

Supplementary Materials

Unraveling the role of *Scutellaria baicalensis* for the treatment of breast cancer using network pharmacology, molecular docking, and molecular dynamics simulation

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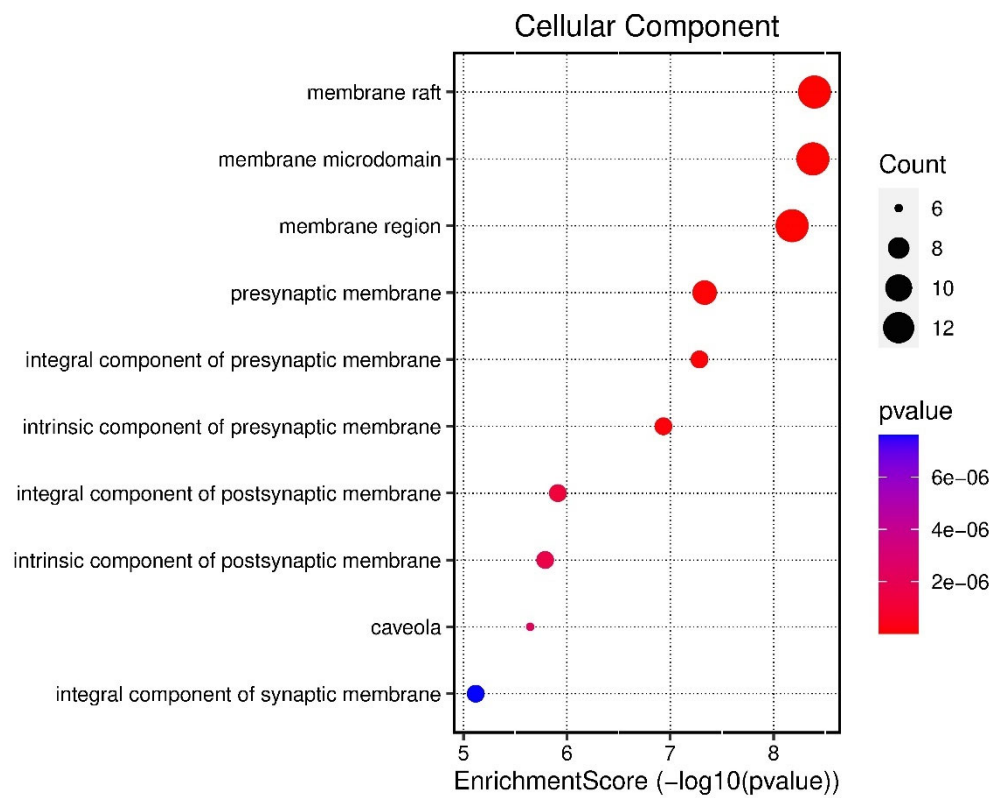


Figure S1 Bubble diagram of Cellular Component (CC) enrichment.

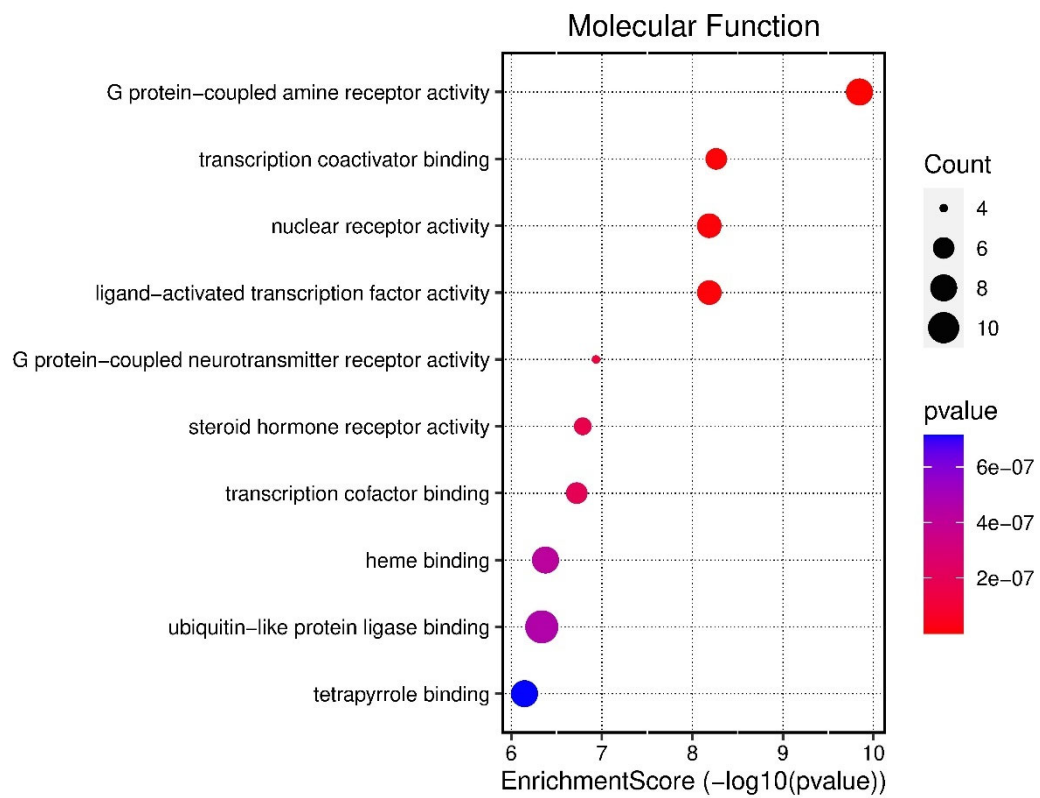


Figure S2 Bubble diagram of Molecular Function (MF) enrichment.

Table S1. Results of BP GO terms enrichment of *Scutellaria baicalensis* in breast cancer.

ID	Description	pvalue	qvalue	Count
GO:00424 93	response to drug	8.16198E- 19	1.47689E- 15	23
GO:00485 45	response to steroid hormone	2.14771E- 16	1.94311E- 13	21
GO:00324 96	response to lipopolysaccharide	1.77376E- 15	1.06986E- 12	20
GO:00069 79	response to oxidative stress	3.59148E- 15	1.62467E- 12	19
GO:00022 37	response to molecule of bacterial origin	5.67948E- 15	2.05538E- 12	19
GO:00075 68	aging	1.83192E- 13	5.52467E- 11	19
GO:00199 32	second-messenger-mediated signaling	4.82922E- 13	1.20972E- 10	18
GO:00725 93	reactive oxygen species metabolic process	5.34839E- 13	1.20972E- 10	18
GO:19012 16	positive regulation of neuron death	1.25039E- 12	2.33344E- 10	18
GO:00621 97	cellular response to chemical stress	1.28957E- 12	2.33344E- 10	17
GO:19012 14	regulation of neuron death	2.79866E- 12	4.55218E- 10	17
GO:00486 08	reproductive structure development	3.27047E- 12	4.55218E- 10	17
GO:00487 32	gland development	3.27047E- 12	4.55218E- 10	16
GO:00614 58	reproductive system development	3.79982E- 12	4.9112E- 10	16
GO:00003 02	response to reactive oxygen species	6.71133E- 12	8.09598E- 10	16
GO:19016 54	response to ketone	1.34143E- 11	1.51705E- 09	16
GO:00709 97	neuron death	1.576E-11	1.67749E- 09	16
GO:00100 38	response to metal ion	2.01817E- 11	2.02879E- 09	16
GO:00345 99	cellular response to oxidative stress	2.18591E- 11	2.08176E- 09	15
GO:00506 73	epithelial cell proliferation	4.89034E- 11	4.42447E- 09	15
GO:00343 49	glial cell apoptotic process	5.14895E- 11	4.43661E- 09	15

GO:00094 11	response to UV	7.20491E- 11	5.92595E- 09	15
GO:00323 55	response to estradiol	7.78408E- 11	6.12395E- 09	14
GO:00308 79	mammary gland development	8.4048E- 11	6.33678E- 09	14
GO:20012 34	negative regulation of apoptotic signaling pathway	9.10494E- 11	6.59006E- 09	14
GO:00030 18	vascular process in circulatory system	1.21104E- 10	8.1953E- 09	14
GO:00513 84	response to glucocorticoid	1.22286E- 10	8.1953E- 09	13
GO:00486 38	regulation of developmental growth	1.35771E- 10	8.77407E- 09	13
GO:00063 52	DNA-templated transcription, initiation	2.07491E- 10	1.27262E- 08	13
GO:00485 11	rhythmic process	2.16252E- 10	1.27262E- 08	13
GO:00096 36	response to toxic substance	2.18026E- 10	1.27262E- 08	13
GO:00423 91	regulation of membrane potential	3.38765E- 10	1.91559E- 08	13
GO:00435 25	positive regulation of neuron apoptotic process	3.88256E- 10	2.11364E- 08	13
GO:00319 60	response to corticosteroid	3.97152E- 10	2.11364E- 08	13
GO:19028 95	positive regulation of pri-miRNA transcription by RNA polymerase II	7.86857E- 10	4.06799E- 08	13
GO:00316 67	response to nutrient levels	8.77387E- 10	4.37367E- 08	13
GO:00447 06	multi-multicellular organism process	8.94326E- 10	4.37367E- 08	13
GO:00971 91	extrinsic apoptotic signaling pathway	1.09256E- 09	5.2025E- 08	12
GO:20012 33	regulation of apoptotic signaling pathway	1.18792E- 09	5.51156E- 08	12
GO:00973 05	response to alcohol	1.32964E- 09	5.93153E- 08	12
GO:00971 93	intrinsic apoptotic signaling pathway	1.344E-09	5.93153E- 08	12
GO:00352 96	regulation of tube diameter	1.73608E- 09	7.30555E- 08	12
GO:00977 46	regulation of blood vessel diameter	1.73608E- 09	7.30555E- 08	12

GO:00063 67	transcription initiation from RNA polymerase II promoter	1.79627E- 09	7.38707E- 08	12
GO:00351 50	regulation of tube size	1.85834E- 09	7.47247E- 08	12
GO:00330 02	muscle cell proliferation	2.13838E- 09	8.41163E- 08	12
GO:20012 37	negative regulation of extrinsic apoptotic signaling pathway	2.29746E- 09	8.84508E- 08	12
GO:00075 65	female pregnancy	2.63575E- 09	9.93609E- 08	12
GO:00380 34	signal transduction in absence of ligand	2.77439E- 09	1.00404E- 07	12
GO:00971 92	extrinsic apoptotic signaling pathway in absence of ligand	2.77439E- 09	1.00404E- 07	12
GO:00199 33	cAMP-mediated signaling	3.09229E- 09	1.09714E- 07	12
GO:00093 14	response to radiation	3.4837E- 09	1.21224E- 07	12
GO:00018 90	placenta development	4.04777E- 09	1.38195E- 07	12
GO:00094 16	response to light stimulus	4.25154E- 09	1.42464E- 07	11
GO:19028 93	regulation of pri-miRNA transcription by RNA polymerase II	4.681E-09	1.54003E- 07	11
GO:00071 87	G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	4.98268E- 09	1.61001E- 07	11
GO:00096 12	response to mechanical stimulus	5.16969E- 09	1.64113E- 07	11
GO:00506 78	regulation of epithelial cell proliferation	6.11762E- 09	1.87395E- 07	11
GO:00616 14	pri-miRNA transcription by RNA polymerase II	6.18384E- 09	1.87395E- 07	11
GO:00481 45	regulation of fibroblast proliferation	6.2861E- 09	1.87395E- 07	11
GO:00704 82	response to oxygen levels	6.31737E- 09	1.87395E- 07	11
GO:00435 23	regulation of neuron apoptotic process	6.61719E- 09	1.93123E- 07	11
GO:00481 44	fibroblast proliferation	6.92061E- 09	1.96406E- 07	11
GO:00432 81	regulation of cysteine-type endopeptidase activity involved in apoptotic process	6.94676E- 09	1.96406E- 07	11
GO:00199 35	cyclic-nucleotide-mediated signaling	1.06415E- 08	2.9624E- 07	11

GO:0043270	positive regulation of ion transport	1.17636E-08	3.22513E-07	11
GO:0031649	heat generation	1.3811E-08	3.72994E-07	11
GO:0007188	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	1.60009E-08	4.25782E-07	11
GO:0001666	response to hypoxia	1.7384E-08	4.55883E-07	11
GO:2000116	regulation of cysteine-type endopeptidase activity	2.07998E-08	5.37667E-07	11
GO:0036293	response to decreased oxygen levels	2.56242E-08	6.38417E-07	11
GO:0060749	mammary gland alveolus development	2.57558E-08	6.38417E-07	11
GO:0061377	mammary gland lobule development	2.57558E-08	6.38417E-07	11
GO:0051402	neuron apoptotic process	2.68429E-08	6.56372E-07	11
GO:0071216	cellular response to biotic stimulus	2.79896E-08	6.75286E-07	11
GO:0018105	peptidyl-serine phosphorylation	3.10234E-08	7.38632E-07	11
GO:0051412	response to corticosterone	3.42107E-08	8.03939E-07	11
GO:0001935	endothelial cell proliferation	4.16246E-08	9.65624E-07	11
GO:2000377	regulation of reactive oxygen species metabolic process	4.36439E-08	9.99651E-07	11
GO:0061180	mammary gland epithelium development	4.97338E-08	1.1249E-06	11
GO:0071887	leukocyte apoptotic process	5.08668E-08	1.13632E-06	11
GO:0018209	peptidyl-serine modification	6.79557E-08	1.49956E-06	11
GO:0050679	positive regulation of epithelial cell proliferation	7.22707E-08	1.57557E-06	11
GO:2001236	regulation of extrinsic apoptotic signaling pathway	8.72146E-08	1.87872E-06	11
GO:0042310	vasoconstriction	9.61378E-08	2.04657E-06	11
GO:0043536	positive regulation of blood vessel endothelial cell migration	1.05074E-07	2.2108E-06	10
GO:0010822	positive regulation of mitochondrion organization	1.0854E-07	2.25748E-06	10

GO:0002064	epithelial cell development	1.11516E-07	2.29302E-06	10
GO:0034614	cellular response to reactive oxygen species	1.31844E-07	2.65366E-06	10
GO:0051222	positive regulation of protein transport	1.31988E-07	2.65366E-06	10
GO:0030099	myeloid cell differentiation	1.46758E-07	2.91818E-06	10
GO:0022612	gland morphogenesis	1.4941E-07	2.93862E-06	10
GO:0048660	regulation of smooth muscle cell proliferation	1.53098E-07	2.97059E-06	10
GO:0032409	regulation of transporter activity	1.54318E-07	2.97059E-06	10
GO:0008637	apoptotic mitochondrial changes	1.59002E-07	3.02852E-06	10
GO:0048146	positive regulation of fibroblast proliferation	1.61197E-07	3.03836E-06	10
GO:0048659	smooth muscle cell proliferation	1.68871E-07	3.15019E-06	10
GO:0010634	positive regulation of epithelial cell migration	1.77275E-07	3.27321E-06	10
GO:0097756	negative regulation of blood vessel diameter	1.89522E-07	3.464E-06	10
GO:0071880	adenylate cyclase-activating adrenergic receptor signaling pathway	2.10364E-07	3.7696E-06	10
GO:0045862	positive regulation of proteolysis	2.12492E-07	3.7696E-06	10
GO:1904951	positive regulation of establishment of protein localization	2.12492E-07	3.7696E-06	10
GO:2001235	positive regulation of apoptotic signaling pathway	2.46984E-07	4.33895E-06	10
GO:0001936	regulation of endothelial cell proliferation	2.58669E-07	4.50053E-06	10
GO:0046683	response to organophosphorus	2.71921E-07	4.66042E-06	10
GO:0051090	regulation of DNA-binding transcription factor activity	2.7301E-07	4.66042E-06	10
GO:0051899	membrane depolarization	2.79977E-07	4.73468E-06	10
GO:0042133	neurotransmitter metabolic process	3.02718E-07	5.07186E-06	10
GO:0001701	in utero embryonic development	3.07557E-07	5.10565E-06	10

GO:00108 21	regulation of mitochondrion organization	3.54783E- 07	5.78351E- 06	10
GO:00352 65	organ growth	3.54783E- 07	5.78351E- 06	10
GO:00525 47	regulation of peptidase activity	3.58282E- 07	5.7884E- 06	10
GO:00075 89	body fluid secretion	3.76315E- 07	5.97309E- 06	10
GO:00971 94	execution phase of apoptosis	3.76315E- 07	5.97309E- 06	10
GO:00513 85	response to mineralocorticoid	4.24533E- 07	6.62226E- 06	10
GO:00718 75	adrenergic receptor signaling pathway	4.24533E- 07	6.62226E- 06	10
GO:00018 36	release of cytochrome c from mitochondria	4.32792E- 07	6.63667E- 06	10
GO:00192 29	regulation of vasoconstriction	4.32792E- 07	6.63667E- 06	10
GO:00714 96	cellular response to external stimulus	4.79114E- 07	7.28525E- 06	10
GO:19037 99	negative regulation of production of miRNAs involved in gene silencing by miRNA	4.8861E- 07	7.36773E- 06	10
GO:00100 39	response to iron ion	4.98445E- 07	7.45391E- 06	10
GO:00109 52	positive regulation of peptidase activity	5.45221E- 07	8.08659E- 06	10
GO:00071 89	adenylate cyclase-activating G protein-coupled receptor signaling pathway	5.52519E- 07	8.1282E- 06	10
GO:00456 39	positive regulation of myeloid cell differentiation	5.72197E- 07	8.29462E- 06	10
GO:00331 57	regulation of intracellular protein transport	5.76705E- 07	8.29462E- 06	9
GO:00427 59	long-chain fatty acid biosynthetic process	5.82167E- 07	8.29462E- 06	9
GO:00459 07	positive regulation of vasoconstriction	5.82167E- 07	8.29462E- 06	9
GO:00305 22	intracellular receptor signaling pathway	5.96973E- 07	8.43911E- 06	9
GO:00140 74	response to purine-containing compound	6.12415E- 07	8.59029E- 06	9
GO:00601 35	maternal process involved in female pregnancy	6.38202E- 07	8.88315E- 06	9
GO:00066 06	protein import into nucleus	6.44387E- 07	8.89821E- 06	9

GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	6.54036E-07	8.89821E-06	9
GO:0048661	positive regulation of smooth muscle cell proliferation	6.54036E-07	8.89821E-06	9
GO:1901030	positive regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	6.76619E-07	9.13675E-06	9
GO:0007200	phospholipase C-activating G protein-coupled receptor signaling pathway	6.98507E-07	9.36244E-06	9
GO:0071222	cellular response to lipopolysaccharide	7.26335E-07	9.66385E-06	9
GO:0002573	myeloid leukocyte differentiation	7.86804E-07	1.03504E-05	9
GO:0032091	negative regulation of protein binding	7.95094E-07	1.03504E-05	9
GO:2000379	positive regulation of reactive oxygen species metabolic process	7.95094E-07	1.03504E-05	9
GO:0002685	regulation of leukocyte migration	8.51585E-07	1.10066E-05	9
GO:0098926	postsynaptic signal transduction	9.01648E-07	1.1571E-05	9
GO:0015980	energy derivation by oxidation of organic compounds	9.23229E-07	1.17645E-05	9
GO:0071276	cellular response to cadmium ion	1.03432E-06	1.3088E-05	9
GO:0007623	circadian rhythm	1.07441E-06	1.35008E-05	9
GO:0043467	regulation of generation of precursor metabolites and energy	1.15432E-06	1.43102E-05	9
GO:0046822	regulation of nucleocytoplasmic transport	1.15464E-06	1.43102E-05	9
GO:0032386	regulation of intracellular transport	1.20214E-06	1.47976E-05	9
GO:0001938	positive regulation of endothelial cell proliferation	1.2261E-06	1.49906E-05	9
GO:0032388	positive regulation of intracellular transport	1.24952E-06	1.50732E-05	9
GO:0071219	cellular response to molecule of bacterial origin	1.24952E-06	1.50732E-05	9
GO:0043535	regulation of blood vessel endothelial cell migration	1.26619E-06	1.51731E-05	9
GO:0008406	gonad development	1.29697E-06	1.53667E-05	9
GO:0022407	regulation of cell-cell adhesion	1.29933E-06	1.53667E-05	9

GO:00436 20	regulation of DNA-templated transcription in response to stress	1.38019E- 06	1.61939E- 05	9
GO:20012 42	regulation of intrinsic apoptotic signaling pathway	1.38718E- 06	1.61939E- 05	9
GO:00359 94	response to muscle stretch	1.47176E- 06	1.70712E- 05	9
GO:00068 01	superoxide metabolic process	1.51717E- 06	1.74859E- 05	9
GO:00511 00	negative regulation of binding	1.58708E- 06	1.81758E- 05	9
GO:00451 37	development of primary sexual characteristics	1.6157E- 06	1.83872E- 05	9
GO:00511 70	import into nucleus	1.73356E- 06	1.96052E- 05	9
GO:19035 24	positive regulation of blood circulation	1.77668E- 06	1.9968E- 05	9
GO:00072 13	G protein-coupled acetylcholine receptor signaling pathway	1.85736E- 06	2.07459E- 05	9
GO:00066 33	fatty acid biosynthetic process	1.8914E- 06	2.08692E- 05	9
GO:00106 32	regulation of epithelial cell migration	1.89146E- 06	2.08692E- 05	9
GO:00086 31	intrinsic apoptotic signaling pathway in response to oxidative stress	1.94626E- 06	2.13436E- 05	9
GO:19035 22	regulation of blood circulation	2.00717E- 06	2.18791E- 05	9
GO:00066 90	icosanoid metabolic process	2.05328E- 06	2.22017E- 05	9
GO:19015 68	fatty acid derivative metabolic process	2.06131E- 06	2.22017E- 05	9
GO:00609 65	negative regulation of gene silencing by miRNA	2.31314E- 06	2.47667E- 05	9
GO:00350 94	response to nicotine	2.45156E- 06	2.59417E- 05	9
GO:19010 28	regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	2.45156E- 06	2.59417E- 05	9
GO:20001 34	negative regulation of G1/S transition of mitotic cell cycle	2.54808E- 06	2.68063E- 05	9
GO:00346 44	cellular response to UV	2.58706E- 06	2.70591E- 05	9
GO:19001 80	regulation of protein localization to nucleus	2.68623E- 06	2.79349E- 05	9
GO:00325 70	response to progesterone	2.74011E- 06	2.83323E- 05	8

GO:00903 16	positive regulation of intracellular protein transport	2.76219E- 06	2.83983E- 05	8
GO:19034 09	reactive oxygen species biosynthetic process	2.83058E- 06	2.89371E- 05	8
GO:00069 53	acute-phase response	3.05469E- 06	3.10527E- 05	8
GO:20000 45	regulation of G1/S transition of mitotic cell cycle	3.11937E- 06	3.15331E- 05	8
GO:00066 31	fatty acid metabolic process	3.18913E- 06	3.1882E- 05	8
GO:00457 87	positive regulation of cell cycle	3.18913E- 06	3.1882E- 05	8
GO:00346 12	response to tumor necrosis factor	3.26709E- 06	3.24819E- 05	8
GO:00082 17	regulation of blood pressure	3.37868E- 06	3.30466E- 05	8
GO:00486 39	positive regulation of developmental growth	3.37868E- 06	3.30466E- 05	8
GO:00611 38	morphogenesis of a branching epithelium	3.37868E- 06	3.30466E- 05	8
GO:00105 95	positive regulation of endothelial cell migration	3.47447E- 06	3.35847E- 05	8
GO:19028 07	negative regulation of cell cycle G1/S phase transition	3.47447E- 06	3.35847E- 05	8
GO:00510 51	negative regulation of transport	3.48937E- 06	3.35847E- 05	8
GO:00098 95	negative regulation of catabolic process	3.54934E- 06	3.39811E- 05	8
GO:00427 70	signal transduction in response to DNA damage	3.65324E- 06	3.44663E- 05	8
GO:00435 34	blood vessel endothelial cell migration	3.65606E- 06	3.44663E- 05	8
GO:00017 76	leukocyte homeostasis	3.6762E- 06	3.44663E- 05	8
GO:00069 19	activation of cysteine-type endopeptidase activity involved in apoptotic process	3.6762E- 06	3.44663E- 05	8
GO:00075 95	lactation	3.76865E- 06	3.4906E- 05	8
GO:00702 31	T cell apoptotic process	3.76865E- 06	3.4906E- 05	8
GO:00459 26	negative regulation of growth	3.78097E- 06	3.4906E- 05	8
GO:00432 80	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	3.83961E- 06	3.52674E- 05	8

GO:00347 65	regulation of ion transmembrane transport	3.95933E- 06	3.61833E- 05	8
GO:00973 00	programmed necrotic cell death	4.17153E- 06	3.72689E- 05	8
GO:00601 49	negative regulation of posttranscriptional gene silencing	4.1811E- 06	3.72689E- 05	8
GO:00609 67	negative regulation of gene silencing by RNA	4.1811E- 06	3.72689E- 05	8
GO:19015 22	positive regulation of transcription from RNA polymerase II promoter involved in cellular response to chemical stimulus	4.1811E- 06	3.72689E- 05	8
GO:19037 98	regulation of production of miRNAs involved in gene silencing by miRNA	4.1811E- 06	3.72689E- 05	8
GO:00712 48	cellular response to metal ion	4.26917E- 06	3.78674E- 05	8
GO:00605 62	epithelial tube morphogenesis	4.40805E- 06	3.85326E- 05	8
GO:00712 14	cellular response to abiotic stimulus	4.40805E- 06	3.85326E- 05	8
GO:01040 04	cellular response to environmental stimulus	4.40805E- 06	3.85326E- 05	8
GO:00018 92	embryonic placenta development	4.49145E- 06	3.8886E- 05	8
GO:00086 25	extrinsic apoptotic signaling pathway via death domain receptors	4.49145E- 06	3.8886E- 05	8
GO:00015 03	ossification	4.65596E- 06	4.01183E- 05	8
GO:19033 51	cellular response to dopamine	4.79374E- 06	4.11097E- 05	8
GO:19033 50	response to dopamine	5.11236E- 06	4.36353E- 05	8
GO:19038 29	positive regulation of cellular protein localization	5.30199E- 06	4.50413E- 05	8
GO:00170 38	protein import	5.55243E- 06	4.69485E- 05	8
GO:00017 63	morphogenesis of a branching structure	5.75998E- 06	4.82525E- 05	8
GO:00310 99	regeneration	5.75998E- 06	4.82525E- 05	8
GO:00158 50	organic hydroxy compound transport	5.84428E- 06	4.8733E- 05	8
GO:00509 27	positive regulation of positive chemotaxis	5.92909E- 06	4.89887E- 05	8
GO:00709 20	regulation of production of small RNA involved in gene silencing by RNA	5.92909E- 06	4.89887E- 05	8

GO:00102 12	response to ionizing radiation	6.18092E- 06	5.08139E- 05	8
GO:00510 91	positive regulation of DNA-binding transcription factor activity	6.20616E- 06	5.08139E- 05	8
GO:00507 27	regulation of inflammatory response	6.2526E- 06	5.09636E- 05	8
GO:00331 35	regulation of peptidyl-serine phosphorylation	6.4692E- 06	5.24926E- 05	8
GO:00105 06	regulation of autophagy	6.67944E- 06	5.37427E- 05	8
GO:00457 85	positive regulation of cell adhesion	6.68267E- 06	5.37427E- 05	8
GO:00973 45	mitochondrial outer membrane permeabilization	6.72042E- 06	5.38072E- 05	8
GO:00425 42	response to hydrogen peroxide	6.76857E- 06	5.3954E- 05	8
GO:19028 06	regulation of cell cycle G1/S phase transition	6.89911E- 06	5.47533E- 05	8
GO:00509 26	regulation of positive chemotaxis	6.98131E- 06	5.51638E- 05	8
GO:00551 23	digestive system development	7.07937E- 06	5.56954E- 05	8
GO:00192 16	regulation of lipid metabolic process	7.13836E- 06	5.59164E- 05	8
GO:00606 88	regulation of morphogenesis of a branching structure	7.35134E- 06	5.7052E- 05	8
GO:00714 56	cellular response to hypoxia	7.40529E- 06	5.7052E- 05	8
GO:00421 00	B cell proliferation	7.40559E- 06	5.7052E- 05	8
GO:00228 98	regulation of transmembrane transporter activity	7.40946E- 06	5.7052E- 05	8
GO:00525 48	regulation of endopeptidase activity	7.62097E- 06	5.82412E- 05	8
GO:00345 04	protein localization to nucleus	7.62828E- 06	5.82412E- 05	8
GO:20012 43	negative regulation of intrinsic apoptotic signaling pathway	7.85819E- 06	5.97445E- 05	8
GO:00347 64	positive regulation of transmembrane transport	7.94254E- 06	5.99805E- 05	8
GO:00069 13	nucleocytoplasmic transport	7.95553E- 06	5.99805E- 05	8
GO:00352 64	multicellular organism growth	8.08382E- 06	6.06948E- 05	8

GO:0001963	synaptic transmission, dopaminergic	8.16529E-06	6.10532E-05	8
GO:0043393	regulation of protein binding	8.22329E-06	6.12338E-05	8
GO:0007548	sex differentiation	8.31828E-06	6.16873E-05	8
GO:0000077	DNA damage checkpoint	8.44383E-06	6.18579E-05	8
GO:0061041	regulation of wound healing	8.44383E-06	6.18579E-05	8
GO:2001056	positive regulation of cysteine-type endopeptidase activity	8.44383E-06	6.18579E-05	8
GO:0051169	nuclear transport	8.56392E-06	6.24846E-05	8
GO:0002763	positive regulation of myeloid leukocyte differentiation	8.75175E-06	6.33443E-05	8
GO:0019369	arachidonic acid metabolic process	8.75175E-06	6.33443E-05	8
GO:0008585	female gonad development	8.83074E-06	6.36613E-05	8
GO:0046651	lymphocyte proliferation	9.06104E-06	6.50624E-05	8
GO:0006006	glucose metabolic process	9.11637E-06	6.52009E-05	8
GO:1901342	regulation of vasculature development	9.44157E-06	6.68095E-05	8
GO:0095500	acetylcholine receptor signaling pathway	9.49111E-06	6.68095E-05	8
GO:0031663	lipopolysaccharide-mediated signaling pathway	9.52589E-06	6.68095E-05	8
GO:0042306	regulation of protein import into nucleus	9.52589E-06	6.68095E-05	8
GO:0046456	icosanoid biosynthetic process	9.52589E-06	6.68095E-05	8
GO:0006936	muscle contraction	9.66751E-06	6.75409E-05	8
GO:0032943	mononuclear cell proliferation	9.85986E-06	6.86199E-05	8
GO:0048754	branching morphogenesis of an epithelial tube	1.00199E-05	6.94663E-05	8
GO:0010631	epithelial cell migration	1.0387E-05	7.17366E-05	8
GO:0036294	cellular response to decreased oxygen levels	1.04335E-05	7.1765E-05	8

GO:19015 70	fatty acid derivative biosynthetic process	1.04704E- 05	7.1765E- 05	8
GO:00510 98	regulation of binding	1.0892E- 05	7.40613E- 05	8
GO:00432 71	negative regulation of ion transport	1.0895E- 05	7.40613E- 05	7
GO:00485 68	embryonic organ development	1.09316E- 05	7.40613E- 05	7
GO:00017 82	B cell homeostasis	1.09692E- 05	7.40613E- 05	7
GO:00020 27	regulation of heart rate	1.10687E- 05	7.44556E- 05	7
GO:00901 32	epithelium migration	1.11523E- 05	7.474E-05	7
GO:19021 10	positive regulation of mitochondrial membrane permeability involved in apoptotic process	1.12342E- 05	7.50109E- 05	7
GO:00712 41	cellular response to inorganic substance	1.15236E- 05	7.66607E- 05	7
GO:00465 45	development of primary female sexual characteristics	1.16944E- 05	7.75115E- 05	7
GO:00620 12	regulation of small molecule metabolic process	1.21177E- 05	7.98094E- 05	7
GO:00022 60	lymphocyte homeostasis	1.21734E- 05	7.98094E- 05	7
GO:19045 89	regulation of protein import	1.21734E- 05	7.98094E- 05	7
GO:00718 68	cellular response to monoamine stimulus	1.23483E- 05	8.01504E- 05	7
GO:00718 70	cellular response to catecholamine stimulus	1.23483E- 05	8.01504E- 05	7
GO:00018 44	protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	1.26102E- 05	8.01504E- 05	7
GO:19051 44	response to acetylcholine	1.26102E- 05	8.01504E- 05	7
GO:19051 45	cellular response to acetylcholine	1.26102E- 05	8.01504E- 05	7
GO:00511 46	striated muscle cell differentiation	1.26279E- 05	8.01504E- 05	7
GO:00016 60	fever generation	1.27126E- 05	8.01504E- 05	7
GO:00196 14	catechol-containing compound catabolic process	1.27126E- 05	8.01504E- 05	7
GO:00320 25	response to cobalt ion	1.27126E- 05	8.01504E- 05	7

GO:00343 50	regulation of glial cell apoptotic process	1.27126E- 05	8.01504E- 05	7
GO:00424 24	catecholamine catabolic process	1.27126E- 05	8.01504E- 05	7
GO:00901 30	tissue migration	1.28301E- 05	8.03683E- 05	7
GO:00315 70	DNA integrity checkpoint	1.2836E- 05	8.03683E- 05	7
GO:00315 71	mitotic G1 DNA damage checkpoint	1.31728E- 05	8.19098E- 05	7
GO:19026 86	mitochondrial outer membrane permeabilization involved in programmed cell death	1.31728E- 05	8.19098E- 05	7
GO:00447 83	G1 DNA damage checkpoint	1.4235E- 05	8.73148E- 05	7
GO:00448 19	mitotic G1/S transition checkpoint	1.4235E- 05	8.73148E- 05	7
GO:00466 86	response to cadmium ion	1.4235E- 05	8.73148E- 05	7
GO:00702 65	necrotic cell death	1.4235E- 05	8.73148E- 05	7
GO:00026 75	positive regulation of acute inflammatory response	1.44251E- 05	8.76881E- 05	7
GO:00069 39	smooth muscle contraction	1.44897E- 05	8.76881E- 05	7
GO:00331 38	positive regulation of peptidyl-serine phosphorylation	1.44897E- 05	8.76881E- 05	7
GO:00436 18	regulation of transcription from RNA polymerase II promoter in response to stress	1.44897E- 05	8.76881E- 05	7
GO:00030 12	muscle system process	1.5128E- 05	9.11434E- 05	7
GO:00508 90	cognition	1.52164E- 05	9.11434E- 05	7
GO:00718 67	response to monoamine	1.52667E- 05	9.11434E- 05	7
GO:00718 69	response to catecholamine	1.52667E- 05	9.11434E- 05	7
GO:00069 40	regulation of smooth muscle contraction	1.53629E- 05	9.11434E- 05	7
GO:00357 94	positive regulation of mitochondrial membrane permeability	1.53629E- 05	9.11434E- 05	7
GO:00025 26	acute inflammatory response	1.6077E- 05	9.49644E- 05	7
GO:00016 54	eye development	1.61119E- 05	9.49644E- 05	7

GO:00342 50	positive regulation of cellular amide metabolic process	1.62784E- 05	9.5634E- 05	7
GO:00101 65	response to X-ray	1.64251E- 05	9.6184E- 05	7
GO:00468 24	positive regulation of nucleocytoplasmic transport	1.65592E- 05	9.63456E- 05	7
GO:19021 08	regulation of mitochondrial membrane permeability involved in apoptotic process	1.65592E- 05	9.63456E- 05	7
GO:00092 66	response to temperature stimulus	1.68964E- 05	9.79923E- 05	7
GO:00316 52	positive regulation of heat generation	1.74188E- 05	0.0001003 78	7
GO:00421 35	neurotransmitter catabolic process	1.74188E- 05	0.0001003 78	7
GO:01500 63	visual system development	1.7614E- 05	0.0001011 81	7
GO:00016 76	long-chain fatty acid metabolic process	1.78018E- 05	0.0001012 96	7
GO:19000 15	regulation of cytokine production involved in inflammatory response	1.78269E- 05	0.0001012 96	7
GO:19057 10	positive regulation of membrane permeability	1.78269E- 05	0.0001012 96	7
GO:00015 05	regulation of neurotransmitter levels	1.79698E- 05	0.0001012 96	7
GO:00454 44	fat cell differentiation	1.79698E- 05	0.0001012 96	7
GO:00714 53	cellular response to oxygen levels	1.79698E- 05	0.0001012 96	7
GO:00313 31	positive regulation of cellular catabolic process	1.84093E- 05	0.0001031 3	7
GO:00426 92	muscle cell differentiation	1.84093E- 05	0.0001031 3	7
GO:00324 11	positive regulation of transporter activity	1.87185E- 05	0.0001045 39	7
GO:00400 14	regulation of multicellular organism growth	1.9169E- 05	0.0001067 25	7
GO:00105 94	regulation of endothelial cell migration	1.96871E- 05	0.0001092 74	7
GO:00016 67	ameboidal-type cell migration	1.98848E- 05	0.0001100 34	7
GO:00488 80	sensory system development	2.0093E- 05	0.0001108 47	7
GO:00706 61	leukocyte proliferation	2.01953E- 05	0.0001110 72	7

GO:0006937	regulation of muscle contraction	2.04512E-05	0.000112139	7
GO:0042698	ovulation cycle	2.05883E-05	0.00011255	7
GO:0010959	regulation of metal ion transport	2.09834E-05	0.000114364	7
GO:0001659	temperature homeostasis	2.12257E-05	0.000114992	7
GO:0010469	regulation of signaling receptor activity	2.12257E-05	0.000114992	7
GO:0018107	peptidyl-threonine phosphorylation	2.16994E-05	0.000117207	7
GO:0002534	cytokine production involved in inflammatory response	2.20882E-05	0.000118952	7
GO:0007569	cell aging	2.27739E-05	0.000122281	7
GO:1904031	positive regulation of cyclin-dependent protein kinase activity	2.36531E-05	0.000126626	7
GO:0046660	female sex differentiation	2.38909E-05	0.000127522	7
GO:0045765	regulation of angiogenesis	2.43724E-05	0.000129709	7
GO:0072330	monocarboxylic acid biosynthetic process	2.49543E-05	0.000132417	7
GO:0048469	cell maturation	2.54705E-05	0.000134761	7
GO:0045742	positive regulation of epidermal growth factor receptor signaling pathway	2.65119E-05	0.000139051	7
GO:1901099	negative regulation of signal transduction in absence of ligand	2.65119E-05	0.000139051	7
GO:2001240	negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	2.65119E-05	0.000139051	7
GO:0070227	lymphocyte apoptotic process	2.71024E-05	0.000140923	6
GO:0072401	signal transduction involved in DNA integrity checkpoint	2.71024E-05	0.000140923	6
GO:0072422	signal transduction involved in DNA damage checkpoint	2.71024E-05	0.000140923	6
GO:0010950	positive regulation of endopeptidase activity	2.73535E-05	0.000141821	6
GO:0045471	response to ethanol	2.75092E-05	0.000142221	6
GO:0051881	regulation of mitochondrial membrane potential	2.89564E-05	0.000148852	6

GO:00723 95	signal transduction involved in cell cycle checkpoint	2.89564E- 05	0.0001488 52	6
GO:00421 13	B cell activation	2.91721E- 05	0.0001495 36	6
GO:19030 34	regulation of response to wounding	2.93498E- 05	0.0001500 22	6
GO:00609 69	negative regulation of gene silencing	2.96162E- 05	0.0001509 57	6
GO:00106 23	programmed cell death involved in cell development	2.9982E- 05	0.0001515 41	6
GO:00193 36	phenol-containing compound catabolic process	2.9982E- 05	0.0001515 41	6
GO:00316 50	regulation of heat generation	2.9982E- 05	0.0001515 41	6
GO:00026 88	regulation of leukocyte chemotaxis	3.01572E- 05	0.0001520 02	6
GO:00359 24	cellular response to vascular endothelial growth factor stimulus	3.09074E- 05	0.0001553 5	6
GO:00193 18	hexose metabolic process	3.13563E- 05	0.0001571 7	6
GO:00019 52	regulation of cell-matrix adhesion	3.15559E- 05	0.0001577 34	6
GO:00430 29	T cell homeostasis	3.29787E- 05	0.0001630 28	6
GO:19011 86	positive regulation of ERBB signaling pathway	3.29787E- 05	0.0001630 28	6
GO:20001 44	positive regulation of DNA-templated transcription, initiation	3.29787E- 05	0.0001630 28	6
GO:00182 10	peptidyl-threonine modification	3.30063E- 05	0.0001630 28	6
GO:00488 72	homeostasis of number of cells	3.31556E- 05	0.0001630 28	6
GO:00902 57	regulation of muscle system process	3.31556E- 05	0.0001630 28	6
GO:00714 78	cellular response to radiation	3.48707E- 05	0.0001709 96	6
GO:00469 02	regulation of mitochondrial membrane permeability	3.51144E- 05	0.0001712 63	6
GO:01500 76	neuroinflammatory response	3.51144E- 05	0.0001712 63	6
GO:00072 10	serotonin receptor signaling pathway	3.66127E- 05	0.0001780 9	6
GO:00714 82	cellular response to light stimulus	3.76817E- 05	0.0001827 99	6

GO:00903 99	replicative senescence	3.80256E- 05	0.0001839 74	6
GO:00459 30	negative regulation of mitotic cell cycle	3.94982E- 05	0.0001905 89	6
GO:00456 37	regulation of myeloid cell differentiation	4.01491E- 05	0.0001927 02	6
GO:00507 30	regulation of peptidyl-tyrosine phosphorylation	4.01491E- 05	0.0001927 02	6
GO:00165 72	histone phosphorylation	4.05312E- 05	0.0001940 22	6
GO:00324 12	regulation of ion transmembrane transporter activity	4.23598E- 05	0.0002022 4	6
GO:00719 02	positive regulation of protein serine/threonine kinase activity	4.32396E- 05	0.0002058 97	6
GO:00507 31	positive regulation of peptidyl-tyrosine phosphorylation	4.40101E- 05	0.0002090 16	6
GO:00723 31	signal transduction by p53 class mediator	4.46712E- 05	0.0002116 01	6
GO:19040 62	regulation of cation transmembrane transport	4.72767E- 05	0.0002224 8	6
GO:19001 19	positive regulation of execution phase of apoptosis	4.73661E- 05	0.0002224 8	6
GO:20004 02	negative regulation of lymphocyte migration	4.73661E- 05	0.0002224 8	6
GO:00226 17	extracellular matrix disassembly	4.75828E- 05	0.0002224 8	6
GO:00301 93	regulation of blood coagulation	4.75828E- 05	0.0002224 8	6
GO:19019 88	negative regulation of cell cycle phase transition	4.83354E- 05	0.0002254 17	6
GO:00485 65	digestive tract development	4.86259E- 05	0.0002261 88	6
GO:19000 46	regulation of hemostasis	5.04416E- 05	0.0002340 32	6
GO:00108 76	lipid localization	5.12107E- 05	0.0002369 93	6
GO:00097 55	hormone-mediated signaling pathway	5.16736E- 05	0.0002385 26	6
GO:00158 44	monoamine transport	5.34313E- 05	0.0002460 12	6
GO:00459 27	positive regulation of growth	5.36084E- 05	0.0002462	6
GO:01500 77	regulation of neuroinflammatory response	5.41309E- 05	0.0002479 71	6

GO:0006970	response to osmotic stress	5.65562E-05	0.000257128	6
GO:0010507	negative regulation of autophagy	5.65562E-05	0.000257128	6
GO:0043154	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	5.65562E-05	0.000257128	6
GO:0043401	steroid hormone mediated signaling pathway	5.72389E-05	0.00025958	6
GO:0002070	epithelial cell maturation	5.80932E-05	0.00026214	6
GO:0019372	lipoxigenase pathway	5.80932E-05	0.00026214	6
GO:1903708	positive regulation of hemopoiesis	5.85635E-05	0.000263605	6
GO:0007193	adenylate cyclase-inhibiting G protein-coupled receptor signaling pathway	5.98204E-05	0.000268594	6
GO:0007586	digestion	6.19806E-05	0.000276919	6
GO:0008584	male gonad development	6.19806E-05	0.000276919	6
GO:0071383	cellular response to steroid hormone stimulus	6.22805E-05	0.000277574	6
GO:0002687	positive regulation of leukocyte migration	6.44664E-05	0.000284921	6
GO:0007292	female gamete generation	6.44664E-05	0.000284921	6
GO:0046546	development of primary male sexual characteristics	6.44664E-05	0.000284921	6
GO:0051204	protein insertion into mitochondrial membrane	6.48739E-05	0.000284921	6
GO:0060443	mammary gland morphogenesis	6.48739E-05	0.000284921	6
GO:0070266	necroptotic process	6.48739E-05	0.000284921	6
GO:0009896	positive regulation of catabolic process	6.65094E-05	0.000291189	6
GO:0050818	regulation of coagulation	6.67838E-05	0.000291189	6
GO:0090559	regulation of membrane permeability	6.67838E-05	0.000291189	6
GO:0050921	positive regulation of chemotaxis	6.96769E-05	0.000302133	6
GO:0060078	regulation of postsynaptic membrane potential	6.96769E-05	0.000302133	6

GO:0006109	regulation of carbohydrate metabolic process	7.02946E-05	0.000302133	6
GO:0010224	response to UV-B	7.02956E-05	0.000302133	6
GO:0070242	thymocyte apoptotic process	7.02956E-05	0.000302133	6
GO:2001267	regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway	7.02956E-05	0.000302133	6
GO:2000142	regulation of DNA-templated transcription, initiation	7.07914E-05	0.000303543	6
GO:0043542	endothelial cell migration	7.23875E-05	0.000309653	6
GO:0000082	G1/S transition of mitotic cell cycle	7.41724E-05	0.00031654	6
GO:1901215	negative regulation of neuron death	7.46069E-05	0.000317645	6
GO:0030225	macrophage differentiation	7.70925E-05	0.000325927	6
GO:0045776	negative regulation of blood pressure	7.70925E-05	0.000325927	6
GO:0046677	response to antibiotic	7.70925E-05	0.000325927	6
GO:0018108	peptidyl-tyrosine phosphorylation	8.0443E-05	0.0003393	6
GO:0070374	positive regulation of ERK1 and ERK2 cascade	8.14787E-05	0.000342869	6
GO:0009409	response to cold	8.37921E-05	0.000350971	6
GO:2001239	regulation of extrinsic apoptotic signaling pathway in absence of ligand	8.37921E-05	0.000350971	6
GO:0042136	neurotransmitter biosynthetic process	8.40603E-05	0.000351282	6
GO:0018212	peptidyl-tyrosine modification	8.54949E-05	0.000356453	6
GO:0010810	regulation of cell-substrate adhesion	8.63406E-05	0.000359152	6
GO:0002532	production of molecular mediator involved in inflammatory response	8.69358E-05	0.000359683	6
GO:2000117	negative regulation of cysteine-type endopeptidase activity	8.69358E-05	0.000359683	6
GO:0060249	anatomical structure homeostasis	8.70646E-05	0.000359683	6
GO:0034976	response to endoplasmic reticulum stress	8.77203E-05	0.000361566	6

GO:00026 73	regulation of acute inflammatory response	9.09052E- 05	0.0003694 6	6
GO:00032 54	regulation of membrane depolarization	9.09052E- 05	0.0003694 6	6
GO:00351 96	production of miRNAs involved in gene silencing by miRNA	9.09052E- 05	0.0003694 6	6
GO:00607 11	labyrinthine layer development	9.09052E- 05	0.0003694 6	6
GO:00901 51	establishment of protein localization to mitochondrial membrane	9.09052E- 05	0.0003694 6	6
GO:00901 99	regulation of release of cytochrome c from mitochondria	9.09052E- 05	0.0003694 6	6
GO:00000 75	cell cycle checkpoint	9.14367E- 05	0.0003694 6	6
GO:00515 91	response to cAMP	9.1473E- 05	0.0003694 6	6
GO:19040 35	regulation of epithelial cell apoptotic process	9.1473E- 05	0.0003694 6	6
GO:00059 96	monosaccharide metabolic process	9.19479E- 05	0.0003705 51	6
GO:00713 56	cellular response to tumor necrosis factor	9.41243E- 05	0.0003784 79	6
GO:00030 73	regulation of systemic arterial blood pressure	9.61902E- 05	0.0003859 28	6
GO:00030 44	regulation of systemic arterial blood pressure mediated by a chemical signal	9.84473E- 05	0.0003932 4	6
GO:00508 73	brown fat cell differentiation	9.84473E- 05	0.0003932 4	6
GO:00022 62	myeloid cell homeostasis	0.0001010 03	0.0004011 48	6
GO:00620 13	positive regulation of small molecule metabolic process	0.0001010 03	0.0004011 48	6
GO:00026 90	positive regulation of leukocyte chemotaxis	0.0001010 92	0.0004011 48	6
GO:00364 73	cell death in response to oxidative stress	0.0001061 84	0.0004204 31	6
GO:00069 84	ER-nucleus signaling pathway	0.0001064 34	0.0004205	6
GO:00485 92	eye morphogenesis	0.0001084 36	0.0004274 77	6
GO:00703 72	regulation of ERK1 and ERK2 cascade	0.0001157 07	0.0004549 51	6
GO:00301 68	platelet activation	0.0001162 97	0.0004549 51	6

GO:00030 85	negative regulation of systemic arterial blood pressure	0.0001166 19	0.0004549 51	6
GO:19020 04	positive regulation of amyloid-beta formation	0.0001166 19	0.0004549 51	6
GO:19019 87	regulation of cell cycle phase transition	0.0001166 62	0.0004549 51	6
GO:00070 44	cell-substrate junction assembly	0.0001169 56	0.0004551 16	6
GO:00509 20	regulation of chemotaxis	0.0001207 35	0.0004688 13	6
GO:00439 49	regulation of cAMP-mediated signaling	0.0001238 02	0.0004785 72	6
GO:00071 60	cell-matrix adhesion	0.0001240 42	0.0004785 72	5
GO:00986 57	import into cell	0.0001240 42	0.0004785 72	5
GO:00160 49	cell growth	0.0001247 47	0.0004802 7	5
GO:00448 43	cell cycle G1/S phase transition	0.0001265 34	0.0004861 16	5
GO:00447 73	mitotic DNA damage checkpoint	0.0001285 48	0.0004928 05	5
GO:00347 67	positive regulation of ion transmembrane transport	0.0001289 3	0.0004932 27	5
GO:00603 26	cell chemotaxis	0.0001293 68	0.0004938 58	5
GO:00308 57	negative regulation of epithelial cell differentiation	0.0001332 15	0.0005053 46	5
GO:00310 50	dsRNA processing	0.0001332 15	0.0005053 46	5
GO:00709 18	production of small RNA involved in gene silencing by RNA	0.0001332 15	0.0005053 46	5
GO:00000 79	regulation of cyclin-dependent protein serine/threonine kinase activity	0.0001346 64	0.0005087 06	5
GO:01501 15	cell-substrate junction organization	0.0001346 64	0.0005087 06	5
GO:00610 42	vascular wound healing	0.0001355 81	0.0005100 44	5
GO:00903 30	regulation of platelet aggregation	0.0001355 81	0.0005100 44	5
GO:00716 95	anatomical structure maturation	0.0001417	0.0005319 55	5
GO:00466 61	male sex differentiation	0.0001426 3	0.0005343 36	5

GO:00432 79	response to alkaloid	0.0001475 62	0.0005516 74	5
GO:00069 77	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	0.0001535 82	0.0005706 41	5
GO:00103 32	response to gamma radiation	0.0001535 82	0.0005706 41	5
GO:19046 45	response to amyloid-beta	0.0001535 82	0.0005706 41	5
GO:00510 00	positive regulation of nitric-oxide synthase activity	0.0001564 42	0.0005788 9	5
GO:00519 00	regulation of mitochondrial depolarization	0.0001564 42	0.0005788 9	5
GO:00711 56	regulation of cell cycle arrest	0.0001613 86	0.0005947 52	5
GO:19040 29	regulation of cyclin-dependent protein kinase activity	0.0001613 86	0.0005947 52	5
GO:00072 04	positive regulation of cytosolic calcium ion concentration	0.0001641 61	0.0006015 75	5
GO:00015 41	ovarian follicle development	0.0001645 67	0.0006015 75	5
GO:00724 31	signal transduction involved in mitotic G1 DNA damage checkpoint	0.0001645 67	0.0006015 75	5
GO:19024 00	intracellular signal transduction involved in G1 DNA damage checkpoint	0.0001645 67	0.0006015 75	5
GO:20002 41	regulation of reproductive process	0.0001734 82	0.0006328 84	5
GO:00703 71	ERK1 and ERK2 cascade	0.0001748 83	0.0006367 14	5
GO:00075 66	embryo implantation	0.0001761 09	0.0006388 57	5
GO:00447 74	mitotic DNA integrity checkpoint	0.0001761 78	0.0006388 57	5
GO:00075 84	response to nutrient	0.0001791	0.0006462 22	5
GO:00351 62	embryonic hemopoiesis	0.0001792 81	0.0006462 22	5
GO:19049 96	positive regulation of leukocyte adhesion to vascular endothelial cell	0.0001792 81	0.0006462 22	5
GO:00508 06	positive regulation of synaptic transmission	0.0001848 62	0.0006650 15	5
GO:00724 13	signal transduction involved in mitotic cell cycle checkpoint	0.0001882 24	0.0006730 95	5
GO:19024 02	signal transduction involved in mitotic DNA damage checkpoint	0.0001882 24	0.0006730 95	5

GO:19024 03	signal transduction involved in mitotic DNA integrity checkpoint	0.0001882 24	0.0006730 95	5
GO:00015 58	regulation of cell growth	0.0001928 1	0.0006881 35	5
GO:00016 55	urogenital system development	0.0001940 35	0.0006911 43	5
GO:00509 94	regulation of lipid catabolic process	0.0002009 29	0.0007142 94	5
GO:00430 10	camera-type eye development	0.0002021 63	0.0007172 73	5
GO:00360 03	positive regulation of transcription from RNA polymerase II promoter in response to stress	0.0002041 78	0.0007173 88	5
GO:00509 95	negative regulation of lipid catabolic process	0.0002041 78	0.0007173 88	5
GO:00518 82	mitochondrial depolarization	0.0002041 78	0.0007173 88	5
GO:00604 44	branching involved in mammary gland duct morphogenesis	0.0002041 78	0.0007173 88	5
GO:19029 93	positive regulation of amyloid precursor protein catabolic process	0.0002041 78	0.0007173 88	5
GO:00162 41	regulation of macroautophagy	0.0002093 89	0.0007342 71	5
GO:19019 91	negative regulation of mitotic cell cycle phase transition	0.0002123 9	0.0007433 54	5
GO:00068 16	calcium ion transport	0.0002142 29	0.0007483 44	5
GO:00487 71	tissue remodeling	0.0002225 79	0.0007757 64	5
GO:00316 68	cellular response to extracellular stimulus	0.0002229 36	0.0007757 64	5
GO:00308 88	regulation of B cell proliferation	0.0002281 77	0.0007870 88	5
GO:00705 27	platelet aggregation	0.0002281 77	0.0007870 88	5
GO:20003 51	regulation of endothelial cell apoptotic process	0.0002281 77	0.0007870 88	5
GO:20012 44	positive regulation of intrinsic apoptotic signaling pathway	0.0002281 77	0.0007870 88	5
GO:20000 27	regulation of animal organ morphogenesis	0.0002283 66	0.0007870 88	5
GO:00158 74	norepinephrine transport	0.0002312 12	0.0007953 84	5
GO:00486 40	negative regulation of developmental growth	0.0002362 38	0.0008111 31	5

GO:00507 96	regulation of insulin secretion	0.0002435 84	0.0008331 91	5
GO:19053 30	regulation of morphogenesis of an epithelium	0.0002435 84	0.0008331 91	5
GO:00313 34	positive regulation of protein-containing complex assembly	0.0002452 97	0.0008374 7	5
GO:00305 18	intracellular steroid hormone receptor signaling pathway	0.0002459 48	0.0008381 11	5
GO:00075 96	blood coagulation	0.0002520 4	0.0008556 46	5
GO:00107 21	negative regulation of cell development	0.0002520 4	0.0008556 46	5
GO:19040 19	epithelial cell apoptotic process	0.0002559 59	0.0008673 26	5
GO:00020 66	columnar/cuboidal epithelial cell development	0.0002579 88	0.0008711 55	5
GO:00063 09	apoptotic DNA fragmentation	0.0002604 6	0.0008711 55	5
GO:00439 51	negative regulation of cAMP-mediated signaling	0.0002604 6	0.0008711 55	5
GO:00603 07	regulation of ventricular cardiac muscle cell membrane repolarization	0.0002604 6	0.0008711 55	5
GO:00607 40	prostate gland epithelium morphogenesis	0.0002604 6	0.0008711 55	5
GO:19007 39	regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	0.0002604 6	0.0008711 55	5
GO:19007 40	positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	0.0002604 6	0.0008711 55	5
GO:00076 11	learning or memory	0.0002632 28	0.0008787 89	5
GO:00335 59	unsaturated fatty acid metabolic process	0.0002662 77	0.0008873 33	5
GO:00018 94	tissue homeostasis	0.0002694 34	0.0008962 01	5
GO:00105 73	vascular endothelial growth factor production	0.0002738 97	0.0009077 11	5
GO:00512 05	protein insertion into membrane	0.0002738 97	0.0009077 11	5
GO:00075 99	hemostasis	0.0002778 3	0.0009190 62	5
GO:00508 17	coagulation	0.0002832 39	0.0009352 45	5
GO:00096 51	response to salt stress	0.0002919 96	0.0009606 54	5

GO:19021 75	regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	0.0002919 96	0.0009606 54	5
GO:00020 65	columnar/cuboidal epithelial cell differentiation	0.0002991 35	0.0009788	5
GO:00109 06	regulation of glucose metabolic process	0.0002991 35	0.0009788	5
GO:01202 54	olefinic compound metabolic process	0.0002991 35	0.0009788	5
GO:00507 08	regulation of protein secretion	0.0002999 86	0.0009798 13	5
GO:00509 18	positive chemotaxis	0.0003078 12	0.0010035 65	5
GO:19019 90	regulation of mitotic cell cycle phase transition	0.0003104 79	0.0010104 38	5
GO:00432 54	regulation of protein-containing complex assembly	0.0003155 89	0.0010252 25	5
GO:00027 61	regulation of myeloid leukocyte differentiation	0.0003226 89	0.0010382 08	5
GO:00326 42	regulation of chemokine production	0.0003258 53	0.0010382 08	5
GO:00725 77	endothelial cell apoptotic process	0.0003258 53	0.0010382 08	5
GO:00023 60	T cell lineage commitment	0.0003258 97	0.0010382 08	5
GO:00104 60	positive regulation of heart rate	0.0003258 97	0.0010382 08	5
GO:00105 75	positive regulation of vascular endothelial growth factor production	0.0003258 97	0.0010382 08	5
GO:00328 00	receptor biosynthetic process	0.0003258 97	0.0010382 08	5
GO:00335 98	mammary gland epithelial cell proliferation	0.0003258 97	0.0010382 08	5
GO:00605 12	prostate gland morphogenesis	0.0003258 97	0.0010382 08	5
GO:00902 00	positive regulation of release of cytochrome c from mitochondria	0.0003258 97	0.0010382 08	5
GO:19907 76	response to angiotensin	0.0003258 97	0.0010382 08	5
GO:00514 80	regulation of cytosolic calcium ion concentration	0.0003296 93	0.0010484 56	5
GO:00508 04	modulation of chemical synaptic transmission	0.0003421 98	0.0010845 13	5
GO:00109 48	negative regulation of cell cycle process	0.0003422 3	0.0010845 13	5

GO:00991 77	regulation of trans-synaptic signaling	0.0003477 36	0.0011000 34	5
GO:00157 21	bile acid and bile salt transport	0.0003622 35	0.0011438 99	5
GO:19054 75	regulation of protein localization to membrane	0.0003631 32	0.0011447 33	5
GO:19054 77	positive regulation of protein localization to membrane	0.0003739 89	0.0011769 09	5
GO:00356 90	cellular response to drug	0.0003845 16	0.0012058 43	5
GO:00429 82	amyloid precursor protein metabolic process	0.0003845 16	0.0012058 43	5
GO:00347 63	negative regulation of transmembrane transport	0.0003877 25	0.0012138 04	5
GO:00093 06	protein secretion	0.0003886 21	0.0012145 06	5
GO:00434 91	protein kinase B signaling	0.0003942 7	0.0012294 86	5
GO:00355 92	establishment of protein localization to extracellular region	0.0003947 73	0.0012294 86	5
GO:00463 94	carboxylic acid biosynthetic process	0.0003963 37	0.0012322 37	5
GO:00059 79	regulation of glycogen biosynthetic process	0.0004010 82	0.0012342 64	5
GO:00109 62	regulation of glucan biosynthetic process	0.0004010 82	0.0012342 64	5
GO:00341 10	regulation of homotypic cell-cell adhesion	0.0004010 82	0.0012342 64	5
GO:00434 57	regulation of cellular respiration	0.0004010 82	0.0012342 64	5
GO:00600 55	angiogenesis involved in wound healing	0.0004010 82	0.0012342 64	5
GO:00996 25	ventricular cardiac muscle cell membrane repolarization	0.0004010 82	0.0012342 64	5
GO:00160 53	organic acid biosynthetic process	0.0004035 65	0.0012397 97	5
GO:00059 77	glycogen metabolic process	0.0004275 88	0.0013113 72	5
GO:00716 92	protein localization to extracellular region	0.0004401 32	0.0013434 72	5
GO:00327 70	positive regulation of monooxygenase activity	0.0004425 09	0.0013434 72	5
GO:00457 37	positive regulation of cyclin-dependent protein serine/threonine kinase activity	0.0004425 09	0.0013434 72	5

GO:00459 87	positive regulation of smooth muscle contraction	0.0004425 09	0.0013434 72	5
GO:00996 23	regulation of cardiac muscle cell membrane repolarization	0.0004425 09	0.0013434 72	5
GO:19001 81	negative regulation of protein localization to nucleus	0.0004425 09	0.0013434 72	5
GO:00011 01	response to acid chemical	0.0004465 2	0.0013524 13	5
GO:00708 38	divalent metal ion transport	0.0004469 49	0.0013524 13	5
GO:00060 73	cellular glucan metabolic process	0.0004503 67	0.0013582 13	5
GO:00440 42	glucan metabolic process	0.0004503 67	0.0013582 13	5
GO:00513 46	negative regulation of hydrolase activity	0.0004608 45	0.0013875	5
GO:00311 00	animal organ regeneration	0.0004739 99	0.0014200 14	5
GO:00326 02	chemokine production	0.0004739 99	0.0014200 14	5
GO:00436 27	response to estrogen	0.0004739 99	0.0014200 14	5
GO:00217 00	developmental maturation	0.0004770 15	0.0014266 88	5
GO:00606 03	mammary gland duct morphogenesis	0.0004865 87	0.0014505 22	5
GO:00988 10	neurotransmitter reuptake	0.0004865 87	0.0014505 22	5
GO:00031 58	endothelium development	0.0004948 5	0.0014727 26	5
GO:00725 11	divalent inorganic cation transport	0.0004971 51	0.0014771 46	5
GO:00468 90	regulation of lipid biosynthetic process	0.0004984 77	0.0014786 56	5
GO:00027 91	regulation of peptide secretion	0.0005077 13	0.0015035 91	5
GO:00457 66	positive regulation of angiogenesis	0.0005113 17	0.0015117 88	5
GO:00614 18	regulation of transcription from RNA polymerase II promoter in response to hypoxia	0.0005238 92	0.0015464 42	5
GO:00400 18	positive regulation of multicellular organism growth	0.0005333 84	0.0015693 39	5
GO:19020 03	regulation of amyloid-beta formation	0.0005333 84	0.0015693 39	5

GO:00421 10	T cell activation	0.0005357 81	0.0015738 33	5
GO:00610 45	negative regulation of wound healing	0.0005501 9	0.0016107 47	5
GO:00723 32	intrinsic apoptotic signaling pathway by p53 class mediator	0.0005501 9	0.0016107 47	5
GO:00705 55	response to interleukin-1	0.0005513 9	0.0016107 47	5
GO:00507 69	positive regulation of neurogenesis	0.0005519 08	0.0016107 47	5
GO:00302 78	regulation of ossification	0.0005652 77	0.0016471 07	5
GO:00513 48	negative regulation of transferase activity	0.0005730 85	0.0016615 94	5
GO:00068 09	nitric oxide biosynthetic process	0.0005774 13	0.0016615 94	5
GO:00310 16	pancreas development	0.0005774 13	0.0016615 94	5
GO:00712 60	cellular response to mechanical stimulus	0.0005774 13	0.0016615 94	5
GO:00903 98	cellular senescence	0.0005774 13	0.0016615 94	5
GO:00300 73	insulin secretion	0.0005794 34	0.0016615 94	5
GO:00902 76	regulation of peptide hormone secretion	0.0005794 34	0.0016615 94	5
GO:00147 06	striated muscle tissue development	0.0005819 84	0.0016615 94	5
GO:00007 37	DNA catabolic process, endonucleolytic	0.0005829 67	0.0016615 94	5
GO:00356 33	maintenance of blood-brain barrier	0.0005829 67	0.0016615 94	5
GO:00432 76	anoikis	0.0005829 67	0.0016615 94	5
GO:00986 64	G protein-coupled serotonin receptor signaling pathway	0.0005829 67	0.0016615 94	5
GO:19026 92	regulation of neuroblast proliferation	0.0005829 67	0.0016615 94	5
GO:00600 48	cardiac muscle contraction	0.0005840 23	0.0016615 94	5
GO:00726 55	establishment of protein localization to mitochondrion	0.0005840 23	0.0016615 94	5
GO:00486 78	response to axon injury	0.0006055 8	0.0017175 26	5

GO:19001 82	positive regulation of protein localization to nucleus	0.0006055 8	0.0017175 26	5
GO:00068 69	lipid transport	0.0006222 9	0.0017610 64	5
GO:00070 06	mitochondrial membrane organization	0.0006228 78	0.0017610 64	5
GO:00711 58	positive regulation of cell cycle arrest	0.0006347 09	0.0017880 93	5
GO:00302 62	apoptotic nuclear changes	0.0006354 02	0.0017880 93	5
GO:00602 51	regulation of glial cell proliferation	0.0006354 02	0.0017880 93	5
GO:19027 49	regulation of cell cycle G2/M phase transition	0.0006388 43	0.0017949 85	5
GO:00082 86	insulin receptor signaling pathway	0.0006430 17	0.0017990 54	5
GO:00455 98	regulation of fat cell differentiation	0.0006430 17	0.0017990 54	5
GO:00301 98	extracellular matrix organization	0.0006432 74	0.0017990 54	5
GO:00900 68	positive regulation of cell cycle process	0.0006452 7	0.0018018 5	5
GO:00430 62	extracellular structure organization	0.0006539 79	0.0018233 55	5
GO:00705 85	protein localization to mitochondrion	0.0006636 41	0.0018474 47	5
GO:00506 70	regulation of lymphocyte proliferation	0.0006702 67	0.0018630 28	5
GO:19016 53	cellular response to peptide	0.0006758 21	0.0018755 83	4
GO:00076 12	learning	0.0006847 56	0.0018945 7	4
GO:00381 27	ERBB signaling pathway	0.0006847 56	0.0018945 7	4
GO:00018 93	maternal placenta development	0.0006907 56	0.0018966 69	4
GO:00105 43	regulation of platelet activation	0.0006907 56	0.0018966 69	4
GO:00425 54	superoxide anion generation	0.0006907 56	0.0018966 69	4
GO:00708 73	regulation of glycogen metabolic process	0.0006907 56	0.0018966 69	4
GO:19053 32	positive regulation of morphogenesis of an epithelium	0.0006907 56	0.0018966 69	4

GO:00480 41	focal adhesion assembly	0.0006959 26	0.0019079 69	4
GO:00329 44	regulation of mononuclear cell proliferation	0.0007028 78	0.0019241 13	4
GO:00197 22	calcium-mediated signaling	0.0007196 37	0.0019670 16	4
GO:00462 09	nitric oxide metabolic process	0.0007280 51	0.0019852 24	4
GO:19040 64	positive regulation of cation transmembrane transport	0.0007284 93	0.0019852 24	4
GO:00069 21	cellular component disassembly involved in execution phase of apoptosis	0.0007490 92	0.0020225 41	4
GO:00715 42	dopaminergic neuron differentiation	0.0007490 92	0.0020225 41	4
GO:00860 10	membrane depolarization during action potential	0.0007490 92	0.0020225 41	4
GO:00900 50	positive regulation of cell migration involved in sprouting angiogenesis	0.0007490 92	0.0020225 41	4
GO:19049 94	regulation of leukocyte adhesion to vascular endothelial cell	0.0007490 92	0.0020225 41	4
GO:20002 73	positive regulation of signaling receptor activity	0.0007490 92	0.0020225 41	4
GO:00106 75	regulation of cellular carbohydrate metabolic process	0.0007511 29	0.0020225 41	4
GO:00719 01	negative regulation of protein serine/threonine kinase activity	0.0007511 29	0.0020225 41	4
GO:00310 56	regulation of histone modification	0.0007742 87	0.0020787 11	4
GO:00435 24	negative regulation of neuron apoptotic process	0.0007742 87	0.0020787 11	4
GO:20010 20	regulation of response to DNA damage stimulus	0.0007897 93	0.0021172	4
GO:00061 12	energy reserve metabolic process	0.0007954 25	0.0021228 62	4
GO:00097 91	post-embryonic development	0.0007954 25	0.0021228 62	4
GO:00341 09	homotypic cell-cell adhesion	0.0007954 25	0.0021228 62	4
GO:00605 37	muscle tissue development	0.0008067 41	0.0021409 19	4
GO:00302 24	monocyte differentiation	0.0008104 73	0.0021409 19	4
GO:00320 94	response to food	0.0008104 73	0.0021409 19	4

GO:00328 85	regulation of polysaccharide biosynthetic process	0.0008104 73	0.0021409 19	4
GO:00457 77	positive regulation of blood pressure	0.0008104 73	0.0021409 19	4
GO:00603 06	regulation of membrane repolarization	0.0008104 73	0.0021409 19	4
GO:19031 31	mononuclear cell differentiation	0.0008104 73	0.0021409 19	4
GO:19047 05	regulation of vascular associated smooth muscle cell proliferation	0.0008307 12	0.0021848 12	4
GO:19908 74	vascular associated smooth muscle cell proliferation	0.0008307 12	0.0021848 12	4
GO:20010 57	reactive nitrogen species metabolic process	0.0008307 12	0.0021848 12	4
GO:00468 89	positive regulation of lipid biosynthetic process	0.0008670 89	0.0022771 77	4
GO:00082 03	cholesterol metabolic process	0.0008722 89	0.0022875 14	4
GO:00342 05	amyloid-beta formation	0.0008749 61	0.0022878 89	4
GO:00860 91	regulation of heart rate by cardiac conduction	0.0008749 61	0.0022878 89	4
GO:00016 49	osteoblast differentiation	0.0008847 99	0.0023069 47	4
GO:00487 38	cardiac muscle tissue development	0.0008847 99	0.0023069 47	4
GO:00305 95	leukocyte chemotaxis	0.0009048 15	0.0023557 39	4
GO:00423 07	positive regulation of protein import into nucleus	0.0009426 18	0.0024381 13	4
GO:00424 17	dopamine metabolic process	0.0009426 18	0.0024381 13	4
GO:19029 91	regulation of amyloid precursor protein catabolic process	0.0009426 18	0.0024381 13	4
GO:00420 58	regulation of epidermal growth factor receptor signaling pathway	0.0009431 91	0.0024381 13	4
GO:00705 42	response to fatty acid	0.0009431 91	0.0024381 13	4
GO:00070 50	cell cycle arrest	0.0009458 93	0.0024416 1	4
GO:00309 02	hindbrain development	0.0009516 48	0.0024529 65	4
GO:19030 39	positive regulation of leukocyte cell-cell adhesion	0.0009669 63	0.0024853 62	4

GO:19040 18	positive regulation of vasculature development	0.0009669 63	0.0024853 62	4
GO:00332 73	response to vitamin	0.0009829 52	0.0025157 37	4
GO:00341 03	regulation of tissue remodeling	0.0009829 52	0.0025157 37	4
GO:20001 77	regulation of neural precursor cell proliferation	0.0009829 52	0.0025157 37	4
GO:00604 02	calcium ion transport into cytosol	0.0010074 59	0.0025577 48	4
GO:00320 70	regulation of deoxyribonuclease activity	0.0010097 83	0.0025577 48	4
GO:00519 01	positive regulation of mitochondrial depolarization	0.0010097 83	0.0025577 48	4
GO:00600 68	vagina development	0.0010097 83	0.0025577 48	4
GO:00703 91	response to lipoteichoic acid	0.0010097 83	0.0025577 48	4
GO:00712 23	cellular response to lipoteichoic acid	0.0010097 83	0.0025577 48	4
GO:00900 37	positive regulation of protein kinase C signaling	0.0010097 83	0.0025577 48	4
GO:00996 22	cardiac muscle cell membrane repolarization	0.0010135 02	0.0025577 48	4
GO:19001 17	regulation of execution phase of apoptosis	0.0010135 02	0.0025577 48	4
GO:19020 42	negative regulation of extrinsic apoptotic signaling pathway via death domain receptors	0.0010135 02	0.0025577 48	4
GO:19004 07	regulation of cellular response to oxidative stress	0.0010238 78	0.0025803 36	4
GO:19021 07	positive regulation of leukocyte differentiation	0.0010362 6	0.0026079 06	4
GO:19030 37	regulation of leukocyte cell-cell adhesion	0.0010644 54	0.0026751 41	4
GO:19030 35	negative regulation of response to wounding	0.0010659 88	0.0026752 81	4
GO:00706 63	regulation of leukocyte proliferation	0.0010777 97	0.0027011 7	4
GO:00015 04	neurotransmitter uptake	0.0010876 73	0.0027146 43	4
GO:19040 37	positive regulation of epithelial cell apoptotic process	0.0010876 73	0.0027146 43	4
GO:19045 91	positive regulation of protein import	0.0010876 73	0.0027146 43	4

GO:0006814	sodium ion transport	0.001101089	0.002743937	4
GO:0032147	activation of protein kinase activity	0.001102443	0.002743937	4
GO:0008202	steroid metabolic process	0.001121834	0.002788364	4
GO:1902652	secondary alcohol metabolic process	0.001126338	0.00279572	4
GO:0006308	DNA catabolic process	0.001165189	0.002884239	4
GO:0045823	positive regulation of heart contraction	0.001165189	0.002884239	4
GO:0034329	cell junction assembly	0.001180932	0.002919215	4
GO:0001820	serotonin secretion	0.001230309	0.003000285	4
GO:0009629	response to gravity	0.001230309	0.003000285	4
GO:0019371	cyclooxygenase pathway	0.001230309	0.003000285	4
GO:0033327	Leydig cell differentiation	0.001230309	0.003000285	4
GO:0033483	gas homeostasis	0.001230309	0.003000285	4
GO:0040015	negative regulation of multicellular organism growth	0.001230309	0.003000285	4
GO:0045899	positive regulation of RNA polymerase II transcription preinitiation complex assembly	0.001230309	0.003000285	4
GO:0060525	prostate glandular acinus development	0.001230309	0.003000285	4
GO:1903800	positive regulation of production of miRNAs involved in gene silencing by miRNA	0.001230309	0.003000285	4
GO:2001269	positive regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway	0.001230309	0.003000285	4
GO:0032881	regulation of polysaccharide metabolic process	0.001246106	0.00301168	4
GO:0033173	calcineurin-NFAT signaling cascade	0.001246106	0.00301168	4
GO:0030516	regulation of axon extension	0.001246632	0.00301168	4
GO:0071674	mononuclear cell migration	0.001246632	0.00301168	4
GO:0120162	positive regulation of cold-induced thermogenesis	0.001246632	0.00301168	4

GO:19011 84	regulation of ERBB signaling pathway	0.0012466 32	0.0030116 8	4
GO:19016 55	cellular response to ketone	0.0012466 32	0.0030116 8	4
GO:00070 93	mitotic cell cycle checkpoint	0.0012553 21	0.0030286 27	4
GO:00458 33	negative regulation of lipid metabolic process	0.0012949 37	0.0031158 97	4
GO:00480 10	vascular endothelial growth factor receptor signaling pathway	0.0012949 37	0.0031158 97	4
GO:00459 31	positive regulation of mitotic cell cycle	0.0013237 62	0.0031760 79	4
GO:00310 18	endocrine pancreas development	0.0013304 8	0.0031760 79	4
GO:00327 22	positive regulation of chemokine production	0.0013304 8	0.0031760 79	4
GO:00427 71	intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	0.0013304 8	0.0031760 79	4
GO:00454 29	positive regulation of nitric oxide biosynthetic process	0.0013304 8	0.0031760 79	4
GO:19046 46	cellular response to amyloid-beta	0.0013304 8	0.0031760 79	4
GO:00161 25	sterol metabolic process	0.0013589 99	0.0032398 85	4
GO:00019 33	negative regulation of protein phosphorylation	0.0013647 91	0.0032494 12	4
GO:00431 22	regulation of I-kappaB kinase/NF-kappaB signaling	0.0013836 49	0.0032899 82	4
GO:00519 24	regulation of calcium ion transport	0.0014118 44	0.0033505 14	4
GO:00059 78	glycogen biosynthetic process	0.0014183 65	0.0033505 14	4
GO:00092 50	glucan biosynthetic process	0.0014183 65	0.0033505 14	4
GO:00610 28	establishment of endothelial barrier	0.0014183 65	0.0033505 14	4
GO:19044 07	positive regulation of nitric oxide metabolic process	0.0014183 65	0.0033505 14	4
GO:00018 19	positive regulation of cytokine production	0.0014241 84	0.0033555	4
GO:00434 34	response to peptide hormone	0.0014241 84	0.0033555	4
GO:00308 56	regulation of epithelial cell differentiation	0.0014315 45	0.0033640 81	4

GO:19059 52	regulation of lipid localization	0.0014315 45	0.0033640 81	4
GO:00326 37	interleukin-8 production	0.0014476 92	0.0033709 85	4
GO:00442 64	cellular polysaccharide metabolic process	0.0014476 92	0.0033709 85	4
GO:19028 82	regulation of response to oxidative stress	0.0014476 92	0.0033709 85	4
GO:00020 24	diet induced thermogenesis	0.0014717 42	0.0033709 85	4
GO:00069 83	ER overload response	0.0014717 42	0.0033709 85	4
GO:00070 77	mitotic nuclear envelope disassembly	0.0014717 42	0.0033709 85	4
GO:00324 94	response to peptidoglycan	0.0014717 42	0.0033709 85	4
GO:00457 60	positive regulation of action potential	0.0014717 42	0.0033709 85	4
GO:00465 41	saliva secretion	0.0014717 42	0.0033709 85	4
GO:00515 83	dopamine uptake involved in synaptic transmission	0.0014717 42	0.0033709 85	4
GO:00519 34	catecholamine uptake involved in synaptic transmission	0.0014717 42	0.0033709 85	4
GO:00604 42	branching involved in prostate gland morphogenesis	0.0014717 42	0.0033709 85	4
GO:00607 36	prostate gland growth	0.0014717 42	0.0033709 85	4
GO:00607 42	epithelial cell differentiation involved in prostate gland development	0.0014717 42	0.0033709 85	4
GO:00702 43	regulation of thymocyte apoptotic process	0.0014717 42	0.0033709 85	4
GO:00901 54	positive regulation of sphingolipid biosynthetic process	0.0014717 42	0.0033709 85	4
GO:00903 31	negative regulation of platelet aggregation	0.0014717 42	0.0033709 85	4
GO:19025 10	regulation of apoptotic DNA fragmentation	0.0014717 42	0.0033709 85	4
GO:19041 81	positive regulation of membrane depolarization	0.0014717 42	0.0033709 85	4
GO:20003 04	positive regulation of ceramide biosynthetic process	0.0014717 42	0.0033709 85	4
GO:00080 16	regulation of heart contraction	0.0014990 71	0.0034278 18	4

GO:0022600	digestive system process	0.001501285	0.003427818	4
GO:0021543	pallium development	0.001506909	0.003427818	4
GO:0022602	ovulation cycle process	0.001509815	0.003427818	4
GO:0045933	positive regulation of muscle contraction	0.001509815	0.003427818	4
GO:0048599	oocyte development	0.001509815	0.003427818	4
GO:0048806	genitalia development	0.001509815	0.003427818	4
GO:0030072	peptide hormone secretion	0.001529042	0.003467119	4
GO:0003205	cardiac chamber development	0.001545669	0.00349606	4
GO:0015718	monocarboxylic acid transport	0.001545669	0.00349606	4
GO:0002042	cell migration involved in sprouting angiogenesis	0.001556246	0.00350247	4
GO:0034766	negative regulation of ion transmembrane transport	0.001556246	0.00350247	4
GO:0060079	excitatory postsynaptic potential	0.001556246	0.00350247	4
GO:0098869	cellular oxidant detoxification	0.001556246	0.00350247	4
GO:0003007	heart morphogenesis	0.001559468	0.003505361	4
GO:0021537	telencephalon development	0.001590353	0.003570349	4
GO:0042220	response to cocaine	0.001604883	0.003598506	4
GO:0006874	cellular calcium ion homeostasis	0.001614817	0.003616298	4
GO:0002067	glandular epithelial cell differentiation	0.001703621	0.003787049	4
GO:0002686	negative regulation of leukocyte migration	0.001703621	0.003787049	4
GO:0030850	prostate gland development	0.001703621	0.003787049	4
GO:0048512	circadian behavior	0.001703621	0.003787049	4
GO:0086009	membrane repolarization	0.001703621	0.003787049	4

GO:00977 20	calcineurin-mediated signaling	0.0017036 21	0.0037870 49	4
GO:00069 41	striated muscle contraction	0.0017080 87	0.0037876 69	4
GO:00604 01	cytosolic calcium ion transport	0.0017080 87	0.0037876 69	4
GO:00324 14	positive regulation of ion transmembrane transporter activity	0.0017295 2	0.0038305 03	4
GO:00423 08	negative regulation of protein import into nucleus	0.0017338 8	0.0038307 82	4
GO:19045 90	negative regulation of protein import	0.0017338 8	0.0038307 82	4
GO:00315 89	cell-substrate adhesion	0.0017551 47	0.0038730 39	4
GO:00313 30	negative regulation of cellular catabolic process	0.0017855 71	0.0039326 74	4
GO:00303 30	DNA damage response, signal transduction by p53 class mediator	0.0017901 36	0.0039326 74	4
GO:00550 17	cardiac muscle tissue growth	0.0017901 36	0.0039326 74	4
GO:19017 96	regulation of signal transduction by p53 class mediator	0.0017938 39	0.0039326 74	4
GO:00017 74	microglial cell activation	0.0018060 79	0.0039326 74	4
GO:00022 69	leukocyte activation involved in inflammatory response	0.0018060 79	0.0039326 74	4
GO:00076 22	rhythmic behavior	0.0018060 79	0.0039326 74	4
GO:00140 09	glial cell proliferation	0.0018060 79	0.0039326 74	4
GO:00301 95	negative regulation of blood coagulation	0.0018060 79	0.0039326 74	4
GO:00429 87	amyloid precursor protein catabolic process	0.0018060 79	0.0039326 74	4
GO:19047 07	positive regulation of vascular associated smooth muscle cell proliferation	0.0018060 79	0.0039326 74	4
GO:00083 61	regulation of cell size	0.0018378 8	0.0039971 11	4
GO:00468 83	regulation of hormone secretion	0.0018545 28	0.0040284 75	4
GO:00713 46	cellular response to interferon-gamma	0.0018827 1	0.0040847 89	4
GO:00071 59	leukocyte cell-cell adhesion	0.0018980 71	0.0041074 14	4

GO:00165 70	histone modification	0.0018999 48	0.0041074 14	4
GO:00550 74	calcium ion homeostasis	0.0018999 48	0.0041074 14	4
GO:00504 35	amyloid-beta metabolic process	0.0019123 07	0.0041219 08	4
GO:19000 47	negative regulation of hemostasis	0.0019123 07	0.0041219 08	4
GO:00189 58	phenol-containing compound metabolic process	0.0019157 64	0.0041219 08	4
GO:00217 61	limbic system development	0.0019157 64	0.0041219 08	4
GO:00905 96	sensory organ morphogenesis	0.0019254 89	0.0041342 09	4
GO:00510 52	regulation of DNA metabolic process	0.0019277 11	0.0041342 09	4
GO:00713 47	cellular response to interleukin-1	0.0019283 36	0.0041342 09	4
GO:00458 98	regulation of RNA polymerase II transcription preinitiation complex assembly	0.0020165 22	0.0042900 3	4
GO:00509 30	induction of positive chemotaxis	0.0020165 22	0.0042900 3	4
GO:00860 69	bundle of His cell to Purkinje myocyte communication	0.0020165 22	0.0042900 3	4
GO:01060 70	regulation of adenylate cyclase-activating G protein-coupled receptor signaling pathway	0.0020165 22	0.0042900 3	4
GO:19036 24	regulation of DNA catabolic process	0.0020165 22	0.0042900 3	4
GO:20012 57	regulation of cation channel activity	0.0020220 1	0.0042900 3	4
GO:00099 94	oocyte differentiation	0.0020223 53	0.0042900 3	4
GO:00311 03	axon regeneration	0.0020223 53	0.0042900 3	4
GO:00509 99	regulation of nitric-oxide synthase activity	0.0020223 53	0.0042900 3	4
GO:00344 40	lipid oxidation	0.0020473 74	0.0043228 35	4
GO:00423 03	molting cycle	0.0020473 74	0.0043228 35	4
GO:00426 33	hair cycle	0.0020473 74	0.0043228 35	4
GO:00613 87	regulation of extent of cell growth	0.0020473 74	0.0043228 35	4

GO:00448 39	cell cycle G2/M phase transition	0.0020735 73	0.0043730 48	4
GO:00059 76	polysaccharide metabolic process	0.0021154 68	0.0044510 27	4
GO:00995 65	chemical synaptic transmission, postsynaptic	0.0021154 68	0.0044510 27	4
GO:00453 33	cellular respiration	0.0021189 72	0.0044532 21	4
GO:00327 31	positive regulation of interleukin-1 beta production	0.0021362 66	0.0044739 79	4
GO:00457 44	negative regulation of G protein-coupled receptor signaling pathway	0.0021362 66	0.0044739 79	4
GO:00617 56	leukocyte adhesion to vascular endothelial cell	0.0021362 66	0.0044739 79	4
GO:00431 23	positive regulation of I-kappaB kinase/NF-kappaB signaling	0.0021687 06	0.0045366 67	4
GO:00329 63	collagen metabolic process	0.0021851 11	0.0045657 05	4
GO:00224 12	cellular process involved in reproduction in multicellular organism	0.0022443 2	0.0046713 43	4
GO:00165 69	covalent chromatin modification	0.0022523 58	0.0046713 43	4
GO:00065 84	catecholamine metabolic process	0.0022540 93	0.0046713 43	4
GO:00097 12	catechol-containing compound metabolic process	0.0022540 93	0.0046713 43	4
GO:00327 57	positive regulation of interleukin-8 production	0.0022540 93	0.0046713 43	4
GO:00220 37	metencephalon development	0.0022563 21	0.0046713 43	4
GO:00432 00	response to amino acid	0.0022563 21	0.0046713 43	4
GO:19907 48	cellular detoxification	0.0022563 21	0.0046713 43	4
GO:00451 65	cell fate commitment	0.0022706 21	0.0046904 32	4
GO:00303 08	negative regulation of cell growth	0.0022707 26	0.0046904 32	4
GO:00224 09	positive regulation of cell-cell adhesion	0.0023116 71	0.0047317 01	4
GO:00060 89	lactate metabolic process	0.0023194 7	0.0047317 01	4
GO:00341 11	negative regulation of homotypic cell-cell adhesion	0.0023194 7	0.0047317 01	4

GO:00448 49	estrous cycle	0.0023194 7	0.0047317 01	4
GO:00456 51	positive regulation of macrophage differentiation	0.0023194 7	0.0047317 01	4
GO:00480 70	regulation of developmental pigmentation	0.0023194 7	0.0047317 01	4
GO:00485 69	post-embryonic animal organ development	0.0023194 7	0.0047317 01	4
GO:00510 44	positive regulation of membrane protein ectodomain proteolysis	0.0023194 7	0.0047317 01	4
GO:19015 50	regulation of endothelial cell development	0.0023194 7	0.0047317 01	4
GO:19031 40	regulation of establishment of endothelial barrier	0.0023194 7	0.0047317 01	4
GO:20010 28	positive regulation of endothelial cell chemotaxis	0.0023194 7	0.0047317 01	4
GO:00224 08	negative regulation of cell-cell adhesion	0.0023230 28	0.0047336 23	4
GO:00604 19	heart growth	0.0023291 17	0.0047406 93	4
GO:00423 26	negative regulation of phosphorylation	0.0023405 63	0.0047586 38	4
GO:00019 54	positive regulation of cell-matrix adhesion	0.0023758 79	0.0048088 26	4
GO:00029 31	response to ischemia	0.0023758 79	0.0048088 26	4
GO:00508 19	negative regulation of coagulation	0.0023758 79	0.0048088 26	4
GO:00513 53	positive regulation of oxidoreductase activity	0.0023758 79	0.0048088 26	4
GO:00466 20	regulation of organ growth	0.0024035 16	0.0048539 05	4
GO:00609 64	regulation of gene silencing by miRNA	0.0024035 16	0.0048539 05	4
GO:00454 46	endothelial cell differentiation	0.0024795 36	0.0050002 29	4
GO:00328 68	response to insulin	0.0024814 98	0.0050002 29	4
GO:00702 28	regulation of lymphocyte apoptotic process	0.0025016 69	0.0050296 72	4
GO:00860 02	cardiac muscle cell action potential involved in contraction	0.0025016 69	0.0050296 72	4
GO:00420 98	T cell proliferation	0.0025410 48	0.0050918 7	4

GO:00508 64	regulation of B cell activation	0.0025410 48	0.0050918 7	4
GO:19022 75	regulation of chromatin organization	0.0025410 48	0.0050918 7	4
GO:00068 05	xenobiotic metabolic process	0.0025571 94	0.0051129 01	4
GO:00219 87	cerebral cortex development	0.0025571 94	0.0051129 01	4
GO:00725 03	cellular divalent inorganic cation homeostasis	0.0025891 21	0.0051710 23	4
GO:00060 66	alcohol metabolic process	0.0025997 78	0.0051860 91	4
GO:00072 49	I-kappaB kinase/NF-kappaB signaling	0.0026149 13	0.0051860 91	4
GO:00305 20	intracellular estrogen receptor signaling pathway	0.0026315 08	0.0051860 91	4
GO:00427 43	hydrogen peroxide metabolic process	0.0026315 08	0.0051860 91	4
GO:00480 16	inositol phosphate-mediated signaling	0.0026315 08	0.0051860 91	4
GO:00989 00	regulation of action potential	0.0026315 08	0.0051860 91	4
GO:00303 97	membrane disassembly	0.0026425 23	0.0051860 91	4
GO:00322 25	regulation of synaptic transmission, dopaminergic	0.0026425 23	0.0051860 91	4
GO:00431 16	negative regulation of vascular permeability	0.0026425 23	0.0051860 91	4
GO:00457 25	positive regulation of glycogen biosynthetic process	0.0026425 23	0.0051860 91	3
GO:00510 81	nuclear envelope disassembly	0.0026425 23	0.0051860 91	3
GO:00517 70	positive regulation of nitric-oxide synthase biosynthetic process	0.0026425 23	0.0051860 91	3
GO:00605 76	intestinal epithelial cell development	0.0026425 23	0.0051860 91	3
GO:00713 91	cellular response to estrogen stimulus	0.0026425 23	0.0051860 91	3
GO:19004 51	positive regulation of glutamate receptor signaling pathway	0.0026425 23	0.0051860 91	3
GO:19037 29	regulation of plasma membrane organization	0.0026425 23	0.0051860 91	3
GO:00600 47	heart contraction	0.0026605 63	0.0052158 37	3

GO:00431 12	receptor metabolic process	0.0027140 55	0.0053101 92	3
GO:00601 47	regulation of posttranscriptional gene silencing	0.0027174 96	0.0053101 92	3
GO:00609 66	regulation of gene silencing by RNA	0.0027174 96	0.0053101 92	3
GO:19037 49	positive regulation of establishment of protein localization to mitochondrion	0.0027654 39	0.0053980 47	3
GO:19037 06	regulation of hemopoiesis	0.0027887 84	0.0054377 5	3
GO:00302 18	erythrocyte differentiation	0.0028001 75	0.0054540 83	3
GO:00309 00	forebrain development	0.0028329 77	0.0055120 4	3
GO:00108 11	positive regulation of cell-substrate adhesion	0.0028845 63	0.0056003 65	3
GO:00972 37	cellular response to toxic substance	0.0028845 63	0.0056003 65	3
GO:00066 36	unsaturated fatty acid biosynthetic process	0.0029035 04	0.0056190 53	3
GO:00311 02	neuron projection regeneration	0.0029035 04	0.0056190 53	3
GO:00480 08	platelet-derived growth factor receptor signaling pathway	0.0029035 04	0.0056190 53	3
GO:00343 41	response to interferon-gamma	0.0029578 28	0.0056685 84	3
GO:00071 73	epidermal growth factor receptor signaling pathway	0.0029706 76	0.0056685 84	3
GO:00486 75	axon extension	0.0029706 76	0.0056685 84	3
GO:00714 66	cellular response to xenobiotic stimulus	0.0029706 76	0.0056685 84	3
GO:00069 78	DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator	0.0029854 87	0.0056685 84	3
GO:00305 40	female genitalia development	0.0029854 87	0.0056685 84	3
GO:00310 65	positive regulation of histone deacetylation	0.0029854 87	0.0056685 84	3
GO:00335 99	regulation of mammary gland epithelial cell proliferation	0.0029854 87	0.0056685 84	3
GO:00431 17	positive regulation of vascular permeability	0.0029854 87	0.0056685 84	3
GO:00459 86	negative regulation of smooth muscle contraction	0.0029854 87	0.0056685 84	3

GO:00506 65	hydrogen peroxide biosynthetic process	0.0029854 87	0.0056685 84	3
GO:00550 12	ventricular cardiac muscle cell differentiation	0.0029854 87	0.0056685 84	3
GO:00606 44	mammary gland epithelial cell differentiation	0.0029854 87	0.0056685 84	3
GO:00708 75	positive regulation of glycogen metabolic process	0.0029854 87	0.0056685 84	3
GO:00718 50	mitotic cell cycle arrest	0.0029854 87	0.0056685 84	3
GO:00903 36	positive regulation of brown fat cell differentiation	0.0029854 87	0.0056685 84	3
GO:00904 94	dopamine uptake	0.0029854 87	0.0056685 84	3
GO:20008 11	negative regulation of anoikis	0.0029854 87	0.0056685 84	3
GO:00442 62	cellular carbohydrate metabolic process	0.0029970 93	0.0056846 55	3
GO:00327 32	positive regulation of interleukin-1 production	0.0030457 45	0.0057504 18	3
GO:00619 00	glial cell activation	0.0030457 45	0.0057504 18	3
GO:00977 55	positive regulation of blood vessel diameter	0.0030457 45	0.0057504 18	3
GO:19034 28	positive regulation of reactive oxygen species biosynthetic process	0.0030457 45	0.0057504 18	3
GO:00507 68	negative regulation of neurogenesis	0.0030476 54	0.0057504 18	3
GO:00421 76	regulation of protein catabolic process	0.0030819 46	0.0058090 63	3
GO:00309 68	endoplasmic reticulum unfolded protein response	0.0031481 49	0.0059078 69	3
GO:00352 70	endocrine system development	0.0031481 49	0.0059078 69	3
GO:00485 93	camera-type eye morphogenesis	0.0031481 49	0.0059078 69	3
GO:19035 78	regulation of ATP metabolic process	0.0031481 49	0.0059078 69	3
GO:00030 15	heart process	0.0031506 92	0.0059078 69	3
GO:00105 74	regulation of vascular endothelial growth factor production	0.0031922 02	0.0059548 52	3
GO:00330 13	tetrapyrrole metabolic process	0.0031922 02	0.0059548 52	3

GO:00336 19	membrane protein proteolysis	0.0031922 02	0.0059548 52	3
GO:00463 24	regulation of glucose import	0.0031922 02	0.0059548 52	3
GO:19020 41	regulation of extrinsic apoptotic signaling pathway via death domain receptors	0.0031922 02	0.0059548 52	3
GO:00550 07	cardiac muscle cell differentiation	0.0032395 44	0.0060369 4	3
GO:00190 79	viral genome replication	0.0033327 32	0.0061820 58	3
GO:00074 05	neuroblast proliferation	0.0033429 16	0.0061820 58	3
GO:00427 72	DNA damage response, signal transduction resulting in transcription	0.0033481 65	0.0061820 58	3
GO:00510 23	regulation of immunoglobulin secretion	0.0033481 65	0.0061820 58	3
GO:00702 30	positive regulation of lymphocyte apoptotic process	0.0033481 65	0.0061820 58	3
GO:00900 36	regulation of protein kinase C signaling	0.0033481 65	0.0061820 58	3
GO:00904 93	catecholamine uptake	0.0033481 65	0.0061820 58	3
GO:01500 78	positive regulation of neuroinflammatory response	0.0033481 65	0.0061820 58	3
GO:20003 03	regulation of ceramide biosynthetic process	0.0033481 65	0.0061820 58	3
GO:00071 62	negative regulation of cell adhesion	0.0033645 62	0.006206 58	3
GO:00140 13	regulation of gliogenesis	0.0034277 33	0.0063160 82	3
GO:00466 22	positive regulation of organ growth	0.0034979 24	0.0064192 71	3
GO:00518 93	regulation of focal adhesion assembly	0.0034979 24	0.0064192 71	3
GO:00700 59	intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	0.0034979 24	0.0064192 71	3
GO:00901 09	regulation of cell-substrate junction assembly	0.0034979 24	0.0064192 71	3
GO:00341 01	erythrocyte homeostasis	0.0035245 61	0.0064616 02	3
GO:00094 10	response to xenobiotic stimulus	0.0036232 35	0.0066357 78	3
GO:00018 85	endothelial cell development	0.0036572 65	0.0066643 75	3

GO:00454 53	bone resorption	0.0036572 65	0.0066643 75	3
GO:00519 26	negative regulation of calcium ion transport	0.0036572 65	0.0066643 75	3
GO:19004 49	regulation of glutamate receptor signaling pathway	0.0036572 65	0.0066643 75	3
GO:20004 01	regulation of lymphocyte migration	0.0036572 65	0.0066643 75	3
GO:00420 63	gliogenesis	0.0037054 57	0.0067097 38	3
GO:00032 06	cardiac chamber morphogenesis	0.0037237 71	0.0067097 38	3
GO:00032 31	cardiac ventricle development	0.0037237 71	0.0067097 38	3
GO:00105 08	positive regulation of autophagy	0.0037237 71	0.0067097 38	3
GO:00105 44	negative regulation of platelet activation	0.0037303 64	0.0067097 38	3
GO:00420 53	regulation of dopamine metabolic process	0.0037303 64	0.0067097 38	3
GO:00420 69	regulation of catecholamine metabolic process	0.0037303 64	0.0067097 38	3
GO:00602 52	positive regulation of glial cell proliferation	0.0037303 64	0.0067097 38	3
GO:00709 89	oxidative demethylation	0.0037303 64	0.0067097 38	3
GO:00901 53	regulation of sphingolipid biosynthetic process	0.0037303 64	0.0067097 38	3
GO:19021 76	negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	0.0037303 64	0.0067097 38	3
GO:19050 38	regulation of membrane lipid metabolic process	0.0037303 64	0.0067097 38	3
GO:20000 10	positive regulation of protein localization to cell surface	0.0037303 64	0.0067097 38	3
GO:19059 53	negative regulation of lipid localization	0.0038209 76	0.0068658 94	3
GO:00162 36	macroautophagy	0.0038852 39	0.0069744 43	3
GO:00327 68	regulation of monooxygenase activity	0.0039890 94	0.0071325 7	3
GO:00466 26	regulation of insulin receptor signaling pathway	0.0039890 94	0.0071325 7	3
GO:01501 16	regulation of cell-substrate junction organization	0.0039890 94	0.0071325 7	3

GO:20003 78	negative regulation of reactive oxygen species metabolic process	0.0039890 94	0.0071325 7	3
GO:00347 54	cellular hormone metabolic process	0.0040367 14	0.0072105 91	3
GO:00072 52	I-kappaB phosphorylation	0.0041318 92	0.0073353 52	3
GO:00193 73	epoxygenase P450 pathway	0.0041318 92	0.0073353 52	3
GO:00324 95	response to muramyl dipeptide	0.0041318 92	0.0073353 52	3
GO:00517 67	nitric-oxide synthase biosynthetic process	0.0041318 92	0.0073353 52	3
GO:00517 69	regulation of nitric-oxide synthase biosynthetic process	0.0041318 92	0.0073353 52	3
GO:19004 09	positive regulation of cellular response to oxidative stress	0.0041318 92	0.0073353 52	3
GO:00468 79	hormone secretion	0.0041349 37	0.0073353 52	3
GO:19036 72	positive regulation of sprouting angiogenesis	0.0041616 54	0.0073755 18	3
GO:00457 27	positive regulation of translation	0.0042549 56	0.0075261 29	3
GO:00506 71	positive regulation of lymphocyte proliferation	0.0042549 56	0.0075261 29	3
GO:00316 69	cellular response to nutrient levels	0.0043363 58	0.0076369 14	3
GO:00424 45	hormone metabolic process	0.0043363 58	0.0076369 14	3
GO:00162 39	positive regulation of macroautophagy	0.0043386 91	0.0076369 14	3
GO:00454 28	regulation of nitric oxide biosynthetic process	0.0043386 91	0.0076369 14	3
GO:00714 79	cellular response to ionizing radiation	0.0043386 91	0.0076369 14	3
GO:00301 83	B cell differentiation	0.0043670 09	0.0076718 32	3
GO:00329 46	positive regulation of mononuclear cell proliferation	0.0043670 09	0.0076718 32	3
GO:00975 29	myeloid leukocyte migration	0.0044196 93	0.0077568 55	3
GO:00519 61	negative regulation of nervous system development	0.0044635 66	0.0078262 64	3
GO:00015 08	action potential	0.0044810 38	0.0078417 03	3

GO:00987 54	detoxification	0.0044810 38	0.0078417 03	3
GO:00600 38	cardiac muscle cell proliferation	0.0045202 39	0.0078754 59	3
GO:00023 63	alpha-beta T cell lineage commitment	0.0045525 56	0.0078754 59	3
GO:00068 37	serotonin transport	0.0045525 56	0.0078754 59	3
GO:00218 54	hypothalamus development	0.0045525 56	0.0078754 59	3
GO:00302 20	platelet formation	0.0045525 56	0.0078754 59	3
GO:00307 28	ovulation	0.0045525 56	0.0078754 59	3
GO:00364 99	PERK-mediated unfolded protein response	0.0045525 56	0.0078754 59	3
GO:00468 23	negative regulation of nucleocytoplasmic transport	0.0045525 56	0.0078754 59	3
GO:00468 27	positive regulation of protein export from nucleus	0.0045525 56	0.0078754 59	3
GO:00483 05	immunoglobulin secretion	0.0045525 56	0.0078754 59	3
GO:00903 12	positive regulation of protein deacetylation	0.0045525 56	0.0078754 59	3
GO:01404 67	integrated stress response signaling	0.0045525 56	0.0078754 59	3
GO:00068 79	cellular iron ion homeostasis	0.0047063 31	0.0081336 98	3
GO:00609 68	regulation of gene silencing	0.0047150 91	0.0081410 62	3
GO:00099 14	hormone transport	0.0047400 72	0.0081763 92	3
GO:00328 69	cellular response to insulin stimulus	0.0047644 92	0.0082106 88	3
GO:00018 89	liver development	0.0048351 46	0.0083245 18	3
GO:00336 92	cellular polysaccharide biosynthetic process	0.0048969 99	0.0084229 95	3
GO:00321 02	negative regulation of response to external stimulus	0.0049461 29	0.0084994 2	3
GO:00069 25	inflammatory cell apoptotic process	0.0049921 67	0.0085138 5	3
GO:00092 35	cobalamin metabolic process	0.0049921 67	0.0085138 5	3

GO:00108 88	negative regulation of lipid storage	0.0049921 67	0.0085138 5	3
GO:00320 69	regulation of nuclease activity	0.0049921 67	0.0085138 5	3
GO:00363 44	platelet morphogenesis	0.0049921 67	0.0085138 5	3
GO:00433 69	CD4-positive or CD8-positive, alpha-beta T cell lineage commitment	0.0049921 67	0.0085138 5	3
GO:19028 84	positive regulation of response to oxidative stress	0.0049921 67	0.0085138 5	3
GO:20004 79	regulation of cAMP-dependent protein kinase activity	0.0049921 67	0.0085138 5	3
GO:00068 36	neurotransmitter transport	0.0050353 61	0.0085713 58	3
GO:00487 62	mesenchymal cell differentiation	0.0050353 61	0.0085713 58	3
GO:00456 00	positive regulation of fat cell differentiation	0.0050922 75	0.0086519 61	3
GO:00519 37	catecholamine transport	0.0050922 75	0.0086519 61	3
GO:00610 08	hepaticobiliary system development	0.0052076 12	0.0088230 69	3
GO:01061 06	cold-induced thermogenesis	0.0052076 12	0.0088230 69	3
GO:01201 61	regulation of cold-induced thermogenesis	0.0052076 12	0.0088230 69	3
GO:00519 66	regulation of synaptic transmission, glutamatergic	0.0052921 91	0.0089496 07	3
GO:19037 47	regulation of establishment of protein localization to mitochondrion	0.0052921 91	0.0089496 07	3
GO:00020 52	positive regulation of neuroblast proliferation	0.0054505 37	0.0091574 78	3
GO:00312 81	positive regulation of cyclase activity	0.0054505 37	0.0091574 78	3
GO:00456 49	regulation of macrophage differentiation	0.0054505 37	0.0091574 78	3
GO:00510 43	regulation of membrane protein ectodomain proteolysis	0.0054505 37	0.0091574 78	3
GO:00860 12	membrane depolarization during cardiac muscle cell action potential	0.0054505 37	0.0091574 78	3
GO:19000 17	positive regulation of cytokine production involved in inflammatory response	0.0054505 37	0.0091574 78	3
GO:20001 78	negative regulation of neural precursor cell proliferation	0.0054505 37	0.0091574 78	3

GO:00346 20	cellular response to unfolded protein	0.0054663 3	0.0091754 92	3
GO:00215 36	diencephalon development	0.0054967 75	0.0092009 89	3
GO:00860 03	cardiac muscle cell contraction	0.0054967 75	0.0092009 89	3
GO:20012 59	positive regulation of cation channel activity	0.0054967 75	0.0092009 89	3
GO:00515 92	response to calcium ion	0.0055988 57	0.0093632 02	3
GO:00463 23	glucose import	0.0057060 57	0.0095045 83	3
GO:00508 05	negative regulation of synaptic transmission	0.0057060 57	0.0095045 83	3
GO:00860 01	cardiac muscle cell action potential	0.0057060 57	0.0095045 83	3
GO:19000 76	regulation of cellular response to insulin stimulus	0.0057060 57	0.0095045 83	3
GO:00605 60	developmental growth involved in morphogenesis	0.0057096 61	0.0095045 83	3
GO:00082 77	regulation of G protein-coupled receptor signaling pathway	0.0057335 16	0.0095355 2	3
GO:00467 77	protein autophosphorylation	0.0058109 43	0.0096465 58	3
GO:00485 88	developmental cell growth	0.0058109 43	0.0096465 58	3
GO:00335 55	multicellular organismal response to stress	0.0059200 66	0.0097594 34	3
GO:00720 91	regulation of stem cell proliferation	0.0059200 66	0.0097594 34	3
GO:19016 16	organic hydroxy compound catabolic process	0.0059200 66	0.0097594 34	3
GO:00106 40	regulation of platelet-derived growth factor receptor signaling pathway	0.0059274 79	0.0097594 34	3
GO:00324 69	endoplasmic reticulum calcium ion homeostasis	0.0059274 79	0.0097594 34	3
GO:00427 38	exogenous drug catabolic process	0.0059274 79	0.0097594 34	3
GO:00903 35	regulation of brown fat cell differentiation	0.0059274 79	0.0097594 34	3
GO:20002 09	regulation of anoikis	0.0059274 79	0.0097594 34	3
GO:20006 37	positive regulation of gene silencing by miRNA	0.0059274 79	0.0097594 34	3

GO:00706 65	positive regulation of leukocyte proliferation	0.0060092 91	0.0098851 4	3
GO:00140 15	positive regulation of gliogenesis	0.0061388 3	0.0100799 01	3
GO:19032 01	regulation of oxidative stress-induced cell death	0.0061388 3	0.0100799 01	3
GO:00512 24	negative regulation of protein transport	0.0061504 36	0.0100898 03	3
GO:00380 93	Fc receptor signaling pathway	0.0062287 84	0.0102090 76	3
GO:00002 71	polysaccharide biosynthetic process	0.0063623 76	0.0104091 78	3
GO:00439 00	regulation of multi-organism process	0.0063623 76	0.0104091 78	3
GO:00107 38	regulation of protein kinase A signaling	0.0064228 07	0.0104325 85	3
GO:00518 94	positive regulation of focal adhesion assembly	0.0064228 07	0.0104325 85	3
GO:00601 48	positive regulation of posttranscriptional gene silencing	0.0064228 07	0.0104325 85	3
GO:00605 71	morphogenesis of an epithelial fold	0.0064228 07	0.0104325 85	3
GO:00605 75	intestinal epithelial cell differentiation	0.0064228 07	0.0104325 85	3
GO:00606 69	embryonic placenta morphogenesis	0.0064228 07	0.0104325 85	3
GO:19043 85	cellular response to angiotensin	0.0064228 07	0.0104325 85	3
GO:20010 26	regulation of endothelial cell chemotaxis	0.0064228 07	0.0104325 85	3
GO:00458 34	positive regulation of lipid metabolic process	0.0064393 16	0.0104500 21	3
GO:00072 65	Ras protein signal transduction	0.0065815 34	0.0106479 92	3
GO:00613 51	neural precursor cell proliferation	0.0065870 8	0.0106479 92	3
GO:00108 27	regulation of glucose transmembrane transport	0.0065907 29	0.0106479 92	3
GO:00422 46	tissue regeneration	0.0065907 29	0.0106479 92	3
GO:00996 01	regulation of neurotransmitter receptor activity	0.0065907 29	0.0106479 92	3
GO:19049 50	negative regulation of establishment of protein localization	0.0067370 79	0.0108650 33	3

GO:19908 45	adaptive thermogenesis	0.0067370 79	0.0108650 33	3
GO:00064 69	negative regulation of protein kinase activity	0.0067803 05	0.0109250 08	3
GO:00031 51	outflow tract morphogenesis	0.0068239 17	0.0109757 32	3
GO:19012 24	positive regulation of NIK/NF-kappaB signaling	0.0068239 17	0.0109757 32	3
GO:00096 15	response to virus	0.0068553 11	0.0110164 34	3
GO:00083 60	regulation of cell shape	0.0068893 27	0.0110612 75	3
GO:00020 68	glandular epithelial cell development	0.0069363 36	0.0110777 73	3
GO:00189 04	ether metabolic process	0.0069363 36	0.0110777 73	3
GO:00194 30	removal of superoxide radicals	0.0069363 36	0.0110777 73	3
GO:00359 02	response to immobilization stress	0.0069363 36	0.0110777 73	3
GO:00427 37	drug catabolic process	0.0069363 36	0.0110777 73	3
GO:00511 23	RNA polymerase II preinitiation complex assembly	0.0069363 36	0.0110777 73	3
GO:00217 66	hippocampus development	0.0070619 63	0.0112684 63	3
GO:00350 51	cardiocyte differentiation	0.0072006 28	0.0114694 95	3
GO:00507 29	positive regulation of inflammatory response	0.0072006 28	0.0114694 95	3
GO:00015 56	oocyte maturation	0.0074678 83	0.0118120 08	3
GO:00020 21	response to dietary excess	0.0074678 83	0.0118120 08	3
GO:00020 26	regulation of the force of heart contraction	0.0074678 83	0.0118120 08	3
GO:00109 71	positive regulation of G2/M transition of mitotic cell cycle	0.0074678 83	0.0118120 08	3
GO:00456 72	positive regulation of osteoclast differentiation	0.0074678 83	0.0118120 08	3
GO:00481 43	astrocyte activation	0.0074678 83	0.0118120 08	3
GO:19032 03	regulation of oxidative stress-induced neuron death	0.0074678 83	0.0118120 08	3

GO:20003 53	positive regulation of endothelial cell apoptotic process	0.0074678 83	0.0118120 08	3
GO:00148 55	striated muscle cell proliferation	0.0075527 29	0.0118942 25	3
GO:00550 13	cardiac muscle cell development	0.0075527 29	0.0118942 25	3
GO:00551 17	regulation of cardiac muscle contraction	0.0075527 29	0.0118942 25	3
GO:00712 77	cellular response to calcium ion	0.0075527 29	0.0118942 25	3
GO:20002 43	positive regulation of reproductive process	0.0075527 29	0.0118942 25	3
GO:00518 96	regulation of protein kinase B signaling	0.0076087 94	0.0119720 98	3
GO:00512 51	positive regulation of lymphocyte activation	0.0076258 08	0.0119884 44	3
GO:00140 31	mesenchymal cell development	0.0078054 95	0.0122390 28	3
GO:00302 79	negative regulation of ossification	0.0078054 95	0.0122390 28	3
GO:00459 13	positive regulation of carbohydrate metabolic process	0.0078054 95	0.0122390 28	3
GO:00459 32	negative regulation of muscle contraction	0.0080172 66	0.0125091 08	3
GO:00714 50	cellular response to oxygen radical	0.0080172 66	0.0125091 08	3
GO:00714 51	cellular response to superoxide	0.0080172 66	0.0125091 08	3
GO:00723 76	protein activation cascade	0.0080172 66	0.0125091 08	3
GO:00723 78	blood coagulation, fibrin clot formation	0.0080172 66	0.0125091 08	3
GO:00092 67	cellular response to starvation	0.0080192 18	0.0125091 08	3
GO:00458 44	positive regulation of striated muscle tissue development	0.0080632 13	0.0125452 89	3
GO:00486 36	positive regulation of muscle organ development	0.0080632 13	0.0125452 89	3
GO:01101 10	positive regulation of animal organ morphogenesis	0.0080632 13	0.0125452 89	3
GO:00109 51	negative regulation of endopeptidase activity	0.0082421 84	0.0128127 28	3
GO:00346 37	cellular carbohydrate biosynthetic process	0.0083259 04	0.0129096 01	3

GO:19018 63	positive regulation of muscle tissue development	0.0083259 04	0.0129096 01	3
GO:20001 06	regulation of leukocyte apoptotic process	0.0083259 04	0.0129096 01	3
GO:00094 08	response to heat	0.0085385 75	0.0132002 33	3
GO:00359 67	cellular response to topologically incorrect protein	0.0085385 75	0.0132002 33	3
GO:00072 63	nitric oxide mediated signal transduction	0.0085843 06	0.0132002 33	3
GO:00190 48	modulation by virus of host process	0.0085843 06	0.0132002 33	3
GO:00310 63	regulation of histone deacetylation	0.0085843 06	0.0132002 33	3
GO:00488 73	homeostasis of number of cells within a tissue	0.0085843 06	0.0132002 33	3
GO:01501 17	positive regulation of cell-substrate junction organization	0.0085843 06	0.0132002 33	3
GO:20001 08	positive regulation of leukocyte apoptotic process	0.0085843 06	0.0132002 33	3
GO:00019 42	hair follicle development	0.0085935 89	0.0132002 33	3
GO:00550 72	iron ion homeostasis	0.0085935 89	0.0132002 33	3
GO:00900 49	regulation of cell migration involved in sprouting angiogenesis	0.0085935 89	0.0132002 33	3
GO:00020 28	regulation of sodium ion transport	0.0088662 89	0.0135960 32	3
GO:00700 98	chemokine-mediated signaling pathway	0.0088662 89	0.0135960 32	3
GO:00458 61	negative regulation of proteolysis	0.0088964 43	0.0136307 19	3
GO:00380 95	Fc-epsilon receptor signaling pathway	0.0090795 18	0.0138834 66	3
GO:00550 02	striated muscle cell development	0.0090795 18	0.0138834 66	3
GO:00224 04	molting cycle process	0.0091440 24	0.0138834 66	3
GO:00224 05	hair cycle process	0.0091440 24	0.0138834 66	3
GO:00550 06	cardiac cell development	0.0091440 24	0.0138834 66	3
GO:00003 03	response to superoxide	0.0091688 22	0.0138834 66	3

GO:00015 16	prostaglandin biosynthetic process	0.0091688 22	0.0138834 66	3
GO:00072 71	synaptic transmission, cholinergic	0.0091688 22	0.0138834 66	3
GO:00199 34	cGMP-mediated signaling	0.0091688 22	0.0138834 66	3
GO:00364 75	neuron death in response to oxidative stress	0.0091688 22	0.0138834 66	3
GO:00464 57	prostanoid biosynthetic process	0.0091688 22	0.0138834 66	3
GO:00481 47	negative regulation of fibroblast proliferation	0.0091688 22	0.0138834 66	3
GO:00714 80	cellular response to gamma radiation	0.0091688 22	0.0138834 66	3
GO:19027 51	positive regulation of cell cycle G2/M phase transition	0.0091688 22	0.0138834 66	3
GO:00434 70	regulation of carbohydrate catabolic process	0.0094268 11	0.0142502 64	3
GO:00987 73	skin epidermis development	0.0094268 11	0.0142502 64	3
GO:00303 07	positive regulation of cell growth	0.0094523 09	0.0142768 82	3
GO:00336 73	negative regulation of kinase activity	0.0096172 88	0.0145139 52	3
GO:00507 14	positive regulation of protein secretion	0.0096423 91	0.0145276 05	3
GO:19901 38	neuron projection extension	0.0096423 91	0.0145276 05	3
GO:00468 49	bone remodeling	0.0097146 7	0.0145992 64	3
GO:00484 77	oogenesis	0.0097146 7	0.0145992 64	3
GO:19040 63	negative regulation of cation transmembrane transport	0.0097146 7	0.0145992 64	3
GO:00003 05	response to oxygen radical	0.0097706 36	0.0145992 64	3
GO:00140 72	response to isoquinoline alkaloid	0.0097706 36	0.0145992 64	3
GO:00432 78	response to morphine	0.0097706 36	0.0145992 64	3
GO:00459 48	positive regulation of translational initiation	0.0097706 36	0.0145992 64	3
GO:00602 61	positive regulation of transcription initiation from RNA polymerase II promoter	0.0097706 36	0.0145992 64	3

GO:00860 11	membrane repolarization during action potential	0.0097706 36	0.0145992 64	3
GO:19022 53	regulation of intrinsic apoptotic signaling pathway by p53 class mediator	0.0097706 36	0.0145992 64	3
GO:00332 09	tumor necrosis factor-mediated signaling pathway	0.0098349 47	0.0146832 32	3
GO:00310 58	positive regulation of histone modification	0.0100076 18	0.0149287 07	3
GO:00357 25	sodium ion transmembrane transport	0.0100299 89	0.0149497 53	3
GO:00068 39	mitochondrial transport	0.0100588 74	0.0149804 68	3
GO:00104 66	negative regulation of peptidase activity	0.0102091 2	0.0151917 21	3
GO:00326 77	regulation of interleukin-8 production	0.0103056 72	0.0153227 96	3
GO:00082 10	estrogen metabolic process	0.0103895 73	0.0153591 98	3
GO:00357 67	endothelial cell chemotaxis	0.0103895 73	0.0153591 98	3
GO:00519 68	positive regulation of synaptic transmission, glutamatergic	0.0103895 73	0.0153591 98	3
GO:00705 28	protein kinase C signaling	0.0103895 73	0.0153591 98	3
GO:00860 19	cell-cell signaling involved in cardiac conduction	0.0103895 73	0.0153591 98	3
GO:00974 21	liver regeneration	0.0103895 73	0.0153591 98	3
GO:19018 89	negative regulation of cell junction assembly	0.0103895 73	0.0153591 98	3
GO:00325 35	regulation of cellular component size	0.0105633 55	0.0156033 58	3
GO:19019 92	positive regulation of mitotic cell cycle phase transition	0.0106088 49	0.0156577 76	3
GO:00303 24	lung development	0.0106301 5	0.0156764 28	3
GO:00072 81	germ cell development	0.0106691 08	0.0157210 67	3
GO:00313 49	positive regulation of defense response	0.0108184 38	0.0159281 35	3
GO:00518 97	positive regulation of protein kinase B signaling	0.0108352 55	0.0159399 26	3
GO:00330 28	myeloid cell apoptotic process	0.0110254 56	0.0161802 7	3

GO:00457 36	negative regulation of cyclin-dependent protein serine/threonine kinase activity	0.0110254 56	0.0161802 7	3
GO:00466 27	negative regulation of insulin receptor signaling pathway	0.0110254 56	0.0161802 7	3
GO:00352 49	synaptic transmission, glutamatergic	0.0112306 35	0.0164680 21	3
GO:00303 23	respiratory tube development	0.0114658 84	0.0167993 65	3
GO:00326 51	regulation of interleukin-1 beta production	0.0115492 73	0.0168805 38	3
GO:19908 68	response to chemokine	0.0115492 73	0.0168805 38	3
GO:19908 69	cellular response to chemokine	0.0115492 73	0.0168805 38	3
GO:00107 65	positive regulation of sodium ion transport	0.0116781 12	0.0169320 8	3
GO:00162 42	negative regulation of macroautophagy	0.0116781 12	0.0169320 8	3
GO:00304 31	sleep	0.0116781 12	0.0169320 8	3
GO:00321 48	activation of protein kinase B activity	0.0116781 12	0.0169320 8	3
GO:00423 11	vasodilation	0.0116781 12	0.0169320 8	3
GO:00456 48	positive regulation of erythrocyte differentiation	0.0116781 12	0.0169320 8	3
GO:00485 66	embryonic digestive tract development	0.0116781 12	0.0169320 8	3
GO:00700 50	neuron cellular homeostasis	0.0116781 12	0.0169320 8	3
GO:00702 32	regulation of T cell apoptotic process	0.0116781 12	0.0169320 8	3
GO:19040 30	negative regulation of cyclin-dependent protein kinase activity	0.0116781 12	0.0169320 8	3
GO:00069 42	regulation of striated muscle contraction	0.0118730 94	0.0171837 59	3
GO:00303 16	osteoclast differentiation	0.0118730 94	0.0171837 59	3
GO:00019 59	regulation of cytokine-mediated signaling pathway	0.0118991 78	0.0171837 59	3
GO:00069 86	response to unfolded protein	0.0118991 78	0.0171837 59	3
GO:00550 01	muscle cell development	0.0118991 78	0.0171837 59	3

GO:0001822	kidney development	0.011964864	0.017251081	3
GO:0016579	protein deubiquitination	0.011964864	0.017251081	3
GO:0022900	electron transport chain	0.012119721	0.017446552	3
GO:0038061	NIK/NF-kappaB signaling	0.012119721	0.017446552	3
GO:0043255	regulation of carbohydrate biosynthetic process	0.012202112	0.017537252	3
GO:0051817	modulation of process of other organism involved in symbiotic interaction	0.012202112	0.017537252	3
GO:0006691	leukotriene metabolic process	0.012347367	0.017661846	3
GO:0060674	placenta blood vessel development	0.012347367	0.017661846	3
GO:0070884	regulation of calcineurin-NFAT signaling cascade	0.012347367	0.017661846	3
GO:0071312	cellular response to alkaloid	0.012347367	0.017661846	3
GO:0110111	negative regulation of animal organ morphogenesis	0.012347367	0.017661846	3
GO:1900077	negative regulation of cellular response to insulin stimulus	0.012347367	0.017661846	3
GO:0045069	regulation of viral genome replication	0.012536338	0.017903847	3
GO:0070301	cellular response to hydrogen peroxide	0.012536338	0.017903847	3
GO:0043488	regulation of mRNA stability	0.012568651	0.017907593	3
GO:0050770	regulation of axonogenesis	0.012568651	0.017907593	3
GO:0051147	regulation of muscle cell differentiation	0.012568651	0.017907593	3
GO:0007215	glutamate receptor signaling pathway	0.012875787	0.018301962	3
GO:0019217	regulation of fatty acid metabolic process	0.012875787	0.018301962	3
GO:0042116	macrophage activation	0.012875787	0.018301962	3
GO:0051783	regulation of nuclear division	0.01302811	0.018409805	3
GO:0001569	branching involved in blood vessel morphogenesis	0.01303305	0.018409805	3

GO:00315 72	G2 DNA damage checkpoint	0.0130330 5	0.0184098 05	3
GO:00344 05	response to fluid shear stress	0.0130330 5	0.0184098 05	3
GO:00433 68	positive T cell selection	0.0130330 5	0.0184098 05	3
GO:00716 34	regulation of transforming growth factor beta production	0.0130330 5	0.0184098 05	3
GO:01060 56	regulation of calcineurin-mediated signaling	0.0130330 5	0.0184098 05	3
GO:20003 10	regulation of NMDA receptor activity	0.0130330 5	0.0184098 05	3
GO:00604 85	mesenchyme development	0.0131833 41	0.0185930 69	3
GO:19021 05	regulation of leukocyte differentiation	0.0131833 41	0.0185930 69	3
GO:00435 02	regulation of muscle adaptation	0.0132204 69	0.0186164 12	3
GO:19030 76	regulation of protein localization to plasma membrane	0.0132204 69	0.0186164 12	3
GO:00510 48	negative regulation of secretion	0.0134981 82	0.0189926 94	3
GO:00720 01	renal system development	0.0135463 45	0.0190456 53	3
GO:00329 41	secretion by tissue	0.0137349 9	0.0192212 71	3
GO:00432 43	positive regulation of protein-containing complex disassembly	0.0137349 9	0.0192212 71	3
GO:00602 60	regulation of transcription initiation from RNA polymerase II promoter	0.0137349 9	0.0192212 71	3
GO:00704 23	nucleotide-binding oligomerization domain containing signaling pathway	0.0137349 9	0.0192212 71	3
GO:00708 97	transcription preinitiation complex assembly	0.0137349 9	0.0192212 71	3
GO:00903 22	regulation of superoxide metabolic process	0.0137349 9	0.0192212 71	3
GO:00026 96	positive regulation of leukocyte activation	0.0137668 81	0.0192510 11	3
GO:00075 17	muscle organ development	0.0139199 94	0.0194500 87	3
GO:00027 93	positive regulation of peptide secretion	0.0142233 63	0.0198586 43	3
GO:00215 49	cerebellum development	0.0142860 26	0.0199244 57	3

GO:00316 47	regulation of protein stability	0.0142925 24	0.0199244 57	3
GO:00358 72	nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway	0.0144530 19	0.0200401 21	3
GO:00440 03	modulation by symbiont of host process	0.0144530 19	0.0200401 21	3
GO:00480 09	insulin-like growth factor receptor signaling pathway	0.0144530 19	0.0200401 21	3
GO:00600 45	positive regulation of cardiac muscle cell proliferation	0.0144530 19	0.0200401 21	3
GO:00713 92	cellular response to estradiol stimulus	0.0144530 19	0.0200401 21	3
GO:00716 04	transforming growth factor beta production	0.0144530 19	0.0200401 21	3
GO:00860 05	ventricular cardiac muscle cell action potential	0.0144530 19	0.0200401 21	3
GO:00192 33	sensory perception of pain	0.0146517 49	0.0202535 94	3
GO:00193 95	fatty acid oxidation	0.0146517 49	0.0202535 94	3
GO:00326 11	interleukin-1 beta production	0.0146517 49	0.0202535 94	3
GO:19052 69	positive regulation of chromatin organization	0.0146517 49	0.0202535 94	3
GO:00434 87	regulation of RNA stability	0.0147203 13	0.0203328 39	3
GO:00020 40	sprouting angiogenesis	0.0149728 66	0.0206501 57	3
GO:00607 59	regulation of response to cytokine stimulus	0.0149728 66	0.0206501 57	3
GO:19034 26	regulation of reactive oxygen species biosynthetic process	0.0150227 57	0.0207031 86	3
GO:00706 46	protein modification by small protein removal	0.0150659 42	0.0207468 99	3
GO:00071 90	activation of adenylate cyclase activity	0.0151869 68	0.0207712 92	3
GO:00107 37	protein kinase A signaling	0.0151869 68	0.0207712 92	3
GO:00108 31	positive regulation of myotube differentiation	0.0151869 68	0.0207712 92	3
GO:00140 37	Schwann cell differentiation	0.0151869 68	0.0207712 92	3
GO:00331 46	regulation of intracellular estrogen receptor signaling pathway	0.0151869 68	0.0207712 92	2

GO:00358 86	vascular associated smooth muscle cell differentiation	0.0151869 68	0.0207712 92	2
GO:00463 26	positive regulation of glucose import	0.0151869 68	0.0207712 92	2
GO:00604 16	response to growth hormone	0.0151869 68	0.0207712 92	2
GO:20002 79	negative regulation of DNA biosynthetic process	0.0151869 68	0.0207712 92	2
GO:00106 39	negative regulation of organelle organization	0.0153521 22	0.0209813 15	2
GO:00325 26	response to retinoic acid	0.0153990 58	0.0210295 78	2
GO:00106 13	positive regulation of cardiac muscle hypertrophy	0.0159366 71	0.0217309 62	2
GO:00439 02	positive regulation of multi-organism process	0.0159366 71	0.0217309 62	2
GO:00103 89	regulation of G2/M transition of mitotic cell cycle	0.0160104 71	0.0217659 85	2
GO:00160 52	carbohydrate catabolic process	0.0160104 71	0.0217659 85	2
GO:00510 54	positive regulation of DNA metabolic process	0.0160104 71	0.0217659 85	2
GO:19018 88	regulation of cell junction assembly	0.0160104 71	0.0217659 85	2
GO:19019 89	positive regulation of cell cycle phase transition	0.0161675 73	0.0219465 85	2
GO:19046 59	glucose transmembrane transport	0.0161675 73	0.0219465 85	2
GO:00508 67	positive regulation of cell activation	0.0161906 04	0.0219613 73	2
GO:00097 46	response to hexose	0.0165458 35	0.0224264 07	2
GO:00326 52	regulation of interleukin-1 production	0.0165598	0.0224285 35	2
GO:00022 51	organ or tissue specific immune response	0.0167019 61	0.0224697 1	2
GO:00072 12	dopamine receptor signaling pathway	0.0167019 61	0.0224697 1	2
GO:00076 18	mating	0.0167019 61	0.0224697 1	2
GO:00147 42	positive regulation of muscle hypertrophy	0.0167019 61	0.0224697 1	2
GO:00308 90	positive regulation of B cell proliferation	0.0167019 61	0.0224697 1	2

GO:00380 83	peptidyl-tyrosine autophosphorylation	0.0167019 61	0.0224697 1	2
GO:00425 96	fear response	0.0167019 61	0.0224697 1	2
GO:00468 25	regulation of protein export from nucleus	0.0167019 61	0.0224697 1	2
GO:20000 08	regulation of protein localization to cell surface	0.0167019 61	0.0224697 1	2
GO:00435 88	skin development	0.0168838 95	0.0226975 96	2
GO:00605 41	respiratory system development	0.0170923 32	0.0229607 46	2
GO:00460 34	ATP metabolic process	0.0173365 68	0.0232643 61	2
GO:00070 09	plasma membrane organization	0.0173602 3	0.0232643 61	2
GO:00358 21	modulation of process of other organism	0.0173602 3	0.0232643 61	2
GO:00359 66	response to topologically incorrect protein	0.0173697 76	0.0232643 61	2
GO:00065 09	membrane protein ectodomain proteolysis	0.0174826 76	0.0233292 34	2
GO:00109 07	positive regulation of glucose metabolic process	0.0174826 76	0.0233292 34	2
GO:00460 06	regulation of activated T cell proliferation	0.0174826 76	0.0233292 34	2
GO:00482 46	macrophage chemotaxis	0.0174826 76	0.0233292 34	2
GO:00714 70	cellular response to osmotic stress	0.0174826 76	0.0233292 34	2
GO:00705 88	calcium ion transmembrane transport	0.0175536 36	0.0234066 63	2
GO:00425 94	response to starvation	0.0176500 27	0.0235178 64	2
GO:00086 45	hexose transmembrane transport	0.0177684 44	0.0236462 32	2
GO:19035 32	positive regulation of secretion by cell	0.0177725 03	0.0236462 32	2
GO:00342 84	response to monosaccharide	0.0179330 94	0.0238423 68	2
GO:00316 23	receptor internalization	0.0181819 97	0.0241555 4	2
GO:00610 13	regulation of mRNA catabolic process	0.0182189 85	0.0241774 4	2

GO:00451 24	regulation of bone resorption	0.0182786 51	0.0241774 4	2
GO:00457 73	positive regulation of axon extension	0.0182786 51	0.0241774 4	2
GO:00903 17	negative regulation of intracellular protein transport	0.0182786 51	0.0241774 4	2
GO:19031 46	regulation of autophagy of mitochondrion	0.0182786 51	0.0241774 4	2
GO:20006 48	positive regulation of stem cell proliferation	0.0182786 51	0.0241774 4	2
GO:00157 49	monosaccharide transmembrane transport	0.0186008 95	0.0245498 4	2
GO:00469 16	cellular transition metal ion homeostasis	0.0186008 95	0.0245498 4	2
GO:19038 28	negative regulation of cellular protein localization	0.0186008 95	0.0245498 4	2
GO:00302 82	bone mineralization	0.0190251 41	0.0250549 44	2
GO:00513 41	regulation of oxidoreductase activity	0.0190251 41	0.0250549 44	2
GO:00726 76	lymphocyte migration	0.0190251 41	0.0250549 44	2
GO:00353 29	hippo signaling	0.0190897 24	0.0251217 12	2
GO:00342 19	carbohydrate transmembrane transport	0.0194547 4	0.0255834 59	2
GO:19012 22	regulation of NIK/NF-kappaB signaling	0.0198896 94	0.0260759 77	2
GO:00108 28	positive regulation of glucose transmembrane transport	0.0199157 36	0.0260759 77	2
GO:00140 02	astrocyte development	0.0199157 36	0.0260759 77	2
GO:00341 05	positive regulation of tissue remodeling	0.0199157 36	0.0260759 77	2
GO:00431 14	regulation of vascular permeability	0.0199157 36	0.0260759 77	2
GO:00903 11	regulation of protein deacetylation	0.0199157 36	0.0260759 77	2
GO:00508 70	positive regulation of T cell activation	0.0199940 45	0.0261595 79	2
GO:00064 70	protein dephosphorylation	0.0200613 99	0.0262287 38	2
GO:00512 35	maintenance of location	0.0203004 32	0.0265220 91	2

GO:00108 63	positive regulation of phospholipase C activity	0.0207565 25	0.0269871 12	2
GO:00171 44	drug metabolic process	0.0207565 25	0.0269871 12	2
GO:00359 87	endodermal cell differentiation	0.0207565 25	0.0269871 12	2
GO:00442 75	cellular carbohydrate catabolic process	0.0207565 25	0.0269871 12	2
GO:00480 66	developmental pigmentation	0.0207565 25	0.0269871 12	2
GO:00507 98	activated T cell proliferation	0.0207565 25	0.0269871 12	2
GO:00326 12	interleukin-1 production	0.0207756 81	0.0269871 12	2
GO:19005 42	regulation of purine nucleotide metabolic process	0.0207756 81	0.0269871 12	2
GO:00507 92	regulation of viral process	0.0209202 85	0.0271554 55	2
GO:00217 82	glial cell development	0.0212267 17	0.0274940 49	2
GO:00427 52	regulation of circadian rhythm	0.0212267 17	0.0274940 49	2
GO:00519 28	positive regulation of calcium ion transport	0.0212267 17	0.0274940 49	2
GO:00305 74	collagen catabolic process	0.0216119 35	0.0279330 19	2
GO:00425 72	retinol metabolic process	0.0216119 35	0.0279330 19	2
GO:00432 68	positive regulation of potassium ion transport	0.0216119 35	0.0279330 19	2
GO:00061 40	regulation of nucleotide metabolic process	0.0216831 18	0.0279650 98	2
GO:00702 52	actin-mediated cell contraction	0.0216831 18	0.0279650 98	2
GO:19043 75	regulation of protein localization to cell periphery	0.0216831 18	0.0279650 98	2
GO:00713 75	cellular response to peptide hormone stimulus	0.0217739 78	0.0280622 8	2
GO:00067 21	terpenoid metabolic process	0.0221448 85	0.0285199 9	2
GO:00508 63	regulation of T cell activation	0.0222802 72	0.0286739 45	2
GO:00319 52	regulation of protein autophosphorylation	0.0224818 06	0.0288512 32	2

GO:0045601	regulation of endothelial cell differentiation	0.022481806	0.028851232	2
GO:0055023	positive regulation of cardiac muscle tissue growth	0.022481806	0.028851232	2
GO:1900274	regulation of phospholipase C activity	0.022481806	0.028851232	2
GO:0034605	cellular response to heat	0.022612018	0.028977232	2
GO:0043500	muscle adaptation	0.022612018	0.028977232	2
GO:0016485	protein processing	0.022851083	0.029262868	2
GO:0006692	prostanoid metabolic process	0.023365985	0.029753789	2
GO:0006693	prostaglandin metabolic process	0.023365985	0.029753789	2
GO:0015695	organic cation transport	0.023365985	0.029753789	2
GO:0015872	dopamine transport	0.023365985	0.029753789	2
GO:0031279	regulation of cyclase activity	0.023365985	0.029753789	2
GO:0042149	cellular response to glucose starvation	0.023365985	0.029753789	2
GO:0045058	T cell selection	0.023365985	0.029753789	2
GO:1900087	positive regulation of G1/S transition of mitotic cell cycle	0.023365985	0.029753789	2
GO:0045732	positive regulation of protein catabolic process	0.023518066	0.029926387	2
GO:0071621	granulocyte chemotaxis	0.023562383	0.029961709	2
GO:0072089	stem cell proliferation	0.024045614	0.03055471	2
GO:0045646	regulation of erythrocyte differentiation	0.024264314	0.030660361	2
GO:0045981	positive regulation of nucleotide metabolic process	0.024264314	0.030660361	2
GO:0046850	regulation of bone remodeling	0.024264314	0.030660361	2
GO:0048546	digestive tract morphogenesis	0.024264314	0.030660361	2
GO:0101023	vascular endothelial cell proliferation	0.024264314	0.030660361	2

GO:19005 44	positive regulation of purine nucleotide metabolic process	0.0242643 14	0.0306603 61	2
GO:19035 80	positive regulation of ATP metabolic process	0.0242643 14	0.0306603 61	2
GO:19055 62	regulation of vascular endothelial cell proliferation	0.0242643 14	0.0306603 61	2
GO:00510 47	positive regulation of secretion	0.0243820 38	0.0307876 17	2
GO:00025 76	platelet degranulation	0.0245342 11	0.0309581 65	2
GO:00434 05	regulation of MAP kinase activity	0.0249268 11	0.0314316 43	2
GO:00352 72	exocrine system development	0.0251766 41	0.0316364 37	2
GO:00380 84	vascular endothelial growth factor signaling pathway	0.0251766 41	0.0316364 37	2
GO:00459 12	negative regulation of carbohydrate metabolic process	0.0251766 41	0.0316364 37	2
GO:00713 54	cellular response to interleukin-6	0.0251766 41	0.0316364 37	2
GO:00716 75	regulation of mononuclear cell migration	0.0251766 41	0.0316364 37	2
GO:00160 42	lipid catabolic process	0.0252021 21	0.0316464 78	2
GO:00100 01	glial cell differentiation	0.0252371 04	0.0316684 29	2
GO:19033 11	regulation of mRNA metabolic process	0.0254793 87	0.0319502 98	2
GO:00067 66	vitamin metabolic process	0.0255274 93	0.0319663 16	2
GO:00441 06	cellular amine metabolic process	0.0255274 93	0.0319663 16	2
GO:00439 03	regulation of symbiotic process	0.0255897 95	0.0320221 71	2
GO:00102 56	endomembrane system organization	0.0256709 46	0.0321015 21	2
GO:00069 98	nuclear envelope organization	0.0261028 12	0.0325067 8	2
GO:00108 83	regulation of lipid storage	0.0261028 12	0.0325067 8	2
GO:00380 66	p38MAPK cascade	0.0261028 12	0.0325067 8	2
GO:00458 39	negative regulation of mitotic nuclear division	0.0261028 12	0.0325067 8	2

GO:00604 21	positive regulation of heart growth	0.0261028 12	0.0325067 8	2
GO:00716 22	regulation of granulocyte chemotaxis	0.0261028 12	0.0325067 8	2
GO:00097 43	response to carbohydrate	0.0263040 98	0.0327349 19	2
GO:00427 42	defense response to bacterium	0.0266080 86	0.0330904 68	2
GO:00431 24	negative regulation of I-kappaB kinase/NF-kappaB signaling	0.0270426 77	0.0335617 37	2
GO:00455 99	negative regulation of fat cell differentiation	0.0270426 77	0.0335617 37	2
GO:00456 61	regulation of myoblast differentiation	0.0270426 77	0.0335617 37	2
GO:00303 36	negative regulation of cell migration	0.0271842 74	0.0336912 53	2
GO:00469 42	carboxylic acid transport	0.0271842 74	0.0336912 53	2
GO:00323 68	regulation of lipid transport	0.0275783 51	0.0341461 29	2
GO:00482 85	organelle fission	0.0275890 39	0.0341461 29	2
GO:00069 68	cellular defense response	0.0279960 84	0.0346025 8	2
GO:20001 79	positive regulation of neural precursor cell proliferation	0.0279960 84	0.0346025 8	2
GO:00158 49	organic acid transport	0.0280634 45	0.0346621 61	2
GO:00330 44	regulation of chromosome organization	0.0289605 74	0.0356514 13	2
GO:00017 06	endoderm formation	0.0289628 84	0.0356514 13	2
GO:00423 04	regulation of fatty acid biosynthetic process	0.0289628 84	0.0356514 13	2
GO:00514 52	intracellular pH reduction	0.0289628 84	0.0356514 13	2
GO:00707 41	response to interleukin-6	0.0289628 84	0.0356514 13	2
GO:00074 09	axonogenesis	0.0290886 44	0.0357818 74	2
GO:00027 05	positive regulation of leukocyte mediated immunity	0.0291726 51	0.0358364 87	2
GO:00550 76	transition metal ion homeostasis	0.0291726 51	0.0358364 87	2

GO:0035304	regulation of protein dephosphorylation	0.02971476	0.03647764	2
GO:0001755	neural crest cell migration	0.029942929	0.036683102	2
GO:0086065	cell communication involved in cardiac conduction	0.029942929	0.036683102	2
GO:0090183	regulation of kidney development	0.029942929	0.036683102	2
GO:0009308	amine metabolic process	0.030262198	0.037024105	2
GO:0097553	calcium ion transmembrane import into cytosol	0.030262198	0.037024105	2
GO:0043312	neutrophil degranulation	0.030378806	0.037141656	2
GO:0042593	glucose homeostasis	0.0308415	0.037670261	2
GO:0019748	secondary metabolic process	0.030936072	0.037670261	2
GO:0032615	interleukin-12 production	0.030936072	0.037670261	2
GO:0061178	regulation of insulin secretion involved in cellular response to glucose stimulus	0.030936072	0.037670261	2
GO:0071398	cellular response to fatty acid	0.030936072	0.037670261	2
GO:1905517	macrophage migration	0.030936072	0.037670261	2
GO:0002283	neutrophil activation involved in immune response	0.031170735	0.03793048	2
GO:0033500	carbohydrate homeostasis	0.031239206	0.037988253	2
GO:0031333	negative regulation of protein-containing complex assembly	0.03137304	0.03812538	2
GO:0016311	dephosphorylation	0.031706163	0.038504341	2
GO:2000146	negative regulation of cell motility	0.031760678	0.038544676	2
GO:0031638	zymogen activation	0.031942166	0.038661209	2
GO:0045851	pH reduction	0.031942166	0.038661209	2
GO:1900408	negative regulation of cellular response to oxidative stress	0.031942166	0.038661209	2
GO:1903202	negative regulation of oxidative stress-induced cell death	0.031942166	0.038661209	2

GO:00067 20	isoprenoid metabolic process	0.0325051 31	0.0392900 33	2
GO:00464 34	organophosphate catabolic process	0.0325051 31	0.0392900 33	2
GO:00016 58	branching involved in ureteric bud morphogenesis	0.0329610 66	0.0397085 1	2
GO:00323 87	negative regulation of intracellular transport	0.0329610 66	0.0397085 1	2
GO:00454 54	cell redox homeostasis	0.0329610 66	0.0397085 1	2
GO:00600 43	regulation of cardiac muscle cell proliferation	0.0329610 66	0.0397085 1	2
GO:00989 30	axonal transport	0.0329610 66	0.0397085 1	2
GO:00226 04	regulation of cell morphogenesis	0.0336276 03	0.0404845 39	2
GO:00715 60	cellular response to transforming growth factor beta stimulus	0.0336891 37	0.0405316 54	2
GO:00108 23	negative regulation of mitochondrion organization	0.0339926 29	0.0407073 24	2
GO:00325 15	negative regulation of phosphoprotein phosphatase activity	0.0339926 29	0.0407073 24	2
GO:00487 47	muscle fiber development	0.0339926 29	0.0407073 24	2
GO:00517 84	negative regulation of nuclear division	0.0339926 29	0.0407073 24	2
GO:00610 98	positive regulation of protein tyrosine kinase activity	0.0339926 29	0.0407073 24	2
GO:19028 08	positive regulation of cell cycle G1/S phase transition	0.0339926 29	0.0407073 24	2
GO:19028 83	negative regulation of response to oxidative stress	0.0339926 29	0.0407073 24	2
GO:00000 86	G2/M transition of mitotic cell cycle	0.0345301 06	0.0413236 23	2
GO:00613 37	cardiac conduction	0.0348328 44	0.0416308 54	2
GO:19036 70	regulation of sprouting angiogenesis	0.0348328 44	0.0416308 54	2
GO:00619 12	selective autophagy	0.0350367 11	0.0417916 98	2
GO:00903 03	positive regulation of wound healing	0.0350367 11	0.0417916 98	2
GO:19030 78	positive regulation of protein localization to plasma membrane	0.0350367 11	0.0417916 98	2

GO:00069 59	humoral immune response	0.0357511 23	0.0426157 55	2
GO:00351 48	tube formation	0.0360283 45	0.0427979 31	2
GO:00600 41	retina development in camera-type eye	0.0360283 45	0.0427979 31	2
GO:00975 30	granulocyte migration	0.0360283 45	0.0427979 31	2
GO:00105 18	positive regulation of phospholipase activity	0.0360931 71	0.0427979 31	2
GO:00106 76	positive regulation of cellular carbohydrate metabolic process	0.0360931 71	0.0427979 31	2
GO:00108 03	regulation of tumor necrosis factor-mediated signaling pathway	0.0360931 71	0.0427979 31	2
GO:00488 57	neural nucleus development	0.0360931 71	0.0427979 31	2
GO:00550 25	positive regulation of cardiac muscle tissue development	0.0360931 71	0.0427979 31	2
GO:00715 59	response to transforming growth factor beta	0.0362486 29	0.0429260 08	2
GO:19016 17	organic hydroxy compound biosynthetic process	0.0362486 29	0.0429260 08	2
GO:00086 43	carbohydrate transport	0.0366339 78	0.0432973 35	2
GO:00163 31	morphogenesis of embryonic epithelium	0.0366339 78	0.0432973 35	2
GO:00508 71	positive regulation of B cell activation	0.0366339 78	0.0432973 35	2
GO:00108 30	regulation of myotube differentiation	0.0371618 68	0.0438353 46	2
GO:00326 13	interleukin-10 production	0.0371618 68	0.0438353 46	2
GO:00550 08	cardiac muscle tissue morphogenesis	0.0371618 68	0.0438353 46	2
GO:00018 37	epithelial to mesenchymal transition	0.0372448 55	0.0438760 32	2
GO:19031 69	regulation of calcium ion transmembrane transport	0.0372448 55	0.0438760 32	2
GO:00162 02	regulation of striated muscle tissue development	0.0378609 66	0.0445438 37	2
GO:00300 48	actin filament-based movement	0.0378609 66	0.0445438 37	2
GO:00024 37	inflammatory response to antigenic stimulus	0.0382426 61	0.0449636 71	2

GO:00140 65	phosphatidylinositol 3-kinase signaling	0.0384823 01	0.0452160 46	2
GO:00434 06	positive regulation of MAP kinase activity	0.0389180 65	0.0456687 51	2
GO:00488 63	stem cell differentiation	0.0389180 65	0.0456687 51	2
GO:00066 87	glycosphingolipid metabolic process	0.0393354 13	0.0460093 05	2
GO:00353 08	negative regulation of protein dephosphorylation	0.0393354 13	0.0460093 05	2
GO:00357 73	insulin secretion involved in cellular response to glucose stimulus	0.0393354 13	0.0460093 05	2
GO:00606 75	ureteric bud morphogenesis	0.0393354 13	0.0460093 05	2
GO:00985 86	cellular response to virus	0.0393354 13	0.0460093 05	2
GO:19018 61	regulation of muscle tissue development	0.0397406 07	0.0464532 19	2
GO:00486 34	regulation of muscle organ development	0.0403775 57	0.0470882 17	2
GO:00987 39	import across plasma membrane	0.0403775 57	0.0470882 17	2
GO:19039 00	regulation of viral life cycle	0.0403775 57	0.0470882 17	2
GO:00329 22	circadian regulation of gene expression	0.0404399 86	0.0470882 17	2
GO:00343 94	protein localization to cell surface	0.0404399 86	0.0470882 17	2
GO:00721 71	mesonephric tubule morphogenesis	0.0404399 86	0.0470882 17	2
GO:00075 19	skeletal muscle tissue development	0.0410196 91	0.0477325 09	2
GO:00025 48	monocyte chemotaxis	0.0415562 42	0.0482018 76	2
GO:00451 23	cellular extravasation	0.0415562 42	0.0482018 76	2
GO:00456 70	regulation of osteoclast differentiation	0.0415562 42	0.0482018 76	2
GO:00465 13	ceramide biosynthetic process	0.0415562 42	0.0482018 76	2
GO:00726 78	T cell migration	0.0415562 42	0.0482018 76	2
GO:00510 92	positive regulation of NF-kappaB transcription factor activity	0.0416669 98	0.0482684 62	2

GO:00550 67	monovalent inorganic cation homeostasis	0.0416669 98	0.0482684 62	2
GO:00302 58	lipid modification	0.0421716 7	0.0488218 35	2
GO:00026 37	regulation of immunoglobulin production	0.0426840 46	0.0492888 7	2
GO:00027 53	cytoplasmic pattern recognition receptor signaling pathway	0.0426840 46	0.0492888 7	2
GO:00507 66	positive regulation of phagocytosis	0.0426840 46	0.0492888 7	2
GO:19043 77	positive regulation of protein localization to cell periphery	0.0426840 46	0.0492888 7	2
GO:00400 13	negative regulation of locomotion	0.0430663 14	0.0496985 73	2
GO:19033 05	regulation of regulated secretory pathway	0.0436398 48	0.0503283 34	2
GO:00486 62	negative regulation of smooth muscle cell proliferation	0.0438232 65	0.0505076 71	2
GO:00512 71	negative regulation of cellular component movement	0.0442360 91	0.0509039 23	2
GO:00066 65	sphingolipid metabolic process	0.0443077 34	0.0509039 23	2
GO:00070 88	regulation of mitotic nuclear division	0.0443077 34	0.0509039 23	2
GO:00312 14	biomineral tissue development	0.0443077 34	0.0509039 23	2
GO:01101 48	biomineralization	0.0443077 34	0.0509039 23	2
GO:00080 88	axo-dendritic transport	0.0449737 63	0.0515788 71	2
GO:00323 70	positive regulation of lipid transport	0.0449737 63	0.0515788 71	2
GO:00072 59	receptor signaling pathway via JAK-STAT	0.0449807 36	0.0515788 71	2
GO:00148 23	response to activity	0.0461354 08	0.0528359 54	2
GO:00425 31	positive regulation of tyrosine phosphorylation of STAT protein	0.0461354 08	0.0528359 54	2
GO:19035 31	negative regulation of secretion by cell	0.0463420 36	0.0528974 92	2
GO:00421 29	regulation of T cell proliferation	0.0470303 09	0.0528974 92	2
GO:00026 76	regulation of chronic inflammatory response	0.0472123 19	0.0528974 92	2

GO:00029 34	desmosome organization	0.0472123 19	0.0528974 92	2
GO:00102 69	response to selenium ion	0.0472123 19	0.0528974 92	2
GO:00107 49	regulation of nitric oxide mediated signal transduction	0.0472123 19	0.0528974 92	2
GO:00140 41	regulation of neuron maturation	0.0472123 19	0.0528974 92	2
GO:00148 77	response to muscle inactivity involved in regulation of muscle adaptation	0.0472123 19	0.0528974 92	2
GO:00148 94	response to denervation involved in regulation of muscle adaptation	0.0472123 19	0.0528974 92	2
GO:00215 48	pons development	0.0472123 19	0.0528974 92	2
GO:00219 36	regulation of cerebellar granule cell precursor proliferation	0.0472123 19	0.0528974 92	2
GO:00425 41	hemoglobin biosynthetic process	0.0472123 19	0.0528974 92	2
GO:00457 92	negative regulation of cell size	0.0472123 19	0.0528974 92	2
GO:00487 39	cardiac muscle fiber development	0.0472123 19	0.0528974 92	2
GO:00513 42	regulation of cyclic-nucleotide phosphodiesterase activity	0.0472123 19	0.0528974 92	2
GO:00515 41	elastin metabolic process	0.0472123 19	0.0528974 92	2
GO:00605 13	prostatic bud formation	0.0472123 19	0.0528974 92	2
GO:00607 68	regulation of epithelial cell proliferation involved in prostate gland development	0.0472123 19	0.0528974 92	2
GO:00700 91	glucagon secretion	0.0472123 19	0.0528974 92	2
GO:00700 92	regulation of glucagon secretion	0.0472123 19	0.0528974 92	2
GO:00700 99	regulation of chemokine-mediated signaling pathway	0.0472123 19	0.0528974 92	2
GO:00713 94	cellular response to testosterone stimulus	0.0472123 19	0.0528974 92	2
GO:00860 70	SA node cell to atrial cardiac muscle cell communication	0.0472123 19	0.0528974 92	2
GO:00970 50	type B pancreatic cell apoptotic process	0.0472123 19	0.0528974 92	2
GO:19002 22	negative regulation of amyloid-beta clearance	0.0472123 19	0.0528974 92	2

GO:19017 25	regulation of histone deacetylase activity	0.0472123 19	0.0528974 92	2
GO:19034 31	positive regulation of cell maturation	0.0472123 19	0.0528974 92	2
GO:19038 62	positive regulation of oxidative phosphorylation	0.0472123 19	0.0528974 92	2
GO:19043 38	regulation of dopaminergic neuron differentiation	0.0472123 19	0.0528974 92	2
GO:19045 26	regulation of microtubule binding	0.0472123 19	0.0528974 92	2
GO:19047 79	regulation of protein localization to centrosome	0.0472123 19	0.0528974 92	2
GO:20000 48	negative regulation of cell-cell adhesion mediated by cadherin	0.0472123 19	0.0528974 92	2
GO:20004 25	regulation of apoptotic cell clearance	0.0472123 19	0.0528974 92	2
GO:20006 59	regulation of interleukin-1-mediated signaling pathway	0.0472123 19	0.0528974 92	2
GO:20010 54	negative regulation of mesenchymal cell apoptotic process	0.0472123 19	0.0528974 92	2
GO:00506 63	cytokine secretion	0.0473080 69	0.0529064 93	2
GO:00709 88	demethylation	0.0473080 69	0.0529064 93	2
GO:19044 27	positive regulation of calcium ion transmembrane transport	0.0473080 69	0.0529064 93	2
GO:00605 38	skeletal muscle organ development	0.0477236 46	0.0533382 83	2
GO:00032 08	cardiac ventricle morphogenesis	0.0484916 15	0.0539964 93	2
GO:00105 17	regulation of phospholipase activity	0.0484916 15	0.0539964 93	2
GO:00106 11	regulation of cardiac muscle hypertrophy	0.0484916 15	0.0539964 93	2
GO:00511 45	smooth muscle cell differentiation	0.0484916 15	0.0539964 93	2
GO:00511 55	positive regulation of striated muscle cell differentiation	0.0484916 15	0.0539964 93	2
GO:00720 78	nephron tubule morphogenesis	0.0484916 15	0.0539964 93	2
GO:00326 35	interleukin-6 production	0.0491254 59	0.0546686 5	2
GO:00514 03	stress-activated MAPK cascade	0.0496488 8	0.0551832 56	2

GO:01400 14	mitotic nuclear division	0.0496488 8	0.0551832 56	2
GO:19030 36	positive regulation of response to wounding	0.0496859 16	0.0551905 2	2
GO:00022 44	hematopoietic progenitor cell differentiation	0.0505473 67	0.0553422 51	2
GO:00331 43	regulation of intracellular steroid hormone receptor signaling pathway	0.0508908 44	0.0553422 51	2
GO:00456 85	regulation of glial cell differentiation	0.0508908 44	0.0553422 51	2
GO:00720 88	nephron epithelium morphogenesis	0.0508908 44	0.0553422 51	2
GO:19019 83	regulation of protein acetylation	0.0508908 44	0.0553422 51	2
GO:00065 27	arginine catabolic process	0.0518105 2	0.0553422 51	2
GO:00070 28	cytoplasm organization	0.0518105 2	0.0553422 51	2
GO:00071 91	adenylate cyclase-activating dopamine receptor signaling pathway	0.0518105 2	0.0553422 51	2
GO:00086 11	ether lipid biosynthetic process	0.0518105 2	0.0553422 51	2
GO:00107 39	positive regulation of protein kinase A signaling	0.0518105 2	0.0553422 51	2
GO:00109 18	positive regulation of mitochondrial membrane potential	0.0518105 2	0.0553422 51	2
GO:00148 70	response to muscle inactivity	0.0518105 2	0.0553422 51	2
GO:00170 85	response to insecticide	0.0518105 2	0.0553422 51	2
GO:00184 01	peptidyl-proline hydroxylation to 4-hydroxy-L-proline	0.0518105 2	0.0553422 51	2
GO:00312 84	positive regulation of guanylate cyclase activity	0.0518105 2	0.0553422 51	2
GO:00314 42	positive regulation of mRNA 3'-end processing	0.0518105 2	0.0553422 51	2
GO:00319 15	positive regulation of synaptic plasticity	0.0518105 2	0.0553422 51	2
GO:00322 53	dense core granule localization	0.0518105 2	0.0553422 51	2
GO:00331 48	positive regulation of intracellular estrogen receptor signaling pathway	0.0518105 2	0.0553422 51	2
GO:00331 97	response to vitamin E	0.0518105 2	0.0553422 51	2

GO:00353 31	negative regulation of hippo signaling	0.0518105 2	0.0553422 51	2
GO:00357 47	natural killer cell chemotaxis	0.0518105 2	0.0553422 51	2
GO:00434 71	regulation of cellular carbohydrate catabolic process	0.0518105 2	0.0553422 51	2
GO:00436 19	regulation of transcription from RNA polymerase II promoter in response to oxidative stress	0.0518105 2	0.0553422 51	2
GO:00456 57	positive regulation of monocyte differentiation	0.0518105 2	0.0553422 51	2
GO:00459 45	positive regulation of transcription by RNA polymerase III	0.0518105 2	0.0553422 51	2
GO:00465 04	glycerol ether biosynthetic process	0.0518105 2	0.0553422 51	2
GO:00487 42	regulation of skeletal muscle fiber development	0.0518105 2	0.0553422 51	2
GO:00488 75	chemical homeostasis within a tissue	0.0518105 2	0.0553422 51	2
GO:00510 24	positive regulation of immunoglobulin secretion	0.0518105 2	0.0553422 51	2
GO:00516 10	serotonin uptake	0.0518105 2	0.0553422 51	2
GO:00517 12	positive regulation of killing of cells of other organism	0.0518105 2	0.0553422 51	2
GO:00519 74	negative regulation of telomerase activity	0.0518105 2	0.0553422 51	2
GO:00602 81	regulation of oocyte development	0.0518105 2	0.0553422 51	2
GO:00603 54	negative regulation of cell adhesion molecule production	0.0518105 2	0.0553422 51	2
GO:00607 67	epithelial cell proliferation involved in prostate gland development	0.0518105 2	0.0553422 51	2
GO:00609 47	cardiac vascular smooth muscle cell differentiation	0.0518105 2	0.0553422 51	2
GO:00706 73	response to interleukin-18	0.0518105 2	0.0553422 51	2
GO:00712 81	cellular response to iron ion	0.0518105 2	0.0553422 51	2
GO:00718 03	positive regulation of podosome assembly	0.0518105 2	0.0553422 51	2
GO:00860 16	AV node cell action potential	0.0518105 2	0.0553422 51	2
GO:00860 27	AV node cell to bundle of His cell signaling	0.0518105 2	0.0553422 51	2

GO:00902 69	fibroblast growth factor production	0.0518105 2	0.0553422 51	2
GO:00902 70	regulation of fibroblast growth factor production	0.0518105 2	0.0553422 51	2
GO:00905 57	establishment of endothelial intestinal barrier	0.0518105 2	0.0553422 51	2
GO:00973 84	cellular lipid biosynthetic process	0.0518105 2	0.0553422 51	2
GO:00995 19	dense core granule cytoskeletal transport	0.0518105 2	0.0553422 51	2
GO:00996 24	atrial cardiac muscle cell membrane repolarization	0.0518105 2	0.0553422 51	2
GO:01060 49	regulation of cellular response to osmotic stress	0.0518105 2	0.0553422 51	2
GO:01060 72	negative regulation of adenylate cyclase-activating G protein-coupled receptor signaling pathway	0.0518105 2	0.0553422 51	2
GO:01400 52	cellular response to oxidised low-density lipoprotein particle stimulus	0.0518105 2	0.0553422 51	2
GO:19010 33	positive regulation of response to reactive oxygen species	0.0518105 2	0.0553422 51	2
GO:19019 50	dense core granule transport	0.0518105 2	0.0553422 51	2
GO:19025 13	regulation of organelle transport along microtubule	0.0518105 2	0.0553422 51	2
GO:19043 21	response to forskolin	0.0518105 2	0.0553422 51	2
GO:19043 22	cellular response to forskolin	0.0518105 2	0.0553422 51	2
GO:19058 79	regulation of oogenesis	0.0518105 2	0.0553422 51	2
GO:19904 40	positive regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress	0.0518105 2	0.0553422 51	2
GO:20004 80	negative regulation of cAMP-dependent protein kinase activity	0.0518105 2	0.0553422 51	2
GO:20005 51	regulation of T-helper 2 cell cytokine production	0.0518105 2	0.0553422 51	2
GO:20005 74	regulation of microtubule motor activity	0.0518105 2	0.0553422 51	2
GO:20006 15	regulation of histone H3-K9 acetylation	0.0518105 2	0.0553422 51	2
GO:20006 28	regulation of miRNA metabolic process	0.0518105 2	0.0553422 51	2
GO:20011 38	regulation of phospholipid transport	0.0518105 2	0.0553422 51	2

GO:20011 40	positive regulation of phospholipid transport	0.0518105 2	0.0553422 51	2
GO:00510 99	positive regulation of binding	0.0519892 57	0.0553965 48	2
GO:00976 96	receptor signaling pathway via STAT	0.0519892 57	0.0553965 48	2
GO:00083 06	associative learning	0.0521062 7	0.0553965 48	2
GO:00147 43	regulation of muscle hypertrophy	0.0521062 7	0.0553965 48	2
GO:00330 77	T cell differentiation in thymus	0.0521062 7	0.0553965 48	2
GO:00601 93	positive regulation of lipase activity	0.0521062 7	0.0553965 48	2
GO:00604 15	muscle tissue morphogenesis	0.0521062 7	0.0553965 48	2
GO:00712 29	cellular response to acid chemical	0.0521062 7	0.0553965 48	2
GO:00506 80	negative regulation of epithelial cell proliferation	0.0527176 59	0.0560136 33	2
GO:00074 22	peripheral nervous system development	0.0533320 68	0.0564675 1	2
GO:00305 00	regulation of bone mineralization	0.0533320 68	0.0564675 1	2
GO:00324 13	negative regulation of ion transmembrane transporter activity	0.0533320 68	0.0564675 1	2
GO:00604 11	cardiac septum morphogenesis	0.0533320 68	0.0564675 1	2
GO:00613 33	renal tubule morphogenesis	0.0533320 68	0.0564675 1	2
GO:00720 28	nephron morphogenesis	0.0533320 68	0.0564675 1	2
GO:00516 04	protein maturation	0.0533733 9	0.0564782 13	2
GO:00603 95	SMAD protein signal transduction	0.0545681 13	0.0577086 87	2
GO:00004 22	autophagy of mitochondrion	0.0558142 79	0.0582697 78	2
GO:00064 46	regulation of translational initiation	0.0558142 79	0.0582697 78	2
GO:00074 92	endoderm development	0.0558142 79	0.0582697 78	2
GO:00165 75	histone deacetylation	0.0558142 79	0.0582697 78	2

GO:00322 72	negative regulation of protein polymerization	0.0558142 79	0.0582697 78	2
GO:00434 62	regulation of ATPase activity	0.0558142 79	0.0582697 78	2
GO:00617 26	mitochondrion disassembly	0.0558142 79	0.0582697 78	2
GO:00002 80	nuclear division	0.0560758 66	0.0582697 78	2
GO:00001 85	activation of MAPKKK activity	0.0563867 73	0.0582697 78	2
GO:00019 76	nervous system process involved in regulation of systemic arterial blood pressure	0.0563867 73	0.0582697 78	2
GO:00025 51	mast cell chemotaxis	0.0563867 73	0.0582697 78	2
GO:00028 63	positive regulation of inflammatory response to antigenic stimulus	0.0563867 73	0.0582697 78	2
GO:00029 23	regulation of humoral immune response mediated by circulating immunoglobulin	0.0563867 73	0.0582697 78	2
GO:00033 34	keratinocyte development	0.0563867 73	0.0582697 78	2
GO:00060 69	ethanol oxidation	0.0563867 73	0.0582697 78	2
GO:00073 20	insemination	0.0563867 73	0.0582697 78	2
GO:00148 31	gastro-intestinal system smooth muscle contraction	0.0563867 73	0.0582697 78	2
GO:00313 92	regulation of prostaglandin biosynthetic process	0.0563867 73	0.0582697 78	2
GO:00332 34	negative regulation of protein sumoylation	0.0563867 73	0.0582697 78	2
GO:00354 04	histone-serine phosphorylation	0.0563867 73	0.0582697 78	2
GO:00364 62	TRAIL-activated apoptotic signaling pathway	0.0563867 73	0.0582697 78	2
GO:00380 03	opioid receptor signaling pathway	0.0563867 73	0.0582697 78	2
GO:00423 68	vitamin D biosynthetic process	0.0563867 73	0.0582697 78	2
GO:00424 16	dopamine biosynthetic process	0.0563867 73	0.0582697 78	2
GO:00463 22	negative regulation of fatty acid oxidation	0.0563867 73	0.0582697 78	2
GO:00510 95	regulation of helicase activity	0.0563867 73	0.0582697 78	2

GO:00515 49	positive regulation of keratinocyte migration	0.0563867 73	0.0582697 78	2
GO:00517 98	positive regulation of hair follicle development	0.0563867 73	0.0582697 78	2
GO:00550 15	ventricular cardiac muscle cell development	0.0563867 73	0.0582697 78	2
GO:00604 53	regulation of gastric acid secretion	0.0563867 73	0.0582697 78	2
GO:00716 79	commissural neuron axon guidance	0.0563867 73	0.0582697 78	2
GO:00725 20	seminiferous tubule development	0.0563867 73	0.0582697 78	2
GO:00725 40	T-helper 17 cell lineage commitment	0.0563867 73	0.0582697 78	2
GO:00860 67	AV node cell to bundle of His cell communication	0.0563867 73	0.0582697 78	2
GO:00972 01	negative regulation of transcription from RNA polymerase II promoter in response to stress	0.0563867 73	0.0582697 78	2
GO:01500 65	regulation of deacetylase activity	0.0563867 73	0.0582697 78	2
GO:19015 03	ether biosynthetic process	0.0563867 73	0.0582697 78	2
GO:19023 37	regulation of apoptotic process involved in morphogenesis	0.0563867 73	0.0582697 78	2
GO:20010 53	regulation of mesenchymal cell apoptotic process	0.0563867 73	0.0582697 78	2
GO:20012 14	positive regulation of vasculogenesis	0.0563867 73	0.0582697 78	2
GO:00061 10	regulation of glycolytic process	0.0570704 42	0.0588418 59	2
GO:00140 32	neural crest cell development	0.0570704 42	0.0588418 59	2
GO:00550 21	regulation of cardiac muscle tissue growth	0.0570704 42	0.0588418 59	2
GO:20003 00	regulation of synaptic vesicle exocytosis	0.0570704 42	0.0588418 59	2
GO:00310 98	stress-activated protein kinase signaling cascade	0.0572467 08	0.0589899 84	2
GO:20012 52	positive regulation of chromosome organization	0.0579542 69	0.0596851 03	2
GO:00019 37	negative regulation of endothelial cell proliferation	0.0583364 79	0.0599422 62	2
GO:00199 15	lipid storage	0.0583364 79	0.0599422 62	2

GO:00332 38	regulation of cellular amine metabolic process	0.0583364 79	0.0599422 62	2
GO:00508 29	defense response to Gram-negative bacterium	0.0583364 79	0.0599422 62	2
GO:00066 11	protein export from nucleus	0.0594942 65	0.0609908 53	2
GO:19029 30	regulation of alcohol biosynthetic process	0.0596122 69	0.0609908 53	2
GO:00015 70	vasculogenesis	0.0608976 9	0.0609908 53	2
GO:00027 18	regulation of cytokine production involved in immune response	0.0608976 9	0.0609908 53	2
GO:00486 44	muscle organ morphogenesis	0.0608976 9	0.0609908 53	2
GO:00487 08	astrocyte differentiation	0.0608976 9	0.0609908 53	2
GO:00007 22	telomere maintenance via recombination	0.0609411 81	0.0609908 53	2
GO:00026 79	respiratory burst involved in defense response	0.0609411 81	0.0609908 53	2
GO:00030 84	positive regulation of systemic arterial blood pressure	0.0609411 81	0.0609908 53	2
GO:00066 84	sphingomyelin metabolic process	0.0609411 81	0.0609908 53	2
GO:00071 71	activation of transmembrane receptor protein tyrosine kinase activity	0.0609411 81	0.0609908 53	2
GO:00098 86	post-embryonic animal morphogenesis	0.0609411 81	0.0609908 53	2
GO:00104 59	negative regulation of heart rate	0.0609411 81	0.0609908 53	2
GO:00106 42	negative regulation of platelet-derived growth factor receptor signaling pathway	0.0609411 81	0.0609908 53	2
GO:00108 70	positive regulation of receptor biosynthetic process	0.0609411 81	0.0609908 53	2
GO:00196 27	urea metabolic process	0.0609411 81	0.0609908 53	2
GO:00219 84	adenohypophysis development	0.0609411 81	0.0609908 53	2
GO:00300 02	cellular anion homeostasis	0.0609411 81	0.0609908 53	2
GO:00303 20	cellular monovalent inorganic anion homeostasis	0.0609411 81	0.0609908 53	2
GO:00306 56	regulation of vitamin metabolic process	0.0609411 81	0.0609908 53	2

GO:00310 53	primary miRNA processing	0.0609411 81	0.0609908 53	2
GO:00311 15	negative regulation of microtubule polymerization	0.0609411 81	0.0609908 53	2
GO:00319 53	negative regulation of protein autophosphorylation	0.0609411 81	0.0609908 53	2
GO:00322 30	positive regulation of synaptic transmission, GABAergic	0.0609411 81	0.0609908 53	2
GO:00323 52	positive regulation of hormone metabolic process	0.0609411 81	0.0609908 53	2
GO:00331 27	regulation of histone phosphorylation	0.0609411 81	0.0609908 53	2
GO:00331 45	positive regulation of intracellular steroid hormone receptor signaling pathway	0.0609411 81	0.0609908 53	2
GO:00426 35	positive regulation of hair cycle	0.0609411 81	0.0609908 53	2
GO:00435 68	positive regulation of insulin-like growth factor receptor signaling pathway	0.0609411 81	0.0609908 53	2
GO:00439 70	histone H3-K9 acetylation	0.0609411 81	0.0609908 53	2
GO:00456 02	negative regulation of endothelial cell differentiation	0.0609411 81	0.0609908 53	2
GO:00457 41	positive regulation of epidermal growth factor-activated receptor activity	0.0609411 81	0.0609908 53	2
GO:00480 96	chromatin-mediated maintenance of transcription	0.0609411 81	0.0609908 53	2
GO:00519 88	regulation of attachment of spindle microtubules to kinetochore	0.0609411 81	0.0609908 53	2
GO:00606 01	lateral sprouting from an epithelium	0.0609411 81	0.0609908 53	2
GO:00610 29	eyelid development in camera-type eye	0.0609411 81	0.0609908 53	2
GO:00610 43	regulation of vascular wound healing	0.0609411 81	0.0609908 53	2
GO:00719 41	nitrogen cycle metabolic process	0.0609411 81	0.0609908 53	2
GO:00726 83	T cell extravasation	0.0609411 81	0.0609908 53	2
GO:00971 52	mesenchymal cell apoptotic process	0.0609411 81	0.0609908 53	2
GO:00975 31	mast cell migration	0.0609411 81	0.0609908 53	2
GO:00989 03	regulation of membrane repolarization during action potential	0.0609411 81	0.0609908 53	2

GO:19001 03	positive regulation of endoplasmic reticulum unfolded protein response	0.0609411 81	0.0609908 53	2
GO:19010 96	regulation of autophagosome maturation	0.0609411 81	0.0609908 53	2
GO:19013 87	positive regulation of voltage-gated calcium channel activity	0.0609411 81	0.0609908 53	2
GO:19036 51	positive regulation of cytoplasmic transport	0.0609411 81	0.0609908 53	2
GO:20001 21	regulation of removal of superoxide radicals	0.0609411 81	0.0609908 53	2
GO:00508 21	protein stabilization	0.0618402 89	0.0618564 82	2
GO:00488 64	stem cell development	0.0621926 21	0.0621745 37	2
GO:00061 63	purine nucleotide metabolic process	0.0626225 51	0.0625697 72	2
GO:00107 69	regulation of cell morphogenesis involved in differentiation	0.0630363 19	0.0629484 33	2
GO:00073 69	gastrulation	0.0634281 29	0.0631991 47	2
GO:00105 65	regulation of cellular ketone metabolic process	0.0634281 29	0.0631991 47	2
GO:00067 67	water-soluble vitamin metabolic process	0.0634969 44	0.0631991 47	2
GO:00320 92	positive regulation of protein binding	0.0634969 44	0.0631991 47	2
GO:00705 09	calcium ion import	0.0634969 44	0.0631991 47	2
GO:00723 84	organelle transport along microtubule	0.0634969 44	0.0631991 47	2
GO:00705 07	regulation of microtubule cytoskeleton organization	0.0642291 44	0.0636610 44	2
GO:00149 10	regulation of smooth muscle cell migration	0.0648105 41	0.0636610 44	2
GO:00425 09	regulation of tyrosine phosphorylation of STAT protein	0.0648105 41	0.0636610 44	2
GO:00454 45	myoblast differentiation	0.0648105 41	0.0636610 44	2
GO:00507 72	positive regulation of axonogenesis	0.0648105 41	0.0636610 44	2
GO:00000 54	ribosomal subunit export from nucleus	0.0654738 47	0.0636610 44	2
GO:00071 00	mitotic centrosome separation	0.0654738 47	0.0636610 44	2

GO:00075 12	adult heart development	0.0654738 47	0.0636610 44	2
GO:00092 14	cyclic nucleotide catabolic process	0.0654738 47	0.0636610 44	2
GO:00102 48	establishment or maintenance of transmembrane electrochemical gradient	0.0654738 47	0.0636610 44	2
GO:00107 52	regulation of cGMP-mediated signaling	0.0654738 47	0.0636610 44	2
GO:00109 17	negative regulation of mitochondrial membrane potential	0.0654738 47	0.0636610 44	2
GO:00148 54	response to inactivity	0.0654738 47	0.0636610 44	2
GO:00148 74	response to stimulus involved in regulation of muscle adaptation	0.0654738 47	0.0636610 44	2
GO:00198 96	axonal transport of mitochondrion	0.0654738 47	0.0636610 44	2
GO:00312 82	regulation of guanylate cyclase activity	0.0654738 47	0.0636610 44	2
GO:00320 42	mitochondrial DNA metabolic process	0.0654738 47	0.0636610 44	2
GO:00323 10	prostaglandin secretion	0.0654738 47	0.0636610 44	2
GO:00336 04	negative regulation of catecholamine secretion	0.0654738 47	0.0636610 44	2
GO:00337 50	ribosome localization	0.0654738 47	0.0636610 44	2
GO:00343 56	NAD biosynthesis via nicotinamide riboside salvage pathway	0.0654738 47	0.0636610 44	2
GO:00351 12	genitalia morphogenesis	0.0654738 47	0.0636610 44	2
GO:00426 59	regulation of cell fate specification	0.0654738 47	0.0636610 44	2
GO:00439 22	negative regulation by host of viral transcription	0.0654738 47	0.0636610 44	2
GO:00460 07	negative regulation of activated T cell proliferation	0.0654738 47	0.0636610 44	2
GO:00474 84	regulation of response to osmotic stress	0.0654738 47	0.0636610 44	2
GO:00515 47	regulation of keratinocyte migration	0.0654738 47	0.0636610 44	2
GO:00517 09	regulation of killing of cells of other organism	0.0654738 47	0.0636610 44	2
GO:00550 64	chloride ion homeostasis	0.0654738 47	0.0636610 44	2

GO:00604 52	positive regulation of cardiac muscle contraction	0.0654738 47	0.0636610 44	2
GO:00702 34	positive regulation of T cell apoptotic process	0.0654738 47	0.0636610 44	2
GO:00704 31	nucleotide-binding oligomerization domain containing 2 signaling pathway	0.0654738 47	0.0636610 44	2
GO:00712 36	cellular response to antibiotic	0.0654738 47	0.0636610 44	2
GO:00724 25	signal transduction involved in G2 DNA damage checkpoint	0.0654738 47	0.0636610 44	2
GO:00902 31	regulation of spindle checkpoint	0.0654738 47	0.0636610 44	2
GO:00902 66	regulation of mitotic cell cycle spindle assembly checkpoint	0.0654738 47	0.0636610 44	2
GO:19018 41	regulation of high voltage-gated calcium channel activity	0.0654738 47	0.0636610 44	2
GO:19028 94	negative regulation of pri-miRNA transcription by RNA polymerase II	0.0654738 47	0.0636610 44	2
GO:19035 04	regulation of mitotic spindle checkpoint	0.0654738 47	0.0636610 44	2
GO:19038 94	regulation of IRE1-mediated unfolded protein response	0.0654738 47	0.0636610 44	2
GO:19047 48	regulation of apoptotic process involved in development	0.0654738 47	0.0636610 44	2
GO:19050 64	negative regulation of vascular associated smooth muscle cell differentiation	0.0654738 47	0.0636610 44	2
GO:20012 79	regulation of unsaturated fatty acid biosynthetic process	0.0654738 47	0.0636610 44	2
GO:00064 13	translational initiation	0.0658452 78	0.0639534 61	2
GO:00480 15	phosphatidylinositol-mediated signaling	0.0658452 78	0.0639534 61	2
GO:00090 60	aerobic respiration	0.0661332 92	0.0640612 7	2
GO:00324 36	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	0.0661332 92	0.0640612 7	2
GO:00514 53	regulation of intracellular pH	0.0661332 92	0.0640612 7	2
GO:00517 81	positive regulation of cell division	0.0661332 92	0.0640612 7	2
GO:00604 20	regulation of heart growth	0.0661332 92	0.0640612 7	2
GO:00064 17	regulation of translation	0.0665509 45	0.0644313 45	2

GO:00140 68	positive regulation of phosphatidylinositol 3-kinase signaling	0.0674650 83	0.0651768 78	2
GO:00324 10	negative regulation of transporter activity	0.0674650 83	0.0651768 78	2
GO:00327 55	positive regulation of interleukin-6 production	0.0674650 83	0.0651768 78	2
GO:00464 70	phosphatidylcholine metabolic process	0.0674650 83	0.0651768 78	2
GO:00072 60	tyrosine phosphorylation of STAT protein	0.0688057 97	0.0661974 84	2
GO:00140 33	neural crest cell differentiation	0.0688057 97	0.0661974 84	2
GO:19010 19	regulation of calcium ion transmembrane transporter activity	0.0688057 97	0.0661974 84	2
GO:00095 66	fertilization	0.0691334 57	0.0661974 84	2
GO:00480 17	inositol lipid-mediated signaling	0.0691334 57	0.0661974 84	2
GO:00718 97	DNA biosynthetic process	0.0691334 57	0.0661974 84	2
GO:00097 49	response to glucose	0.0699670 44	0.0661974 84	2
GO:00512 16	cartilage development	0.0699670 44	0.0661974 84	2
GO:00061 22	mitochondrial electron transport, ubiquinol to cytochrome c	0.0699848 74	0.0661974 84	2
GO:00094 04	toxin metabolic process	0.0699848 74	0.0661974 84	2
GO:00107 63	positive regulation of fibroblast migration	0.0699848 74	0.0661974 84	2
GO:00200 27	hemoglobin metabolic process	0.0699848 74	0.0661974 84	2
GO:00219 24	cell proliferation in external granule layer	0.0699848 74	0.0661974 84	2
GO:00219 30	cerebellar granule cell precursor proliferation	0.0699848 74	0.0661974 84	2
GO:00302 38	male sex determination	0.0699848 74	0.0661974 84	2
GO:00322 52	secretory granule localization	0.0699848 74	0.0661974 84	2
GO:00336 89	negative regulation of osteoblast proliferation	0.0699848 74	0.0661974 84	2
GO:00356 35	entry of bacterium into host cell	0.0699848 74	0.0661974 84	2

GO:00357 45	T-helper 2 cell cytokine production	0.0699848 74	0.0661974 84	2
GO:00423 62	fat-soluble vitamin biosynthetic process	0.0699848 74	0.0661974 84	2
GO:00433 74	CD8-positive, alpha-beta T cell differentiation	0.0699848 74	0.0661974 84	2
GO:00454 75	locomotor rhythm	0.0699848 74	0.0661974 84	2
GO:00457 79	negative regulation of bone resorption	0.0699848 74	0.0661974 84	2
GO:00458 37	negative regulation of membrane potential	0.0699848 74	0.0661974 84	2
GO:00464 79	glycosphingolipid catabolic process	0.0699848 74	0.0661974 84	2
GO:00507 46	regulation of lipoprotein metabolic process	0.0699848 74	0.0661974 84	2
GO:00508 62	positive regulation of T cell receptor signaling pathway	0.0699848 74	0.0661974 84	2
GO:00512 99	centrosome separation	0.0699848 74	0.0661974 84	2
GO:00601 34	prepulse inhibition	0.0699848 74	0.0661974 84	2
GO:00603 47	heart trabecula formation	0.0699848 74	0.0661974 84	2
GO:00608 41	venous blood vessel development	0.0699848 74	0.0661974 84	2
GO:00708 85	negative regulation of calcineurin-NFAT signaling cascade	0.0699848 74	0.0661974 84	2
GO:00714 28	rRNA-containing ribonucleoprotein complex export from nucleus	0.0699848 74	0.0661974 84	2
GO:00718 01	regulation of podosome assembly	0.0699848 74	0.0661974 84	2
GO:00725 67	chemokine (C-X-C motif) ligand 2 production	0.0699848 74	0.0661974 84	2
GO:00905 94	inflammatory response to wounding	0.0699848 74	0.0661974 84	2
GO:00972 02	activation of cysteine-type endopeptidase activity	0.0699848 74	0.0661974 84	2
GO:01060 57	negative regulation of calcineurin-mediated signaling	0.0699848 74	0.0661974 84	2
GO:19039 60	negative regulation of anion transmembrane transport	0.0699848 74	0.0661974 84	2
GO:20003 41	regulation of chemokine (C-X-C motif) ligand 2 production	0.0699848 74	0.0661974 84	2

GO:00464 27	positive regulation of receptor signaling pathway via JAK-STAT	0.0701553 19	0.0663240 36	2
GO:00076 26	locomotory behavior	0.0708052 12	0.0669034 82	2
GO:00424 75	odontogenesis of dentin-containing tooth	0.0715135 36	0.0674670 81	2
GO:00603 33	interferon-gamma-mediated signaling pathway	0.0715135 36	0.0674670 81	2
GO:00973 06	cellular response to alcohol	0.0715135 36	0.0674670 81	2
GO:19033 21	negative regulation of protein modification by small protein conjugation or removal	0.0728803 35	0.0687207 13	2
GO:00026 83	negative regulation of immune system process	0.0732239 27	0.0689306 4	2
GO:00022 21	pattern recognition receptor signaling pathway	0.0733470 06	0.0689306 4	2
GO:00071 79	transforming growth factor beta receptor signaling pathway	0.0742033 05	0.0689306 4	2
GO:00068 98	receptor-mediated endocytosis	0.0742066 86	0.0689306 4	2
GO:00149 09	smooth muscle cell migration	0.0742556 02	0.0689306 4	2
GO:00517 02	interaction with symbiont	0.0742556 02	0.0689306 4	2
GO:00610 97	regulation of protein tyrosine kinase activity	0.0742556 02	0.0689306 4	2
GO:00720 80	nephron tubule development	0.0742556 02	0.0689306 4	2
GO:19048 94	positive regulation of receptor signaling pathway via STAT	0.0742556 02	0.0689306 4	2
GO:00017 80	neutrophil homeostasis	0.0744743 64	0.0689306 4	2
GO:00022 95	T-helper cell lineage commitment	0.0744743 64	0.0689306 4	2
GO:00028 30	positive regulation of type 2 immune response	0.0744743 64	0.0689306 4	2
GO:00060 98	pentose-phosphate shunt	0.0744743 64	0.0689306 4	2
GO:00102 25	response to UV-C	0.0744743 64	0.0689306 4	2
GO:00140 61	regulation of norepinephrine secretion	0.0744743 64	0.0689306 4	2
GO:00170 14	protein nitrosylation	0.0744743 64	0.0689306 4	2

GO:00181 19	peptidyl-cysteine S-nitrosylation	0.0744743 64	0.0689306 4	2
GO:00195 11	peptidyl-proline hydroxylation	0.0744743 64	0.0689306 4	2
GO:00215 34	cell proliferation in hindbrain	0.0744743 64	0.0689306 4	2
GO:00330 33	negative regulation of myeloid cell apoptotic process	0.0744743 64	0.0689306 4	2
GO:00341 16	positive regulation of heterotypic cell-cell adhesion	0.0744743 64	0.0689306 4	2
GO:00343 74	low-density lipoprotein particle remodeling	0.0744743 64	0.0689306 4	2
GO:00458 38	positive regulation of membrane potential	0.0744743 64	0.0689306 4	2
GO:00459 89	positive regulation of striated muscle contraction	0.0744743 64	0.0689306 4	2
GO:00463 25	negative regulation of glucose import	0.0744743 64	0.0689306 4	2
GO:00605 72	morphogenesis of an epithelial bud	0.0744743 64	0.0689306 4	2
GO:00614 50	trophoblast cell migration	0.0744743 64	0.0689306 4	2
GO:00708 86	positive regulation of calcineurin-NFAT signaling cascade	0.0744743 64	0.0689306 4	2
GO:00713 80	cellular response to prostaglandin E stimulus	0.0744743 64	0.0689306 4	2
GO:00991 70	postsynaptic modulation of chemical synaptic transmission	0.0744743 64	0.0689306 4	2
GO:01060 58	positive regulation of calcineurin-mediated signaling	0.0744743 64	0.0689306 4	2
GO:19011 63	regulation of trophoblast cell migration	0.0744743 64	0.0689306 4	2
GO:19021 66	negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	0.0744743 64	0.0689306 4	2
GO:19025 14	regulation of calcium ion transmembrane transport via high voltage-gated calcium channel	0.0744743 64	0.0689306 4	2
GO:19050 50	positive regulation of metallopeptidase activity	0.0744743 64	0.0689306 4	2
GO:20012 12	regulation of vasculogenesis	0.0744743 64	0.0689306 4	2
GO:00064 73	protein acetylation	0.0750640 89	0.0694409 48	2
GO:00106 60	regulation of muscle cell apoptotic process	0.0756392 27	0.0697590 17	2

GO:00306 41	regulation of cellular pH	0.0756392 27	0.0697590 17	2
GO:00343 08	primary alcohol metabolic process	0.0756392 27	0.0697590 17	2
GO:00457 78	positive regulation of ossification	0.0756392 27	0.0697590 17	2
GO:00609 93	kidney morphogenesis	0.0756392 27	0.0697590 17	2
GO:19059 54	positive regulation of lipid localization	0.0756392 27	0.0697590 17	2
GO:00511 68	nuclear export	0.0759293 4	0.0699909 03	2
GO:00507 09	negative regulation of protein secretion	0.0770310 99	0.0708620 98	2
GO:00613 26	renal tubule development	0.0770310 99	0.0708620 98	2
GO:00701 67	regulation of biomineral tissue development	0.0770310 99	0.0708620 98	2
GO:01101 49	regulation of biomineralization	0.0770310 99	0.0708620 98	2
GO:00356 37	multicellular organismal signaling	0.0776731 59	0.0714164 32	2
GO:00725 21	purine-containing compound metabolic process	0.0780521 78	0.0716729 7	2
GO:00508 66	negative regulation of cell activation	0.0785516 9	0.0716729 7	2
GO:19013 43	negative regulation of vasculature development	0.0785516 9	0.0716729 7	2
GO:00031 84	pulmonary valve morphogenesis	0.0789424 19	0.0716729 7	2
GO:00083 40	determination of adult lifespan	0.0789424 19	0.0716729 7	2
GO:00092 99	mRNA transcription	0.0789424 19	0.0716729 7	2
GO:00107 15	regulation of extracellular matrix disassembly	0.0789424 19	0.0716729 7	2
GO:00157 32	prostaglandin transport	0.0789424 19	0.0716729 7	2
GO:00193 77	glycolipid catabolic process	0.0789424 19	0.0716729 7	2
GO:00307 30	sequestering of triglyceride	0.0789424 19	0.0716729 7	2
GO:00308 89	negative regulation of B cell proliferation	0.0789424 19	0.0716729 7	2

GO:00309 49	positive regulation of vascular endothelial growth factor receptor signaling pathway	0.0789424 19	0.0716729 7	2
GO:00326 82	negative regulation of chemokine production	0.0789424 19	0.0716729 7	2
GO:00329 66	negative regulation of collagen biosynthetic process	0.0789424 19	0.0716729 7	2
GO:00357 29	cellular response to hepatocyte growth factor stimulus	0.0789424 19	0.0716729 7	2
GO:00439 23	positive regulation by host of viral transcription	0.0789424 19	0.0716729 7	2
GO:00445 39	long-chain fatty acid import into cell	0.0789424 19	0.0716729 7	2
GO:00460 68	cGMP metabolic process	0.0789424 19	0.0716729 7	2
GO:00468 51	negative regulation of bone remodeling	0.0789424 19	0.0716729 7	2
GO:00482 43	norepinephrine secretion	0.0789424 19	0.0716729 7	2
GO:00901 41	positive regulation of mitochondrial fission	0.0789424 19	0.0716729 7	2
GO:00901 85	negative regulation of kidney development	0.0789424 19	0.0716729 7	2
GO:01403 54	lipid import into cell	0.0789424 19	0.0716729 7	2
GO:19032 09	positive regulation of oxidative stress-induced cell death	0.0789424 19	0.0716729 7	1
GO:19053 31	negative regulation of morphogenesis of an epithelium	0.0789424 19	0.0716729 7	1
GO:00064 76	protein deacetylation	0.0798391 48	0.0723057 24	1
GO:00427 75	mitochondrial ATP synthesis coupled electron transport	0.0798391 48	0.0723057 24	1
GO:00507 64	regulation of phagocytosis	0.0798391 48	0.0723057 24	1
GO:00986 59	inorganic cation import across plasma membrane	0.0798391 48	0.0723057 24	1
GO:00995 87	inorganic ion import across plasma membrane	0.0798391 48	0.0723057 24	1
GO:00353 03	regulation of dephosphorylation	0.0803218 92	0.0727065 28	1
GO:00085 44	epidermis development	0.0808076 95	0.0731096 99	1
GO:00452 16	cell-cell junction organization	0.0812135 25	0.0732946 05	1

GO:00016 57	ureteric bud development	0.0812551 07	0.0732946 05	1
GO:00106 57	muscle cell apoptotic process	0.0812551 07	0.0732946 05	1
GO:00140 20	primary neural tube formation	0.0812551 07	0.0732946 05	1
GO:00427 73	ATP synthesis coupled electron transport	0.0812551 07	0.0732946 05	1
GO:00508 10	regulation of steroid biosynthetic process	0.0812551 07	0.0732946 05	1
GO:00027 03	regulation of leukocyte mediated immunity	0.0821094 84	0.0738934 64	1
GO:00434 73	pigmentation	0.0826788 8	0.0738934 64	1
GO:00508 30	defense response to Gram-positive bacterium	0.0826788 8	0.0738934 64	1
GO:00721 63	mesonephric epithelium development	0.0826788 8	0.0738934 64	1
GO:00721 64	mesonephric tubule development	0.0826788 8	0.0738934 64	1
GO:00190 58	viral life cycle	0.0828602 16	0.0738934 64	1
GO:00066 43	membrane lipid metabolic process	0.0830097 5	0.0738934 64	1
GO:00517 01	interaction with host	0.0830097 5	0.0738934 64	1
GO:00063 49	regulation of gene expression by genetic imprinting	0.0833891 39	0.0738934 64	1
GO:00066 77	glycosylceramide metabolic process	0.0833891 39	0.0738934 64	1
GO:00067 40	NADPH regeneration	0.0833891 39	0.0738934 64	1
GO:00105 23	negative regulation of calcium ion transport into cytosol	0.0833891 39	0.0738934 64	1
GO:00107 13	negative regulation of collagen metabolic process	0.0833891 39	0.0738934 64	1
GO:00312 93	membrane protein intracellular domain proteolysis	0.0833891 39	0.0738934 64	1
GO:00327 40	positive regulation of interleukin-17 production	0.0833891 39	0.0738934 64	1
GO:00327 80	negative regulation of ATPase activity	0.0833891 39	0.0738934 64	1
GO:00331 94	response to hydroperoxide	0.0833891 39	0.0738934 64	1

GO:00353 30	regulation of hippo signaling	0.0833891 39	0.0738934 64	1
GO:00432 17	myelin maintenance	0.0833891 39	0.0738934 64	1
GO:00451 87	regulation of circadian sleep/wake cycle, sleep	0.0833891 39	0.0738934 64	1
GO:00468 85	regulation of hormone biosynthetic process	0.0833891 39	0.0738934 64	1
GO:00518 95	negative regulation of focal adhesion assembly	0.0833891 39	0.0738934 64	1
GO:00600 04	reflex	0.0833891 39	0.0738934 64	1
GO:00600 33	anatomical structure regression	0.0833891 39	0.0738934 64	1
GO:00604 57	negative regulation of digestive system process	0.0833891 39	0.0738934 64	1
GO:00609 77	coronary vasculature morphogenesis	0.0833891 39	0.0738934 64	1
GO:00612 98	retina vasculature development in camera-type eye	0.0833891 39	0.0738934 64	1
GO:00615 77	calcium ion transmembrane transport via high voltage-gated calcium channel	0.0833891 39	0.0738934 64	1
GO:00713 18	cellular response to ATP	0.0833891 39	0.0738934 64	1
GO:00716 05	monocyte chemotactic protein-1 production	0.0833891 39	0.0738934 64	1
GO:00716 37	regulation of monocyte chemotactic protein-1 production	0.0833891 39	0.0738934 64	1
GO:00901 90	positive regulation of branching involved in ureteric bud morphogenesis	0.0833891 39	0.0738934 64	1
GO:01501 18	negative regulation of cell-substrate junction organization	0.0833891 39	0.0738934 64	1
GO:19002 21	regulation of amyloid-beta clearance	0.0833891 39	0.0738934 64	1
GO:19015 24	regulation of mitophagy	0.0833891 39	0.0738934 64	1
GO:19021 65	regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	0.0833891 39	0.0738934 64	1
GO:00901 50	establishment of protein localization to membrane	0.0835458 18	0.0739960 64	1
GO:00160 51	carbohydrate biosynthetic process	0.0839143 03	0.0742860 68	1
GO:00066 72	ceramide metabolic process	0.0841103 61	0.0743868 45	1

GO:00508 48	regulation of calcium-mediated signaling	0.0841103 61	0.0743868 45	1
GO:00027 92	negative regulation of peptide secretion	0.0855494 43	0.0754751 17	1
GO:00105 22	regulation of calcium ion transport into cytosol	0.0855494 43	0.0754751 17	1
GO:00159 08	fatty acid transport	0.0855494 43	0.0754751 17	1
GO:00421 02	positive regulation of T cell proliferation	0.0855494 43	0.0754751 17	1
GO:00601 91	regulation of lipase activity	0.0855494 43	0.0754751 17	1
GO:00516 51	maintenance of location in cell	0.0866534 75	0.0762101 95	1
GO:00550 24	regulation of cardiac muscle tissue development	0.0869960 23	0.0762101 95	1
GO:20000 60	positive regulation of ubiquitin-dependent protein catabolic process	0.0869960 23	0.0762101 95	1
GO:00016 96	gastric acid secretion	0.0878146 27	0.0762101 95	1
GO:00020 76	osteoblast development	0.0878146 27	0.0762101 95	1
GO:00029 22	positive regulation of humoral immune response	0.0878146 27	0.0762101 95	1
GO:00031 59	morphogenesis of an endothelium	0.0878146 27	0.0762101 95	1
GO:00106 63	positive regulation of striated muscle cell apoptotic process	0.0878146 27	0.0762101 95	1
GO:00106 66	positive regulation of cardiac muscle cell apoptotic process	0.0878146 27	0.0762101 95	1
GO:00107 59	positive regulation of macrophage chemotaxis	0.0878146 27	0.0762101 95	1
GO:00190 54	modulation by virus of host cellular process	0.0878146 27	0.0762101 95	1
GO:00300 11	maintenance of cell polarity	0.0878146 27	0.0762101 95	1
GO:00320 26	response to magnesium ion	0.0878146 27	0.0762101 95	1
GO:00320 95	regulation of response to food	0.0878146 27	0.0762101 95	1
GO:00329 30	positive regulation of superoxide anion generation	0.0878146 27	0.0762101 95	1
GO:00357 28	response to hepatocyte growth factor	0.0878146 27	0.0762101 95	1

GO:00433 73	CD4-positive, alpha-beta T cell lineage commitment	0.0878146 27	0.0762101 95	1
GO:00450 91	regulation of single stranded viral RNA replication via double stranded DNA intermediate	0.0878146 27	0.0762101 95	1
GO:00457 80	positive regulation of bone resorption	0.0878146 27	0.0762101 95	1
GO:00464 85	ether lipid metabolic process	0.0878146 27	0.0762101 95	1
GO:00468 52	positive regulation of bone remodeling	0.0878146 27	0.0762101 95	1
GO:00482 45	eosinophil chemotaxis	0.0878146 27	0.0762101 95	1
GO:00484 90	anterograde synaptic vesicle transport	0.0878146 27	0.0762101 95	1
GO:00515 46	keratinocyte migration	0.0878146 27	0.0762101 95	1
GO:00606 02	branch elongation of an epithelium	0.0878146 27	0.0762101 95	1
GO:00611 54	endothelial tube morphogenesis	0.0878146 27	0.0762101 95	1
GO:00702 33	negative regulation of T cell apoptotic process	0.0878146 27	0.0762101 95	1
GO:00718 00	podosome assembly	0.0878146 27	0.0762101 95	1
GO:00976 23	potassium ion export across plasma membrane	0.0878146 27	0.0762101 95	1
GO:00989 15	membrane repolarization during ventricular cardiac muscle cell action potential	0.0878146 27	0.0762101 95	1
GO:00995 14	synaptic vesicle cytoskeletal transport	0.0878146 27	0.0762101 95	1
GO:00995 17	synaptic vesicle transport along microtubule	0.0878146 27	0.0762101 95	1
GO:20006 47	negative regulation of stem cell proliferation	0.0878146 27	0.0762101 95	1
GO:20006 96	regulation of epithelial cell differentiation involved in kidney development	0.0878146 27	0.0762101 95	1
GO:00018 23	mesonephros development	0.0884499 95	0.0765779 61	1
GO:00068 85	regulation of pH	0.0884499 95	0.0765779 61	1
GO:00305 93	neutrophil chemotaxis	0.0884499 95	0.0765779 61	1
GO:00704 98	interleukin-1-mediated signaling pathway	0.0884499 95	0.0765779 61	1

GO:19018 90	positive regulation of cell junction assembly	0.0884499 95	0.0765779 61	1
GO:00301 78	negative regulation of Wnt signaling pathway	0.0894304 84	0.0773898 17	1
GO:00023 67	cytokine production involved in immune response	0.0899112 58	0.0776573 06	1
GO:00033 00	cardiac muscle hypertrophy	0.0899112 58	0.0776573 06	1
GO:00109 23	negative regulation of phosphatase activity	0.0899112 58	0.0776573 06	1
GO:00485 25	negative regulation of viral process	0.0899112 58	0.0776573 06	1
GO:00028 24	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	0.0913797 1	0.0784004 11	1
GO:00076 31	feeding behavior	0.0913797 1	0.0784004 11	1
GO:00440 70	regulation of anion transport	0.0913797 1	0.0784004 11	1
GO:00620 14	negative regulation of small molecule metabolic process	0.0913797 1	0.0784004 11	1
GO:00023 20	lymphoid progenitor cell differentiation	0.0922189 81	0.0784004 11	1
GO:00025 44	chronic inflammatory response	0.0922189 81	0.0784004 11	1
GO:00026 89	negative regulation of leukocyte chemotaxis	0.0922189 81	0.0784004 11	1
GO:00027 26	positive regulation of T cell cytokine production	0.0922189 81	0.0784004 11	1
GO:00029 02	regulation of B cell apoptotic process	0.0922189 81	0.0784004 11	1
GO:00033 23	type B pancreatic cell development	0.0922189 81	0.0784004 11	1
GO:00065 25	arginine metabolic process	0.0922189 81	0.0784004 11	1
GO:00076 20	copulation	0.0922189 81	0.0784004 11	1
GO:00100 42	response to manganese ion	0.0922189 81	0.0784004 11	1
GO:00108 75	positive regulation of cholesterol efflux	0.0922189 81	0.0784004 11	1
GO:00312 90	retinal ganglion cell axon guidance	0.0922189 81	0.0784004 11	1
GO:00319 98	regulation of fatty acid beta-oxidation	0.0922189 81	0.0784004 11	1

GO:00323 32	positive regulation of chondrocyte differentiation	0.0922189 81	0.0784004 11	1
GO:00327 93	positive regulation of CREB transcription factor activity	0.0922189 81	0.0784004 11	1
GO:00341 38	toll-like receptor 3 signaling pathway	0.0922189 81	0.0784004 11	1
GO:00363 03	lymph vessel morphogenesis	0.0922189 81	0.0784004 11	1
GO:00396 92	single stranded viral RNA replication via double stranded DNA intermediate	0.0922189 81	0.0784004 11	1
GO:00439 50	positive regulation of cAMP-mediated signaling	0.0922189 81	0.0784004 11	1
GO:00603 53	regulation of cell adhesion molecule production	0.0922189 81	0.0784004 11	1
GO:00605 46	negative regulation of necroptotic process	0.0922189 81	0.0784004 11	1
GO:00620 99	negative regulation of programmed necrotic cell death	0.0922189 81	0.0784004 11	1
GO:00716 36	positive regulation of transforming growth factor beta production	0.0922189 81	0.0784004 11	1
GO:00717 31	response to nitric oxide	0.0922189 81	0.0784004 11	1
GO:00860 14	atrial cardiac muscle cell action potential	0.0922189 81	0.0784004 11	1
GO:00860 26	atrial cardiac muscle cell to AV node cell signaling	0.0922189 81	0.0784004 11	1
GO:00860 66	atrial cardiac muscle cell to AV node cell communication	0.0922189 81	0.0784004 11	1
GO:00977 09	connective tissue replacement	0.0922189 81	0.0784004 11	1
GO:00987 03	calcium ion import across plasma membrane	0.0922189 81	0.0784004 11	1
GO:19017 41	positive regulation of myoblast fusion	0.0922189 81	0.0784004 11	1
GO:00171 57	regulation of exocytosis	0.0922447 65	0.0784004 11	1
GO:00018 41	neural tube formation	0.0928552 47	0.0787343 61	1
GO:00027 08	positive regulation of lymphocyte mediated immunity	0.0928552 47	0.0787343 61	1
GO:00148 12	muscle cell migration	0.0928552 47	0.0787343 61	1
GO:00466 32	alpha-beta T cell differentiation	0.0928552 47	0.0787343 61	1

GO:00469 28	regulation of neurotransmitter secretion	0.0928552 47	0.0787343 61	1
GO:00026 99	positive regulation of immune effector process	0.0931910 42	0.0789820 79	1
GO:00148 97	striated muscle hypertrophy	0.0943377 71	0.0798044 48	1
GO:00301 48	sphingolipid biosynthetic process	0.0943377 71	0.0798044 48	1
GO:00356 01	protein deacylation	0.0943377 71	0.0798044 48	1
GO:00432 66	regulation of potassium ion transport	0.0943377 71	0.0798044 48	1
GO:00456 65	negative regulation of neuron differentiation	0.0950957 45	0.0801464 12	1
GO:00071 78	transmembrane receptor protein serine/threonine kinase signaling pathway	0.0956268 87	0.0801464 12	1
GO:00015 23	retinoid metabolic process	0.0958271 81	0.0801464 12	1
GO:00020 62	chondrocyte differentiation	0.0958271 81	0.0801464 12	1
GO:19027 50	negative regulation of cell cycle G2/M phase transition	0.0958271 81	0.0801464 12	1
GO:00015 02	cartilage condensation	0.0966023 03	0.0801464 12	1
GO:00020 29	desensitization of G protein-coupled receptor signaling pathway	0.0966023 03	0.0801464 12	1
GO:00031 77	pulmonary valve development	0.0966023 03	0.0801464 12	1
GO:00061 23	mitochondrial electron transport, cytochrome c to oxygen	0.0966023 03	0.0801464 12	1
GO:00066 62	glycerol ether metabolic process	0.0966023 03	0.0801464 12	1
GO:00091 10	vitamin biosynthetic process	0.0966023 03	0.0801464 12	1
GO:00097 13	catechol-containing compound biosynthetic process	0.0966023 03	0.0801464 12	1
GO:00108 29	negative regulation of glucose transmembrane transport	0.0966023 03	0.0801464 12	1
GO:00108 93	positive regulation of steroid biosynthetic process	0.0966023 03	0.0801464 12	1
GO:00148 21	phasic smooth muscle contraction	0.0966023 03	0.0801464 12	1
GO:00193 70	leukotriene biosynthetic process	0.0966023 03	0.0801464 12	1

GO:00196 46	aerobic electron transport chain	0.0966023 03	0.0801464 12	1
GO:00224 01	negative adaptation of signaling pathway	0.0966023 03	0.0801464 12	1
GO:00305 02	negative regulation of bone mineralization	0.0966023 03	0.0801464 12	1
GO:00353 57	peroxisome proliferator activated receptor signaling pathway	0.0966023 03	0.0801464 12	1
GO:00424 23	catecholamine biosynthetic process	0.0966023 03	0.0801464 12	1
GO:00436 51	linoleic acid metabolic process	0.0966023 03	0.0801464 12	1
GO:00465 14	ceramide catabolic process	0.0966023 03	0.0801464 12	1
GO:00467 16	muscle cell cellular homeostasis	0.0966023 03	0.0801464 12	1
GO:00517 97	regulation of hair follicle development	0.0966023 03	0.0801464 12	1
GO:00600 65	uterus development	0.0966023 03	0.0801464 12	1
GO:00607 13	labyrinthine layer morphogenesis	0.0966023 03	0.0801464 12	1
GO:00607 16	labyrinthine layer blood vessel development	0.0966023 03	0.0801464 12	1
GO:00612 13	positive regulation of mesonephros development	0.0966023 03	0.0801464 12	1
GO:00714 98	cellular response to fluid shear stress	0.0966023 03	0.0801464 12	1
GO:00725 74	hepatocyte proliferation	0.0966023 03	0.0801464 12	1
GO:00725 75	epithelial cell proliferation involved in liver morphogenesis	0.0966023 03	0.0801464 12	1
GO:00902 01	negative regulation of release of cytochrome c from mitochondria	0.0966023 03	0.0801464 12	1
GO:00902 80	positive regulation of calcium ion import	0.0966023 03	0.0801464 12	1
GO:19026 56	calcium ion import into cytosol	0.0966023 03	0.0801464 12	1
GO:19030 55	positive regulation of extracellular matrix organization	0.0966023 03	0.0801464 12	1
GO:19032 04	negative regulation of oxidative stress-induced neuron death	0.0966023 03	0.0801464 12	1
GO:19035 99	positive regulation of autophagy of mitochondrion	0.0966023 03	0.0801464 12	1

GO:19039 78	regulation of microglial cell activation	0.0966023 03	0.0801464 12	1
GO:19048 86	beta-catenin destruction complex disassembly	0.0966023 03	0.0801464 12	1
GO:20000 47	regulation of cell-cell adhesion mediated by cadherin	0.0966023 03	0.0801464 12	1
GO:20002 69	regulation of fibroblast apoptotic process	0.0966023 03	0.0801464 12	1
GO:00022 86	T cell activation involved in immune response	0.0973233 77	0.0806337 41	1
GO:00148 96	muscle hypertrophy	0.0973233 77	0.0806337 41	1
GO:20002 78	regulation of DNA biosynthetic process	0.0973233 77	0.0806337 41	1
GO:00028 21	positive regulation of adaptive immune response	0.0988262 62	0.0817292 14	1
GO:00066 64	glycolipid metabolic process	0.0988262 62	0.0817292 14	1
GO:00720 09	nephron epithelium development	0.0988262 62	0.0817292 14	1
GO:19018 00	positive regulation of proteasomal protein catabolic process	0.0988262 62	0.0817292 14	1
GO:00508 07	regulation of synapse organization	0.0989531 42	0.0817967 59	1
GO:00353 05	negative regulation of dephosphorylation	0.1003357 39	0.0823683 27	1
GO:00511 49	positive regulation of muscle cell differentiation	0.1003357 39	0.0823683 27	1
GO:00987 32	macromolecule deacylation	0.1003357 39	0.0823683 27	1
GO:19030 08	organelle disassembly	0.1003357 39	0.0823683 27	1
GO:19035 09	liposaccharide metabolic process	0.1003357 39	0.0823683 27	1
GO:00020 89	lens morphogenesis in camera-type eye	0.1009646 9	0.0823683 27	1
GO:00023 13	mature B cell differentiation involved in immune response	0.1009646 9	0.0823683 27	1
GO:00059 80	glycogen catabolic process	0.1009646 9	0.0823683 27	1
GO:00060 67	ethanol metabolic process	0.1009646 9	0.0823683 27	1
GO:00063 12	mitotic recombination	0.1009646 9	0.0823683 27	1

GO:00073 42	fusion of sperm to egg plasma membrane involved in single fertilization	0.1009646 9	0.0823683 27	1
GO:00230 58	adaptation of signaling pathway	0.1009646 9	0.0823683 27	1
GO:00329 28	regulation of superoxide anion generation	0.1009646 9	0.0823683 27	1
GO:00341 04	negative regulation of tissue remodeling	0.1009646 9	0.0823683 27	1
GO:00350 24	negative regulation of Rho protein signal transduction	0.1009646 9	0.0823683 27	1
GO:00355 84	calcium-mediated signaling using intracellular calcium source	0.1009646 9	0.0823683 27	1
GO:00423 59	vitamin D metabolic process	0.1009646 9	0.0823683 27	1
GO:00427 49	regulation of circadian sleep/wake cycle	0.1009646 9	0.0823683 27	1
GO:00456 55	regulation of monocyte differentiation	0.1009646 9	0.0823683 27	1
GO:00456 63	positive regulation of myoblast differentiation	0.1009646 9	0.0823683 27	1
GO:00460 58	cAMP metabolic process	0.1009646 9	0.0823683 27	1
GO:00508 02	circadian sleep/wake cycle, sleep	0.1009646 9	0.0823683 27	1
GO:00550 93	response to hyperoxia	0.1009646 9	0.0823683 27	1
GO:00603 52	cell adhesion molecule production	0.1009646 9	0.0823683 27	1
GO:00711 57	negative regulation of cell cycle arrest	0.1009646 9	0.0823683 27	1
GO:00713 79	cellular response to prostaglandin stimulus	0.1009646 9	0.0823683 27	1
GO:00725 76	liver morphogenesis	0.1009646 9	0.0823683 27	1
GO:00901 89	regulation of branching involved in ureteric bud morphogenesis	0.1009646 9	0.0823683 27	1
GO:19017 39	regulation of myoblast fusion	0.1009646 9	0.0823683 27	1
GO:00062 75	regulation of DNA replication	0.1018517 09	0.0830545 24	1
GO:00300 98	lymphocyte differentiation	0.1023409 33	0.0834158 67	1
GO:00022 23	stimulatory C-type lectin receptor signaling pathway	0.1033740 78	0.0842200 25	1

GO:0003279	cardiac septum development	0.104902751	0.084500609	1
GO:0016101	diterpenoid metabolic process	0.104902751	0.084500609	1
GO:0030004	cellular monovalent inorganic cation homeostasis	0.104902751	0.084500609	1
GO:0098693	regulation of synaptic vesicle cycle	0.104902751	0.084500609	1
GO:0000002	mitochondrial genome maintenance	0.105306242	0.084500609	1
GO:0001919	regulation of receptor recycling	0.105306242	0.084500609	1
GO:0006359	regulation of transcription by RNA polymerase III	0.105306242	0.084500609	1
GO:0006582	melanin metabolic process	0.105306242	0.084500609	1
GO:0007274	neuromuscular synaptic transmission	0.105306242	0.084500609	1
GO:0007413	axonal fasciculation	0.105306242	0.084500609	1
GO:0007617	mating behavior	0.105306242	0.084500609	1
GO:0009251	glucan catabolic process	0.105306242	0.084500609	1
GO:0010226	response to lithium ion	0.105306242	0.084500609	1
GO:0010288	response to lead ion	0.105306242	0.084500609	1
GO:0030539	male genitalia development	0.105306242	0.084500609	1
GO:0031639	plasminogen activation	0.105306242	0.084500609	1
GO:0032098	regulation of appetite	0.105306242	0.084500609	1
GO:0034643	establishment of mitochondrion localization, microtubule-mediated	0.105306242	0.084500609	1
GO:0035743	CD4-positive, alpha-beta T cell cytokine production	0.105306242	0.084500609	1
GO:0045723	positive regulation of fatty acid biosynthetic process	0.105306242	0.084500609	1
GO:0047497	mitochondrion transport along microtubule	0.105306242	0.084500609	1
GO:0051151	negative regulation of smooth muscle cell differentiation	0.105306242	0.084500609	1

GO:00604 45	branching involved in salivary gland morphogenesis	0.1053062 42	0.0845006 09	1
GO:00605 47	negative regulation of necrotic cell death	0.1053062 42	0.0845006 09	1
GO:00705 84	mitochondrion morphogenesis	0.1053062 42	0.0845006 09	1
GO:00709 35	3'-UTR-mediated mRNA stabilization	0.1053062 42	0.0845006 09	1
GO:00726 77	eosinophil migration	0.1053062 42	0.0845006 09	1
GO:00903 43	positive regulation of cell aging	0.1053062 42	0.0845006 09	1
GO:01060 30	neuron projection fasciculation	0.1053062 42	0.0845006 09	1
GO:19019 84	negative regulation of protein acetylation	0.1053062 42	0.0845006 09	1
GO:19020 01	fatty acid transmembrane transport	0.1053062 42	0.0845006 09	1
GO:19022 54	negative regulation of intrinsic apoptotic signaling pathway by p53 class mediator	0.1053062 42	0.0845006 09	1
GO:19035 89	positive regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis	0.1053062 42	0.0845006 09	1
GO:20008 10	regulation of bicellular tight junction assembly	0.1053062 42	0.0845006 09	1
GO:00060 96	glycolytic process	0.1064376 31	0.0853706 08	1
GO:00328 72	regulation of stress-activated MAPK cascade	0.1068550 21	0.0856674 12	1
GO:00301 11	regulation of Wnt signaling pathway	0.1077105 89	0.0863150 92	1
GO:00022 20	innate immune response activating cell surface receptor signaling pathway	0.1079786 26	0.0864150 74	1
GO:00067 57	ATP generation from ADP	0.1079786 26	0.0864150 74	1
GO:00229 04	respiratory electron transport chain	0.1079786 26	0.0864150 74	1
GO:00064 02	mRNA catabolic process	0.1084880 44	0.0867843 77	1
GO:00027 58	innate immune response-activating signal transduction	0.1095256 44	0.0868508 22	1
GO:00149 02	myotube differentiation	0.1095256 44	0.0868508 22	1
GO:00436 66	regulation of phosphoprotein phosphatase activity	0.1095256 44	0.0868508 22	1

GO:00017 59	organ induction	0.1096270 58	0.0868508 22	1
GO:00024 38	acute inflammatory response to antigenic stimulus	0.1096270 58	0.0868508 22	1
GO:00027 19	negative regulation of cytokine production involved in immune response	0.1096270 58	0.0868508 22	1
GO:00070 95	mitotic G2 DNA damage checkpoint	0.1096270 58	0.0868508 22	1
GO:00108 69	regulation of receptor biosynthetic process	0.1096270 58	0.0868508 22	1
GO:00148 50	response to muscle activity	0.1096270 58	0.0868508 22	1
GO:00328 91	negative regulation of organic acid transport	0.1096270 58	0.0868508 22	1
GO:00336 22	integrin activation	0.1096270 58	0.0868508 22	1
GO:00346 95	response to prostaglandin E	0.1096270 58	0.0868508 22	1
GO:00442 47	cellular polysaccharide catabolic process	0.1096270 58	0.0868508 22	1
GO:00443 21	response to leptin	0.1096270 58	0.0868508 22	1
GO:00443 46	fibroblast apoptotic process	0.1096270 58	0.0868508 22	1
GO:00445 50	secondary metabolite biosynthetic process	0.1096270 58	0.0868508 22	1
GO:00458 21	positive regulation of glycolytic process	0.1096270 58	0.0868508 22	1
GO:00466 28	positive regulation of insulin receptor signaling pathway	0.1096270 58	0.0868508 22	1
GO:00513 49	positive regulation of lyase activity	0.1096270 58	0.0868508 22	1
GO:00987 43	cell aggregation	0.1096270 58	0.0868508 22	1
GO:19033 06	negative regulation of regulated secretory pathway	0.1096270 58	0.0868508 22	1
GO:19034 29	regulation of cell maturation	0.1096270 58	0.0868508 22	1
GO:00328 86	regulation of microtubule-based process	0.1098807 22	0.0869375 93	1
GO:00508 03	regulation of synapse structure or activity	0.1098807 22	0.0869375 93	1
GO:00703 02	regulation of stress-activated protein kinase signaling cascade	0.1098807 22	0.0869375 93	1

GO:00512 09	release of sequestered calcium ion into cytosol	0.1110785 9	0.0878469 34	1
GO:00456 66	positive regulation of neuron differentiation	0.1116234 35	0.0882392 61	1
GO:19033 20	regulation of protein modification by small protein conjugation or removal	0.1119163 11	0.0884321 48	1
GO:00511 53	regulation of striated muscle cell differentiation	0.1126373 75	0.0889242 43	1
GO:00512 83	negative regulation of sequestering of calcium ion	0.1126373 75	0.0889242 43	1
GO:00004 23	mitophagy	0.1139272 35	0.0892803 53	1
GO:00020 53	positive regulation of mesenchymal cell proliferation	0.1139272 35	0.0892803 53	1
GO:00020 92	positive regulation of receptor internalization	0.1139272 35	0.0892803 53	1
GO:00033 09	type B pancreatic cell differentiation	0.1139272 35	0.0892803 53	1
GO:00075 30	sex determination	0.1139272 35	0.0892803 53	1
GO:00148 29	vascular associated smooth muscle contraction	0.1139272 35	0.0892803 53	1
GO:00224 10	circadian sleep/wake cycle process	0.1139272 35	0.0892803 53	1
GO:00321 04	regulation of response to extracellular stimulus	0.1139272 35	0.0892803 53	1
GO:00321 07	regulation of response to nutrient levels	0.1139272 35	0.0892803 53	1
GO:00456 62	negative regulation of myoblast differentiation	0.1139272 35	0.0892803 53	1
GO:00466 97	decidualization	0.1139272 35	0.0892803 53	1
GO:00508 57	positive regulation of antigen receptor-mediated signaling pathway	0.1139272 35	0.0892803 53	1
GO:00612 17	regulation of mesonephros development	0.1139272 35	0.0892803 53	1
GO:00614 36	establishment of skin barrier	0.1139272 35	0.0892803 53	1
GO:00716 77	positive regulation of mononuclear cell migration	0.1139272 35	0.0892803 53	1
GO:19055 64	positive regulation of vascular endothelial cell proliferation	0.1139272 35	0.0892803 53	1
GO:20003 11	regulation of AMPA receptor activity	0.1139272 35	0.0892803 53	1

GO:00515 88	regulation of neurotransmitter transport	0.1142019 06	0.0894568 59	1
GO:00076 13	memory	0.1157720 95	0.0905692	1
GO:00160 79	synaptic vesicle exocytosis	0.1157720 95	0.0905692	1
GO:00512 82	regulation of sequestering of calcium ion	0.1157720 95	0.0905692	1
GO:00432 44	regulation of protein-containing complex disassembly	0.1173478 51	0.0913288 74	1
GO:19902 66	neutrophil migration	0.1173478 51	0.0913288 74	1
GO:00435 43	protein acylation	0.1181096 92	0.0913288 74	1
GO:00002 72	polysaccharide catabolic process	0.1182068 71	0.0913288 74	1
GO:00017 83	B cell apoptotic process	0.1182068 71	0.0913288 74	1
GO:00019 45	lymph vessel development	0.1182068 71	0.0913288 74	1
GO:00022 27	innate immune response in mucosa	0.1182068 71	0.0913288 74	1
GO:00303 18	melanocyte differentiation	0.1182068 71	0.0913288 74	1
GO:00308 10	positive regulation of nucleotide biosynthetic process	0.1182068 71	0.0913288 74	1
GO:00316 64	regulation of lipopolysaccharide-mediated signaling pathway	0.1182068 71	0.0913288 74	1
GO:00332 33	regulation of protein sumoylation	0.1182068 71	0.0913288 74	1
GO:00341 14	regulation of heterotypic cell-cell adhesion	0.1182068 71	0.0913288 74	1
GO:00421 04	positive regulation of activated T cell proliferation	0.1182068 71	0.0913288 74	1
GO:00427 30	fibrinolysis	0.1182068 71	0.0913288 74	1
GO:00435 67	regulation of insulin-like growth factor receptor signaling pathway	0.1182068 71	0.0913288 74	1
GO:00440 68	modulation by symbiont of host cellular process	0.1182068 71	0.0913288 74	1
GO:00450 26	plasma membrane fusion	0.1182068 71	0.0913288 74	1
GO:00486 43	positive regulation of skeletal muscle tissue development	0.1182068 71	0.0913288 74	1

GO:00511 56	glucose 6-phosphate metabolic process	0.1182068 71	0.0913288 74	1
GO:00516 54	establishment of mitochondrion localization	0.1182068 71	0.0913288 74	1
GO:00550 83	monovalent inorganic anion homeostasis	0.1182068 71	0.0913288 74	1
GO:00603 43	trabecula formation	0.1182068 71	0.0913288 74	1
GO:00605 61	apoptotic process involved in morphogenesis	0.1182068 71	0.0913288 74	1
GO:00607 06	cell differentiation involved in embryonic placenta development	0.1182068 71	0.0913288 74	1
GO:00900 23	positive regulation of neutrophil chemotaxis	0.1182068 71	0.0913288 74	1
GO:00970 66	response to thyroid hormone	0.1182068 71	0.0913288 74	1
GO:19003 73	positive regulation of purine nucleotide biosynthetic process	0.1182068 71	0.0913288 74	1
GO:19036 49	regulation of cytoplasmic transport	0.1182068 71	0.0913288 74	1
GO:19055 23	positive regulation of macrophage migration	0.1182068 71	0.0913288 74	1
GO:00319 29	TOR signaling	0.1205157 13	0.0929539 69	1
GO:00460 31	ADP metabolic process	0.1205157 13	0.0929539 69	1
GO:00511 01	regulation of DNA binding	0.1205157 13	0.0929539 69	1
GO:00512 08	sequestering of calcium ion	0.1205157 13	0.0929539 69	1
GO:00028 33	positive regulation of response to biotic stimulus	0.1212539 85	0.0934835 51	1
GO:00018 38	embryonic epithelial tube formation	0.1221076 43	0.0936598 13	1
GO:00030 14	renal system process	0.1221076 43	0.0936598 13	1
GO:00067 06	steroid catabolic process	0.1224660 63	0.0936598 13	1
GO:00080 53	mitochondrial fusion	0.1224660 63	0.0936598 13	1
GO:00090 65	glutamine family amino acid catabolic process	0.1224660 63	0.0936598 13	1
GO:00181 26	protein hydroxylation	0.1224660 63	0.0936598 13	1

GO:00319 54	positive regulation of protein autophosphorylation	0.1224660 63	0.0936598 13	1
GO:00328 97	negative regulation of viral transcription	0.1224660 63	0.0936598 13	1
GO:00360 37	CD8-positive, alpha-beta T cell activation	0.1224660 63	0.0936598 13	1
GO:00509 96	positive regulation of lipid catabolic process	0.1224660 63	0.0936598 13	1
GO:00519 53	negative regulation of amine transport	0.1224660 63	0.0936598 13	1
GO:00605 44	regulation of necroptotic process	0.1224660 63	0.0936598 13	1
GO:00620 98	regulation of programmed necrotic cell death	0.1224660 63	0.0936598 13	1
GO:00715 14	genetic imprinting	0.1224660 63	0.0936598 13	1
GO:00725 39	T-helper 17 cell differentiation	0.1224660 63	0.0936598 13	1
GO:00901 40	regulation of mitochondrial fission	0.1224660 63	0.0936598 13	1
GO:19000 78	positive regulation of cellular response to insulin stimulus	0.1224660 63	0.0936598 13	1
GO:19001 20	regulation of receptor binding	0.1224660 63	0.0936598 13	1
GO:19016 23	regulation of lymphocyte chemotaxis	0.1224660 63	0.0936598 13	1
GO:00302 17	T cell differentiation	0.1233673 93	0.0943092 74	1
GO:00017 04	formation of primary germ layer	0.1253070 69	0.0954890 44	1
GO:00140 66	regulation of phosphatidylinositol 3-kinase signaling	0.1253070 69	0.0954890 44	1
GO:00510 53	negative regulation of DNA metabolic process	0.1253070 69	0.0954890 44	1
GO:19030 52	positive regulation of proteolysis involved in cellular protein catabolic process	0.1253070 69	0.0954890 44	1
GO:00004 70	maturation of LSU-rRNA	0.1267049 07	0.0954890 44	1
GO:00019 64	startle response	0.1267049 07	0.0954890 44	1
GO:00023 35	mature B cell differentiation	0.1267049 07	0.0954890 44	1
GO:00031 80	aortic valve morphogenesis	0.1267049 07	0.0954890 44	1

GO:0006929	substrate-dependent cell migration	0.126704907	0.095489044	1
GO:0007205	protein kinase C-activating G protein-coupled receptor signaling pathway	0.126704907	0.095489044	1
GO:0022011	myelination in peripheral nervous system	0.126704907	0.095489044	1
GO:0030194	positive regulation of blood coagulation	0.126704907	0.095489044	1
GO:0031069	hair follicle morphogenesis	0.126704907	0.095489044	1
GO:0031440	regulation of mRNA 3'-end processing	0.126704907	0.095489044	1
GO:0032292	peripheral nervous system axon ensheathment	0.126704907	0.095489044	1
GO:0033561	regulation of water loss via skin	0.126704907	0.095489044	1
GO:0035883	enteroendocrine cell differentiation	0.126704907	0.095489044	1
GO:0042745	circadian sleep/wake cycle	0.126704907	0.095489044	1
GO:0044331	cell-cell adhesion mediated by cadherin	0.126704907	0.095489044	1
GO:0045745	positive regulation of G protein-coupled receptor signaling pathway	0.126704907	0.095489044	1
GO:0048753	pigment granule organization	0.126704907	0.095489044	1
GO:0060143	positive regulation of syncytium formation by plasma membrane fusion	0.126704907	0.095489044	1
GO:0071168	protein localization to chromatin	0.126704907	0.095489044	1
GO:0071280	cellular response to copper ion	0.126704907	0.095489044	1
GO:0086013	membrane repolarization during cardiac muscle cell action potential	0.126704907	0.095489044	1
GO:0099560	synaptic membrane adhesion	0.126704907	0.095489044	1
GO:1900048	positive regulation of hemostasis	0.126704907	0.095489044	1
GO:1900101	regulation of endoplasmic reticulum unfolded protein response	0.126704907	0.095489044	1
GO:1902932	positive regulation of alcohol biosynthetic process	0.126704907	0.095489044	1
GO:1903579	negative regulation of ATP metabolic process	0.126704907	0.095489044	1

GO:19050 63	regulation of vascular associated smooth muscle cell differentiation	0.1267049 07	0.0954890 44	1
GO:19055 63	negative regulation of vascular endothelial cell proliferation	0.1267049 07	0.0954890 44	1
GO:20001 91	regulation of fatty acid transport	0.1267049 07	0.0954890 44	1
GO:20004 63	positive regulation of excitatory postsynaptic potential	0.1267049 07	0.0954890 44	1
GO:00516 07	defense response to virus	0.1287098 34	0.0969386 75	1
GO:00091 50	purine ribonucleotide metabolic process	0.1287355 76	0.0969386 75	1
GO:00421 80	cellular ketone metabolic process	0.1308698 97	0.0979341 17	1
GO:00082 09	androgen metabolic process	0.1309235	0.0979341 17	1
GO:00094 35	NAD biosynthetic process	0.1309235	0.0979341 17	1
GO:00323 73	positive regulation of sterol transport	0.1309235	0.0979341 17	1
GO:00323 76	positive regulation of cholesterol transport	0.1309235	0.0979341 17	1
GO:00330 32	regulation of myeloid cell apoptotic process	0.1309235	0.0979341 17	1
GO:00362 96	response to increased oxygen levels	0.1309235	0.0979341 17	1
GO:00426 34	regulation of hair cycle	0.1309235	0.0979341 17	1
GO:00431 53	entrainment of circadian clock by photoperiod	0.1309235	0.0979341 17	1
GO:00458 22	negative regulation of heart contraction	0.1309235	0.0979341 17	1
GO:00508 20	positive regulation of coagulation	0.1309235	0.0979341 17	1
GO:00509 01	leukocyte tethering or rolling	0.1309235	0.0979341 17	1
GO:00550 75	potassium ion homeostasis	0.1309235	0.0979341 17	1
GO:00604 41	epithelial tube branching involved in lung morphogenesis	0.1309235	0.0979341 17	1
GO:00716 24	positive regulation of granulocyte chemotaxis	0.1309235	0.0979341 17	1
GO:00801 54	regulation of fertilization	0.1309235	0.0979341 17	1

GO:00192 18	regulation of steroid metabolic process	0.1317658 03	0.0984420 94	1
GO:00324 34	regulation of proteasomal ubiquitin-dependent protein catabolic process	0.1317658 03	0.0984420 94	1
GO:00456 67	regulation of osteoblast differentiation	0.1317658 03	0.0984420 94	1
GO:00435 47	positive regulation of GTPase activity	0.1329652 82	0.0992972 26	1
GO:00614 48	connective tissue development	0.1330428 79	0.0993141 86	1
GO:00424 76	odontogenesis	0.1333924 74	0.0995340 91	1
GO:00061 65	nucleoside diphosphate phosphorylation	0.1350237 76	0.1000816 99	1
GO:00069 97	nucleus organization	0.1350237 76	0.1000816 99	1
GO:00421 77	negative regulation of protein catabolic process	0.1350237 76	0.1000816 99	1
GO:00721 75	epithelial tube formation	0.1350237 76	0.1000816 99	1
GO:00034 01	axis elongation	0.1351219 38	0.1000816 99	1
GO:00071 76	regulation of epidermal growth factor-activated receptor activity	0.1351219 38	0.1000816 99	1
GO:00105 86	miRNA metabolic process	0.1351219 38	0.1000816 99	1
GO:00107 58	regulation of macrophage chemotaxis	0.1351219 38	0.1000816 99	1
GO:00190 98	reproductive behavior	0.1351219 38	0.1000816 99	1
GO:00331 37	negative regulation of peptidyl-serine phosphorylation	0.1351219 38	0.1000816 99	1
GO:00336 88	regulation of osteoblast proliferation	0.1351219 38	0.1000816 99	1
GO:00356 66	TRIF-dependent toll-like receptor signaling pathway	0.1351219 38	0.1000816 99	1
GO:00482 65	response to pain	0.1351219 38	0.1000816 99	1
GO:00601 42	regulation of syncytium formation by plasma membrane fusion	0.1351219 38	0.1000816 99	1
GO:00701 68	negative regulation of biomineral tissue development	0.1351219 38	0.1000816 99	1
GO:00707 23	response to cholesterol	0.1351219 38	0.1000816 99	1

GO:01101 50	negative regulation of biomineralization	0.1351219 38	0.1000816 99	1
GO:01200 33	negative regulation of plasma membrane bounded cell projection assembly	0.1351219 38	0.1000816 99	1
GO:00713 33	cellular response to glucose stimulus	0.1366596 27	0.1011792 14	1
GO:00091 65	nucleotide biosynthetic process	0.1374268 59	0.1017056 38	1
GO:00469 39	nucleotide phosphorylation	0.1382999 47	0.1022681 3	1
GO:00508 53	B cell receptor signaling pathway	0.1382999 47	0.1022681 3	1
GO:00028 28	regulation of type 2 immune response	0.1393003 14	0.1023387 14	1
GO:00091 54	purine ribonucleotide catabolic process	0.1393003 14	0.1023387 14	1
GO:00140 44	Schwann cell development	0.1393003 14	0.1023387 14	1
GO:00343 68	protein-lipid complex remodeling	0.1393003 14	0.1023387 14	1
GO:00343 69	plasma lipoprotein particle remodeling	0.1393003 14	0.1023387 14	1
GO:00431 71	peptide catabolic process	0.1393003 14	0.1023387 14	1
GO:00459 40	positive regulation of steroid metabolic process	0.1393003 14	0.1023387 14	1
GO:00487 10	regulation of astrocyte differentiation	0.1393003 14	0.1023387 14	1
GO:00702 29	negative regulation of lymphocyte apoptotic process	0.1393003 14	0.1023387 14	1
GO:00715 39	protein localization to centrosome	0.1393003 14	0.1023387 14	1
GO:00715 49	cellular response to dexamethasone stimulus	0.1393003 14	0.1023387 14	1
GO:00725 38	T-helper 17 type immune response	0.1393003 14	0.1023387 14	1
GO:19007 45	positive regulation of p38MAPK cascade	0.1393003 14	0.1023387 14	1
GO:19022 30	negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage	0.1393003 14	0.1023387 14	1
GO:19026 24	positive regulation of neutrophil migration	0.1393003 14	0.1023387 14	1
GO:19037 92	negative regulation of anion transport	0.1393003 14	0.1023387 14	1

GO:00091 35	purine nucleoside diphosphate metabolic process	0.1399446 56	0.1026870 12	1
GO:00091 79	purine ribonucleoside diphosphate metabolic process	0.1399446 56	0.1026870 12	1
GO:00713 31	cellular response to hexose stimulus	0.1399446 56	0.1026870 12	1
GO:00064 01	RNA catabolic process	0.1407224 09	0.1031923 38	1
GO:19012 93	nucleoside phosphate biosynthetic process	0.1407473 86	0.1031923 38	1
GO:00713 26	cellular response to monosaccharide stimulus	0.1415936 75	0.1036880 91	1
GO:19030 38	negative regulation of leukocyte cell-cell adhesion	0.1415936 75	0.1036880 91	1
GO:00092 59	ribonucleotide metabolic process	0.1415954 68	0.1036880 91	1
GO:00020 82	regulation of oxidative phosphorylation	0.1434587 25	0.1040837 16	1
GO:00027 24	regulation of T cell cytokine production	0.1434587 25	0.1040837 16	1
GO:00031 76	aortic valve development	0.1434587 25	0.1040837 16	1
GO:00092 61	ribonucleotide catabolic process	0.1434587 25	0.1040837 16	1
GO:00193 59	nicotinamide nucleotide biosynthetic process	0.1434587 25	0.1040837 16	1
GO:00193 63	pyridine nucleotide biosynthetic process	0.1434587 25	0.1040837 16	1
GO:00323 50	regulation of hormone metabolic process	0.1434587 25	0.1040837 16	1
GO:00343 67	protein-containing complex remodeling	0.1434587 25	0.1040837 16	1
GO:00346 94	response to prostaglandin	0.1434587 25	0.1040837 16	1
GO:00381 28	ERBB2 signaling pathway	0.1434587 25	0.1040837 16	1
GO:00427 44	hydrogen peroxide catabolic process	0.1434587 25	0.1040837 16	1
GO:00448 18	mitotic G2/M transition checkpoint	0.1434587 25	0.1040837 16	1
GO:00463 20	regulation of fatty acid oxidation	0.1434587 25	0.1040837 16	1
GO:00469 49	fatty-acyl-CoA biosynthetic process	0.1434587 25	0.1040837 16	1

GO:00487 30	epidermis morphogenesis	0.1434587 25	0.1040837 16	1
GO:00487 41	skeletal muscle fiber development	0.1434587 25	0.1040837 16	1
GO:00488 41	regulation of axon extension involved in axon guidance	0.1434587 25	0.1040837 16	1
GO:00508 49	negative regulation of calcium-mediated signaling	0.1434587 25	0.1040837 16	1
GO:00508 69	negative regulation of B cell activation	0.1434587 25	0.1040837 16	1
GO:00610 36	positive regulation of cartilage development	0.1434587 25	0.1040837 16	1
GO:00713 53	cellular response to interleukin-4	0.1434587 25	0.1040837 16	1
GO:19019 76	regulation of cell cycle checkpoint	0.1434587 25	0.1040837 16	1
GO:19039 59	regulation of anion transmembrane transport	0.1434587 25	0.1040837 16	1
GO:00091 85	ribonucleoside diphosphate metabolic process	0.1449043 29	0.1050904 09	1
GO:00062 60	DNA replication	0.1452169 63	0.1052749 49	1
GO:00072 66	Rho protein signal transduction	0.1465658 09	0.1061499 87	1
GO:00028 61	regulation of inflammatory response to antigenic stimulus	0.1475972 65	0.1061499 87	1
GO:00093 03	rRNA transcription	0.1475972 65	0.1061499 87	1
GO:00096 48	photoperiodism	0.1475972 65	0.1061499 87	1
GO:00104 64	regulation of mesenchymal cell proliferation	0.1475972 65	0.1061499 87	1
GO:00301 49	sphingolipid catabolic process	0.1475972 65	0.1061499 87	1
GO:00400 20	regulation of meiotic nuclear division	0.1475972 65	0.1061499 87	1
GO:00425 73	retinoic acid metabolic process	0.1475972 65	0.1061499 87	1
GO:00427 55	eating behavior	0.1475972 65	0.1061499 87	1
GO:00459 20	negative regulation of exocytosis	0.1475972 65	0.1061499 87	1
GO:00480 11	neurotrophin TRK receptor signaling pathway	0.1475972 65	0.1061499 87	1

GO:00483 84	retinoic acid receptor signaling pathway	0.1475972 65	0.1061499 87	1
GO:00506 85	positive regulation of mRNA processing	0.1475972 65	0.1061499 87	1
GO:00519 84	positive regulation of chromosome segregation	0.1475972 65	0.1061499 87	1
GO:00900 22	regulation of neutrophil chemotaxis	0.1475972 65	0.1061499 87	1
GO:01202 55	olefinic compound biosynthetic process	0.1475972 65	0.1061499 87	1
GO:19013 80	negative regulation of potassium ion transmembrane transport	0.1475972 65	0.1061499 87	1
GO:19017 97	negative regulation of signal transduction by p53 class mediator	0.1475972 65	0.1061499 87	1
GO:19050 48	regulation of metalloproteinase activity	0.1475972 65	0.1061499 87	1
GO:19055 08	protein localization to microtubule organizing center	0.1475972 65	0.1061499 87	1
GO:00300 10	establishment of cell polarity	0.1482312 89	0.1065636 14	1
GO:00464 25	regulation of receptor signaling pathway via JAK-STAT	0.1499006 92	0.1076781 89	1
GO:00720 73	kidney epithelium development	0.1499006 92	0.1076781 89	1
GO:00196 93	ribose phosphate metabolic process	0.1513417 89	0.1078264 57	1
GO:00720 06	nephron development	0.1515739 44	0.1078264 57	1
GO:00018 81	receptor recycling	0.1517160 27	0.1078264 57	1
GO:00027 56	MyD88-independent toll-like receptor signaling pathway	0.1517160 27	0.1078264 57	1
GO:00070 94	mitotic spindle assembly checkpoint	0.1517160 27	0.1078264 57	1
GO:00072 02	activation of phospholipase C activity	0.1517160 27	0.1078264 57	1
GO:00081 56	negative regulation of DNA replication	0.1517160 27	0.1078264 57	1
GO:00086 08	attachment of spindle microtubules to kinetochore	0.1517160 27	0.1078264 57	1
GO:00096 49	entrainment of circadian clock	0.1517160 27	0.1078264 57	1
GO:00107 62	regulation of fibroblast migration	0.1517160 27	0.1078264 57	1

GO:00181 49	peptide cross-linking	0.1517160 27	0.1078264 57	1
GO:00192 28	neuronal action potential	0.1517160 27	0.1078264 57	1
GO:00308 51	granulocyte differentiation	0.1517160 27	0.1078264 57	1
GO:00315 77	spindle checkpoint	0.1517160 27	0.1078264 57	1
GO:00331 98	response to ATP	0.1517160 27	0.1078264 57	1
GO:00357 74	positive regulation of insulin secretion involved in cellular response to glucose stimulus	0.1517160 27	0.1078264 57	1
GO:00435 16	regulation of DNA damage response, signal transduction by p53 class mediator	0.1517160 27	0.1078264 57	1
GO:00466 85	response to arsenic-containing substance	0.1517160 27	0.1078264 57	1
GO:00485 36	spleen development	0.1517160 27	0.1078264 57	1
GO:00488 54	brain morphogenesis	0.1517160 27	0.1078264 57	1
GO:00507 15	positive regulation of cytokine secretion	0.1517160 27	0.1078264 57	1
GO:00550 94	response to lipoprotein particle	0.1517160 27	0.1078264 57	1
GO:00613 84	heart trabecula morphogenesis	0.1517160 27	0.1078264 57	1
GO:00701 02	interleukin-6-mediated signaling pathway	0.1517160 27	0.1078264 57	1
GO:00711 73	spindle assembly checkpoint	0.1517160 27	0.1078264 57	1
GO:00711 74	mitotic spindle checkpoint	0.1517160 27	0.1078264 57	1
GO:20003 52	negative regulation of endothelial cell apoptotic process	0.1517160 27	0.1078264 57	1
GO:00022 18	activation of innate immune response	0.1532509 7	0.1088318 67	1
GO:00027 00	regulation of production of molecular mediator of immune response	0.1532509 7	0.1088318 67	1
GO:00726 59	protein localization to plasma membrane	0.1542953 08	0.1095305 22	1
GO:00713 22	cellular response to carbohydrate stimulus	0.1549316 95	0.1096064 92	1
GO:00160 54	organic acid catabolic process	0.1554427 02	0.1096064 92	1

GO:00463 95	carboxylic acid catabolic process	0.1554427 02	0.1096064 92	1
GO:00067 39	NADP metabolic process	0.1558151 05	0.1096064 92	1
GO:00074 35	salivary gland morphogenesis	0.1558151 05	0.1096064 92	1
GO:00102 59	multicellular organism aging	0.1558151 05	0.1096064 92	1
GO:00149 04	myotube cell development	0.1558151 05	0.1096064 92	1
GO:00193 62	pyridine nucleotide metabolic process	0.1558151 05	0.1096064 92	1
GO:00309 47	regulation of vascular endothelial growth factor receptor signaling pathway	0.1558151 05	0.1096064 92	1
GO:00322 28	regulation of synaptic transmission, GABAergic	0.1558151 05	0.1096064 92	1
GO:00327 35	positive regulation of interleukin-12 production	0.1558151 05	0.1096064 92	1
GO:00336 87	osteoblast proliferation	0.1558151 05	0.1096064 92	1
GO:00363 14	response to sterol	0.1558151 05	0.1096064 92	1
GO:00396 94	viral RNA genome replication	0.1558151 05	0.1096064 92	1
GO:00424 62	eye photoreceptor cell development	0.1558151 05	0.1096064 92	1
GO:00459 22	negative regulation of fatty acid metabolic process	0.1558151 05	0.1096064 92	1
GO:00464 96	nicotinamide nucleotide metabolic process	0.1558151 05	0.1096064 92	1
GO:00703 06	lens fiber cell differentiation	0.1558151 05	0.1096064 92	1
GO:00706 70	response to interleukin-4	0.1558151 05	0.1096064 92	1
GO:00725 25	pyridine-containing compound biosynthetic process	0.1558151 05	0.1096064 92	1
GO:19000 16	negative regulation of cytokine production involved in inflammatory response	0.1558151 05	0.1096064 92	1
GO:19010 20	negative regulation of calcium ion transmembrane transporter activity	0.1558151 05	0.1096064 92	1
GO:19012 23	negative regulation of NIK/NF-kappaB signaling	0.1558151 05	0.1096064 92	1
GO:00516 56	establishment of organelle localization	0.1558560 95	0.1096064 92	1

GO:00443 44	cellular response to fibroblast growth factor stimulus	0.1566160 46	0.1100126 61	1
GO:00466 31	alpha-beta T cell activation	0.1566160 46	0.1100126 61	1
GO:00488 13	dendrite morphogenesis	0.1566160 46	0.1100126 61	1
GO:00508 08	synapse organization	0.1567650 94	0.1100746 26	1
GO:00070 43	cell-cell junction assembly	0.1583039 5	0.1110689 54	1
GO:00464 67	membrane lipid biosynthetic process	0.1583039 5	0.1110689 54	1
GO:00004 60	maturation of 5.8S rRNA	0.1598945 93	0.1116654 02	1
GO:00027 01	negative regulation of production of molecular mediator of immune response	0.1598945 93	0.1116654 02	1
GO:00033 82	epithelial cell morphogenesis	0.1598945 93	0.1116654 02	1
GO:00060 07	glucose catabolic process	0.1598945 93	0.1116654 02	1
GO:00100 92	specification of animal organ identity	0.1598945 93	0.1116654 02	1
GO:00311 28	developmental induction	0.1598945 93	0.1116654 02	1
GO:00332 80	response to vitamin D	0.1598945 93	0.1116654 02	1
GO:00458 41	negative regulation of mitotic metaphase/anaphase transition	0.1598945 93	0.1116654 02	1
GO:00466 76	negative regulation of insulin secretion	0.1598945 93	0.1116654 02	1
GO:00509 31	pigment cell differentiation	0.1598945 93	0.1116654 02	1
GO:00714 02	cellular response to lipoprotein particle stimulus	0.1598945 93	0.1116654 02	1
GO:19013 85	regulation of voltage-gated calcium channel activity	0.1598945 93	0.1116654 02	1
GO:00316 44	regulation of nervous system process	0.1599953 35	0.1116926 5	1
GO:00061 19	oxidative phosphorylation	0.1616901 29	0.1127887 56	1
GO:19033 64	positive regulation of cellular protein catabolic process	0.1616901 29	0.1127887 56	1
GO:00302 12	hyaluronan metabolic process	0.1639545 82	0.1140167 18	1

GO:00457 30	respiratory burst	0.1639545 82	0.1140167 18	1
GO:00488 46	axon extension involved in axon guidance	0.1639545 82	0.1140167 18	1
GO:00972 42	amyloid-beta clearance	0.1639545 82	0.1140167 18	1
GO:19021 00	negative regulation of metaphase/anaphase transition of cell cycle	0.1639545 82	0.1140167 18	1
GO:19022 84	neuron projection extension involved in neuron projection guidance	0.1639545 82	0.1140167 18	1
GO:19035 14	release of sequestered calcium ion into cytosol by endoplasmic reticulum	0.1639545 82	0.1140167 18	1
GO:19053 14	semi-lunar valve development	0.1639545 82	0.1140167 18	1
GO:19048 92	regulation of receptor signaling pathway via STAT	0.1650896 61	0.1147619 66	1
GO:00022 24	toll-like receptor signaling pathway	0.1667942 59	0.1158578 97	1
GO:00060 90	pyruvate metabolic process	0.1667942 59	0.1158578 97	1
GO:00023 85	mucosal immune response	0.1679951 64	0.1160682 81	1
GO:00031 56	regulation of animal organ formation	0.1679951 64	0.1160682 81	1
GO:00032 98	physiological muscle hypertrophy	0.1679951 64	0.1160682 81	1
GO:00033 01	physiological cardiac muscle hypertrophy	0.1679951 64	0.1160682 81	1
GO:00060 84	acetyl-CoA metabolic process	0.1679951 64	0.1160682 81	1
GO:00072 23	Wnt signaling pathway, calcium modulating pathway	0.1679951 64	0.1160682 81	1
GO:00106 61	positive regulation of muscle cell apoptotic process	0.1679951 64	0.1160682 81	1
GO:00327 33	positive regulation of interleukin-10 production	0.1679951 64	0.1160682 81	1
GO:00459 23	positive regulation of fatty acid metabolic process	0.1679951 64	0.1160682 81	1
GO:00464 66	membrane lipid catabolic process	0.1679951 64	0.1160682 81	1
GO:00519 30	regulation of sensory perception of pain	0.1679951 64	0.1160682 81	1
GO:00610 49	cell growth involved in cardiac muscle cell development	0.1679951 64	0.1160682 81	1

GO:19035 23	negative regulation of blood circulation	0.1679951 64	0.1160682 81	1
GO:19058 98	positive regulation of response to endoplasmic reticulum stress	0.1679951 64	0.1160682 81	1
GO:00016 78	cellular glucose homeostasis	0.1685019 84	0.1162852 43	1
GO:00028 22	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	0.1685019 84	0.1162852 43	1
GO:00717 74	response to fibroblast growth factor	0.1685019 84	0.1162852 43	1
GO:00027 06	regulation of lymphocyte mediated immunity	0.1702127 7	0.1174210 93	1
GO:00091 32	nucleoside diphosphate metabolic process	0.1719265 46	0.1179012 15	1
GO:00016 62	behavioral fear response	0.1720164 33	0.1179012 15	1
GO:00066 56	phosphatidylcholine biosynthetic process	0.1720164 33	0.1179012 15	1
GO:00067 78	porphyrin-containing compound metabolic process	0.1720164 33	0.1179012 15	1
GO:00074 31	salivary gland development	0.1720164 33	0.1179012 15	1
GO:00104 53	regulation of cell fate commitment	0.1720164 33	0.1179012 15	1
GO:00308 66	cortical actin cytoskeleton organization	0.1720164 33	0.1179012 15	1
GO:00311 11	negative regulation of microtubule polymerization or depolymerization	0.1720164 33	0.1179012 15	1
GO:00326 60	regulation of interleukin-17 production	0.1720164 33	0.1179012 15	1
GO:00381 79	neurotrophin signaling pathway	0.1720164 33	0.1179012 15	1
GO:00420 92	type 2 immune response	0.1720164 33	0.1179012 15	1
GO:00463 29	negative regulation of JNK cascade	0.1720164 33	0.1179012 15	1
GO:00519 31	regulation of sensory perception	0.1720164 33	0.1179012 15	1
GO:19010 21	positive regulation of calcium ion transmembrane transporter activity	0.1720164 33	0.1179012 15	1
GO:19022 29	regulation of intrinsic apoptotic signaling pathway in response to DNA damage	0.1720164 33	0.1179012 15	1
GO:19047 06	negative regulation of vascular associated smooth muscle cell proliferation	0.1720164 33	0.1179012 15	1

GO:20008 16	negative regulation of mitotic sister chromatid separation	0.1720164 33	0.1179012 15	1
GO:00001 87	activation of MAPK activity	0.1736432 47	0.1189261 49	1
GO:19029 04	negative regulation of supramolecular fiber organization	0.1736432 47	0.1189261 49	1
GO:00442 82	small molecule catabolic process	0.1744082 11	0.1194048 69	1
GO:00107 70	positive regulation of cell morphogenesis involved in differentiation	0.1753628 04	0.1197371 44	1
GO:00022 09	behavioral defense response	0.1760184 78	0.1197371 44	1
GO:00027 14	positive regulation of B cell mediated immunity	0.1760184 78	0.1197371 44	1
GO:00028 91	positive regulation of immunoglobulin mediated immune response	0.1760184 78	0.1197371 44	1
GO:00091 87	cyclic nucleotide metabolic process	0.1760184 78	0.1197371 44	1
GO:00109 39	regulation of necrotic cell death	0.1760184 78	0.1197371 44	1
GO:00305 01	positive regulation of bone mineralization	0.1760184 78	0.1197371 44	1
GO:00457 40	positive regulation of DNA replication	0.1760184 78	0.1197371 44	1
GO:00457 46	negative regulation of Notch signaling pathway	0.1760184 78	0.1197371 44	1
GO:00508 92	intestinal absorption	0.1760184 78	0.1197371 44	1
GO:00512 81	positive regulation of release of sequestered calcium ion into cytosol	0.1760184 78	0.1197371 44	1
GO:00901 84	positive regulation of kidney development	0.1760184 78	0.1197371 44	1
GO:00973 52	autophagosome maturation	0.1760184 78	0.1197371 44	1
GO:01403 53	lipid export from cell	0.1760184 78	0.1197371 44	1
GO:19013 81	positive regulation of potassium ion transmembrane transport	0.1760184 78	0.1197371 44	1
GO:19027 42	apoptotic process involved in development	0.1760184 78	0.1197371 44	1
GO:19058 19	negative regulation of chromosome separation	0.1760184 78	0.1197371 44	1
GO:00165 73	histone acetylation	0.1788102 24	0.1214992 09	1

GO:00326 75	regulation of interleukin-6 production	0.1788102 24	0.1214992 09	1
GO:20000 58	regulation of ubiquitin-dependent protein catabolic process	0.1788102 24	0.1214992 09	1
GO:00067 34	NADH metabolic process	0.1800013 91	0.1218054 52	1
GO:00335 74	response to testosterone	0.1800013 91	0.1218054 52	1
GO:00353 37	fatty-acyl-CoA metabolic process	0.1800013 91	0.1218054 52	1
GO:00432 67	negative regulation of potassium ion transport	0.1800013 91	0.1218054 52	1
GO:00482 86	lung alveolus development	0.1800013 91	0.1218054 52	1
GO:00504 34	positive regulation of viral transcription	0.1800013 91	0.1218054 52	1
GO:00508 32	defense response to fungus	0.1800013 91	0.1218054 52	1
GO:00703 17	negative regulation of G0 to G1 transition	0.1800013 91	0.1218054 52	1
GO:00715 48	response to dexamethasone	0.1800013 91	0.1218054 52	1
GO:00725 24	pyridine-containing compound metabolic process	0.1800013 91	0.1218054 52	1
GO:19031 70	negative regulation of calcium ion transmembrane transport	0.1800013 91	0.1218054 52	1
GO:00109 70	transport along microtubule	0.1822682 8	0.1232933 3	1
GO:00002 66	mitochondrial fission	0.1839652 62	0.1239096 44	1
GO:00017 09	cell fate determination	0.1839652 62	0.1239096 44	1
GO:00219 83	pituitary gland development	0.1839652 62	0.1239096 44	1
GO:00330 48	negative regulation of mitotic sister chromatid segregation	0.1839652 62	0.1239096 44	1
GO:00440 58	regulation of digestive system process	0.1839652 62	0.1239096 44	1
GO:00466 21	negative regulation of organ growth	0.1839652 62	0.1239096 44	1
GO:00725 95	maintenance of protein localization in organelle	0.1839652 62	0.1239096 44	1
GO:00902 78	negative regulation of peptide hormone secretion	0.1839652 62	0.1239096 44	1

GO:00902 79	regulation of calcium ion import	0.1839652 62	0.1239096 44	1
GO:19003 71	regulation of purine nucleotide biosynthetic process	0.1839652 62	0.1239096 44	1
GO:19026 22	regulation of neutrophil migration	0.1839652 62	0.1239096 44	1
GO:00073 38	single fertilization	0.1840011 36	0.1239096 44	1
GO:00219 15	neural tube development	0.1857364 58	0.1249852 11	1
GO:00514 94	negative regulation of cytoskeleton organization	0.1857364 58	0.1249852 11	1
GO:00017 64	neuron migration	0.1874741 82	0.1256071 4	1
GO:00183 93	internal peptidyl-lysine acetylation	0.1874741 82	0.1256071 4	1
GO:00461 65	alcohol biosynthetic process	0.1874741 82	0.1256071 4	1
GO:00019 53	negative regulation of cell-matrix adhesion	0.1879101 81	0.1256071 4	1
GO:00023 69	T cell cytokine production	0.1879101 81	0.1256071 4	1
GO:00171 58	regulation of calcium ion-dependent exocytosis	0.1879101 81	0.1256071 4	1
GO:00217 62	substantia nigra development	0.1879101 81	0.1256071 4	1
GO:00305 17	negative regulation of axon extension	0.1879101 81	0.1256071 4	1
GO:00305 21	androgen receptor signaling pathway	0.1879101 81	0.1256071 4	1
GO:00308 08	regulation of nucleotide biosynthetic process	0.1879101 81	0.1256071 4	1
GO:00400 19	positive regulation of embryonic development	0.1879101 81	0.1256071 4	1
GO:00466 88	response to copper ion	0.1879101 81	0.1256071 4	1
GO:00467 17	acid secretion	0.1879101 81	0.1256071 4	1
GO:00508 50	positive regulation of calcium-mediated signaling	0.1879101 81	0.1256071 4	1
GO:00508 56	regulation of T cell receptor signaling pathway	0.1879101 81	0.1256071 4	1
GO:00713 64	cellular response to epidermal growth factor stimulus	0.1879101 81	0.1256071 4	1

GO:00860 04	regulation of cardiac muscle cell contraction	0.1879101 81	0.1256071 4	1
GO:19010 31	regulation of response to reactive oxygen species	0.1879101 81	0.1256071 4	1
GO:00064 75	internal protein amino acid acetylation	0.1909565 92	0.1274780 11	1
GO:00061 95	purine nucleotide catabolic process	0.1918362 38	0.1274780 11	1
GO:00104 63	mesenchymal cell proliferation	0.1918362 38	0.1274780 11	1
GO:00316 70	cellular response to nutrient	0.1918362 38	0.1274780 11	1
GO:00326 20	interleukin-17 production	0.1918362 38	0.1274780 11	1
GO:00329 65	regulation of collagen biosynthetic process	0.1918362 38	0.1274780 11	1
GO:00330 46	negative regulation of sister chromatid segregation	0.1918362 38	0.1274780 11	1
GO:00353 07	positive regulation of protein dephosphorylation	0.1918362 38	0.1274780 11	1
GO:00453 32	phospholipid translocation	0.1918362 38	0.1274780 11	1
GO:00456 84	positive regulation of epidermis development	0.1918362 38	0.1274780 11	1
GO:00456 87	positive regulation of glial cell differentiation	0.1918362 38	0.1274780 11	1
GO:00484 89	synaptic vesicle transport	0.1918362 38	0.1274780 11	1
GO:19026 67	regulation of axon guidance	0.1918362 38	0.1274780 11	1
GO:19030 53	regulation of extracellular matrix organization	0.1918362 38	0.1274780 11	1
GO:19055 21	regulation of macrophage migration	0.1918362 38	0.1274780 11	1
GO:20004 04	regulation of T cell migration	0.1918362 38	0.1274780 11	1
GO:00903 05	nucleic acid phosphodiester bond hydrolysis	0.1922498 47	0.1277059 61	1
GO:00028 19	regulation of adaptive immune response	0.1944478 7	0.1291186 44	1
GO:00019 74	blood vessel remodeling	0.1957435 23	0.1294091 17	1
GO:00026 39	positive regulation of immunoglobulin production	0.1957435 23	0.1294091 17	1

GO:00067 75	fat-soluble vitamin metabolic process	0.1957435 23	0.1294091 17	1
GO:00075 20	myoblast fusion	0.1957435 23	0.1294091 17	1
GO:00106 77	negative regulation of cellular carbohydrate metabolic process	0.1957435 23	0.1294091 17	1
GO:00341 98	cellular response to amino acid starvation	0.1957435 23	0.1294091 17	1
GO:00461 89	phenol-containing compound biosynthetic process	0.1957435 23	0.1294091 17	1
GO:00519 85	negative regulation of chromosome segregation	0.1957435 23	0.1294091 17	1
GO:00523 72	modulation by symbiont of entry into host	0.1957435 23	0.1294091 17	1
GO:00604 12	ventricular septum morphogenesis	0.1957435 23	0.1294091 17	1
GO:00703 16	regulation of G0 to G1 transition	0.1957435 23	0.1294091 17	1
GO:00988 15	modulation of excitatory postsynaptic potential	0.1957435 23	0.1294091 17	1
GO:00328 74	positive regulation of stress-activated MAPK cascade	0.1979475 3	0.1308184 25	1
GO:00017 54	eye photoreceptor cell differentiation	0.1996321 22	0.1314009 22	1
GO:00107 61	fibroblast migration	0.1996321 22	0.1314009 22	1
GO:00108 74	regulation of cholesterol efflux	0.1996321 22	0.1314009 22	1
GO:00316 41	regulation of myelination	0.1996321 22	0.1314009 22	1
GO:00320 07	negative regulation of TOR signaling	0.1996321 22	0.1314009 22	1
GO:00323 09	icosanoid secretion	0.1996321 22	0.1314009 22	1
GO:00450 23	G0 to G1 transition	0.1996321 22	0.1314009 22	1
GO:00485 38	thymus development	0.1996321 22	0.1314009 22	1
GO:00514 89	regulation of filopodium assembly	0.1996321 22	0.1314009 22	1
GO:00516 46	mitochondrion localization	0.1996321 22	0.1314009 22	1
GO:19007 44	regulation of p38MAPK cascade	0.1996321 22	0.1314009 22	1

GO:0051302	regulation of cell division	0.199700354	0.131400922	1
GO:0018394	peptidyl-lysine acetylation	0.201455095	0.132459191	1
GO:0070304	positive regulation of stress-activated protein kinase signaling cascade	0.201455095	0.132459191	1
GO:0002429	immune response-activating cell surface receptor signaling pathway	0.202578942	0.132983656	1
GO:0002757	immune response-activating signal transduction	0.202578942	0.132983656	1
GO:0043087	regulation of GTPase activity	0.202578942	0.132983656	1
GO:0006383	transcription by RNA polymerase III	0.203502127	0.132983656	1
GO:0007080	mitotic metaphase plate congression	0.203502127	0.132983656	1
GO:0008542	visual learning	0.203502127	0.132983656	1
GO:0010559	regulation of glycoprotein biosynthetic process	0.203502127	0.132983656	1
GO:0010569	regulation of double-strand break repair via homologous recombination	0.203502127	0.132983656	1
GO:0030261	chromosome condensation	0.203502127	0.132983656	1
GO:0032369	negative regulation of lipid transport	0.203502127	0.132983656	1
GO:0034204	lipid translocation	0.203502127	0.132983656	1
GO:0035850	epithelial cell differentiation involved in kidney development	0.203502127	0.132983656	1
GO:0042551	neuron maturation	0.203502127	0.132983656	1
GO:0048483	autonomic nervous system development	0.203502127	0.132983656	1
GO:0051150	regulation of smooth muscle cell differentiation	0.203502127	0.132983656	1
GO:0070849	response to epidermal growth factor	0.203502127	0.132983656	1
GO:1903115	regulation of actin filament-based movement	0.203502127	0.132983656	1
GO:0007269	neurotransmitter secretion	0.206730239	0.134625376	1
GO:0010921	regulation of phosphatase activity	0.206730239	0.134625376	1

GO:00996 43	signal release from synapse	0.2067302 39	0.1346253 76	1
GO:00508 51	antigen receptor-mediated signaling pathway	0.2070565 69	0.1346253 76	1
GO:00080 89	anterograde axonal transport	0.2073536 23	0.1346253 76	1
GO:00149 11	positive regulation of smooth muscle cell migration	0.2073536 23	0.1346253 76	1
GO:00336 28	regulation of cell adhesion mediated by integrin	0.2073536 23	0.1346253 76	1
GO:00424 61	photoreceptor cell development	0.2073536 23	0.1346253 76	1
GO:00519 32	synaptic transmission, GABAergic	0.2073536 23	0.1346253 76	1
GO:00519 72	regulation of telomerase activity	0.2073536 23	0.1346253 76	1
GO:00550 10	ventricular cardiac muscle tissue morphogenesis	0.2073536 23	0.1346253 76	1
GO:00606 32	regulation of microtubule-based movement	0.2073536 23	0.1346253 76	1
GO:00701 69	positive regulation of biomineral tissue development	0.2073536 23	0.1346253 76	1
GO:01101 51	positive regulation of biomineralization	0.2073536 23	0.1346253 76	1
GO:19002 71	regulation of long-term synaptic potentiation	0.2073536 23	0.1346253 76	1
GO:19040 36	negative regulation of epithelial cell apoptotic process	0.2073536 23	0.1346253 76	1
GO:19905 73	potassium ion import across plasma membrane	0.2073536 23	0.1346253 76	1
GO:19909 28	response to amino acid starvation	0.2073536 23	0.1346253 76	1
GO:00093 95	phospholipid catabolic process	0.2111866 99	0.1366726 66	1
GO:00107 12	regulation of collagen metabolic process	0.2111866 99	0.1366726 66	1
GO:00181 98	peptidyl-cysteine modification	0.2111866 99	0.1366726 66	1
GO:00474 96	vesicle transport along microtubule	0.2111866 99	0.1366726 66	1
GO:00486 41	regulation of skeletal muscle tissue development	0.2111866 99	0.1366726 66	1
GO:00613 83	trabecula morphogenesis	0.2111866 99	0.1366726 66	1

GO:00616 47	histone H3-K9 modification	0.2111866 99	0.1366726 66	1
GO:19900 90	cellular response to nerve growth factor stimulus	0.2111866 99	0.1366726 66	1
GO:20001 07	negative regulation of leukocyte apoptotic process	0.2111866 99	0.1366726 66	1
GO:00329 84	protein-containing complex disassembly	0.2133030 78	0.1379929 59	1
GO:00019 61	positive regulation of cytokine-mediated signaling pathway	0.2150014 41	0.1385961 7	1
GO:00027 11	positive regulation of T cell mediated immunity	0.2150014 41	0.1385961 7	1
GO:00080 38	neuron recognition	0.2150014 41	0.1385961 7	1
GO:00107 18	positive regulation of epithelial to mesenchymal transition	0.2150014 41	0.1385961 7	1
GO:00196 74	NAD metabolic process	0.2150014 41	0.1385961 7	1
GO:00455 40	regulation of cholesterol biosynthetic process	0.2150014 41	0.1385961 7	1
GO:00717 15	icosanoid transport	0.2150014 41	0.1385961 7	1
GO:01061 18	regulation of sterol biosynthetic process	0.2150014 41	0.1385961 7	1
GO:19015 71	fatty acid derivative transport	0.2150014 41	0.1385961 7	1
GO:19037 27	positive regulation of phospholipid metabolic process	0.2150014 41	0.1385961 7	1
GO:00311 13	regulation of microtubule polymerization	0.2187979 37	0.1405428 15	1
GO:00328 73	negative regulation of stress-activated MAPK cascade	0.2187979 37	0.1405428 15	1
GO:00351 76	social behavior	0.2187979 37	0.1405428 15	1
GO:00432 77	apoptotic cell clearance	0.2187979 37	0.1405428 15	1
GO:00482 55	mRNA stabilization	0.2187979 37	0.1405428 15	1
GO:00609 76	coronary vasculature development	0.2187979 37	0.1405428 15	1
GO:00703 03	negative regulation of stress-activated protein kinase signaling cascade	0.2187979 37	0.1405428 15	1
GO:00718 27	plasma lipoprotein particle organization	0.2187979 37	0.1405428 15	1

GO:00725 23	purine-containing compound catabolic process	0.2187979 37	0.1405428 15	1
GO:19035 87	regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis	0.2187979 37	0.1405428 15	1
GO:00434 33	negative regulation of DNA-binding transcription factor activity	0.2208674 23	0.1418217 85	1
GO:00019 12	positive regulation of leukocyte mediated cytotoxicity	0.2225762 73	0.1422537 38	1
GO:00031 79	heart valve morphogenesis	0.2225762 73	0.1422537 38	1
GO:00323 30	regulation of chondrocyte differentiation	0.2225762 73	0.1422537 38	1
GO:00330 59	cellular pigmentation	0.2225762 73	0.1422537 38	1
GO:00465 80	negative regulation of Ras protein signal transduction	0.2225762 73	0.1422537 38	1
GO:00482 60	positive regulation of receptor-mediated endocytosis	0.2225762 73	0.1422537 38	1
GO:00513 39	regulation of lyase activity	0.2225762 73	0.1422537 38	1
GO:00514 45	regulation of meiotic cell cycle	0.2225762 73	0.1422537 38	1
GO:00604 25	lung morphogenesis	0.2225762 73	0.1422537 38	1
GO:19900 89	response to nerve growth factor	0.2225762 73	0.1422537 38	1
GO:20012 38	positive regulation of extrinsic apoptotic signaling pathway	0.2225762 73	0.1422537 38	1
GO:20012 58	negative regulation of cation channel activity	0.2225762 73	0.1422537 38	1
GO:00463 28	regulation of JNK cascade	0.2226407 54	0.1422537 38	1
GO:00900 90	negative regulation of canonical Wnt signaling pathway	0.2226407 54	0.1422537 38	1
GO:19907 78	protein localization to cell periphery	0.2259175 77	0.1439543 07	1
GO:00076 32	visual behavior	0.2263365 34	0.1439543 07	1
GO:00083 33	endosome to lysosome transport	0.2263365 34	0.1439543 07	1
GO:00329 64	collagen biosynthetic process	0.2263365 34	0.1439543 07	1
GO:00353 84	thioester biosynthetic process	0.2263365 34	0.1439543 07	1

GO:00433 92	negative regulation of DNA binding	0.2263365 34	0.1439543 07	1
GO:00456 68	negative regulation of osteoblast differentiation	0.2263365 34	0.1439543 07	1
GO:00517 03	intraspecies interaction between organisms	0.2263365 34	0.1439543 07	1
GO:00713 20	cellular response to cAMP	0.2263365 34	0.1439543 07	1
GO:00716 16	acyl-CoA biosynthetic process	0.2263365 34	0.1439543 07	1
GO:00726 98	protein localization to microtubule cytoskeleton	0.2263365 34	0.1439543 07	1
GO:00970 35	regulation of membrane lipid distribution	0.2263365 34	0.1439543 07	1
GO:20007 72	regulation of cellular senescence	0.2263365 34	0.1439543 07	1
GO:00022 85	lymphocyte activation involved in immune response	0.2279677 17	0.1448899 14	1
GO:00434 09	negative regulation of MAPK cascade	0.2279677 17	0.1448899 14	1
GO:00313 45	negative regulation of cell projection organization	0.2297455 22	0.1459685 66	1
GO:00096 20	response to fungus	0.2300788 07	0.1460264 98	1
GO:00105 24	positive regulation of calcium ion transport into cytosol	0.2300788 07	0.1460264 98	1
GO:19030 18	regulation of glycoprotein metabolic process	0.2300788 07	0.1460264 98	1
GO:00991 11	microtubule-based transport	0.2333040 54	0.1479233 2	1
GO:00027 20	positive regulation of cytokine production involved in immune response	0.2338031 76	0.1479233 2	1
GO:00032 29	ventricular cardiac muscle tissue development	0.2338031 76	0.1479233 2	1
GO:00083 47	glial cell migration	0.2338031 76	0.1479233 2	1
GO:00326 55	regulation of interleukin-12 production	0.2338031 76	0.1479233 2	1
GO:00327 81	positive regulation of ATPase activity	0.2338031 76	0.1479233 2	1
GO:00350 65	regulation of histone acetylation	0.2338031 76	0.1479233 2	1
GO:00504 33	regulation of catecholamine secretion	0.2338031 76	0.1479233 2	1

GO:00718 25	protein-lipid complex subunit organization	0.2338031 76	0.1479233 2	1
GO:00481 67	regulation of synaptic plasticity	0.2350846 8	0.1486821 19	1
GO:00165 25	negative regulation of angiogenesis	0.2368661 48	0.1497564 85	1
GO:00027 12	regulation of B cell mediated immunity	0.2375097 26	0.1497970 02	1
GO:00028 89	regulation of immunoglobulin mediated immune response	0.2375097 26	0.1497970 02	1
GO:00106 65	regulation of cardiac muscle cell apoptotic process	0.2375097 26	0.1497970 02	1
GO:00193 20	hexose catabolic process	0.2375097 26	0.1497970 02	1
GO:00300 71	regulation of mitotic metaphase/anaphase transition	0.2375097 26	0.1497970 02	1
GO:00312 95	T cell costimulation	0.2375097 26	0.1497970 02	1
GO:00507 32	negative regulation of peptidyl-tyrosine phosphorylation	0.2375097 26	0.1497970 02	1
GO:00611 36	regulation of proteasomal protein catabolic process	0.2386484 07	0.1504627 22	1
GO:20001 81	negative regulation of blood vessel morphogenesis	0.2404314 1	0.1515340 68	1
GO:00020 90	regulation of receptor internalization	0.2411985 41	0.1515951 42	1
GO:00065 76	cellular biogenic amine metabolic process	0.2411985 41	0.1515951 42	1
GO:00443 80	protein localization to cytoskeleton	0.2411985 41	0.1515951 42	1
GO:00458 40	positive regulation of mitotic nuclear division	0.2411985 41	0.1515951 42	1
GO:00504 32	catecholamine secretion	0.2411985 41	0.1515951 42	1
GO:00607 60	positive regulation of response to cytokine stimulus	0.2411985 41	0.1515951 42	1
GO:00610 05	cell differentiation involved in kidney development	0.2411985 41	0.1515951 42	1
GO:00974 79	synaptic vesicle localization	0.2411985 41	0.1515951 42	1
GO:19011 36	carbohydrate derivative catabolic process	0.2422151 09	0.1521812 03	1
GO:00507 28	negative regulation of inflammatory response	0.2439994 56	0.1531047 99	1

GO:00007 68	syncytium formation by plasma membrane fusion	0.2448697 06	0.1531047 99	1
GO:00020 43	blood vessel endothelial cell proliferation involved in sprouting angiogenesis	0.2448697 06	0.1531047 99	1
GO:00070 91	metaphase/anaphase transition of mitotic cell cycle	0.2448697 06	0.1531047 99	1
GO:00106 56	negative regulation of muscle cell apoptotic process	0.2448697 06	0.1531047 99	1
GO:00106 62	regulation of striated muscle cell apoptotic process	0.2448697 06	0.1531047 99	1
GO:00312 94	lymphocyte costimulation	0.2448697 06	0.1531047 99	1
GO:00353 06	positive regulation of dephosphorylation	0.2448697 06	0.1531047 99	1
GO:00434 89	RNA stabilization	0.2448697 06	0.1531047 99	1
GO:01402 53	cell-cell fusion	0.2448697 06	0.1531047 99	1
GO:19020 99	regulation of metaphase/anaphase transition of cell cycle	0.2448697 06	0.1531047 99	1
GO:19023 73	negative regulation of mRNA catabolic process	0.2448697 06	0.1531047 99	1
GO:19037 93	positive regulation of anion transport	0.2448697 06	0.1531047 99	1
GO:20002 72	negative regulation of signaling receptor activity	0.2448697 06	0.1531047 99	1
GO:00061 64	purine nucleotide biosynthetic process	0.2457844 04	0.1535705 84	1
GO:00066 94	steroid biosynthetic process	0.2457844 04	0.1535705 84	1
GO:00106 59	cardiac muscle cell apoptotic process	0.2485233 03	0.1549074 67	1
GO:00430 30	regulation of macrophage activation	0.2485233 03	0.1549074 67	1
GO:00458 15	positive regulation of gene expression, epigenetic	0.2485233 03	0.1549074 67	1
GO:00466 05	regulation of centrosome cycle	0.2485233 03	0.1549074 67	1
GO:00507 07	regulation of cytokine secretion	0.2485233 03	0.1549074 67	1
GO:00510 58	negative regulation of small GTPase mediated signal transduction	0.2485233 03	0.1549074 67	1
GO:00713 85	cellular response to glucocorticoid stimulus	0.2485233 03	0.1549074 67	1

GO:00995 04	synaptic vesicle cycle	0.2493559 16	0.1553729 23	1
GO:00307 05	cytoskeleton-dependent intracellular transport	0.2511423 87	0.1564322	1
GO:00069 49	syncytium formation	0.2521594 16	0.1565805 86	1
GO:00182 08	peptidyl-proline modification	0.2521594 16	0.1565805 86	1
GO:00308 65	cortical cytoskeleton organization	0.2521594 16	0.1565805 86	1
GO:00326 53	regulation of interleukin-10 production	0.2521594 16	0.1565805 86	1
GO:00420 93	T-helper cell differentiation	0.2521594 16	0.1565805 86	1
GO:00433 88	positive regulation of DNA binding	0.2521594 16	0.1565805 86	1
GO:00439 66	histone H3 acetylation	0.2521594 16	0.1565805 86	1
GO:00447 84	metaphase/anaphase transition of cell cycle	0.2521594 16	0.1565805 86	1
GO:00718 06	protein transmembrane transport	0.2521594 16	0.1565805 86	1
GO:00436 87	post-translational protein modification	0.2554457 03	0.1581762 79	1
GO:00031 70	heart valve development	0.2557781 28	0.1581762 79	1
GO:00106 58	striated muscle cell apoptotic process	0.2557781 28	0.1581762 79	1
GO:00109 65	regulation of mitotic sister chromatid separation	0.2557781 28	0.1581762 79	1
GO:00313 43	positive regulation of cell killing	0.2557781 28	0.1581762 79	1
GO:00427 33	embryonic digit morphogenesis	0.2557781 28	0.1581762 79	1
GO:00450 71	negative regulation of viral genome replication	0.2557781 28	0.1581762 79	1
GO:00468 47	filopodium assembly	0.2557781 28	0.1581762 79	1
GO:00468 88	negative regulation of hormone secretion	0.2557781 28	0.1581762 79	1
GO:00513 10	metaphase plate congression	0.2557781 28	0.1581762 79	1
GO:00903 42	regulation of cell aging	0.2557781 28	0.1581762 79	1

GO:20007 56	regulation of peptidyl-lysine acetylation	0.2557781 28	0.1581762 79	1
GO:00024 49	lymphocyte mediated immunity	0.2593406 47	0.1600205 99	1
GO:00022 94	CD4-positive, alpha-beta T cell differentiation involved in immune response	0.2593795 2	0.1600205 99	1
GO:00341 13	heterotypic cell-cell adhesion	0.2593795 2	0.1600205 99	1
GO:00518 51	modulation by host of symbiont process	0.2593795 2	0.1600205 99	1
GO:00550 81	anion homeostasis	0.2593795 2	0.1600205 99	1
GO:00713 84	cellular response to corticosteroid stimulus	0.2593795 2	0.1600205 99	1
GO:01401 15	export across plasma membrane	0.2593795 2	0.1600205 99	1
GO:00022 87	alpha-beta T cell activation involved in immune response	0.2629636 76	0.1620108 45	1
GO:00022 93	alpha-beta T cell differentiation involved in immune response	0.2629636 76	0.1620108 45	1
GO:00060 81	cellular aldehyde metabolic process	0.2629636 76	0.1620108 45	1
GO:00465 30	photoreceptor cell differentiation	0.2629636 76	0.1620108 45	1
GO:00024 60	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	0.2645467 62	0.1629307 03	1
GO:00725 22	purine-containing compound biosynthetic process	0.2654454 24	0.1634285 5	1
GO:00019 47	heart looping	0.2665306 76	0.1637068 04	1
GO:00325 07	maintenance of protein location in cell	0.2665306 76	0.1637068 04	1
GO:00328 35	glomerulus development	0.2665306 76	0.1637068 04	1
GO:00333 44	cholesterol efflux	0.2665306 76	0.1637068 04	1
GO:00421 30	negative regulation of T cell proliferation	0.2665306 76	0.1637068 04	1
GO:00513 06	mitotic sister chromatid separation	0.2665306 76	0.1637068 04	1
GO:00518 98	negative regulation of protein kinase B signaling	0.2665306 76	0.1637068 04	1
GO:00400 29	regulation of gene expression, epigenetic	0.2672340 57	0.1640831 33	1

GO:00023 77	immunoglobulin production	0.2690227 16	0.1651253 48	1
GO:00075 88	excretion	0.2700806 02	0.1651584 13	1
GO:00171 56	calcium-ion regulated exocytosis	0.2700806 02	0.1651584 13	1
GO:00308 37	negative regulation of actin filament polymerization	0.2700806 02	0.1651584 13	1
GO:00316 40	killing of cells of other organism	0.2700806 02	0.1651584 13	1
GO:00316 46	positive regulation of nervous system process	0.2700806 02	0.1651584 13	1
GO:00327 29	positive regulation of interferon-gamma production	0.2700806 02	0.1651584 13	1
GO:00467 82	regulation of viral transcription	0.2700806 02	0.1651584 13	1
GO:00482 47	lymphocyte chemotaxis	0.2700806 02	0.1651584 13	1
GO:00486 45	animal organ formation	0.2700806 02	0.1651584 13	1
GO:00901 81	regulation of cholesterol metabolic process	0.2700806 02	0.1651584 13	1
GO:19023 05	regulation of sodium ion transmembrane transport	0.2700806 02	0.1651584 13	1
GO:00313 96	regulation of protein ubiquitination	0.2708113 59	0.1655493 34	1
GO:00327 15	negative regulation of interleukin-6 production	0.2736135 35	0.1669802 67	1
GO:00456 69	positive regulation of osteoblast differentiation	0.2736135 35	0.1669802 67	1
GO:00463 65	monosaccharide catabolic process	0.2736135 35	0.1669802 67	1
GO:00509 22	negative regulation of chemotaxis	0.2736135 35	0.1669802 67	1
GO:19058 18	regulation of chromosome separation	0.2736135 35	0.1669802 67	1
GO:00072 54	JNK cascade	0.2743884 35	0.1673402 94	1
GO:00450 89	positive regulation of innate immune response	0.2743884 35	0.1673402 94	1
GO:00091 66	nucleotide catabolic process	0.2771295 55	0.1685008 86	1
GO:00328 90	regulation of organic acid transport	0.2771295 55	0.1685008 86	1

GO:00338 66	nucleoside bisphosphate biosynthetic process	0.2771295 55	0.1685008 86	1
GO:00340 30	ribonucleoside bisphosphate biosynthetic process	0.2771295 55	0.1685008 86	1
GO:00340 33	purine nucleoside bisphosphate biosynthetic process	0.2771295 55	0.1685008 86	1
GO:00343 32	adherens junction organization	0.2771295 55	0.1685008 86	1
GO:00364 98	IRE1-mediated unfolded protein response	0.2771295 55	0.1685008 86	1
GO:00422 55	ribosome assembly	0.2771295 55	0.1685008 86	1
GO:00713 00	cellular response to retinoic acid	0.2771295 55	0.1685008 86	1
GO:00069 09	phagocytosis	0.2802417 61	0.1701710 2	1
GO:00066 25	protein targeting to peroxisome	0.2806287 41	0.1701710 2	1
GO:00108 12	negative regulation of cell-substrate adhesion	0.2806287 41	0.1701710 2	1
GO:00424 46	hormone biosynthetic process	0.2806287 41	0.1701710 2	1
GO:00511 48	negative regulation of muscle cell differentiation	0.2806287 41	0.1701710 2	1
GO:00726 62	protein localization to peroxisome	0.2806287 41	0.1701710 2	1
GO:00726 63	establishment of protein localization to peroxisome	0.2806287 41	0.1701710 2	1
GO:19023 69	negative regulation of RNA catabolic process	0.2806287 41	0.1701710 2	1
GO:00359 14	skeletal muscle cell differentiation	0.2841111 75	0.1720521 06	1
GO:00508 54	regulation of antigen receptor-mediated signaling pathway	0.2841111 75	0.1720521 06	1
GO:00613 71	determination of heart left/right asymmetry	0.2841111 75	0.1720521 06	1
GO:00712 30	cellular response to amino acid stimulus	0.2841111 75	0.1720521 06	1
GO:00071 63	establishment or maintenance of cell polarity	0.2869018 06	0.1736258 42	1
GO:00990 03	vesicle-mediated transport in synapse	0.2869018 06	0.1736258 42	1
GO:00017 56	somitogenesis	0.2875769 34	0.1736858 79	1

GO:00031 43	embryonic heart tube morphogenesis	0.2875769 34	0.1736858 79	1
GO:00323 74	regulation of cholesterol transport	0.2875769 34	0.1736858 79	1
GO:00439 67	histone H4 acetylation	0.2875769 34	0.1736858 79	1
GO:00507 71	negative regulation of axonogenesis	0.2875769 34	0.1736858 79	1
GO:00507 95	regulation of behavior	0.2875769 34	0.1736858 79	1
GO:00022 92	T cell differentiation involved in immune response	0.2910260 99	0.1754761 97	1
GO:00323 71	regulation of sterol transport	0.2910260 99	0.1754761 97	1
GO:00336 27	cell adhesion mediated by integrin	0.2910260 99	0.1754761 97	1
GO:00508 91	multicellular organismal water homeostasis	0.2910260 99	0.1754761 97	1
GO:00517 85	positive regulation of nuclear division	0.2910260 99	0.1754761 97	1
GO:00192 26	transmission of nerve impulse	0.2944587 47	0.1772506 17	1
GO:00330 47	regulation of mitotic sister chromatid segregation	0.2944587 47	0.1772506 17	1
GO:00424 40	pigment metabolic process	0.2944587 47	0.1772506 17	1
GO:00435 74	peroxisomal transport	0.2944587 47	0.1772506 17	1
GO:00610 35	regulation of cartilage development	0.2944587 47	0.1772506 17	1
GO:19030 50	regulation of proteolysis involved in cellular protein catabolic process	0.2958284 52	0.1780158 96	1
GO:00027 09	regulation of T cell mediated immunity	0.2978749 57	0.1790687 36	1
GO:19012 92	nucleoside phosphate catabolic process	0.2978749 57	0.1790687 36	1
GO:19021 17	positive regulation of organelle assembly	0.2978749 57	0.1790687 36	1
GO:00160 64	immunoglobulin mediated immune response	0.2993952 24	0.1799228 76	1
GO:00063 05	DNA alkylation	0.3012748 07	0.1805726 52	1
GO:00063 06	DNA methylation	0.3012748 07	0.1805726 52	1

GO:00066 35	fatty acid beta-oxidation	0.3012748 07	0.1805726 52	1
GO:00320 24	positive regulation of insulin secretion	0.3012748 07	0.1805726 52	1
GO:00324 81	positive regulation of type I interferon production	0.3012748 07	0.1805726 52	1
GO:00341 21	regulation of toll-like receptor signaling pathway	0.3012748 07	0.1805726 52	1
GO:00422 73	ribosomal large subunit biogenesis	0.3012748 07	0.1805726 52	1
GO:00435 07	positive regulation of JUN kinase activity	0.3012748 07	0.1805726 52	1
GO:00019 10	regulation of leukocyte mediated cytotoxicity	0.3046583 74	0.1821068 72	1
GO:00066 95	cholesterol biosynthetic process	0.3046583 74	0.1821068 72	1
GO:00090 64	glutamine family amino acid metabolic process	0.3046583 74	0.1821068 72	1
GO:00159 09	long-chain fatty acid transport	0.3046583 74	0.1821068 72	1
GO:00488 44	artery morphogenesis	0.3046583 74	0.1821068 72	1
GO:00618 44	antimicrobial humoral immune response mediated by antimicrobial peptide	0.3046583 74	0.1821068 72	1
GO:00995 18	vesicle cytoskeletal trafficking	0.3046583 74	0.1821068 72	1
GO:19026 53	secondary alcohol biosynthetic process	0.3046583 74	0.1821068 72	1
GO:00197 24	B cell mediated immunity	0.3047403 3	0.1821068 72	1
GO:00322 71	regulation of protein polymerization	0.3065205 47	0.1831102 22	1
GO:00032 81	ventricular septum development	0.3080257 36	0.1838879 79	1
GO:00062 78	RNA-dependent DNA biosynthetic process	0.3080257 36	0.1838879 79	1
GO:00182 05	peptidyl-lysine modification	0.3105499 95	0.1853337 88	1
GO:00467 85	microtubule polymerization	0.3113769 68	0.1857048 22	1
GO:00708 30	bicellular tight junction assembly	0.3113769 68	0.1857048 22	1
GO:00433 67	CD4-positive, alpha-beta T cell differentiation	0.3147121 48	0.1876320 76	1

GO:00442 42	cellular lipid catabolic process	0.3154089 81	0.1879855 9	1
GO:00028 31	regulation of response to biotic stimulus	0.3158390 8	0.1881799 49	1
GO:00068 26	iron ion transport	0.3180313 52	0.1889262 51	1
GO:00070 32	endosome organization	0.3180313 52	0.1889262 51	1
GO:00301 04	water homeostasis	0.3180313 52	0.1889262 51	1
GO:00434 07	negative regulation of MAP kinase activity	0.3180313 52	0.1889262 51	1
GO:00500 00	chromosome localization	0.3180313 52	0.1889262 51	1
GO:00506 72	negative regulation of lymphocyte proliferation	0.3180313 52	0.1889262 51	1
GO:00513 03	establishment of chromosome localization	0.3180313 52	0.1889262 51	1
GO:01201 92	tight junction assembly	0.3180313 52	0.1889262 51	1
GO:19000 34	regulation of cellular response to heat	0.3180313 52	0.1889262 51	1
GO:00023 12	B cell activation involved in immune response	0.3213346 54	0.1906382 3	1
GO:00313 97	negative regulation of protein ubiquitination	0.3213346 54	0.1906382 3	1
GO:00329 45	negative regulation of mononuclear cell proliferation	0.3213346 54	0.1906382 3	1
GO:00350 50	embryonic heart tube development	0.3213346 54	0.1906382 3	1
GO:00063 23	DNA packaging	0.3225025 96	0.1912684 24	1
GO:00019 60	negative regulation of cytokine-mediated signaling pathway	0.3246221 31	0.1922733 89	1
GO:00161 26	sterol biosynthetic process	0.3246221 31	0.1922733 89	1
GO:00432 42	negative regulation of protein-containing complex disassembly	0.3246221 31	0.1922733 89	1
GO:00512 79	regulation of release of sequestered calcium ion into cytosol	0.3246221 31	0.1922733 89	1
GO:00068 13	potassium ion transport	0.3260429 99	0.1930517 76	1
GO:00650 04	protein-DNA complex assembly	0.3278114 92	0.1937672 46	1

GO:00169 25	protein sumoylation	0.3278938 58	0.1937672 46	1
GO:00219 54	central nervous system neuron development	0.3278938 58	0.1937672 46	1
GO:00456 52	regulation of megakaryocyte differentiation	0.3278938 58	0.1937672 46	1
GO:01201 93	tight junction organization	0.3278938 58	0.1937672 46	1
GO:19033 13	positive regulation of mRNA metabolic process	0.3278938 58	0.1937672 46	1
GO:00020 88	lens development in camera-type eye	0.3311499 09	0.1954360 88	1
GO:00070 31	peroxisome organization	0.3311499 09	0.1954360 88	1
GO:00311 45	anaphase-promoting complex-dependent catabolic process	0.3311499 09	0.1954360 88	1
GO:20010 21	negative regulation of response to DNA damage stimulus	0.3311499 09	0.1954360 88	1
GO:00330 45	regulation of sister chromatid segregation	0.3343903 58	0.1972841 71	1
GO:00163 58	dendrite development	0.3348733 82	0.1975047 5	1
GO:00431 61	proteasome-mediated ubiquitin-dependent protein catabolic process	0.3356879 6	0.1979206 68	1
GO:00301 01	natural killer cell activation	0.3376152 8	0.1987332 35	1
GO:00311 10	regulation of microtubule polymerization or depolymerization	0.3376152 8	0.1987332 35	1
GO:00345 02	protein localization to chromosome	0.3376152 8	0.1987332 35	1
GO:00432 97	apical junction assembly	0.3376152 8	0.1987332 35	1
GO:20007 79	regulation of double-strand break repair	0.3376152 8	0.1987332 35	1
GO:00350 23	regulation of Rho protein signal transduction	0.3408247 47	0.2004268 48	1
GO:00706 64	negative regulation of leukocyte proliferation	0.3408247 47	0.2004268 48	1
GO:19039 01	negative regulation of viral life cycle	0.3408247 47	0.2004268 48	1
GO:00305 12	negative regulation of transforming growth factor beta receptor signaling pathway	0.3440188 34	0.2019114 59	1
GO:00480 13	ephrin receptor signaling pathway	0.3440188 34	0.2019114 59	1

GO:00512 62	protein tetramerization	0.3440188 34	0.2019114 59	1
GO:00602 18	hematopoietic stem cell differentiation	0.3440188 34	0.2019114 59	1
GO:00602 91	long-term synaptic potentiation	0.3440188 34	0.2019114 59	1
GO:00607 61	negative regulation of response to cytokine stimulus	0.3440188 34	0.2019114 59	1
GO:19033 12	negative regulation of mRNA metabolic process	0.3471976 13	0.2037110 71	1
GO:00435 06	regulation of JUN kinase activity	0.3503611 56	0.2053009 37	1
GO:00435 37	negative regulation of blood vessel endothelial cell migration	0.3503611 56	0.2053009 37	1
GO:00610 53	somite development	0.3503611 56	0.2053009 37	1
GO:19038 45	negative regulation of cellular response to transforming growth factor beta stimulus	0.3503611 56	0.2053009 37	1
GO:00016 56	metanephros development	0.3566428 25	0.2085091 46	1
GO:00018 43	neural tube closure	0.3566428 25	0.2085091 46	1
GO:00159 14	phospholipid transport	0.3566428 25	0.2085091 46	1
GO:00309 01	midbrain development	0.3566428 25	0.2085091 46	1
GO:00456 82	regulation of epidermis development	0.3566428 25	0.2085091 46	1
GO:00519 52	regulation of amine transport	0.3566428 25	0.2085091 46	1
GO:19013 79	regulation of potassium ion transmembrane transport	0.3566428 25	0.2085091 46	1
GO:19033 62	regulation of cellular protein catabolic process	0.3576723 01	0.2090434 81	1
GO:00313 41	regulation of cell killing	0.3597610 94	0.2099929 78	1
GO:00606 06	tube closure	0.3597610 94	0.2099929 78	1
GO:01060 27	neuron projection organization	0.3597610 94	0.2099929 78	1
GO:19058 97	regulation of response to endoplasmic reticulum stress	0.3597610 94	0.2099929 78	1
GO:00063 02	double-strand break repair	0.3611566 2	0.2107395 68	1

GO:00451 85	maintenance of protein location	0.3628644 15	0.2116678 3	1
GO:00513 04	chromosome separation	0.3659528 58	0.2134006 01	1
GO:00488 14	regulation of dendrite morphogenesis	0.3690264 94	0.2150543 41	1
GO:19037 25	regulation of phospholipid metabolic process	0.3690264 94	0.2150543 41	1
GO:00109 72	negative regulation of G2/M transition of mitotic cell cycle	0.3720853 92	0.2167671 36	1
GO:00313 48	negative regulation of defense response	0.3732972 37	0.2174031 3	1
GO:00357 10	CD4-positive, alpha-beta T cell activation	0.3751296 24	0.2183999 95	1
GO:00066 44	phospholipid metabolic process	0.3766026 46	0.2191165 84	1
GO:00073 89	pattern specification process	0.3766026 46	0.2191165 84	1
GO:00107 71	negative regulation of cell morphogenesis involved in differentiation	0.3781592 58	0.2196690 94	1
GO:00352 78	miRNA mediated inhibition of translation	0.3781592 58	0.2196690 94	1
GO:00400 33	negative regulation of translation, ncRNA-mediated	0.3781592 58	0.2196690 94	1
GO:00447 28	DNA methylation or demethylation	0.3781592 58	0.2196690 94	1
GO:00459 74	regulation of translation, ncRNA-mediated	0.3781592 58	0.2196690 94	1
GO:00107 17	regulation of epithelial to mesenchymal transition	0.3811743 64	0.2211365 76	1
GO:00158 37	amine transport	0.3811743 64	0.2211365 76	1
GO:00622 07	regulation of pattern recognition receptor signaling pathway	0.3811743 64	0.2211365 76	1
GO:00902 77	positive regulation of peptide hormone secretion	0.3811743 64	0.2211365 76	1
GO:00027 02	positive regulation of production of molecular mediator of immune response	0.3841750 11	0.2225206 7	1
GO:00302 19	megakaryocyte differentiation	0.3841750 11	0.2225206 7	1
GO:00352 82	segmentation	0.3841750 11	0.2225206 7	1
GO:00458 07	positive regulation of endocytosis	0.3841750 11	0.2225206 7	1

GO:00616 40	cytoskeleton-dependent cytokinesis	0.3841750 11	0.2225206 7	1
GO:00015 78	microtubule bundle formation	0.3871612 66	0.2240352 17	1
GO:00017 08	cell fate specification	0.3871612 66	0.2240352 17	1
GO:00311 24	mRNA 3'-end processing	0.3871612 66	0.2240352 17	1
GO:00320 06	regulation of TOR signaling	0.3901331 99	0.2256106 61	1
GO:00608 40	artery development	0.3901331 99	0.2256106 61	1
GO:00718 24	protein-DNA complex subunit organization	0.3955976 02	0.2285849 34	1
GO:00024 56	T cell mediated immunity	0.3960343 69	0.2285849 34	1
GO:00066 37	acyl-CoA metabolic process	0.3960343 69	0.2285849 34	1
GO:00326 49	regulation of interferon-gamma production	0.3960343 69	0.2285849 34	1
GO:00353 83	thioester metabolic process	0.3960343 69	0.2285849 34	1
GO:19016 06	alpha-amino acid catabolic process	0.3960343 69	0.2285849 34	1
GO:00026 97	regulation of immune effector process	0.3962503 25	0.2286366 5	1
GO:00303 01	cholesterol transport	0.3989637 41	0.2298553 87	1
GO:00482 59	regulation of receptor-mediated endocytosis	0.3989637 41	0.2298553 87	1
GO:00970 06	regulation of plasma lipoprotein particle levels	0.3989637 41	0.2298553 87	1
GO:20010 22	positive regulation of response to DNA damage stimulus	0.3989637 41	0.2298553 87	1
GO:00074 11	axon guidance	0.3989976 62	0.2298553 87	1
GO:00974 85	neuron projection guidance	0.4006944 57	0.2307594 13	1
GO:00072 18	neuropeptide signaling pathway	0.4018790 6	0.2312943 97	1
GO:00344 46	substrate adhesion-dependent cell spreading	0.4018790 6	0.2312943 97	1
GO:00000 18	regulation of DNA recombination	0.4047803 93	0.2324466 74	1

GO:00105 96	negative regulation of endothelial cell migration	0.4047803 93	0.2324466 74	1
GO:00344 04	nucleobase-containing small molecule biosynthetic process	0.4047803 93	0.2324466 74	1
GO:00485 24	positive regulation of viral process	0.4047803 93	0.2324466 74	1
GO:00509 05	neuromuscular process	0.4047803 93	0.2324466 74	1
GO:00519 83	regulation of chromosome segregation	0.4047803 93	0.2324466 74	1
GO:00991 75	regulation of postsynapse organization	0.4047803 93	0.2324466 74	1
GO:00019 09	leukocyte mediated cytotoxicity	0.4076678 06	0.2338821 08	1
GO:00072 29	integrin-mediated signaling pathway	0.4076678 06	0.2338821 08	1
GO:00085 93	regulation of Notch signaling pathway	0.4076678 06	0.2338821 08	1
GO:00109 76	positive regulation of neuron projection development	0.4091453 47	0.2346553 85	1
GO:00215 10	spinal cord development	0.4105413 66	0.2353068 73	1
GO:00987 81	ncRNA transcription	0.4105413 66	0.2353068 73	1
GO:00104 98	proteasomal protein catabolic process	0.4131538 97	0.2367210 38	1
GO:00062 89	nucleotide-excision repair	0.4134011 37	0.2367210 38	1
GO:00070 41	lysosomal transport	0.4134011 37	0.2367210 38	1
GO:00608 28	regulation of canonical Wnt signaling pathway	0.4175394 6	0.2390150 79	1
GO:19035 10	mucopolysaccharide metabolic process	0.4218983 77	0.2414339 06	1
GO:00063 10	DNA recombination	0.4242124 45	0.2426813 96	1
GO:00090 62	fatty acid catabolic process	0.4247036 48	0.2428856 12	1
GO:00512 58	protein polymerization	0.4258746 8	0.2434783 65	1
GO:00346 60	ncRNA metabolic process	0.4260613 11	0.2435081 27	1
GO:00326 09	interferon-gamma production	0.4274954 55	0.2442506 4	1

GO:00323 92	DNA geometric change	0.4302738 63	0.2457604 9	1
GO:00311 09	microtubule polymerization or depolymerization	0.4330389 33	0.2472617 72	1
GO:00070 52	mitotic spindle organization	0.4357907 31	0.2484442 81	1
GO:00159 18	sterol transport	0.4357907 31	0.2484442 81	1
GO:00508 68	negative regulation of T cell activation	0.4357907 31	0.2484442 81	1
GO:00024 40	production of molecular mediator of immune response	0.4357964 16	0.2484442 81	1
GO:00302 16	keratinocyte differentiation	0.4357964 16	0.2484442 81	1
GO:00450 88	regulation of innate immune response	0.4374412 88	0.2493034 64	1
GO:00063 04	DNA modification	0.4412547 59	0.2513976 31	1
GO:00902 87	regulation of cellular response to growth factor stimulus	0.4423606 19	0.2519483 47	1
GO:00313 98	positive regulation of protein ubiquitination	0.4439671 15	0.2527837 67	1
GO:00026 98	negative regulation of immune effector process	0.4520262 92	0.2571297 33	1
GO:00090 63	cellular amino acid catabolic process	0.4520262 92	0.2571297 33	1
GO:00106 33	negative regulation of epithelial cell migration	0.4520262 92	0.2571297 33	1
GO:00070 98	centrosome cycle	0.4546869 26	0.2583995 06	1
GO:00073 68	determination of left/right symmetry	0.4546869 26	0.2583995 06	1
GO:00324 79	regulation of type I interferon production	0.4546869 26	0.2583995 06	1
GO:00170 15	regulation of transforming growth factor beta receptor signaling pathway	0.4599699 24	0.2610738 62	1
GO:00303 26	embryonic limb morphogenesis	0.4599699 24	0.2610738 62	1
GO:00326 06	type I interferon production	0.4599699 24	0.2610738 62	1
GO:00351 13	embryonic appendage morphogenesis	0.4599699 24	0.2610738 62	1
GO:00000 41	transition metal ion transport	0.4652022 97	0.2638781 55	1

GO:19038 44	regulation of cellular response to transforming growth factor beta stimulus	0.4652022 97	0.2638781 55	1
GO:00714 26	ribonucleoprotein complex export from nucleus	0.4677996 49	0.2652683 03	1
GO:00468 87	positive regulation of hormone secretion	0.4703845 25	0.2665669 96	1
GO:00711 66	ribonucleoprotein complex localization	0.4703845 25	0.2665669 96	1
GO:00062 82	regulation of DNA repair	0.4729569 83	0.2679408 94	1
GO:00901 01	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	0.4755170 84	0.2693069 32	1
GO:00029 20	regulation of humoral immune response	0.4780648 84	0.2704113 24	1
GO:00074 98	mesoderm development	0.4780648 84	0.2704113 24	1
GO:00098 55	determination of bilateral symmetry	0.4780648 84	0.2704113 24	1
GO:00459 95	regulation of embryonic development	0.4780648 84	0.2704113 24	1
GO:00097 99	specification of symmetry	0.4806004 43	0.2715908 35	1
GO:00157 48	organophosphate ester transport	0.4806004 43	0.2715908 35	1
GO:00421 57	lipoprotein metabolic process	0.4806004 43	0.2715908 35	1
GO:00310 23	microtubule organizing center organization	0.4831238 19	0.2729315 76	1
GO:00197 30	antimicrobial humoral response	0.4856350 7	0.2740935 37	1
GO:00305 34	adult behavior	0.4856350 7	0.2740935 37	1
GO:00425 52	myelination	0.4856350 7	0.2740935 37	1
GO:00007 24	double-strand break repair via homologous recombination	0.4881342 54	0.2749894 42	1
GO:00338 65	nucleoside bisphosphate metabolic process	0.4881342 54	0.2749894 42	1
GO:00338 75	ribonucleoside bisphosphate metabolic process	0.4881342 54	0.2749894 42	1
GO:00340 32	purine nucleoside bisphosphate metabolic process	0.4881342 54	0.2749894 42	1
GO:00463 30	positive regulation of JNK cascade	0.4881342 54	0.2749894 42	1

GO:00723 29	monocarboxylic acid catabolic process	0.4881342 54	0.2749894 42	1
GO:00600 70	canonical Wnt signaling pathway	0.4886684 71	0.2752047 12	1
GO:00160 50	vesicle organization	0.4902232 1	0.2758752 52	1
GO:00024 33	immune response-regulating cell surface receptor signaling pathway involved in phagocytosis	0.4906214 27	0.2758752 52	1
GO:00072 72	ensheathment of neurons	0.4906214 27	0.2758752 52	1
GO:00083 66	axon ensheathment	0.4906214 27	0.2758752 52	1
GO:00380 96	Fc-gamma receptor signaling pathway involved in phagocytosis	0.4906214 27	0.2758752 52	1
GO:00007 25	recombinational repair	0.4930966 48	0.2770948 47	1
GO:00482 84	organelle fusion	0.4930966 48	0.2770948 47	1
GO:00066 50	glycerophospholipid metabolic process	0.4948699 65	0.2780050 23	1
GO:19033 22	positive regulation of protein modification by small protein conjugation or removal	0.4955599 72	0.2783062 47	1
GO:00380 94	Fc-gamma receptor signaling pathway	0.4980114 56	0.2795962 22	1
GO:00064 05	RNA export from nucleus	0.5028791 3	0.2821539 7	1
GO:19028 50	microtubule cytoskeleton organization involved in mitosis	0.5028791 3	0.2821539 7	1
GO:00024 31	Fc receptor mediated stimulatory signaling pathway	0.5052954 32	0.2834218 18	1
GO:00444 09	entry into host	0.5100932 41	0.2860242 63	1
GO:20012 51	negative regulation of chromosome organization	0.5124748 6	0.2872706 85	1
GO:00030 02	regionalization	0.5131912 85	0.2874941 56	1
GO:00711 03	DNA conformation change	0.5131912 85	0.2874941 56	1
GO:00070 34	vacuolar transport	0.5172037 97	0.2893836 3	1
GO:00351 07	appendage morphogenesis	0.5172037 97	0.2893836 3	1
GO:00351 08	limb morphogenesis	0.5172037 97	0.2893836 3	1

GO:19050 39	carboxylic acid transmembrane transport	0.5172037 97	0.2893836 3	1
GO:00355 67	non-canonical Wnt signaling pathway	0.5195512 25	0.2905173 88	1
GO:19038 25	organic acid transmembrane transport	0.5195512 25	0.2905173 88	1
GO:00018 18	negative regulation of cytokine production	0.5206976 85	0.2910685 07	1
GO:00076 05	sensory perception of sound	0.5218873 64	0.2915533 96	1
GO:00506 84	regulation of mRNA processing	0.5218873 64	0.2915533 96	1
GO:00311 23	RNA 3'-end processing	0.5242122 67	0.2927618 22	1
GO:00109 77	negative regulation of neuron projection development	0.5265259 9	0.2938725 86	1
GO:00512 50	negative regulation of lymphocyte activation	0.5265259 9	0.2938725 86	1
GO:00099 13	epidermal cell differentiation	0.5281279 42	0.2946757 98	1
GO:00024 55	humoral immune response mediated by circulating immunoglobulin	0.5288285 83	0.2948848 71	1
GO:00507 73	regulation of dendrite development	0.5288285 83	0.2948848 71	1
GO:00344 01	chromatin organization involved in regulation of transcription	0.5311201 02	0.2960714 26	1
GO:00070 18	microtubule-based movement	0.5325492 62	0.2967766 79	1
GO:00302 03	glycosaminoglycan metabolic process	0.5356701 22	0.2984239 5	1
GO:00322 59	methylation	0.5369427 92	0.2990408 9	1
GO:00507 77	negative regulation of immune response	0.5379287 29	0.2994056 84	1
GO:19026 00	proton transmembrane transport	0.5379287 29	0.2994056 84	1
GO:19029 03	regulation of supramolecular fiber organization	0.5398563 11	0.3003861 58	1
GO:00000 70	mitotic sister chromatid segregation	0.5424133 96	0.3016234 68	1
GO:00007 23	telomere maintenance	0.5424133 96	0.3016234 68	1
GO:00164 82	cytosolic transport	0.5512539 81	0.3064453 37	1

GO:00485 15	spermatid differentiation	0.5534376 02	0.3075647 35	1
GO:00521 26	movement in host environment	0.5599256 07	0.3109793 28	1
GO:00610 25	membrane fusion	0.5599256 07	0.3109793 28	1
GO:00009 10	cytokinesis	0.5663203 7	0.3142415 84	1
GO:00019 06	cell killing	0.5663203 7	0.3142415 84	1
GO:00060 22	aminoglycan metabolic process	0.5663203 7	0.3142415 84	1
GO:00091 52	purine ribonucleotide biosynthetic process	0.5684314 67	0.3151230 95	1
GO:00509 54	sensory perception of mechanical stimulus	0.5684314 67	0.3151230 95	1
GO:00991 73	postsynapse organization	0.5684314 67	0.3151230 95	1
GO:00313 46	positive regulation of cell projection organization	0.5696915 54	0.3157249 23	1
GO:00308 33	regulation of actin filament polymerization	0.5705324	0.3159973 56	1
GO:00322 00	telomere organization	0.5705324	0.3159973 56	1
GO:01400 13	meiotic nuclear division	0.5767746 96	0.3193569 87	1
GO:00344 70	ncRNA processing	0.5779597 64	0.3199152 59	1
GO:00190 83	viral transcription	0.5788354 54	0.3203019 94	1
GO:00329 70	regulation of actin filament-based process	0.5847623 41	0.3233934 54	1
GO:00487 36	appendage development	0.5849583 69	0.3233934 54	1
GO:00601 73	limb development	0.5849583 69	0.3233934 54	1
GO:00902 88	negative regulation of cellular response to growth factor stimulus	0.5869797 12	0.3244118 33	1
GO:00070 51	spindle organization	0.5889913 18	0.3253248 75	1
GO:01200 32	regulation of plasma membrane bounded cell projection assembly	0.5889913 18	0.3253248 75	1
GO:00026 95	negative regulation of leukocyte activation	0.5909932 34	0.3262314 53	1

GO:00074 16	synapse assembly	0.5909932 34	0.3262314 53	1
GO:00604 91	regulation of cell projection assembly	0.5929855 05	0.3272313 71	1
GO:00092 60	ribonucleotide biosynthetic process	0.5949681 78	0.3282253 85	1
GO:00091 00	glycoprotein metabolic process	0.5981279 54	0.3298679 65	1
GO:00080 64	regulation of actin polymerization or depolymerization	0.6028038	0.3323454 03	1
GO:00308 32	regulation of actin filament length	0.6047391 64	0.3333108 75	1
GO:00219 53	central nervous system neuron differentiation	0.6066652 01	0.3341688 63	1
GO:00442 72	sulfur compound biosynthetic process	0.6066652 01	0.3341688 63	1
GO:00300 41	actin filament polymerization	0.6085819 55	0.3350206 97	1
GO:19030 46	meiotic cell cycle process	0.6085819 55	0.3350206 97	1
GO:00463 90	ribose phosphate biosynthetic process	0.6104894 71	0.3357643 26	1
GO:00465 78	regulation of Ras protein signal transduction	0.6104894 71	0.3357643 26	1
GO:19021 15	regulation of organelle assembly	0.6104894 71	0.3357643 26	1
GO:00072 19	Notch signaling pathway	0.6123877 92	0.3365015 47	1
GO:00190 80	viral gene expression	0.6123877 92	0.3365015 47	1
GO:00314 97	chromatin assembly	0.6123877 92	0.3365015 47	1
GO:00008 19	sister chromatid segregation	0.6142769 63	0.3374371 58	1
GO:00506 57	nucleic acid transport	0.6217430 11	0.3413311 95	1
GO:00506 58	RNA transport	0.6217430 11	0.3413311 95	1
GO:00070 15	actin filament organization	0.6226414 22	0.3416171 22	1
GO:00464 86	glycerolipid metabolic process	0.6226414 22	0.3416171 22	1
GO:19016 05	alpha-amino acid metabolic process	0.6254222 57	0.3430388 35	1

GO:00512 36	establishment of RNA localization	0.6272485 84	0.3439363 05	1
GO:00603 48	bone development	0.6290661 05	0.3448284 04	1
GO:00068 88	endoplasmic reticulum to Golgi vesicle-mediated transport	0.6326748 91	0.3465965 99	1
GO:00508 52	T cell receptor signaling pathway	0.6326748 91	0.3465965 99	1
GO:00301 00	regulation of endocytosis	0.6397886 12	0.3503876 08	1
GO:00516 50	establishment of vesicle localization	0.6432942 04	0.3522008 88	1
GO:00063 38	chromatin remodeling	0.6536097 92	0.3576322 1	1
GO:00718 05	potassium ion transmembrane transport	0.6536097 92	0.3576322 1	1
GO:00099 52	anterior/posterior pattern specification	0.6553001 34	0.3584487 15	1
GO:00063 33	chromatin assembly or disassembly	0.6569823 18	0.3591517 27	1
GO:00171 48	negative regulation of translation	0.6569823 18	0.3591517 27	1
GO:00081 54	actin polymerization or depolymerization	0.6586563 83	0.3599581 37	1
GO:00435 83	ear development	0.6636302 46	0.3625668 68	1
GO:00080 37	cell recognition	0.6669062 63	0.3642467 05	1
GO:00063 64	rRNA processing	0.6685324 19	0.3650246 89	1
GO:00487 05	skeletal system morphogenesis	0.6701507 22	0.3657979 17	1
GO:00516 48	vesicle localization	0.6717612 1	0.3665664 15	1
GO:00064 57	protein folding	0.6733639 21	0.3672194 98	1
GO:00464 74	glycerophospholipid biosynthetic process	0.6733639 21	0.3672194 98	1
GO:00512 59	protein complex oligomerization	0.6749588 92	0.3679784 13	1
GO:00226 18	ribonucleoprotein complex assembly	0.6781257 62	0.3695935 91	1
GO:00064 03	RNA localization	0.6828189 35	0.3720394 14	1

GO:00160 72	rRNA metabolic process	0.6859100 52	0.3734987 03	1
GO:00342 49	negative regulation of cellular amide metabolic process	0.6859100 52	0.3734987 03	1
GO:00718 26	ribonucleoprotein complex subunit organization	0.6889713 72	0.3750528 18	1
GO:00513 21	meiotic cell cycle	0.7095898 26	0.3860445 33	1
GO:00900 92	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	0.7095898 26	0.3860445 33	1
GO:00159 31	nucleobase-containing compound transport	0.7193861 3	0.3912564 68	1
GO:00450 17	glycerolipid biosynthetic process	0.7315024 87	0.3977267 13	1
GO:00086 54	phospholipid biosynthetic process	0.7328163 87	0.3983214 08	1
GO:00988 13	nuclear chromosome segregation	0.7341239 27	0.3989122 9	1
GO:00987 42	cell-cell adhesion via plasma-membrane adhesion molecules	0.7405672 98	0.4022927 16	1
GO:01100 53	regulation of actin filament organization	0.7418373 17	0.4028616 76	1
GO:00315 03	protein-containing complex localization	0.7577985 59	0.4114061 06	1
GO:00485 62	embryonic organ morphogenesis	0.7705389 9	0.4181973 68	1
GO:00422 54	ribosome biogenesis	0.7793862 2	0.4228722 2	1
GO:00986 56	anion transmembrane transport	0.7847435 25	0.4256513 06	1
GO:00434 14	macromolecule methylation	0.7878959 35	0.4272331 32	1
GO:00510 56	regulation of small GTPase mediated signal transduction	0.7930487 94	0.4298984 19	1
GO:00070 59	chromosome segregation	0.8039533 03	0.4356790 49	1
GO:00002 09	protein polyubiquitination	0.8096596 55	0.4385087 81	1
GO:00065 20	cellular amino acid metabolic process	0.8096596 55	0.4385087 81	1
GO:00091 01	glycoprotein biosynthetic process	0.8115250 22	0.4393875 44	1
GO:00329 56	regulation of actin cytoskeleton organization	0.8275200 98	0.4479138 02	1

GO:00067 90	sulfur compound metabolic process	0.8366260 03	0.4527071 58	1
GO:00481 93	Golgi vesicle transport	0.8390258 09	0.4538699 91	1
GO:00066 05	protein targeting	0.8861054 63	0.4791944 16	1
GO:00076 08	sensory perception of smell	0.8905301 17	0.4814433 26	1
GO:00226 13	ribonucleoprotein complex biogenesis	0.9056597 7	0.4894765 6	1

Table S2. Results of CC GO terms enrichment of *Scutellaria baicalensis* in breast cancer.

ID	Description	pvalue	qvalue	Count
GO:0045121	membrane raft	4.02216E-09	3.66649E-07	13
GO:0098857	membrane microdomain	4.17145E-09	3.66649E-07	13
GO:0098589	membrane region	6.62638E-09	3.88282E-07	13
GO:0042734	presynaptic membrane	4.64859E-08	1.83355E-06	10
GO:0099056	integral component of presynaptic membrane	5.21519E-08	1.83355E-06	9
GO:0098889	intrinsic component of presynaptic membrane	1.16317E-07	3.40789E-06	9
GO:0099055	integral component of postsynaptic membrane	1.22265E-06	3.07043E-05	8
GO:0098936	intrinsic component of postsynaptic membrane	1.62059E-06	3.56104E-05	8
GO:0005901	caveola	2.26278E-06	4.41969E-05	8
GO:0099699	integral component of synaptic membrane	7.61425E-06	0.000126047	8
GO:0031968	organelle outer membrane	8.04921E-06	0.000126047	8
GO:0019867	outer membrane	8.60442E-06	0.000126047	7
GO:0099240	intrinsic component of synaptic membrane	1.24327E-05	0.00015894	7
GO:0097060	synaptic membrane	1.26581E-05	0.00015894	7
GO:0044853	plasma membrane raft	1.45482E-05	0.000170495	7
GO:0005741	mitochondrial outer membrane	3.17801E-05	0.000349163	7
GO:0045211	postsynaptic membrane	4.85648E-05	0.000502187	7
GO:0005667	transcription regulator complex	0.000130061	0.001270191	7
GO:0098978	glutamatergic synapse	0.000279469	0.002585673	7
GO:0034399	nuclear periphery	0.000366184	0.003218569	7
GO:0042383	sarcolemma	0.00042043	0.003519391	6
GO:0060205	cytoplasmic vesicle lumen	0.00081931	0.006489825	6
GO:0031983	vesicle lumen	0.000849118	0.006489825	6
GO:0090575	RNA polymerase II transcription regulator complex	0.000934121	0.006842024	6
GO:0000307	cyclin-dependent protein kinase holoenzyme complex	0.001050845	0.007389098	5
GO:0098691	dopaminergic synapse	0.001615165	0.010561098	5
GO:0005635	nuclear envelope	0.001622109	0.010561098	5
GO:0030315	T-tubule	0.002035625	0.012780054	5
GO:0031965	nuclear membrane	0.002820252	0.017095536	5
GO:0031093	platelet alpha granule lumen	0.003764251	0.022057189	4
GO:0034774	secretory granule lumen	0.003925275	0.022258777	4
GO:0046930	pore complex	0.005082967	0.02792288	4
GO:0032809	neuronal cell body membrane	0.007480715	0.039849423	4
GO:0120111	neuron projection cytoplasm	0.007791766	0.0402856	4
GO:1902554	serine/threonine protein kinase complex	0.008292834	0.041651228	4
GO:0031091	platelet alpha granule	0.008812476	0.043031682	4
GO:0044298	cell body membrane	0.009119741	0.0433285	4
GO:0032839	dendrite cytoplasm	0.010903724	0.050441049	4
GO:1902911	protein kinase complex	0.012651981	0.057027824	4
GO:0016363	nuclear matrix	0.014345947	0.06304666	3
GO:0034703	cation channel complex	0.019752972	0.082446891	3

GO:0101002	ficolin-1-rich granule	0.020167398	0.082446891	3
GO:1904813	ficolin-1-rich granule lumen	0.020167398	0.082446891	3
GO:0099061	integral component of postsynaptic density membrane	0.023550587	0.094089666	3
GO:0099146	intrinsic component of postsynaptic density membrane	0.026196402	0.102334482	3
GO:1904724	tertiary granule lumen	0.027103969	0.103578097	3
GO:0061695	transferase complex, transferring phosphorus-containing groups	0.030473829	0.113978264	3
GO:0072562	blood microparticle	0.031811899	0.116504104	3
GO:0070820	tertiary granule	0.041156192	0.147649496	3
GO:0098981	cholinergic synapse	0.045574055	0.15703743	3
GO:0099060	integral component of postsynaptic specialization membrane	0.046591354	0.15703743	3
GO:0005775	vacuolar lumen	0.046955673	0.15703743	3
GO:0017053	transcription repressor complex	0.048871309	0.15703743	3
GO:0062023	collagen-containing extracellular matrix	0.049067084	0.15703743	3
GO:0005652	nuclear lamina	0.050016879	0.15703743	3
GO:0098948	intrinsic component of postsynaptic specialization membrane	0.050026295	0.15703743	3
GO:0034702	ion channel complex	0.050927576	0.157061962	3
GO:0030877	beta-catenin destruction complex	0.054439247	0.159497444	3
GO:1990454	L-type voltage-gated calcium channel complex	0.054439247	0.159497444	3
GO:1990909	Wnt signalosome	0.054439247	0.159497444	3
GO:0005788	endoplasmic reticulum lumen	0.05563261	0.160321757	3
GO:0098685	Schaffer collateral - CA1 synapse	0.058380686	0.161619892	3
GO:0033391	chromatoid body	0.058841254	0.161619892	2
GO:0044292	dendrite terminus	0.058841254	0.161619892	2
GO:0000940	condensed chromosome outer kinetochore	0.063222992	0.168875319	2
GO:1902495	transmembrane transporter complex	0.063404087	0.168875319	2
GO:0035578	azurophil granule lumen	0.067179564	0.17444094	2
GO:1990351	transporter complex	0.06808959	0.17444094	2
GO:0098839	postsynaptic density membrane	0.068470681	0.17444094	2
GO:0014069	postsynaptic density	0.072333495	0.176361972	2
GO:0032838	plasma membrane bounded cell projection cytoplasm	0.075532841	0.176361972	2
GO:0032279	asymmetric synapse	0.076076985	0.176361972	2
GO:0000778	condensed nuclear chromosome kinetochore	0.076247511	0.176361972	2
GO:0001518	voltage-gated sodium channel complex	0.076247511	0.176361972	2
GO:0043083	synaptic cleft	0.076247511	0.176361972	2
GO:0043194	axon initial segment	0.076247511	0.176361972	2
GO:0005911	cell-cell junction	0.080010581	0.181534389	2
GO:0097440	apical dendrite	0.080549091	0.181534389	2
GO:0000794	condensed nuclear chromosome	0.083193345	0.182806429	2
GO:0005604	basement membrane	0.083193345	0.182806429	2
GO:0000159	protein phosphatase type 2A complex	0.084830859	0.18410336	2
GO:0099572	postsynaptic specialization	0.08788261	0.18840046	2
GO:0071682	endocytic vesicle lumen	0.089092906	0.188693916	2
GO:0098984	neuron to neuron synapse	0.092701629	0.193027846	2

GO:0005697	telomerase holoenzyme complex	0.093335321	0.193027846	2
GO:0030687	preribosome, large subunit precursor	0.101761613	0.208007214	2
GO:0099634	postsynaptic specialization membrane	0.104638306	0.211428882	2
GO:0035327	transcriptionally active chromatin	0.105945668	0.211637877	2
GO:0034706	sodium channel complex	0.114256036	0.224644757	2
GO:0099568	cytoplasmic region	0.115012735	0.224644757	2
GO:0001891	phagocytic cup	0.118382524	0.226200018	2
GO:0034364	high-density lipoprotein particle	0.118382524	0.226200018	2
GO:0030018	Z disc	0.11967757	0.226215666	2
GO:0005640	nuclear outer membrane	0.122489999	0.227134243	2
GO:0043679	axon terminus	0.122747697	0.227134243	2
GO:0031674	I band	0.13837551	0.251417879	2
GO:0000780	condensed nuclear chromosome, centromeric region	0.138731482	0.251417879	2
GO:0005669	transcription factor TFIID complex	0.146740373	0.260559727	2
GO:0005719	nuclear euchromatin	0.146740373	0.260559727	1
GO:0044306	neuron projection terminus	0.152791731	0.266571986	1
GO:0034358	plasma lipoprotein particle	0.154675601	0.266571986	1
GO:1990777	lipoprotein particle	0.154675601	0.266571986	1
GO:0043198	dendritic shaft	0.162537836	0.272157877	1
GO:0005766	primary lysosome	0.162561366	0.272157877	1
GO:0042582	azurophil granule	0.162561366	0.272157877	1
GO:0043204	perikaryon	0.164200762	0.27230911	1
GO:0032994	protein-lipid complex	0.166441788	0.273445929	1
GO:0150034	distal axon	0.174229708	0.282940811	1
GO:0000781	chromosome, telomeric region	0.17741905	0.282940811	1
GO:0000791	euchromatin	0.178045975	0.282940811	1
GO:0000922	spindle pole	0.179083314	0.282940811	1
GO:0005891	voltage-gated calcium channel complex	0.181878419	0.282940811	1
GO:0032590	dendrite membrane	0.181878419	0.282940811	1
GO:0043209	myelin sheath	0.197032264	0.303826298	1
GO:0008287	protein serine/threonine phosphatase complex	0.211908446	0.313035917	1
GO:0009925	basal plasma membrane	0.211908446	0.313035917	1
GO:0014704	intercalated disc	0.211908446	0.313035917	1
GO:0098878	neurotransmitter receptor complex	0.211908446	0.313035917	1
GO:1903293	phosphatase complex	0.211908446	0.313035917	1
GO:0005782	peroxisomal matrix	0.215584698	0.31320265	1
GO:0031907	microbody lumen	0.215584698	0.31320265	1
GO:0098687	chromosomal region	0.222883761	0.318545385	1
GO:0032154	cleavage furrow	0.222886397	0.318545385	1
GO:1904115	axon cytoplasm	0.233713084	0.331325001	1
GO:0005819	spindle	0.243818993	0.337838653	1
GO:0005637	nuclear inner membrane	0.24439057	0.337838653	1
GO:0032993	protein-DNA complex	0.247101393	0.337838653	1

GO:0032589	neuron projection membrane	0.247916928	0.337838653	1
GO:0035861	site of double-strand break	0.247916928	0.337838653	1
GO:0030017	sarcomere	0.250546735	0.33879599	1
GO:0005769	early endosome	0.2562852	0.343910232	1
GO:0016328	lateral plasma membrane	0.26186033	0.348729467	1
GO:0034704	calcium channel complex	0.268735845	0.355194984	1
GO:0044304	main axon	0.272149812	0.356834412	1
GO:0045178	basal part of cell	0.275548015	0.356834412	1
GO:0000793	condensed chromosome	0.276416242	0.356834412	1
GO:0005657	replication fork	0.282297415	0.356834412	1
GO:0016529	sarcoplasmic reticulum	0.282297415	0.356834412	1
GO:0030016	myofibril	0.285037082	0.356834412	1
GO:0032153	cell division site	0.285648756	0.356834412	1
GO:0016607	nuclear speck	0.286540008	0.356834412	1
GO:0070821	tertiary granule membrane	0.28898462	0.356834412	1
GO:0044291	cell-cell contact zone	0.292305075	0.356834412	1
GO:0098982	GABA-ergic synapse	0.292305075	0.356834412	1
GO:0031594	neuromuscular junction	0.298900046	0.362368839	1
GO:0043292	contractile fiber	0.303966926	0.362784608	1
GO:0005925	focal adhesion	0.304336974	0.362784608	1
GO:0030684	preribosome	0.305434227	0.362784608	1
GO:0016591	RNA polymerase II, holoenzyme	0.308678695	0.363113733	1
GO:0005758	mitochondrial intermembrane space	0.311908174	0.363113733	1
GO:0016528	sarcoplasm	0.311908174	0.363113733	1
GO:0030055	cell-substrate junction	0.314534455	0.363361904	1
GO:0016323	basolateral plasma membrane	0.317683524	0.363361904	1
GO:0090734	site of DNA damage	0.318322435	0.363361904	1
GO:0008076	voltage-gated potassium channel complex	0.33721252	0.382441364	1
GO:0001750	photoreceptor outer segment	0.340310135	0.383480382	1
GO:0031970	organelle envelope lumen	0.343393432	0.384490131	1
GO:0035579	specific granule membrane	0.346462475	0.385471241	1
GO:1905368	peptidase complex	0.34951733	0.386424323	1
GO:0034705	potassium channel complex	0.361596161	0.394812415	1
GO:0043202	lysosomal lumen	0.361596161	0.394812415	1
GO:0070469	respirasome	0.376383166	0.399442072	1
GO:0005759	mitochondrial matrix	0.378229003	0.399442072	1
GO:0016605	PML body	0.379299659	0.399442072	1
GO:0005796	Golgi lumen	0.382202662	0.399442072	1
GO:0055029	nuclear DNA-directed RNA polymerase complex	0.382202662	0.399442072	1
GO:0000428	DNA-directed RNA polymerase complex	0.385092237	0.399442072	1
GO:0042470	melanosome	0.387968444	0.399442072	1
GO:0048770	pigment granule	0.387968444	0.399442072	1
GO:0000777	condensed chromosome kinetochore	0.390831344	0.399442072	1

GO:0030175	filopodium	0.390831344	0.399442072	1
GO:0030863	cortical cytoskeleton	0.390831344	0.399442072	1
GO:0030880	RNA polymerase complex	0.396517471	0.402910968	1
GO:0022626	cytosolic ribosome	0.402151099	0.406286954	1
GO:0098802	plasma membrane signaling receptor complex	0.419403855	0.420958119	1
GO:0097733	photoreceptor cell cilium	0.42146226	0.420958119	1
GO:0030665	clathrin-coated vesicle membrane	0.424170157	0.421269201	1
GO:0000779	condensed chromosome, centromeric region	0.434876959	0.427077049	1
GO:0005923	bicellular tight junction	0.434876959	0.427077049	1
GO:0070160	tight junction	0.453142153	0.442542336	1
GO:0005793	endoplasmic reticulum-Golgi intermediate compartment	0.45570335	0.442584818	1
GO:0000776	kinetochore	0.473302563	0.452182654	1
GO:0005777	peroxisome	0.473302563	0.452182654	1
GO:0042579	microbody	0.473302563	0.452182654	1
GO:0097731	9+0 non-motile cilium	0.478226712	0.454285067	1
GO:0045335	phagocytic vesicle	0.480671684	0.454285067	1
GO:0043296	apical junction complex	0.48793882	0.458687211	1
GO:0016324	apical plasma membrane	0.502858043	0.47019761	1
GO:0036064	ciliary basal body	0.516015148	0.479947255	1
GO:0005875	microtubule associated complex	0.525031252	0.485270246	1
GO:0042581	specific granule	0.527259199	0.485270246	1
GO:0005912	adherens junction	0.540411464	0.494185238	1
GO:0097730	non-motile cilium	0.542568045	0.494185238	1
GO:0031225	anchored component of membrane	0.551094734	0.499364192	1
GO:0031256	leading edge membrane	0.559464198	0.501775086	1
GO:0043197	dendritic spine	0.559464198	0.501775086	1
GO:0044309	neuron spine	0.563590868	0.502910366	1
GO:0030662	coated vesicle membrane	0.575742865	0.510350765	1
GO:0030426	growth cone	0.577735402	0.510350765	1
GO:0009897	external side of plasma membrane	0.580974744	0.510646222	1
GO:0055037	recycling endosome	0.589497738	0.514685795	1
GO:0030427	site of polarized growth	0.591426371	0.514685795	1
GO:0030136	clathrin-coated vesicle	0.597158665	0.515881161	1
GO:0000775	chromosome, centromeric region	0.60093593	0.515881161	1
GO:0045177	apical part of cell	0.601603929	0.515881161	1
GO:0031514	motile cilium	0.606536243	0.517585859	1
GO:0005882	intermediate filament	0.635117365	0.539357234	1
GO:0098858	actin-based cell projection	0.643620454	0.543950485	1
GO:0036464	cytoplasmic ribonucleoprotein granule	0.664822204	0.559180599	1
GO:0035770	ribonucleoprotein granule	0.680277935	0.569455715	1
GO:0045111	intermediate filament cytoskeleton	0.69213321	0.576633804	1
GO:0098798	mitochondrial protein complex	0.711842886	0.590257011	1
GO:0005840	ribosome	0.718575231	0.593042074	1

GO:0030135	coated vesicle	0.753499607	0.618959342	1
GO:0005938	cell cortex	0.761538462	0.62068781	1
GO:0030667	secretory granule membrane	0.762665501	0.62068781	1
GO:0030139	endocytic vesicle	0.77040861	0.624100111	1
GO:0031253	cell projection membrane	0.801802754	0.646552679	1
GO:0031252	cell leading edge	0.862584809	0.692389633	1
GO:0005874	microtubule	0.868982236	0.694354227	1
GO:0005743	mitochondrial inner membrane	0.900681688	0.716426968	1

Table S3. Results of MF GO terms enrichment of *Scutellaria baicalensis* in breast cancer.

ID	Description	pvalue	qvalue	Count
GO:000 8227	G protein-coupled amine receptor activity	1.4282E -10	3.35252 E-08	11
GO:000 1223	transcription coactivator binding	5.45016 E-09	3.81772 E-07	11
GO:000 4879	nuclear receptor activity	6.50553 E-09	3.81772 E-07	10
GO:009 8531	ligand-activated transcription factor activity	6.50553 E-09	3.81772 E-07	10
GO:009 9528	G protein-coupled neurotransmitter receptor activity	1.16114 E-07	5.45124 E-06	10
GO:000 3707	steroid hormone receptor activity	1.62524 E-07	6.34906 E-06	9
GO:000 1221	transcription cofactor binding	1.89333 E-07	6.34906 E-06	8
GO:002 0037	heme binding	4.19123 E-07	1.2023E -05	8
GO:004 4389	ubiquitin-like protein ligase binding	4.6097E -07	1.2023E -05	8
GO:004 6906	tetrapyrrole binding	7.14631 E-07	1.6775E -05	8
GO:006 1629	RNA polymerase II-specific DNA-binding transcription factor binding	8.19321 E-07	1.74841 E-05	8
GO:014 0297	DNA-binding transcription factor binding	1.1571E -06	2.26344 E-05	8
GO:000 1091	RNA polymerase II general transcription initiation factor binding	2.07114 E-06	3.59193 E-05	7
GO:003 1625	ubiquitin protein ligase binding	2.14227 E-06	3.59193 E-05	7
GO:004 6982	protein heterodimerization activity	4.27855 E-06	6.69556 E-05	7
GO:000 2020	protease binding	5.31956 E-06	7.80436 E-05	7
GO:000 8144	drug binding	1.29264 E-05	0.00017 8124	7
GO:009 7199	cysteine-type endopeptidase activity involved in apoptotic signaling pathway	1.38015 E-05	0.00017 8124	7
GO:000 5496	steroid binding	1.44177 E-05	0.00017 8124	7
GO:005 1721	protein phosphatase 2A binding	1.82911 E-05	0.00019 2984	7
GO:001	sodium:chloride symporter activity	1.8909E	0.00019	6

5378		-05	2984	
GO:005 1400	BH domain binding	1.8909E -05	0.00019 2984	6
GO:007 0513	death domain binding	1.8909E -05	0.00019 2984	6
GO:001 5373	anion:sodium symporter activity	4.12666 E-05	0.00038 7472	6
GO:190 1338	catecholamine binding	4.12666 E-05	0.00038 7472	6
GO:001 7171	serine hydrolase activity	4.58734 E-05	0.00041 416	6
GO:009 7153	cysteine-type endopeptidase activity involved in apoptotic process	5.13981 E-05	0.00044 6853	6
GO:005 1879	Hsp90 protein binding	5.48182 E-05	0.00045 9566	6
GO:000 5126	cytokine receptor binding	6.01205 E-05	0.00048 6638	6
GO:014 0296	general transcription initiation factor binding	6.59834 E-05	0.00051 6291	6
GO:001 5377	cation:chloride symporter activity	7.62645 E-05	0.00055 9441	6
GO:003 5173	histone kinase activity	7.62645 E-05	0.00055 9441	6
GO:003 2813	tumor necrosis factor receptor superfamily binding	9.31579 E-05	0.00066 2654	6
GO:000 5326	neurotransmitter transmembrane transporter activity	0.00010 7899	0.00073 3913	6
GO:001 6538	cyclin-dependent protein serine/threonine kinase regulator activity	0.00010 9429	0.00073 3913	6
GO:000 5123	death receptor binding	0.00012 6485	0.00082 4739	5
GO:001 6705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	0.00015 4792	0.00098 2039	5
GO:001 5296	anion:cation symporter activity	0.00016 9643	0.00100 12	5
GO:001 5464	acetylcholine receptor activity	0.00016 9643	0.00100 12	5
GO:000 1085	RNA polymerase II transcription factor binding	0.00017 0608	0.00100 12	5
GO:004 7485	protein N-terminus binding	0.00019 1556	0.00108 8927	5
GO:000 4252	serine-type endopeptidase activity	0.00019 4835	0.00108 8927	5

GO:003 0594	neurotransmitter receptor activity	0.00022 7377	0.00124 1251	5
GO:009 8960	postsynaptic neurotransmitter receptor activity	0.00030 3982	0.00162 1723	5
GO:001 9887	protein kinase regulator activity	0.00031 7199	0.00164 3029	5
GO:000 2039	p53 binding	0.00032 2375	0.00164 3029	4
GO:000 4175	endopeptidase activity	0.00033 2633	0.00164 3029	4
GO:000 8236	serine-type peptidase activity	0.00033 5974	0.00164 3029	4
GO:003 1072	heat shock protein binding	0.00042 3871	0.00203 0577	4
GO:000 1098	basal transcription machinery binding	0.00044 9878	0.00207 0644	4
GO:000 1099	basal RNA polymerase II transcription machinery binding	0.00044 9878	0.00207 0644	4
GO:000 5164	tumor necrosis factor receptor binding	0.00047 9429	0.00212 3389	4
GO:003 0291	protein serine/threonine kinase inhibitor activity	0.00047 9429	0.00212 3389	4
GO:000 4993	G protein-coupled serotonin receptor activity	0.00063 142	0.00269 4865	4
GO:009 9589	serotonin receptor activity	0.00063 142	0.00269 4865	4
GO:001 9207	kinase regulator activity	0.00071 9535	0.00301 6096	4
GO:003 5257	nuclear hormone receptor binding	0.00075 0819	0.00309 2016	4
GO:001 9903	protein phosphatase binding	0.00087 5542	0.00354 3482	4
GO:000 8081	phosphoric diester hydrolase activity	0.00100 1481	0.00398 4482	4
GO:000 1094	TFIID-class transcription factor complex binding	0.00106 6388	0.00403 743	4
GO:001 6725	oxidoreductase activity, acting on CH or CH2 groups	0.00106 6388	0.00403 743	4
GO:001 6803	ether hydrolase activity	0.00106 6388	0.00403 743	4
GO:005 1213	dioxygenase activity	0.00108 8032	0.00405 3988	4
GO:000 5125	cytokine activity	0.00111 3529	0.00408 4161	4

GO:001 6801	hydrolase activity, acting on ether bonds	0.00129 9162	0.00469 1709	4
GO:000 1046	core promoter sequence-specific DNA binding	0.00153 4468	0.00528 6579	4
GO:000 4861	cyclin-dependent protein serine/threonine kinase inhibitor activity	0.00155 397	0.00528 6579	4
GO:004 3176	amine binding	0.00155 397	0.00528 6579	4
GO:005 1378	serotonin binding	0.00155 397	0.00528 6579	4
GO:001 6922	nuclear receptor binding	0.00160 0829	0.00536 8195	3
GO:190 1618	organic hydroxy compound transmembrane transporter activity	0.00173 5919	0.00572 9435	3
GO:005 1087	chaperone binding	0.00178 2633	0.00572 9435	3
GO:000 1162	RNA polymerase II intronic transcription regulatory region sequence-specific DNA binding	0.00183 0593	0.00572 9435	3
GO:003 4236	protein kinase A catalytic subunit binding	0.00183 0593	0.00572 9435	3
GO:004 2166	acetylcholine binding	0.00183 0593	0.00572 9435	3
GO:005 1427	hormone receptor binding	0.00187 8782	0.00580 2885	3
GO:005 0998	nitric-oxide synthase binding	0.00212 8814	0.00648 9755	3
GO:000 4601	peroxidase activity	0.00218 663	0.00658 0546	3
GO:005 0661	NADP binding	0.00243 6724	0.00724 0366	3
GO:004 2826	histone deacetylase binding	0.00257 185	0.00746 1089	3
GO:001 5267	channel activity	0.00260 0455	0.00746 1089	3
GO:002 2803	passive transmembrane transporter activity	0.00263 3959	0.00746 1089	3
GO:001 6684	oxidoreductase activity, acting on peroxide as acceptor	0.00270 3839	0.00746 1089	3
GO:000 1161	intronic transcription regulatory region sequence-specific DNA binding	0.00278 9186	0.00746 1089	3
GO:000 4697	protein kinase C activity	0.00278 9186	0.00746 1089	3
GO:000 4698	calcium-dependent protein kinase C activity	0.00278 9186	0.00746 1089	3

GO:001 6641	oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen as acceptor	0.00278 9186	0.00746 1089	3
GO:001 9902	phosphatase binding	0.00279 7072	0.00746 1089	3
GO:003 3218	amide binding	0.00285 7665	0.00753 707	3
GO:009 7110	scaffold protein binding	0.00329 0617	0.00858 2546	3
GO:000 4860	protein kinase inhibitor activity	0.00412 6195	0.01064 3625	3
GO:001 6638	oxidoreductase activity, acting on the CH-NH2 group of donors	0.00435 9691	0.01100 4088	3
GO:003 1690	adrenergic receptor binding	0.00435 9691	0.01100 4088	3
GO:004 2165	neurotransmitter binding	0.00480 3129	0.01199 4376	3
GO:001 9210	kinase inhibitor activity	0.00487 9444	0.01205 6688	3
GO:000 5518	collagen binding	0.00507 9838	0.01242 1096	3
GO:004 6873	metal ion transmembrane transporter activity	0.00538 6065	0.01303 4102	3
GO:001 5370	solute:sodium symporter activity	0.00549 5362	0.01316 2896	3
GO:000 5178	integrin binding	0.00573 3607	0.01323 164	3
GO:000 4114	3',5'-cyclic-nucleotide phosphodiesterase activity	0.00574 9533	0.01323 164	3
GO:000 9931	calcium-dependent protein serine/threonine kinase activity	0.00574 9533	0.01323 164	3
GO:007 0412	R-SMAD binding	0.00574 9533	0.01323 164	3
GO:000 0979	RNA polymerase II core promoter sequence-specific DNA binding	0.00625 2094	0.01411 1508	3
GO:001 0857	calcium-dependent protein kinase activity	0.00625 2094	0.01411 1508	3
GO:000 5261	cation channel activity	0.00634 2654	0.01417 9567	3
GO:000 5506	iron ion binding	0.00676 6927	0.01458 8053	3
GO:000 4112	cyclic-nucleotide phosphodiesterase activity	0.00677 3959	0.01458 8053	3
GO:001 6702	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	0.00677 3959	0.01458 8053	3

GO:007 0330	aromatase activity	0.00677 3959	0.01458 8053	3
GO:001 5081	sodium ion transmembrane transporter activity	0.00692 394	0.01477 5489	3
GO:000 4435	phosphatidylinositol phospholipase C activity	0.00731 4928	0.01515 176	3
GO:001 6701	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	0.00731 4928	0.01515 176	3
GO:001 7025	TBP-class protein binding	0.00731 4928	0.01515 176	3
GO:003 3613	activating transcription factor binding	0.00735 8456	0.01515 176	3
GO:005 0660	flavin adenine dinucleotide binding	0.00761 4424	0.01554 2486	3
GO:003 0295	protein kinase activator activity	0.00787 5609	0.01593 7031	3
GO:000 4629	phospholipase C activity	0.00845 339	0.01681 6289	3
GO:003 5035	histone acetyltransferase binding	0.00845 339	0.01681 6289	3
GO:000 8013	beta-catenin binding	0.00869 0696	0.01714 308	3
GO:001 6209	antioxidant activity	0.00897 2977	0.01755 2403	3
GO:005 1117	ATPase binding	0.00955 3547	0.01853 3631	3
GO:001 9209	kinase activator activity	0.00985 1875	0.01895 5721	3
GO:004 2578	phosphoric ester hydrolase activity	0.01010 156	0.01927 8117	3
GO:005 1059	NF-kappaB binding	0.01029 9463	0.01949 7285	3
GO:004 8018	receptor ligand activity	0.01059 2597	0.01989 1782	3
GO:003 0546	signaling receptor activator activity	0.01115 9932	0.02079 085	3
GO:005 1019	mitogen-activated protein kinase binding	0.01162 0189	0.02144 7154	3
GO:001 5077	monovalent inorganic cation transmembrane transporter activity	0.01169 495	0.02144 7154	2
GO:001 5294	solute:cation symporter activity	0.01278 1317	0.02325 7721	2
GO:001 6712	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen	0.01301 1159	0.02349 3833	2

GO:009 7718	disordered domain specific binding	0.01373 252	0.02460 7086	2
GO:000 4497	monooxygenase activity	0.01385 6787	0.02464 1654	2
GO:001 5108	chloride transmembrane transporter activity	0.01422 6388	0.02510 8703	2
GO:000 8395	steroid hydroxylase activity	0.01522 6074	0.02647 4967	2
GO:004 3539	protein serine/threonine kinase activator activity	0.01522 6074	0.02647 4967	2
GO:000 5244	voltage-gated ion channel activity	0.01667 837	0.02857 6845	2
GO:002 2832	voltage-gated channel activity	0.01667 837	0.02857 6845	2
GO:000 5516	calmodulin binding	0.01753 0026	0.02981 8428	2
GO:000 9055	electron transfer activity	0.01780 4729	0.03006 7811	2
GO:003 0331	estrogen receptor binding	0.01841 145	0.03087 0325	2
GO:004 2277	peptide binding	0.01857 3441	0.03092 1069	2
GO:000 4197	cysteine-type endopeptidase activity	0.01909 8862	0.03157 1877	2
GO:000 5245	voltage-gated calcium channel activity	0.02010 0426	0.03299 5179	2
GO:000 5216	ion channel activity	0.02026 4799	0.03303 3992	2
GO:000 4712	protein serine/threonine/tyrosine kinase activity	0.02096 8375	0.03345 97	2
GO:001 6709	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen	0.02096 8375	0.03345 97	2
GO:004 8156	tau protein binding	0.02096 8375	0.03345 97	2
GO:000 4674	protein serine/threonine kinase activity	0.02109 6116	0.03345 97	2
GO:000 1102	RNA polymerase II activating transcription factor binding	0.02275 0334	0.03584 1219	2
GO:000 8009	chemokine activity	0.02459 2577	0.03848 5226	2
GO:007 0888	E-box binding	0.02553 5886	0.03943 5614	2
GO:009 9529	neurotransmitter receptor activity involved in regulation of postsynaptic membrane potential	0.02553 5886	0.03943 5614	2

GO:002 2836	gated channel activity	0.02615 4389	0.04012 6789	2
GO:005 1018	protein kinase A binding	0.02649 3766	0.04038 3525	2
GO:003 0374	nuclear receptor transcription coactivator activity	0.02945 3189	0.04460 483	2
GO:000 8234	cysteine-type peptidase activity	0.03186 5404	0.04794 8617	2
GO:002 2843	voltage-gated cation channel activity	0.03244 9462	0.04803 6764	2
GO:004 3621	protein self-association	0.03253 7907	0.04803 6764	2
GO:005 0840	extracellular matrix binding	0.03253 7907	0.04803 6764	2
GO:001 5293	symporter activity	0.03423 5214	0.05022 6663	2
GO:001 9842	vitamin binding	0.03484 1632	0.05079 8848	2
GO:001 5103	inorganic anion transmembrane transporter activity	0.03545 3618	0.05137 2039	2
GO:000 8083	growth factor activity	0.04669 9463	0.06725 2051	2
GO:004 2379	chemokine receptor binding	0.04725 0621	0.06737 3043	2
GO:000 2162	dystroglycan binding	0.04850 5569	0.06737 3043	2
GO:000 4955	prostaglandin receptor activity	0.04850 5569	0.06737 3043	2
GO:000 8603	cAMP-dependent protein kinase regulator activity	0.04850 5569	0.06737 3043	2
GO:001 8455	alcohol dehydrogenase [NAD(P)+] activity	0.04850 5569	0.06737 3043	2
GO:004 3560	insulin receptor substrate binding	0.04850 5569	0.06737 3043	2
GO:000 8201	heparin binding	0.05178 3854	0.07139 5157	2
GO:007 0491	repressing transcription factor binding	0.05218 385	0.07139 5157	2
GO:000 4312	fatty acid synthase activity	0.05322 621	0.07139 5157	2
GO:000 4954	prostanoid receptor activity	0.05322 621	0.07139 5157	2
GO:000 5527	macrolide binding	0.05322 621	0.07139 5157	2

GO:003 1996	thioesterase binding	0.05322 621	0.07139 5157	2
GO:000 1540	amyloid-beta binding	0.05599 928	0.07310 12	2
GO:000 1664	G protein-coupled receptor binding	0.05791 6639	0.07310 12	2
GO:000 3964	RNA-directed DNA polymerase activity	0.05792 3687	0.07310 12	2
GO:000 4115	3',5'-cyclic-AMP phosphodiesterase activity	0.05792 3687	0.07310 12	2
GO:001 6004	phospholipase activator activity	0.05792 3687	0.07310 12	2
GO:003 1543	peptidyl-proline dioxygenase activity	0.05792 3687	0.07310 12	2
GO:003 4452	dynactin binding	0.05792 3687	0.07310 12	2
GO:004 2301	phosphate ion binding	0.05792 3687	0.07310 12	2
GO:004 3023	ribosomal large subunit binding	0.05792 3687	0.07310 12	2
GO:004 7555	3',5'-cyclic-GMP phosphodiesterase activity	0.05792 3687	0.07310 12	2
GO:190 2282	voltage-gated potassium channel activity involved in ventricular cardiac muscle cell action potential repolarization	0.05792 3687	0.07310 12	2
GO:004 6332	SMAD binding	0.05859 5863	0.07355 4053	2
GO:003 5258	steroid hormone receptor binding	0.06123 3572	0.07645 6252	2
GO:000 8179	adenylate cyclase binding	0.06259 8111	0.07653 1682	2
GO:001 6175	superoxide-generating NAD(P)H oxidase activity	0.06259 8111	0.07653 1682	2
GO:001 6653	oxidoreductase activity, acting on NAD(P)H, heme protein as acceptor	0.06259 8111	0.07653 1682	2
GO:003 1005	filamin binding	0.06259 8111	0.07653 1682	2
GO:000 5172	vascular endothelial growth factor receptor binding	0.06724 9595	0.08054 06	2
GO:003 2794	GTPase activating protein binding	0.06724 9595	0.08054 06	2
GO:003 5497	cAMP response element binding	0.06724 9595	0.08054 06	2
GO:006 0229	lipase activator activity	0.06724 9595	0.08054 06	2

GO:000 8237	metallopeptidase activity	0.06770 907	0.08067 9256	2
GO:000 4953	icosanoid receptor activity	0.07187 8251	0.08352 7097	2
GO:000 5161	platelet-derived growth factor receptor binding	0.07187 8251	0.08352 7097	2
GO:003 0553	cGMP binding	0.07187 8251	0.08352 7097	2
GO:004 2809	vitamin D receptor binding	0.07187 8251	0.08352 7097	2
GO:008 6008	voltage-gated potassium channel activity involved in cardiac muscle cell action potential repolarization	0.07187 8251	0.08352 7097	2
GO:000 5159	insulin-like growth factor receptor binding	0.07648 4189	0.08673 2642	2
GO:000 8392	arachidonic acid epoxygenase activity	0.07648 4189	0.08673 2642	2
GO:001 0181	FMN binding	0.07648 4189	0.08673 2642	2
GO:007 0402	NADPH binding	0.07648 4189	0.08673 2642	2
GO:007 1837	HMG box domain binding	0.07648 4189	0.08673 2642	2
GO:000 4708	MAP kinase kinase activity	0.08562 8351	0.09526 1273	2
GO:004 5236	CXCR chemokine receptor binding	0.08562 8351	0.09526 1273	2
GO:004 6965	retinoid X receptor binding	0.08562 8351	0.09526 1273	2
GO:007 0064	proline-rich region binding	0.08562 8351	0.09526 1273	2
GO:003 1406	carboxylic acid binding	0.08843 0236	0.09791 4313	2
GO:001 6722	oxidoreductase activity, oxidizing metal ions	0.09016 6794	0.09890 4059	1
GO:005 0664	oxidoreductase activity, acting on NAD(P)H, oxygen as acceptor	0.09016 6794	0.09890 4059	1
GO:000 1972	retinoic acid binding	0.09468 2957	0.09966 6271	1
GO:000 4707	MAP kinase activity	0.09468 2957	0.09966 6271	1
GO:000 4745	retinol dehydrogenase activity	0.09468 2957	0.09966 6271	1
GO:000 8320	protein transmembrane transporter activity	0.09468 2957	0.09966 6271	1

GO:000 8391	arachidonic acid monooxygenase activity	0.09468 2957	0.09966 6271	1
GO:003 0506	ankyrin binding	0.09468 2957	0.09966 6271	1
GO:003 1418	L-ascorbic acid binding	0.09468 2957	0.09966 6271	1
GO:003 1681	G-protein beta-subunit binding	0.09468 2957	0.09966 6271	1
GO:014 0318	protein transporter activity	0.09468 2957	0.09966 6271	1
GO:000 4620	phospholipase activity	0.09572 8593	0.09987 1233	1
GO:001 6407	acetyltransferase activity	0.09572 8593	0.09987 1233	1
GO:003 1490	chromatin DNA binding	0.09726 6438	0.10102 6622	1
GO:004 3177	organic acid binding	0.10018 2299	0.10287 7514	1
GO:000 4222	metalloendopeptidase activity	0.10036 3243	0.10287 7514	1
GO:009 9094	ligand-gated cation channel activity	0.10036 3243	0.10287 7514	1
GO:001 6651	oxidoreductase activity, acting on NAD(P)H	0.10192 1991	0.10397 5256	1
GO:000 5242	inward rectifier potassium channel activity	0.10364 8876	0.10397 5256	1
GO:002 2884	macromolecule transmembrane transporter activity	0.10364 8876	0.10397 5256	1
GO:005 0321	tau-protein kinase activity	0.10364 8876	0.10397 5256	1
GO:007 0034	telomerase RNA binding	0.10364 8876	0.10397 5256	1
GO:002 2853	active ion transmembrane transporter activity	0.10525 6483	0.10513 8615	1
GO:000 5158	insulin receptor binding	0.10809 8846	0.10597 3127	1
GO:000 5248	voltage-gated sodium channel activity	0.10809 8846	0.10597 3127	1
GO:001 7134	fibroblast growth factor binding	0.10809 8846	0.10597 3127	1
GO:003 0552	cAMP binding	0.10809 8846	0.10597 3127	1
GO:000 5539	glycosaminoglycan binding	0.10834 9206	0.10597 3127	1

GO:001 5101	organic cation transmembrane transporter activity	0.11252 6966	0.10870 1255	1
GO:007 0006	metalloaminopeptidase activity	0.11252 6966	0.10870 1255	1
GO:001 5291	secondary active transmembrane transporter activity	0.11252 7734	0.10870 1255	1
GO:000 5262	calcium channel activity	0.11624 2595	0.11157 9525	1
GO:000 1671	ATPase activator activity	0.11693 3341	0.11157 9525	1
GO:000 4190	aspartic-type endopeptidase activity	0.11693 3341	0.11157 9525	1
GO:001 6616	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	0.11949 1899	0.11211 7411	1
GO:000 1965	G-protein alpha-subunit binding	0.12131 8078	0.11211 7411	1
GO:000 8198	ferrous iron binding	0.12131 8078	0.11211 7411	1
GO:001 5252	proton channel activity	0.12131 8078	0.11211 7411	1
GO:001 6628	oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor	0.12131 8078	0.11211 7411	1
GO:001 7075	syntaxin-1 binding	0.12131 8078	0.11211 7411	1
GO:004 2923	neuropeptide binding	0.12131 8078	0.11211 7411	1
GO:007 0001	aspartic-type peptidase activity	0.12131 8078	0.11211 7411	1
GO:000 1968	fibronectin binding	0.12568 128	0.11524 2293	1
GO:004 2974	retinoic acid receptor binding	0.12568 128	0.11524 2293	1
GO:004 3236	laminin binding	0.13434 3503	0.12270 5718	1
GO:001 6298	lipase activity	0.13606 3462	0.12331 7017	1
GO:001 6614	oxidoreductase activity, acting on CH-OH group of donors	0.13606 3462	0.12331 7017	1
GO:003 0332	cyclin binding	0.13864 273	0.12469 1788	1
GO:004 3325	phosphatidylinositol-3,4-bisphosphate binding	0.13864 273	0.12469 1788	1
GO:190 1681	sulfur compound binding	0.14111 2039	0.12642 8223	1

GO:001 5085	calcium ion transmembrane transporter activity	0.14283 0226	0.12707 8736	1
GO:190 4680	peptide transmembrane transporter activity	0.14292 0839	0.12707 8736	1
GO:000 4713	protein tyrosine kinase activity	0.14453 3157	0.12802 7385	1
GO:001 9838	growth factor binding	0.14624 0415	0.12843 1535	1
GO:001 6417	S-acyltransferase activity	0.14717 7932	0.12843 1535	1
GO:004 8019	receptor antagonist activity	0.14717 7932	0.12843 1535	1
GO:007 1889	14-3-3 protein binding	0.14717 7932	0.12843 1535	1
GO:001 5276	ligand-gated ion channel activity	0.15138 7316	0.13067 0847	1
GO:002 2834	ligand-gated channel activity	0.15138 7316	0.13067 0847	1
GO:000 5251	delayed rectifier potassium channel activity	0.15141 4112	0.13067 0847	1
GO:007 0851	growth factor receptor binding	0.15483 8707	0.13313 681	1
GO:005 2689	carboxylic ester hydrolase activity	0.15830 5445	0.13562 0877	1
GO:000 5501	retinoid binding	0.16399 8182	0.13847 6314	1
GO:003 4061	DNA polymerase activity	0.16399 8182	0.13847 6314	1
GO:004 2805	actinin binding	0.16399 8182	0.13847 6314	1
GO:004 3394	proteoglycan binding	0.16399 8182	0.13847 6314	1
GO:001 6247	channel regulator activity	0.16703 5322	0.13947 4923	1
GO:001 9840	isoprenoid binding	0.16815 1718	0.13947 4923	1
GO:003 0551	cyclic nucleotide binding	0.16815 1718	0.13947 4923	1
GO:004 2056	chemoattractant activity	0.16815 1718	0.13947 4923	1
GO:004 8487	beta-tubulin binding	0.16815 1718	0.13947 4923	1
GO:003 2451	demethylase activity	0.17228 4843	0.14190 0351	1

GO:004 3014	alpha-tubulin binding	0.17228 4843	0.14190 0351	1
GO:000 5547	phosphatidylinositol-3,4,5-trisphosphate binding	0.17639 7657	0.14427 5363	1
GO:001 6248	channel inhibitor activity	0.17639 7657	0.14427 5363	1
GO:001 6504	peptidase activator activity	0.18049 0259	0.14660 1085	1
GO:001 6790	thiolester hydrolase activity	0.18049 0259	0.14660 1085	1
GO:003 0547	receptor inhibitor activity	0.18456 2746	0.14887 8613	1
GO:006 0590	ATPase regulator activity	0.18456 2746	0.14887 8613	1
GO:003 0544	Hsp70 protein binding	0.18861 5217	0.15162 6508	1
GO:007 2509	divalent inorganic cation transmembrane transporter activity	0.19188 8526	0.15373 1422	1
GO:000 5272	sodium channel activity	0.19666 0497	0.15701 8585	1
GO:000 8188	neuropeptide receptor activity	0.20065 35	0.15966 3624	1
GO:000 4177	aminopeptidase activity	0.20462 6873	0.16118 6127	1
GO:000 4715	non-membrane spanning protein tyrosine kinase activity	0.20462 6873	0.16118 6127	1
GO:001 6706	2-oxoglutarate-dependent dioxygenase activity	0.20462 6873	0.16118 6127	1
GO:004 8020	CCR chemokine receptor binding	0.20858 071	0.16375 1095	1
GO:001 5485	cholesterol binding	0.21643 0161	0.16934 7108	1
GO:000 3743	translation initiation factor activity	0.22420 2607	0.17426 6927	1
GO:004 2887	amide transmembrane transporter activity	0.22420 2607	0.17426 6927	1
GO:004 5296	cadherin binding	0.22756 0059	0.17629 2837	1
GO:001 5459	potassium channel regulator activity	0.23189 8794	0.17906 3127	1
GO:000 4402	histone acetyltransferase activity	0.23951 9463	0.18254 5592	1
GO:000 5080	protein kinase C binding	0.23951 9463	0.18254 5592	1

GO:003 0170	pyridoxal phosphate binding	0.23951 9463	0.18254 5592	1
GO:007 0279	vitamin B6 binding	0.23951 9463	0.18254 5592	1
GO:000 8022	protein C-terminus binding	0.24095 2947	0.18304 3799	1
GO:002 2804	active transmembrane transporter activity	0.24334 0179	0.18426 0984	1
GO:004 3022	ribosome binding	0.24706 5347	0.18588 2498	1
GO:006 1733	peptide-lysine-N-acetyltransferase activity	0.24706 5347	0.18588 2498	1
GO:199 0841	promoter-specific chromatin binding	0.25081 0471	0.18809 731	1
GO:001 6597	amino acid binding	0.25453 7171	0.18848 3444	1
GO:001 6627	oxidoreductase activity, acting on the CH-CH group of donors	0.25453 7171	0.18848 3444	1
GO:001 6836	hydro-lyase activity	0.25453 7171	0.18848 3444	1
GO:003 2934	sterol binding	0.25453 7171	0.18848 3444	1
GO:000 5507	copper ion binding	0.25824 5536	0.18943 6693	1
GO:002 2824	transmitter-gated ion channel activity	0.25824 5536	0.18943 6693	1
GO:002 2835	transmitter-gated channel activity	0.25824 5536	0.18943 6693	1
GO:000 8509	anion transmembrane transporter activity	0.26063 4683	0.19059 3652	1
GO:000 4714	transmembrane receptor protein tyrosine kinase activity	0.26193 5655	0.19095 0151	1
GO:000 8235	metalloexopeptidase activity	0.27289 7423	0.19832 5323	1
GO:003 4212	peptide N-acetyltransferase activity	0.27651 5442	0.20033 4449	1
GO:004 8029	monosaccharide binding	0.29081 0321	0.21004 2758	1
GO:000 4857	enzyme inhibitor activity	0.29566 4851	0.21289 3968	1
GO:003 0971	receptor tyrosine kinase binding	0.30134 7827	0.21566 2918	1
GO:003 3293	monocarboxylic acid binding	0.30134 7827	0.21566 2918	1

GO:000 5230	extracellular ligand-gated ion channel activity	0.30828 6649	0.21929 1619	1
GO:001 6835	carbon-oxygen lyase activity	0.30828 6649	0.21929 1619	1
GO:000 4722	protein serine/threonine phosphatase activity	0.31173 0456	0.22107 1368	1
GO:001 6747	transferase activity, transferring acyl groups other than amino-acyl groups	0.31437 1103	0.22227 253	1
GO:001 9905	syntaxin binding	0.32196 046	0.22695 49	1
GO:001 9199	transmembrane receptor protein kinase activity	0.32869 6769	0.23100 9705	1
GO:000 8080	N-acetyltransferase activity	0.34197 1438	0.23819 969	1
GO:000 8135	translation factor activity, RNA binding	0.34197 1438	0.23819 969	1
GO:004 2562	hormone binding	0.34197 1438	0.23819 969	1
GO:003 0165	PDZ domain binding	0.34524 9334	0.23977 1415	1
GO:004 3178	alcohol binding	0.34851 108	0.24132 2685	1
GO:000 5249	voltage-gated potassium channel activity	0.35498 6436	0.24508 3514	1
GO:007 2341	modified amino acid binding	0.36139 8132	0.24877 8464	1
GO:001 6746	transferase activity, transferring acyl groups	0.36855 1653	0.25296 0968	1
GO:000 8238	exopeptidase activity	0.37715 2905	0.25810 986	1
GO:000 3713	transcription coactivator activity	0.38274 2805	0.26117 3946	1
GO:199 0782	protein tyrosine kinase binding	0.38642 0602	0.26291 9281	1
GO:001 6791	phosphatase activity	0.40029 2853	0.27157 0752	1
GO:001 6410	N-acyltransferase activity	0.41341 3172	0.27966 3696	1
GO:009 0079	translation regulator activity, nucleic acid binding	0.41925 0139	0.28279 7281	1
GO:000 0149	SNARE binding	0.43641 8573	0.29269 5765	1
GO:000 5088	Ras guanyl-nucleotide exchange factor activity	0.43641 8573	0.29269 5765	1

GO:000 3730	mRNA 3'-UTR binding	0.44202 9074	0.29561 3986	1
GO:009 9106	ion channel regulator activity	0.44758 433	0.29763 3236	1
GO:190 2936	phosphatidylinositol biphosphate binding	0.44758 433	0.29763 3236	1
GO:000 3712	transcription coregulator activity	0.45025 8379	0.29777 9494	1
GO:000 5267	potassium channel activity	0.45034 1409	0.29777 9494	1
GO:000 5179	hormone activity	0.45581 4804	0.30055 2044	1
GO:001 5078	proton transmembrane transporter activity	0.46926 3583	0.30855 3086	1
GO:001 7124	SH3 domain binding	0.47978 5482	0.31459 0304	1
GO:004 4325	ion channel binding	0.48238 3557	0.31534 6383	1
GO:001 6779	nucleotidyltransferase activity	0.48496 8798	0.31534 6383	1
GO:004 3021	ribonucleoprotein complex binding	0.48496 8798	0.31534 6383	1
GO:000 5319	lipid transporter activity	0.48754 1268	0.31614 3364	1
GO:000 1227	DNA-binding transcription repressor activity, RNA polymerase II-specific	0.49701 6593	0.32139 974	1
GO:000 1217	DNA-binding transcription repressor activity	0.49859 874	0.32153 7071	1
GO:004 5182	translation regulator activity	0.50021 4231	0.32169 5093	1
GO:006 0589	nucleoside-triphosphatase regulator activity	0.51733 9176	0.33179 9356	1
GO:000 8528	G protein-coupled peptide receptor activity	0.52224 9314	0.33403 5844	1
GO:000 1653	peptide receptor activity	0.53173 1611	0.33917 6628	1
GO:001 5079	potassium ion transmembrane transporter activity	0.54102 7732	0.34417 1115	1
GO:001 5631	tubulin binding	0.54309 595	0.34455 3049	1
GO:000 5201	extracellular matrix structural constituent	0.56999 7583	0.36064 5371	1
GO:000 4721	phosphoprotein phosphatase activity	0.59104 4652	0.37195 6984	1

GO:190 1981	phosphatidylinositol phosphate binding	0.59104 4652	0.37195 6984	1
GO:001 6829	lyase activity	0.61107 2313	0.38353 258	1
GO:000 3714	transcription corepressor activity	0.62071 9223	0.38854 8454	1
GO:001 6758	transferase activity, transferring hexosyl groups	0.63382 8507	0.39569 9208	1
GO:000 3779	actin binding	0.64148 9924	0.39924 9438	1
GO:005 1015	actin filament binding	0.64291 6921	0.39924 9438	1
GO:014 0097	catalytic activity, acting on DNA	0.64826 2504	0.40150 6842	1
GO:000 5085	guanyl-nucleotide exchange factor activity	0.65871 7356	0.40690 8505	1
GO:000 5543	phospholipid binding	0.66217 7938	0.40797 2593	1
GO:006 1134	peptidase regulator activity	0.68193 183	0.41904 3257	1
GO:003 5091	phosphatidylinositol binding	0.73065 3118	0.44780 9936	1
GO:000 8017	microtubule binding	0.73469 7698	0.44911 6192	1
GO:003 0246	carbohydrate binding	0.73736 0654	0.44957 3276	1
GO:000 5096	GTPase activator activity	0.74775 0676	0.45355 2021	1
GO:001 6757	transferase activity, transferring glycosyl groups	0.74775 0676	0.45355 2021	1
GO:003 0695	GTPase regulator activity	0.78539 8356	0.47515 9613	1
GO:001 9001	guanyl nucleotide binding	0.86400 186	0.52003 3508	1
GO:003 2561	guanyl ribonucleotide binding	0.86400 186	0.52003 3508	1
GO:001 7016	Ras GTPase binding	0.87589 3789	0.52584 2819	1
GO:003 1267	small GTPase binding	0.88383 6971	0.52925 7907	1

Table S4. Results of KEGG terms enrichment of *Scutellaria baicalensis* in breast cancer.

ID	Description	pvalue	qvalue	Count
hsa05417	Lipid and atherosclerosis	4.61314E-19	3.88475E-17	24
hsa05161	Hepatitis B	8.59501E-17	2.51817E-15	22
hsa04933	AGE-RAGE signaling pathway in diabetic complications	8.97098E-17	2.51817E-15	20
hsa05163	Human cytomegalovirus infection	3.09276E-16	6.51108E-15	20
hsa05167	Kaposi sarcoma-associated herpesvirus infection	3.05986E-15	5.15345E-14	18
hsa04657	IL-17 signaling pathway	1.83733E-14	2.57871E-13	18
hsa05222	Small cell lung cancer	2.92941E-13	3.5241E-12	17
hsa05162	Measles	6.74265E-12	7.09752E-11	17
hsa05205	Proteoglycans in cancer	1.68193E-11	1.57373E-10	17
hsa05170	Human immunodeficiency virus 1 infection	2.88299E-11	2.20707E-10	17
hsa05207	Chemical carcinogenesis - receptor activation	2.88299E-11	2.20707E-10	15
hsa04932	Non-alcoholic fatty liver disease	3.30637E-11	2.32026E-10	15
hsa05210	Colorectal cancer	4.80082E-11	3.10984E-10	15
hsa04210	Apoptosis	6.93656E-11	4.17237E-10	15
hsa04115	p53 signaling pathway	1.38225E-10	7.76001E-10	15
hsa01522	Endocrine resistance	2.31256E-10	1.21714E-09	14
hsa05142	Chagas disease	3.72245E-10	1.84394E-09	14
hsa05160	Hepatitis C	4.80952E-10	2.25007E-09	14
hsa04668	TNF signaling pathway	1.12154E-09	4.9708E-09	14
hsa05169	Epstein-Barr virus infection	1.42444E-09	5.89244E-09	14
hsa05164	Influenza A	1.4934E-09	5.89244E-09	13
hsa04936	Alcoholic liver disease	1.5394E-09	5.89244E-09	13
hsa01524	Platinum drug resistance	2.65084E-09	9.70558E-09	13
hsa05215	Prostate cancer	3.17274E-09	1.11324E-08	13
hsa05135	Yersinia infection	1.15047E-08	3.83807E-08	13
hsa04151	PI3K-Akt signaling pathway	1.185E-08	3.83807E-08	13
hsa04915	Estrogen signaling pathway	1.24977E-08	3.89791E-08	12
hsa05418	Fluid shear stress and atherosclerosis	1.3567E-08	4.08032E-08	12
hsa05224	Breast cancer	2.55584E-08	7.42168E-08	12
hsa04919	Thyroid hormone signaling pathway	3.34334E-08	9.38483E-08	12
hsa05133	Pertussis	6.43187E-08	1.7472E-07	12
hsa05130	Pathogenic Escherichia coli infection	8.15295E-08	2.14551E-07	12
hsa04625	C-type lectin receptor signaling pathway	8.62348E-08	2.20057E-07	12
hsa05134	Legionellosis	9.35542E-08	2.31713E-07	12
hsa04066	HIF-1 signaling pathway	1.35165E-07	3.25208E-07	12
hsa05219	Bladder cancer	1.53837E-07	3.59852E-07	12
hsa05145	Toxoplasmosis	1.75034E-07	3.98369E-07	11
hsa04010	MAPK signaling pathway	2.24107E-07	4.85612E-07	11
hsa04726	Serotonergic synapse	2.24899E-07	4.85612E-07	11
hsa05152	Tuberculosis	2.4158E-07	5.08588E-07	11
hsa04722	Neurotrophin signaling pathway	3.10584E-07	6.37913E-07	11

hsa05166	Human T-cell leukemia virus 1 infection	3.29132E-07	6.59913E-07	11
hsa04218	Cellular senescence	4.56566E-07	8.94131E-07	11
hsa04917	Prolactin signaling pathway	4.80073E-07	9.18801E-07	11
hsa05223	Non-small cell lung cancer	5.98694E-07	1.12036E-06	10
hsa04926	Relaxin signaling pathway	6.60946E-07	1.20997E-06	10
hsa04215	Apoptosis - multiple species	6.98678E-07	1.25183E-06	10
hsa05212	Pancreatic cancer	9.12531E-07	1.60093E-06	10
hsa04620	Toll-like receptor signaling pathway	9.84121E-07	1.69129E-06	10
hsa05022	Pathways of neurodegeneration - multiple diseases	1.04326E-06	1.75707E-06	10
hsa05132	Salmonella infection	1.22078E-06	1.99461E-06	10
hsa01521	EGFR tyrosine kinase inhibitor resistance	1.23167E-06	1.99461E-06	10
hsa04659	Th17 cell differentiation	1.35545E-06	2.15365E-06	10
hsa05213	Endometrial cancer	1.78891E-06	2.78972E-06	10
hsa04370	VEGF signaling pathway	2.0131E-06	3.08225E-06	10
hsa04261	Adrenergic signaling in cardiomyocytes	2.64281E-06	3.97415E-06	10
hsa05323	Rheumatoid arthritis	4.28311E-06	6.32778E-06	9
hsa05165	Human papillomavirus infection	5.5165E-06	7.99153E-06	9
hsa04380	Osteoclast differentiation	5.59907E-06	7.99153E-06	9
hsa05131	Shigellosis	6.8843E-06	9.66217E-06	9
hsa05146	Amoebiasis	8.56232E-06	1.18203E-05	9
hsa04660	T cell receptor signaling pathway	9.89228E-06	1.3436E-05	9
hsa05140	Leishmaniasis	1.22387E-05	1.63591E-05	9
hsa04024	cAMP signaling pathway	1.37223E-05	1.80557E-05	9
hsa04621	NOD-like receptor signaling pathway	1.63037E-05	2.11222E-05	8
hsa04725	Cholinergic synapse	1.82455E-05	2.32797E-05	8
hsa04923	Regulation of lipolysis in adipocytes	2.05854E-05	2.58733E-05	8
hsa05202	Transcriptional misregulation in cancer	2.46873E-05	3.05725E-05	8
hsa04071	Sphingolipid signaling pathway	2.66112E-05	3.24774E-05	8
hsa04020	Calcium signaling pathway	2.96542E-05	3.56743E-05	8
hsa05235	PD-L1 expression and PD-1 checkpoint pathway in cancer	3.1774E-05	3.7686E-05	8
hsa05216	Thyroid cancer	3.34167E-05	3.90838E-05	8
hsa04728	Dopaminergic synapse	5.61263E-05	6.47455E-05	8
hsa05031	Amphetamine addiction	6.83731E-05	7.67698E-05	8
hsa05211	Renal cell carcinoma	6.83731E-05	7.67698E-05	8
hsa05208	Chemical carcinogenesis - reactive oxygen species	8.43683E-05	9.34828E-05	8
hsa05214	Glioma	0.000109378	0.000118768	8
hsa04931	Insulin resistance	0.000110009	0.000118768	8
hsa05171	Coronavirus disease - COVID-19	0.00011726	0.000123991	8
hsa05220	Chronic myeloid leukemia	0.000117791	0.000123991	8
hsa05010	Alzheimer disease	0.000125842	0.00013083	7
hsa05226	Gastric cancer	0.00013184	0.000134731	7
hsa05030	Cocaine addiction	0.000132794	0.000134731	7
hsa04921	Oxytocin signaling pathway	0.000165786	0.000166202	7

hsa04662	B cell receptor signaling pathway	0.000179687	0.000178018	7
hsa04510	Focal adhesion	0.000197598	0.000193486	7
hsa05203	Viral carcinogenesis	0.000220845	0.000213764	7
hsa01523	Antifolate resistance	0.000227715	0.000217909	7
hsa04022	cGMP-PKG signaling pathway	0.000288997	0.000273445	7
hsa05206	MicroRNAs in cancer	0.000292599	0.000273777	7
hsa05225	Hepatocellular carcinoma	0.000300955	0.000278501	6
hsa05416	Viral myocarditis	0.000348324	0.000318832	6
hsa04970	Salivary secretion	0.000357723	0.000323914	6
hsa04068	FoxO signaling pathway	0.000364607	0.000326636	6
hsa00590	Arachidonic acid metabolism	0.000376407	0.000333657	6
hsa05321	Inflammatory bowel disease	0.000506186	0.000444022	6
hsa05143	African trypanosomiasis	0.000519737	0.000451209	6
hsa04064	NF-kappa B signaling pathway	0.000651315	0.00055967	6
hsa04622	RIG-I-like receptor signaling pathway	0.000712702	0.00060017	6
hsa05120	Epithelial cell signaling in Helicobacter pylori infection	0.000712702	0.00060017	6
hsa00982	Drug metabolism - cytochrome P450	0.000810878	0.000669455	6
hsa05218	Melanoma	0.000810878	0.000669455	6
hsa04080	Neuroactive ligand-receptor interaction	0.000874286	0.000714797	6
hsa05168	Herpes simplex virus 1 infection	0.001429049	0.001157124	6
hsa04310	Wnt signaling pathway	0.001539529	0.00123471	5
hsa05144	Malaria	0.001638647	0.001301805	5
hsa04012	ErbB signaling pathway	0.00171407	0.001348998	5
hsa04110	Cell cycle	0.001769035	0.001379364	5
hsa05020	Prion disease	0.001798459	0.001389442	5
hsa04658	Th1 and Th2 cell differentiation	0.002430703	0.001860825	5
hsa05231	Choline metabolism in cancer	0.003200496	0.002428067	5
hsa05217	Basal cell carcinoma	0.003833453	0.002882295	5
hsa04928	Parathyroid hormone synthesis, secretion and action	0.004482388	0.003340392	5
hsa05415	Diabetic cardiomyopathy	0.004603171	0.003400311	5
hsa05221	Acute myeloid leukemia	0.00478303	0.003502448	5
hsa04664	Fc epsilon RI signaling pathway	0.005042988	0.003660971	5
hsa04920	Adipocytokine signaling pathway	0.005312274	0.003823499	5
hsa04217	Necroptosis	0.005613054	0.003998083	5
hsa05012	Parkinson disease	0.005649791	0.003998083	5
hsa00350	Tyrosine metabolism	0.005776591	0.004053748	5
hsa04630	JAK-STAT signaling pathway	0.006140253	0.004264068	5
hsa04137	Mitophagy - animal	0.006177569	0.004264068	5
hsa04935	Growth hormone synthesis, secretion and action	0.007288291	0.004989844	4
hsa00380	Tryptophan metabolism	0.008889092	0.005988441	4
hsa05332	Graft-versus-host disease	0.008889092	0.005988441	4
hsa04014	Ras signaling pathway	0.009378244	0.006267832	4
hsa04650	Natural killer cell mediated cytotoxicity	0.010802383	0.00716279	4

hsa00360	Phenylalanine metabolism	0.011301709	0.007435335	4
hsa05014	Amyotrophic lateral sclerosis	0.011683758	0.007627096	4
hsa04211	Longevity regulating pathway	0.0128685	0.00833587	4
hsa04062	Chemokine signaling pathway	0.013569946	0.008723147	4
hsa05032	Morphine addiction	0.013872307	0.008849957	4
hsa04912	GnRH signaling pathway	0.01492469	0.009449744	4
hsa00330	Arginine and proline metabolism	0.015101139	0.009490111	4
hsa04750	Inflammatory mediator regulation of TRP channels	0.017772846	0.011086376	4
hsa04061	Viral protein interaction with cytokine and cytokine receptor	0.01900071	0.011765145	4
hsa04340	Hedgehog signaling pathway	0.019383861	0.011914782	4
hsa04914	Progesterone-mediated oocyte maturation	0.0202801	0.012286316	4
hsa04972	Pancreatic secretion	0.0202801	0.012286316	4
hsa00340	Histidine metabolism	0.020911778	0.012578513	4
hsa04929	GnRH secretion	0.027494153	0.016420547	4
hsa00830	Retinol metabolism	0.032129778	0.019053982	4
hsa04924	Renin secretion	0.033348755	0.019502196	4
hsa05204	Chemical carcinogenesis - DNA adducts	0.033348755	0.019502196	4
hsa04152	AMPK signaling pathway	0.034188768	0.019855546	4
hsa05230	Central carbon metabolism in cancer	0.034591638	0.019951918	4
hsa00591	Linoleic acid metabolism	0.035104237	0.020109839	3
hsa04613	Neutrophil extracellular trap formation	0.044727514	0.025310717	3
hsa04114	Oocyte meiosis	0.044869847	0.025310717	3
hsa00980	Metabolism of xenobiotics by cytochrome P450	0.045385279	0.025310717	3
hsa04721	Synaptic vesicle cycle	0.045385279	0.025310717	3
hsa04270	Vascular smooth muscle contraction	0.048073579	0.026633562	3
hsa04910	Insulin signaling pathway	0.051401678	0.028291257	3
hsa04960	Aldosterone-regulated sodium reabsorption	0.054657485	0.029887893	3
hsa04140	Autophagy - animal	0.056031875	0.030441766	3
hsa05330	Allograft rejection	0.05732035	0.030942159	3
hsa00260	Glycine, serine and threonine metabolism	0.062778544	0.033672702	3
hsa04015	Rap1 signaling pathway	0.063480294	0.033833601	3
hsa05410	Hypertrophic cardiomyopathy	0.064315953	0.034063398	3
hsa04940	Type I diabetes mellitus	0.071279805	0.037515687	3
hsa04934	Cushing syndrome	0.073947977	0.038678249	3
hsa05414	Dilated cardiomyopathy	0.074947168	0.038916487	3
hsa04150	mTOR signaling pathway	0.075327725	0.038916487	3
hsa04666	Fc gamma R-mediated phagocytosis	0.076790863	0.039430482	3
hsa04930	Type II diabetes mellitus	0.080131306	0.04089636	3
hsa05016	Huntington disease	0.092545419	0.046947581	3
hsa04961	Endocrine and other factor-regulated calcium reabsorption	0.101989153	0.051428505	3
hsa04670	Leukocyte transendothelial migration	0.111037866	0.055658078	3
hsa05034	Alcoholism	0.124278678	0.061926467	2
hsa04611	Platelet activation	0.13348481	0.066122507	2

hsa04623	Cytosolic DNA-sensing pathway	0.135603311	0.066779101	2
hsa00061	Fatty acid biosynthesis	0.169100639	0.082644468	2
hsa04371	Apelin signaling pathway	0.169782728	0.082644468	2
hsa03320	PPAR signaling pathway	0.178593433	0.086083161	2
hsa04550	Signaling pathways regulating pluripotency of stem cells	0.179913806	0.086083161	2
hsa05017	Spinocerebellar ataxia	0.179913806	0.086083161	2
hsa04971	Gastric acid secretion	0.182270379	0.086387152	2
hsa04810	Regulation of actin cytoskeleton	0.183583265	0.086387152	2
hsa04060	Cytokine-cytokine receptor interaction	0.18362669	0.086387152	2
hsa04072	Phospholipase D signaling pathway	0.192805833	0.089703208	2
hsa04723	Retrograde endocannabinoid signaling	0.192805833	0.089703208	2
hsa00220	Arginine biosynthesis	0.202655714	0.093767826	2
hsa04610	Complement and coagulation cascades	0.215808788	0.099308042	2
hsa04742	Taste transduction	0.219574432	0.099948532	2
hsa04911	Insulin secretion	0.219574432	0.099948532	2
hsa04540	Gap junction	0.227122808	0.102828662	2
hsa04713	Circadian entrainment	0.261276811	0.117659133	2
hsa04640	Hematopoietic cell lineage	0.268886457	0.120441862	2
hsa05310	Asthma	0.273337689	0.121787887	2
hsa04916	Melanogenesis	0.276496053	0.122546727	2
hsa04974	Protein digestion and absorption	0.284102485	0.125258742	2
hsa04922	Glucagon signaling pathway	0.299294019	0.131269307	2
hsa00500	Starch and sucrose metabolism	0.309892276	0.135213428	2
hsa04216	Ferroptosis	0.344629041	0.149594809	2
hsa00071	Fatty acid degradation	0.35803492	0.154616969	1
hsa00230	Purine metabolism	0.377829162	0.162332615	1
hsa00620	Pyruvate metabolism	0.384039132	0.163334028	1
hsa04973	Carbohydrate digestion and absorption	0.384039132	0.163334028	1
hsa04672	Intestinal immune network for IgA production	0.396648184	0.167849007	1
hsa05110	Vibrio cholerae infection	0.402856738	0.16962389	1
hsa04913	Ovarian steroidogenesis	0.409002168	0.171354666	1
hsa05320	Autoimmune thyroid disease	0.421106183	0.175552343	1
hsa01212	Fatty acid metabolism	0.444584197	0.184426942	1
hsa04730	Long-term depression	0.461572993	0.190535807	1
hsa00140	Steroid hormone biosynthesis	0.46712103	0.191885404	1
hsa04213	Longevity regulating pathway - multiple species	0.472612582	0.193198807	1
hsa04390	Hippo signaling pathway	0.479827553	0.195200632	1
hsa00010	Glycolysis / Gluconeogenesis	0.499242736	0.201155472	1
hsa04720	Long-term potentiation	0.499242736	0.201155472	1
hsa04530	Tight junction	0.519044427	0.208138116	1
hsa04141	Protein processing in endoplasmic reticulum	0.52539125	0.20968471	1
hsa04918	Thyroid hormone synthesis	0.539113484	0.214146369	1
hsa05100	Bacterial invasion of epithelial cells	0.548580768	0.215870445	1

hsa05412	Arrhythmogenic right ventricular cardiomyopathy	0.548580768	0.215870445	1
hsa04612	Antigen processing and presentation	0.553242101	0.216692133	1
hsa04360	Axon guidance	0.559298765	0.218050201	1
hsa00983	Drug metabolism - other enzymes	0.562422571	0.218257607	1
hsa04146	Peroxisome	0.571416617	0.220730707	1
hsa04260	Cardiac muscle contraction	0.593110493	0.228064597	1
hsa04512	ECM-receptor interaction	0.597317248	0.228157811	1
hsa04727	GABAergic synapse	0.601481028	0.228157811	1
hsa04976	Bile secretion	0.601481028	0.228157811	1
hsa04350	TGF-beta signaling pathway	0.621670349	0.234758687	1
hsa04070	Phosphatidylinositol signaling system	0.633295351	0.237388494	1
hsa00564	Glycerophospholipid metabolism	0.637091371	0.237388494	1
hsa04925	Aldosterone synthesis and secretion	0.637091371	0.237388494	1
hsa03008	Ribosome biogenesis in eukaryotes	0.676369431	0.25091377	1
hsa04724	Glutamatergic synapse	0.692804957	0.255883641	1
hsa00190	Oxidative phosphorylation	0.750695304	0.276054352	1
hsa05322	Systemic lupus erythematosus	0.75585405	0.276742902	1
hsa04145	Phagosome	0.793500231	0.28926871	1
hsa04714	Thermogenesis	0.911069204	0.330696626	1