	1.000	G-protein signaling, coupled to cAMP nucleotide second messenger
GO:0019992	FUNCTION	64	5	3.79E-01	1.000	diacylglycerol binding
GO:0007600	PROCESS	703	18	3.82E-01	1.000	sensory perception
GO:0030695	FUNCTION	364	18	3.83E-01	1.000	GTPase regulator activity
GO:0045637	PROCESS	53	2	3.83E-01	1.000	regulation of myeloid cell differentiation
GO:0051223	PROCESS	90	3	3.84E-01	1.000	regulation of protein transport
GO:0010975	PROCESS	42	3	3.86E-01	1.000	regulation of neuron projection development
GO:0050804	PROCESS	65	4	3.87E-01	1.000	regulation of synaptic transmission
GO:0016462	FUNCTION	684	23	3.87E-01	1.000	pyrophosphatase activity
GO:0009605	PROCESS	677	21	3.89E-01	1.000	response to external stimulus
GO:0050727	PROCESS	53	2	3.90E-01	1.000	regulation of inflammatory response
GO:0030659	CELLULAR	112	5	3.91E-01	1.000	cytoplasmic vesicle membrane
GO:0003677	FUNCTION	2132	48	3.91E-01	1.000	DNA binding
GO:0016811	FUNCTION	54	2	3.92E-01	1.000	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides
GO:0016887	FUNCTION	299	12	3.93E-01	1.000	ATPase activity
GO:0051094	PROCESS	504	17	3.94E-01	1.000	positive regulation of developmental process
GO:0080090	PROCESS	2941	73	3.94E-01	1.000	regulation of primary metabolic process
GO:0015837	PROCESS	97	4	3.95E-01	1.000	amine transport
GO:0006355	PROCESS	1570	38	3.95E-01	1.000	regulation of transcription, DNA-dependent
GO:0007254	PROCESS	47	2	3.97E-01	1.000	JNK cascade
GO:0060589	FUNCTION	373	18	3.98E-01	1.000	nucleoside-triphosphatase regulator activity
GO:0016818	FUNCTION	687	23	3.99E-01	1.000	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides
GO:0016798	FUNCTION	103	3	3.99E-01	1.000	hydrolase activity, acting on glycosyl bonds
GO:0007599	PROCESS	86	3	3.99E-01	1.000	hemostasis
GO:0050921	PROCESS	24	2	4.01E-01	1.000	positive regulation of chemotaxis
GO:0040017	PROCESS	24	2	4.01E-01	1.000	positive regulation of locomotion
GO:0004012	FUNCTION	14	2	4.02E-01	1.000	phospholipid-translocating ATPase activity
GO:0015247	FUNCTION	14	2	4.02E-01	1.000	aminophospholipid transporter activity
GO:0006397	PROCESS	296	7	4.02E-01	1.000	mRNA processing
GO:0042157	PROCESS	68	2	4.03E-01	1.000	lipoprotein metabolic process
GO:0042127	PROCESS	603	18	4.03E-01	1.000	regulation of cell proliferation
GO:0003014	PROCESS	19	2	4.03E-01	1.000	renal system process
GO:0005083	FUNCTION	235	12	4.04E-01	1.000	small GTPase regulator activity
GO:0015630	CELLULAR	467	14	4.04E-01	1.000	microtubule cytoskeleton
GO:0016817	FUNCTION	691	23	4.05E-01	1.000	hydrolase activity, acting on acid anhydrides

GO:0046982	FUNCTION	139	5	4.05E-01	1.000	protein heterodimerization activity
GO:0043069	PROCESS	277	8	4.05E-01	1.000	negative regulation of programmed cell death
GO:0060548	PROCESS	277	8	4.05E-01	1.000	negative regulation of cell death
GO:0015698	PROCESS	73	3	4.06E-01	1.000	inorganic anion transport
GO:0005739	CELLULAR	949	21	4.06E-01	1.000	mitochondrion
GO:0044429	CELLULAR	517	11	4.07E-01	1.000	mitochondrial part
GO:0005044	FUNCTION	39	2	4.09E-01	1.000	scavenger receptor activity
GO:0005529	FUNCTION	172	6	4.09E-01	1.000	sugar binding
GO:0010605	PROCESS	589	17	4.11E-01	1.000	negative regulation of macromolecule metabolic process
GO:0042981	PROCESS	607	18	4.12E-01	1.000	regulation of apoptosis
GO:0030323	PROCESS	69	3	4.14E-01	1.000	respiratory tube development
GO:0070201	PROCESS	96	3	4.14E-01	1.000	regulation of establishment of protein localization
GO:0009314	PROCESS	146	5	4.15E-01	1.000	response to radiation
GO:0045017	PROCESS	69	2	4.16E-01	1.000	glycerolipid biosynthetic process
GO:0009790	PROCESS	405	13	4.16E-01	1.000	embryonic development
GO:0007200	PROCESS	43	2	4.17E-01	1.000	activation of phospholipase C activity by G-protein coupled receptor protein signaling pathway coupled to IP3 second messenger
GO:0009205	PROCESS	100	4	4.17E-01	1.000	purine ribonucleoside triphosphate metabolic process
GO:0048520	PROCESS	27	2	4.17E-01	1.000	positive regulation of behavior
GO:0010769	PROCESS	49	3	4.18E-01	1.000	regulation of cell morphogenesis involved in differentiation
GO:0009199	PROCESS	101	4	4.20E-01	1.000	ribonucleoside triphosphate metabolic process
GO:0050920	PROCESS	27	2	4.20E-01	1.000	regulation of chemotaxis
GO:0042221	PROCESS	868	27	4.21E-01	1.000	response to chemical stimulus
GO:0004866	FUNCTION	134	4	4.21E-01	1.000	endopeptidase inhibitor activity
GO:0006974	PROCESS	329	8	4.21E-01	1.000	response to DNA damage stimulus
GO:0046649	PROCESS	135	5	4.21E-01	1.000	lymphocyte activation
GO:0008033	PROCESS	72	2	4.21E-01	1.000	tRNA processing
GO:0009144	PROCESS	101	4	4.21E-01	1.000	purine nucleoside triphosphate metabolic process
GO:0051969	PROCESS	72	4	4.22E-01	1.000	regulation of transmission of nerve impulse
GO:0060541	PROCESS	73	3	4.22E-01	1.000	respiratory system development
GO:0031098	PROCESS	50	2	4.23E-01	1.000	stress-activated protein kinase signaling pathway
GO:0016071	PROCESS	339	8	4.25E-01	1.000	mRNA metabolic process
GO:0044430	CELLULAR	797	24	4.27E-01	1.000	cytoskeletal part
GO:0004252	FUNCTION	150	4	4.28E-01	1.000	serine-type endopeptidase activity
GO:0055085	PROCESS	204	6	4.28E-01	1.000	transmembrane transport
GO:0007050	PROCESS	95	3	4.29E-01	1.000	cell cycle arrest
GO:0030099	PROCESS	64	2	4.29E-01	1.000	myeloid cell differentiation
GO:0007166	PROCESS	1577	46	4.30E-01	1.000	cell surface receptor linked signal transduction
GO:0043176	FUNCTION	80	3	4.30E-01	1.000	amine binding
GO:0032269	PROCESS	126	4	4.31E-01	1.000	negative regulation of cellular protein metabolic process
GO:0019932	PROCESS	199	7	4.31E-01	1.000	second-messenger-mediated signaling
GO:0031644	PROCESS	75	4	4.33E-01	1.000	regulation of neurological system process
GO:0051028	PROCESS	75	2	4.33E-01	1.000	mRNA transport
GO:0016568	PROCESS	246	7	4.33E-01	1.000	chromatin modification
GO:0005743	CELLULAR	243	5	4.34E-01	1.000	mitochondrial inner membrane
GO:0007155	PROCESS	647	34	4.35E-01	1.000	cell adhesion
GO:0001936	PROCESS	29	2	4.35E-01	1.000	regulation of endothelial cell proliferation
GO:0022610	PROCESS	648	34	4.36E-01	1.000	biological adhesion
GO:0009755	PROCESS	48	2	4.39E-01	1.000	hormone-mediated signaling
GO:0012506	CELLULAR	120	5	4.39E-01	1.000	vesicle membrane
GO:0048754	PROCESS	42	2	4.43E-01	1.000	branching morphogenesis of a tube
GO:0006396	PROCESS	509	11	4.43E-01	1.000	RNA processing
GO:0022603	PROCESS	231	9	4.46E-01	1.000	regulation of anatomical structure morphogenesis
GO:0005516	FUNCTION	130	7	4.47E-01	1.000	calmodulin binding
GO:0006865	PROCESS	74	3	4.48E-01	1.000	amino acid transport
GO:0033559	PROCESS	50	2	4.50E-01	1.000	unsaturated fatty acid metabolic process
GO:0005795	CELLULAR	40	2	4.51E-01	1.000	Golgi stack
GO:0046907	PROCESS	548	15	4.51E-01	1.000	intracellular transport
GO:0004713	FUNCTION	147	7	4.52E-01	1.000	protein tyrosine kinase activity
GO:0035239	PROCESS	70	3	4.52E-01	1.000	tube morphogenesis
GO:0031344	PROCESS	54	3	4.52E-01	1.000	regulation of cell projection organization
GO:0010646	PROCESS	801	28	4.53E-01	1.000	regulation of cell communication
GO:0050795	PROCESS	33	2	4.53E-01	1.000	regulation of behavior
GO:0016604	CELLULAR	150	4	4.53E-01	1.000	nuclear body
GO:0009141	PROCESS	107	4	4.54E-01	1.000	nucleoside triphosphate metabolic process
GO:0050870	PROCESS	57	2	4.55E-01	1.000	positive regulation of T cell activation
GO:0019205	FUNCTION	39	2	4.56E-01	1.000	nucleobase, nucleoside, nucleotide kinase activity
GO:0030528	FUNCTION	1359	36	4.57E-01	1.000	transcription regulator activity
GO:0042578	FUNCTION	313	13	4.58E-01	1.000	phosphoric ester hydrolase activity
GO:0032787	PROCESS	266	8	4.59E-01	1.000	monocarboxylic acid metabolic process
GO:0006936	PROCESS	123	6	4.60E-01	1.000	muscle contraction
GO:0046395	PROCESS	98	3	4.60E-01	1.000	carboxylic acid catabolic process
GO:0016054	PROCESS	98	3	4.60E-01	1.000	organic acid catabolic process
GO:0045211	CELLULAR	119	9	4.60E-01	1.000	postsynaptic membrane
GO:0050900	PROCESS	48	2	4.61E-01	1.000	leukocyte migration
GO:0022604	PROCESS	97	5	4.61E-01	1.000	regulation of cell morphogenesis
GO:0019933	PROCESS	73	3	4.61E-01	1.000	cAMP-mediated signaling
GO:0043254	PROCESS	62	2	4.62E-01	1.000	regulation of protein complex assembly
GO:0015082	FUNCTION	31	2	4.62E-01	1.000	di-, tri-valent inorganic cation transmembrane transporter activity

GO:0019222	PROCESS	3218	79	4.64E-01	1.000	regulation of metabolic process
GO:0030098	PROCESS	69	3	4.64E-01	1.000	lymphocyte differentiation
GO:0030855	PROCESS	57	2	4.66E-01	1.000	epithelial cell differentiation
GO:0006650	PROCESS	95	3	4.67E-01	1.000	glycerophospholipid metabolic process
GO:0035295	PROCESS	130	5	4.67E-01	1.000	tube development
GO:0007160	PROCESS	79	4	4.68E-01	1.000	cell-matrix adhesion
GO:0048193	PROCESS	110	3	4.69E-01	1.000	Golgi vesicle transport
GO:0035257	FUNCTION	69	2	4.70E-01	1.000	nuclear hormone receptor binding
GO:0030817	PROCESS	83	4	4.72E-01	1.000	regulation of cAMP biosynthetic process
GO:0051247	PROCESS	163	5	4.73E-01	1.000	positive regulation of protein metabolic process
GO:0031667	PROCESS	102	3	4.76E-01	1.000	response to nutrient levels
GO:0048534	PROCESS	183	6	4.77E-01	1.000	hemopoietic or lymphoid organ development
GO:0032313	PROCESS	43	2	4.79E-01	1.000	regulation of Rab GTPase activity
GO:0032483	PROCESS	43	2	4.79E-01	1.000	regulation of Rab protein signal transduction
GO:0004175	FUNCTION	354	10	4.79E-01	1.000	endopeptidase activity
GO:0045765	PROCESS	83	3	4.79E-01	1.000	regulation of angiogenesis
GO:0003723	FUNCTION	655	15	4.80E-01	1.000	RNA binding
GO:0006357	PROCESS	592	16	4.81E-01	1.000	regulation of transcription from RNA polymerase II promoter
GO:0005097	FUNCTION	44	2	4.81E-01	1.000	Rab GTPase activator activity
GO:0009165	PROCESS	165	6	4.82E-01	1.000	nucleotide biosynthetic process
GO:0005262	FUNCTION	73	6	4.82E-01	1.000	calcium channel activity
GO:0017038	PROCESS	108	3	4.82E-01	1.000	protein import
GO:0016879	FUNCTION	203	6	4.83E-01	1.000	ligase activity, forming carbon-nitrogen bonds
GO:0009150	PROCESS	118	4	4.84E-01	1.000	purine ribonucleotide metabolic process
GO:0006937	PROCESS	54	3	4.84E-01	1.000	regulation of muscle contraction
GO:0006511	PROCESS	207	5	4.85E-01	1.000	ubiquitin-dependent protein catabolic process
GO:0003824	FUNCTION	4762	134	4.85E-01	1.000	catalytic activity
GO:0046930	CELLULAR	86	2	4.85E-01	1.000	pore complex
GO:0006576	PROCESS	81	3	4.85E-01	1.000	biogenic amine metabolic process
GO:0009791	PROCESS	39	2	4.86E-01	1.000	post-embryonic development
GO:0014706	PROCESS	95	4	4.87E-01	1.000	striated muscle tissue development
GO:0001822	PROCESS	64	3	4.88E-01	1.000	kidney development
GO:0051649	PROCESS	697	20	4.89E-01	1.000	establishment of localization in cell
GO:0006940	PROCESS	27	2	4.89E-01	1.000	regulation of smooth muscle contraction
GO:0006725	PROCESS	107	4	4.92E-01	1.000	cellular aromatic compound metabolic process
GO:0019866	CELLULAR	259	5	4.92E-01	1.000	organelle inner membrane
GO:0000075	PROCESS	74	2	4.93E-01	1.000	cell cycle checkpoint
GO:0050793	PROCESS	1051	33	4.93E-01	1.000	regulation of developmental process
GO:0032501	PROCESS	3427	108	4.95E-01	1.000	multicellular organismal process
GO:0004518	FUNCTION	147	3	4.95E-01	1.000	nuclease activity
GO:0007601	PROCESS	205	8	4.95E-01	1.000	visual perception
GO:0050953	PROCESS	205	8	4.95E-01	1.000	sensory perception of light stimulus
GO:0030529	CELLULAR	442	7	4.96E-01	1.000	ribonucleoprotein complex
GO:0010468	PROCESS	2575	60	4.97E-01	1.000	regulation of gene expression
GO:0050890	PROCESS	760	19	4.97E-01	1.000	cognition
GO:0032880	PROCESS	107	3	4.97E-01	1.000	regulation of protein localization
GO:0009187	PROCESS	31	2	4.98E-01	1.000	cyclic nucleotide metabolic process
GO:0007049	PROCESS	696	15	4.98E-01	1.000	cell cycle
GO:0060249	PROCESS	45	2	4.99E-01	1.000	anatomical structure homeostasis
GO:0050880	PROCESS	41	2	5.00E-01	1.000	regulation of blood vessel size
GO:0035150	PROCESS	41	2	5.00E-01	1.000	regulation of tube size
GO:0005891	CELLULAR	21	2	5.00E-01	1.000	voltage-gated calcium channel complex
GO:0030814	PROCESS	86	4	5.02E-01	1.000	regulation of cAMP metabolic process
GO:0006606	PROCESS	71	2	5.02E-01	1.000	protein import into nucleus
GO:0008509	FUNCTION	131	6	5.04E-01	1.000	anion transmembrane transporter activity
GO:0007584	PROCESS	66	2	5.05E-01	1.000	response to nutrient
GO:0005576	CELLULAR	1837	53	5.06E-01	1.000	extracellular region
GO:0007242	PROCESS	1082	35	5.06E-01	1.000	intracellular signaling cascade
GO:0051251	PROCESS	68	2	5.07E-01	1.000	positive regulation of lymphocyte activation
GO:0009124	PROCESS	45	2	5.08E-01	1.000	nucleoside monophosphate biosynthetic process
GO:0051170	PROCESS	73	2	5.08E-01	1.000	nuclear import
GO:0046394	PROCESS	139	4	5.10E-01	1.000	carboxylic acid biosynthetic process
GO:0016053	PROCESS	139	4	5.10E-01	1.000	organic acid biosynthetic process
GO:0006259	PROCESS	444	10	5.11E-01	1.000	DNA metabolic process
GO:0005925	CELLULAR	89	4	5.14E-01	1.000	focal adhesion
GO:0000904	PROCESS	158	9	5.14E-01	1.000	cell morphogenesis involved in differentiation
GO:0060537	PROCESS	100	4	5.15E-01	1.000	muscle tissue development
GO:0051427	FUNCTION	75	2	5.15E-01	1.000	hormone receptor binding
GO:0002520	PROCESS	194	6	5.20E-01	1.000	immune system development
GO:0030336	PROCESS	49	2	5.22E-01	1.000	negative regulation of cell migration
GO:0045202	CELLULAR	266	17	5.23E-01	1.000	synapse
GO:0031967	CELLULAR	520	11	5.23E-01	1.000	organelle envelope
GO:0008022	FUNCTION	114	4	5.23E-01	1.000	protein C-terminus binding
GO:0043066	PROCESS	271	7	5.23E-01	1.000	negative regulation of apoptosis
GO:0001763	PROCESS	48	2	5.25E-01	1.000	morphogenesis of a branching structure
GO:0031328	PROCESS	536	16	5.25E-01	1.000	positive regulation of cellular biosynthetic process
GO:0005102	FUNCTION	771	22	5.26E-01	1.000	receptor binding
GO:0031975	CELLULAR	522	11	5.26E-01	1.000	envelope
GO:0005788	CELLULAR	75	2	5.27E-01	1.000	endoplasmic reticulum lumen

GO:0032555	FUNCTION	1693	53	5.28E-01	1.000	purine ribonucleotide binding
GO:0032553	FUNCTION	1693	53	5.28E-01	1.000	ribonucleotide binding
GO:0019899	FUNCTION	405	14	5.29E-01	1.000	enzyme binding
GO:0004725	FUNCTION	92	5	5.29E-01	1.000	protein tyrosine phosphatase activity
GO:0030203	PROCESS	47	2	5.29E-01	1.000	glycosaminoglycan metabolic process
GO:0001655	PROCESS	74	3	5.30E-01	1.000	urogenital system development
GO:0006575	PROCESS	138	4	5.31E-01	1.000	cellular amino acid derivative metabolic process
GO:0044444	CELLULAR	4282	107	5.33E-01	1.000	cytoplasmic part
GO:0031323	PROCESS	3082	74	5.33E-01	1.000	regulation of cellular metabolic process
GO:0009891	PROCESS	539	16	5.34E-01	1.000	positive regulation of biosynthetic process
GO:0007283	PROCESS	229	5	5.34E-01	1.000	spermatogenesis
GO:0048232	PROCESS	229	5	5.34E-01	1.000	male gamete generation
GO:0003018	PROCESS	44	2	5.37E-01	1.000	vascular process in circulatory system
GO:0007190	PROCESS	47	2	5.38E-01	1.000	activation of adenylate cyclase activity
GO:0007202	PROCESS	55	2	5.39E-01	1.000	activation of phospholipase C activity
GO:0010863	PROCESS	55	2	5.39E-01	1.000	positive regulation of phospholipase C activity
GO:0051641	PROCESS	764	22	5.40E-01	1.000	cellular localization
GO:0016324	CELLULAR	81	4	5.40E-01	1.000	apical plasma membrane
GO:0033365	PROCESS	119	3	5.40E-01	1.000	protein localization in organelle
GO:0010518	PROCESS	56	2	5.42E-01	1.000	positive regulation of phospholipase activity
GO:0045762	PROCESS	48	2	5.45E-01	1.000	positive regulation of adenylate cyclase activity
GO:0048167	PROCESS	29	2	5.45E-01	1.000	regulation of synaptic plasticity
GO:0007264	PROCESS	248	7	5.45E-01	1.000	small GTPase mediated signal transduction
GO:0045595	PROCESS	352	12	5.46E-01	1.000	regulation of cell differentiation
GO:0031589	PROCESS	89	4	5.47E-01	1.000	cell-substrate adhesion
GO:0032559	FUNCTION	1380	46	5.48E-01	1.000	adenyl ribonucleotide binding
GO:0050839	FUNCTION	21	3	5.48E-01	1.000	cell adhesion molecule binding
GO:0016477	PROCESS	196	8	5.48E-01	1.000	cell migration
GO:0051186	PROCESS	169	4	5.49E-01	1.000	cofactor metabolic process
GO:0031281	PROCESS	49	2	5.50E-01	1.000	positive regulation of cyclase activity
GO:0051093	PROCESS	445	13	5.50E-01	1.000	negative regulation of developmental process
GO:0008380	PROCESS	258	5	5.50E-01	1.000	RNA splicing
GO:0004553	FUNCTION	81	2	5.51E-01	1.000	hydrolase activity, hydrolyzing O-glycosyl compounds
GO:0010517	PROCESS	58	2	5.51E-01	1.000	regulation of phospholipase activity
GO:0007010	PROCESS	355	12	5.52E-01	1.000	cytoskeleton organization
GO:0032386	PROCESS	60	2	5.52E-01	1.000	regulation of intracellular transport
GO:0046483	PROCESS	280	9	5.53E-01	1.000	heterocycle metabolic process
GO:0019219	PROCESS	2514	59	5.53E-01	1.000	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
GO:0006310	PROCESS	88	2	5.56E-01	1.000	DNA recombination
GO:0004222	FUNCTION	98	4	5.57E-01	1.000	metalloendopeptidase activity
GO:0005912	CELLULAR	130	7	5.58E-01	1.000	adherens junction
GO:0016829	FUNCTION	139	4	5.58E-01	1.000	lyase activity
GO:0034504	PROCESS	79	2	5.59E-01	1.000	protein localization in nucleus
GO:0015294	FUNCTION	74	3	5.61E-01	1.000	solute:cation symporter activity
GO:0051349	PROCESS	51	2	5.61E-01	1.000	positive regulation of lyase activity
GO:0005178	FUNCTION	51	2	5.61E-01	1.000	integrin binding
GO:0006886	PROCESS	323	8	5.61E-01	1.000	intracellular protein transport
GO:0009206	PROCESS	87	3	5.61E-01	1.000	purine ribonucleoside triphosphate biosynthetic process
GO:0009145	PROCESS	87	3	5.61E-01	1.000	purine nucleoside triphosphate biosynthetic process
GO:0048598	PROCESS	220	6	5.61E-01	1.000	embryonic morphogenesis
GO:0005924	CELLULAR	93	4	5.63E-01	1.000	cell-substrate adherens junction
GO:0009201	PROCESS	88	3	5.64E-01	1.000	ribonucleoside triphosphate biosynthetic process
GO:0009142	PROCESS	88	3	5.64E-01	1.000	nucleoside triphosphate biosynthetic process
GO:0046700	PROCESS	56	2	5.65E-01	1.000	heterocycle catabolic process
GO:0006820	PROCESS	116	4	5.66E-01	1.000	anion transport
GO:0016791	FUNCTION	231	8	5.68E-01	1.000	phosphatase activity
GO:0031324	PROCESS	567	15	5.68E-01	1.000	negative regulation of cellular metabolic process
GO:0002696	PROCESS	76	2	5.68E-01	1.000	positive regulation of leukocyte activation
GO:0051015	FUNCTION	38	2	5.70E-01	1.000	actin filament binding
GO:0007565	PROCESS	76	2	5.71E-01	1.000	female pregnancy
GO:0042623	FUNCTION	238	8	5.72E-01	1.000	ATPase activity, coupled
GO:0051129	PROCESS	114	3	5.72E-01	1.000	negative regulation of cellular component organization
GO:0051239	PROCESS	689	22	5.72E-01	1.000	regulation of multicellular organismal process
GO:0007215	PROCESS	22	2	5.74E-01	1.000	glutamate signaling pathway
GO:0005783	CELLULAR	867	23	5.74E-01	1.000	endoplasmic reticulum
GO:0032956	PROCESS	66	2	5.75E-01	1.000	regulation of actin cytoskeleton organization
GO:0051241	PROCESS	100	3	5.75E-01	1.000	negative regulation of multicellular organismal process
GO:0009991	PROCESS	118	3	5.75E-01	1.000	response to extracellular stimulus
GO:0048870	PROCESS	223	9	5.76E-01	1.000	cell motility
GO:0045182	FUNCTION	106	2	5.79E-01	1.000	translation regulator activity
GO:0030097	PROCESS	163	5	5.79E-01	1.000	hemopoiesis
GO:0003012	PROCESS	153	6	5.80E-01	1.000	muscle system process
GO:0030326	PROCESS	54	2	5.80E-01	1.000	embryonic limb morphogenesis
GO:0035113	PROCESS	54	2	5.80E-01	1.000	embryonic appendage morphogenesis
GO:0051171	PROCESS	2531	59	5.81E-01	1.000	regulation of nitrogen compound metabolic process
GO:0009893	PROCESS	681	20	5.81E-01	1.000	positive regulation of metabolic process
GO:0006519	PROCESS	316	8	5.82E-01	1.000	cellular amino acid and derivative metabolic process
GO:0048646	PROCESS	244	9	5.82E-01	1.000	anatomical structure formation involved in morphogenesis

GO:0000166	FUNCTION	2046	61	5.83E-01	1.000	nucleotide binding
GO:0017076	FUNCTION	1768	54	5.85E-01	1.000	purine nucleotide binding
GO:0032970	PROCESS	69	2	5.85E-01	1.000	regulation of actin filament-based process
GO:0051051	PROCESS	96	3	5.85E-01	1.000	negative regulation of transport
GO:0005125	FUNCTION	191	3	5.85E-01	1.000	cytokine activity
GO:0019216	PROCESS	86	3	5.86E-01	1.000	regulation of lipid metabolic process
GO:0030055	CELLULAR	96	4	5.86E-01	1.000	cell-substrate junction
GO:0030136	CELLULAR	101	4	5.86E-01	1.000	clathrin-coated vesicle
GO:0009259	PROCESS	127	4	5.87E-01	1.000	ribonucleotide metabolic process
GO:0046777	PROCESS	57	2	5.90E-01	1.000	protein amino acid autophosphorylation
GO:0015631	FUNCTION	72	2	5.90E-01	1.000	tubulin binding
GO:0009966	PROCESS	716	23	5.92E-01	1.000	regulation of signal transduction
GO:0009581	PROCESS	60	2	5.93E-01	1.000	detection of external stimulus
GO:0006022	PROCESS	57	2	5.94E-01	1.000	aminoglycan metabolic process
GO:0051716	PROCESS	604	15	5.95E-01	1.000	cellular response to stimulus
GO:0045321	PROCESS	168	5	5.96E-01	1.000	leukocyte activation
GO:0050867	PROCESS	79	2	5.97E-01	1.000	positive regulation of cell activation
GO:0004970	FUNCTION	17	2	5.98E-01	1.000	ionotropic glutamate receptor activity
GO:0005234	FUNCTION	18	2	5.99E-01	1.000	extracellular-glutamate-gated ion channel activity
GO:0003676	FUNCTION	2957	62	6.01E-01	1.000	nucleic acid binding
GO:0045935	PROCESS	484	14	6.01E-01	1.000	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
GO:0031327	PROCESS	459	12	6.01E-01	1.000	negative regulation of cellular biosynthetic process
GO:0010033	PROCESS	417	12	6.01E-01	1.000	response to organic substance
GO:0010038	PROCESS	67	3	6.02E-01	1.000	response to metal ion
GO:0010647	PROCESS	253	7	6.02E-01	1.000	positive regulation of cell communication
GO:0042493	PROCESS	84	3	6.03E-01	1.000	response to drug
GO:0030554	FUNCTION	1453	47	6.04E-01	1.000	adenyl nucleotide binding
GO:0006730	PROCESS	89	2	6.05E-01	1.000	one-carbon metabolic process
GO:0030036	PROCESS	188	7	6.05E-01	1.000	actin cytoskeleton organization
GO:0042445	PROCESS	87	3	6.06E-01	1.000	hormone metabolic process
GO:0040011	PROCESS	333	11	6.07E-01	1.000	locomotion
GO:0046034	PROCESS	89	3	6.08E-01	1.000	ATP metabolic process
GO:0010629	PROCESS	420	11	6.08E-01	1.000	negative regulation of gene expression
GO:0010740	PROCESS	145	3	6.10E-01	1.000	positive regulation of protein kinase cascade
GO:0045944	PROCESS	273	8	6.11E-01	1.000	positive regulation of transcription from RNA polymerase II promoter
GO:0032403	FUNCTION	126	4	6.12E-01	1.000	protein complex binding
GO:0007346	PROCESS	138	3	6.12E-01	1.000	regulation of mitotic cell cycle
GO:0008146	FUNCTION	45	2	6.12E-01	1.000	sulfotransferase activity
GO:0006325	PROCESS	332	7	6.14E-01	1.000	chromatin organization
GO:0009890	PROCESS	465	12	6.16E-01	1.000	negative regulation of biosynthetic process
GO:0005089	FUNCTION	66	4	6.17E-01	1.000	Rho guanyl-nucleotide exchange factor activity
GO:0045893	PROCESS	378	11	6.20E-01	1.000	positive regulation of transcription, DNA-dependent
GO:0031981	CELLULAR	1297	26	6.21E-01	1.000	nuclear lumen
GO:0010035	PROCESS	72	3	6.22E-01	1.000	response to inorganic substance
GO:0031326	PROCESS	2641	61	6.24E-01	1.000	regulation of cellular biosynthetic process
GO:0050863	PROCESS	84	2	6.25E-01	1.000	regulation of T cell activation
GO:0050770	PROCESS	36	2	6.26E-01	1.000	regulation of axonogenesis
GO:0051254	PROCESS	381	11	6.28E-01	1.000	positive regulation of RNA metabolic process
GO:0001883	FUNCTION	1469	47	6.28E-01	1.000	purine nucleoside binding
GO:0006928	PROCESS	361	15	6.29E-01	1.000	cell motion
GO:0051674	PROCESS	361	15	6.29E-01	1.000	localization of cell
GO:0010627	PROCESS	225	5	6.29E-01	1.000	regulation of protein kinase cascade
GO:0005245	FUNCTION	24	2	6.30E-01	1.000	voltage-gated calcium channel activity
GO:0048705	PROCESS	74	2	6.30E-01	1.000	skeletal system morphogenesis
GO:0051173	PROCESS	495	14	6.31E-01	1.000	positive regulation of nitrogen compound metabolic process
GO:0008654	PROCESS	91	2	6.31E-01	1.000	phospholipid biosynthetic process
GO:0043168	FUNCTION	78	3	6.32E-01	1.000	anion binding
GO:0005524	FUNCTION	1366	44	6.34E-01	1.000	ATP binding
GO:0008360	PROCESS	48	2	6.34E-01	1.000	regulation of cell shape
GO:0009889	PROCESS	2649	61	6.34E-01	1.000	regulation of biosynthetic process
GO:0051098	PROCESS	118	3	6.35E-01	1.000	regulation of binding
GO:0032147	PROCESS	83	3	6.35E-01	1.000	activation of protein kinase activity
GO:0007411	PROCESS	71	5	6.36E-01	1.000	axon guidance
GO:0006470	PROCESS	118	5	6.36E-01	1.000	protein amino acid dephosphorylation
GO:0032270	PROCESS	158	4	6.37E-01	1.000	positive regulation of cellular protein metabolic process
GO:0007219	PROCESS	43	2	6.39E-01	1.000	Notch signaling pathway
GO:0050865	PROCESS	125	3	6.40E-01	1.000	regulation of cell activation
GO:0016782	FUNCTION	54	2	6.40E-01	1.000	transferase activity, transferring sulfur-containing groups
GO:0031252	CELLULAR	108	4	6.41E-01	1.000	cell leading edge
GO:0000226	PROCESS	108	2	6.41E-01	1.000	microtubule cytoskeleton organization
GO:0043687	PROCESS	1043	33	6.41E-01	1.000	post-translational protein modification
GO:0051188	PROCESS	88	2	6.41E-01	1.000	cofactor biosynthetic process
GO:0051052	PROCESS	101	2	6.41E-01	1.000	regulation of DNA metabolic process
GO:0016607	CELLULAR	95	2	6.42E-01	1.000	nuclear speck
GO:0015171	FUNCTION	52	2	6.42E-01	1.000	amino acid transmembrane transporter activity
GO:0009967	PROCESS	241	6	6.43E-01	1.000	positive regulation of signal transduction
GO:0007423	PROCESS	159	5	6.45E-01	1.000	sensory organ development
GO:0051271	PROCESS	54	2	6.46E-01	1.000	negative regulation of cell motion

GO:0045449	PROCESS	2339	52	6.47E-01	1.000	regulation of transcription
GO:0001882	FUNCTION	1478	47	6.47E-01	1.000	nucleoside binding
GO:0009416	PROCESS	108	3	6.47E-01	1.000	response to light stimulus
GO:0005911	CELLULAR	156	6	6.47E-01	1.000	cell-cell junction
GO:0031325	PROCESS	658	18	6.49E-01	1.000	positive regulation of cellular metabolic process
GO:0009308	PROCESS	351	9	6.52E-01	1.000	amine metabolic process
GO:0006399	PROCESS	114	2	6.52E-01	1.000	tRNA metabolic process
GO:0005509	FUNCTION	865	38	6.53E-01	1.000	calcium ion binding
GO:0055067	PROCESS	32	2	6.53E-01	1.000	monovalent inorganic cation homeostasis
GO:0048015	PROCESS	75	2	6.57E-01	1.000	phosphoinositide-mediated signaling
GO:0009152	PROCESS	105	3	6.58E-01	1.000	purine ribonucleotide biosynthetic process
GO:0015662	FUNCTION	44	2	6.59E-01	1.000	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism
GO:0043009	PROCESS	229	6	6.59E-01	1.000	chordate embryonic development
GO:0046906	FUNCTION	119	3	6.61E-01	1.000	tetrapyrrole binding
GO:0030135	CELLULAR	126	4	6.62E-01	1.000	coated vesicle
GO:0006633	PROCESS	74	2	6.62E-01	1.000	fatty acid biosynthetic process
GO:0030029	PROCESS	204	7	6.63E-01	1.000	actin filament-based process
GO:0016616	FUNCTION	96	2	6.64E-01	1.000	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
GO:0031974	CELLULAR	1668	33	6.64E-01	1.000	membrane-enclosed lumen
GO:0030016	CELLULAR	91	3	6.65E-01	1.000	myofibril
GO:0019752	PROCESS	497	12	6.65E-01	1.000	carboxylic acid metabolic process
GO:0043436	PROCESS	497	12	6.65E-01	1.000	oxoacid metabolic process
GO:0009792	PROCESS	231	6	6.66E-01	1.000	embryonic development ending in birth or egg hatching
GO:0008544	PROCESS	153	3	6.66E-01	1.000	epidermis development
GO:0043005	CELLULAR	171	9	6.67E-01	1.000	neuron projection
GO:0051253	PROCESS	288	7	6.68E-01	1.000	negative regulation of RNA metabolic process
GO:0006082	PROCESS	500	12	6.69E-01	1.000	organic acid metabolic process
GO:0048469	PROCESS	53	2	6.69E-01	1.000	cell maturation
GO:0048609	PROCESS	68	2	6.70E-01	1.000	reproductive process in a multicellular organism
GO:0032504	PROCESS	68	2	6.70E-01	1.000	multicellular organism reproduction
GO:0006665	PROCESS	67	2	6.72E-01	1.000	sphingolipid metabolic process
GO:0009628	PROCESS	242	7	6.72E-01	1.000	response to abiotic stimulus
GO:0034613	PROCESS	355	8	6.73E-01	1.000	cellular protein localization
GO:0051259	PROCESS	106	3	6.73E-01	1.000	protein oligomerization
GO:0005625	CELLULAR	199	5	6.75E-01	1.000	soluble fraction
GO:0010604	PROCESS	646	18	6.75E-01	1.000	positive regulation of macromolecule metabolic process
GO:0009101	PROCESS	144	5	6.77E-01	1.000	glycoprotein biosynthetic process
GO:0031090	CELLULAR	931	23	6.78E-01	1.000	organelle membrane
GO:0005856	CELLULAR	1187	37	6.79E-01	1.000	cytoskeleton
GO:0043408	PROCESS	83	2	6.80E-01	1.000	regulation of MAPKKK cascade
GO:0070161	CELLULAR	149	7	6.83E-01	1.000	anchoring junction
GO:0042180	PROCESS	507	12	6.86E-01	1.000	cellular ketone metabolic process
GO:0022613	PROCESS	164	2	6.86E-01	1.000	ribonucleoprotein complex biogenesis
GO:0005794	CELLULAR	774	24	6.88E-01	1.000	Golgi apparatus
GO:0070727	PROCESS	358	8	6.91E-01	1.000	cellular macromolecule localization
GO:0043292	CELLULAR	99	3	6.92E-01	1.000	contractile fiber
GO:0009968	PROCESS	195	5	6.94E-01	1.000	negative regulation of signal transduction
GO:0005829	CELLULAR	1075	25	6.95E-01	1.000	cytosol
GO:0051249	PROCESS	102	2	6.95E-01	1.000	regulation of lymphocyte activation
GO:0009617	PROCESS	127	2	6.95E-01	1.000	response to bacterium
GO:0031347	PROCESS	94	2	6.96E-01	1.000	regulation of defense response
GO:0035108	PROCESS	63	2	6.99E-01	1.000	limb morphogenesis
GO:0035107	PROCESS	63	2	6.99E-01	1.000	appendage morphogenesis
GO:0043233	CELLULAR	1637	32	7.01E-01	1.000	organelle lumen
GO:0050878	PROCESS	109	3	7.01E-01	1.000	regulation of body fluid levels
GO:0043269	PROCESS	67	2	7.03E-01	1.000	regulation of ion transport
GO:0016311	PROCESS	133	5	7.03E-01	1.000	dephosphorylation
GO:0007169	PROCESS	186	7	7.04E-01	1.000	transmembrane receptor protein tyrosine kinase signaling pathway
GO:0048812	PROCESS	131	7	7.04E-01	1.000	neuron projection morphogenesis
GO:0001775	PROCESS	201	5	7.05E-01	1.000	cell activation
GO:0009123	PROCESS	55	2	7.06E-01	1.000	nucleoside monophosphate metabolic process
GO:0007178	PROCESS	83	2	7.06E-01	1.000	transmembrane receptor protein serine/threonine kinase signaling pathway
GO:0005099	FUNCTION	80	3	7.06E-01	1.000	Ras GTPase activator activity
GO:0006643	PROCESS	73	2	7.07E-01	1.000	membrane lipid metabolic process
GO:0022414	PROCESS	547	12	7.07E-01	1.000	reproductive process
GO:0050662	FUNCTION	154	4	7.08E-01	1.000	coenzyme binding
GO:0051726	PROCESS	270	5	7.09E-01	1.000	regulation of cell cycle
GO:0010817	PROCESS	111	3	7.10E-01	1.000	regulation of hormone levels
GO:0000003	PROCESS	551	12	7.10E-01	1.000	reproduction
GO:0016614	FUNCTION	108	2	7.13E-01	1.000	oxidoreductase activity, acting on CH-OH group of donors
GO:0005923	CELLULAR	65	2	7.14E-01	1.000	tight junction
GO:0070160	CELLULAR	65	2	7.14E-01	1.000	occluding junction
GO:0009100	PROCESS	181	6	7.15E-01	1.000	glycoprotein metabolic process
GO:0060173	PROCESS	65	2	7.15E-01	1.000	limb development
GO:0048736	PROCESS	65	2	7.15E-01	1.000	appendage development
GO:0007398	PROCESS	167	3	7.15E-01	1.000	ectoderm development

GO:0004930	FUNCTION	743	14	7.15E-01	1.000	G-protein coupled receptor activity
GO:0005088	FUNCTION	78	4	7.16E-01	1.000	Ras guanyl-nucleotide exchange factor activity
GO:0048667	PROCESS	133	7	7.17E-01	1.000	cell morphogenesis involved in neuron differentiation
GO:0005200	FUNCTION	71	2	7.18E-01	1.000	structural constituent of cytoskeleton
GO:0042625	FUNCTION	61	2	7.20E-01	1.000	ATPase activity, coupled to transmembrane movement of ions
GO:0050658	PROCESS	84	2	7.20E-01	1.000	RNA transport
GO:0050657	PROCESS	84	2	7.20E-01	1.000	nucleic acid transport
GO:0051236	PROCESS	84	2	7.20E-01	1.000	establishment of RNA localization
GO:0051276	PROCESS	423	8	7.21E-01	1.000	chromosome organization
GO:0034660	PROCESS	217	3	7.21E-01	1.000	ncRNA metabolic process
GO:0045597	PROCESS	169	5	7.21E-01	1.000	positive regulation of cell differentiation
GO:0044432	CELLULAR	302	7	7.21E-01	1.000	endoplasmic reticulum part
GO:0003924	FUNCTION	181	3	7.22E-01	1.000	GTPase activity
GO:0019199	FUNCTION	80	4	7.23E-01	1.000	transmembrane receptor protein kinase activity
GO:0014069	CELLULAR	43	3	7.23E-01	1.000	postsynaptic density
GO:0004672	FUNCTION	559	19	7.26E-01	1.000	protein kinase activity
GO:0010648	PROCESS	204	5	7.27E-01	1.000	negative regulation of cell communication
GO:0009117	PROCESS	247	7	7.27E-01	1.000	nucleotide metabolic process
GO:0006753	PROCESS	247	7	7.27E-01	1.000	nucleoside phosphate metabolic process
GO:0048858	PROCESS	138	7	7.29E-01	1.000	cell projection morphogenesis
GO:0042110	PROCESS	80	2	7.30E-01	1.000	T cell activation
GO:0044267	PROCESS	2072	51	7.32E-01	1.000	cellular protein metabolic process
GO:0016874	FUNCTION	355	8	7.32E-01	1.000	ligase activity
GO:0019887	FUNCTION	73	2	7.36E-01	1.000	protein kinase regulator activity
GO:0006457	PROCESS	153	2	7.36E-01	1.000	protein folding
GO:0045934	PROCESS	420	10	7.38E-01	1.000	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
GO:0007608	PROCESS	363	4	7.38E-01	1.000	sensory perception of smell
GO:0048523	PROCESS	1309	33	7.38E-01	1.000	negative regulation of cellular process
GO:0004721	FUNCTION	150	5	7.40E-01	1.000	phosphoprotein phosphatase activity
GO:0051172	PROCESS	421	10	7.41E-01	1.000	negative regulation of nitrogen compound metabolic process
GO:0009260	PROCESS	112	3	7.41E-01	1.000	ribonucleotide biosynthetic process
GO:0016070	PROCESS	830	15	7.42E-01	1.000	RNA metabolic process
GO:0031225	CELLULAR	208	8	7.42E-01	1.000	anchored to membrane
GO:0021700	PROCESS	66	2	7.43E-01	1.000	developmental maturation
GO:0004497	FUNCTION	88	2	7.44E-01	1.000	monooxygenase activity
GO:0046942	PROCESS	115	3	7.45E-01	1.000	carboxylic acid transport
GO:0032990	PROCESS	145	7	7.45E-01	1.000	cell part morphogenesis
GO:0010608	PROCESS	184	3	7.45E-01	1.000	posttranscriptional regulation of gene expression
GO:0015849	PROCESS	116	3	7.45E-01	1.000	organic acid transport
GO:0045596	PROCESS	157	4	7.46E-01	1.000	negative regulation of cell differentiation
GO:0007267	PROCESS	497	16	7.46E-01	1.000	cell-cell signaling
GO:0048513	PROCESS	1319	40	7.48E-01	1.000	organ development
GO:0051493	PROCESS	101	2	7.51E-01	1.000	regulation of cytoskeleton organization
GO:0005901	CELLULAR	30	2	7.51E-01	1.000	caveola
GO:0006403	PROCESS	86	2	7.52E-01	1.000	RNA localization
GO:0030674	FUNCTION	84	2	7.54E-01	1.000	protein binding, bridging
GO:0044249	PROCESS	1587	36	7.54E-01	1.000	cellular biosynthetic process
GO:0040008	PROCESS	244	5	7.55E-01	1.000	regulation of growth
GO:0007167	PROCESS	282	10	7.55E-01	1.000	enzyme linked receptor protein signaling pathway
GO:0090066	PROCESS	222	5	7.55E-01	1.000	regulation of anatomical structure size
GO:0044451	CELLULAR	470	9	7.56E-01	1.000	nucleoplasm part
GO:0006351	PROCESS	226	4	7.57E-01	1.000	transcription, DNA-dependent
GO:0045664	PROCESS	85	3	7.57E-01	1.000	regulation of neuron differentiation
GO:0010556	PROCESS	2541	54	7.58E-01	1.000	regulation of macromolecule biosynthetic process
GO:0005730	CELLULAR	628	11	7.59E-01	1.000	nucleolus
GO:0016740	FUNCTION	1568	44	7.62E-01	1.000	transferase activity
GO:0009887	PROCESS	521	15	7.63E-01	1.000	organ morphogenesis
GO:0070013	CELLULAR	1601	30	7.66E-01	1.000	intracellular organelle lumen
GO:0016564	FUNCTION	261	6	7.66E-01	1.000	transcription repressor activity
GO:0016337	PROCESS	256	11	7.67E-01	1.000	cell-cell adhesion
GO:0010628	PROCESS	455	12	7.67E-01	1.000	positive regulation of gene expression
GO:0005085	FUNCTION	140	6	7.68E-01	1.000	guanyl-nucleotide exchange factor activity
GO:0032774	PROCESS	230	4	7.70E-01	1.000	RNA biosynthetic process
GO:0000902	PROCESS	218	9	7.71E-01	1.000	cell morphogenesis
GO:0044270	PROCESS	85	2	7.72E-01	1.000	nitrogen compound catabolic process
GO:0005001	FUNCTION	18	2	7.72E-01	1.000	transmembrane receptor protein tyrosine phosphatase activity
GO:0019198	FUNCTION	18	2	7.72E-01	1.000	transmembrane receptor protein phosphatase activity
GO:0044087	PROCESS	108	2	7.73E-01	1.000	regulation of cellular component biogenesis
GO:0030031	PROCESS	60	2	7.73E-01	1.000	cell projection assembly
GO:0044237	PROCESS	4589	106	7.73E-01	1.000	cellular metabolic process
GO:0006754	PROCESS	78	2	7.74E-01	1.000	ATP biosynthetic process
GO:0008283	PROCESS	302	7	7.74E-01	1.000	cell proliferation
GO:0045941	PROCESS	440	11	7.75E-01	1.000	positive regulation of transcription
GO:0055086	PROCESS	267	7	7.75E-01	1.000	nucleobase, nucleoside and nucleotide metabolic process
GO:0006412	PROCESS	273	3	7.76E-01	1.000	translation
GO:0019207	FUNCTION	83	2	7.77E-01	1.000	kinase regulator activity
GO:0005813	CELLULAR	191	4	7.77E-01	1.000	centrosome
GO:0003712	FUNCTION	325	7	7.77E-01	1.000	transcription cofactor activity

GO:0004674	FUNCTION	395	12	7.80E-01	1.000	protein serine/threonine kinase activity
GO:0032870	PROCESS	96	2	7.80E-01	1.000	cellular response to hormone stimulus
GO:0043062	PROCESS	104	3	7.81E-01	1.000	extracellular structure organization
GO:0007409	PROCESS	123	6	7.81E-01	1.000	axonogenesis
GO:0044456	CELLULAR	182	10	7.82E-01	1.000	synapse part
GO:0033043	PROCESS	179	3	7.84E-01	1.000	regulation of organelle organization
GO:0005789	CELLULAR	228	5	7.86E-01	1.000	endoplasmic reticulum membrane
GO:0051707	PROCESS	219	3	7.89E-01	1.000	response to other organism
GO:0008083	FUNCTION	151	3	7.90E-01	1.000	growth factor activity
GO:0045892	PROCESS	283	6	7.91E-01	1.000	negative regulation of transcription, DNA-dependent
GO:0008037	PROCESS	47	3	7.91E-01	1.000	cell recognition
GO:0044446	CELLULAR	3686	79	7.95E-01	1.000	intracellular organelle part
GO:0016323	CELLULAR	150	5	7.95E-01	1.000	basolateral plasma membrane
GO:0031404	FUNCTION	66	2	7.96E-01	1.000	chloride ion binding
GO:0005654	CELLULAR	781	14	7.98E-01	1.000	nucleoplasm
GO:0006366	PROCESS	176	3	8.01E-01	1.000	transcription from RNA polymerase II promoter
GO:0045296	FUNCTION	13	2	8.02E-01	1.000	cadherin binding
GO:0030027	CELLULAR	57	2	8.02E-01	1.000	lamellipodium
GO:0006520	PROCESS	213	4	8.02E-01	1.000	cellular amino acid metabolic process
GO:0044106	PROCESS	213	4	8.02E-01	1.000	cellular amine metabolic process
GO:0001817	PROCESS	130	2	8.03E-01	1.000	regulation of cytokine production
GO:0044428	CELLULAR	1605	30	8.04E-01	1.000	nuclear part
GO:0007606	PROCESS	405	4	8.06E-01	1.000	sensory perception of chemical stimulus
GO:0009058	PROCESS	1657	37	8.07E-01	1.000	biosynthetic process
GO:0015931	PROCESS	99	2	8.07E-01	1.000	nucleobase, nucleoside, nucleotide and nucleic acid transport
GO:0030534	PROCESS	59	2	8.09E-01	1.000	adult behavior
GO:0042995	CELLULAR	464	18	8.11E-01	1.000	cell projection
GO:0012505	CELLULAR	680	18	8.12E-01	1.000	endomembrane system
GO:0003777	FUNCTION	72	2	8.12E-01	1.000	microtubule motor activity
GO:0005254	FUNCTION	63	2	8.13E-01	1.000	chloride channel activity
GO:0030900	PROCESS	88	2	8.14E-01	1.000	forebrain development
GO:0005976	PROCESS	97	2	8.14E-01	1.000	polysaccharide metabolic process
GO:0020037	FUNCTION	111	2	8.14E-01	1.000	heme binding
GO:0005634	CELLULAR	4571	94	8.15E-01	1.000	nucleus
GO:0005253	FUNCTION	67	2	8.21E-01	1.000	anion channel activity
GO:0007276	PROCESS	286	5	8.21E-01	1.000	gamete generation
GO:0048519	PROCESS	1431	36	8.23E-01	1.000	negative regulation of biological process
GO:0007017	PROCESS	207	4	8.23E-01	1.000	microtubule-based process
GO:0051050	PROCESS	159	3	8.24E-01	1.000	positive regulation of transport
GO:0006486	PROCESS	119	3	8.24E-01	1.000	protein amino acid glycosylation
GO:0043413	PROCESS	119	3	8.24E-01	1.000	biopolymer glycosylation
GO:0070085	PROCESS	119	3	8.24E-01	1.000	glycosylation
GO:0006913	PROCESS	132	2	8.24E-01	1.000	nucleocytoplasmic transport
GO:0005694	CELLULAR	386	5	8.25E-01	1.000	chromosome
GO:0051240	PROCESS	147	3	8.26E-01	1.000	positive regulation of multicellular organismal process
GO:0051169	PROCESS	134	2	8.28E-01	1.000	nuclear transport
GO:0043405	PROCESS	115	2	8.29E-01	1.000	regulation of MAP kinase activity
GO:0032989	PROCESS	246	9	8.29E-01	1.000	cellular component morphogenesis
GO:0010557	PROCESS	513	12	8.29E-01	1.000	positive regulation of macromolecule biosynthetic process
GO:0055114	PROCESS	570	12	8.30E-01	1.000	oxidation reduction
GO:0002694	PROCESS	119	2	8.30E-01	1.000	regulation of leukocyte activation
GO:0016301	FUNCTION	717	22	8.31E-01	1.000	kinase activity
GO:0050767	PROCESS	110	3	8.31E-01	1.000	regulation of neurogenesis
GO:0006807	PROCESS	1885	39	8.33E-01	1.000	nitrogen compound metabolic process
GO:0006732	PROCESS	132	2	8.35E-01	1.000	coenzyme metabolic process
GO:0042175	CELLULAR	241	5	8.35E-01	1.000	nuclear envelope-endoplasmic reticulum network
GO:0044422	CELLULAR	3708	79	8.37E-01	1.000	organelle part
GO:0003714	FUNCTION	124	2	8.37E-01	1.000	transcription corepressor activity
GO:0044260	PROCESS	3304	73	8.38E-01	1.000	cellular macromolecule metabolic process
GO:0044449	CELLULAR	91	2	8.38E-01	1.000	contractile fiber part
GO:0005201	FUNCTION	76	2	8.40E-01	1.000	extracellular matrix structural constituent
GO:0009607	PROCESS	304	4	8.41E-01	1.000	response to biotic stimulus
GO:0044092	PROCESS	277	5	8.42E-01	1.000	negative regulation of molecular function
GO:0016481	PROCESS	378	8	8.42E-01	1.000	negative regulation of transcription
GO:0005815	CELLULAR	213	4	8.43E-01	1.000	microtubule organizing center
GO:0000139	CELLULAR	172	4	8.43E-01	1.000	Golgi membrane
GO:0030030	PROCESS	239	10	8.44E-01	1.000	cell projection organization
GO:0031175	PROCESS	155	7	8.47E-01	1.000	neuron projection development
GO:0005874	CELLULAR	240	5	8.48E-01	1.000	microtubule
GO:0006605	PROCESS	180	3	8.49E-01	1.000	protein targeting
GO:0070887	PROCESS	197	4	8.49E-01	1.000	cellular response to chemical stimulus
GO:0006139	PROCESS	1548	30	8.51E-01	1.000	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
GO:0032535	PROCESS	184	3	8.51E-01	1.000	regulation of cellular component size
GO:0001666	PROCESS	72	2	8.52E-01	1.000	response to hypoxia
GO:0006464	PROCESS	1290	36	8.52E-01	1.000	protein modification process
GO:0043086	PROCESS	233	4	8.52E-01	1.000	negative regulation of catalytic activity
GO:0006350	PROCESS	268	4	8.53E-01	1.000	transcription
GO:0043412	PROCESS	1356	37	8.53E-01	1.000	biopolymer modification
GO:0045761	PROCESS	79	2	8.53E-01	1.000	regulation of adenylate cyclase activity

GO:0034641	PROCESS	224	4	8.53E-01	1.000	cellular nitrogen compound metabolic process
GO:0000122	PROCESS	205	4	8.54E-01	1.000	negative regulation of transcription from RNA polymerase II promoter
GO:0060429	PROCESS	117	2	8.54E-01	1.000	epithelium development
GO:0045860	PROCESS	172	4	8.54E-01	1.000	positive regulation of protein kinase activity
GO:0016773	FUNCTION	667	20	8.54E-01	1.000	phosphotransferase activity, alcohol group as acceptor
GO:0001501	PROCESS	243	5	8.55E-01	1.000	skeletal system development
GO:0034960	PROCESS	3187	70	8.55E-01	1.000	cellular biopolymer metabolic process
GO:0070482	PROCESS	74	2	8.55E-01	1.000	response to oxygen levels
GO:0033674	PROCESS	173	4	8.56E-01	1.000	positive regulation of kinase activity
GO:0046943	FUNCTION	80	2	8.58E-01	1.000	carboxylic acid transmembrane transporter activity
GO:0005342	FUNCTION	81	2	8.59E-01	1.000	organic acid transmembrane transporter activity
GO:0007610	PROCESS	349	9	8.59E-01	1.000	behavior
GO:0031279	PROCESS	81	2	8.60E-01	1.000	regulation of cyclase activity
GO:0005578	CELLULAR	290	10	8.61E-01	1.000	proteinaceous extracellular matrix
GO:0048666	PROCESS	211	8	8.61E-01	1.000	neuron development
GO:0051339	PROCESS	83	2	8.64E-01	1.000	regulation of lyase activity
GO:0010558	PROCESS	450	9	8.64E-01	1.000	negative regulation of macromolecule biosynthetic process
GO:0051960	PROCESS	125	3	8.66E-01	1.000	regulation of nervous system development
GO:0017124	FUNCTION	83	2	8.71E-01	1.000	SH3 domain binding
GO:0007018	PROCESS	98	2	8.71E-01	1.000	microtubule-based movement
GO:0008066	FUNCTION	29	2	8.71E-01	1.000	glutamate receptor activity
GO:0042626	FUNCTION	93	3	8.74E-01	1.000	ATPase activity, coupled to transmembrane movement of substances
GO:0051347	PROCESS	180	4	8.75E-01	1.000	positive regulation of transferase activity
GO:0044420	CELLULAR	97	3	8.77E-01	1.000	extracellular matrix part
GO:0043492	FUNCTION	94	3	8.77E-01	1.000	ATPase activity, coupled to movement of substances
GO:0044271	PROCESS	132	2	8.78E-01	1.000	nitrogen compound biosynthetic process
GO:0016820	FUNCTION	95	3	8.78E-01	1.000	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances
GO:0048037	FUNCTION	214	4	8.80E-01	1.000	cofactor binding
GO:0048468	PROCESS	587	18	8.81E-01	1.000	cell development
GO:0018193	PROCESS	122	2	8.82E-01	1.000	peptidyl-amino acid modification
GO:0016772	FUNCTION	833	23	8.85E-01	1.000	transferase activity, transferring phosphorus-containing groups
GO:0043296	CELLULAR	89	2	8.85E-01	1.000	apical junction complex
GO:0015405	FUNCTION	104	3	8.85E-01	1.000	P-P-bond-hydrolysis-driven transmembrane transporter activity
GO:0015399	FUNCTION	104	3	8.85E-01	1.000	primary active transmembrane transporter activity
GO:0004984	FUNCTION	346	2	8.86E-01	1.000	olfactory receptor activity
GO:0003713	FUNCTION	196	3	8.89E-01	1.000	transcription coactivator activity
GO:0005496	FUNCTION	112	2	8.90E-01	1.000	steroid binding
GO:0007275	PROCESS	2322	69	8.92E-01	1.000	multicellular organismal development
GO:0031012	CELLULAR	308	10	8.94E-01	1.000	extracellular matrix
GO:0048699	PROCESS	367	12	8.96E-01	1.000	generation of neurons
GO:0009653	PROCESS	843	24	8.98E-01	1.000	anatomical structure morphogenesis
GO:0043284	PROCESS	741	11	9.01E-01	1.000	biopolymer biosynthetic process
GO:0019953	PROCESS	343	5	9.03E-01	1.000	sexual reproduction
GO:0016327	CELLULAR	92	2	9.05E-01	1.000	apicolateral plasma membrane
GO:0009059	PROCESS	930	16	9.05E-01	1.000	macromolecule biosynthetic process
GO:0008285	PROCESS	288	6	9.07E-01	1.000	negative regulation of cell proliferation
GO:0060284	PROCESS	138	3	9.08E-01	1.000	regulation of cell development
GO:0044427	CELLULAR	314	3	9.08E-01	1.000	chromosomal part
GO:0001558	PROCESS	134	2	9.10E-01	1.000	regulation of cell growth
GO:0016563	FUNCTION	341	6	9.10E-01	1.000	transcription activator activity
GO:0009719	PROCESS	200	4	9.10E-01	1.000	response to endogenous stimulus
GO:0009725	PROCESS	186	3	9.10E-01	1.000	response to hormone stimulus
GO:0045859	PROCESS	278	5	9.12E-01	1.000	regulation of protein kinase activity
GO:0043232	CELLULAR	2236	50	9.13E-01	1.000	intracellular non-membrane-bounded organelle
GO:0043228	CELLULAR	2236	50	9.13E-01	1.000	non-membrane-bounded organelle
GO:0000165	PROCESS	142	2	9.13E-01	1.000	MAPKKK cascade
GO:0043549	PROCESS	283	5	9.14E-01	1.000	regulation of kinase activity
GO:0019900	FUNCTION	124	2	9.15E-01	1.000	kinase binding
GO:0016491	FUNCTION	624	12	9.15E-01	1.000	oxidoreductase activity
GO:0007507	PROCESS	158	3	9.16E-01	1.000	heart development
GO:0009055	FUNCTION	198	3	9.16E-01	1.000	electron carrier activity
GO:0006468	PROCESS	588	16	9.20E-01	1.000	protein amino acid phosphorylation
GO:0030154	PROCESS	1245	35	9.20E-01	1.000	cell differentiation
GO:0034645	PROCESS	912	15	9.22E-01	1.000	cellular macromolecule biosynthetic process
GO:0022008	PROCESS	392	12	9.24E-01	1.000	neurogenesis
GO:0009888	PROCESS	537	10	9.25E-01	1.000	tissue development
GO:0008134	FUNCTION	450	8	9.27E-01	1.000	transcription factor binding
GO:0048729	PROCESS	134	2	9.28E-01	1.000	tissue morphogenesis
GO:0006796	PROCESS	848	23	9.29E-01	1.000	phosphate metabolic process
GO:0006793	PROCESS	848	23	9.29E-01	1.000	phosphorus metabolic process
GO:0004714	FUNCTION	64	2	9.29E-01	1.000	transmembrane receptor protein tyrosine kinase activity
GO:0051338	PROCESS	294	5	9.30E-01	1.000	regulation of transferase activity
GO:0009898	CELLULAR	292	6	9.31E-01	1.000	internal side of plasma membrane
GO:0005759	CELLULAR	210	2	9.32E-01	1.000	mitochondrial matrix
GO:0031980	CELLULAR	210	2	9.32E-01	1.000	mitochondrial lumen
GO:0034961	PROCESS	731	10	9.34E-01	1.000	cellular biopolymer biosynthetic process
GO:0051130	PROCESS	137	2	9.36E-01	1.000	positive regulation of cellular component organization
GO:0048471	CELLULAR	223	4	9.36E-01	1.000	perinuclear region of cytoplasm

GO:0030182	PROCESS	283	9	9.36E-01	1.000	neuron differentiation
GO:0048869	PROCESS	1286	35	9.45E-01	1.000	cellular developmental process
GO:0044463	CELLULAR	134	3	9.46E-01	1.000	cell projection part
GO:0016310	PROCESS	696	17	9.47E-01	1.000	phosphorylation
GO:0005635	CELLULAR	176	2	9.49E-01	1.000	nuclear envelope
GO:0044431	CELLULAR	257	5	9.56E-01	1.000	Golgi apparatus part
GO:0007626	PROCESS	216	4	9.57E-01	1.000	locomotory behavior
GO:0032502	PROCESS	2538	71	9.59E-01	1.000	developmental process
GO:0042325	PROCESS	373	6	9.59E-01	1.000	regulation of phosphorylation
GO:0005506	FUNCTION	278	4	9.59E-01	1.000	iron ion binding
GO:0005198	FUNCTION	555	9	9.60E-01	1.000	structural molecule activity
GO:0048731	PROCESS	1804	51	9.67E-01	1.000	system development
GO:0007156	PROCESS	131	3	9.69E-01	1.000	homophilic cell adhesion
GO:0005975	PROCESS	455	7	9.70E-01	1.000	carbohydrate metabolic process
GO:0007420	PROCESS	184	4	9.72E-01	1.000	brain development
GO:0019220	PROCESS	387	6	9.73E-01	1.000	regulation of phosphate metabolic process
GO:0051174	PROCESS	387	6	9.73E-01	1.000	regulation of phosphorus metabolic process
GO:0007417	PROCESS	293	8	9.78E-01	1.000	central nervous system development
GO:0048856	PROCESS	1940	53	9.80E-01	1.000	anatomical structure development
GO:0007243	PROCESS	292	4	9.81E-01	1.000	protein kinase cascade
GO:0044262	PROCESS	257	3	9.83E-01	1.000	cellular carbohydrate metabolic process
GO:0019904	FUNCTION	253	4	9.86E-01	1.000	protein domain specific binding
GO:0007399	PROCESS	802	21	9.98E-01	1.000	nervous system development