

Emotion COR positive

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0015012	heparan sulfate proteoglycan biosynthetic process	9	0.099673677	< 0.001	< 0.001

Emotion SUBC positive

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0006607	NLS-bearing protein import into nucleus	5	0.554800515	< 0.001	< 0.001
GO:0070757	interleukin-35-mediated signaling pathway	5	0.519433719	< 0.001	< 0.001
GO:0098792	xenophagy	7	0.48758963	< 0.001	< 0.001
GO:1905098	negative regulation of guanyl-nucleotide exchange factor activity	5	0.486589447	< 0.001	< 0.001
GO:0098703	calcium ion import across plasma membrane	5	0.466306306	< 0.001	< 0.001
GO:1990035	calcium ion import into cell	5	0.466306306	< 0.001	< 0.001
GO:0006054	N-acetylneuraminate metabolic process	5	0.462445302	< 0.001	< 0.001
GO:0051024	positive regulation of immunoglobulin secretion	5	0.461621622	0.0002	0.000356582
GO:0031646	positive regulation of neurological system process	6	0.459244959	< 0.001	< 0.001
GO:0021877	forebrain neuron fate commitment	7	0.459238831	0.0072	0.008495371
GO:1900246	positive regulation of RIG-I signaling pathway	5	0.457760618	< 0.001	< 0.001
GO:0002692	negative regulation of cellular extravasation	5	0.451480051	0.0048	0.005840847
GO:0035493	SNARE complex assembly	6	0.451051051	0.0005	0.000791911
GO:0072160	nephron tubule epithelial cell differentiation	5	0.44967825	< 0.001	< 0.001
GO:0019433	triglyceride catabolic process	7	0.448097077	< 0.001	< 0.001
GO:0046461	neutral lipid catabolic process	7	0.448097077	< 0.001	< 0.001
GO:0046464	acylglycerol catabolic process	7	0.448097077	< 0.001	< 0.001
GO:0006525	arginine metabolic process	6	0.448005148	< 0.001	< 0.001
GO:0072087	renal vesicle development	6	0.447275847	< 0.001	< 0.001
GO:0010919	regulation of inositol phosphate biosynthetic process	6	0.443200343	< 0.001	< 0.001
GO:0060732	positive regulation of inositol phosphate biosynthetic process	6	0.443200343	< 0.001	< 0.001
GO:0018410	C-terminal protein amino acid modification	6	0.442900043	0.0001	0.000192793
GO:0051000	positive regulation of nitric-oxide synthase activity	7	0.442801986	< 0.001	< 0.001
GO:0018065	protein-cofactor linkage	6	0.442170742	< 0.001	< 0.001
GO:2000696	regulation of epithelial cell differentiation involved in kidney development	5	0.4402574	< 0.001	< 0.001
GO:0048566	embryonic digestive tract development	7	0.438058467	< 0.001	< 0.001
GO:0009415	response to water	6	0.436979837	0.0001	0.000192793
GO:0032226	positive regulation of synaptic transmission, dopaminergic	5	0.436138996	< 0.001	< 0.001
GO:0060439	trachea morphogenesis	6	0.434963535	0.0001	0.000192793
GO:0031547	brain-derived neurotrophic factor receptor signaling pathway	5	0.434954955	0.0005	0.000791911
GO:0098659	inorganic cation import into cell	6	0.434706135	< 0.001	< 0.001
GO:0099587	inorganic ion import into cell	6	0.434706135	< 0.001	< 0.001
GO:0021902	commitment of neuronal cell to specific neuron type in forebrain	5	0.434697555	0.0084	0.009757868
GO:1990709	presynaptic active zone organization	6	0.431746032	0.0025	0.003237479
GO:0007202	activation of phospholipase C activity	11	0.427963028	< 0.001	< 0.001
GO:0090036	regulation of protein kinase C signaling	6	0.427027027	< 0.001	< 0.001
GO:0006474	N-terminal protein amino acid acetylation	8	0.426898327	< 0.001	< 0.001
GO:0045176	apical protein localization	7	0.426291598	< 0.001	< 0.001
GO:1903044	protein localization to membrane raft	5	0.425431145	0.0002	0.000356582
GO:1905097	regulation of guanyl-nucleotide exchange factor activity	6	0.424281424	< 0.001	< 0.001
GO:1902932	positive regulation of alcohol biosynthetic process	7	0.423607281	0.0004	0.000648934
GO:0014049	positive regulation of glutamate secretion	7	0.423570509	0.0006	0.000927725
GO:0033540	fatty acid beta-oxidation using acyl-CoA oxidase	6	0.422565423	< 0.001	< 0.001
GO:0032211	negative regulation of telomere maintenance via telomerase	8	0.421235521	< 0.001	< 0.001
GO:0051957	positive regulation of amino acid transport	8	0.41994852	0.0002	0.000356582
GO:0001958	endochondral ossification	10	0.419459459	< 0.001	< 0.001
GO:0036075	replacement ossification	10	0.419459459	< 0.001	< 0.001
GO:0050718	positive regulation of interleukin-1 beta secretion	10	0.417734878	< 0.001	< 0.001
GO:0002076	osteoblast development	5	0.417657658	< 0.001	< 0.001
GO:0072077	renal vesicle morphogenesis	5	0.417451737	< 0.001	< 0.001
GO:0072283	metanephric renal vesicle morphogenesis	5	0.417451737	< 0.001	< 0.001
GO:0071107	response to parathyroid hormone	5	0.416628057	0.0001	0.000192793
GO:0060767	epithelial cell proliferation involved in prostate gland development	5	0.416370656	< 0.001	< 0.001
GO:0071498	cellular response to fluid shear stress	6	0.414886315	0.0007	0.001063182
GO:0060330	regulation of response to interferon-gamma	9	0.414414414	0.0001	0.000192793
GO:0060334	regulation of interferon-gamma-mediated signaling pathway	9	0.414414414	0.0001	0.000192793
GO:0050995	negative regulation of lipid catabolic process	5	0.411068211	0.0002	0.000356582
GO:1904321	response to forskolin	5	0.410604891	< 0.001	< 0.001
GO:1904322	cellular response to forskolin	5	0.410604891	< 0.001	< 0.001
GO:0006195	purine nucleotide catabolic process	12	0.409202059	< 0.001	< 0.001
GO:0097094	craniofacial suture morphogenesis	6	0.408365508	< 0.001	< 0.001
GO:0051152	positive regulation of smooth muscle cell differentiation	6	0.408065208	0.0002	0.000356582
GO:0002689	negative regulation of leukocyte chemotaxis	6	0.407893608	< 0.001	< 0.001
GO:0071318	cellular response to ATP	9	0.407693408	< 0.001	< 0.001
GO:0035589	G-protein coupled purinergic nucleotide receptor signaling pathway	6	0.407507508	0.0004	0.000648934
GO:0060534	trachea cartilage development	5	0.407104247	< 0.001	< 0.001
GO:0003351	epithelial cilium movement	7	0.406618864	0.0006	0.000927725
GO:0050951	sensory perception of temperature stimulus	8	0.406467181	< 0.001	< 0.001
GO:0006048	UDP-N-acetylglucosamine biosynthetic process	6	0.406349206	< 0.001	< 0.001
GO:1902414	protein localization to cell junction	5	0.405817246	< 0.001	< 0.001
GO:0071569	protein ufmylation	5	0.405611326	< 0.001	< 0.001
GO:1990564	protein polyufmylation	5	0.405611326	< 0.001	< 0.001
GO:1990592	protein K69-linked ufmylation	5	0.405611326	< 0.001	< 0.001
GO:1903997	positive regulation of non-membrane spanning protein tyrosine kinase activity	5	0.405508366	0.0003	0.000505993
GO:0002833	positive regulation of response to biotic stimulus	20	0.405495495	< 0.001	< 0.001
GO:0045063	T-helper 1 cell differentiation	5	0.404890605	< 0.001	< 0.001
GO:0060438	trachea development	8	0.404150579	0.0011	0.001576346
GO:1903995	regulation of non-membrane spanning protein tyrosine kinase activity	6	0.403732304	< 0.001	< 0.001
GO:0034114	regulation of heterotypic cell-cell adhesion	6	0.403088803	< 0.001	< 0.001
GO:0032516	positive regulation of phosphoprotein phosphatase activity	8	0.402574003	0.0001	0.000192793
GO:0035162	embryonic hemopoiesis	5	0.401750322	< 0.001	< 0.001

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GO:0021960	anterior commissure morphogenesis	5	0.401750322	0.0059	0.007066401
GO:0032700	negative regulation of interleukin-17 production	6	0.401501502	< 0.001	< 0.001
GO:0006359	regulation of transcription from RNA polymerase III promoter	9	0.401401401	< 0.001	< 0.001
GO:0010992	ubiquitin homeostasis	5	0.401132561	0.0001	0.000192793
GO:0033561	regulation of water loss via skin	7	0.400551572	0.0001	0.000192793
GO:0050961	detection of temperature stimulus involved in sensory perception	6	0.4001287	< 0.001	< 0.001
GO:0050965	detection of temperature stimulus involved in sensory perception of pain	6	0.4001287	< 0.001	< 0.001
GO:0021895	cerebral cortex neuron differentiation	15	0.39955384	0.0004	0.000648934
GO:0031115	negative regulation of microtubule polymerization	8	0.398938224	< 0.001	< 0.001
GO:0070885	negative regulation of calcineurin-NFAT signaling cascade	7	0.39823497	0.0004	0.000648934
GO:1904357	negative regulation of telomere maintenance via telomere lengthening	10	0.397400257	< 0.001	< 0.001
GO:0008105	asymmetric protein localization	8	0.396750322	< 0.001	< 0.001
GO:1904429	regulation of t-circle formation	5	0.396499356	0.0014	0.00194839
GO:0033004	negative regulation of mast cell activation	6	0.395967396	< 0.001	< 0.001
GO:0099558	maintenance of synapse structure	11	0.395928396	0.0048	0.005840847
GO:0070102	interleukin-6-mediated signaling pathway	7	0.395918367	0.0001	0.000192793
GO:0003407	neural retina development	22	0.395858196	0.0002	0.000356582
GO:0046325	negative regulation of glucose import	6	0.395795796	< 0.001	< 0.001
GO:0072574	hepatocyte proliferation	5	0.393770914	< 0.001	< 0.001
GO:0072575	epithelial cell proliferation involved in liver morphogenesis	5	0.393770914	< 0.001	< 0.001
GO:0016081	synaptic vesicle docking	8	0.392664093	0.0012	0.001702047
GO:0016191	synaptic vesicle uncoating	5	0.392123552	0.0011	0.001576346
GO:0072318	clathrin coat disassembly	5	0.392123552	0.0011	0.001576346
GO:0050999	regulation of nitric-oxide synthase activity	16	0.391924067	< 0.001	< 0.001
GO:1990504	dense core granule exocytosis	5	0.391248391	0.0018	0.002428764
GO:0032620	interleukin-17 production	9	0.390847991	< 0.001	< 0.001
GO:0040019	positive regulation of embryonic development	11	0.390803791	< 0.001	< 0.001
GO:0010807	regulation of synaptic vesicle priming	5	0.39047619	0.0063	0.007507211
GO:0034616	response to laminar fluid shear stress	5	0.39032175	< 0.001	< 0.001
GO:0051954	positive regulation of amine transport	17	0.38958286	0.0001	0.000192793
GO:0099640	axo-dendritic protein transport	6	0.389146289	0.0016	0.002186748
GO:0099641	anterograde axonal protein transport	6	0.389146289	0.0016	0.002186748
GO:0031915	positive regulation of synaptic plasticity	6	0.389060489	0.0006	0.000927725
GO:0036037	CD8-positive, alpha-beta T cell activation	5	0.388880309	< 0.001	< 0.001
GO:0072321	chaperone-mediated protein transport	7	0.388564074	0.0003	0.000505993
GO:0006040	amino sugar metabolic process	16	0.387612613	< 0.001	< 0.001
GO:1901071	glucosamine-containing compound metabolic process	7	0.386615187	< 0.001	< 0.001
GO:0039531	regulation of viral-induced cytoplasmic pattern recognition receptor signaling pathway	9	0.386414986	< 0.001	< 0.001
GO:0043162	ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway	6	0.385971686	< 0.001	< 0.001
GO:0010454	negative regulation of cell fate commitment	5	0.385379665	0.0024	0.003116943
GO:0045161	neuronal ion channel clustering	5	0.384658945	0.0018	0.002428764
GO:0010226	response to lithium ion	6	0.384255684	< 0.001	< 0.001
GO:0070106	interleukin-27-mediated signaling pathway	6	0.383998284	0.0011	0.001576346
GO:0050716	positive regulation of interleukin-1 secretion	13	0.383704584	< 0.001	< 0.001
GO:2001169	regulation of ATP biosynthetic process	6	0.383354783	0.0001	0.000192793
GO:0042416	dopamine biosynthetic process	6	0.383097383	< 0.001	< 0.001
GO:0032958	inositol phosphate biosynthetic process	10	0.383011583	0.0016	0.002186748
GO:0033006	regulation of mast cell activation involved in immune response	12	0.382990133	< 0.001	< 0.001
GO:1905050	positive regulation of metallopeptidase activity	5	0.382960103	0.0019	0.00254969
GO:0009249	protein lipoylation	5	0.382548263	0.0005	0.000791911
GO:0006904	vesicle docking involved in exocytosis	21	0.381638782	< 0.001	< 0.001
GO:1904376	negative regulation of protein localization to cell periphery	9	0.381467181	< 0.001	< 0.001
GO:0090148	membrane fission	6	0.381295581	0.001	0.001450349
GO:0001682	tRNA 5'-leader removal	6	0.381166881	< 0.001	< 0.001
GO:0009084	glutamine family amino acid biosynthetic process	8	0.381048906	< 0.001	< 0.001
GO:0007288	sperm axoneme assembly	5	0.380643501	0.0113	0.012793882
GO:0060004	reflex	8	0.380212355	0.0002	0.000356582
GO:0032594	protein transport within lipid bilayer	6	0.38005148	0.009	0.010394529
GO:0031111	negative regulation of microtubule polymerization or depolymerization	19	0.379800853	< 0.001	< 0.001
GO:0010453	regulation of cell fate commitment	7	0.379738923	0.0035	0.004390436
GO:0060425	lung morphogenesis	15	0.37971686	0.0011	0.001576346
GO:0030857	negative regulation of epithelial cell differentiation	7	0.379628608	< 0.001	< 0.001
GO:1901985	positive regulation of protein acetylation	16	0.379472329	0.0001	0.000192793
GO:1901841	regulation of high voltage-gated calcium channel activity	8	0.379343629	0.0022	0.002896881
GO:0002820	negative regulation of adaptive immune response	12	0.379279279	< 0.001	< 0.001
GO:0010092	specification of animal organ identity	7	0.378709322	0.0015	0.002069969
GO:0021892	cerebral cortex GABAergic interneuron differentiation	7	0.37841515	0.0073	0.008600218
GO:0097154	GABAergic neuron differentiation	7	0.37841515	0.0073	0.008600218
GO:0048278	vesicle docking	24	0.378389103	< 0.001	< 0.001
GO:0042462	eye photoreceptor cell development	13	0.378239778	< 0.001	< 0.001
GO:0061436	establishment of skin barrier	5	0.378172458	0.0011	0.001576346
GO:0072576	liver morphogenesis	6	0.378078078	< 0.001	< 0.001
GO:0002701	negative regulation of production of molecular mediator of immune response	9	0.376662377	< 0.001	< 0.001
GO:1905048	regulation of metallopeptidase activity	8	0.376190476	0.0001	0.000192793
GO:0099560	synaptic membrane adhesion	17	0.376167764	0.0014	0.00194839
GO:0032225	regulation of synaptic transmission, dopaminergic	10	0.376113256	< 0.001	< 0.001
GO:0046349	amino sugar biosynthetic process	7	0.376025005	< 0.001	< 0.001
GO:0032715	negative regulation of interleukin-6 production	12	0.375439725	< 0.001	< 0.001
GO:0048643	positive regulation of skeletal muscle tissue development	6	0.375375375	0.0001	0.000192793
GO:0070528	protein kinase C signaling	12	0.375010725	< 0.001	< 0.001
GO:0007435	salivary gland morphogenesis	12	0.374817675	< 0.001	< 0.001
GO:0051445	regulation of meiotic cell cycle	10	0.374594595	< 0.001	< 0.001
GO:0031342	negative regulation of cell killing	5	0.374568855	< 0.001	< 0.001

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GO:2000104	negative regulation of DNA-dependent DNA replication	8	0.374259974	0.0013	0.001826625
GO:0070493	thrombin-activated receptor signaling pathway	5	0.373899614	< 0.001	< 0.001
GO:0060413	atrial septum morphogenesis	7	0.373230373	< 0.001	< 0.001
GO:0042762	regulation of sulfur metabolic process	7	0.372936202	0.0109	0.012398148
GO:1903421	regulation of synaptic vesicle recycling	16	0.372747748	0.0011	0.001576346
GO:0010470	regulation of gastrulation	10	0.372689833	< 0.001	< 0.001
GO:0031579	membrane raft organization	7	0.37238463	< 0.001	< 0.001
GO:1903959	regulation of anion transmembrane transport	6	0.372114972	< 0.001	< 0.001
GO:0072202	cell differentiation involved in metanephros development	6	0.372072072	< 0.001	< 0.001
GO:0014048	regulation of glutamate secretion	10	0.372046332	0.0029	0.003693519
GO:0032768	regulation of monooxygenase activity	20	0.371917632	< 0.001	< 0.001
GO:0098501	polynucleotide dephosphorylation	5	0.371891892	< 0.001	< 0.001
GO:0072673	lamellipodium morphogenesis	5	0.371891892	0.0036	0.004505419
GO:0016082	synaptic vesicle priming	11	0.371802972	0.0062	0.00739947
GO:0048715	negative regulation of oligodendrocyte differentiation	5	0.370965251	0.0107	0.012191187
GO:0015874	norepinephrine transport	10	0.370553411	0.0002	0.000356582
GO:1905476	negative regulation of protein localization to membrane	12	0.37035607	< 0.001	< 0.001
GO:1904263	positive regulation of TORC1 signaling	5	0.36983269	0.0049	0.005958506
GO:0009154	purine ribonucleotide catabolic process	8	0.368918919	< 0.001	< 0.001
GO:0002704	negative regulation of leukocyte mediated immunity	11	0.368831169	< 0.001	< 0.001
GO:0042403	thyroid hormone metabolic process	5	0.368803089	0.0004	0.000648934
GO:0045671	negative regulation of osteoclast differentiation	7	0.368707483	< 0.001	< 0.001
GO:0090185	negative regulation of kidney development	5	0.368545689	< 0.001	< 0.001
GO:0010310	regulation of hydrogen peroxide metabolic process	8	0.368532819	< 0.001	< 0.001
GO:0072319	vesicle uncoating	6	0.368425568	0.0011	0.001576346
GO:0010829	negative regulation of glucose transport	9	0.368396968	< 0.001	< 0.001
GO:0072523	purine-containing compound catabolic process	15	0.368168168	< 0.001	< 0.001
GO:0031365	N-terminal protein amino acid modification	11	0.367871768	< 0.001	< 0.001
GO:0032325	positive regulation of protein sumoylation	7	0.367089539	< 0.001	< 0.001
GO:0002686	negative regulation of leukocyte migration	18	0.367052767	< 0.001	< 0.001
GO:0002828	regulation of type 2 immune response	7	0.367015996	0.0004	0.000648934
GO:0061437	renal system vasculature development	7	0.366685052	< 0.001	< 0.001
GO:0061440	kidney vasculature development	7	0.366685052	< 0.001	< 0.001
GO:0072012	glomerulus vasculature development	7	0.366685052	< 0.001	< 0.001
GO:0060080	inhibitory postsynaptic potential	6	0.366580867	0.0112	0.012688637
GO:0031666	positive regulation of lipopolysaccharide-mediated signaling pathway	5	0.366486486	< 0.001	< 0.001
GO:0032770	positive regulation of monooxygenase activity	10	0.366229086	0.0001	0.000192793
GO:0018146	keratan sulfate biosynthetic process	9	0.365851566	0.0001	0.000192793
GO:0043951	negative regulation of cAMP-mediated signaling	7	0.365839309	0.0008	0.001193265
GO:0060536	cartilage morphogenesis	5	0.364942085	< 0.001	< 0.001
GO:1901983	regulation of protein acetylation	28	0.364892443	< 0.001	< 0.001
GO:0061014	positive regulation of mRNA catabolic process	9	0.364764765	< 0.001	< 0.001
GO:0033623	regulation of integrin activation	5	0.364375804	< 0.001	< 0.001
GO:0046039	GTP metabolic process	12	0.364242814	< 0.001	< 0.001
GO:0043304	regulation of mast cell degranulation	11	0.364151164	< 0.001	< 0.001
GO:0071435	potassium ion export	5	0.363912484	0.0004	0.000648934
GO:0097623	potassium ion export across plasma membrane	5	0.363912484	0.0004	0.000648934
GO:0090197	positive regulation of chemokine secretion	8	0.363352638	< 0.001	< 0.001
GO:0039528	cytoplasmic pattern recognition receptor signaling pathway in response to virus	10	0.363140283	< 0.001	< 0.001
GO:0098779	mitophagy in response to mitochondrial depolarization	9	0.362877163	0.0001	0.000192793
GO:0021680	cerebellar Purkinje cell layer development	6	0.362419562	0.0027	0.003470695
GO:0034405	response to fluid shear stress	10	0.362316602	< 0.001	< 0.001
GO:0003171	atrioventricular valve development	9	0.362219362	< 0.001	< 0.001
GO:0003181	atrioventricular valve morphogenesis	9	0.362219362	< 0.001	< 0.001
GO:0006290	pyrimidine dimer repair	6	0.361861862	0.0012	0.001702047
GO:2000756	regulation of peptidyl-lysine acetylation	21	0.361720905	< 0.001	< 0.001
GO:0032201	telomere maintenance via semi-conservative replication	10	0.361647362	0.0023	0.003013139
GO:0023019	signal transduction involved in regulation of gene expression	8	0.361615187	0.0003	0.000505993
GO:0035590	purinergic nucleotide receptor signaling pathway	10	0.361338481	< 0.001	< 0.001
GO:0010922	positive regulation of phosphatase activity	13	0.361290961	< 0.001	< 0.001
GO:0006596	polyamine biosynthetic process	7	0.360801618	0.0001	0.000192793
GO:0045932	negative regulation of muscle contraction	11	0.360734761	< 0.001	< 0.001
GO:0043696	dedifferentiation	5	0.360669241	< 0.001	< 0.001
GO:0043697	cell dedifferentiation	5	0.360669241	< 0.001	< 0.001
GO:0060441	epithelial tube branching involved in lung morphogenesis	8	0.360456885	< 0.001	< 0.001
GO:0016048	detection of temperature stimulus	7	0.360397132	< 0.001	< 0.001
GO:0001754	eye photoreceptor cell differentiation	15	0.36006864	< 0.001	< 0.001
GO:0010592	positive regulation of lamellipodium assembly	10	0.36002574	< 0.001	< 0.001
GO:0015813	L-glutamate transport	11	0.35984556	0.0008	0.001193265
GO:0060219	camera-type eye photoreceptor cell differentiation	5	0.35984556	0.0023	0.003013139
GO:0003128	heart field specification	5	0.35958816	0.0153	0.01697069
GO:0003139	secondary heart field specification	5	0.35958816	0.0153	0.01697069
GO:0032660	regulation of interleukin-17 production	7	0.359367531	< 0.001	< 0.001
GO:0002279	mast cell activation involved in immune response	18	0.359244959	< 0.001	< 0.001
GO:0002823	negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	10	0.358944659	0.0001	0.000192793
GO:1902745	positive regulation of lamellipodium organization	12	0.358880309	< 0.001	< 0.001
GO:0035850	epithelial cell differentiation involved in kidney development	11	0.358722359	0.0001	0.000192793
GO:1903077	negative regulation of protein localization to plasma membrane	8	0.358365508	< 0.001	< 0.001
GO:1904888	cranial skeletal system development	19	0.358301158	< 0.001	< 0.001
GO:0051955	regulation of amino acid transport	15	0.358266838	0.0017	0.00231289
GO:0003215	cardiac right ventricle morphogenesis	7	0.358264387	0.0015	0.002069969
GO:0050849	negative regulation of calcium-mediated signaling	13	0.358202158	0.0002	0.000356582

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0032731	positive regulation of interleukin-1 beta production	15	0.358112398	< 0.001	< 0.001
GO:0044331	cell-cell adhesion mediated by cadherin	11	0.358043758	< 0.001	< 0.001
GO:0009268	response to pH	13	0.357984358	< 0.001	< 0.001
GO:0001829	trophectodermal cell differentiation	5	0.357889318	0.0131	0.01468722
GO:0015804	neutral amino acid transport	7	0.3576025	< 0.001	< 0.001
GO:0034393	positive regulation of smooth muscle cell apoptotic process	7	0.357234786	0.0018	0.002428764
GO:0015936	coenzyme A metabolic process	6	0.356499356	< 0.001	< 0.001
GO:0009445	putrescine metabolic process	5	0.356447876	0.0003	0.000505993
GO:0021762	substantia nigra development	18	0.356413556	< 0.001	< 0.001
GO:2001171	positive regulation of ATP biosynthetic process	5	0.356241956	0.0001	0.000192793
GO:0048701	embryonic cranial skeleton morphogenesis	13	0.355925156	< 0.001	< 0.001
GO:0006047	UDP-N-acetylglucosamine metabolic process	7	0.35583747	< 0.001	< 0.001
GO:0034390	smooth muscle cell apoptotic process	12	0.355619906	0.0014	0.00194839
GO:0034391	regulation of smooth muscle cell apoptotic process	12	0.355619906	0.0014	0.00194839
GO:0034058	endosomal vesicle fusion	6	0.355126555	0.0002	0.000356582
GO:0008272	sulfate transport	6	0.354826255	0.01	0.011478335
GO:1902358	sulfate transmembrane transport	6	0.354826255	0.01	0.011478335
GO:1901385	regulation of voltage-gated calcium channel activity	13	0.354459954	< 0.001	< 0.001
GO:0060180	female mating behavior	6	0.354397254	0.0007	0.001063182
GO:0019228	neuronal action potential	8	0.354054054	< 0.001	< 0.001
GO:0045746	negative regulation of Notch signaling pathway	14	0.354035668	< 0.001	< 0.001
GO:0045622	regulation of T-helper cell differentiation	7	0.353925354	< 0.001	< 0.001
GO:2000758	positive regulation of peptidyl-lysine acetylation	11	0.353340353	< 0.001	< 0.001
GO:0035137	hindlimb morphogenesis	11	0.353340353	< 0.001	< 0.001
GO:0039535	regulation of RIG-I signaling pathway	8	0.352863578	< 0.001	< 0.001
GO:0032892	positive regulation of organic acid transport	14	0.352748667	< 0.001	< 0.001
GO:0072215	regulation of metanephros development	6	0.352509653	0.0037	0.004617737
GO:0051546	keratinocyte migration	5	0.352432432	< 0.001	< 0.001
GO:0051547	regulation of keratinocyte migration	5	0.352432432	< 0.001	< 0.001
GO:1902743	regulation of lamellipodium organization	17	0.352396094	< 0.001	< 0.001
GO:0010591	regulation of lamellipodium assembly	15	0.352295152	< 0.001	< 0.001
GO:0090342	regulation of cell aging	22	0.352275652	< 0.001	< 0.001
GO:2000279	negative regulation of DNA biosynthetic process	13	0.352004752	< 0.001	< 0.001
GO:0043923	positive regulation by host of viral transcription	7	0.351939695	0.0005	0.000791911
GO:0003333	amino acid transmembrane transport	12	0.351887602	< 0.001	< 0.001
GO:0061179	negative regulation of insulin secretion involved in cellular response to glucose stimulus	6	0.351265551	< 0.001	< 0.001
GO:0033206	meiotic cytokinesis	5	0.351145431	< 0.001	< 0.001
GO:2000341	regulation of chemokine (C-X-C motif) ligand 2 production	6	0.351136851	< 0.001	< 0.001
GO:0048747	muscle fiber development	18	0.351065351	< 0.001	< 0.001
GO:0001956	positive regulation of neurotransmitter secretion	16	0.351061776	0.0121	0.013633945
GO:0006312	mitotic recombination	8	0.350740026	< 0.001	< 0.001
GO:0060350	endochondral bone morphogenesis	17	0.350624574	0.0011	0.001576346
GO:0048172	regulation of short-term neuronal synaptic plasticity	11	0.35048555	0.0077	0.00902229
GO:0009166	nucleotide catabolic process	19	0.350457224	< 0.001	< 0.001
GO:1905383	protein localization to presynapse	8	0.3502574	0.0054	0.006510843
GO:0061013	regulation of mRNA catabolic process	12	0.3498284	< 0.001	< 0.001
GO:2000772	regulation of cellular senescence	19	0.349359886	0.0002	0.000356582
GO:0010863	positive regulation of phospholipase C activity	16	0.349308237	0.0001	0.000192793
GO:0048488	synaptic vesicle endocytosis	31	0.349209117	0.0005	0.000791911
GO:0016577	histone demethylation	8	0.348938224	0.0078	0.009125612
GO:0070076	histone lysine demethylation	8	0.348938224	0.0078	0.009125612
GO:0046530	photoreceptor cell differentiation	22	0.348894349	< 0.001	< 0.001
GO:0050812	regulation of acyl-CoA biosynthetic process	5	0.348880309	0.0093	0.010727257
GO:0009954	proximal/distal pattern formation	8	0.348777349	0.0043	0.005276385
GO:1900120	regulation of receptor binding	5	0.348571429	< 0.001	< 0.001
GO:0034214	protein hexamerization	6	0.348562849	< 0.001	< 0.001
GO:0040020	regulation of meiotic nuclear division	5	0.348365508	< 0.001	< 0.001
GO:1901032	negative regulation of response to reactive oxygen species	7	0.348078691	< 0.001	< 0.001
GO:1903206	negative regulation of hydrogen peroxide-induced cell death	7	0.348078691	< 0.001	< 0.001
GO:0051127	positive regulation of actin nucleation	8	0.348069498	0.0003	0.000505993
GO:1902894	negative regulation of pri-miRNA transcription from RNA polymerase II promoter	7	0.348005148	0.0006	0.000927725
GO:0051590	positive regulation of neurotransmitter transport	18	0.347890748	0.0109	0.012398148
GO:0043330	response to exogenous dsRNA	10	0.347850708	< 0.001	< 0.001
GO:0007026	negative regulation of microtubule depolymerization	12	0.347833548	0.0002	0.000356582
GO:0051023	regulation of immunoglobulin secretion	7	0.34756389	< 0.001	< 0.001
GO:1902992	negative regulation of amyloid precursor protein catabolic process	8	0.347522523	< 0.001	< 0.001
GO:0050706	regulation of interleukin-1 beta secretion	15	0.347387387	< 0.001	< 0.001
GO:0001660	fever generation	5	0.347335907	< 0.001	< 0.001
GO:0036119	response to platelet-derived growth factor	6	0.347275847	< 0.001	< 0.001
GO:0045668	negative regulation of osteoblast differentiation	13	0.347252747	0.0011	0.001576346
GO:0007193	adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway	32	0.346927284	0.0008	0.001193265
GO:0007431	salivary gland development	13	0.346896347	< 0.001	< 0.001
GO:0010839	negative regulation of keratinocyte proliferation	6	0.346803947	< 0.001	< 0.001
GO:0070200	establishment of protein localization to telomere	7	0.346387204	0.0005	0.000791911
GO:1900151	regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	7	0.346129803	< 0.001	< 0.001
GO:1900153	positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	7	0.346129803	< 0.001	< 0.001
GO:0009595	detection of biotic stimulus	5	0.345842986	< 0.001	< 0.001
GO:1900242	regulation of synaptic vesicle endocytosis	12	0.345817246	0.001	0.001450349
GO:0043303	mast cell degranulation	17	0.345658263	< 0.001	< 0.001
GO:2001258	negative regulation of cation channel activity	13	0.345648946	< 0.001	< 0.001
GO:0045822	negative regulation of heart contraction	9	0.345602746	< 0.001	< 0.001
GO:0051150	regulation of smooth muscle cell differentiation	9	0.345431145	0.0001	0.000192793
GO:0046503	glycerolipid catabolic process	12	0.345280995	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0014047	glutamate secretion	30	0.345208065	0.0019	0.00254969
GO:0010971	positive regulation of G2/M transition of mitotic cell cycle	12	0.345023595	0.0005	0.000791911
GO:2001212	regulation of vasculogenesis	5	0.344916345	0.0002	0.000356582
GO:0001963	synaptic transmission, dopaminergic	14	0.344787645	< 0.001	< 0.001
GO:0000083	regulation of transcription involved in G1/S transition of mitotic cell cycle	10	0.344607465	< 0.001	< 0.001
GO:0007019	microtubule depolymerization	17	0.344552956	< 0.001	< 0.001
GO:0032695	negative regulation of interleukin-12 production	5	0.344401544	0.0003	0.000505993
GO:0006482	protein demethylation	10	0.344375804	0.0066	0.007843941
GO:0008214	protein dealkylation	10	0.344375804	0.0066	0.007843941
GO:0051145	smooth muscle cell differentiation	16	0.344288932	< 0.001	< 0.001
GO:0044068	modulation by symbiont of host cellular process	17	0.344234991	< 0.001	< 0.001
GO:0043508	negative regulation of JUN kinase activity	5	0.344195624	0.0001	0.000192793
GO:2000343	positive regulation of chemokine (C-X-C motif) ligand 2 production	5	0.343680824	< 0.001	< 0.001
GO:0032732	positive regulation of interleukin-1 production	18	0.343472043	< 0.001	< 0.001
GO:0090382	phagosome maturation	19	0.342979069	< 0.001	< 0.001
GO:0043084	penile erection	5	0.342805663	0.0019	0.00254969
GO:0051353	positive regulation of oxidoreductase activity	17	0.34256946	< 0.001	< 0.001
GO:0051123	RNA polymerase II transcriptional preinitiation complex assembly	5	0.342548263	0.0016	0.002186748
GO:0070527	platelet aggregation	27	0.342523476	< 0.001	< 0.001
GO:0033028	myeloid cell apoptotic process	8	0.342213642	0.0008	0.001193265
GO:0033032	regulation of myeloid cell apoptotic process	8	0.342213642	0.0008	0.001193265
GO:0006865	amino acid transport	56	0.342195256	0.0001	0.000192793
GO:0071157	negative regulation of cell cycle arrest	8	0.341859717	< 0.001	< 0.001
GO:0015837	amine transport	36	0.341727442	< 0.001	< 0.001
GO:0042461	photoreceptor cell development	18	0.341698842	< 0.001	< 0.001
GO:0006144	purine nucleobase metabolic process	7	0.341680456	< 0.001	< 0.001
GO:0032927	positive regulation of activin receptor signaling pathway	6	0.341527242	< 0.001	< 0.001
GO:0002739	regulation of cytokine secretion involved in immune response	8	0.341505792	< 0.001	< 0.001
GO:0090239	regulation of histone H4 acetylation	7	0.341165655	< 0.001	< 0.001
GO:0070741	response to interleukin-6	14	0.341110498	< 0.001	< 0.001
GO:0048490	anterograde synaptic vesicle transport	13	0.340995941	< 0.001	< 0.001
GO:0099514	synaptic vesicle cytoskeletal transport	13	0.340995941	< 0.001	< 0.001
GO:0099517	synaptic vesicle transport along microtubule	13	0.340995941	< 0.001	< 0.001
GO:0033198	response to ATP	15	0.340849421	< 0.001	< 0.001
GO:0033137	negative regulation of peptidyl-serine phosphorylation	11	0.340587341	< 0.001	< 0.001
GO:0071354	cellular response to interleukin-6	13	0.340580141	< 0.001	< 0.001
GO:0035518	histone H2A monoubiquitination	8	0.340540541	< 0.001	< 0.001
GO:0043247	telomere maintenance in response to DNA damage	7	0.34028314	0.006	0.007178216
GO:0051764	actin crosslink formation	6	0.34019734	0.0002	0.000356582
GO:0031114	regulation of microtubule depolymerization	13	0.34016434	0.0001	0.000192793
GO:0036465	synaptic vesicle recycling	36	0.34016159	0.0004	0.000648934
GO:0051953	negative regulation of amine transport	11	0.34011934	0.0037	0.004617737
GO:0001710	mesodermal cell fate commitment	5	0.34007722	0.0071	0.008390203
GO:0043653	mitochondrial fragmentation involved in apoptotic process	5	0.34002574	< 0.001	< 0.001
GO:0014046	dopamine secretion	9	0.33996854	< 0.001	< 0.001
GO:0014059	regulation of dopamine secretion	9	0.33996854	< 0.001	< 0.001
GO:0060795	cell fate commitment involved in formation of primary germ layer	7	0.339915426	0.0021	0.002780108
GO:0097320	membrane tubulation	5	0.33976834	0.0038	0.004725081
GO:0003338	metanephros morphogenesis	11	0.33955774	< 0.001	< 0.001
GO:0070229	negative regulation of lymphocyte apoptotic process	9	0.339339339	< 0.001	< 0.001
GO:0032205	negative regulation of telomere maintenance	17	0.339086986	0.0001	0.000192793
GO:0002377	immunoglobulin production	32	0.338972008	< 0.001	< 0.001
GO:0051382	kinetochore assembly	7	0.338849053	< 0.001	< 0.001
GO:0090281	negative regulation of calcium ion import	10	0.338532819	0.0003	0.000505993
GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	34	0.338451056	< 0.001	< 0.001
GO:2000010	positive regulation of protein localization to cell surface	8	0.338256113	0.0004	0.000648934
GO:0007379	segment specification	5	0.338172458	0.0081	0.00945
GO:0007157	heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	11	0.337755938	0.0007	0.001063182
GO:0048305	immunoglobulin secretion	9	0.337709138	< 0.001	< 0.001
GO:2000369	regulation of clathrin-dependent endocytosis	20	0.337696268	0.001	0.001450349
GO:1905523	positive regulation of macrophage migration	9	0.337680538	< 0.001	< 0.001
GO:0042092	type 2 immune response	8	0.337483912	< 0.001	< 0.001
GO:0019933	cAMP-mediated signaling	25	0.337431145	0.0001	0.000192793
GO:0010447	response to acidic pH	8	0.337226512	< 0.001	< 0.001
GO:0033233	regulation of protein sumoylation	8	0.337226512	< 0.001	< 0.001
GO:0071542	dopaminergic neuron differentiation	9	0.337108537	< 0.001	< 0.001
GO:0090383	phagosome acidification	14	0.337065637	0.0018	0.002428764
GO:0035067	negative regulation of histone acetylation	9	0.337022737	< 0.001	< 0.001
GO:2000757	negative regulation of peptidyl-lysine acetylation	9	0.337022737	< 0.001	< 0.001
GO:0043301	negative regulation of leukocyte degranulation	5	0.336782497	0.0004	0.000648934
GO:1901299	negative regulation of hydrogen peroxide-mediated programmed cell death	5	0.336731017	< 0.001	< 0.001
GO:0071260	cellular response to mechanical stimulus	20	0.336679537	< 0.001	< 0.001
GO:0072583	clathrin-dependent endocytosis	45	0.336668097	0.0003	0.000505993
GO:1900274	regulation of phospholipase C activity	17	0.336573548	< 0.001	< 0.001
GO:0010452	histone H3-K36 methylation	7	0.336532451	0.0022	0.002896881
GO:0035735	intracellular transport involved in cilium assembly	22	0.336410436	< 0.001	< 0.001
GO:0051125	regulation of actin nucleation	11	0.336398736	0.0016	0.002186748
GO:0060338	regulation of type I interferon-mediated signaling pathway	11	0.336258336	< 0.001	< 0.001
GO:1902042	negative regulation of extrinsic apoptotic signaling pathway via death domain receptors	8	0.336164736	< 0.001	< 0.001
GO:0090557	establishment of endothelial intestinal barrier	5	0.336164736	0.0015	0.002069969
GO:0042088	T-helper 1 type immune response	11	0.336047736	< 0.001	< 0.001
GO:0051058	negative regulation of small GTPase mediated signal transduction	29	0.336013846	< 0.001	< 0.001
GO:0098840	protein transport along microtubule	31	0.335923942	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0099118	microtubule-based protein transport	31	0.335923942	< 0.001	< 0.001
GO:0051770	positive regulation of nitric-oxide synthase biosynthetic process	7	0.335907336	< 0.001	< 0.001
GO:0007076	mitotic chromosome condensation	6	0.335649936	0.0007	0.001063182
GO:1901298	regulation of hydrogen peroxide-mediated programmed cell death	6	0.335564136	0.0001	0.000192793
GO:0046173	polyol biosynthetic process	17	0.335543947	< 0.001	< 0.001
GO:0035307	positive regulation of protein dephosphorylation	20	0.335469755	0.0001	0.000192793
GO:0015012	heparan sulfate proteoglycan biosynthetic process	9	0.335220935	0.0013	0.001826625
GO:0048857	neural nucleus development	23	0.335202283	< 0.001	< 0.001
GO:0003188	heart valve formation	5	0.335083655	< 0.001	< 0.001
GO:0042475	odontogenesis of dentin-containing tooth	19	0.335080946	< 0.001	< 0.001
GO:0035065	regulation of histone acetylation	19	0.334945472	< 0.001	< 0.001
GO:0001768	establishment of T cell polarity	5	0.334929215	< 0.001	< 0.001
GO:0070199	establishment of protein localization to chromosome	10	0.334903475	0.0003	0.000505993
GO:0014812	muscle cell migration	31	0.33476149	< 0.001	< 0.001
GO:0035588	G-protein coupled purinergic receptor signaling pathway	8	0.33458816	0.0001	0.000192793
GO:0035025	positive regulation of Rho protein signal transduction	6	0.334534535	< 0.001	< 0.001
GO:0050704	regulation of interleukin-1 secretion	18	0.334534535	< 0.001	< 0.001
GO:0006293	nucleotide-excision repair, preincision complex stabilization	10	0.334388674	0.0002	0.000356582
GO:0006295	nucleotide-excision repair, DNA incision, 3'-to lesion	10	0.334388674	0.0002	0.000356582
GO:0038179	neurotrophin signaling pathway	18	0.334205634	0.0012	0.001702047
GO:0051952	regulation of amine transport	34	0.334060111	0.0002	0.000356582
GO:0048308	organelle inheritance	7	0.334031991	0.0229	0.024839743
GO:0048313	Golgi inheritance	7	0.334031991	0.0229	0.024839743
GO:0098787	mRNA cleavage involved in mRNA processing	5	0.333951094	0.0001	0.000192793
GO:0042744	hydrogen peroxide catabolic process	9	0.333905334	< 0.001	< 0.001
GO:0046854	phosphatidylinositol phosphorylation	15	0.333830974	0.0011	0.001576346
GO:1903975	regulation of glial cell migration	6	0.333719434	0.0009	0.001319479
GO:1904948	midbrain dopaminergic neuron differentiation	5	0.333539254	< 0.001	< 0.001
GO:0043984	histone H4-K16 acetylation	10	0.333487773	< 0.001	< 0.001
GO:0046640	regulation of alpha-beta T cell proliferation	6	0.333462033	0.0002	0.000356582
GO:0008090	retrograde axonal transport	7	0.333370105	0.0022	0.002896881
GO:0090329	regulation of DNA-dependent DNA replication	18	0.333290433	0.0019	0.00254969
GO:0071295	cellular response to vitamin	8	0.333236808	< 0.001	< 0.001
GO:0070202	regulation of establishment of protein localization to chromosome	7	0.333112705	0.0004	0.000648934
GO:0072210	metanephric nephron development	12	0.333097383	< 0.001	< 0.001
GO:2000651	positive regulation of sodium ion transmembrane transporter activity	6	0.333033033	0.0005	0.000791911
GO:0033598	mammary gland epithelial cell proliferation	13	0.333016533	< 0.001	< 0.001
GO:0016445	somatic diversification of immunoglobulins	19	0.332940459	0.0002	0.000356582
GO:0072170	metanephric tubule development	8	0.332915058	< 0.001	< 0.001
GO:0072207	metanephric epithelium development	8	0.332915058	< 0.001	< 0.001
GO:0072234	metanephric nephron tubule development	8	0.332915058	< 0.001	< 0.001
GO:0072243	metanephric nephron epithelium development	8	0.332915058	< 0.001	< 0.001
GO:0090195	chemokine secretion	9	0.332875733	< 0.001	< 0.001
GO:0090196	regulation of chemokine secretion	9	0.332875733	< 0.001	< 0.001
GO:0015800	acidic amino acid transport	13	0.332858133	0.0001	0.000192793
GO:0060397	JAK-STAT cascade involved in growth hormone signaling pathway	7	0.332855304	< 0.001	< 0.001
GO:1903393	positive regulation of adherens junction organization	14	0.332726604	< 0.001	< 0.001
GO:0043949	regulation of cAMP-mediated signaling	15	0.332715573	0.0001	0.000192793
GO:0055093	response to hyperoxia	7	0.332450818	0.0007	0.001063182
GO:0010421	hydrogen peroxide-mediated programmed cell death	7	0.332340504	< 0.001	< 0.001
GO:0097468	programmed cell death in response to reactive oxygen species	7	0.332340504	< 0.001	< 0.001
GO:0019935	cyclic-nucleotide-mediated signaling	34	0.332243168	0.0001	0.000192793
GO:0042308	negative regulation of protein import into nucleus	17	0.332243168	< 0.001	< 0.001
GO:1904590	negative regulation of protein import	17	0.332243168	< 0.001	< 0.001
GO:0018200	peptidyl-glutamic acid modification	9	0.332017732	< 0.001	< 0.001
GO:0046337	phosphatidylethanolamine metabolic process	10	0.331969112	0.0001	0.000192793
GO:0033003	regulation of mast cell activation	17	0.331955485	< 0.001	< 0.001
GO:0002576	platelet degranulation	49	0.331883487	< 0.001	< 0.001
GO:0043244	regulation of protein complex disassembly	43	0.331824848	< 0.001	< 0.001
GO:0046823	negative regulation of nucleocytoplasmic transport	22	0.331718732	< 0.001	< 0.001
GO:0045686	negative regulation of glial cell differentiation	8	0.331402831	0.0137	0.015318601
GO:0051261	protein depolymerization	52	0.331402831	< 0.001	< 0.001
GO:0046580	negative regulation of Ras protein signal transduction	26	0.331323631	< 0.001	< 0.001
GO:2001267	regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway	7	0.331274131	0.0083	0.009660392
GO:0050702	interleukin-1 beta secretion	16	0.331241956	< 0.001	< 0.001
GO:0060349	bone morphogenesis	28	0.33123736	< 0.001	< 0.001
GO:1902188	positive regulation of viral release from host cell	7	0.331163817	0.001	0.001450349
GO:0070884	regulation of calcineurin-NFAT signaling cascade	16	0.331145431	< 0.001	< 0.001
GO:0048243	norepinephrine secretion	8	0.331081081	0.0004	0.000648934
GO:0016578	histone deubiquitination	12	0.330973831	0.0012	0.001702047
GO:0090343	positive regulation of cell aging	5	0.330965251	0.0001	0.000192793
GO:2000774	positive regulation of cellular senescence	5	0.330965251	0.0001	0.000192793
GO:0042743	hydrogen peroxide metabolic process	17	0.33074419	< 0.001	< 0.001
GO:0039529	RIG-I signaling pathway	9	0.330730731	< 0.001	< 0.001
GO:1901292	nucleoside phosphate catabolic process	21	0.330710302	< 0.001	< 0.001
GO:0048706	embryonic skeletal system development	31	0.330634782	< 0.001	< 0.001
GO:1902259	regulation of delayed rectifier potassium channel activity	9	0.330616331	0.0031	0.003925117
GO:0006919	activation of cysteine-type endopeptidase activity involved in apoptotic process	23	0.330501931	< 0.001	< 0.001
GO:0003283	atrial septum development	8	0.330469755	< 0.001	< 0.001
GO:0001881	receptor recycling	15	0.33041613	< 0.001	< 0.001
GO:0045010	actin nucleation	22	0.33036153	0.0009	0.001319479
GO:0051220	cytoplasmic sequestering of protein	20	0.33029601	< 0.001	< 0.001
GO:0043650	dicarboxylic acid biosynthetic process	8	0.330276705	0.0001	0.000192793

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0002374	cytokine secretion involved in immune response	10	0.33019305	< 0.001	< 0.001
GO:0075733	intracellular transport of virus	28	0.330161794	< 0.001	< 0.001
GO:0009261	ribonucleotide catabolic process	9	0.33007293	0.0001	0.000192793
GO:0002711	positive regulation of T cell mediated immunity	6	0.32990133	0.0006	0.000927725
GO:0051938	L-glutamate import	6	0.32990133	0.0322	0.03424022
GO:0060914	heart formation	6	0.32968683	0.0019	0.00254969
GO:0019054	modulation by virus of host process	16	0.329649292	< 0.001	< 0.001
GO:2000144	positive regulation of DNA-templated transcription, initiation	8	0.329633205	0.0003	0.000505993
GO:0042073	intraciliary transport	23	0.329550669	< 0.001	< 0.001
GO:0002448	mast cell mediated immunity	18	0.32954383	< 0.001	< 0.001
GO:0002691	regulation of cellular extravasation	12	0.32953668	0.0003	0.000505993
GO:0015807	L-amino acid transport	18	0.329386529	< 0.001	< 0.001
GO:1905521	regulation of macrophage migration	14	0.329343629	< 0.001	< 0.001
GO:1904037	positive regulation of epithelial cell apoptotic process	8	0.329182754	< 0.001	< 0.001
GO:0030011	maintenance of cell polarity	6	0.329172029	< 0.001	< 0.001
GO:0030201	heparan sulfate proteoglycan metabolic process	12	0.329129129	0.0016	0.002186748
GO:0031110	regulation of microtubule polymerization or depolymerization	33	0.329121329	< 0.001	< 0.001
GO:0006361	transcription initiation from RNA polymerase I promoter	22	0.329097929	< 0.001	< 0.001
GO:0014911	positive regulation of smooth muscle cell migration	14	0.329031072	< 0.001	< 0.001
GO:0051930	regulation of sensory perception of pain	11	0.328957529	0.0001	0.000192793
GO:0051931	regulation of sensory perception	11	0.328957529	0.0001	0.000192793
GO:0033127	regulation of histone phosphorylation	6	0.328871729	< 0.001	< 0.001
GO:0009994	oocyte differentiation	14	0.3288656	< 0.001	< 0.001
GO:0032024	positive regulation of insulin secretion	27	0.328862196	0.0004	0.000648934
GO:0006835	dicarboxylic acid transport	46	0.328851211	0.0007	0.001063182
GO:0045978	negative regulation of nucleoside metabolic process	8	0.328700129	0.0001	0.000192793
GO:1903579	negative regulation of ATP metabolic process	8	0.328700129	0.0001	0.000192793
GO:0015988	energy coupled proton transmembrane transport, against electrochemical gradient	13	0.328581329	0.0023	0.003013139
GO:0015991	ATP hydrolysis coupled proton transport	13	0.328581329	0.0023	0.003013139
GO:0090662	ATP hydrolysis coupled transmembrane transport	13	0.328581329	0.0023	0.003013139
GO:0014909	smooth muscle cell migration	27	0.328547595	< 0.001	< 0.001
GO:0010464	regulation of mesenchymal cell proliferation	8	0.328539254	< 0.001	< 0.001
GO:1900181	negative regulation of protein localization to nucleus	23	0.328465111	< 0.001	< 0.001
GO:0090183	regulation of kidney development	15	0.328219648	< 0.001	< 0.001
GO:0000726	non-recombinational repair	28	0.328203714	0.0001	0.000192793
GO:0045576	mast cell activation	21	0.328148557	< 0.001	< 0.001
GO:0003209	cardiac atrium morphogenesis	12	0.328142428	< 0.001	< 0.001
GO:0031650	regulation of heat generation	5	0.328082368	< 0.001	< 0.001
GO:0031652	positive regulation of heat generation	5	0.328082368	< 0.001	< 0.001
GO:0016559	peroxisome fission	7	0.328001471	0.0002	0.000356582
GO:0051341	regulation of oxidoreductase activity	28	0.327817614	< 0.001	< 0.001
GO:0090241	negative regulation of histone H4 acetylation	5	0.327722008	< 0.001	< 0.001
GO:0070207	protein homotrimerization	11	0.327670528	0.0002	0.000356582
GO:0018198	peptidyl-cysteine modification	19	0.327670528	< 0.001	< 0.001
GO:0033605	positive regulation of catecholamine secretion	8	0.327606178	0.0001	0.000192793
GO:2000107	negative regulation of leukocyte apoptotic process	11	0.327459927	< 0.001	< 0.001
GO:0034113	heterotypic cell-cell adhesion	16	0.327445302	< 0.001	< 0.001
GO:0035306	positive regulation of dephosphorylation	25	0.327423423	< 0.001	< 0.001
GO:0098930	axonal transport	34	0.327375274	0.0001	0.000192793
GO:1903727	positive regulation of phospholipid metabolic process	19	0.327264106	< 0.001	< 0.001
GO:0021695	cerebellar cortex development	15	0.327241527	0.0002	0.000356582
GO:0060042	retina morphogenesis in camera-type eye	12	0.327220077	0.0003	0.000505993
GO:1902581	multi-organism cellular localization	29	0.32708472	< 0.001	< 0.001
GO:1902583	multi-organism intracellular transport	29	0.32708472	< 0.001	< 0.001
GO:0072425	signal transduction involved in G2 DNA damage checkpoint	6	0.327069927	0.0005	0.000791911
GO:0002639	positive regulation of immunoglobulin production	16	0.326978764	0.0006	0.000927725
GO:0008089	anterograde axonal transport	30	0.326924067	< 0.001	< 0.001
GO:0033599	regulation of mammary gland epithelial cell proliferation	8	0.326833977	< 0.001	< 0.001
GO:1901880	negative regulation of protein depolymerization	29	0.326809568	< 0.001	< 0.001
GO:0010518	positive regulation of phospholipase activity	21	0.326677698	< 0.001	< 0.001
GO:0043552	positive regulation of phosphatidylinositol 3-kinase activity	13	0.326660727	< 0.001	< 0.001
GO:0060231	mesenchymal to epithelial transition	5	0.326589447	< 0.001	< 0.001
GO:2000380	regulation of mesoderm development	6	0.326426426	< 0.001	< 0.001
GO:0042635	positive regulation of hair cycle	5	0.326383526	< 0.001	< 0.001
GO:0051798	positive regulation of hair follicle development	5	0.326383526	< 0.001	< 0.001
GO:1903423	positive regulation of synaptic vesicle recycling	7	0.326346755	0.0088	0.010185307
GO:0050777	negative regulation of immune response	40	0.326274131	< 0.001	< 0.001
GO:0051897	positive regulation of protein kinase B signaling	64	0.326242761	< 0.001	< 0.001
GO:0030168	platelet activation	64	0.326234717	0.0002	0.000356582
GO:0016188	synaptic vesicle maturation	5	0.326229086	0.0193	0.021134184
GO:0043114	regulation of vascular permeability	14	0.326126126	< 0.001	< 0.001
GO:2000047	regulation of cell-cell adhesion mediated by cadherin	9	0.326126126	< 0.001	< 0.001
GO:0002700	regulation of production of molecular mediator of immune response	43	0.326078238	< 0.001	< 0.001
GO:0044766	multi-organism transport	32	0.326029601	< 0.001	< 0.001
GO:1902579	multi-organism localization	32	0.326029601	< 0.001	< 0.001
GO:0016925	protein sumoylation	29	0.325824347	< 0.001	< 0.001
GO:0035456	response to interferon-beta	6	0.325782926	< 0.001	< 0.001
GO:0035458	cellular response to interferon-beta	6	0.325782926	< 0.001	< 0.001
GO:1901068	guanosine-containing compound metabolic process	21	0.325684869	< 0.001	< 0.001
GO:0072395	signal transduction involved in cell cycle checkpoint	25	0.325436293	< 0.001	< 0.001
GO:0072401	signal transduction involved in DNA integrity checkpoint	25	0.325436293	< 0.001	< 0.001
GO:0072422	signal transduction involved in DNA damage checkpoint	25	0.325436293	< 0.001	< 0.001
GO:0019377	glycolipid catabolic process	5	0.325302445	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0043242	negative regulation of protein complex disassembly	30	0.325199485	< 0.001	< 0.001
GO:0002707	negative regulation of lymphocyte mediated immunity	6	0.325096525	< 0.001	< 0.001
GO:0098739	import across plasma membrane	14	0.325059754	< 0.001	< 0.001
GO:0042339	keratan sulfate metabolic process	11	0.325026325	0.0001	0.000192793
GO:0070897	DNA-templated transcriptional preinitiation complex assembly	12	0.325010725	0.0003	0.000505993
GO:0030219	megakaryocyte differentiation	25	0.324983269	< 0.001	< 0.001
GO:0035690	cellular response to drug	27	0.324982125	< 0.001	< 0.001
GO:0001953	negative regulation of cell-matrix adhesion	15	0.324976405	< 0.001	< 0.001
GO:0035272	exocrine system development	16	0.324887387	< 0.001	< 0.001
GO:0045292	mRNA cis splicing, via spliceosome	6	0.324753325	0.0003	0.000505993
GO:0002762	negative regulation of myeloid leukocyte differentiation	15	0.324736165	< 0.001	< 0.001
GO:0042501	serine phosphorylation of STAT protein	5	0.324581725	0.0002	0.000356582
GO:0006953	acute-phase response	14	0.324563339	< 0.001	< 0.001
GO:0000460	maturation of 5.8S rRNA	5	0.324478764	0.0001	0.000192793
GO:0071379	cellular response to prostaglandin stimulus	10	0.324324324	< 0.001	< 0.001
GO:0071380	cellular response to prostaglandin E stimulus	10	0.324324324	< 0.001	< 0.001
GO:0016239	positive regulation of macroautophagy	34	0.324082065	< 0.001	< 0.001
GO:0031503	protein complex localization	38	0.32398564	< 0.001	< 0.001
GO:1901879	regulation of protein depolymerization	39	0.323928324	< 0.001	< 0.001
GO:0014014	negative regulation of gliogenesis	12	0.323788074	0.0034	0.00427293
GO:0002287	alpha-beta T cell activation involved in immune response	14	0.323754367	< 0.001	< 0.001
GO:0002292	T cell differentiation involved in immune response	14	0.323754367	< 0.001	< 0.001
GO:0002293	alpha-beta T cell differentiation involved in immune response	14	0.323754367	< 0.001	< 0.001
GO:0002294	CD4-positive, alpha-beta T cell differentiation involved in immune response	14	0.323754367	< 0.001	< 0.001
GO:0042093	T-helper cell differentiation	14	0.323754367	< 0.001	< 0.001
GO:0006270	DNA replication initiation	13	0.323690724	0.0008	0.001193265
GO:0042769	DNA damage response, detection of DNA damage	18	0.323666524	0.0001	0.000192793
GO:0045429	positive regulation of nitric oxide biosynthetic process	13	0.323552124	< 0.001	< 0.001
GO:1904407	positive regulation of nitric oxide metabolic process	13	0.323552124	< 0.001	< 0.001
GO:0042430	indole-containing compound metabolic process	7	0.323515352	0.001	0.001450349
GO:0032835	glomerulus development	18	0.323437723	< 0.001	< 0.001
GO:0002440	production of molecular mediator of immune response	58	0.323263658	< 0.001	< 0.001
GO:0002118	aggressive behavior	6	0.323208923	0.0051	0.006185009
GO:0050850	positive regulation of calcium-mediated signaling	19	0.323186344	< 0.001	< 0.001
GO:0002328	pro-B cell differentiation	6	0.323080223	< 0.001	< 0.001
GO:0072148	epithelial cell fate commitment	5	0.323037323	0.0005	0.000791911
GO:0006012	galactose metabolic process	5	0.322985843	0.0112	0.012688637
GO:0021542	dentate gyrus development	9	0.322980123	0.0021	0.002780108
GO:0007260	tyrosine phosphorylation of STAT protein	26	0.322859123	0.0001	0.000192793
GO:0009065	glutamine family amino acid catabolic process	13	0.322760123	< 0.001	< 0.001
GO:1904896	ESCRT complex disassembly	7	0.32270638	0.0002	0.000356582
GO:1904903	ESCRT III complex disassembly	7	0.32270638	0.0002	0.000356582
GO:0010573	vascular endothelial growth factor production	10	0.322651223	< 0.001	< 0.001
GO:0008088	axo-dendritic transport	38	0.322651223	0.0001	0.000192793
GO:0021955	central nervous system neuron axonogenesis	22	0.322639523	< 0.001	< 0.001
GO:0051280	negative regulation of release of sequestered calcium ion into cytosol	8	0.322522523	0.002	0.002664694
GO:0015682	ferric iron transport	19	0.322522523	0.0026	0.003356522
GO:0033572	transferrin transport	19	0.322522523	0.0026	0.003356522
GO:0072512	trivalent inorganic cation transport	19	0.322522523	0.0026	0.003356522
GO:2000786	positive regulation of autophagosome assembly	8	0.322490347	0.0002	0.000356582
GO:1902774	late endosome to lysosome transport	5	0.322419562	< 0.001	< 0.001
GO:0003382	epithelial cell morphogenesis	13	0.322185922	< 0.001	< 0.001
GO:0048025	negative regulation of mRNA splicing, via spliceosome	11	0.322124722	0.0004	0.000648934
GO:0043388	positive regulation of DNA binding	23	0.322097253	< 0.001	< 0.001
GO:0042401	cellular biogenic amine biosynthetic process	8	0.321943372	0.0001	0.000192793
GO:0044786	cell cycle DNA replication	20	0.321917632	0.0005	0.000791911
GO:0044803	multi-organism membrane organization	17	0.321780604	0.0001	0.000192793
GO:1901655	cellular response to ketone	30	0.321604462	< 0.001	< 0.001
GO:0021894	cerebral cortex GABAergic interneuron development	5	0.321544402	0.0083	0.009660392
GO:0001960	negative regulation of cytokine-mediated signaling pathway	21	0.321505179	< 0.001	< 0.001
GO:0070671	response to interleukin-12	20	0.321454311	< 0.001	< 0.001
GO:0021952	central nervous system projection neuron axonogenesis	16	0.321364221	0.0008	0.001193265
GO:0070233	negative regulation of T cell apoptotic process	5	0.321338481	< 0.001	< 0.001
GO:1904589	regulation of protein import	40	0.321287001	< 0.001	< 0.001
GO:0042573	retinoic acid metabolic process	6	0.321278421	0.0001	0.000192793
GO:0098962	regulation of postsynaptic neurotransmitter receptor activity	6	0.321278421	0.0227	0.024637638
GO:0050432	catecholamine secretion	19	0.321276163	< 0.001	< 0.001
GO:0008156	negative regulation of DNA replication	15	0.321252681	0.0012	0.001702047
GO:0014832	urinary bladder smooth muscle contraction	5	0.321184041	0.0004	0.000648934
GO:0014848	urinary tract smooth muscle contraction	5	0.321184041	0.0004	0.000648934
GO:0051293	establishment of spindle localization	17	0.321129533	< 0.001	< 0.001
GO:0030206	chondroitin sulfate biosynthetic process	14	0.32107005	< 0.001	< 0.001
GO:0072171	mesonephric tubule morphogenesis	18	0.321063921	< 0.001	< 0.001
GO:0098880	maintenance of postsynaptic specialization structure	5	0.320926641	0.0182	0.020002603
GO:0031113	regulation of microtubule polymerization	23	0.32079906	0.0006	0.000927725
GO:0006362	transcription elongation from RNA polymerase I promoter	18	0.320692121	< 0.001	< 0.001
GO:0000132	establishment of mitotic spindle orientation	11	0.320650521	0.0047	0.005730776
GO:0061025	membrane fusion	57	0.32060331	< 0.001	< 0.001
GO:1902106	negative regulation of leukocyte differentiation	29	0.320569831	< 0.001	< 0.001
GO:1900027	regulation of ruffle assembly	10	0.32048906	0.0001	0.000192793
GO:0035587	purinergic receptor signaling pathway	12	0.32042042	< 0.001	< 0.001
GO:0098586	cellular response to virus	20	0.32034749	< 0.001	< 0.001
GO:0033260	nuclear DNA replication	16	0.320286358	0.0013	0.001826625

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0048199	vesicle targeting, to, from or within Golgi	35	0.3202574	< 0.001	< 0.001
GO:0032786	positive regulation of DNA-templated transcription, elongation	10	0.32007722	0.0003	0.000505993
GO:0046794	transport of virus	29	0.319886389	< 0.001	< 0.001
GO:2000738	positive regulation of stem cell differentiation	8	0.319851995	< 0.001	< 0.001
GO:0048569	post-embryonic animal organ development	5	0.31984556	< 0.001	< 0.001
GO:0007213	G-protein coupled acetylcholine receptor signaling pathway	11	0.31980812	0.0016	0.002186748
GO:0035082	axoneme assembly	17	0.319797108	0.0128	0.014368758
GO:0033238	regulation of cellular amine metabolic process	52	0.31974557	0.0001	0.000192793
GO:0002320	lymphoid progenitor cell differentiation	7	0.319544034	< 0.001	< 0.001
GO:1902667	regulation of axon guidance	14	0.319415334	0.0001	0.000192793
GO:0090218	positive regulation of lipid kinase activity	15	0.319399399	< 0.001	< 0.001
GO:0061098	positive regulation of protein tyrosine kinase activity	28	0.319378562	< 0.001	< 0.001
GO:0007000	nucleolus organization	6	0.319347919	< 0.001	< 0.001
GO:0030574	collagen catabolic process	6	0.319305019	0.0002	0.000356582
GO:0044243	multicellular organism catabolic process	6	0.319305019	0.0002	0.000356582
GO:0061005	cell differentiation involved in kidney development	14	0.319286634	< 0.001	< 0.001
GO:0022408	negative regulation of cell-cell adhesion	55	0.319166959	< 0.001	< 0.001
GO:0045989	positive regulation of striated muscle contraction	5	0.319124839	< 0.001	< 0.001
GO:0060452	positive regulation of cardiac muscle contraction	5	0.319124839	< 0.001	< 0.001
GO:0051969	regulation of transmission of nerve impulse	6	0.319004719	< 0.001	< 0.001
GO:0016447	somatic recombination of immunoglobulin gene segments	18	0.318961819	0.0006	0.000927725
GO:0007270	neuron-neuron synaptic transmission	65	0.318910999	0.0001	0.000192793
GO:0000729	DNA double-strand break processing	9	0.318833119	0.0003	0.000505993
GO:0050688	regulation of defense response to virus	37	0.318703259	< 0.001	< 0.001
GO:0010758	regulation of macrophage chemotaxis	10	0.318687259	0.0001	0.000192793
GO:0043154	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	33	0.318427518	< 0.001	< 0.001
GO:0035116	embryonic hindlimb morphogenesis	9	0.318346918	< 0.001	< 0.001
GO:0051894	positive regulation of focal adhesion assembly	11	0.318310518	0.0002	0.000356582
GO:0090161	Golgi ribbon formation	5	0.318249678	0.0001	0.000192793
GO:0021796	cerebral cortex regionalization	5	0.318249678	0.0004	0.000648934
GO:0002031	G-protein coupled receptor internalization	6	0.318232518	< 0.001	< 0.001
GO:0060850	regulation of transcription involved in cell fate commitment	8	0.318018018	< 0.001	< 0.001
GO:0050974	detection of mechanical stimulus involved in sensory perception	9	0.317975118	0.0016	0.002186748
GO:0071377	cellular response to glucagon stimulus	12	0.317975118	0.0001	0.000192793
GO:0034587	piRNA metabolic process	6	0.317932218	0.0041	0.005057384
GO:0035864	response to potassium ion	7	0.317926089	0.0013	0.001826625
GO:0035865	cellular response to potassium ion	7	0.317926089	0.0013	0.001826625
GO:0021819	layer formation in cerebral cortex	9	0.317917918	0.0047	0.005730776
GO:0033604	negative regulation of catecholamine secretion	6	0.317889318	0.0015	0.002069969
GO:1903428	positive regulation of reactive oxygen species biosynthetic process	16	0.31787323	< 0.001	< 0.001
GO:0042306	regulation of protein import into nucleus	39	0.317770518	< 0.001	< 0.001
GO:0006646	phosphatidylethanolamine biosynthetic process	6	0.317760618	< 0.001	< 0.001
GO:0071514	genetic imprinting	10	0.317657658	< 0.001	< 0.001
GO:0032272	negative regulation of protein polymerization	32	0.317438867	< 0.001	< 0.001
GO:0048207	vesicle targeting, rough ER to cis-Golgi	33	0.317436917	< 0.001	< 0.001
GO:0048208	COPII vesicle coating	33	0.317436917	< 0.001	< 0.001
GO:0010517	regulation of phospholipase activity	24	0.317428142	< 0.001	< 0.001
GO:0030042	actin filament depolymerization	28	0.317374517	< 0.001	< 0.001
GO:0030834	regulation of actin filament depolymerization	25	0.317302445	< 0.001	< 0.001
GO:1902430	negative regulation of beta-amyloid formation	7	0.317264203	< 0.001	< 0.001
GO:0050860	negative regulation of T cell receptor signaling pathway	8	0.317245817	< 0.001	< 0.001
GO:0048820	hair follicle maturation	6	0.317245817	0.0006	0.000927725
GO:0043367	CD4-positive, alpha-beta T cell differentiation	20	0.317232947	< 0.001	< 0.001
GO:0002718	regulation of cytokine production involved in immune response	21	0.317166146	< 0.001	< 0.001
GO:0002053	positive regulation of mesenchymal cell proliferation	6	0.317160017	< 0.001	< 0.001
GO:0071711	basement membrane organization	6	0.317074217	0.0002	0.000356582
GO:0034629	cellular protein complex localization	10	0.316705277	< 0.001	< 0.001
GO:0071257	cellular response to electrical stimulus	5	0.316550837	0.0012	0.001702047
GO:0097091	synaptic vesicle clustering	11	0.316461916	0.0033	0.004153051
GO:0090331	negative regulation of platelet aggregation	5	0.316396396	< 0.001	< 0.001
GO:0070986	left/right axis specification	6	0.316302016	< 0.001	< 0.001
GO:0014910	regulation of smooth muscle cell migration	25	0.316272844	< 0.001	< 0.001
GO:0031954	positive regulation of protein autophosphorylation	15	0.316190476	0.0013	0.001826625
GO:0032418	lysosome localization	35	0.316124288	< 0.001	< 0.001
GO:0035774	positive regulation of insulin secretion involved in cellular response to glucose stimulus	14	0.316124288	0.0001	0.000192793
GO:0001702	gastrulation with mouth forming second	10	0.316113256	< 0.001	< 0.001
GO:0051386	regulation of neurotrophin TRK receptor signaling pathway	7	0.316050745	0.0112	0.012688637
GO:0042417	dopamine metabolic process	14	0.315977202	< 0.001	< 0.001
GO:0042551	neuron maturation	18	0.315858716	< 0.001	< 0.001
GO:0032434	regulation of proteasomal ubiquitin-dependent protein catabolic process	55	0.315708436	< 0.001	< 0.001
GO:0006521	regulation of cellular amino acid metabolic process	42	0.315689159	0.0003	0.000505993
GO:0030641	regulation of cellular pH	27	0.315677582	< 0.001	< 0.001
GO:0030279	negative regulation of ossification	23	0.315662246	< 0.001	< 0.001
GO:0030858	positive regulation of epithelial cell differentiation	18	0.315644216	< 0.001	< 0.001
GO:0071391	cellular response to estrogen stimulus	5	0.315624196	0.0005	0.000791911
GO:0006473	protein acetylation	84	0.315609487	< 0.001	< 0.001
GO:0098926	postsynaptic signal transduction	5	0.315521236	0.0001	0.000192793
GO:0099527	postsynapse to nucleus signaling pathway	5	0.315521236	0.0001	0.000192793
GO:0014066	regulation of phosphatidylinositol 3-kinase signaling	53	0.315441587	< 0.001	< 0.001
GO:0006349	regulation of gene expression by genetic imprinting	6	0.315401115	0.0003	0.000505993
GO:1901984	negative regulation of protein acetylation	11	0.315385515	< 0.001	< 0.001
GO:0051409	response to nitrosative stress	7	0.315352087	< 0.001	< 0.001
GO:0050650	chondroitin sulfate proteoglycan biosynthetic process	16	0.315315315	0.0002	0.000356582

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0006303	double-strand break repair via nonhomologous end joining	26	0.315285615	0.0001	0.000192793
GO:0006901	vesicle coating	34	0.31512605	< 0.001	< 0.001
GO:0031952	regulation of protein autophosphorylation	21	0.315070172	0.0002	0.000356582
GO:0035635	entry of bacterium into host cell	5	0.315057915	0.0014	0.00194839
GO:0071670	smooth muscle cell chemotaxis	5	0.315057915	0.0006	0.000927725
GO:0043921	modulation by host of viral transcription	8	0.315057915	0.0023	0.003013139
GO:0052472	modulation by host of symbiont transcription	8	0.315057915	0.0023	0.003013139
GO:0071599	otic vesicle development	5	0.314954955	0.0001	0.000192793
GO:0043116	negative regulation of vascular permeability	6	0.314843415	0.0001	0.000192793
GO:0002699	positive regulation of immune effector process	68	0.314819441	< 0.001	< 0.001
GO:0031958	corticosteroid receptor signaling pathway	9	0.314800515	0.0003	0.000505993
GO:0042220	response to cocaine	22	0.314765415	< 0.001	< 0.001
GO:0010466	negative regulation of peptidase activity	62	0.314746544	< 0.001	< 0.001
GO:2000049	positive regulation of cell-cell adhesion mediated by cadherin	5	0.314697555	0.0171	0.018858857
GO:0060117	auditory receptor cell development	8	0.31463964	0.0001	0.000192793
GO:0018196	peptidyl-asparagine modification	14	0.314451186	< 0.001	< 0.001
GO:0060428	lung epithelium development	8	0.314414414	< 0.001	< 0.001
GO:0051294	establishment of spindle orientation	12	0.314392964	0.0033	0.004153051
GO:1905522	negative regulation of macrophage migration	5	0.314337194	0.0001	0.000192793
GO:0046834	lipid phosphorylation	21	0.314236686	0.0029	0.003693519
GO:0010649	regulation of cell communication by electrical coupling	5	0.314182754	< 0.001	< 0.001
GO:1901844	regulation of cell communication by electrical coupling involved in cardiac conduction	5	0.314182754	< 0.001	< 0.001
GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	88	0.314133614	0.0001	0.000192793
GO:0051193	regulation of cofactor metabolic process	36	0.314071214	< 0.001	< 0.001
GO:1904385	cellular response to angiotensin	7	0.314065085	0.021	0.022870617
GO:0097581	lamellipodium organization	38	0.314028314	< 0.001	< 0.001
GO:0045986	negative regulation of smooth muscle contraction	7	0.313918	0.0041	0.005057384
GO:0010951	negative regulation of endopeptidase activity	60	0.313916774	< 0.001	< 0.001
GO:0048011	neurotrophin TRK receptor signaling pathway	15	0.313908194	0.0013	0.001826625
GO:0044241	lipid digestion	5	0.313873874	< 0.001	< 0.001
GO:0045910	negative regulation of DNA recombination	13	0.313850114	0.0041	0.005057384
GO:0045652	regulation of megakaryocyte differentiation	21	0.313770914	< 0.001	< 0.001
GO:0072567	chemokine (C-X-C motif) ligand 2 production	7	0.313697371	< 0.001	< 0.001
GO:0046068	cGMP metabolic process	8	0.313642214	0.0001	0.000192793
GO:0042246	tissue regeneration	14	0.313495128	0.0009	0.001319479
GO:0071526	semaphorin-plexin signaling pathway	10	0.313436293	< 0.001	< 0.001
GO:0030890	positive regulation of B cell proliferation	13	0.313295713	< 0.001	< 0.001
GO:0032332	positive regulation of chondrocyte differentiation	9	0.313284713	0.0007	0.001063182
GO:1901800	positive regulation of proteasomal protein catabolic process	44	0.313174213	< 0.001	< 0.001
GO:0046755	viral budding	15	0.313101673	0.0003	0.000505993
GO:1902590	multi-organism organelle organization	15	0.313101673	0.0003	0.000505993
GO:1902592	multi-organism membrane budding	15	0.313101673	0.0003	0.000505993
GO:0007162	negative regulation of cell adhesion	85	0.3129866	< 0.001	< 0.001
GO:0097479	synaptic vesicle localization	111	0.312952335	0.001	0.001450349
GO:1902083	negative regulation of peptidyl-cysteine S-nitrosylation	5	0.312947233	< 0.001	< 0.001
GO:0007253	cytoplasmic sequestering of NF-kappaB	5	0.312947233	0.0002	0.000356582
GO:0042345	regulation of NF-kappaB import into nucleus	5	0.312947233	0.0002	0.000356582
GO:0042347	negative regulation of NF-kappaB import into nucleus	5	0.312947233	0.0002	0.000356582
GO:0042348	NF-kappaB import into nucleus	5	0.312947233	0.0002	0.000356582
GO:0072273	metanephric nephron morphogenesis	9	0.312941513	< 0.001	< 0.001
GO:2000370	positive regulation of clathrin-dependent endocytosis	8	0.312934363	0.0114	0.012893596
GO:0032536	regulation of cell projection size	5	0.312895753	0.0193	0.021134184
GO:0019233	sensory perception of pain	41	0.312791537	< 0.001	< 0.001
GO:0051968	positive regulation of synaptic transmission, glutamatergic	12	0.312741313	0.0018	0.002428764
GO:0060856	establishment of blood-brain barrier	5	0.312741313	0.0021	0.002780108
GO:0051882	mitochondrial depolarization	7	0.31266777	< 0.001	< 0.001
GO:0070206	protein trimerization	17	0.312605042	< 0.001	< 0.001
GO:0046822	regulation of nucleocytoplasmic transport	59	0.312584255	< 0.001	< 0.001
GO:1904591	positive regulation of protein import	18	0.312512513	< 0.001	< 0.001
GO:0001188	RNA polymerase I transcriptional preinitiation complex assembly	7	0.312483912	0.0001	0.000192793
GO:0070268	cornification	19	0.312416176	< 0.001	< 0.001
GO:0021871	forebrain regionalization	11	0.312390312	0.0017	0.00231289
GO:1903170	negative regulation of calcium ion transmembrane transport	14	0.312373598	0.0001	0.000192793
GO:0060193	positive regulation of lipase activity	25	0.312339768	< 0.001	< 0.001
GO:0033119	negative regulation of RNA splicing	14	0.312226512	0.0002	0.000356582
GO:0034350	regulation of glial cell apoptotic process	5	0.312226512	0.0045	0.005509289
GO:2000807	regulation of synaptic vesicle clustering	6	0.312097812	0.0006	0.000927725
GO:0050433	regulation of catecholamine secretion	18	0.312040612	< 0.001	< 0.001
GO:0030835	negative regulation of actin filament depolymerization	17	0.311969112	< 0.001	< 0.001
GO:0034219	carbohydrate transmembrane transport	10	0.311943372	< 0.001	< 0.001
GO:0021549	cerebellum development	31	0.311877776	< 0.001	< 0.001
GO:1901661	quinone metabolic process	9	0.311854712	< 0.001	< 0.001
GO:0072111	cell proliferation involved in kidney development	7	0.311822026	< 0.001	< 0.001
GO:0033622	integrin activation	8	0.311808237	< 0.001	< 0.001
GO:0030901	midbrain development	29	0.31169396	< 0.001	< 0.001
GO:0043090	amino acid import	8	0.311647362	0.0187	0.020510412
GO:0043092	L-amino acid import	8	0.311647362	0.0187	0.020510412
GO:0021826	substrate-independent telencephalic tangential migration	6	0.311583012	0.0016	0.002186748
GO:0021830	interneuron migration from the subpallium to the cortex	6	0.311583012	0.0016	0.002186748
GO:0021843	substrate-independent telencephalic tangential interneuron migration	6	0.311583012	0.0016	0.002186748
GO:0060315	negative regulation of ryanodine-sensitive calcium-release channel activity	6	0.311497211	0.0132	0.014787065
GO:0010882	regulation of cardiac muscle contraction by calcium ion signaling	13	0.311434511	< 0.001	< 0.001
GO:0006363	termination of RNA polymerase I transcription	18	0.311425711	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0032890	regulation of organic acid transport	24	0.311336336	< 0.001	< 0.001
GO:0006261	DNA-dependent DNA replication	53	0.31131347	0.0005	0.000791911
GO:0060021	palate development	27	0.311273178	< 0.001	< 0.001
GO:0099550	trans-synaptic signalling, modulating synaptic transmission	5	0.311248391	0.0411	0.043118695
GO:2000169	regulation of peptidyl-cysteine S-nitrosylation	6	0.311239811	0.0004	0.000648934
GO:0002702	positive regulation of production of molecular mediator of immune response	33	0.311220311	< 0.001	< 0.001
GO:0006541	glutamine metabolic process	10	0.311171171	< 0.001	< 0.001
GO:0090174	organelle membrane fusion	30	0.311136851	< 0.001	< 0.001
GO:0030517	negative regulation of axon extension	15	0.311093951	< 0.001	< 0.001
GO:0090493	catecholamine uptake	8	0.311036036	0.0001	0.000192793
GO:0032435	negative regulation of proteasomal ubiquitin-dependent protein catabolic process	14	0.310994668	0.0002	0.000356582
GO:1900016	negative regulation of cytokine production involved in inflammatory response	8	0.310971686	< 0.001	< 0.001
GO:0060761	negative regulation of response to cytokine stimulus	23	0.310905937	0.0002	0.000356582
GO:0090231	regulation of spindle checkpoint	5	0.310888031	0.0459	0.047857148
GO:0090266	regulation of mitotic cell cycle spindle assembly checkpoint	5	0.310888031	0.0459	0.047857148
GO:1903504	regulation of mitotic spindle checkpoint	5	0.310888031	0.0459	0.047857148
GO:0045907	positive regulation of vasoconstriction	9	0.310882311	< 0.001	< 0.001
GO:0001836	release of cytochrome c from mitochondria	29	0.310770869	< 0.001	< 0.001
GO:0008045	motor neuron axon guidance	14	0.310700496	0.0045	0.005509289
GO:0006383	transcription from RNA polymerase III promoter	25	0.310692407	0.0002	0.000356582
GO:2001251	negative regulation of chromosome organization	33	0.310635311	0.0005	0.000791911
GO:0045744	negative regulation of G-protein coupled receptor protein signaling pathway	19	0.310600826	< 0.001	< 0.001
GO:0048489	synaptic vesicle transport	104	0.310570736	0.0014	0.00194839
GO:0097480	establishment of synaptic vesicle localization	104	0.310570736	0.0014	0.00194839
GO:2001234	negative regulation of apoptotic signaling pathway	80	0.310472973	< 0.001	< 0.001
GO:0046825	regulation of protein export from nucleus	13	0.31042471	< 0.001	< 0.001
GO:1903313	positive regulation of mRNA metabolic process	17	0.310364146	< 0.001	< 0.001
GO:0048705	skeletal system morphogenesis	61	0.310331878	< 0.001	< 0.001
GO:0071709	membrane assembly	16	0.310312098	< 0.001	< 0.001
GO:0051583	dopamine uptake involved in synaptic transmission	6	0.31025311	0.0031	0.003925117
GO:0051934	catecholamine uptake involved in synaptic transmission	6	0.31025311	0.0031	0.003925117
GO:0050701	interleukin-1 secretion	20	0.31019305	< 0.001	< 0.001
GO:0043124	negative regulation of I-kappaB kinase/NF-kappaB signaling	22	0.31016731	< 0.001	< 0.001
GO:1903205	regulation of hydrogen peroxide-induced cell death	9	0.31011011	< 0.001	< 0.001
GO:0016572	histone phosphorylation	15	0.30994423	0.0055	0.006618125
GO:0006296	nucleotide-excision repair, DNA incision, 5'-to lesion	16	0.30990991	0.0002	0.000356582
GO:0044106	cellular amine metabolic process	65	0.30985843	< 0.001	< 0.001
GO:0019043	establishment of viral latency	6	0.30978121	< 0.001	< 0.001
GO:0075713	establishment of integrated proviral latency	6	0.30978121	< 0.001	< 0.001
GO:1903825	organic acid transmembrane transport	21	0.309762824	0.0003	0.000505993
GO:1905039	carboxylic acid transmembrane transport	21	0.309762824	0.0003	0.000505993
GO:0071467	cellular response to pH	5	0.30970399	< 0.001	< 0.001
GO:0061178	regulation of insulin secretion involved in cellular response to glucose stimulus	26	0.30963271	< 0.001	< 0.001
GO:0010574	regulation of vascular endothelial growth factor production	9	0.30962391	< 0.001	< 0.001
GO:0046425	regulation of JAK-STAT cascade	38	0.309503488	< 0.001	< 0.001
GO:0051937	catecholamine transport	26	0.309434709	< 0.001	< 0.001
GO:0061136	regulation of proteasomal protein catabolic process	77	0.309401795	< 0.001	< 0.001
GO:0043543	protein acylation	99	0.309392509	< 0.001	< 0.001
GO:0060041	retina development in camera-type eye	49	0.309337326	< 0.001	< 0.001
GO:0071349	cellular response to interleukin-12	19	0.309327372	< 0.001	< 0.001
GO:0048741	skeletal muscle fiber development	12	0.309287859	0.002	0.002664694
GO:0050715	positive regulation of cytokine secretion	43	0.309275388	< 0.001	< 0.001
GO:0050909	sensory perception of taste	10	0.309240669	0.0009	0.001319479
GO:0090656	t-circle formation	9	0.309194909	0.0001	0.000192793
GO:0001889	liver development	37	0.309123796	< 0.001	< 0.001
GO:0061008	hepaticobiliary system development	37	0.309123796	< 0.001	< 0.001
GO:0002793	positive regulation of peptide secretion	33	0.309090909	< 0.001	< 0.001
GO:0051653	spindle localization	20	0.309021879	0.0003	0.000505993
GO:1902043	positive regulation of extrinsic apoptotic signaling pathway via death domain receptors	6	0.309009009	0.0001	0.000192793
GO:0099504	synaptic vesicle cycle	99	0.308997309	0.001	0.001450349
GO:0051693	actin filament capping	15	0.308863149	0.0006	0.000927725
GO:0051383	kinetochore organization	8	0.308848134	< 0.001	< 0.001
GO:1903955	positive regulation of protein targeting to mitochondrion	21	0.30883128	< 0.001	< 0.001
GO:0070198	protein localization to chromosome, telomeric region	14	0.308825152	0.0003	0.000505993
GO:0009649	entrainment of circadian clock	12	0.308815959	0.0123	0.013827585
GO:0090184	positive regulation of kidney development	11	0.308810109	< 0.001	< 0.001
GO:0099003	vesicle-mediated transport in synapse	110	0.308807769	0.001	0.001450349
GO:0014061	regulation of norepinephrine secretion	7	0.308733223	0.0001	0.000192793
GO:0019226	transmission of nerve impulse	22	0.308716509	< 0.001	< 0.001
GO:0008542	visual learning	22	0.308622909	0.0037	0.004617737
GO:2000106	regulation of leukocyte apoptotic process	24	0.308526384	< 0.001	< 0.001
GO:2000074	regulation of type B pancreatic cell development	5	0.308519949	0.0101	0.011583277
GO:0006885	regulation of pH	34	0.308501779	< 0.001	< 0.001
GO:0008593	regulation of Notch signaling pathway	31	0.308481754	< 0.001	< 0.001
GO:1900034	regulation of cellular response to heat	35	0.308416988	< 0.001	< 0.001
GO:0001706	endoderm formation	12	0.308344058	< 0.001	< 0.001
GO:0001709	cell fate determination	17	0.308274661	0.0047	0.005730776
GO:0095500	acetylcholine receptor signaling pathway	15	0.308211068	< 0.001	< 0.001
GO:1903831	signal transduction involved in cellular response to ammonium ion	15	0.308211068	< 0.001	< 0.001
GO:0010954	positive regulation of protein processing	7	0.30814488	< 0.001	< 0.001
GO:0035249	synaptic transmission, glutamatergic	35	0.308071337	0.0033	0.004153051
GO:0090114	COPII-coated vesicle budding	38	0.308067466	< 0.001	< 0.001
GO:0018279	protein N-linked glycosylation via asparagine	13	0.308048708	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0051966	regulation of synaptic transmission, glutamatergic	26	0.308048708	0.0014	0.00194839
GO:0034394	protein localization to cell surface	24	0.307947233	< 0.001	< 0.001
GO:0031570	DNA integrity checkpoint	58	0.307886211	< 0.001	< 0.001
GO:0050848	regulation of calcium-mediated signaling	47	0.307724746	< 0.001	< 0.001
GO:1902751	positive regulation of cell cycle G2/M phase transition	15	0.307696268	0.0004	0.000648934
GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	60	0.307687688	< 0.001	< 0.001
GO:0034332	adherens junction organization	60	0.307666238	< 0.001	< 0.001
GO:0002831	regulation of response to biotic stimulus	67	0.307631726	< 0.001	< 0.001
GO:2000117	negative regulation of cysteine-type endopeptidase activity	35	0.307600662	< 0.001	< 0.001
GO:0006534	cysteine metabolic process	7	0.307593308	< 0.001	< 0.001
GO:0007188	adenylate cyclase-modulating G-protein coupled receptor signaling pathway	55	0.307588628	< 0.001	< 0.001
GO:0046427	positive regulation of JAK-STAT cascade	20	0.307554698	< 0.001	< 0.001
GO:0030166	proteoglycan biosynthetic process	25	0.307490347	< 0.001	< 0.001
GO:0032228	regulation of synaptic transmission, GABAergic	15	0.307456027	0.0002	0.000356582
GO:0021879	forebrain neuron differentiation	24	0.307410982	0.0045	0.005509289
GO:0007259	JAK-STAT cascade	46	0.307341503	< 0.001	< 0.001
GO:0071305	cellular response to vitamin D	5	0.307284427	0.0004	0.000648934
GO:0090201	negative regulation of release of cytochrome c from mitochondria	12	0.307228657	< 0.001	< 0.001
GO:0006152	purine nucleoside catabolic process	5	0.307129987	0.0003	0.000505993
GO:0046130	purine ribonucleoside catabolic process	5	0.307129987	0.0003	0.000505993
GO:0006903	vesicle targeting	45	0.307101387	< 0.001	< 0.001
GO:0032891	negative regulation of organic acid transport	5	0.307078507	0.0053	0.006400268
GO:0033262	regulation of nuclear cell cycle DNA replication	5	0.307027027	< 0.001	< 0.001
GO:1901136	carbohydrate derivative catabolic process	64	0.306986004	< 0.001	< 0.001
GO:1901976	regulation of cell cycle checkpoint	11	0.306984907	0.0068	0.008063902
GO:2000042	negative regulation of double-strand break repair via homologous recombination	5	0.306975547	0.0001	0.000192793
GO:0002819	regulation of adaptive immune response	41	0.306883887	< 0.001	< 0.001
GO:0009301	snRNA transcription	36	0.306799657	< 0.001	< 0.001
GO:0042795	snRNA transcription from RNA polymerase II promoter	36	0.306799657	< 0.001	< 0.001
GO:0032728	positive regulation of interferon-beta production	9	0.306792507	0.0014	0.00194839
GO:0021697	cerebellar cortex formation	8	0.306756757	0.0072	0.008495371
GO:0044801	single-organism membrane fusion	41	0.306752048	< 0.001	< 0.001
GO:0035722	interleukin-12-mediated signaling pathway	18	0.306692407	< 0.001	< 0.001
GO:0010569	regulation of double-strand break repair via homologous recombination	17	0.306639413	< 0.001	< 0.001
GO:0006294	nucleotide-excision repair, preincision complex assembly	14	0.306637249	0.0001	0.000192793
GO:0002637	regulation of immunoglobulin production	22	0.306587107	0.0004	0.000648934
GO:0060993	kidney morphogenesis	29	0.306572582	< 0.001	< 0.001
GO:0021761	limbic system development	49	0.306474404	< 0.001	< 0.001
GO:0006497	protein lipidation	30	0.306366366	< 0.001	< 0.001
GO:0070203	regulation of establishment of protein localization to telomere	6	0.306306306	0.002	0.002664694
GO:1903405	protein localization to nuclear body	6	0.306306306	0.002	0.002664694
GO:1904816	positive regulation of protein localization to chromosome, telomeric region	6	0.306306306	0.002	0.002664694
GO:1904851	positive regulation of establishment of protein localization to telomere	6	0.306306306	0.002	0.002664694
GO:1904867	protein localization to Cajal body	6	0.306306306	0.002	0.002664694
GO:1904869	regulation of protein localization to Cajal body	6	0.306306306	0.002	0.002664694
GO:1904871	positive regulation of protein localization to Cajal body	6	0.306306306	0.002	0.002664694
GO:1900117	regulation of execution phase of apoptosis	9	0.306220506	0.0024	0.003116943
GO:0006370	7-methylguanosine mRNA capping	17	0.306200318	0.0003	0.000505993
GO:1902600	hydrogen ion transmembrane transport	38	0.306157285	< 0.001	< 0.001
GO:1903523	negative regulation of blood circulation	12	0.306134706	< 0.001	< 0.001
GO:0009308	amine metabolic process	67	0.306129584	0.0001	0.000192793
GO:0030318	melanocyte differentiation	7	0.306085678	0.0001	0.000192793
GO:0006611	protein export from nucleus	28	0.306076485	0.0002	0.000356582
GO:0050655	dermatan sulfate proteoglycan metabolic process	7	0.306048906	0.019	0.020831
GO:0021800	cerebral cortex tangential migration	6	0.306006006	0.0051	0.006185009
GO:0045793	positive regulation of cell size	6	0.305963106	0.0007	0.001063182
GO:1905517	macrophage migration	19	0.305954074	< 0.001	< 0.001
GO:0072331	signal transduction by p53 class mediator	106	0.305937204	0.0004	0.000648934
GO:0051057	positive regulation of small GTPase mediated signal transduction	24	0.305920206	< 0.001	< 0.001
GO:0051648	vesicle localization	180	0.305918776	0.0001	0.000192793
GO:0006906	vesicle fusion	28	0.305763927	< 0.001	< 0.001
GO:0035136	forelimb morphogenesis	12	0.305705706	0.0001	0.000192793
GO:0051196	regulation of coenzyme metabolic process	35	0.3056959	< 0.001	< 0.001
GO:0050798	activated T cell proliferation	12	0.305598456	< 0.001	< 0.001
GO:0043627	response to estrogen	21	0.30555862	< 0.001	< 0.001
GO:0031297	replication fork processing	12	0.305491205	0.0005	0.000791911
GO:0045005	DNA-dependent DNA replication maintenance of fidelity	12	0.305491205	0.0005	0.000791911
GO:0050714	positive regulation of protein secretion	93	0.305404022	< 0.001	< 0.001
GO:0071392	cellular response to estradiol stimulus	7	0.305313477	0.0001	0.000192793
GO:0006367	transcription initiation from RNA polymerase II promoter	67	0.305299756	< 0.001	< 0.001
GO:0003230	cardiac atrium development	13	0.305296505	< 0.001	< 0.001
GO:0018394	peptidyl-lysine acetylation	70	0.305210517	< 0.001	< 0.001
GO:0035909	aorta morphogenesis	10	0.305199485	0.0039	0.004841626
GO:0006026	aminoglycan catabolic process	22	0.305183105	0.0001	0.000192793
GO:0006027	glycosaminoglycan catabolic process	22	0.305183105	0.0001	0.000192793
GO:0017145	stem cell division	18	0.305176605	< 0.001	< 0.001
GO:1901020	negative regulation of calcium ion transmembrane transporter activity	12	0.305169455	0.0009	0.001319479
GO:2000402	negative regulation of lymphocyte migration	7	0.305166391	0.0006	0.000927725
GO:0033762	response to glucagon	14	0.305074462	< 0.001	< 0.001
GO:0072413	signal transduction involved in mitotic cell cycle checkpoint	17	0.305004164	0.0008	0.001193265
GO:0072431	signal transduction involved in mitotic G1 DNA damage checkpoint	17	0.305004164	0.0008	0.001193265
GO:1902400	intracellular signal transduction involved in G1 DNA damage checkpoint	17	0.305004164	0.0008	0.001193265
GO:1902402	signal transduction involved in mitotic DNA damage checkpoint	17	0.305004164	0.0008	0.001193265

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1902403	signal transduction involved in mitotic DNA integrity checkpoint	17	0.305004164	0.0008	0.001193265
GO:0001959	regulation of cytokine-mediated signaling pathway	60	0.304869155	< 0.001	< 0.001
GO:0033522	histone H2A ubiquitination	12	0.304869155	< 0.001	< 0.001
GO:0060675	ureteric bud morphogenesis	17	0.304867893	< 0.001	< 0.001
GO:1900180	regulation of protein localization to nucleus	62	0.304770208	< 0.001	< 0.001
GO:0016574	histone ubiquitination	20	0.304749035	< 0.001	< 0.001
GO:0043403	skeletal muscle tissue regeneration	11	0.304668305	0.001	0.001450349
GO:0021533	cell differentiation in hindbrain	6	0.304633205	0.0028	0.003584743
GO:0021872	forebrain generation of neurons	28	0.304633205	0.0041	0.005057384
GO:0098751	bone cell development	10	0.304607465	< 0.001	< 0.001
GO:0051168	nuclear export	74	0.304598421	0.0001	0.000192793
GO:0006278	RNA-dependent DNA biosynthetic process	35	0.304585402	0.0001	0.000192793
GO:0009064	glutamine family amino acid metabolic process	30	0.304564565	< 0.001	< 0.001
GO:0006406	mRNA export from nucleus	39	0.304550705	0.0009	0.001319479
GO:0071427	mRNA-containing ribonucleoprotein complex export from nucleus	39	0.304550705	0.0009	0.001319479
GO:0006635	fatty acid beta-oxidation	20	0.304504505	< 0.001	< 0.001
GO:0086011	membrane repolarization during action potential	9	0.304504505	0.0024	0.003116943
GO:0007200	phospholipase C-activating G-protein coupled receptor signaling pathway	25	0.30436036	0.0009	0.001319479
GO:0007221	positive regulation of transcription of Notch receptor target	5	0.304350064	0.0001	0.000192793
GO:0031338	regulation of vesicle fusion	9	0.304304304	0.0083	0.009660392
GO:0048546	digestive tract morphogenesis	12	0.304290004	< 0.001	< 0.001
GO:0000077	DNA damage checkpoint	57	0.304247104	< 0.001	< 0.001
GO:0001825	blastocyst formation	14	0.304173561	0.0152	0.016877091
GO:0007187	G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	62	0.304122556	< 0.001	< 0.001
GO:0021954	central nervous system neuron development	45	0.304069784	< 0.001	< 0.001
GO:0042752	regulation of circadian rhythm	52	0.304034254	0.0007	0.001063182
GO:0030705	cytoskeleton-dependent intracellular transport	85	0.304032099	< 0.001	< 0.001
GO:1905144	response to acetylcholine	17	0.304004845	< 0.001	< 0.001
GO:1905145	cellular response to acetylcholine	17	0.304004845	< 0.001	< 0.001
GO:0061213	positive regulation of mesonephros development	7	0.303989704	< 0.001	< 0.001
GO:0061217	regulation of mesonephros development	7	0.303989704	< 0.001	< 0.001
GO:0097530	granulocyte migration	29	0.303936449	< 0.001	< 0.001
GO:0001656	metanephros development	23	0.303933747	< 0.001	< 0.001
GO:0042307	positive regulation of protein import into nucleus	17	0.303929139	< 0.001	< 0.001
GO:0000018	regulation of DNA recombination	40	0.303880309	0.0002	0.000356582
GO:0006388	tRNA splicing, via endonucleolytic cleavage and ligation	5	0.303835264	0.0038	0.004725081
GO:0032436	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	36	0.303782354	0.0001	0.000192793
GO:0050686	negative regulation of mRNA processing	15	0.303749464	0.0001	0.000192793
GO:2000001	regulation of DNA damage checkpoint	6	0.303732304	0.0002	0.000356582
GO:0034109	homotypic cell-cell adhesion	36	0.303710854	< 0.001	< 0.001
GO:0009310	amine catabolic process	10	0.303680824	< 0.001	< 0.001
GO:1901890	positive regulation of cell junction assembly	13	0.303653104	< 0.001	< 0.001
GO:0019217	regulation of fatty acid metabolic process	34	0.303641457	< 0.001	< 0.001
GO:0046717	acid secretion	50	0.303624196	0.0001	0.000192793
GO:0007004	telomere maintenance via telomerase	34	0.303580892	0.0003	0.000505993
GO:0006297	nucleotide-excision repair, DNA gap filling	8	0.303507079	0.0135	0.015116867
GO:0002204	somatic recombination of immunoglobulin genes involved in immune response	16	0.303458816	0.0008	0.001193265
GO:0002208	somatic diversification of immunoglobulins involved in immune response	16	0.303458816	0.0008	0.001193265
GO:0045190	isotype switching	16	0.303458816	0.0008	0.001193265
GO:0060122	inner ear receptor stereocilium organization	10	0.303423423	< 0.001	< 0.001
GO:2000178	negative regulation of neural precursor cell proliferation	9	0.303417703	0.0001	0.000192793
GO:0006638	neutral lipid metabolic process	31	0.303391871	< 0.001	< 0.001
GO:0090199	regulation of release of cytochrome c from mitochondria	24	0.303335478	< 0.001	< 0.001
GO:0003299	muscle hypertrophy in response to stress	9	0.303274703	0.0029	0.003693519
GO:0014887	cardiac muscle adaptation	9	0.303274703	0.0029	0.003693519
GO:0014898	cardiac muscle hypertrophy in response to stress	9	0.303274703	0.0029	0.003693519
GO:0015872	dopamine transport	15	0.303251823	< 0.001	< 0.001
GO:0051895	negative regulation of focal adhesion assembly	9	0.303217503	< 0.001	< 0.001
GO:1903392	negative regulation of adherens junction organization	9	0.303217503	< 0.001	< 0.001
GO:0043486	histone exchange	15	0.303200343	0.0068	0.008063902
GO:1990266	neutrophil migration	20	0.303166023	< 0.001	< 0.001
GO:0048709	oligodendrocyte differentiation	27	0.30315077	< 0.001	< 0.001
GO:1901524	regulation of macromitophagy	6	0.303088803	0.0004	0.000648934
GO:0045123	cellular extravasation	25	0.303063063	< 0.001	< 0.001
GO:0030534	adult behavior	63	0.303062246	< 0.001	< 0.001
GO:0033135	regulation of peptidyl-serine phosphorylation	60	0.303007293	< 0.001	< 0.001
GO:0050690	regulation of defense response to virus by virus	17	0.303005527	< 0.001	< 0.001
GO:0042273	ribosomal large subunit biogenesis	13	0.302979903	0.003	0.003811001
GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	16	0.302960103	0.0008	0.001193265
GO:0043491	protein kinase B signaling	91	0.30290636	< 0.001	< 0.001
GO:0071300	cellular response to retinoic acid	17	0.302869256	0.0028	0.003584743
GO:0015849	organic acid transport	106	0.302865399	< 0.001	< 0.001
GO:0046942	carboxylic acid transport	106	0.302865399	< 0.001	< 0.001
GO:1902805	positive regulation of synaptic vesicle transport	14	0.302813017	0.0111	0.012593827
GO:0048713	regulation of oligodendrocyte differentiation	12	0.302745603	< 0.001	< 0.001
GO:0051004	regulation of lipoprotein lipase activity	6	0.302745603	0.0013	0.001826625
GO:1903146	regulation of mitophagy	19	0.302743345	0.0004	0.000648934
GO:0010833	telomere maintenance via telomere lengthening	37	0.302695746	0.0001	0.000192793
GO:0001824	blastocyst development	35	0.302592388	0.0004	0.000648934
GO:1903792	negative regulation of anion transport	7	0.302555617	0.0001	0.000192793
GO:0009070	serine family amino acid biosynthetic process	7	0.302518845	0.0018	0.002428764
GO:0046578	regulation of Ras protein signal transduction	100	0.30236036	< 0.001	< 0.001
GO:0002200	somatic diversification of immune receptors	23	0.302333389	0.0014	0.00194839

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0002092	positive regulation of receptor internalization	10	0.302290862	0.0004	0.000648934
GO:0034661	ncRNA catabolic process	6	0.302230802	0.0013	0.001826625
GO:0031146	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	49	0.302172143	0.0003	0.000505993
GO:0051767	nitric-oxide synthase biosynthetic process	8	0.302155727	< 0.001	< 0.001
GO:0051769	regulation of nitric-oxide synthase biosynthetic process	8	0.302155727	< 0.001	< 0.001
GO:0045026	plasma membrane fusion	6	0.302145002	0.025	0.026960686
GO:0006353	DNA-templated transcription, termination	34	0.302134908	< 0.001	< 0.001
GO:0006405	RNA export from nucleus	44	0.302100152	0.0002	0.000356582
GO:0050482	arachidonic acid secretion	9	0.301959102	< 0.001	< 0.001
GO:1903963	arachidonate transport	9	0.301959102	< 0.001	< 0.001
GO:0043525	positive regulation of neuron apoptotic process	21	0.301795673	< 0.001	< 0.001
GO:2000679	positive regulation of transcription regulatory region DNA binding	10	0.301776062	< 0.001	< 0.001
GO:0043624	cellular protein complex disassembly	101	0.301741912	< 0.001	< 0.001
GO:1902041	regulation of extrinsic apoptotic signaling pathway via death domain receptors	17	0.301733666	< 0.001	< 0.001
GO:0019048	modulation by virus of host morphology or physiology	21	0.301697616	< 0.001	< 0.001
GO:0046579	positive regulation of Ras protein signal transduction	23	0.301684293	< 0.001	< 0.001
GO:0090277	positive regulation of peptide hormone secretion	32	0.301681145	< 0.001	< 0.001
GO:0050796	regulation of insulin secretion	64	0.301661036	0.0007	0.001063182
GO:0044030	regulation of DNA methylation	7	0.30163633	0.0011	0.001576346
GO:0010970	transport along microtubule	76	0.301629073	< 0.001	< 0.001
GO:0099111	microtubule-based transport	76	0.301629073	< 0.001	< 0.001
GO:0001845	phagolysosome assembly	5	0.301621622	< 0.001	< 0.001
GO:0006968	cellular defense response	9	0.301615902	< 0.001	< 0.001
GO:0021766	hippocampus development	42	0.301611816	< 0.001	< 0.001
GO:1904356	regulation of telomere maintenance via telomere lengthening	28	0.301599559	< 0.001	< 0.001
GO:0036445	neuronal stem cell division	6	0.301587302	0.0029	0.003693519
GO:0055057	neuroblast division	6	0.301587302	0.0029	0.003693519
GO:0014029	neural crest formation	7	0.301562787	0.0002	0.000356582
GO:0030204	chondroitin sulfate metabolic process	20	0.301557272	0.0003	0.000505993
GO:0042531	positive regulation of tyrosine phosphorylation of STAT protein	17	0.301445984	0.0002	0.000356582
GO:0060478	acrosomal vesicle exocytosis	5	0.301415701	0.0117	0.013205263
GO:0047496	vesicle transport along microtubule	25	0.301405405	0.0001	0.000192793
GO:0006368	transcription elongation from RNA polymerase II promoter	36	0.301379951	0.0003	0.000505993
GO:0010831	positive regulation of myotube differentiation	6	0.301372801	0.0046	0.0056228
GO:0030032	lamellipodium assembly	32	0.301359395	< 0.001	< 0.001
GO:1902803	regulation of synaptic vesicle transport	58	0.301340257	0.0027	0.003470695
GO:0070534	protein K63-linked ubiquitination	18	0.301315601	0.0001	0.000192793
GO:0072006	nephron development	42	0.30129313	< 0.001	< 0.001
GO:0006940	regulation of smooth muscle contraction	22	0.301287001	< 0.001	< 0.001
GO:0034314	Arp2/3 complex-mediated actin nucleation	17	0.301264289	0.0047	0.005730776
GO:0000086	G2/M transition of mitotic cell cycle	121	0.301254029	< 0.001	< 0.001
GO:0097202	activation of cysteine-type endopeptidase activity	8	0.301190476	0.0006	0.000927725
GO:0001822	kidney development	86	0.30110742	< 0.001	< 0.001
GO:0006516	glycoprotein catabolic process	9	0.301072501	0.001	0.001450349
GO:0044003	modification by symbiont of host morphology or physiology	23	0.301068771	< 0.001	< 0.001
GO:0046633	alpha-beta T cell proliferation	7	0.301047987	0.0007	0.001063182
GO:0002286	T cell activation involved in immune response	21	0.30103573	< 0.001	< 0.001
GO:1903426	regulation of reactive oxygen species biosynthetic process	29	0.300892025	< 0.001	< 0.001
GO:0030207	chondroitin sulfate catabolic process	8	0.300772201	0.0282	0.030230669
GO:0015732	prostaglandin transport	6	0.300772201	< 0.001	< 0.001
GO:0032310	prostaglandin secretion	6	0.300772201	< 0.001	< 0.001
GO:2000008	regulation of protein localization to cell surface	16	0.300659588	0.0001	0.000192793
GO:0051650	establishment of vesicle localization	171	0.300623932	0.0001	0.000192793
GO:1902410	mitotic cytokinetic process	5	0.300540541	< 0.001	< 0.001
GO:0048148	behavioral response to cocaine	8	0.300514801	0.0075	0.008822377
GO:0043241	protein complex disassembly	115	0.300491299	< 0.001	< 0.001
GO:0033683	nucleotide-excision repair, DNA incision	17	0.300461806	0.0002	0.000356582
GO:0051099	positive regulation of binding	76	0.300433516	< 0.001	< 0.001
GO:0010463	mesenchymal cell proliferation	11	0.3004329	< 0.001	< 0.001
GO:0043371	negative regulation of CD4-positive, alpha-beta T cell differentiation	5	0.3003861	0.0022	0.002896881
GO:0046639	negative regulation of alpha-beta T cell differentiation	5	0.3003861	0.0022	0.002896881
GO:0051453	regulation of intracellular pH	24	0.30036465	< 0.001	< 0.001
GO:0006826	iron ion transport	26	0.3003267	< 0.001	< 0.001
GO:0009408	response to heat	72	0.300239525	< 0.001	< 0.001
GO:0009118	regulation of nucleoside metabolic process	42	0.300239015	< 0.001	< 0.001
GO:1903578	regulation of ATP metabolic process	42	0.300239015	< 0.001	< 0.001
GO:0001662	behavioral fear response	26	0.3001584	0.0002	0.000356582
GO:0002209	behavioral defense response	26	0.3001584	0.0002	0.000356582
GO:0016073	snRNA metabolic process	37	0.300045219	< 0.001	< 0.001
GO:0090344	negative regulation of cell aging	12	0.3000429	< 0.001	< 0.001
GO:0043029	T cell homeostasis	12	0.30002145	< 0.001	< 0.001
GO:0055007	cardiac muscle cell differentiation	38	0.299878074	< 0.001	< 0.001
GO:0035107	appendage morphogenesis	42	0.299852914	< 0.001	< 0.001
GO:0035108	limb morphogenesis	42	0.299852914	< 0.001	< 0.001
GO:0031109	microtubule polymerization or depolymerization	43	0.299811439	< 0.001	< 0.001
GO:1901673	regulation of mitotic spindle assembly	8	0.2997426	0.0013	0.001826625
GO:0051354	negative regulation of oxidoreductase activity	5	0.2996139	0.0024	0.003116943
GO:0072080	nephron tubule development	27	0.299604366	< 0.001	< 0.001
GO:1901796	regulation of signal transduction by p53 class mediator	81	0.299537633	0.0005	0.000791911
GO:0014065	phosphatidylinositol 3-kinase signaling	64	0.299521396	< 0.001	< 0.001
GO:0097049	motor neuron apoptotic process	5	0.29951094	0.0048	0.005840847
GO:2000671	regulation of motor neuron apoptotic process	5	0.29951094	0.0048	0.005840847
GO:0090200	positive regulation of release of cytochrome c from mitochondria	12	0.299442299	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0072009	nephron epithelium development	30	0.299407979	< 0.001	< 0.001
GO:0006022	aminoglycan metabolic process	62	0.299377257	< 0.001	< 0.001
GO:0030203	glycosaminoglycan metabolic process	62	0.299377257	< 0.001	< 0.001
GO:0051284	positive regulation of sequestering of calcium ion	9	0.299356499	0.0054	0.006510843
GO:1902950	regulation of dendritic spine maintenance	7	0.299282956	0.0048	0.005840847
GO:0009219	pyrimidine deoxyribonucleotide metabolic process	5	0.299253539	0.0009	0.001319479
GO:0006582	melanin metabolic process	13	0.299198099	< 0.001	< 0.001
GO:0042438	melanin biosynthetic process	13	0.299198099	< 0.001	< 0.001
GO:0044550	secondary metabolite biosynthetic process	13	0.299198099	< 0.001	< 0.001
GO:0098657	import into cell	29	0.299187858	< 0.001	< 0.001
GO:0032410	negative regulation of transporter activity	30	0.299167739	< 0.001	< 0.001
GO:0050654	chondroitin sulfate proteoglycan metabolic process	22	0.299145899	0.0004	0.000648934
GO:0050651	dermatan sulfate proteoglycan biosynthetic process	6	0.299141999	0.0193	0.021134184
GO:0014904	myotube cell development	14	0.299135871	0.0026	0.003356522
GO:0046683	response to organophosphorus	54	0.299132466	< 0.001	< 0.001
GO:0099623	regulation of cardiac muscle cell membrane repolarization	9	0.299127699	0.0001	0.000192793
GO:0042310	vasoconstriction	21	0.299086842	< 0.001	< 0.001
GO:0051896	regulation of protein kinase B signaling	83	0.299068087	< 0.001	< 0.001
GO:0021953	central nervous system neuron differentiation	82	0.29899865	0.0001	0.000192793
GO:0019229	regulation of vasoconstriction	19	0.298868794	< 0.001	< 0.001
GO:0048736	appendage development	51	0.298781134	< 0.001	< 0.001
GO:0060173	limb development	51	0.298781134	< 0.001	< 0.001
GO:0042098	T cell proliferation	52	0.298722899	< 0.001	< 0.001
GO:1903050	regulation of proteolysis involved in cellular protein catabolic process	90	0.298715859	0.0001	0.000192793
GO:0071426	ribonucleoprotein complex export from nucleus	44	0.298707149	0.0004	0.000648934
GO:0035023	regulation of Rho protein signal transduction	54	0.298693932	< 0.001	< 0.001
GO:1903312	negative regulation of mRNA metabolic process	19	0.298692678	< 0.001	< 0.001
GO:0036120	cellular response to platelet-derived growth factor stimulus	5	0.298687259	0.0002	0.000356582
GO:0035710	CD4-positive, alpha-beta T cell activation	22	0.298677899	< 0.001	< 0.001
GO:1901658	glycosyl compound catabolic process	14	0.298676227	0.0002	0.000356582
GO:0007212	dopamine receptor signaling pathway	15	0.298635779	< 0.001	< 0.001
GO:0042053	regulation of dopamine metabolic process	10	0.298635779	< 0.001	< 0.001
GO:0042069	regulation of catecholamine metabolic process	10	0.298635779	< 0.001	< 0.001
GO:0015844	monoamine transport	31	0.298617512	< 0.001	< 0.001
GO:0048012	hepatocyte growth factor receptor signaling pathway	10	0.298584299	0.0004	0.000648934
GO:0021801	cerebral cortex radial glia guided migration	14	0.298529141	0.0017	0.00231289
GO:0022030	telencephalon glial cell migration	14	0.298529141	0.0017	0.00231289
GO:0046824	positive regulation of nucleocytoplasmic transport	26	0.298495198	< 0.001	< 0.001
GO:0021544	subpallium development	11	0.298490698	0.0046	0.0056228
GO:0099622	cardiac muscle cell membrane repolarization	13	0.298485298	0.0005	0.000791911
GO:0008333	endosome to lysosome transport	31	0.298468053	< 0.001	< 0.001
GO:0071242	cellular response to ammonium ion	37	0.298340812	0.0001	0.000192793
GO:0048704	embryonic skeletal system morphogenesis	21	0.298326898	< 0.001	< 0.001
GO:0071786	endoplasmic reticulum tubular network organization	10	0.298301158	< 0.001	< 0.001
GO:0017014	protein nitrosylation	9	0.298269698	< 0.001	< 0.001
GO:0018119	peptidyl-cysteine S-nitrosylation	9	0.298269698	< 0.001	< 0.001
GO:0061326	renal tubule development	28	0.298198198	< 0.001	< 0.001
GO:0071166	ribonucleoprotein complex localization	45	0.298143858	0.0006	0.000927725
GO:0044346	fibroblast apoptotic process	10	0.298120978	< 0.001	< 0.001
GO:0040001	establishment of mitotic spindle localization	13	0.298109098	0.0015	0.002069969
GO:0008217	regulation of blood pressure	47	0.298053068	< 0.001	< 0.001
GO:0000244	spliceosomal tri-snRNP complex assembly	8	0.298037323	0.0003	0.000505993
GO:0006120	mitochondrial electron transport, NADH to ubiquinone	22	0.298034398	0.0018	0.002428764
GO:0060191	regulation of lipase activity	34	0.297978651	< 0.001	< 0.001
GO:2000269	regulation of fibroblast apoptotic process	9	0.297955098	< 0.001	< 0.001
GO:0021799	cerebral cortex radially oriented cell migration	18	0.297912198	0.0007	0.001063182
GO:0006900	membrane budding	63	0.297861126	< 0.001	< 0.001
GO:0045428	regulation of nitric oxide biosynthetic process	19	0.29785274	< 0.001	< 0.001
GO:0006023	aminoglycan biosynthetic process	46	0.297840076	< 0.001	< 0.001
GO:0006024	glycosaminoglycan biosynthetic process	46	0.297840076	< 0.001	< 0.001
GO:0006595	polyamine metabolic process	9	0.297783498	0.0006	0.000927725
GO:0045995	regulation of embryonic development	37	0.297714703	< 0.001	< 0.001
GO:0021575	hindbrain morphogenesis	11	0.297695098	0.0024	0.003116943
GO:0021587	cerebellum morphogenesis	11	0.297695098	0.0024	0.003116943
GO:0007632	visual behavior	25	0.29762677	0.0046	0.0056228
GO:0010565	regulation of cellular ketone metabolic process	83	0.29758571	< 0.001	< 0.001
GO:1903052	positive regulation of proteolysis involved in cellular protein catabolic process	50	0.297580438	0.0001	0.000192793
GO:0050872	white fat cell differentiation	7	0.297517926	0.0009	0.001319479
GO:0009264	deoxyribonucleotide catabolic process	7	0.297297297	0.0002	0.000356582
GO:0060307	regulation of ventricular cardiac muscle cell membrane repolarization	7	0.297223754	< 0.001	< 0.001
GO:0009309	amine biosynthetic process	9	0.297211497	0.0003	0.000505993
GO:0035773	insulin secretion involved in cellular response to glucose stimulus	29	0.297199663	< 0.001	< 0.001
GO:2000272	negative regulation of receptor activity	20	0.297155727	0.0004	0.000648934
GO:1900408	negative regulation of cellular response to oxidative stress	17	0.297145885	< 0.001	< 0.001
GO:1902883	negative regulation of response to oxidative stress	17	0.297145885	< 0.001	< 0.001
GO:1903202	negative regulation of oxidative stress-induced cell death	17	0.297145885	< 0.001	< 0.001
GO:0030330	DNA damage response, signal transduction by p53 class mediator	35	0.297120794	< 0.001	< 0.001
GO:0002697	regulation of immune effector process	129	0.297069827	< 0.001	< 0.001
GO:0034776	response to histamine	6	0.297039897	0.0243	0.026242446
GO:0071420	cellular response to histamine	6	0.297039897	0.0243	0.026242446
GO:1904837	beta-catenin-TCF complex assembly	12	0.296996997	0.0001	0.000192793
GO:0008306	associative learning	39	0.296947497	0.0024	0.003116943
GO:0042158	lipoprotein biosynthetic process	31	0.296907045	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0035024	negative regulation of Rho protein signal transduction	13	0.296901297	< 0.001	< 0.001
GO:0036005	response to macrophage colony-stimulating factor	8	0.296879022	< 0.001	< 0.001
GO:0036006	cellular response to macrophage colony-stimulating factor stimulus	8	0.296879022	< 0.001	< 0.001
GO:0032252	secretory granule localization	9	0.296839697	0.0094	0.010831045
GO:0043476	pigment accumulation	8	0.296718147	< 0.001	< 0.001
GO:0043482	cellular pigment accumulation	8	0.296718147	< 0.001	< 0.001
GO:0010661	positive regulation of muscle cell apoptotic process	14	0.296672182	0.0022	0.002896881
GO:0042770	signal transduction in response to DNA damage	50	0.296658945	< 0.001	< 0.001
GO:0050657	nucleic acid transport	70	0.296646442	< 0.001	< 0.001
GO:0050658	RNA transport	70	0.296646442	< 0.001	< 0.001
GO:0034122	negative regulation of toll-like receptor signaling pathway	17	0.296631085	0.0006	0.000927725
GO:0002534	cytokine production involved in inflammatory response	17	0.296585661	< 0.001	< 0.001
GO:0097696	STAT cascade	49	0.296577627	< 0.001	< 0.001
GO:0032608	interferon-beta production	17	0.296509955	< 0.001	< 0.001
GO:0032648	regulation of interferon-beta production	17	0.296509955	< 0.001	< 0.001
GO:0010923	negative regulation of phosphatase activity	57	0.296493486	0.0007	0.001063182
GO:1904892	regulation of STAT cascade	41	0.29648115	< 0.001	< 0.001
GO:0002791	regulation of peptide secretion	75	0.29648048	0.0001	0.000192793
GO:0090087	regulation of peptide transport	75	0.29648048	0.0001	0.000192793
GO:0099072	regulation of postsynaptic specialization membrane neurotransmitter receptor levels	16	0.296428571	0.0078	0.009125612
GO:0006000	fructose metabolic process	5	0.296422136	0.0007	0.001063182
GO:0044839	cell cycle G2/M phase transition	132	0.296351546	< 0.001	< 0.001
GO:1902884	positive regulation of response to oxidative stress	7	0.296304468	0.0003	0.000505993
GO:2000027	regulation of organ morphogenesis	102	0.296207132	< 0.001	< 0.001
GO:0072088	nephron epithelium morphogenesis	22	0.296138996	< 0.001	< 0.001
GO:0032486	Rap protein signal transduction	9	0.296096096	< 0.001	< 0.001
GO:0030220	platelet formation	7	0.296083839	0.0002	0.000356582
GO:0036344	platelet morphogenesis	7	0.296083839	0.0002	0.000356582
GO:0051056	regulation of small GTPase mediated signal transduction	149	0.296070759	< 0.001	< 0.001
GO:0006475	internal protein amino acid acetylation	70	0.29606913	< 0.001	< 0.001
GO:0033138	positive regulation of peptidyl-serine phosphorylation	47	0.296010296	< 0.001	< 0.001
GO:0044843	cell cycle G1/S phase transition	105	0.295975976	< 0.001	< 0.001
GO:0042304	regulation of fatty acid biosynthetic process	16	0.295833333	< 0.001	< 0.001
GO:0032509	endosome transport via multivesicular body sorting pathway	7	0.295789667	0.0011	0.001576346
GO:0032984	macromolecular complex disassembly	129	0.295754891	< 0.001	< 0.001
GO:2000050	regulation of non-canonical Wnt signaling pathway	6	0.295709996	0.0088	0.010185307
GO:0043300	regulation of leukocyte degranulation	19	0.295698706	< 0.001	< 0.001
GO:0061180	mammary gland epithelium development	26	0.295663796	< 0.001	< 0.001
GO:0009226	nucleotide-sugar biosynthetic process	11	0.295659296	< 0.001	< 0.001
GO:0030521	androgen receptor signaling pathway	20	0.295649936	0.0012	0.001702047
GO:0048013	ephrin receptor signaling pathway	53	0.295616911	0.0001	0.000192793
GO:0032305	positive regulation of icosanoid secretion	7	0.29560581	< 0.001	< 0.001
GO:2000193	positive regulation of fatty acid transport	7	0.29560581	< 0.001	< 0.001
GO:0001570	vasculogenesis	28	0.295596617	< 0.001	< 0.001
GO:0003298	physiological muscle hypertrophy	14	0.295587424	0.0011	0.001576346
GO:0003301	physiological cardiac muscle hypertrophy	14	0.295587424	0.0011	0.001576346
GO:0061049	cell growth involved in cardiac muscle cell development	14	0.295587424	0.0011	0.001576346
GO:0017156	calcium ion regulated exocytosis	78	0.295558196	0.0027	0.003470695
GO:0002260	lymphocyte homeostasis	21	0.295507753	< 0.001	< 0.001
GO:0098661	inorganic anion transmembrane transport	34	0.295503066	< 0.001	< 0.001
GO:0007265	Ras protein signal transduction	156	0.295488895	< 0.001	< 0.001
GO:1903533	regulation of protein targeting	85	0.295480354	< 0.001	< 0.001
GO:0006654	phosphatidic acid biosynthetic process	14	0.29534841	< 0.001	< 0.001
GO:0046473	phosphatidic acid metabolic process	14	0.29534841	< 0.001	< 0.001
GO:1904645	response to beta-amyloid	18	0.295323895	0.0003	0.000505993
GO:0035567	non-canonical Wnt signaling pathway	79	0.295316293	< 0.001	< 0.001
GO:0032204	regulation of telomere maintenance	38	0.295305832	0.0002	0.000356582
GO:1903311	regulation of mRNA metabolic process	50	0.295299871	< 0.001	< 0.001
GO:0060037	pharyngeal system development	5	0.295289575	< 0.001	< 0.001
GO:0045651	positive regulation of macrophage differentiation	8	0.29520592	< 0.001	< 0.001
GO:0048103	somatic stem cell division	10	0.295109395	0.0001	0.000192793
GO:0051236	establishment of RNA localization	71	0.295096706	< 0.001	< 0.001
GO:0042634	regulation of hair cycle	8	0.29501287	< 0.001	< 0.001
GO:0035066	positive regulation of histone acetylation	9	0.294952095	0.0002	0.000356582
GO:0060445	branching involved in salivary gland morphogenesis	7	0.294943924	< 0.001	< 0.001
GO:0032271	regulation of protein polymerization	88	0.294939745	< 0.001	< 0.001
GO:0022037	metencephalon development	34	0.294859565	< 0.001	< 0.001
GO:0060765	regulation of androgen receptor signaling pathway	9	0.294837695	0.0038	0.004725081
GO:0006734	NADH metabolic process	18	0.294823395	0.0001	0.000192793
GO:0048538	thymus development	16	0.294787645	0.0002	0.000356582
GO:0002228	natural killer cell mediated immunity	17	0.294783859	< 0.001	< 0.001
GO:0042730	fibrinolysis	7	0.294723295	< 0.001	< 0.001
GO:0055002	striated muscle cell development	46	0.294661742	< 0.001	< 0.001
GO:0002753	cytoplasmic pattern recognition receptor signaling pathway	22	0.294653095	0.0001	0.000192793
GO:0034383	low-density lipoprotein particle clearance	11	0.294606295	0.0013	0.001826625
GO:0090169	regulation of spindle assembly	9	0.294580295	0.0009	0.001319479
GO:0001736	establishment of planar polarity	73	0.294518785	< 0.001	< 0.001
GO:0007164	establishment of tissue polarity	73	0.294518785	< 0.001	< 0.001
GO:0030324	lung development	51	0.294516365	< 0.001	< 0.001
GO:0098781	ncRNA transcription	52	0.294510445	< 0.001	< 0.001
GO:1904380	endoplasmic reticulum mannose trimming	9	0.294465894	0.001	0.001450349
GO:0005513	detection of calcium ion	7	0.294465894	0.0133	0.014896
GO:1905209	positive regulation of cardiocyte differentiation	12	0.294444444	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0000737	DNA catabolic process, endonucleolytic	9	0.294437294	0.0013	0.001826625
GO:0006308	DNA catabolic process	9	0.294437294	0.0013	0.001826625
GO:0006309	apoptotic DNA fragmentation	9	0.294437294	0.0013	0.001826625
GO:0018393	internal peptidyl-lysine acetylation	67	0.294415951	< 0.001	< 0.001
GO:0031348	negative regulation of defense response	58	0.294399325	< 0.001	< 0.001
GO:0060964	regulation of gene silencing by miRNA	36	0.294372944	< 0.001	< 0.001
GO:1904526	regulation of microtubule binding	5	0.294362934	0.009	0.010394529
GO:0042509	regulation of tyrosine phosphorylation of STAT protein	24	0.294294294	0.0004	0.000648934
GO:0032495	response to muramyl dipeptide	7	0.294282037	< 0.001	< 0.001
GO:0030004	cellular monovalent inorganic cation homeostasis	31	0.294266617	< 0.001	< 0.001
GO:0046324	regulation of glucose import	23	0.294264451	0.0001	0.000192793
GO:0006310	DNA recombination	97	0.294216455	< 0.001	< 0.001
GO:0043981	histone H4-K5 acetylation	7	0.294208494	< 0.001	< 0.001
GO:0043982	histone H4-K8 acetylation	7	0.294208494	< 0.001	< 0.001
GO:0031987	locomotion involved in locomotory behavior	5	0.294208494	< 0.001	< 0.001
GO:0090263	positive regulation of canonical Wnt signaling pathway	66	0.294110994	0.0001	0.000192793
GO:0003018	vascular process in circulatory system	47	0.294098962	< 0.001	< 0.001
GO:0048385	regulation of retinoic acid receptor signaling pathway	7	0.29409818	< 0.001	< 0.001
GO:0030323	respiratory tube development	53	0.294087079	< 0.001	< 0.001
GO:0039702	viral budding via host ESCRT complex	12	0.294079794	0.0005	0.000791911
GO:0060147	regulation of posttranscriptional gene silencing	37	0.294055445	< 0.001	< 0.001
GO:0060966	regulation of gene silencing by RNA	37	0.294055445	< 0.001	< 0.001
GO:0021591	ventricular system development	13	0.293990694	0.0002	0.000356582
GO:0050708	regulation of protein secretion	159	0.293983471	< 0.001	< 0.001
GO:0009755	hormone-mediated signaling pathway	78	0.293927994	< 0.001	< 0.001
GO:0051642	centrosome localization	10	0.293925354	0.0019	0.00254969
GO:0050891	multicellular organismal water homeostasis	24	0.293918919	< 0.001	< 0.001
GO:0006735	NADH regeneration	13	0.293911494	0.0006	0.000927725
GO:0061621	canonical glycolysis	13	0.293911494	0.0006	0.000927725
GO:0061718	glucose catabolic process to pyruvate	13	0.293911494	0.0006	0.000927725
GO:1903391	regulation of adherens junction organization	32	0.293910875	< 0.001	< 0.001
GO:0061318	renal filtration cell differentiation	5	0.293899614	0.0076	0.008916717
GO:0072010	glomerular epithelium development	5	0.293899614	0.0076	0.008916717
GO:0072112	glomerular visceral epithelial cell differentiation	5	0.293899614	0.0076	0.008916717
GO:0072311	glomerular epithelial cell differentiation	5	0.293899614	0.0076	0.008916717
GO:0060968	regulation of gene silencing	43	0.293891233	< 0.001	< 0.001
GO:0000082	G1/S transition of mitotic cell cycle	100	0.293868726	< 0.001	< 0.001
GO:1903793	positive regulation of anion transport	21	0.293853037	< 0.001	< 0.001
GO:0018023	peptidyl-lysine trimethylation	15	0.293745174	0.0005	0.000791911
GO:0008286	insulin receptor signaling pathway	52	0.293743194	< 0.001	< 0.001
GO:0002093	auditory receptor cell morphogenesis	6	0.293693694	0.0003	0.000505993
GO:0060088	auditory receptor cell stereocilium organization	6	0.293693694	0.0003	0.000505993
GO:0098877	neurotransmitter receptor transport to plasma membrane	8	0.293693694	0.0006	0.000927725
GO:0098969	neurotransmitter receptor transport to postsynaptic membrane	8	0.293693694	0.0006	0.000927725
GO:0099637	neurotransmitter receptor transport	8	0.293693694	0.0006	0.000927725
GO:1903540	establishment of protein localization to postsynaptic membrane	8	0.293693694	0.0006	0.000927725
GO:0061517	macrophage proliferation	5	0.293693694	< 0.001	< 0.001
GO:0061518	microglial cell proliferation	5	0.293693694	< 0.001	< 0.001
GO:0060831	smoothened signaling pathway involved in dorsal/ventral neural tube patterning	7	0.293693694	0.0016	0.002186748
GO:1903729	regulation of plasma membrane organization	50	0.293688546	< 0.001	< 0.001
GO:0008154	actin polymerization or depolymerization	88	0.293681994	< 0.001	< 0.001
GO:1903169	regulation of calcium ion transmembrane transport	60	0.293603604	0.0013	0.001826625
GO:0051258	protein polymerization	113	0.293586633	< 0.001	< 0.001
GO:0070979	protein K11-linked ubiquitination	19	0.293571767	0.0002	0.000356582
GO:0045861	negative regulation of proteolysis	92	0.293509037	< 0.001	< 0.001
GO:0090330	regulation of platelet aggregation	9	0.293464893	0.0007	0.001063182
GO:0051797	regulation of hair follicle development	6	0.293393393	< 0.001	< 0.001
GO:0006639	acylglycerol metabolic process	30	0.293341913	< 0.001	< 0.001
GO:2001237	negative regulation of extrinsic apoptotic signaling pathway	24	0.293339768	< 0.001	< 0.001
GO:0002741	positive regulation of cytokine secretion involved in immune response	6	0.293264693	< 0.001	< 0.001
GO:0045923	positive regulation of fatty acid metabolic process	9	0.293236093	0.0002	0.000356582
GO:0051155	positive regulation of striated muscle cell differentiation	20	0.293217503	< 0.001	< 0.001
GO:0006352	DNA-templated transcription, initiation	91	0.293210007	< 0.001	< 0.001
GO:0033363	secretory granule organization	14	0.293197279	< 0.001	< 0.001
GO:0006409	tRNA export from nucleus	12	0.293178893	0.0001	0.000192793
GO:0051031	tRNA transport	12	0.293178893	0.0001	0.000192793
GO:0071431	tRNA-containing ribonucleoprotein complex export from nucleus	12	0.293178893	0.0001	0.000192793
GO:0042771	intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	18	0.293178893	0.0009	0.001319479
GO:1902750	negative regulation of cell cycle G2/M phase transition	55	0.293141453	0.0004	0.000648934
GO:0002934	desmosome organization	5	0.293127413	0.0004	0.000648934
GO:0090276	regulation of peptide hormone secretion	74	0.293105847	0.0002	0.000356582
GO:0060359	response to ammonium ion	71	0.293091885	< 0.001	< 0.001
GO:0014074	response to purine-containing compound	61	0.293073401	< 0.001	< 0.001
GO:0072001	renal system development	92	0.293069778	< 0.001	< 0.001
GO:0060713	labyrinthine layer morphogenesis	7	0.293068579	0.0001	0.000192793
GO:0045071	negative regulation of viral genome replication	16	0.293066281	< 0.001	< 0.001
GO:0032720	negative regulation of tumor necrosis factor production	20	0.293024453	< 0.001	< 0.001
GO:0006489	dolichyl diphosphate biosynthetic process	5	0.293024453	0.0179	0.019692915
GO:0046465	dolichyl diphosphate metabolic process	5	0.293024453	0.0179	0.019692915
GO:0008064	regulation of actin polymerization or depolymerization	74	0.293004974	< 0.001	< 0.001
GO:0030832	regulation of actin filament length	74	0.293004974	< 0.001	< 0.001
GO:0000724	double-strand break repair via homologous recombination	45	0.292955813	< 0.001	< 0.001
GO:0000725	recombinational repair	45	0.292955813	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0046189	phenol-containing compound biosynthetic process	22	0.292909793	< 0.001	< 0.001
GO:0051494	negative regulation of cytoskeleton organization	63	0.292835693	< 0.001	< 0.001
GO:0032526	response to retinoic acid	29	0.292761727	0.0007	0.001063182
GO:0009225	nucleotide-sugar metabolic process	17	0.292739799	< 0.001	< 0.001
GO:0048246	macrophage chemotaxis	15	0.292612613	< 0.001	< 0.001
GO:0010972	negative regulation of G2/M transition of mitotic cell cycle	48	0.292535393	0.0009	0.001319479
GO:0055013	cardiac muscle cell development	25	0.292530245	0.0002	0.000356582
GO:0043370	regulation of CD4-positive, alpha-beta T cell differentiation	11	0.292476892	< 0.001	< 0.001
GO:0007338	single fertilization	42	0.292449592	< 0.001	< 0.001
GO:0006577	amino-acid betaine metabolic process	9	0.292406692	0.0005	0.000791911
GO:0035150	regulation of tube size	35	0.29238463	< 0.001	< 0.001
GO:0050880	regulation of blood vessel size	35	0.29238463	< 0.001	< 0.001
GO:0007156	homophilic cell adhesion via plasma membrane adhesion molecules	46	0.292350736	0.0001	0.000192793
GO:0006165	nucleoside diphosphate phosphorylation	48	0.292347705	< 0.001	< 0.001
GO:0002381	immunoglobulin production involved in immunoglobulin mediated immune response	17	0.292346128	0.0012	0.001702047
GO:0052547	regulation of peptidase activity	127	0.292345889	< 0.001	< 0.001
GO:0035305	negative regulation of dephosphorylation	62	0.29232366	0.0003	0.000505993
GO:0006354	DNA-templated transcription, elongation	52	0.292287892	< 0.001	< 0.001
GO:1900424	regulation of defense response to bacterium	8	0.292245817	< 0.001	< 0.001
GO:0009306	protein secretion	199	0.292221726	< 0.001	< 0.001
GO:0048641	regulation of skeletal muscle tissue development	15	0.292200772	< 0.001	< 0.001
GO:0045023	G0 to G1 transition	13	0.292149292	0.0001	0.000192793
GO:0070316	regulation of G0 to G1 transition	13	0.292149292	0.0001	0.000192793
GO:0007626	locomotory behavior	84	0.292094135	< 0.001	< 0.001
GO:0050922	negative regulation of chemotaxis	16	0.292084942	< 0.001	< 0.001
GO:0060260	regulation of transcription initiation from RNA polymerase II promoter	7	0.292002206	0.0025	0.003237479
GO:0019932	second-messenger-mediated signaling	114	0.291991239	< 0.001	< 0.001
GO:0018205	peptidyl-lysine modification	152	0.291981643	< 0.001	< 0.001
GO:0072538	T-helper 17 type immune response	5	0.291943372	< 0.001	< 0.001
GO:0098976	excitatory chemical synaptic transmission	5	0.291943372	0.0067	0.007954042
GO:0031334	positive regulation of protein complex assembly	102	0.291934792	< 0.001	< 0.001
GO:0032210	regulation of telomere maintenance via telomerase	26	0.291872092	0.0002	0.000356582
GO:1905606	regulation of presynapse assembly	17	0.291816186	0.001	0.001450349
GO:0052312	modulation of transcription in other organism involved in symbiotic interaction	9	0.291806092	0.0017	0.00231289
GO:0001655	urogenital system development	104	0.291778042	< 0.001	< 0.001
GO:0032103	positive regulation of response to external stimulus	108	0.291698842	< 0.001	< 0.001
GO:0021696	cerebellar cortex morphogenesis	10	0.291685972	0.0028	0.003584743
GO:0006369	termination of RNA polymerase II transcription	16	0.291682754	0.0002	0.000356582
GO:0002888	positive regulation of myeloid leukocyte mediated immunity	8	0.291666667	< 0.001	< 0.001
GO:0060071	Wnt signaling pathway, planar cell polarity pathway	64	0.291646557	0.0001	0.000192793
GO:0090175	regulation of establishment of planar polarity	64	0.291646557	0.0001	0.000192793
GO:0045324	late endosome to vacuole transport	6	0.291591592	< 0.001	< 0.001
GO:0035296	regulation of tube diameter	33	0.291509692	< 0.001	< 0.001
GO:0097746	regulation of blood vessel diameter	33	0.291509692	< 0.001	< 0.001
GO:0051817	modification of morphology or physiology of other organism involved in symbiotic interaction	44	0.291505792	< 0.001	< 0.001
GO:0007292	female gamete generation	34	0.291407374	< 0.001	< 0.001
GO:0002367	cytokine production involved in immune response	25	0.291366795	< 0.001	< 0.001
GO:0002822	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	35	0.291362383	< 0.001	< 0.001
GO:0046339	diacylglycerol metabolic process	5	0.291325611	0.0004	0.000648934
GO:0047484	regulation of response to osmotic stress	7	0.291303548	0.0036	0.004505419
GO:0043243	positive regulation of protein complex disassembly	16	0.291296654	< 0.001	< 0.001
GO:0097485	neuron projection guidance	109	0.291207066	0.0001	0.000192793
GO:0015740	C4-dicarboxylate transport	8	0.291184041	0.0112	0.012688637
GO:0090311	regulation of protein deacetylation	19	0.291146786	0.0003	0.000505993
GO:0002715	regulation of natural killer cell mediated immunity	8	0.291119691	< 0.001	< 0.001
GO:0070507	regulation of microtubule cytoskeleton organization	80	0.291100386	< 0.001	< 0.001
GO:0046785	microtubule polymerization	34	0.291074268	0.0001	0.000192793
GO:0046883	regulation of hormone secretion	90	0.291065351	0.0001	0.000192793
GO:0043302	positive regulation of leukocyte degranulation	8	0.291055341	< 0.001	< 0.001
GO:0002931	response to ischemia	25	0.291037323	< 0.001	< 0.001
GO:0019098	reproductive behavior	19	0.290997765	0.0001	0.000192793
GO:0097306	cellular response to alcohol	20	0.290926641	< 0.001	< 0.001
GO:1903038	negative regulation of leukocyte cell-cell adhesion	32	0.29090251	< 0.001	< 0.001
GO:0090494	dopamine uptake	7	0.290899062	< 0.001	< 0.001
GO:0070669	response to interleukin-2	6	0.290819391	< 0.001	< 0.001
GO:0000075	cell cycle checkpoint	83	0.290806469	< 0.001	< 0.001
GO:0000394	RNA splicing, via endonucleolytic cleavage and ligation	6	0.290776491	0.0029	0.003693519
GO:0061418	regulation of transcription from RNA polymerase II promoter in response to hypoxia	45	0.290747891	0.0012	0.001702047
GO:0042596	fear response	27	0.290747891	0.0006	0.000927725
GO:0007411	axon guidance	107	0.290691493	< 0.001	< 0.001
GO:0008637	apoptotic mitochondrial changes	58	0.29064927	< 0.001	< 0.001
GO:0050707	regulation of cytokine secretion	63	0.290633491	< 0.001	< 0.001
GO:0046031	ADP metabolic process	47	0.290582984	< 0.001	< 0.001
GO:0006739	NADP metabolic process	10	0.290579151	< 0.001	< 0.001
GO:0007018	microtubule-based movement	108	0.290564374	< 0.001	< 0.001
GO:1904063	negative regulation of cation transmembrane transport	28	0.290522155	< 0.001	< 0.001
GO:0048675	axon extension	65	0.290517771	< 0.001	< 0.001
GO:0033627	cell adhesion mediated by integrin	23	0.290504169	< 0.001	< 0.001
GO:0050858	negative regulation of antigen receptor-mediated signaling pathway	10	0.290501931	< 0.001	< 0.001
GO:1904894	positive regulation of STAT cascade	22	0.29047619	< 0.001	< 0.001
GO:1903510	mucopolysaccharide metabolic process	44	0.29047034	< 0.001	< 0.001
GO:0033173	calcineurin-NFAT signaling cascade	21	0.290470062	0.0001	0.000192793

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0097720	calcineurin-mediated signaling	21	0.290470062	0.0001	0.000192793
GO:0006096	glycolytic process	41	0.290447939	< 0.001	< 0.001
GO:0010614	negative regulation of cardiac muscle hypertrophy	10	0.29042471	0.0003	0.000505993
GO:0043523	regulation of neuron apoptotic process	93	0.290413916	< 0.001	< 0.001
GO:0006836	neurotransmitter transport	104	0.29039699	0.0018	0.002428764
GO:0052548	regulation of endopeptidase activity	115	0.290363158	< 0.001	< 0.001
GO:0015711	organic anion transport	148	0.290352708	< 0.001	< 0.001
GO:0001501	skeletal system development	169	0.290350537	< 0.001	< 0.001
GO:0090670	RNA localization to Cajal body	11	0.29034749	0.0024	0.003116943
GO:0090671	telomerase RNA localization to Cajal body	11	0.29034749	0.0024	0.003116943
GO:0090672	telomerase RNA localization	11	0.29034749	0.0024	0.003116943
GO:1904872	regulation of telomerase RNA localization to Cajal body	11	0.29034749	0.0024	0.003116943
GO:0010950	positive regulation of endopeptidase activity	56	0.290315315	< 0.001	< 0.001
GO:0030593	neutrophil chemotaxis	19	0.290279753	< 0.001	< 0.001
GO:0030837	negative regulation of actin filament polymerization	24	0.290272415	0.0001	0.000192793
GO:0099518	vesicle cytoskeletal trafficking	28	0.290246369	0.0005	0.000791911
GO:0010771	negative regulation of cell morphogenesis involved in differentiation	44	0.29024219	0.0013	0.001826625
GO:0097529	myeloid leukocyte migration	55	0.29021645	< 0.001	< 0.001
GO:0043280	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	40	0.290199485	< 0.001	< 0.001
GO:0007140	male meiosis	12	0.29011154	< 0.001	< 0.001
GO:0018108	peptidyl-tyrosine phosphorylation	127	0.290057662	< 0.001	< 0.001
GO:0038003	opioid receptor signaling pathway	5	0.29003861	< 0.001	< 0.001
GO:0006888	ER to Golgi vesicle-mediated transport	84	0.290037997	0.0002	0.000356582
GO:0071277	cellular response to calcium ion	28	0.289988969	< 0.001	< 0.001
GO:0042698	ovulation cycle	33	0.28997309	0.0023	0.003013139
GO:0008033	tRNA processing	48	0.289950665	0.0002	0.000356582
GO:0014075	response to amine	21	0.289943004	< 0.001	< 0.001
GO:0010801	negative regulation of peptidyl-threonine phosphorylation	9	0.28991849	0.0064	0.007617974
GO:0010921	regulation of phosphatase activity	94	0.28984912	0.0003	0.000505993
GO:0006576	cellular biogenic amine metabolic process	17	0.28983269	< 0.001	< 0.001
GO:0015672	monovalent inorganic cation transport	164	0.289812286	< 0.001	< 0.001
GO:0003148	outflow tract septum morphogenesis	7	0.289795918	0.0068	0.008063902
GO:0016573	histone acetylation	65	0.28977725	< 0.001	< 0.001
GO:0035987	endodermal cell differentiation	11	0.28973909	< 0.001	< 0.001
GO:0045117	azole transport	5	0.28972973	0.0001	0.000192793
GO:0051932	synaptic transmission, GABAergic	18	0.28971829	0.0002	0.000356582
GO:0033555	multicellular organismal response to stress	38	0.289690442	0.0004	0.000648934
GO:0048477	oogenesis	26	0.28965449	< 0.001	< 0.001
GO:0031670	cellular response to nutrient	12	0.28963964	0.0038	0.004725081
GO:0055117	regulation of cardiac muscle contraction	31	0.289633412	< 0.001	< 0.001
GO:0060759	regulation of response to cytokine stimulus	67	0.289632916	< 0.001	< 0.001
GO:0018209	peptidyl-serine modification	128	0.289617519	< 0.001	< 0.001
GO:0006818	hydrogen transport	44	0.28961624	0.0001	0.000192793
GO:0015992	proton transport	44	0.28961624	0.0001	0.000192793
GO:0045980	negative regulation of nucleotide metabolic process	15	0.28959245	< 0.001	< 0.001
GO:1900543	negative regulation of purine nucleotide metabolic process	15	0.28959245	< 0.001	< 0.001
GO:0044091	membrane biogenesis	21	0.28957529	< 0.001	< 0.001
GO:0007224	smoothened signaling pathway	44	0.28956944	0.0017	0.00231289
GO:0002562	somatic diversification of immune receptors via germline recombination within a single locus	22	0.28950509	0.0039	0.004841626
GO:0016444	somatic cell DNA recombination	22	0.28950509	0.0039	0.004841626
GO:2000727	positive regulation of cardiac muscle cell differentiation	10	0.289472329	< 0.001	< 0.001
GO:1903358	regulation of Golgi organization	10	0.289472329	0.0021	0.002780108
GO:0010952	positive regulation of peptidase activity	67	0.289398567	< 0.001	< 0.001
GO:0006403	RNA localization	86	0.289392715	< 0.001	< 0.001
GO:0000422	mitophagy	31	0.289392618	0.0002	0.000356582
GO:0061726	mitochondrion disassembly	31	0.289392618	0.0002	0.000356582
GO:0031572	G2 DNA damage checkpoint	13	0.289377289	0.0004	0.000648934
GO:0042102	positive regulation of T cell proliferation	23	0.289373846	< 0.001	< 0.001
GO:0032651	regulation of interleukin-1 beta production	27	0.289365556	< 0.001	< 0.001
GO:0060026	convergent extension	6	0.289360789	0.0001	0.000192793
GO:0008344	adult locomotory behavior	31	0.289276373	< 0.001	< 0.001
GO:0030177	positive regulation of Wnt signaling pathway	82	0.289223718	0.0001	0.000192793
GO:0048599	oocyte development	12	0.289189189	< 0.001	< 0.001
GO:0035725	sodium ion transmembrane transport	43	0.289162252	< 0.001	< 0.001
GO:0006821	chloride transport	35	0.289111969	< 0.001	< 0.001
GO:0021543	pallium development	82	0.289110714	< 0.001	< 0.001
GO:0010827	regulation of glucose transport	32	0.289108752	0.0001	0.000192793
GO:0001578	microtubule bundle formation	30	0.289094809	0.0002	0.000356582
GO:2001057	reactive nitrogen species metabolic process	28	0.289023718	< 0.001	< 0.001
GO:0018212	peptidyl-tyrosine modification	129	0.289016591	< 0.001	< 0.001
GO:0002495	antigen processing and presentation of peptide antigen via MHC class II	47	0.2890112	< 0.001	< 0.001
GO:0002504	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	47	0.2890112	< 0.001	< 0.001
GO:0022612	gland morphogenesis	38	0.2890063	< 0.001	< 0.001
GO:0000723	telomere maintenance	63	0.289003289	0.0003	0.000505993
GO:0032200	telomere organization	63	0.289003289	0.0003	0.000505993
GO:2000278	regulation of DNA biosynthetic process	46	0.288998937	0.0001	0.000192793
GO:0043524	negative regulation of neuron apoptotic process	71	0.288911849	< 0.001	< 0.001
GO:0070988	demethylation	20	0.288893179	0.0031	0.003925117
GO:0070672	response to interleukin-15	5	0.288854569	< 0.001	< 0.001
GO:0046037	GMP metabolic process	7	0.28883986	< 0.001	< 0.001
GO:0035303	regulation of dephosphorylation	113	0.288821312	< 0.001	< 0.001
GO:0003281	ventricular septum development	25	0.288813385	< 0.001	< 0.001
GO:0045446	endothelial cell differentiation	33	0.288756289	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0051169	nuclear transport	149	0.288733988	< 0.001	< 0.001
GO:0018105	peptidyl-serine phosphorylation	121	0.288692471	< 0.001	< 0.001
GO:0016233	telomere capping	20	0.288661519	0.0026	0.003356522
GO:0050434	positive regulation of viral transcription	22	0.288650989	0.001	0.001450349
GO:0061333	renal tubule morphogenesis	23	0.28864641	< 0.001	< 0.001
GO:0048469	cell maturation	48	0.288583226	< 0.001	< 0.001
GO:0045738	negative regulation of DNA repair	13	0.288565489	< 0.001	< 0.001
GO:0031333	negative regulation of protein complex assembly	55	0.288508249	< 0.001	< 0.001
GO:0051047	positive regulation of secretion	162	0.288499611	< 0.001	< 0.001
GO:0031397	negative regulation of protein ubiquitination	41	0.288495464	0.0001	0.000192793
GO:0099531	presynaptic process involved in chemical synaptic transmission	90	0.288482768	0.0042	0.005168936
GO:0032652	regulation of interleukin-1 production	31	0.288454353	< 0.001	< 0.001
GO:0050728	negative regulation of inflammatory response	41	0.288413849	< 0.001	< 0.001
GO:0006641	triglyceride metabolic process	26	0.288347688	< 0.001	< 0.001
GO:0002675	positive regulation of acute inflammatory response	10	0.288339768	0.0105	0.011988591
GO:1903409	reactive oxygen species biosynthetic process	34	0.288333712	< 0.001	< 0.001
GO:0045601	regulation of endothelial cell differentiation	6	0.288331188	0.0001	0.000192793
GO:0036152	phosphatidylethanolamine acyl-chain remodeling	6	0.288288288	0.0053	0.006400268
GO:0002698	negative regulation of immune effector process	31	0.288279985	< 0.001	< 0.001
GO:0006110	regulation of glycolytic process	28	0.288269903	< 0.001	< 0.001
GO:0048146	positive regulation of fibroblast proliferation	20	0.288262548	< 0.001	< 0.001
GO:0017158	regulation of calcium ion-dependent exocytosis	53	0.288244579	0.002	0.002664694
GO:0042095	interferon-gamma biosynthetic process	5	0.288185328	< 0.001	< 0.001
GO:0045072	regulation of interferon-gamma biosynthetic process	5	0.288185328	< 0.001	< 0.001
GO:0044351	macropinocytosis	5	0.288185328	0.0002	0.000356582
GO:0030900	forebrain development	168	0.288151927	< 0.001	< 0.001
GO:0051028	mRNA transport	57	0.288143783	0.0002	0.000356582
GO:0086013	membrane repolarization during cardiac muscle cell action potential	7	0.288104431	0.0033	0.004153051
GO:1990126	retrograde transport, endosome to plasma membrane	9	0.288088088	0.0003	0.000505993
GO:0051410	detoxification of nitrogen compound	5	0.288082368	0.0378	0.039873355
GO:0070317	negative regulation of G0 to G1 transition	12	0.288073788	0.0001	0.000192793
GO:0051402	neuron apoptotic process	102	0.288071265	< 0.001	< 0.001
GO:2000785	regulation of autophagosome assembly	20	0.288069498	< 0.001	< 0.001
GO:0000186	activation of MAPKK activity	20	0.288056628	< 0.001	< 0.001
GO:2000573	positive regulation of DNA biosynthetic process	32	0.288022844	0.0003	0.000505993
GO:0060969	negative regulation of gene silencing	7	0.287957345	0.0057	0.006849633
GO:0042129	regulation of T cell proliferation	39	0.287918688	< 0.001	< 0.001
GO:2000271	positive regulation of fibroblast apoptotic process	6	0.287902188	< 0.001	< 0.001
GO:1904375	regulation of protein localization to cell periphery	45	0.287870728	< 0.001	< 0.001
GO:0042711	maternal behavior	8	0.287870013	0.0007	0.001063182
GO:0060746	parental behavior	8	0.287870013	0.0007	0.001063182
GO:0042476	odontogenesis	32	0.287845882	< 0.001	< 0.001
GO:0007041	lysosomal transport	52	0.287837838	< 0.001	< 0.001
GO:0051222	positive regulation of protein transport	171	0.287826172	< 0.001	< 0.001
GO:0031571	mitotic G1 DNA damage checkpoint	20	0.287824968	0.0023	0.003013139
GO:0044819	mitotic G1/S transition checkpoint	20	0.287824968	0.0023	0.003013139
GO:0019934	cGMP-mediated signaling	9	0.287802088	0.0338	0.03585693
GO:0016079	synaptic vesicle exocytosis	65	0.287761608	0.0055	0.006618125
GO:0045620	negative regulation of lymphocyte differentiation	15	0.287756328	0.0001	0.000192793
GO:0042311	vasodilation	10	0.287722008	0.0054	0.006510843
GO:0032413	negative regulation of ion transmembrane transporter activity	25	0.287701416	< 0.001	< 0.001
GO:1904951	positive regulation of establishment of protein localization	191	0.287667024	< 0.001	< 0.001
GO:0043087	regulation of GTPase activity	187	0.287650982	< 0.001	< 0.001
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	182	0.287634888	0.0001	0.000192793
GO:0034134	toll-like receptor 2 signaling pathway	9	0.287630488	0.0001	0.000192793
GO:0007623	circadian rhythm	87	0.287622598	< 0.001	< 0.001
GO:0050853	B cell receptor signaling pathway	10	0.287567568	< 0.001	< 0.001
GO:0006606	protein import into nucleus	60	0.287533248	< 0.001	< 0.001
GO:0044744	protein targeting to nucleus	60	0.287533248	< 0.001	< 0.001
GO:1902593	single-organism nuclear import	60	0.287533248	< 0.001	< 0.001
GO:0030041	actin filament polymerization	72	0.287523238	< 0.001	< 0.001
GO:0051149	positive regulation of muscle cell differentiation	42	0.287430287	< 0.001	< 0.001
GO:0002230	positive regulation of defense response to virus by host	7	0.287405773	0.0023	0.003013139
GO:0050670	regulation of lymphocyte proliferation	52	0.287387387	< 0.001	< 0.001
GO:0070661	leukocyte proliferation	79	0.287314077	< 0.001	< 0.001
GO:0016601	Rac protein signal transduction	14	0.287313844	0.0006	0.000927725
GO:0051924	regulation of calcium ion transport	95	0.287302039	< 0.001	< 0.001
GO:0030856	regulation of epithelial cell differentiation	36	0.287087087	< 0.001	< 0.001
GO:1901216	positive regulation of neuron death	39	0.287054087	< 0.001	< 0.001
GO:0010390	histone monoubiquitination	11	0.287001287	0.0002	0.000356582
GO:1903201	regulation of oxidative stress-induced cell death	24	0.287001287	< 0.001	< 0.001
GO:0045445	myoblast differentiation	33	0.286985687	< 0.001	< 0.001
GO:2000780	negative regulation of double-strand break repair	11	0.286977887	< 0.001	< 0.001
GO:0003085	negative regulation of systemic arterial blood pressure	7	0.286964516	< 0.001	< 0.001
GO:0050671	positive regulation of lymphocyte proliferation	35	0.286957161	< 0.001	< 0.001
GO:0048678	response to axon injury	33	0.286876487	< 0.001	< 0.001
GO:0070232	regulation of T cell apoptotic process	8	0.286872587	< 0.001	< 0.001
GO:0001913	T cell mediated cytotoxicity	8	0.286872587	0.0003	0.000505993
GO:1903076	regulation of protein localization to plasma membrane	41	0.286806667	< 0.001	< 0.001
GO:0070663	regulation of leukocyte proliferation	55	0.286795367	< 0.001	< 0.001
GO:0060541	respiratory system development	57	0.286784529	< 0.001	< 0.001
GO:0003341	cilium movement	19	0.286784529	0.0023	0.003013139
GO:0010765	positive regulation of sodium ion transport	16	0.286776062	0.0004	0.000648934

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0006813	potassium ion transport	74	0.286733452	0.0003	0.000505993
GO:0072348	sulfur compound transport	14	0.286707115	< 0.001	< 0.001
GO:0051346	negative regulation of hydrolase activity	156	0.286704287	< 0.001	< 0.001
GO:0002703	regulation of leukocyte mediated immunity	54	0.28666762	< 0.001	< 0.001
GO:0010389	regulation of G2/M transition of mitotic cell cycle	102	0.286665657	0.0001	0.000192793
GO:1901215	negative regulation of neuron death	97	0.286653664	< 0.001	< 0.001
GO:0035428	hexose transmembrane transport	9	0.286629487	0.0002	0.000356582
GO:1904659	glucose transmembrane transport	9	0.286629487	0.0002	0.000356582
GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	71	0.286627875	< 0.001	< 0.001
GO:0009452	7-methylguanosine RNA capping	19	0.286581318	0.0003	0.000505993
GO:0036260	RNA capping	19	0.286581318	0.0003	0.000505993
GO:0045471	response to ethanol	46	0.28655923	< 0.001	< 0.001
GO:0006939	smooth muscle contraction	39	0.286559087	< 0.001	< 0.001
GO:0007096	regulation of exit from mitosis	6	0.286529387	< 0.001	< 0.001
GO:0006913	nucleocytoplasmic transport	146	0.286504117	< 0.001	< 0.001
GO:0009914	hormone transport	114	0.286500034	< 0.001	< 0.001
GO:0048021	regulation of melanin biosynthetic process	8	0.286486486	0.0001	0.000192793
GO:1900376	regulation of secondary metabolite biosynthetic process	8	0.286486486	0.0001	0.000192793
GO:0055001	muscle cell development	51	0.286476392	< 0.001	< 0.001
GO:0045979	positive regulation of nucleoside metabolic process	17	0.286456204	< 0.001	< 0.001
GO:1903580	positive regulation of ATP metabolic process	17	0.286456204	< 0.001	< 0.001
GO:0006656	phosphatidylcholine biosynthetic process	12	0.286443586	< 0.001	< 0.001
GO:1903305	regulation of regulated secretory pathway	73	0.286405388	0.0001	0.000192793
GO:0048017	inositol lipid-mediated signaling	76	0.286391655	< 0.001	< 0.001
GO:0001946	lymphangiogenesis	6	0.286357786	0.0012	0.001702047
GO:0007214	gamma-aminobutyric acid signaling pathway	6	0.286357786	0.0226	0.024538959
GO:0002824	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	23	0.286307425	0.0001	0.000192793
GO:0001832	blastocyst growth	7	0.286302629	0.0001	0.000192793
GO:0014003	oligodendrocyte development	11	0.286275886	< 0.001	< 0.001
GO:0033182	regulation of histone ubiquitination	6	0.286229086	0.0001	0.000192793
GO:0050730	regulation of peptidyl-tyrosine phosphorylation	85	0.286229086	< 0.001	< 0.001
GO:0035304	regulation of protein dephosphorylation	74	0.28615604	0.0003	0.000505993
GO:0007584	response to nutrient	51	0.286143286	< 0.001	< 0.001
GO:0031329	regulation of cellular catabolic process	157	0.286140554	< 0.001	< 0.001
GO:0015931	nucleobase-containing compound transport	82	0.286128637	< 0.001	< 0.001
GO:0001658	branching involved in ureteric bud morphogenesis	15	0.286091806	0.0001	0.000192793
GO:1903532	positive regulation of secretion by cell	154	0.286061943	< 0.001	< 0.001
GO:0014741	negative regulation of muscle hypertrophy	11	0.286041886	0.0001	0.000192793
GO:0034389	lipid particle organization	8	0.286036036	0.0009	0.001319479
GO:0098974	postsynaptic actin cytoskeleton organization	5	0.286023166	0.0035	0.004390436
GO:0034766	negative regulation of ion transmembrane transport	32	0.286019949	< 0.001	< 0.001
GO:0032655	regulation of interleukin-12 production	17	0.28601711	< 0.001	< 0.001
GO:0051452	intracellular pH reduction	22	0.285971686	< 0.001	< 0.001
GO:1903321	negative regulation of protein modification by small protein conjugation or removal	42	0.285965557	0.0001	0.000192793
GO:0007413	axonal fasciculation	16	0.285955598	0.0001	0.000192793
GO:0010948	negative regulation of cell cycle process	135	0.285937366	0.0001	0.000192793
GO:2000241	regulation of reproductive process	42	0.2858675	< 0.001	< 0.001
GO:0022412	cellular process involved in reproduction in multicellular organism	86	0.285848972	< 0.001	< 0.001
GO:0071375	cellular response to peptide hormone stimulus	123	0.285816827	< 0.001	< 0.001
GO:0006757	ATP generation from ADP	42	0.2857817	< 0.001	< 0.001
GO:0031349	positive regulation of defense response	180	0.285727156	< 0.001	< 0.001
GO:0001738	morphogenesis of a polarized epithelium	80	0.285698198	< 0.001	< 0.001
GO:0043254	regulation of protein complex assembly	176	0.285680648	< 0.001	< 0.001
GO:0046651	lymphocyte proliferation	70	0.285666483	< 0.001	< 0.001
GO:0071361	cellular response to ethanol	7	0.285603971	0.0003	0.000505993
GO:0060065	uterus development	7	0.285603971	0.0166	0.018341116
GO:0015698	inorganic anion transport	49	0.285588212	< 0.001	< 0.001
GO:0048821	erythrocyte development	11	0.285573886	0.0005	0.000791911
GO:0030049	muscle filament sliding	16	0.285505148	< 0.001	< 0.001
GO:0033275	actin-myosin filament sliding	16	0.285505148	< 0.001	< 0.001
GO:0072028	nephron morphogenesis	23	0.285456885	< 0.001	< 0.001
GO:0023061	signal release	189	0.285429647	0.0001	0.000192793
GO:0046879	hormone secretion	110	0.285410085	< 0.001	< 0.001
GO:0071280	cellular response to copper ion	9	0.285399685	0.0013	0.001826625
GO:0070071	proton-transporting two-sector ATPase complex assembly	6	0.285242385	0.0062	0.00739947
GO:0006688	glycosphingolipid biosynthetic process	12	0.285242385	0.0073	0.008600218
GO:0031644	regulation of neurological system process	26	0.285209385	< 0.001	< 0.001
GO:0050663	cytokine secretion	67	0.285191802	< 0.001	< 0.001
GO:0030888	regulation of B cell proliferation	15	0.285182325	< 0.001	< 0.001
GO:0046148	pigment biosynthetic process	27	0.285170885	< 0.001	< 0.001
GO:0022407	regulation of cell-cell adhesion	140	0.285164552	< 0.001	< 0.001
GO:0046466	membrane lipid catabolic process	7	0.285162714	< 0.001	< 0.001
GO:0055012	ventricular cardiac muscle cell differentiation	5	0.285148005	0.0037	0.004617737
GO:0010742	macrophage derived foam cell differentiation	7	0.285089171	0.0083	0.009660392
GO:0090077	foam cell differentiation	7	0.285089171	0.0083	0.009660392
GO:0007269	neurotransmitter secretion	87	0.285019009	0.006	0.007178216
GO:0099643	signal release from synapse	87	0.285019009	0.006	0.007178216
GO:1904029	regulation of cyclin-dependent protein kinase activity	39	0.284961885	< 0.001	< 0.001
GO:0051289	protein homotetramerization	33	0.284934285	< 0.001	< 0.001
GO:0072078	nephron tubule morphogenesis	21	0.284929828	< 0.001	< 0.001
GO:1903214	regulation of protein targeting to mitochondrion	27	0.284923018	0.0001	0.000192793
GO:0051281	positive regulation of release of sequestered calcium ion into cytosol	17	0.284896661	0.0023	0.003013139

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0046939	nucleotide phosphorylation	50	0.284859717	< 0.001	< 0.001
GO:0002089	lens morphogenesis in camera-type eye	6	0.284770485	< 0.001	< 0.001
GO:0007160	cell-matrix adhesion	82	0.284766299	< 0.001	< 0.001
GO:1905330	regulation of morphogenesis of an epithelium	85	0.284748278	< 0.001	< 0.001
GO:0018242	protein O-linked glycosylation via serine	5	0.284736165	0.006	0.007178216
GO:0070228	regulation of lymphocyte apoptotic process	14	0.28470307	< 0.001	< 0.001
GO:0001952	regulation of cell-matrix adhesion	47	0.284701114	< 0.001	< 0.001
GO:0030073	insulin secretion	77	0.28469137	< 0.001	< 0.001
GO:0046474	glycerophospholipid biosynthetic process	90	0.284681825	< 0.001	< 0.001
GO:0001649	osteoblast differentiation	74	0.284681206	< 0.001	< 0.001
GO:0043966	histone H3 acetylation	26	0.284674785	< 0.001	< 0.001
GO:0001818	negative regulation of cytokine production	85	0.284669543	< 0.001	< 0.001
GO:1901988	negative regulation of cell cycle phase transition	101	0.284664297	0.0001	0.000192793
GO:0050673	epithelial cell proliferation	136	0.284631691	< 0.001	< 0.001
GO:0030878	thyroid gland development	9	0.284627485	0.0013	0.001826625
GO:0008053	mitochondrial fusion	11	0.284567685	< 0.001	< 0.001
GO:0032611	interleukin-1 beta production	29	0.284560422	< 0.001	< 0.001
GO:0030833	regulation of actin filament polymerization	63	0.284500827	< 0.001	< 0.001
GO:0051973	positive regulation of telomerase activity	16	0.284459459	< 0.001	< 0.001
GO:0045589	regulation of regulatory T cell differentiation	5	0.284427284	0.0004	0.000648934
GO:0051568	histone H3-K4 methylation	23	0.284427284	0.0001	0.000192793
GO:0051893	regulation of focal adhesion assembly	29	0.284427284	< 0.001	< 0.001
GO:0090109	regulation of cell-substrate junction assembly	29	0.284427284	< 0.001	< 0.001
GO:0032330	regulation of chondrocyte differentiation	15	0.284410124	< 0.001	< 0.001
GO:0043044	ATP-dependent chromatin remodeling	25	0.284406692	0.0035	0.004390436
GO:1902514	regulation of calcium ion transmembrane transport via high voltage-gated calcium channel	7	0.284390513	0.0121	0.013633945
GO:0051965	positive regulation of synapse assembly	33	0.284349284	0.002	0.002664694
GO:0032309	icosanoid secretion	14	0.284335356	< 0.001	< 0.001
GO:0071715	icosanoid transport	14	0.284335356	< 0.001	< 0.001
GO:1901571	fatty acid derivative transport	14	0.284335356	< 0.001	< 0.001
GO:0006029	proteoglycan metabolic process	36	0.284291434	< 0.001	< 0.001
GO:0010575	positive regulation of vascular endothelial growth factor production	7	0.284243427	< 0.001	< 0.001
GO:0006289	nucleotide-excision repair	53	0.28423302	0.0001	0.000192793
GO:0010001	glial cell differentiation	62	0.284228007	< 0.001	< 0.001
GO:0070665	positive regulation of leukocyte proliferation	37	0.284225538	< 0.001	< 0.001
GO:0034199	activation of protein kinase A activity	11	0.284216684	< 0.001	< 0.001
GO:0006929	substrate-dependent cell migration	10	0.284195624	< 0.001	< 0.001
GO:0050680	negative regulation of epithelial cell proliferation	50	0.284175032	< 0.001	< 0.001
GO:2001044	regulation of integrin-mediated signaling pathway	5	0.284169884	0.0248	0.026750339
GO:1901031	regulation of response to reactive oxygen species	10	0.284144144	< 0.001	< 0.001
GO:1902749	regulation of cell cycle G2/M phase transition	112	0.28404578	< 0.001	< 0.001
GO:1902036	regulation of hematopoietic stem cell differentiation	42	0.284004413	0.0008	0.001193265
GO:0050691	regulation of defense response to virus by host	9	0.283941084	0.0007	0.001063182
GO:1901992	positive regulation of mitotic cell cycle phase transition	31	0.283937394	0.0002	0.000356582
GO:0060325	face morphogenesis	7	0.283912484	0.0004	0.000648934
GO:0070571	negative regulation of neuron projection regeneration	8	0.283912484	0.0334	0.035446504
GO:1903828	negative regulation of cellular protein localization	60	0.283895324	< 0.001	< 0.001
GO:0036296	response to increased oxygen levels	12	0.283891034	0.0001	0.000192793
GO:0099625	ventricular cardiac muscle cell membrane repolarization	9	0.283855284	0.0002	0.000356582
GO:0007569	cell aging	48	0.283853496	< 0.001	< 0.001
GO:0032615	interleukin-12 production	18	0.283840984	< 0.001	< 0.001
GO:0009713	catechol-containing compound biosynthetic process	9	0.283826684	< 0.001	< 0.001
GO:0042423	catecholamine biosynthetic process	9	0.283826684	< 0.001	< 0.001
GO:0015696	ammonium transport	28	0.28380217	< 0.001	< 0.001
GO:1901991	negative regulation of mitotic cell cycle phase transition	94	0.283759139	0.0001	0.000192793
GO:0019722	calcium-mediated signaling	75	0.283754612	< 0.001	< 0.001
GO:0097421	liver regeneration	7	0.283728627	0.0042	0.005168936
GO:0006820	anion transport	186	0.283709055	< 0.001	< 0.001
GO:0042267	natural killer cell mediated cytotoxicity	16	0.283687259	< 0.001	< 0.001
GO:0009205	purine ribonucleoside triphosphate metabolic process	115	0.283641654	0.0001	0.000192793
GO:1902570	protein localization to nucleolus	6	0.283612184	0.0002	0.000356582
GO:0006779	porphyrin-containing compound biosynthetic process	9	0.283597884	0.0015	0.002069969
GO:0006783	heme biosynthetic process	9	0.283597884	0.0015	0.002069969
GO:0001767	establishment of lymphocyte polarity	6	0.283569284	0.0004	0.000648934
GO:0001541	ovarian follicle development	13	0.283556084	0.0017	0.00231289
GO:0050806	positive regulation of synaptic transmission	89	0.28354229	0.0031	0.003925117
GO:0032944	regulation of mononuclear cell proliferation	53	0.283528812	< 0.001	< 0.001
GO:0002062	chondrocyte differentiation	35	0.283522706	< 0.001	< 0.001
GO:0097194	execution phase of apoptosis	24	0.283494208	0.0002	0.000356582
GO:1902882	regulation of response to oxidative stress	28	0.283480419	< 0.001	< 0.001
GO:2000779	regulation of double-strand break repair	32	0.283437902	< 0.001	< 0.001
GO:0071548	response to dexamethasone	13	0.283437283	< 0.001	< 0.001
GO:1900182	positive regulation of protein localization to nucleus	30	0.283414843	0.0001	0.000192793
GO:0019372	lipoxygenase pathway	5	0.283397683	0.0001	0.000192793
GO:0009048	dosage compensation by inactivation of X chromosome	6	0.283397683	0.0037	0.004617737
GO:0031345	negative regulation of cell projection organization	82	0.283360015	0.0008	0.001193265
GO:0060712	spermatogonial germ cell development	5	0.283346203	< 0.001	< 0.001
GO:0007044	cell-substrate junction assembly	39	0.283344883	< 0.001	< 0.001
GO:0043568	positive regulation of insulin-like growth factor receptor signaling pathway	5	0.283294723	0.0208	0.022657367
GO:0060749	mammary gland alveolus development	5	0.283294723	< 0.001	< 0.001
GO:0061377	mammary gland lobule development	5	0.283294723	< 0.001	< 0.001
GO:2000479	regulation of cAMP-dependent protein kinase activity	11	0.283280683	< 0.001	< 0.001
GO:0042180	cellular ketone metabolic process	108	0.283264217	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1900015	regulation of cytokine production involved in inflammatory response	16	0.283252896	< 0.001	< 0.001
GO:0046887	positive regulation of hormone secretion	41	0.283221898	< 0.001	< 0.001
GO:0002886	regulation of myeloid leukocyte mediated immunity	19	0.283221567	< 0.001	< 0.001
GO:0090189	regulation of branching involved in ureteric bud morphogenesis	6	0.283183183	0.0008	0.001193265
GO:0090190	positive regulation of branching involved in ureteric bud morphogenesis	6	0.283183183	0.0008	0.001193265
GO:0070987	error-free translesion synthesis	9	0.283168883	0.0003	0.000505993
GO:0048284	organelle fusion	59	0.283166459	< 0.001	< 0.001
GO:0043455	regulation of secondary metabolic process	10	0.283166023	0.0003	0.000505993
GO:0007266	Rho protein signal transduction	72	0.283147433	< 0.001	< 0.001
GO:0071549	cellular response to dexamethasone stimulus	9	0.283083083	0.0002	0.000356582
GO:0050954	sensory perception of mechanical stimulus	59	0.283061754	< 0.001	< 0.001
GO:0007283	spermatogenesis	167	0.283004647	< 0.001	< 0.001
GO:0098656	anion transmembrane transport	65	0.283001683	< 0.001	< 0.001
GO:0010676	positive regulation of cellular carbohydrate metabolic process	25	0.282996139	< 0.001	< 0.001
GO:0036159	inner dynein arm assembly	7	0.282993197	0.0477	0.049647689
GO:1901565	organonitrogen compound catabolic process	115	0.282985843	< 0.001	< 0.001
GO:0043967	histone H4 acetylation	27	0.282968683	< 0.001	< 0.001
GO:0048259	regulation of receptor-mediated endocytosis	44	0.282947233	< 0.001	< 0.001
GO:0030202	heparin metabolic process	6	0.282925783	0.0021	0.002780108
GO:0009144	purine nucleoside triphosphate metabolic process	118	0.282922147	0.0001	0.000192793
GO:0043401	steroid hormone mediated signaling pathway	64	0.282858752	< 0.001	< 0.001
GO:0032943	mononuclear cell proliferation	71	0.282810376	< 0.001	< 0.001
GO:0048015	phosphatidylinositol-mediated signaling	75	0.282745603	< 0.001	< 0.001
GO:2000142	regulation of DNA-templated transcription, initiation	12	0.282732733	0.0005	0.000791911
GO:0043516	regulation of DNA damage response, signal transduction by p53 class mediator	15	0.282728443	< 0.001	< 0.001
GO:0048659	smooth muscle cell proliferation	54	0.282682683	< 0.001	< 0.001
GO:0017157	regulation of exocytosis	99	0.282659283	0.0001	0.000192793
GO:0015833	peptide transport	98	0.282643868	< 0.001	< 0.001
GO:0035195	gene silencing by miRNA	50	0.282620335	< 0.001	< 0.001
GO:0016042	lipid catabolic process	83	0.282594471	< 0.001	< 0.001
GO:1903977	positive regulation of glial cell migration	5	0.282574003	0.0203	0.022152908
GO:0030518	intracellular steroid hormone receptor signaling pathway	47	0.282521427	< 0.001	< 0.001
GO:0016241	regulation of macroautophagy	91	0.282520825	< 0.001	< 0.001
GO:0035019	somatic stem cell population maintenance	28	0.282496782	< 0.001	< 0.001
GO:0090066	regulation of anatomical structure size	194	0.282464939	< 0.001	< 0.001
GO:0048002	antigen processing and presentation of peptide antigen	89	0.282457739	0.0002	0.000356582
GO:0031998	regulation of fatty acid beta-oxidation	6	0.282410982	0.0002	0.000356582
GO:1901653	cellular response to peptide	148	0.282376778	< 0.001	< 0.001
GO:0019369	arachidonic acid metabolic process	11	0.282368082	< 0.001	< 0.001
GO:0006140	regulation of nucleotide metabolic process	70	0.282334988	< 0.001	< 0.001
GO:1905037	autophagosome organization	39	0.282295482	0.0001	0.000192793
GO:0035308	negative regulation of protein dephosphorylation	35	0.282243059	0.0022	0.002896881
GO:1900244	positive regulation of synaptic vesicle endocytosis	6	0.282239382	0.0187	0.020510412
GO:0070588	calcium ion transmembrane transport	110	0.282157482	< 0.001	< 0.001
GO:0050729	positive regulation of inflammatory response	38	0.282110682	< 0.001	< 0.001
GO:0019896	axonal transport of mitochondrion	5	0.282110682	0.0003	0.000505993
GO:0060142	regulation of syncytium formation by plasma membrane fusion	6	0.282067782	0.0006	0.000927725
GO:0060143	positive regulation of syncytium formation by plasma membrane fusion	6	0.282067782	0.0006	0.000927725
GO:0002821	positive regulation of adaptive immune response	26	0.282021582	0.0001	0.000192793
GO:0048661	positive regulation of smooth muscle cell proliferation	36	0.281989132	< 0.001	< 0.001
GO:0006163	purine nucleotide metabolic process	182	0.281936725	< 0.001	< 0.001
GO:0099054	presynapse assembly	25	0.281904762	0.0009	0.001319479
GO:0009266	response to temperature stimulus	93	0.281886495	< 0.001	< 0.001
GO:2000379	positive regulation of reactive oxygen species metabolic process	32	0.281861326	< 0.001	< 0.001
GO:0097553	calcium ion transmembrane import into cytosol	56	0.281857878	0.0011	0.001576346
GO:1902656	calcium ion import into cytosol	56	0.281857878	0.0011	0.001576346
GO:0003214	cardiac left ventricle morphogenesis	6	0.281853282	0.0395	0.041520716
GO:2000134	negative regulation of G1/S transition of mitotic cell cycle	32	0.281845238	< 0.001	< 0.001
GO:0002902	regulation of B cell apoptotic process	6	0.281810382	< 0.001	< 0.001
GO:0006376	mRNA splice site selection	10	0.281801802	0.001	0.001450349
GO:0035115	embryonic forelimb morphogenesis	9	0.281738882	0.0001	0.000192793
GO:0045665	negative regulation of neuron differentiation	97	0.281683451	< 0.001	< 0.001
GO:0034605	cellular response to heat	56	0.281674021	< 0.001	< 0.001
GO:0036473	cell death in response to oxidative stress	35	0.28166207	< 0.001	< 0.001
GO:0048663	neuron fate commitment	19	0.281609429	0.0009	0.001319479
GO:0048016	inositol phosphate-mediated signaling	25	0.281606178	< 0.001	< 0.001
GO:0071156	regulation of cell cycle arrest	38	0.281595882	< 0.001	< 0.001
GO:0019886	antigen processing and presentation of exogenous peptide antigen via MHC class II	45	0.281584442	< 0.001	< 0.001
GO:0001516	prostaglandin biosynthetic process	12	0.281552982	0.0002	0.000356582
GO:0046457	prostanoid biosynthetic process	12	0.281552982	0.0002	0.000356582
GO:0008608	attachment of spindle microtubules to kinetochore	11	0.281549082	< 0.001	< 0.001
GO:2001056	positive regulation of cysteine-type endopeptidase activity	51	0.281520176	< 0.001	< 0.001
GO:0032802	low-density lipoprotein particle receptor catabolic process	10	0.281441441	0.0056	0.006732458
GO:0007628	adult walking behavior	11	0.281432081	0.0014	0.00194839
GO:0090659	walking behavior	11	0.281432081	0.0014	0.00194839
GO:0001764	neuron migration	77	0.281428739	0.0001	0.000192793
GO:0090312	positive regulation of protein deacetylation	9	0.281424281	0.0016	0.002186748
GO:0048232	male gamete generation	168	0.281422749	< 0.001	< 0.001
GO:2000177	regulation of neural precursor cell proliferation	31	0.281404907	0.0001	0.000192793
GO:0002478	antigen processing and presentation of exogenous peptide antigen	84	0.281390574	0.0002	0.000356582
GO:0035194	posttranscriptional gene silencing by RNA	53	0.281377334	< 0.001	< 0.001
GO:0010977	negative regulation of neuron projection development	69	0.281372055	0.0006	0.000927725
GO:0051053	negative regulation of DNA metabolic process	54	0.281371848	0.0004	0.000648934

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1902166	negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	8	0.281370656	0.0409	0.042933877
GO:0006360	transcription from RNA polymerase I promoter	33	0.281307281	0.0001	0.000192793
GO:0016236	macroautophagy	152	0.281294452	0.0002	0.000356582
GO:032946	positive regulation of mononuclear cell proliferation	36	0.281288431	< 0.001	< 0.001
GO:0006970	response to osmotic stress	30	0.281261261	< 0.001	< 0.001
GO:0045061	thymic T cell selection	5	0.281235521	0.0108	0.012299937
GO:1903362	regulation of cellular protein catabolic process	103	0.281231023	< 0.001	< 0.001
GO:0006809	nitric oxide biosynthetic process	23	0.281215377	0.0002	0.000356582
GO:0009952	anterior/posterior pattern specification	54	0.281176415	< 0.001	< 0.001
GO:0002479	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	38	0.281175913	0.0014	0.00194839
GO:0042590	antigen processing and presentation of exogenous peptide antigen via MHC class I	39	0.281166881	0.0015	0.002069969
GO:0034763	negative regulation of transmembrane transport	36	0.281109681	< 0.001	< 0.001
GO:0046627	negative regulation of insulin receptor signaling pathway	11	0.281104481	0.0048	0.005840847
GO:0016180	snRNA processing	5	0.281081081	0.0002	0.000356582
GO:0061615	glycolytic process through fructose-6-phosphate	14	0.281081081	0.001	0.001450349
GO:0061620	glycolytic process through glucose-6-phosphate	14	0.281081081	0.001	0.001450349
GO:0051701	interaction with host	75	0.281067353	< 0.001	< 0.001
GO:0044070	regulation of anion transport	36	0.281066781	< 0.001	< 0.001
GO:0002790	peptide secretion	95	0.281040439	< 0.001	< 0.001
GO:0045684	positive regulation of epidermis development	11	0.281034281	< 0.001	< 0.001
GO:0032515	negative regulation of phosphoprotein phosphatase activity	31	0.281014655	0.0038	0.004725081
GO:0097066	response to thyroid hormone	6	0.280995281	0.0042	0.005168936
GO:0045862	positive regulation of proteolysis	131	0.280986766	< 0.001	< 0.001
GO:0070498	interleukin-1-mediated signaling pathway	54	0.280985748	0.0006	0.000927725
GO:0045661	regulation of myoblast differentiation	21	0.280983024	< 0.001	< 0.001
GO:0097305	response to alcohol	63	0.280974852	< 0.001	< 0.001
GO:0006650	glycerophospholipid metabolic process	125	0.280963707	< 0.001	< 0.001
GO:0071621	granulocyte chemotaxis	27	0.280947614	< 0.001	< 0.001
GO:0007281	germ cell development	71	0.280943318	< 0.001	< 0.001
GO:0051580	regulation of neurotransmitter uptake	9	0.280938081	0.0076	0.008916717
GO:0051310	metaphase plate congression	25	0.280936937	0.0002	0.000356582
GO:0009798	axis specification	25	0.280916345	< 0.001	< 0.001
GO:0051926	negative regulation of calcium ion transport	22	0.280870481	< 0.001	< 0.001
GO:1904706	negative regulation of vascular smooth muscle cell proliferation	7	0.280860452	0.0043	0.005276385
GO:0042493	response to drug	107	0.280859765	< 0.001	< 0.001
GO:0002709	regulation of T cell mediated immunity	12	0.280845131	0.0002	0.000356582
GO:0050920	regulation of chemotaxis	73	0.280844837	< 0.001	< 0.001
GO:0090398	cellular senescence	34	0.280831251	0.0004	0.000648934
GO:0071322	cellular response to carbohydrate stimulus	62	0.280827832	< 0.001	< 0.001
GO:0006733	oxidoreduction coenzyme metabolic process	71	0.280827306	< 0.001	< 0.001
GO:0035372	protein localization to microtubule	6	0.280823681	0.0206	0.022453086
GO:0032675	regulation of interleukin-6 production	37	0.280802811	< 0.001	< 0.001
GO:0003013	circulatory system process	174	0.280800012	< 0.001	< 0.001
GO:0031498	chromatin disassembly	8	0.280791506	0.0233	0.025253349
GO:0070555	response to interleukin-1	82	0.280767178	0.0002	0.000356582
GO:0042472	inner ear morphogenesis	27	0.280718814	< 0.001	< 0.001
GO:0010639	negative regulation of organelle organization	139	0.280705166	< 0.001	< 0.001
GO:0035051	cardiocyte differentiation	49	0.280697607	< 0.001	< 0.001
GO:0035767	endothelial cell chemotaxis	10	0.280694981	0.0025	0.003237479
GO:1902186	regulation of viral release from host cell	14	0.280694981	0.0003	0.000505993
GO:0060828	regulation of canonical Wnt signaling pathway	116	0.280690543	< 0.001	< 0.001
GO:0051881	regulation of mitochondrial membrane potential	25	0.280689833	0.0001	0.000192793
GO:0045191	regulation of isotype switching	13	0.280665281	0.0056	0.006732458
GO:0071229	cellular response to acid chemical	74	0.280614978	< 0.001	< 0.001
GO:1904950	negative regulation of establishment of protein localization	87	0.280586991	< 0.001	< 0.001
GO:0006090	pyruvate metabolic process	52	0.280586081	< 0.001	< 0.001
GO:0048660	regulation of smooth muscle cell proliferation	53	0.280585707	< 0.001	< 0.001
GO:0042402	cellular biogenic amine catabolic process	9	0.280566281	0.0002	0.000356582
GO:0044342	type B pancreatic cell proliferation	8	0.280534106	0.0101	0.011583277
GO:0016050	vesicle organization	139	0.280523689	< 0.001	< 0.001
GO:0006283	transcription-coupled nucleotide-excision repair	39	0.280506881	0.0006	0.000927725
GO:0006302	double-strand break repair	80	0.280501931	< 0.001	< 0.001
GO:0006007	glucose catabolic process	15	0.28049764	0.0021	0.002780108
GO:0032844	regulation of homeostatic process	181	0.28044398	< 0.001	< 0.001
GO:0051131	chaperone-mediated protein complex assembly	8	0.28043758	0.0003	0.000505993
GO:0034381	plasma lipoprotein particle clearance	17	0.280414869	0.0002	0.000356582
GO:0033046	negative regulation of sister chromatid segregation	16	0.280405405	0.0012	0.001702047
GO:0033048	negative regulation of mitotic sister chromatid segregation	16	0.280405405	0.0012	0.001702047
GO:0051985	negative regulation of chromosome segregation	16	0.280405405	0.0012	0.001702047
GO:0050852	T cell receptor signaling pathway	80	0.280379665	0.0002	0.000356582
GO:0007599	hemostasis	126	0.280368123	< 0.001	< 0.001
GO:0034968	histone lysine methylation	46	0.280342454	0.0003	0.000505993
GO:0046386	deoxyribose phosphate catabolic process	8	0.280341055	0.0002	0.000356582
GO:0043551	regulation of phosphatidylinositol 3-kinase activity	21	0.280333395	< 0.001	< 0.001
GO:0001505	regulation of neurotransmitter levels	109	0.280320688	0.0009	0.001319479
GO:0007612	learning	79	0.28030888	0.0035	0.004390436
GO:1901214	regulation of neuron death	142	0.280303442	< 0.001	< 0.001
GO:0042471	ear morphogenesis	36	0.28030173	< 0.001	< 0.001
GO:2001233	regulation of apoptotic signaling pathway	154	0.280298852	< 0.001	< 0.001
GO:0006949	syncytium formation	16	0.280292793	0.0098	0.011263122
GO:0048732	gland development	141	0.280286974	< 0.001	< 0.001
GO:0002638	negative regulation of immunoglobulin production	5	0.2802574	0.0036	0.004505419

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0050000	chromosome localization	31	0.280209241	0.0001	0.000192793
GO:0051303	establishment of chromosome localization	31	0.280209241	0.0001	0.000192793
GO:0061577	calcium ion transmembrane transport via high voltage-gated calcium channel	8	0.28018018	0.0195	0.021348865
GO:0007015	actin filament organization	154	0.28015678	< 0.001	< 0.001
GO:0051660	establishment of centrosome localization	6	0.28013728	0.0136	0.015222535
GO:1900029	positive regulation of ruffle assembly	7	0.280125023	0.0003	0.000505993
GO:0032387	negative regulation of intracellular transport	42	0.280118894	< 0.001	< 0.001
GO:0009199	ribonucleoside triphosphate metabolic process	117	0.28009768	0.0001	0.000192793
GO:0007045	cell-substrate adherens junction assembly	37	0.280086264	< 0.001	< 0.001
GO:0048041	focal adhesion assembly	37	0.280086264	< 0.001	< 0.001
GO:2000778	positive regulation of interleukin-6 secretion	8	0.280083655	0.0016	0.002186748
GO:0045216	cell-cell junction organization	94	0.280056957	< 0.001	< 0.001
GO:0042276	error-prone translesion synthesis	9	0.28005148	0.0073	0.008600218
GO:0032507	maintenance of protein location in cell	36	0.28004433	< 0.001	< 0.001
GO:0030072	peptide hormone secretion	93	0.280029338	< 0.001	< 0.001
GO:0090279	regulation of calcium ion import	51	0.279945492	0.0009	0.001319479
GO:1904705	regulation of vascular smooth muscle cell proliferation	23	0.279928376	< 0.001	< 0.001
GO:1990874	vascular smooth muscle cell proliferation	23	0.279928376	< 0.001	< 0.001
GO:0015909	long-chain fatty acid transport	21	0.279904394	< 0.001	< 0.001
GO:0070252	actin-mediated cell contraction	44	0.27989353	< 0.001	< 0.001
GO:0016579	protein deubiquitination	148	0.279870604	0.0001	0.000192793
GO:0034080	CENP-A containing nucleosome assembly	13	0.27983368	0.0141	0.015736555
GO:0061641	CENP-A containing chromatin organization	13	0.27983368	0.0141	0.015736555
GO:0002532	production of molecular mediator involved in inflammatory response	23	0.279749315	< 0.001	< 0.001
GO:1903556	negative regulation of tumor necrosis factor superfamily cytokine production	21	0.279745051	< 0.001	< 0.001
GO:0030178	negative regulation of Wnt signaling pathway	86	0.279737212	< 0.001	< 0.001
GO:0009886	post-embryonic animal morphogenesis	5	0.27969112	0.0002	0.000356582
GO:0032703	negative regulation of interleukin-2 production	8	0.27966538	< 0.001	< 0.001
GO:1905332	positive regulation of morphogenesis of an epithelium	9	0.27965108	0.0004	0.000648934
GO:0090317	negative regulation of intracellular protein transport	32	0.279641248	< 0.001	< 0.001
GO:0000041	transition metal ion transport	35	0.27963964	< 0.001	< 0.001
GO:0070997	neuron death	154	0.279636965	< 0.001	< 0.001
GO:0018958	phenol-containing compound metabolic process	42	0.279628608	< 0.001	< 0.001
GO:0019884	antigen processing and presentation of exogenous antigen	85	0.279615414	0.0002	0.000356582
GO:0033628	regulation of cell adhesion mediated by integrin	19	0.27953668	< 0.001	< 0.001
GO:1904031	positive regulation of cyclin-dependent protein kinase activity	17	0.27953668	0.0003	0.000505993
GO:1904707	positive regulation of vascular smooth muscle cell proliferation	16	0.279520592	< 0.001	< 0.001
GO:0010800	positive regulation of peptidyl-threonine phosphorylation	18	0.27950808	< 0.001	< 0.001
GO:1904814	regulation of protein localization to chromosome, telomeric region	7	0.279499908	0.0026	0.003356522
GO:0031331	positive regulation of cellular catabolic process	100	0.279472329	< 0.001	< 0.001
GO:0060402	calcium ion transport into cytosol	63	0.279434537	0.0008	0.001193265
GO:2000300	regulation of synaptic vesicle exocytosis	43	0.279387028	0.0055	0.006618125
GO:0071352	cellular response to interleukin-2	5	0.279382239	< 0.001	< 0.001
GO:0038095	Fc-epsilon receptor signaling pathway	69	0.279353888	0.0002	0.000356582
GO:0045667	regulation of osteoblast differentiation	42	0.279328308	< 0.001	< 0.001
GO:0046128	purine ribonucleoside metabolic process	143	0.279309879	0.0001	0.000192793
GO:0021537	telencephalon development	116	0.27929925	< 0.001	< 0.001
GO:0043550	regulation of lipid kinase activity	24	0.279290004	0.0001	0.000192793
GO:0072332	intrinsic apoptotic signaling pathway by p53 class mediator	29	0.279288155	0.0014	0.00194839
GO:1900077	negative regulation of cellular response to insulin stimulus	12	0.279257829	0.002	0.002664694
GO:0060412	ventricular septum morphogenesis	17	0.279248997	< 0.001	< 0.001
GO:0090090	negative regulation of canonical Wnt signaling pathway	77	0.279182336	0.0001	0.000192793
GO:0036507	protein demannosylation	12	0.279150579	< 0.001	< 0.001
GO:0036508	protein alpha-1,2-demannosylation	12	0.279150579	< 0.001	< 0.001
GO:1903749	positive regulation of establishment of protein localization to mitochondrion	36	0.279150579	< 0.001	< 0.001
GO:0071383	cellular response to steroid hormone stimulus	80	0.279140927	< 0.001	< 0.001
GO:1904062	regulation of cation transmembrane transport	125	0.279106306	0.0012	0.001702047
GO:2000116	regulation of cysteine-type endopeptidase activity	84	0.279034136	< 0.001	< 0.001
GO:0044773	mitotic DNA damage checkpoint	30	0.278996139	0.0006	0.000927725
GO:0044774	mitotic DNA integrity checkpoint	30	0.278996139	0.0006	0.000927725
GO:0060218	hematopoietic stem cell differentiation	44	0.278992629	0.0008	0.001193265
GO:0033005	positive regulation of mast cell activation	6	0.278978979	0.0003	0.000505993
GO:0007141	male meiosis I	5	0.278918919	0.0001	0.000192793
GO:0022038	corpus callosum development	12	0.278893179	0.0005	0.000791911
GO:0009150	purine ribonucleotide metabolic process	176	0.278828829	< 0.001	< 0.001
GO:0006513	protein monoubiquitination	35	0.278815959	< 0.001	< 0.001
GO:0044783	G1 DNA damage checkpoint	21	0.27880125	0.0027	0.003470695
GO:0030522	intracellular receptor signaling pathway	98	0.27874084	< 0.001	< 0.001
GO:0060259	regulation of feeding behavior	10	0.278738739	0.0089	0.010294435
GO:0030433	ER-associated ubiquitin-dependent protein catabolic process	31	0.278714659	0.0001	0.000192793
GO:0014888	striated muscle adaptation	15	0.278712999	< 0.001	< 0.001
GO:0043666	regulation of phosphoprotein phosphatase activity	62	0.278702205	0.0009	0.001319479
GO:1990776	response to angiotensin	11	0.278694279	0.0107	0.012191187
GO:0032612	interleukin-1 production	34	0.278666061	< 0.001	< 0.001
GO:0007034	vacuolar transport	58	0.278649092	< 0.001	< 0.001
GO:0006266	DNA ligation	6	0.278635779	0.0281	0.030129444
GO:0030336	negative regulation of cell migration	111	0.278634619	< 0.001	< 0.001
GO:0003254	regulation of membrane depolarization	13	0.278625879	< 0.001	< 0.001
GO:0070886	positive regulation of calcineurin-NFAT signaling cascade	7	0.278617393	0.0001	0.000192793
GO:0021795	cerebral cortex cell migration	24	0.278603604	0.0009	0.001319479
GO:0007405	neuroblast proliferation	18	0.278592879	0.004	0.004954389
GO:0007596	blood coagulation	124	0.278567277	< 0.001	< 0.001
GO:0050817	coagulation	124	0.278567277	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0008015	blood circulation	172	0.278560953	< 0.001	< 0.001
GO:0018904	ether metabolic process	5	0.278558559	0.0005	0.000791911
GO:0002695	negative regulation of leukocyte activation	47	0.278556368	< 0.001	< 0.001
GO:1901889	negative regulation of cell junction assembly	11	0.278530479	< 0.001	< 0.001
GO:0045581	negative regulation of T cell differentiation	12	0.278528529	0.0005	0.000791911
GO:0051154	negative regulation of striated muscle cell differentiation	10	0.278507079	0.0002	0.000356582
GO:0032306	regulation of prostaglandin secretion	5	0.278507079	< 0.001	< 0.001
GO:0032308	positive regulation of prostaglandin secretion	5	0.278507079	< 0.001	< 0.001
GO:0051101	regulation of DNA binding	45	0.278501359	< 0.001	< 0.001
GO:0006338	chromatin remodeling	53	0.278443943	0.0009	0.001319479
GO:0051224	negative regulation of protein transport	85	0.278422288	< 0.001	< 0.001
GO:0006775	fat-soluble vitamin metabolic process	12	0.278399828	< 0.001	< 0.001
GO:0009141	nucleoside triphosphate metabolic process	124	0.27838253	0.0001	0.000192793
GO:0007223	Wnt signaling pathway, calcium modulating pathway	16	0.278378378	0.0094	0.010831045
GO:0009566	fertilization	54	0.278368845	< 0.001	< 0.001
GO:0045663	positive regulation of myoblast differentiation	11	0.278366678	0.002	0.002664694
GO:0071347	cellular response to interleukin-1	69	0.278331748	0.0003	0.000505993
GO:0043462	regulation of ATPase activity	27	0.278325945	< 0.001	< 0.001
GO:0033280	response to vitamin D	10	0.278275418	< 0.001	< 0.001
GO:0001556	oocyte maturation	7	0.278212907	< 0.001	< 0.001
GO:0090002	establishment of protein localization to plasma membrane	25	0.278198198	< 0.001	< 0.001
GO:0008209	androgen metabolic process	5	0.278198198	0.0081	0.00945
GO:0072659	protein localization to plasma membrane	118	0.278162424	< 0.001	< 0.001
GO:1904035	regulation of epithelial cell apoptotic process	19	0.278141299	< 0.001	< 0.001
GO:0002250	adaptive immune response	96	0.278096847	< 0.001	< 0.001
GO:0060078	regulation of postsynaptic membrane potential	63	0.27808625	0.0036	0.004505419
GO:0050865	regulation of cell activation	170	0.278055871	< 0.001	< 0.001
GO:0051588	regulation of neurotransmitter transport	63	0.278012707	0.0047	0.005730776
GO:0098780	response to mitochondrial depolarisation	13	0.277992278	0.0021	0.002780108
GO:0055123	digestive system development	35	0.277984924	< 0.001	< 0.001
GO:0009063	cellular amino acid catabolic process	39	0.277959278	0.0007	0.001063182
GO:0045930	negative regulation of mitotic cell cycle	130	0.277940798	0.0001	0.000192793
GO:0009135	purine nucleoside diphosphate metabolic process	55	0.277931438	< 0.001	< 0.001
GO:0009179	purine ribonucleoside diphosphate metabolic process	55	0.277931438	< 0.001	< 0.001
GO:0042278	purine nucleoside metabolic process	145	0.277770381	0.0001	0.000192793
GO:0003205	cardiac chamber development	69	0.277749799	< 0.001	< 0.001
GO:0050770	regulation of axonogenesis	87	0.277743754	0.0002	0.000356582
GO:0070646	protein modification by small protein removal	156	0.277687028	0.0001	0.000192793
GO:0051147	regulation of muscle cell differentiation	69	0.277663999	< 0.001	< 0.001
GO:1900542	regulation of purine nucleotide metabolic process	68	0.277647816	< 0.001	< 0.001
GO:0015908	fatty acid transport	31	0.277626936	< 0.001	< 0.001
GO:0036303	lymph vessel morphogenesis	8	0.277606178	0.009	0.010394529
GO:0043547	positive regulation of GTPase activity	146	0.277593836	< 0.001	< 0.001
GO:0031047	gene silencing by RNA	63	0.277567363	< 0.001	< 0.001
GO:0090075	relaxation of muscle	10	0.277554698	0.0002	0.000356582
GO:2000146	negative regulation of cell motility	115	0.277546864	< 0.001	< 0.001
GO:0048841	regulation of axon extension involved in axon guidance	8	0.277541828	< 0.001	< 0.001
GO:1900407	regulation of cellular response to oxidative stress	25	0.277539254	< 0.001	< 0.001
GO:0042100	B cell proliferation	17	0.277538042	< 0.001	< 0.001
GO:0038128	ERBB2 signaling pathway	17	0.277492619	< 0.001	< 0.001
GO:0055006	cardiac cell development	28	0.277459092	0.0001	0.000192793
GO:0001776	leukocyte homeostasis	28	0.277440706	0.0001	0.000192793
GO:0097178	ruffle assembly	19	0.277396193	< 0.001	< 0.001
GO:0046486	glycerolipid metabolic process	147	0.277395179	< 0.001	< 0.001
GO:1905475	regulation of protein localization to membrane	88	0.277389727	< 0.001	< 0.001
GO:0050878	regulation of body fluid levels	183	0.277352294	< 0.001	< 0.001
GO:0048260	positive regulation of receptor-mediated endocytosis	23	0.27733199	0.0006	0.000927725
GO:0009437	carnitine metabolic process	7	0.277330392	0.0016	0.002186748
GO:0090502	RNA phosphodiester bond hydrolysis, endonucleolytic	27	0.277315411	0.001	0.001450349
GO:0061097	regulation of protein tyrosine kinase activity	40	0.277297297	0.0001	0.000192793
GO:0003231	cardiac ventricle development	54	0.277291577	< 0.001	< 0.001
GO:0050851	antigen receptor-mediated signaling pathway	87	0.277225994	0.0001	0.000192793
GO:0036257	multivesicular body organization	17	0.277204936	0.0008	0.001193265
GO:0036258	multivesicular body assembly	17	0.277204936	0.0008	0.001193265
GO:0042110	T cell activation	142	0.277185636	< 0.001	< 0.001
GO:0070489	T cell aggregation	142	0.277185636	< 0.001	< 0.001
GO:0071593	lymphocyte aggregation	142	0.277185636	< 0.001	< 0.001
GO:0050863	regulation of T cell activation	93	0.277175793	< 0.001	< 0.001
GO:1902930	regulation of alcohol biosynthetic process	36	0.277170027	< 0.001	< 0.001
GO:0010959	regulation of metal ion transport	142	0.277158446	< 0.001	< 0.001
GO:0042692	muscle cell differentiation	135	0.277151437	< 0.001	< 0.001
GO:0071897	DNA biosynthetic process	80	0.277129987	0.0002	0.000356582
GO:0016570	histone modification	177	0.277129914	< 0.001	< 0.001
GO:0060560	developmental growth involved in morphogenesis	113	0.277119851	0.0001	0.000192793
GO:0046323	glucose import	25	0.277096525	0.0002	0.000356582
GO:0048568	embryonic organ development	126	0.277083206	< 0.001	< 0.001
GO:0006487	protein N-linked glycosylation	22	0.277079677	< 0.001	< 0.001
GO:0003015	heart process	105	0.27707054	< 0.001	< 0.001
GO:0097164	ammonium ion metabolic process	69	0.277067129	< 0.001	< 0.001
GO:0044273	sulfur compound catabolic process	16	0.277043115	0.0015	0.002069969
GO:2001026	regulation of endothelial cell chemotaxis	8	0.277027027	0.0015	0.002069969
GO:2001028	positive regulation of endothelial cell chemotaxis	8	0.277027027	0.0015	0.002069969
GO:1901989	positive regulation of cell cycle phase transition	35	0.276999448	0.0003	0.000505993

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0043616	keratinocyte proliferation	17	0.276947536	< 0.001	< 0.001
GO:1903319	positive regulation of protein maturation	8	0.276930502	0.0001	0.000192793
GO:0016569	covalent chromatin modification	180	0.276894037	< 0.001	< 0.001
GO:1903035	negative regulation of response to wounding	32	0.276874196	< 0.001	< 0.001
GO:0060119	inner ear receptor cell development	16	0.276850064	< 0.001	< 0.001
GO:0001835	blastocyst hatching	10	0.276833977	< 0.001	< 0.001
GO:0035188	hatching	10	0.276833977	< 0.001	< 0.001
GO:0071684	organism emergence from protective structure	10	0.276833977	< 0.001	< 0.001
GO:0099565	chemical synaptic transmission, postsynaptic	56	0.276815591	0.0028	0.003584743
GO:0043407	negative regulation of MAP kinase activity	34	0.276796124	0.0005	0.000791911
GO:0090313	regulation of protein targeting to membrane	20	0.276782497	< 0.001	< 0.001
GO:0050684	regulation of mRNA processing	39	0.276744877	< 0.001	< 0.001
GO:0034330	cell junction organization	107	0.27673655	< 0.001	< 0.001
GO:0060396	growth hormone receptor signaling pathway	13	0.276725077	0.0002	0.000356582
GO:0002792	negative regulation of peptide secretion	19	0.276718824	0.0019	0.00254969
GO:0090278	negative regulation of peptide hormone secretion	19	0.276718824	0.0019	0.00254969
GO:0034142	toll-like receptor 4 signaling pathway	16	0.276673102	< 0.001	< 0.001
GO:0046033	AMP metabolic process	6	0.276662377	0.0021	0.002780108
GO:0001659	temperature homeostasis	14	0.276631734	< 0.001	< 0.001
GO:1903599	positive regulation of mitophagy	7	0.276631734	0.0003	0.000505993
GO:0016441	posttranscriptional gene silencing	54	0.276609943	< 0.001	< 0.001
GO:0010524	positive regulation of calcium ion transport into cytosol	21	0.276545934	0.0021	0.002780108
GO:0030104	water homeostasis	28	0.276539805	< 0.001	< 0.001
GO:0009303	rRNA transcription	15	0.276533677	0.0002	0.000356582
GO:0002694	regulation of leukocyte activation	156	0.276528727	< 0.001	< 0.001
GO:1903725	regulation of phospholipid metabolic process	36	0.276512227	< 0.001	< 0.001
GO:0006004	fucose metabolic process	8	0.276512227	< 0.001	< 0.001
GO:0045088	regulation of innate immune response	159	0.276483492	< 0.001	< 0.001
GO:2000773	negative regulation of cellular senescence	9	0.276476476	0.0002	0.000356582
GO:0032011	ARF protein signal transduction	10	0.276473616	0.0053	0.006400268
GO:0032012	regulation of ARF protein signal transduction	10	0.276473616	0.0053	0.006400268
GO:0001101	response to acid chemical	121	0.276458513	< 0.001	< 0.001
GO:0032886	regulation of microtubule-based process	93	0.276398057	< 0.001	< 0.001
GO:0043434	response to peptide hormone	162	0.276370021	< 0.001	< 0.001
GO:0035265	organ growth	60	0.276336336	< 0.001	< 0.001
GO:0001508	action potential	48	0.276303089	0.0002	0.000356582
GO:0060348	bone development	67	0.27626347	< 0.001	< 0.001
GO:0048745	smooth muscle tissue development	5	0.276241956	0.0023	0.003013139
GO:0071248	cellular response to metal ion	70	0.276205185	< 0.001	< 0.001
GO:0045851	pH reduction	24	0.276179751	0.0002	0.000356582
GO:0001654	eye development	121	0.276147931	< 0.001	< 0.001
GO:0006937	regulation of muscle contraction	69	0.276119598	< 0.001	< 0.001
GO:0034762	regulation of transmembrane transport	183	0.276117335	0.0003	0.000505993
GO:0042921	glucocorticoid receptor signaling pathway	8	0.276093951	0.0008	0.001193265
GO:0042326	negative regulation of phosphorylation	192	0.276072501	< 0.001	< 0.001
GO:0046329	negative regulation of JNK cascade	19	0.276041455	0.0002	0.000356582
GO:0006260	DNA replication	107	0.276041328	0.0001	0.000192793
GO:0001954	positive regulation of cell-matrix adhesion	20	0.275997426	< 0.001	< 0.001
GO:0002285	lymphocyte activation involved in immune response	43	0.27595702	< 0.001	< 0.001
GO:1903037	regulation of leukocyte cell-cell adhesion	102	0.275940647	< 0.001	< 0.001
GO:0050771	negative regulation of axonogenesis	32	0.275868726	0.0013	0.001826625
GO:0006658	phosphatidylserine metabolic process	9	0.275847276	0.0003	0.000505993
GO:0002244	hematopoietic progenitor cell differentiation	68	0.27579302	0.0001	0.000192793
GO:1901990	regulation of mitotic cell cycle phase transition	190	0.275724446	0.0001	0.000192793
GO:0071326	cellular response to monosaccharide stimulus	58	0.275720055	< 0.001	< 0.001
GO:0071331	cellular response to hexose stimulus	58	0.275720055	< 0.001	< 0.001
GO:0071333	cellular response to glucose stimulus	58	0.275720055	< 0.001	< 0.001
GO:0007263	nitric oxide mediated signal transduction	10	0.275701416	< 0.001	< 0.001
GO:0070374	positive regulation of ERK1 and ERK2 cascade	75	0.275644788	< 0.001	< 0.001
GO:0030838	positive regulation of actin filament polymerization	39	0.275570076	0.0005	0.000791911
GO:0000423	macromitophagy	14	0.27552859	0.0007	0.001063182
GO:0003334	keratinocyte development	5	0.275521236	0.0036	0.004505419
GO:0060271	cilium assembly	151	0.275517144	< 0.001	< 0.001
GO:0072384	organelle transport along microtubule	42	0.275479561	0.0001	0.000192793
GO:0032535	regulation of cellular component size	164	0.275473208	< 0.001	< 0.001
GO:0071872	cellular response to epinephrine stimulus	5	0.275469755	< 0.001	< 0.001
GO:0042990	regulation of transcription factor import into nucleus	9	0.275446875	0.0003	0.000505993
GO:0042991	transcription factor import into nucleus	9	0.275446875	0.0003	0.000505993
GO:0042992	negative regulation of transcription factor import into nucleus	9	0.275446875	0.0003	0.000505993
GO:0042994	cytoplasmic sequestering of transcription factor	9	0.275446875	0.0003	0.000505993
GO:0042063	gliogenesis	100	0.275446589	< 0.001	< 0.001
GO:0061003	positive regulation of dendritic spine morphogenesis	11	0.275441675	0.0015	0.002069969
GO:0032784	regulation of DNA-templated transcription, elongation	17	0.275433417	0.0003	0.000505993
GO:0031099	regeneration	55	0.275408915	< 0.001	< 0.001
GO:1990778	protein localization to cell periphery	129	0.275388345	< 0.001	< 0.001
GO:0010721	negative regulation of cell development	132	0.275379275	< 0.001	< 0.001
GO:0042249	establishment of planar polarity of embryonic epithelium	5	0.275366795	0.0018	0.002428764
GO:0009126	purine nucleoside monophosphate metabolic process	117	0.275363275	0.0001	0.000192793
GO:0009167	purine ribonucleoside monophosphate metabolic process	117	0.275363275	0.0001	0.000192793
GO:0007605	sensory perception of sound	51	0.275362758	< 0.001	< 0.001
GO:1901652	response to peptide	192	0.275348563	< 0.001	< 0.001
GO:0032206	positive regulation of telomere maintenance	27	0.275294342	0.0001	0.000192793
GO:0051250	negative regulation of lymphocyte activation	35	0.275293252	0.0001	0.000192793

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0007286	spermatid development	39	0.275292875	< 0.001	< 0.001
GO:0051170	nuclear import	73	0.275273708	< 0.001	< 0.001
GO:0032845	negative regulation of homeostatic process	83	0.275272519	< 0.001	< 0.001
GO:0051782	negative regulation of cell division	5	0.275263835	0.0003	0.000505993
GO:0060766	negative regulation of androgen receptor signaling pathway	6	0.275246675	0.031	0.033048728
GO:0030111	regulation of Wnt signaling pathway	147	0.275239671	< 0.001	< 0.001
GO:0008299	isoprenoid biosynthetic process	8	0.275225225	0.0057	0.006849633
GO:0050890	cognition	143	0.275166275	0.0014	0.00194839
GO:0034333	adherens junction assembly	41	0.275160875	< 0.001	< 0.001
GO:0009259	ribonucleotide metabolic process	183	0.275124305	< 0.001	< 0.001
GO:0046928	regulation of neurotransmitter secretion	57	0.275106686	0.0075	0.008822377
GO:0002683	negative regulation of immune system process	138	0.275026579	< 0.001	< 0.001
GO:0002685	regulation of leukocyte migration	63	0.275013789	< 0.001	< 0.001
GO:0045475	locomotor rhythm	5	0.275006435	0.0155	0.017160828
GO:0046632	alpha-beta T cell differentiation	27	0.274998808	< 0.001	< 0.001
GO:0009651	response to salt stress	12	0.274989275	0.0002	0.000356582
GO:0006284	base-excision repair	16	0.274967825	0.0143	0.015940017
GO:0060563	neuroepithelial cell differentiation	19	0.274944117	< 0.001	< 0.001
GO:1902807	negative regulation of cell cycle G1/S phase transition	33	0.274942475	< 0.001	< 0.001
GO:0071241	cellular response to inorganic substance	78	0.274933175	< 0.001	< 0.001
GO:0038111	interleukin-7-mediated signaling pathway	8	0.274903475	< 0.001	< 0.001
GO:1902806	regulation of cell cycle G1/S phase transition	57	0.274903475	0.0001	0.000192793
GO:1900409	positive regulation of cellular response to oxidative stress	6	0.274903475	0.0009	0.001319479
GO:1903209	positive regulation of oxidative stress-induced cell death	6	0.274903475	0.0009	0.001319479
GO:0019362	pyridine nucleotide metabolic process	67	0.274895791	< 0.001	< 0.001
GO:0046496	nicotinamide nucleotide metabolic process	67	0.274895791	< 0.001	< 0.001
GO:0044782	cilium organization	152	0.274879767	< 0.001	< 0.001
GO:0072521	purine-containing compound metabolic process	192	0.2748713	< 0.001	< 0.001
GO:1902307	positive regulation of sodium ion transmembrane transport	10	0.274851995	< 0.001	< 0.001
GO:0051146	striated muscle cell differentiation	85	0.274848967	< 0.001	< 0.001
GO:0048515	spermatid differentiation	42	0.274829932	< 0.001	< 0.001
GO:0071396	cellular response to lipid	195	0.274822955	< 0.001	< 0.001
GO:0001933	negative regulation of protein phosphorylation	177	0.274820583	< 0.001	< 0.001
GO:0060070	canonical Wnt signaling pathway	132	0.274804025	< 0.001	< 0.001
GO:0007568	aging	127	0.274796056	< 0.001	< 0.001
GO:0007620	copulation	7	0.274793161	0.0012	0.001702047
GO:0045844	positive regulation of striated muscle tissue development	24	0.2747855	< 0.001	< 0.001
GO:0048636	positive regulation of muscle organ development	24	0.2747855	< 0.001	< 0.001
GO:1901863	positive regulation of muscle tissue development	24	0.2747855	< 0.001	< 0.001
GO:0007094	mitotic spindle assembly checkpoint	13	0.274764875	0.0018	0.002428764
GO:0031577	spindle checkpoint	13	0.274764875	0.0018	0.002428764
GO:0071173	spindle assembly checkpoint	13	0.274764875	0.0018	0.002428764
GO:0071174	mitotic spindle checkpoint	13	0.274764875	0.0018	0.002428764
GO:0043372	positive regulation of CD4-positive, alpha-beta T cell differentiation	5	0.274749035	< 0.001	< 0.001
GO:2000516	positive regulation of CD4-positive, alpha-beta T cell activation	5	0.274749035	< 0.001	< 0.001
GO:0045956	positive regulation of calcium ion-dependent exocytosis	16	0.2747426	0.018	0.019794872
GO:0010799	regulation of peptidyl-threonine phosphorylation	25	0.274728443	0.0003	0.000505993
GO:0031623	receptor internalization	41	0.274683743	< 0.001	< 0.001
GO:0002758	innate immune response-activating signal transduction	117	0.274650475	0.0001	0.000192793
GO:0019076	viral release from host cell	17	0.274646075	0.0006	0.000927725
GO:0035890	exit from host	17	0.274646075	0.0006	0.000927725
GO:0035891	exit from host cell	17	0.274646075	0.0006	0.000927725
GO:0052126	movement in host environment	17	0.274646075	0.0006	0.000927725
GO:0052192	movement in environment of other organism involved in symbiotic interaction	17	0.274646075	0.0006	0.000927725
GO:0009612	response to mechanical stimulus	64	0.274646075	< 0.001	< 0.001
GO:0070486	leukocyte aggregation	144	0.2746282	< 0.001	< 0.001
GO:0006816	calcium ion transport	154	0.27460596	< 0.001	< 0.001
GO:0042759	long-chain fatty acid biosynthetic process	6	0.274603175	0.0006	0.000927725
GO:1990138	neuron projection extension	91	0.274564046	0.0001	0.000192793
GO:0001937	negative regulation of endothelial cell proliferation	9	0.274560275	< 0.001	< 0.001
GO:0010522	regulation of calcium ion transport into cytosol	46	0.274550948	0.0011	0.001576346
GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	46	0.274545353	0.0007	0.001063182
GO:0015758	glucose transport	44	0.274540775	0.0001	0.000192793
GO:0022029	telencephalon cell migration	30	0.274508795	0.0009	0.001319479
GO:0021978	telencephalon regionalization	7	0.274498989	0.0001	0.000192793
GO:0042440	pigment metabolic process	29	0.274477433	< 0.001	< 0.001
GO:0006282	regulation of DNA repair	49	0.27446747	< 0.001	< 0.001
GO:0018022	peptidyl-lysine methylation	49	0.274462217	0.0002	0.000356582
GO:0030488	tRNA methylation	9	0.274445874	0.0004	0.000648934
GO:0032729	positive regulation of interferon-gamma production	17	0.274434098	< 0.001	< 0.001
GO:0007009	plasma membrane organization	143	0.274428274	< 0.001	< 0.001
GO:0045948	positive regulation of translational initiation	7	0.274425446	0.0002	0.000356582
GO:0034612	response to tumor necrosis factor	117	0.274395274	0.0001	0.000192793
GO:0050868	negative regulation of T cell activation	28	0.274351903	0.0001	0.000192793
GO:0021885	forebrain cell migration	33	0.274349674	0.0016	0.002186748
GO:0045913	positive regulation of carbohydrate metabolic process	34	0.274343251	< 0.001	< 0.001
GO:0032102	negative regulation of response to external stimulus	111	0.274337658	< 0.001	< 0.001
GO:0046112	nucleobase biosynthetic process	5	0.274337194	< 0.001	< 0.001
GO:0021772	olfactory bulb development	14	0.274315131	0.0449	0.046859714
GO:0021988	olfactory lobe development	14	0.274315131	0.0449	0.046859714
GO:0048520	positive regulation of behavior	13	0.274309474	0.0028	0.003584743
GO:0097193	intrinsic apoptotic signaling pathway	114	0.274300616	< 0.001	< 0.001
GO:0033209	tumor necrosis factor-mediated signaling pathway	81	0.274296519	0.0001	0.000192793

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0006399	tRNA metabolic process	71	0.274287164	0.0002	0.000356582
GO:0045165	cell fate commitment	71	0.274269038	< 0.001	< 0.001
GO:0019882	antigen processing and presentation	102	0.274267545	0.0002	0.000356582
GO:2000649	regulation of sodium ion transmembrane transporter activity	18	0.274259974	0.0024	0.003116943
GO:0051702	interaction with symbiont	28	0.274241589	< 0.001	< 0.001
GO:0030809	negative regulation of nucleotide biosynthetic process	8	0.274227799	0.0001	0.000192793
GO:1900372	negative regulation of purine nucleotide biosynthetic process	8	0.274227799	0.0001	0.000192793
GO:0009132	nucleoside diphosphate metabolic process	59	0.274196715	< 0.001	< 0.001
GO:0060491	regulation of cell projection assembly	75	0.274189618	< 0.001	< 0.001
GO:0031124	mRNA 3'-end processing	35	0.274182754	0.0014	0.00194839
GO:0010523	negative regulation of calcium ion transport into cytosol	10	0.274182754	0.0021	0.002780108
GO:0060416	response to growth hormone	18	0.274159874	< 0.001	< 0.001
GO:0031102	neuron projection regeneration	23	0.274153657	0.0011	0.001576346
GO:0007618	mating	19	0.274131274	0.0009	0.001319479
GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	40	0.274099099	< 0.001	< 0.001
GO:0071320	cellular response to cAMP	24	0.274088374	< 0.001	< 0.001
GO:1902476	chloride transmembrane transport	27	0.274074074	< 0.001	< 0.001
GO:0031589	cell-substrate adhesion	119	0.274072872	< 0.001	< 0.001
GO:0043010	camera-type eye development	105	0.274062634	< 0.001	< 0.001
GO:0051249	regulation of lymphocyte activation	127	0.27405831	< 0.001	< 0.001
GO:0048863	stem cell differentiation	98	0.274041972	< 0.001	< 0.001
GO:0045815	positive regulation of gene expression, epigenetic	22	0.274037674	0.0001	0.000192793
GO:0070838	divalent metal ion transport	160	0.273978443	< 0.001	< 0.001
GO:0072511	divalent inorganic cation transport	160	0.273978443	< 0.001	< 0.001
GO:0051052	regulation of DNA metabolic process	173	0.273972073	< 0.001	< 0.001
GO:2000736	regulation of stem cell differentiation	58	0.273936005	0.0004	0.000648934
GO:0050994	regulation of lipid catabolic process	17	0.273889015	< 0.001	< 0.001
GO:0071214	cellular response to abiotic stimulus	101	0.273871325	< 0.001	< 0.001
GO:0002706	regulation of lymphocyte mediated immunity	33	0.273866074	< 0.001	< 0.001
GO:0006814	sodium ion transport	67	0.273858507	< 0.001	< 0.001
GO:0030195	negative regulation of blood coagulation	18	0.273816674	< 0.001	< 0.001
GO:0050819	negative regulation of coagulation	18	0.273816674	< 0.001	< 0.001
GO:1900047	negative regulation of hemostasis	18	0.273816674	< 0.001	< 0.001
GO:0034765	regulation of ion transmembrane transport	175	0.273809156	0.0004	0.000648934
GO:0031647	regulation of protein stability	124	0.273801221	< 0.001	< 0.001
GO:0046209	nitric oxide metabolic process	25	0.27378121	< 0.001	< 0.001
GO:1990416	cellular response to brain-derived neurotrophic factor stimulus	5	0.273770914	0.0302	0.032240379
GO:0060419	heart growth	34	0.273730033	< 0.001	< 0.001
GO:0000266	mitochondrial fission	12	0.273702274	0.0008	0.001193265
GO:1904862	inhibitory synapse assembly	7	0.273616474	0.018	0.019794872
GO:0097106	postsynaptic density organization	13	0.273596674	0.0055	0.006618125
GO:0099084	postsynaptic specialization organization	13	0.273596674	0.0055	0.006618125
GO:0002082	regulation of oxidative phosphorylation	9	0.273559274	0.0006	0.000927725
GO:0001657	ureteric bud development	30	0.273539254	< 0.001	< 0.001
GO:0048545	response to steroid hormone	120	0.273522094	< 0.001	< 0.001
GO:0007059	chromosome segregation	108	0.27349254	< 0.001	< 0.001
GO:0030149	sphingolipid catabolic process	5	0.273462033	0.0025	0.003237479
GO:0002768	immune response-regulating cell surface receptor signaling pathway	145	0.273407003	< 0.001	< 0.001
GO:0033157	regulation of intracellular protein transport	122	0.27340549	< 0.001	< 0.001
GO:0042255	ribosome assembly	13	0.273398673	0.0022	0.002896881
GO:0007611	learning or memory	130	0.273370953	0.0017	0.00231289
GO:0090022	regulation of neutrophil chemotaxis	10	0.273359073	< 0.001	< 0.001
GO:1902622	regulation of neutrophil migration	10	0.273359073	< 0.001	< 0.001
GO:0009185	ribonucleoside diphosphate metabolic process	56	0.273313109	< 0.001	< 0.001
GO:0002757	immune response-activating signal transduction	184	0.273301718	< 0.001	< 0.001
GO:0046034	ATP metabolic process	105	0.273292885	0.0003	0.000505993
GO:0060047	heart contraction	103	0.273259112	< 0.001	< 0.001
GO:0051051	negative regulation of transport	192	0.273242439	< 0.001	< 0.001
GO:0001885	endothelial cell development	21	0.273236502	< 0.001	< 0.001
GO:1901657	glycosyl compound metabolic process	166	0.27322262	0.0001	0.000192793
GO:0045017	glycerolipid biosynthetic process	99	0.273164073	< 0.001	< 0.001
GO:1904646	cellular response to beta-amyloid	16	0.273149936	0.0001	0.000192793
GO:0002446	neutrophil mediated immunity	190	0.273149089	< 0.001	< 0.001
GO:0030278	regulation of ossification	73	0.273133407	< 0.001	< 0.001
GO:0009615	response to virus	113	0.273117618	< 0.001	< 0.001
GO:0010657	muscle cell apoptotic process	34	0.273116814	< 0.001	< 0.001
GO:0051271	negative regulation of cellular component movement	123	0.273116322	< 0.001	< 0.001
GO:1903531	negative regulation of secretion by cell	74	0.273115587	< 0.001	< 0.001
GO:0048565	digestive tract development	33	0.273093873	< 0.001	< 0.001
GO:0051591	response to cAMP	38	0.273081352	< 0.001	< 0.001
GO:0044057	regulation of system process	194	0.273080444	< 0.001	< 0.001
GO:0007189	adenylate cyclase-activating G-protein coupled receptor signaling pathway	25	0.273029601	< 0.001	< 0.001
GO:0002720	positive regulation of cytokine production involved in immune response	15	0.272981553	< 0.001	< 0.001
GO:0032846	positive regulation of homeostatic process	93	0.272974357	< 0.001	< 0.001
GO:0002283	neutrophil activation involved in immune response	185	0.272969495	< 0.001	< 0.001
GO:0043312	neutrophil degranulation	185	0.272969495	< 0.001	< 0.001
GO:0044827	modulation by host of viral genome replication	8	0.272940798	0.0001	0.000192793
GO:0071804	cellular potassium ion transport	56	0.272917816	0.0004	0.000648934
GO:0071805	potassium ion transmembrane transport	56	0.272917816	0.0004	0.000648934
GO:0002764	immune response-regulating signaling pathway	199	0.272905066	< 0.001	< 0.001
GO:0022406	membrane docking	82	0.272850551	< 0.001	< 0.001
GO:0010460	positive regulation of heart rate	8	0.272844273	0.0114	0.012893596
GO:0072350	tricarboxylic acid metabolic process	11	0.272820873	0.0005	0.000791911

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0051016	barbed-end actin filament capping	7	0.272807501	< 0.001	< 0.001
GO:0006336	DNA replication-independent nucleosome assembly	15	0.272792793	0.0203	0.022152908
GO:0034724	DNA replication-independent nucleosome organization	15	0.272792793	0.0203	0.022152908
GO:1903747	regulation of establishment of protein localization to mitochondrion	44	0.272774073	< 0.001	< 0.001
GO:0051607	defense response to virus	84	0.27277073	< 0.001	< 0.001
GO:0032722	positive regulation of chemokine production	20	0.272767053	< 0.001	< 0.001
GO:0046607	positive regulation of centrosome cycle	6	0.272758473	0.0083	0.009660392
GO:0030048	actin filament-based movement	51	0.272743332	< 0.001	< 0.001
GO:0098722	asymmetric stem cell division	7	0.272733958	0.0024	0.003116943
GO:0006644	phospholipid metabolic process	166	0.272678358	< 0.001	< 0.001
GO:0008654	phospholipid biosynthetic process	110	0.272675793	< 0.001	< 0.001
GO:0042491	auditory receptor cell differentiation	12	0.272672673	< 0.001	< 0.001
GO:0032925	regulation of activin receptor signaling pathway	10	0.272664093	< 0.001	< 0.001
GO:0060048	cardiac muscle contraction	53	0.272645152	< 0.001	< 0.001
GO:0031532	actin cytoskeleton reorganization	38	0.272634288	0.0001	0.000192793
GO:1901019	regulation of calcium ion transmembrane transporter activity	40	0.272631918	0.0008	0.001193265
GO:0002063	chondrocyte development	10	0.272612613	< 0.001	< 0.001
GO:0036474	cell death in response to hydrogen peroxide	12	0.272608323	< 0.001	< 0.001
GO:0060333	interferon-gamma-mediated signaling pathway	23	0.272598064	< 0.001	< 0.001
GO:0007159	leukocyte cell-cell adhesion	162	0.272597995	< 0.001	< 0.001
GO:0002090	regulation of receptor internalization	20	0.272561133	< 0.001	< 0.001
GO:0045648	positive regulation of erythrocyte differentiation	10	0.272561133	< 0.001	< 0.001
GO:0046165	alcohol biosynthetic process	60	0.272561133	< 0.001	< 0.001
GO:0050900	leukocyte migration	124	0.272539129	< 0.001	< 0.001
GO:0046434	organophosphate catabolic process	41	0.272517814	< 0.001	< 0.001
GO:0043046	DNA methylation involved in gamete generation	7	0.27251333	0.0211	0.022970266
GO:0048588	developmental cell growth	113	0.272498035	0.0001	0.000192793
GO:0015893	drug transport	7	0.272476558	< 0.001	< 0.001
GO:0033865	nucleoside bisphosphate metabolic process	13	0.272468072	< 0.001	< 0.001
GO:0033875	ribonucleoside bisphosphate metabolic process	13	0.272468072	< 0.001	< 0.001
GO:0034032	purine nucleoside bisphosphate metabolic process	13	0.272468072	< 0.001	< 0.001
GO:0003002	regionalization	112	0.272458172	0.0001	0.000192793
GO:0001678	cellular glucose homeostasis	64	0.272454151	< 0.001	< 0.001
GO:0009127	purine nucleoside monophosphate biosynthetic process	29	0.272409355	0.0001	0.000192793
GO:0009168	purine ribonucleoside monophosphate biosynthetic process	29	0.272409355	0.0001	0.000192793
GO:0002705	positive regulation of leukocyte mediated immunity	32	0.272401866	< 0.001	< 0.001
GO:1901685	glutathione derivative metabolic process	8	0.272393822	0.0097	0.01115531
GO:1901687	glutathione derivative biosynthetic process	8	0.272393822	0.0097	0.01115531
GO:0071679	commissural neuron axon guidance	6	0.272372372	0.0047	0.005730776
GO:0051091	positive regulation of sequence-specific DNA binding transcription factor activity	98	0.272360991	< 0.001	< 0.001
GO:0042886	amide transport	108	0.272355689	< 0.001	< 0.001
GO:0048562	embryonic organ morphogenesis	77	0.272322787	< 0.001	< 0.001
GO:0001503	ossification	140	0.272290862	< 0.001	< 0.001
GO:0019079	viral genome replication	48	0.272270485	< 0.001	< 0.001
GO:0048333	mesodermal cell differentiation	7	0.272255929	0.0001	0.000192793
GO:1903429	regulation of cell maturation	5	0.272226512	0.0026	0.003356522
GO:0061515	myeloid cell development	22	0.272200772	< 0.001	< 0.001
GO:0030325	adrenal gland development	6	0.272200772	0.0001	0.000192793
GO:0060323	head morphogenesis	10	0.272123552	< 0.001	< 0.001
GO:1900119	positive regulation of execution phase of apoptosis	7	0.272108844	0.0024	0.003116943
GO:0050931	pigment cell differentiation	13	0.272091872	< 0.001	< 0.001
GO:0002429	immune response-activating cell surface receptor signaling pathway	131	0.272089756	< 0.001	< 0.001
GO:0060602	branch elongation of an epithelium	5	0.272072072	< 0.001	< 0.001
GO:0000045	autophagosome assembly	38	0.272058525	0.0001	0.000192793
GO:0007423	sensory organ development	177	0.27205753	< 0.001	< 0.001
GO:0000079	regulation of cyclin-dependent protein serine/threonine kinase activity	36	0.272050622	< 0.001	< 0.001
GO:0032680	regulation of tumor necrosis factor production	45	0.272032032	< 0.001	< 0.001
GO:0071941	nitrogen cycle metabolic process	5	0.272020592	0.002	0.002664694
GO:0045089	positive regulation of innate immune response	138	0.272017981	< 0.001	< 0.001
GO:0051592	response to calcium ion	54	0.271914772	< 0.001	< 0.001
GO:0019693	ribose phosphate metabolic process	188	0.271891344	< 0.001	< 0.001
GO:0008645	hexose transport	45	0.271889032	0.0001	0.000192793
GO:0015749	monosaccharide transport	45	0.271889032	0.0001	0.000192793
GO:0097503	sialylation	9	0.271871872	0.0001	0.000192793
GO:0014745	negative regulation of muscle adaptation	5	0.271866152	0.0002	0.000356582
GO:1990173	protein localization to nucleoplasm	7	0.271851443	0.0029	0.003693519
GO:0032388	positive regulation of intracellular transport	107	0.271833917	< 0.001	< 0.001
GO:0033143	regulation of intracellular steroid hormone receptor signaling pathway	31	0.271756549	< 0.001	< 0.001
GO:0008585	female gonad development	26	0.271755272	0.0009	0.001319479
GO:0051491	positive regulation of filopodium assembly	17	0.271754107	0.0056	0.006732458
GO:0043470	regulation of carbohydrate catabolic process	31	0.271748246	< 0.001	< 0.001
GO:0003401	axis elongation	7	0.271704357	0.0002	0.000356582
GO:2000243	positive regulation of reproductive process	21	0.271679843	0.0009	0.001319479
GO:0007204	positive regulation of cytosolic calcium ion concentration	109	0.271677707	< 0.001	< 0.001
GO:0060046	regulation of acrosome reaction	5	0.271660232	0.0406	0.042635523
GO:1903320	regulation of protein modification by small protein conjugation or removal	121	0.271638108	< 0.001	< 0.001
GO:0048511	rhythmic process	131	0.271612288	0.0004	0.000648934
GO:0035904	aorta development	19	0.271611461	0.0007	0.001063182
GO:0006891	intra-Golgi vesicle-mediated transport	10	0.271608752	0.0004	0.000648934
GO:0002218	activation of innate immune response	127	0.271607941	0.0001	0.000192793
GO:0008406	gonad development	64	0.271529118	< 0.001	< 0.001
GO:0048525	negative regulation of viral process	30	0.271488631	< 0.001	< 0.001
GO:0001910	regulation of leukocyte mediated cytotoxicity	13	0.271458271	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0031145	anaphase-promoting complex-dependent catabolic process	54	0.271457171	0.0014	0.00194839
GO:0042176	regulation of protein catabolic process	169	0.271455225	< 0.001	< 0.001
GO:1903008	organelle disassembly	40	0.271435006	0.0001	0.000192793
GO:0050678	regulation of epithelial cell proliferation	118	0.271417665	< 0.001	< 0.001
GO:0009066	aspartate family amino acid metabolic process	18	0.271399971	0.0003	0.000505993
GO:0045879	negative regulation of smoothened signaling pathway	12	0.271342771	< 0.001	< 0.001
GO:0032688	negative regulation of interferon-beta production	6	0.271342771	0.0001	0.000192793
GO:0034695	response to prostaglandin E	13	0.271339471	< 0.001	< 0.001
GO:0051048	negative regulation of secretion	79	0.271280322	< 0.001	< 0.001
GO:0070911	global genome nucleotide-excision repair	13	0.271280071	0.0004	0.000648934
GO:0072337	modified amino acid transport	9	0.271271271	0.0048	0.005840847
GO:0003279	cardiac septum development	36	0.271264121	< 0.001	< 0.001
GO:0061138	morphogenesis of a branching epithelium	54	0.271261738	< 0.001	< 0.001
GO:0018345	protein palmitoylation	13	0.271240471	< 0.001	< 0.001
GO:0008334	histone mRNA metabolic process	12	0.271235521	0.0002	0.000356582
GO:1903364	positive regulation of cellular protein catabolic process	61	0.271228137	< 0.001	< 0.001
GO:0006479	protein methylation	75	0.271217503	< 0.001	< 0.001
GO:0008213	protein alkylation	75	0.271217503	< 0.001	< 0.001
GO:0045069	regulation of viral genome replication	34	0.271178742	< 0.001	< 0.001
GO:0070936	protein K48-linked ubiquitination	24	0.271128271	0.0004	0.000648934
GO:1904358	positive regulation of telomere maintenance via telomere lengthening	19	0.271123755	0.0005	0.000791911
GO:0009896	positive regulation of catabolic process	126	0.271099671	< 0.001	< 0.001
GO:0043620	regulation of DNA-templated transcription in response to stress	55	0.271065871	0.0016	0.002186748
GO:0010660	regulation of muscle cell apoptotic process	31	0.271050774	< 0.001	< 0.001
GO:0016322	neuron remodeling	7	0.270932157	0.0003	0.000505993
GO:0009636	response to toxic substance	65	0.270931591	< 0.001	< 0.001
GO:0070391	response to lipoteichoic acid	5	0.270888031	0.0001	0.000192793
GO:0071223	cellular response to lipoteichoic acid	5	0.270888031	0.0001	0.000192793
GO:1904019	epithelial cell apoptotic process	30	0.270862291	< 0.001	< 0.001
GO:0009116	nucleoside metabolic process	161	0.270833034	0.0001	0.000192793
GO:0050866	negative regulation of cell activation	56	0.270821842	< 0.001	< 0.001
GO:0002115	store-operated calcium entry	8	0.270785071	0.0005	0.000791911
GO:2001256	regulation of store-operated calcium entry	8	0.270785071	0.0005	0.000791911
GO:0007190	activation of adenylate cyclase activity	13	0.270785071	0.0053	0.006400268
GO:0003208	cardiac ventricle morphogenesis	33	0.270769471	< 0.001	< 0.001
GO:0032273	positive regulation of protein polymerization	52	0.270755371	0.0004	0.000648934
GO:0098727	maintenance of cell number	53	0.270751075	< 0.001	< 0.001
GO:0001779	natural killer cell differentiation	8	0.270720721	0.001	0.001450349
GO:0022602	ovulation cycle process	25	0.270702703	0.0055	0.006618125
GO:0043954	cellular component maintenance	32	0.270688546	< 0.001	< 0.001
GO:0045947	negative regulation of translational initiation	8	0.270688546	0.0002	0.000356582
GO:0086003	cardiac muscle cell contraction	24	0.270656371	0.0004	0.000648934
GO:2000179	positive regulation of neural precursor cell proliferation	17	0.2706488	0.0111	0.012593827
GO:0045137	development of primary sexual characteristics	67	0.270616032	< 0.001	< 0.001
GO:0001909	leukocyte mediated cytotoxicity	28	0.270582828	< 0.001	< 0.001
GO:0046322	negative regulation of fatty acid oxidation	6	0.270570571	0.0032	0.004042263
GO:0051260	protein homooligomerization	148	0.270546802	< 0.001	< 0.001
GO:1903522	regulation of blood circulation	111	0.270525352	< 0.001	< 0.001
GO:0048193	Golgi vesicle transport	152	0.270502269	0.0002	0.000356582
GO:1902513	regulation of organelle transport along microtubule	5	0.27047619	0.0088	0.010185307
GO:0042060	wound healing	180	0.27044902	< 0.001	< 0.001
GO:0009119	ribonucleoside metabolic process	150	0.270410982	0.0001	0.000192793
GO:0010508	positive regulation of autophagy	50	0.270409266	< 0.001	< 0.001
GO:0035601	protein deacylation	34	0.270406541	< 0.001	< 0.001
GO:0098732	macromolecule deacylation	34	0.270406541	< 0.001	< 0.001
GO:0071158	positive regulation of cell cycle arrest	28	0.270371392	0.0002	0.000356582
GO:0030516	regulation of axon extension	47	0.270363372	< 0.001	< 0.001
GO:0003073	regulation of systemic arterial blood pressure	24	0.270280995	< 0.001	< 0.001
GO:0045185	maintenance of protein location	38	0.270229628	< 0.001	< 0.001
GO:0046888	negative regulation of hormone secretion	26	0.27013167	0.0024	0.003116943
GO:0050727	regulation of inflammatory response	104	0.27013167	< 0.001	< 0.001
GO:0050805	negative regulation of synaptic transmission	32	0.270085264	0.0022	0.002896881
GO:0042119	neutrophil activation	188	0.27006079	< 0.001	< 0.001
GO:0003158	endothelium development	39	0.27004587	< 0.001	< 0.001
GO:0030210	heparin biosynthetic process	5	0.27001287	0.0007	0.001063182
GO:0046631	alpha-beta T cell activation	32	0.269964607	< 0.001	< 0.001
GO:0050768	negative regulation of neurogenesis	119	0.26996312	0.0001	0.000192793
GO:0043405	regulation of MAP kinase activity	142	0.269949426	< 0.001	< 0.001
GO:0000209	protein polyubiquitination	159	0.26992707	0.0002	0.000356582
GO:2001236	regulation of extrinsic apoptotic signaling pathway	43	0.269893149	< 0.001	< 0.001
GO:0010762	regulation of fibroblast migration	13	0.26987427	< 0.001	< 0.001
GO:0010675	regulation of cellular carbohydrate metabolic process	54	0.269860337	< 0.001	< 0.001
GO:0009161	ribonucleoside monophosphate metabolic process	125	0.269837838	0.0003	0.000505993
GO:0008544	epidermis development	111	0.269834313	< 0.001	< 0.001
GO:0042987	amyloid precursor protein catabolic process	21	0.269829013	< 0.001	< 0.001
GO:0021700	developmental maturation	100	0.269801802	< 0.001	< 0.001
GO:0033002	muscle cell proliferation	70	0.269795918	< 0.001	< 0.001
GO:0070371	ERK1 and ERK2 cascade	113	0.269730413	< 0.001	< 0.001
GO:0032869	cellular response to insulin stimulus	80	0.269697555	< 0.001	< 0.001
GO:0032635	interleukin-6 production	41	0.269655021	< 0.001	< 0.001
GO:0046545	development of primary female sexual characteristics	29	0.269622332	0.0011	0.001576346
GO:0007638	mechanosensory behavior	5	0.26960103	0.0123	0.013827585
GO:0031223	auditory behavior	5	0.26960103	0.0123	0.013827585

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0072524	pyridine-containing compound metabolic process	71	0.269559701	< 0.001	< 0.001
GO:0008356	asymmetric cell division	10	0.26954955	0.0037	0.004617737
GO:0002064	epithelial cell development	66	0.26950977	< 0.001	< 0.001
GO:0018026	peptidyl-lysine monomethylation	5	0.269446589	0.0016	0.002186748
GO:1901838	positive regulation of transcription of nuclear large rRNA transcript from RNA polymerase I promoter	5	0.269446589	0.032	0.034034245
GO:0043618	regulation of transcription from RNA polymerase II promoter in response to stress	53	0.269405794	0.0021	0.002780108
GO:0060149	negative regulation of posttranscriptional gene silencing	6	0.269369369	0.0024	0.003116943
GO:0060965	negative regulation of gene silencing by miRNA	6	0.269369369	0.0024	0.003116943
GO:0060967	negative regulation of gene silencing by RNA	6	0.269369369	0.0024	0.003116943
GO:0010817	regulation of hormone levels	163	0.269322785	< 0.001	< 0.001
GO:0030501	positive regulation of bone mineralization	18	0.269312169	< 0.001	< 0.001
GO:0045931	positive regulation of mitotic cell cycle	58	0.269307238	< 0.001	< 0.001
GO:0006921	cellular component disassembly involved in execution phase of apoptosis	12	0.269283569	0.0011	0.001576346
GO:0030262	apoptotic nuclear changes	12	0.269283569	0.0011	0.001576346
GO:0072176	nephric duct development	7	0.269277441	0.0001	0.000192793
GO:0071356	cellular response to tumor necrosis factor	108	0.269259736	0.0001	0.000192793
GO:0038093	Fc receptor signaling pathway	102	0.269255581	0.0001	0.000192793
GO:0043112	receptor metabolic process	77	0.269223955	< 0.001	< 0.001
GO:0051090	regulation of sequence-specific DNA binding transcription factor activity	162	0.269202536	< 0.001	< 0.001
GO:0007219	Notch signaling pathway	62	0.269186698	< 0.001	< 0.001
GO:0042407	cristae formation	14	0.269185512	0.0071	0.008390203
GO:0060079	excitatory postsynaptic potential	53	0.269133824	0.0026	0.003356522
GO:0019827	stem cell population maintenance	52	0.269131769	< 0.001	< 0.001
GO:0018158	protein oxidation	6	0.269111969	0.0002	0.000356582
GO:1904350	regulation of protein catabolic process in the vacuole	5	0.269086229	0.0093	0.010727257
GO:0001975	response to amphetamine	16	0.269079794	< 0.001	< 0.001
GO:0043687	post-translational protein modification	182	0.269061055	< 0.001	< 0.001
GO:0048645	animal organ formation	18	0.269054769	< 0.001	< 0.001
GO:0032259	methylation	126	0.269040469	< 0.001	< 0.001
GO:0002221	pattern recognition receptor signaling pathway	69	0.269028034	< 0.001	< 0.001
GO:0046599	regulation of centriole replication	9	0.268954669	< 0.001	< 0.001
GO:0051209	release of sequestered calcium ion into cytosol	49	0.268951751	0.0007	0.001063182
GO:0051282	regulation of sequestering of calcium ion	49	0.268951751	0.0007	0.001063182
GO:0051283	negative regulation of sequestering of calcium ion	49	0.268951751	0.0007	0.001063182
GO:0042391	regulation of membrane potential	160	0.268933398	0.0002	0.000356582
GO:0030308	negative regulation of cell growth	70	0.268924435	< 0.001	< 0.001
GO:0045933	positive regulation of muscle contraction	17	0.268892422	< 0.001	< 0.001
GO:2000045	regulation of G1/S transition of mitotic cell cycle	52	0.268824869	0.0003	0.000505993
GO:0008016	regulation of heart contraction	92	0.268795814	< 0.001	< 0.001
GO:0036230	granulocyte activation	191	0.268685439	< 0.001	< 0.001
GO:0009948	anterior/posterior axis specification	12	0.268682969	0.0001	0.000192793
GO:0035637	multicellular organismal signaling	72	0.268665094	0.0001	0.000192793
GO:0051443	positive regulation of ubiquitin-protein transferase activity	15	0.268657229	0.0004	0.000648934
GO:0031638	zymogen activation	16	0.268613256	< 0.001	< 0.001
GO:0000381	regulation of alternative mRNA splicing, via spliceosome	20	0.268584299	0.0001	0.000192793
GO:0010543	regulation of platelet activation	14	0.268578783	0.0001	0.000192793
GO:0001919	regulation of receptor recycling	9	0.268554269	0.0009	0.001319479
GO:0006400	tRNA modification	27	0.268535202	0.0001	0.000192793
GO:0043950	positive regulation of cAMP-mediated signaling	6	0.268511369	0.0074	0.008712331
GO:0048024	regulation of mRNA splicing, via spliceosome	29	0.268503972	< 0.001	< 0.001
GO:0002360	T cell lineage commitment	5	0.268468468	0.0025	0.003237479
GO:0061045	negative regulation of wound healing	26	0.268458568	< 0.001	< 0.001
GO:0000768	syncytium formation by plasma membrane fusion	15	0.268434148	0.0173	0.01905998
GO:0040029	regulation of gene expression, epigenetic	113	0.26840241	0.0002	0.000356582
GO:0008347	glial cell migration	26	0.268399168	< 0.001	< 0.001
GO:0045821	positive regulation of glycolytic process	10	0.268365508	0.0103	0.011785137
GO:0051194	positive regulation of cofactor metabolic process	10	0.268365508	0.0103	0.011785137
GO:0051197	positive regulation of coenzyme metabolic process	10	0.268365508	0.0103	0.011785137
GO:0098876	vesicle-mediated transport to the plasma membrane	33	0.268351468	0.0002	0.000356582
GO:0051279	regulation of release of sequestered calcium ion into cytosol	38	0.268346542	0.003	0.003811001
GO:0021670	lateral ventricle development	6	0.268339768	0.039	0.041027059
GO:0033146	regulation of intracellular estrogen receptor signaling pathway	17	0.268317057	< 0.001	< 0.001
GO:0008643	carbohydrate transport	54	0.268311168	< 0.001	< 0.001
GO:0009164	nucleoside catabolic process	11	0.268304668	0.0005	0.000791911
GO:0045777	positive regulation of blood pressure	10	0.268288288	< 0.001	< 0.001
GO:0006520	cellular amino acid metabolic process	145	0.268282075	0.0001	0.000192793
GO:0003206	cardiac chamber morphogenesis	55	0.268271908	< 0.001	< 0.001
GO:0060561	apoptotic process involved in morphogenesis	7	0.26824784	0.0007	0.001063182
GO:0000226	microtubule cytoskeleton organization	200	0.268227799	< 0.001	< 0.001
GO:0045785	positive regulation of cell adhesion	138	0.268151381	< 0.001	< 0.001
GO:0034205	beta-amyloid formation	15	0.268142428	0.0001	0.000192793
GO:0048738	cardiac muscle tissue development	75	0.268121836	< 0.001	< 0.001
GO:1902808	positive regulation of cell cycle G1/S phase transition	17	0.26810508	0.0021	0.002780108
GO:0032956	regulation of actin cytoskeleton organization	139	0.268098108	< 0.001	< 0.001
GO:1990823	response to leukemia inhibitory factor	38	0.268089142	< 0.001	< 0.001
GO:1990830	cellular response to leukemia inhibitory factor	38	0.268089142	< 0.001	< 0.001
GO:0031396	regulation of protein ubiquitination	109	0.268074103	0.0001	0.000192793
GO:1901607	alpha-amino acid biosynthetic process	26	0.268052668	< 0.001	< 0.001
GO:0043368	positive T cell selection	8	0.268050193	0.0123	0.013827585
GO:0038065	collagen-activated signaling pathway	5	0.268005148	< 0.001	< 0.001
GO:0009743	response to carbohydrate	89	0.267930531	< 0.001	< 0.001
GO:0002220	innate immune response activating cell surface receptor signaling pathway	56	0.267861739	0.0004	0.000648934
GO:0002223	stimulatory C-type lectin receptor signaling pathway	56	0.267861739	0.0004	0.000648934

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0051013	microtubule severing	5	0.267850708	< 0.001	< 0.001
GO:0044242	cellular lipid catabolic process	55	0.267836668	< 0.001	< 0.001
GO:0009746	response to hexose	76	0.267818194	< 0.001	< 0.001
GO:0030808	regulation of nucleotide biosynthetic process	32	0.267816924	0.0001	0.000192793
GO:1900371	regulation of purine nucleotide biosynthetic process	32	0.267816924	0.0001	0.000192793
GO:0016571	histone methylation	56	0.267815775	0.0003	0.000505993
GO:0006476	protein deacetylation	33	0.267805468	< 0.001	< 0.001
GO:0002065	columnar/cuboidal epithelial cell differentiation	36	0.267803518	< 0.001	< 0.001
GO:0071887	leukocyte apoptotic process	29	0.267793902	< 0.001	< 0.001
GO:0048598	embryonic morphogenesis	184	0.267756421	< 0.001	< 0.001
GO:0051216	cartilage development	65	0.267739828	< 0.001	< 0.001
GO:0031663	lipopolysaccharide-mediated signaling pathway	27	0.267724868	< 0.001	< 0.001
GO:0046660	female sex differentiation	33	0.267719668	0.0012	0.001702047
GO:0051983	regulation of chromosome segregation	39	0.267709468	0.0001	0.000192793
GO:0051054	positive regulation of DNA metabolic process	106	0.267708409	< 0.001	< 0.001
GO:0051153	regulation of striated muscle cell differentiation	34	0.267696268	< 0.001	< 0.001
GO:0045920	negative regulation of exocytosis	15	0.267679108	< 0.001	< 0.001
GO:2001020	regulation of response to DNA damage stimulus	85	0.267665985	< 0.001	< 0.001
GO:0060326	cell chemotaxis	79	0.267653911	< 0.001	< 0.001
GO:0007422	peripheral nervous system development	23	0.267651502	0.0009	0.001319479
GO:0042594	response to starvation	72	0.267546118	< 0.001	< 0.001
GO:1904668	positive regulation of ubiquitin protein ligase activity	6	0.267524668	0.0003	0.000505993
GO:0031103	axon regeneration	19	0.267520152	0.0015	0.002069969
GO:0001945	lymph vessel development	11	0.267509068	0.0028	0.003584743
GO:0050808	synapse organization	179	0.267497825	0.0003	0.000505993
GO:0030850	prostate gland development	15	0.267438867	< 0.001	< 0.001
GO:0045717	negative regulation of fatty acid biosynthetic process	7	0.267438867	< 0.001	< 0.001
GO:0006099	tricarboxylic acid cycle	6	0.267353067	0.015	0.016665296
GO:1905269	positive regulation of chromatin organization	37	0.267313646	0.0007	0.001063182
GO:0071397	cellular response to cholesterol	8	0.267310167	< 0.001	< 0.001
GO:0043433	negative regulation of sequence-specific DNA binding transcription factor activity	60	0.267267267	< 0.001	< 0.001
GO:2000273	positive regulation of receptor activity	24	0.267235092	0.0003	0.000505993
GO:0031294	lymphocyte costimulation	21	0.267156953	< 0.001	< 0.001
GO:0031295	T cell costimulation	21	0.267156953	< 0.001	< 0.001
GO:0050774	negative regulation of dendrite morphogenesis	10	0.267155727	0.0019	0.00254969
GO:0006991	response to sterol depletion	6	0.267138567	< 0.001	< 0.001
GO:0035329	hippo signaling	11	0.267111267	< 0.001	< 0.001
GO:0006469	negative regulation of protein kinase activity	99	0.267095667	< 0.001	< 0.001
GO:1902224	ketone body metabolic process	5	0.267078507	0.0043	0.005276385
GO:0051900	regulation of mitochondrial depolarization	6	0.267052767	0.0001	0.000192793
GO:0051384	response to glucocorticoid	46	0.267047171	< 0.001	< 0.001
GO:0050709	negative regulation of protein secretion	49	0.266960838	< 0.001	< 0.001
GO:0072163	mesonephric epithelium development	31	0.266924067	< 0.001	< 0.001
GO:0072164	mesonephric tubule development	31	0.266924067	< 0.001	< 0.001
GO:0040013	negative regulation of locomotion	131	0.266843507	< 0.001	< 0.001
GO:0090316	positive regulation of intracellular protein transport	78	0.266841567	< 0.001	< 0.001
GO:0035315	hair cell differentiation	13	0.266825067	< 0.001	< 0.001
GO:0038202	TORC1 signaling	21	0.266813753	< 0.001	< 0.001
GO:0007616	long-term memory	16	0.266811454	0.0113	0.012793882
GO:2000108	positive regulation of leukocyte apoptotic process	9	0.266809667	< 0.001	< 0.001
GO:0016525	negative regulation of angiogenesis	36	0.266788217	< 0.001	< 0.001
GO:2000181	negative regulation of blood vessel morphogenesis	36	0.266788217	< 0.001	< 0.001
GO:0060236	regulation of mitotic spindle organization	17	0.266787796	0.0017	0.00231289
GO:1903322	positive regulation of protein modification by small protein conjugation or removal	73	0.266772448	< 0.001	< 0.001
GO:0043331	response to dsRNA	32	0.266771236	< 0.001	< 0.001
GO:0033120	positive regulation of RNA splicing	12	0.266752467	0.0003	0.000505993
GO:1901532	regulation of hematopoietic progenitor cell differentiation	48	0.266725654	0.0011	0.001576346
GO:0060401	cytosolic calcium ion transport	70	0.266699761	0.0004	0.000648934
GO:0010469	regulation of receptor activity	197	0.266698025	< 0.001	< 0.001
GO:0006625	protein targeting to peroxisome	32	0.266690798	0.0004	0.000648934
GO:0043574	peroxisomal transport	32	0.266690798	0.0004	0.000648934
GO:0072662	protein localization to peroxisome	32	0.266690798	0.0004	0.000648934
GO:0072663	establishment of protein localization to peroxisome	32	0.266690798	0.0004	0.000648934
GO:2001032	regulation of double-strand break repair via nonhomologous end joining	7	0.266666667	0.0024	0.003116943
GO:0043414	macromolecule methylation	108	0.266638067	< 0.001	< 0.001
GO:0030851	granulocyte differentiation	12	0.266623767	< 0.001	< 0.001
GO:0032042	mitochondrial DNA metabolic process	5	0.266615187	0.0168	0.018543137
GO:0007131	reciprocal meiotic recombination	9	0.266609467	0.0004	0.000648934
GO:0035825	reciprocal DNA recombination	9	0.266609467	0.0004	0.000648934
GO:0070266	necroptotic process	9	0.266609467	0.0018	0.002428764
GO:0032970	regulation of actin filament-based process	153	0.266584231	< 0.001	< 0.001
GO:0009069	serine family amino acid metabolic process	16	0.266554054	0.0002	0.000356582
GO:0006954	inflammatory response	191	0.266541336	< 0.001	< 0.001
GO:0070286	axonemal dynein complex assembly	10	0.266435006	0.0408	0.042837226
GO:0030217	T cell differentiation	66	0.266381966	< 0.001	< 0.001
GO:0030500	regulation of bone mineralization	25	0.266357786	< 0.001	< 0.001
GO:0071243	cellular response to arsenic-containing substance	8	0.266312741	< 0.001	< 0.001
GO:0034284	response to monosaccharide	77	0.266278895	< 0.001	< 0.001
GO:0007566	embryo implantation	17	0.266272996	0.0001	0.000192793
GO:0006337	nucleosome disassembly	7	0.266262181	0.0316	0.033622052
GO:0072089	stem cell proliferation	38	0.266260245	0.0008	0.001193265
GO:0007416	synapse assembly	92	0.266252588	0.001	0.001450349
GO:0051262	protein tetramerization	54	0.2662472	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1903900	regulation of viral life cycle	74	0.266190128	0.0003	0.000505993
GO:0090314	positive regulation of protein targeting to membrane	17	0.266151866	< 0.001	< 0.001
GO:0060113	inner ear receptor cell differentiation	19	0.266138319	< 0.001	< 0.001
GO:0006109	regulation of carbohydrate metabolic process	79	0.266129059	< 0.001	< 0.001
GO:0043279	response to alkaloid	59	0.2660777	< 0.001	< 0.001
GO:0007218	neuropeptide signaling pathway	33	0.266050466	0.0004	0.000648934
GO:0090224	regulation of spindle organization	18	0.266037466	0.001	0.001450349
GO:0009123	nucleoside monophosphate metabolic process	131	0.266030043	0.0002	0.000356582
GO:0043270	positive regulation of ion transport	105	0.266024392	< 0.001	< 0.001
GO:0043271	negative regulation of ion transport	49	0.266010033	< 0.001	< 0.001
GO:0071901	negative regulation of protein serine/threonine kinase activity	58	0.2659921	< 0.001	< 0.001
GO:0002708	positive regulation of lymphocyte mediated immunity	24	0.265980266	0.0001	0.000192793
GO:0043457	regulation of cellular respiration	12	0.265958816	0.0001	0.000192793
GO:0031629	synaptic vesicle fusion to presynaptic active zone membrane	5	0.265945946	0.0388	0.040832561
GO:0099500	vesicle fusion to plasma membrane	5	0.265945946	0.0388	0.040832561
GO:0098754	detoxification	36	0.265930216	< 0.001	< 0.001
GO:0051480	regulation of cytosolic calcium ion concentration	118	0.265916279	< 0.001	< 0.001
GO:0006415	translational termination	48	0.265830116	0.0009	0.001319479
GO:0071230	cellular response to amino acid stimulus	33	0.265816466	< 0.001	< 0.001
GO:0051098	regulation of binding	157	0.265789538	< 0.001	< 0.001
GO:0010043	response to zinc ion	14	0.265784151	0.0013	0.001826625
GO:0045830	positive regulation of isotype switching	11	0.265777466	0.0059	0.007066401
GO:1902305	regulation of sodium ion transmembrane transport	24	0.265776491	0.001	0.001450349
GO:0032506	cytokinetic process	14	0.265765766	0.0005	0.000791911
GO:0034315	regulation of Arp2/3 complex-mediated actin nucleation	8	0.265765766	0.014	0.015631405
GO:0045066	regulatory T cell differentiation	7	0.26574738	0.001	0.001450349
GO:1901030	positive regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	18	0.265694266	0.0023	0.003013139
GO:0019068	virion assembly	20	0.265649936	0.0016	0.002186748
GO:0014013	regulation of gliogenesis	43	0.26563108	< 0.001	< 0.001
GO:0006898	receptor-mediated endocytosis	111	0.265588368	< 0.001	< 0.001
GO:0055067	monovalent inorganic cation homeostasis	45	0.265545546	< 0.001	< 0.001
GO:0032481	positive regulation of type I interferon production	35	0.265526751	0.0002	0.000356582
GO:0071398	cellular response to fatty acid	23	0.265525152	< 0.001	< 0.001
GO:0051208	sequestering of calcium ion	51	0.265510889	0.0005	0.000791911
GO:0033044	regulation of chromosome organization	73	0.265404348	0.0003	0.000505993
GO:0009749	response to glucose	74	0.265390101	< 0.001	< 0.001
GO:0010035	response to inorganic substance	189	0.26536877	< 0.001	< 0.001
GO:1901654	response to ketone	68	0.265353168	< 0.001	< 0.001
GO:0046475	glycerophospholipid catabolic process	6	0.265336765	0.0002	0.000356582
GO:0046321	positive regulation of fatty acid oxidation	6	0.265336765	0.0072	0.008495371
GO:0007031	peroxisome organization	38	0.265318702	0.0004	0.000648934
GO:0042269	regulation of natural killer cell mediated cytotoxicity	7	0.26523258	< 0.001	< 0.001
GO:0042726	flavin-containing compound metabolic process	5	0.265173745	0.0287	0.030748374
GO:0010212	response to ionizing radiation	63	0.265167208	0.0001	0.000192793
GO:0098900	regulation of action potential	22	0.265157365	0.0002	0.000356582
GO:0016458	gene silencing	85	0.265140435	0.0002	0.000356582
GO:0010506	regulation of autophagy	150	0.265110253	< 0.001	< 0.001
GO:2000725	regulation of cardiac muscle cell differentiation	16	0.265057915	0.0001	0.000192793
GO:0042451	purine nucleoside biosynthetic process	36	0.265057915	0.0002	0.000356582
GO:0046129	purine ribonucleoside biosynthetic process	36	0.265057915	0.0002	0.000356582
GO:0042490	mechanoreceptor differentiation	21	0.265024208	< 0.001	< 0.001
GO:0048167	regulation of synaptic plasticity	100	0.265006435	0.0072	0.008495371
GO:0030902	hindbrain development	47	0.26498535	< 0.001	< 0.001
GO:0001701	in utero embryonic development	130	0.264940105	< 0.001	< 0.001
GO:0006470	protein dephosphorylation	166	0.264936193	< 0.001	< 0.001
GO:0031529	ruffle organization	24	0.264929215	< 0.001	< 0.001
GO:0071902	positive regulation of protein serine/threonine kinase activity	144	0.26492564	< 0.001	< 0.001
GO:0032640	tumor necrosis factor production	47	0.264903201	< 0.001	< 0.001
GO:2000021	regulation of ion homeostasis	75	0.264895753	< 0.001	< 0.001
GO:2000514	regulation of CD4-positive, alpha-beta T cell activation	13	0.264884665	0.0001	0.000192793
GO:0016266	O-glycan processing	14	0.264846479	< 0.001	< 0.001
GO:0051225	spindle assembly	35	0.264813385	< 0.001	< 0.001
GO:0036297	interstrand cross-link repair	24	0.26474689	0.0016	0.002186748
GO:0010769	regulation of cell morphogenesis involved in differentiation	144	0.264707565	0.0002	0.000356582
GO:0010631	epithelial cell migration	116	0.264698442	< 0.001	< 0.001
GO:0090130	tissue migration	116	0.264698442	< 0.001	< 0.001
GO:0090132	epithelium migration	116	0.264698442	< 0.001	< 0.001
GO:0019395	fatty acid oxidation	33	0.264677665	< 0.001	< 0.001
GO:0032355	response to estradiol	41	0.264663967	< 0.001	< 0.001
GO:0070125	mitochondrial translational elongation	41	0.264638855	0.0007	0.001063182
GO:0070126	mitochondrial translational termination	41	0.264638855	0.0007	0.001063182
GO:0032212	positive regulation of telomere maintenance via telomerase	18	0.264636065	0.0005	0.000791911
GO:2000648	positive regulation of stem cell proliferation	11	0.264607465	0.0272	0.029199205
GO:0048846	axon extension involved in axon guidance	13	0.264607465	0.0001	0.000192793
GO:1902284	neuron projection extension involved in neuron projection guidance	13	0.264607465	0.0001	0.000192793
GO:0001755	neural crest cell migration	11	0.264584065	< 0.001	< 0.001
GO:1902165	regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	9	0.264578865	0.0475	0.049449046
GO:0031123	RNA 3'-end processing	41	0.264576074	0.0006	0.000927725
GO:0043583	ear development	71	0.26456396	< 0.001	< 0.001
GO:0036294	cellular response to decreased oxygen levels	94	0.26454996	0.0003	0.000505993
GO:0017038	protein import	75	0.264545689	0.0001	0.000192793
GO:0010544	negative regulation of platelet activation	9	0.264521665	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0006997	nucleus organization	55	0.264518545	< 0.001	< 0.001
GO:2001259	positive regulation of cation channel activity	25	0.264442728	0.0004	0.000648934
GO:0007548	sex differentiation	80	0.264440154	< 0.001	< 0.001
GO:0051238	sequestering of metal ion	54	0.264435864	0.0005	0.000791911
GO:0021681	cerebellar granular layer development	6	0.264392964	< 0.001	< 0.001
GO:0033081	regulation of T cell differentiation in thymus	9	0.264378664	0.0076	0.008916717
GO:2000398	regulation of thymocyte aggregation	9	0.264378664	0.0076	0.008916717
GO:0045839	negative regulation of mitotic nuclear division	21	0.264350064	0.0001	0.000192793
GO:0051784	negative regulation of nuclear division	21	0.264350064	0.0001	0.000192793
GO:1904064	positive regulation of cation transmembrane transport	48	0.264317889	0.0004	0.000648934
GO:0030514	negative regulation of BMP signaling pathway	12	0.264264264	0.0041	0.005057384
GO:0061448	connective tissue development	81	0.26421342	< 0.001	< 0.001
GO:0043248	proteasome assembly	9	0.264207064	0.0046	0.0056228
GO:0050711	negative regulation of interleukin-1 secretion	5	0.264144144	0.0104	0.011884458
GO:0050713	negative regulation of interleukin-1 beta secretion	5	0.264144144	0.0104	0.011884458
GO:0031664	regulation of lipopolysaccharide-mediated signaling pathway	12	0.264135564	< 0.001	< 0.001
GO:0071453	cellular response to oxygen levels	103	0.264095163	0.0003	0.000505993
GO:0010165	response to X-ray	11	0.264092664	0.006	0.007178216
GO:1901606	alpha-amino acid catabolic process	34	0.264085093	0.0008	0.001193265
GO:1901888	regulation of cell junction assembly	37	0.264030053	< 0.001	< 0.001
GO:0007389	pattern specification process	141	0.264021468	< 0.001	< 0.001
GO:0048387	negative regulation of retinoic acid receptor signaling pathway	5	0.263989704	< 0.001	< 0.001
GO:0050732	negative regulation of peptidyl-tyrosine phosphorylation	17	0.263971535	0.0012	0.001702047
GO:0051851	modification by host of symbiont morphology or physiology	26	0.263963964	< 0.001	< 0.001
GO:0048839	inner ear development	59	0.263944332	< 0.001	< 0.001
GO:0036475	neuron death in response to oxidative stress	12	0.263942514	< 0.001	< 0.001
GO:0048485	sympathetic nervous system development	6	0.263921064	0.0265	0.028498706
GO:0030282	bone mineralization	40	0.263873874	< 0.001	< 0.001
GO:1903902	positive regulation of viral life cycle	49	0.263866782	0.0009	0.001319479
GO:0034504	protein localization to nucleus	107	0.263866537	< 0.001	< 0.001
GO:0030258	lipid modification	74	0.26382135	< 0.001	< 0.001
GO:0001504	neurotransmitter uptake	17	0.263774699	0.0005	0.000791911
GO:0072073	kidney epithelium development	44	0.263753364	< 0.001	< 0.001
GO:0007173	epidermal growth factor receptor signaling pathway	49	0.263751215	< 0.001	< 0.001
GO:0010823	negative regulation of mitochondrion organization	24	0.263738739	0.0001	0.000192793
GO:0010812	negative regulation of cell-substrate adhesion	22	0.263729964	< 0.001	< 0.001
GO:0001895	retina homeostasis	22	0.263718264	< 0.001	< 0.001
GO:0038127	ERBB signaling pathway	64	0.263690476	< 0.001	< 0.001
GO:0061387	regulation of extent of cell growth	51	0.263628334	< 0.001	< 0.001
GO:0007158	neuron cell-cell adhesion	11	0.263601264	0.0212	0.023069835
GO:0060148	positive regulation of posttranscriptional gene silencing	11	0.263577864	< 0.001	< 0.001
GO:1904036	negative regulation of epithelial cell apoptotic process	9	0.263577864	0.0004	0.000648934
GO:0002456	T cell mediated immunity	20	0.263564994	0.0001	0.000192793
GO:0007126	meiotic nuclear division	48	0.263556414	< 0.001	< 0.001
GO:0007050	cell cycle arrest	99	0.263546664	< 0.001	< 0.001
GO:1903046	meiotic cell cycle process	52	0.263538264	< 0.001	< 0.001
GO:0008631	intrinsic apoptotic signaling pathway in response to oxidative stress	21	0.263528835	0.0001	0.000192793
GO:0050792	regulation of viral process	79	0.263483375	0.0003	0.000505993
GO:0071456	cellular response to hypoxia	89	0.263433257	0.0004	0.000648934
GO:1901798	positive regulation of signal transduction by p53 class mediator	7	0.263394006	0.0088	0.010185307
GO:0034644	cellular response to UV	29	0.263355967	< 0.001	< 0.001
GO:0009895	negative regulation of catabolic process	70	0.263346203	< 0.001	< 0.001
GO:0045921	positive regulation of exocytosis	44	0.263338013	0.0001	0.000192793
GO:0071353	cellular response to interleukin-4	13	0.263300663	< 0.001	< 0.001
GO:0010761	fibroblast migration	17	0.263290181	< 0.001	< 0.001
GO:0007250	activation of NF-kappaB-inducing kinase activity	5	0.263268983	0.0128	0.014368758
GO:0032147	activation of protein kinase activity	128	0.263233993	< 0.001	< 0.001
GO:0046488	phosphatidylinositol metabolic process	72	0.263209638	< 0.001	< 0.001
GO:0031016	pancreas development	20	0.263191763	< 0.001	< 0.001
GO:0030198	extracellular matrix organization	105	0.263188086	< 0.001	< 0.001
GO:0043062	extracellular structure organization	105	0.263188086	< 0.001	< 0.001
GO:0046782	regulation of viral transcription	29	0.263169574	0.0005	0.000791911
GO:0090280	positive regulation of calcium ion import	24	0.263148863	< 0.001	< 0.001
GO:1902275	regulation of chromatin organization	61	0.263113699	< 0.001	< 0.001
GO:0045600	positive regulation of fat cell differentiation	26	0.263063063	< 0.001	< 0.001
GO:0001667	ameboidal-type cell migration	149	0.263045788	< 0.001	< 0.001
GO:0002526	acute inflammatory response	36	0.263041613	< 0.001	< 0.001
GO:0043487	regulation of RNA stability	90	0.263040183	0.0003	0.000505993
GO:1903555	regulation of tumor necrosis factor superfamily cytokine production	47	0.26303568	< 0.001	< 0.001
GO:0010810	regulation of cell-substrate adhesion	76	0.263032581	< 0.001	< 0.001
GO:0030836	positive regulation of actin filament depolymerization	9	0.262948663	< 0.001	< 0.001
GO:0071294	cellular response to zinc ion	9	0.262891463	0.0148	0.01645324
GO:0050772	positive regulation of axonogenesis	38	0.262880173	< 0.001	< 0.001
GO:0051148	negative regulation of muscle cell differentiation	20	0.262857143	< 0.001	< 0.001
GO:0042753	positive regulation of circadian rhythm	6	0.262848563	0.0013	0.001826625
GO:0060986	endocrine hormone secretion	13	0.262785863	< 0.001	< 0.001
GO:2000677	regulation of transcription regulatory region DNA binding	19	0.262765021	< 0.001	< 0.001
GO:0032963	collagen metabolic process	23	0.262749706	< 0.001	< 0.001
GO:0044259	multicellular organismal macromolecule metabolic process	23	0.262749706	< 0.001	< 0.001
GO:0050821	protein stabilization	79	0.262747015	0.0001	0.000192793
GO:0043488	regulation of mRNA stability	89	0.262721791	0.0003	0.000505993
GO:0033673	negative regulation of kinase activity	107	0.262704627	< 0.001	< 0.001
GO:0008360	regulation of cell shape	48	0.262666238	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0031960	response to corticosteroid	50	0.262646075	< 0.001	< 0.001
GO:0009394	2'-deoxyribonucleotide metabolic process	12	0.262634063	0.0001	0.000192793
GO:0006692	prostanoid metabolic process	17	0.262623969	< 0.001	< 0.001
GO:0006693	prostaglandin metabolic process	17	0.262623969	< 0.001	< 0.001
GO:0007586	digestion	41	0.262541984	< 0.001	< 0.001
GO:1903901	negative regulation of viral life cycle	29	0.262521635	< 0.001	< 0.001
GO:0031018	endocrine pancreas development	15	0.262496782	< 0.001	< 0.001
GO:0031069	hair follicle morphogenesis	8	0.262483912	< 0.001	< 0.001
GO:0048730	epidermis morphogenesis	8	0.262483912	< 0.001	< 0.001
GO:0032922	circadian regulation of gene expression	25	0.262455598	0.0016	0.002186748
GO:0097119	postsynaptic density protein 95 clustering	7	0.262437948	0.0067	0.007954042
GO:0035418	protein localization to synapse	33	0.262423462	0.0091	0.010505533
GO:0065004	protein-DNA complex assembly	73	0.262403695	0.0002	0.000356582
GO:0060999	positive regulation of dendritic spine development	21	0.262376662	0.004	0.004954389
GO:0007614	short-term memory	5	0.262342342	0.0148	0.01645324
GO:0032760	positive regulation of tumor necrosis factor production	24	0.262280137	< 0.001	< 0.001
GO:0033273	response to vitamin	24	0.262183612	< 0.001	< 0.001
GO:0030326	embryonic limb morphogenesis	33	0.262150462	< 0.001	< 0.001
GO:0035113	embryonic appendage morphogenesis	33	0.262150462	< 0.001	< 0.001
GO:0060998	regulation of dendritic spine development	39	0.262066462	0.0083	0.009660392
GO:0070536	protein K63-linked deubiquitination	19	0.262060557	< 0.001	< 0.001
GO:0050870	positive regulation of T cell activation	59	0.262042187	< 0.001	< 0.001
GO:0045747	positive regulation of Notch signaling pathway	14	0.262033462	< 0.001	< 0.001
GO:0060972	left/right pattern formation	9	0.262004862	< 0.001	< 0.001
GO:0010935	regulation of macrophage cytokine production	5	0.261981982	0.0002	0.000356582
GO:0061684	chaperone-mediated autophagy	5	0.261981982	0.0003	0.000505993
GO:0071774	response to fibroblast growth factor	56	0.261890973	< 0.001	< 0.001
GO:0046777	protein autophosphorylation	94	0.261863687	0.0005	0.000791911
GO:1904377	positive regulation of protein localization to cell periphery	27	0.261861862	0.0001	0.000192793
GO:0045103	intermediate filament-based process	12	0.261861862	< 0.001	< 0.001
GO:0045104	intermediate filament cytoskeleton organization	12	0.261861862	< 0.001	< 0.001
GO:0003091	renal water homeostasis	16	0.261856499	< 0.001	< 0.001
GO:0007084	mitotic nuclear envelope reassembly	7	0.261849605	0.0038	0.004725081
GO:0031440	regulation of mRNA 3'-end processing	8	0.261840412	0.0058	0.006954338
GO:0030260	entry into host cell	38	0.261837025	< 0.001	< 0.001
GO:0044409	entry into host	38	0.261837025	< 0.001	< 0.001
GO:0051806	entry into cell of other organism involved in symbiotic interaction	38	0.261837025	< 0.001	< 0.001
GO:0051828	entry into other organism involved in symbiotic interaction	38	0.261837025	< 0.001	< 0.001
GO:0051961	negative regulation of nervous system development	131	0.261823219	< 0.001	< 0.001
GO:0070841	inclusion body assembly	8	0.261808237	0.0009	0.001319479
GO:0060324	face development	14	0.261794448	0.0001	0.000192793
GO:0007617	mating behavior	15	0.261793222	< 0.001	< 0.001
GO:0016054	organic acid catabolic process	80	0.261782497	< 0.001	< 0.001
GO:0046395	carboxylic acid catabolic process	80	0.261782497	< 0.001	< 0.001
GO:0051865	protein autoubiquitination	31	0.261767759	< 0.001	< 0.001
GO:0033630	positive regulation of cell adhesion mediated by integrin	9	0.261747462	0.0003	0.000505993
GO:0010759	positive regulation of macrophage chemotaxis	7	0.26173929	0.0001	0.000192793
GO:0060294	cilium movement involved in cell motility	5	0.261724582	< 0.001	< 0.001
GO:0045669	positive regulation of osteoblast differentiation	27	0.261690262	< 0.001	< 0.001
GO:1901343	negative regulation of vasculature development	38	0.26168123	< 0.001	< 0.001
GO:0090257	regulation of muscle system process	96	0.261676855	< 0.001	< 0.001
GO:2000637	positive regulation of gene silencing by miRNA	10	0.261673102	< 0.001	< 0.001
GO:0036150	phosphatidylserine acyl-chain remodeling	5	0.261673102	0.0001	0.000192793
GO:0010560	positive regulation of glycoprotein biosynthetic process	6	0.261561562	< 0.001	< 0.001
GO:1903020	positive regulation of glycoprotein metabolic process	6	0.261561562	< 0.001	< 0.001
GO:0045824	negative regulation of innate immune response	13	0.261558262	< 0.001	< 0.001
GO:1903306	negative regulation of regulated secretory pathway	10	0.261518662	< 0.001	< 0.001
GO:0097061	dendritic spine organization	47	0.261513185	0.0041	0.005057384
GO:0071824	protein-DNA complex subunit organization	81	0.261483706	0.0004	0.000648934
GO:0044344	cellular response to fibroblast growth factor stimulus	55	0.261439101	< 0.001	< 0.001
GO:0002449	lymphocyte mediated immunity	63	0.261420604	< 0.001	< 0.001
GO:0006661	phosphatidylinositol biosynthetic process	56	0.261371576	< 0.001	< 0.001
GO:1904874	positive regulation of telomerase RNA localization to Cajal body	10	0.261338481	0.0052	0.006299215
GO:0001676	long-chain fatty acid metabolic process	30	0.261329901	< 0.001	< 0.001
GO:0008361	regulation of cell size	81	0.261321639	< 0.001	< 0.001
GO:0060840	artery development	25	0.261271557	< 0.001	< 0.001
GO:0061028	establishment of endothelial barrier	16	0.261245174	< 0.001	< 0.001
GO:0002712	regulation of B cell mediated immunity	14	0.261206104	0.0016	0.002186748
GO:0002889	regulation of immunoglobulin mediated immune response	14	0.261206104	0.0016	0.002186748
GO:0036503	ERAD pathway	42	0.261187718	0.0001	0.000192793
GO:1902991	regulation of amyloid precursor protein catabolic process	16	0.261164736	0.0004	0.000648934
GO:0048813	dendrite morphogenesis	82	0.261123144	0.002	0.002664694
GO:0003300	cardiac muscle hypertrophy	35	0.261040632	0.0004	0.000648934
GO:0016358	dendrite development	129	0.261037782	0.0004	0.000648934
GO:0007600	sensory perception	186	0.261024619	< 0.001	< 0.001
GO:0045732	positive regulation of protein catabolic process	90	0.261012441	0.0001	0.000192793
GO:0044745	amino acid transmembrane import	5	0.260952381	0.0417	0.043705741
GO:0089718	amino acid import across plasma membrane	5	0.260952381	0.0417	0.043705741
GO:0010822	positive regulation of mitochondrion organization	68	0.260901658	0.0001	0.000192793
GO:0043392	negative regulation of DNA binding	19	0.260895482	0.0006	0.000927725
GO:0042773	ATP synthesis coupled electron transport	33	0.260879061	0.0069	0.008171729
GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	92	0.260872363	< 0.001	< 0.001
GO:0009152	purine ribonucleotide biosynthetic process	67	0.260838664	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0048844	artery morphogenesis	16	0.260810811	< 0.001	< 0.001
GO:0014031	mesenchymal cell development	26	0.260805861	< 0.001	< 0.001
GO:0014032	neural crest cell development	26	0.260805861	< 0.001	< 0.001
GO:0045787	positive regulation of cell cycle	136	0.260769173	< 0.001	< 0.001
GO:0009314	response to radiation	172	0.260768908	< 0.001	< 0.001
GO:0031100	animal organ regeneration	19	0.260760008	< 0.001	< 0.001
GO:0031056	regulation of histone modification	54	0.260717861	< 0.001	< 0.001
GO:0072393	microtubule anchoring at microtubule organizing center	7	0.260672918	0.014	0.015631405
GO:0061050	regulation of cell growth involved in cardiac muscle cell development	9	0.260660661	0.0074	0.008712331
GO:0008625	extrinsic apoptotic signaling pathway via death domain receptors	28	0.260636146	0.0001	0.000192793
GO:1901799	negative regulation of proteasomal protein catabolic process	18	0.260632061	0.0006	0.000927725
GO:0032868	response to insulin	100	0.260617761	< 0.001	< 0.001
GO:0060996	dendritic spine development	54	0.260603461	0.0043	0.005276385
GO:0050867	positive regulation of cell activation	100	0.260576577	< 0.001	< 0.001
GO:0009799	specification of symmetry	42	0.260574861	< 0.001	< 0.001
GO:0009855	determination of bilateral symmetry	42	0.260574861	< 0.001	< 0.001
GO:0042775	mitochondrial ATP synthesis coupled electron transport	32	0.260553411	0.0077	0.00902229
GO:0098915	membrane repolarization during ventricular cardiac muscle cell action potential	5	0.260540541	0.0042	0.005168936
GO:0043410	positive regulation of MAPK cascade	199	0.260539506	< 0.001	< 0.001
GO:0001912	positive regulation of leukocyte mediated cytotoxicity	8	0.260521236	< 0.001	< 0.001
GO:0014896	muscle hypertrophy	36	0.260517661	0.0006	0.000927725
GO:0014897	striated muscle hypertrophy	36	0.260517661	0.0006	0.000927725
GO:0038061	NIK/NF-kappaB signaling	70	0.260496415	0.0005	0.000791911
GO:0060216	definitive hemopoiesis	6	0.26048906	< 0.001	< 0.001
GO:0046470	phosphatidylcholine metabolic process	26	0.26047916	0.0001	0.000192793
GO:0010811	positive regulation of cell-substrate adhesion	43	0.26045913	< 0.001	< 0.001
GO:0043001	Golgi to plasma membrane protein transport	13	0.26044946	0.0002	0.000356582
GO:0071496	cellular response to external stimulus	112	0.260443096	< 0.001	< 0.001
GO:0090596	sensory organ morphogenesis	74	0.260440363	< 0.001	< 0.001
GO:0043542	endothelial cell migration	85	0.260428496	< 0.001	< 0.001
GO:0021987	cerebral cortex development	56	0.260383343	< 0.001	< 0.001
GO:0009187	cyclic nucleotide metabolic process	33	0.26037206	0.0009	0.001319479
GO:0046541	saliva secretion	5	0.26033462	0.0242	0.026144902
GO:0042542	response to hydrogen peroxide	50	0.26030888	< 0.001	< 0.001
GO:0070509	calcium ion import	78	0.26029106	0.0008	0.001193265
GO:0034349	glial cell apoptotic process	6	0.26027456	0.0007	0.001063182
GO:2001021	negative regulation of response to DNA damage stimulus	38	0.260245208	< 0.001	< 0.001
GO:0050982	detection of mechanical stimulus	12	0.26023166	0.0009	0.001319479
GO:0022617	extracellular matrix disassembly	24	0.26023166	0.0016	0.002186748
GO:0000578	embryonic axis specification	11	0.26023166	< 0.001	< 0.001
GO:0070570	regulation of neuron projection regeneration	15	0.2602145	0.0077	0.00902229
GO:0070372	regulation of ERK1 and ERK2 cascade	106	0.260207377	< 0.001	< 0.001
GO:0032303	regulation of icosanoid secretion	8	0.260199485	< 0.001	< 0.001
GO:0014850	response to muscle activity	7	0.260194889	0.0054	0.006510843
GO:0001819	positive regulation of cytokine production	151	0.26016177	< 0.001	< 0.001
GO:0048514	blood vessel morphogenesis	182	0.260100132	< 0.001	< 0.001
GO:0072595	maintenance of protein localization in organelle	16	0.260054698	< 0.001	< 0.001
GO:0006091	generation of precursor metabolites and energy	183	0.26002349	< 0.001	< 0.001
GO:0046513	ceramide biosynthetic process	14	0.25997426	0.0002	0.000356582
GO:0001539	cilium or flagellum-dependent cell motility	10	0.25997426	0.0062	0.00739947
GO:0060285	cilium-dependent cell motility	10	0.25997426	0.0062	0.00739947
GO:1903078	positive regulation of protein localization to plasma membrane	25	0.259953668	0.0008	0.001193265
GO:0000289	nuclear-transcribed mRNA poly(A) tail shortening	11	0.25995086	0.0018	0.002428764
GO:0035278	miRNA mediated inhibition of translation	7	0.259937489	0.0001	0.000192793
GO:0040033	negative regulation of translation, ncRNA-mediated	7	0.259937489	0.0001	0.000192793
GO:0045974	regulation of translation, ncRNA-mediated	7	0.259937489	0.0001	0.000192793
GO:0007549	dosage compensation	7	0.259863946	0.0001	0.000192793
GO:0007093	mitotic cell cycle checkpoint	56	0.25984556	0.0002	0.000356582
GO:0002027	regulation of heart rate	35	0.259841883	0.0003	0.000505993
GO:0043409	negative regulation of MAPK cascade	74	0.259835125	0.0006	0.000927725
GO:0060669	embryonic placenta morphogenesis	8	0.259813385	0.0001	0.000192793
GO:0001823	mesonephros development	33	0.25977146	< 0.001	< 0.001
GO:0007143	female meiotic division	14	0.259735245	0.0005	0.000791911
GO:0071378	cellular response to growth hormone stimulus	14	0.259698474	< 0.001	< 0.001
GO:0048384	retinoic acid receptor signaling pathway	11	0.25964666	< 0.001	< 0.001
GO:0045454	cell redox homeostasis	30	0.25963964	< 0.001	< 0.001
GO:0070341	fat cell proliferation	6	0.25963106	0.0349	0.036944094
GO:0070344	regulation of fat cell proliferation	6	0.25963106	0.0349	0.036944094
GO:1901797	negative regulation of signal transduction by p53 class mediator	17	0.259626013	< 0.001	< 0.001
GO:0048872	homeostasis of number of cells	98	0.259619678	< 0.001	< 0.001
GO:0034501	protein localization to kinetochore	5	0.2596139	0.0109	0.012398148
GO:0071459	protein localization to chromosome, centromeric region	5	0.2596139	0.0109	0.012398148
GO:0032253	dense core granule localization	6	0.25958816	0.0265	0.028498706
GO:0099519	dense core granule cytoskeletal transport	6	0.25958816	0.0265	0.028498706
GO:1901950	dense core granule transport	6	0.25958816	0.0265	0.028498706
GO:0034446	substrate adhesion-dependent cell spreading	32	0.259547941	< 0.001	< 0.001
GO:2000059	negative regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process	6	0.25950236	0.0116	0.013103344
GO:0051321	meiotic cell cycle	70	0.259481522	< 0.001	< 0.001
GO:2001243	negative regulation of intrinsic apoptotic signaling pathway	40	0.259388674	< 0.001	< 0.001
GO:0008584	male gonad development	39	0.259360459	< 0.001	< 0.001
GO:0046546	development of primary male sexual characteristics	39	0.259360459	< 0.001	< 0.001
GO:0036295	cellular response to increased oxygen levels	9	0.259345059	0.0002	0.000356582
GO:0006458	'de novo' protein folding	15	0.259287859	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0033500	carbohydrate homeostasis	93	0.259282324	< 0.001	< 0.001
GO:0042593	glucose homeostasis	93	0.259282324	< 0.001	< 0.001
GO:0009101	glycoprotein biosynthetic process	121	0.259280768	< 0.001	< 0.001
GO:0007368	determination of left/right symmetry	41	0.259271118	< 0.001	< 0.001
GO:0071384	cellular response to corticosteroid stimulus	18	0.259259259	< 0.001	< 0.001
GO:1904666	regulation of ubiquitin protein ligase activity	13	0.259241659	0.0001	0.000192793
GO:0042149	cellular response to glucose starvation	10	0.259227799	0.0022	0.002896881
GO:0021884	forebrain neuron development	15	0.259219219	0.0026	0.003356522
GO:0051963	regulation of synapse assembly	56	0.259202059	0.0011	0.001576346
GO:0032941	secretion by tissue	30	0.259193479	< 0.001	< 0.001
GO:0097502	mannosylation	14	0.259165288	< 0.001	< 0.001
GO:0000187	activation of MAPK activity	68	0.259156636	< 0.001	< 0.001
GO:0046629	gamma-delta T cell activation	6	0.259116259	0.0002	0.000356582
GO:0055098	response to low-density lipoprotein particle	6	0.259116259	0.0302	0.032240379
GO:0071404	cellular response to low-density lipoprotein particle stimulus	6	0.259116259	0.0302	0.032240379
GO:0034440	lipid oxidation	34	0.2590885	< 0.001	< 0.001
GO:0051348	negative regulation of transferase activity	121	0.259074423	< 0.001	< 0.001
GO:1902254	negative regulation of intrinsic apoptotic signaling pathway by p53 class mediator	12	0.259073359	0.0206	0.022453086
GO:0030101	natural killer cell activation	17	0.259050647	< 0.001	< 0.001
GO:0009100	glycoprotein metabolic process	139	0.259005768	< 0.001	< 0.001
GO:0071474	cellular hyperosmotic response	5	0.258944659	0.0179	0.019692915
GO:0007369	gastrulation	58	0.258935783	< 0.001	< 0.001
GO:0009109	coenzyme catabolic process	5	0.258893179	0.0002	0.000356582
GO:0043648	dicarboxylic acid metabolic process	40	0.258886744	< 0.001	< 0.001
GO:0006164	purine nucleotide biosynthetic process	68	0.258853812	< 0.001	< 0.001
GO:2000191	regulation of fatty acid transport	10	0.258841699	< 0.001	< 0.001
GO:0042303	molting cycle	33	0.258804259	< 0.001	< 0.001
GO:0042633	hair cycle	33	0.258804259	< 0.001	< 0.001
GO:1900087	positive regulation of G1/S transition of mitotic cell cycle	16	0.258751609	0.002	0.002664694
GO:0060314	regulation of ryanodine-sensitive calcium-release channel activity	17	0.258747823	0.0015	0.002069969
GO:2000601	positive regulation of Arp2/3 complex-mediated actin nucleation	6	0.258730159	0.0157	0.01736447
GO:0098542	defense response to other organism	134	0.258700705	< 0.001	< 0.001
GO:0001763	morphogenesis of a branching structure	60	0.258682969	< 0.001	< 0.001
GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	62	0.258629136	< 0.001	< 0.001
GO:0032479	regulation of type I interferon production	49	0.258597957	0.0001	0.000192793
GO:0051899	membrane depolarization	26	0.258588259	< 0.001	< 0.001
GO:0007340	acrosome reaction	12	0.258537109	0.0006	0.000927725
GO:0015718	monocarboxylic acid transport	45	0.258509939	< 0.001	< 0.001
GO:0043255	regulation of carbohydrate biosynthetic process	40	0.258507079	< 0.001	< 0.001
GO:0055081	anion homeostasis	14	0.258485016	0.0003	0.000505993
GO:0002433	immune response-regulating cell surface receptor signaling pathway involved in phagocytosis	44	0.258435708	0.0001	0.000192793
GO:0038094	Fc-gamma receptor signaling pathway	44	0.258435708	0.0001	0.000192793
GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis	44	0.258435708	0.0001	0.000192793
GO:0048285	organelle fission	163	0.258425121	< 0.001	< 0.001
GO:0006677	glycosylceramide metabolic process	7	0.258393087	0.0274	0.029402224
GO:0007520	myoblast fusion	11	0.258383058	0.0312	0.033235719
GO:1903054	negative regulation of extracellular matrix organization	5	0.258378378	0.0001	0.000192793
GO:0061640	cytoskeleton-dependent cytokinesis	32	0.258365508	< 0.001	< 0.001
GO:0070302	regulation of stress-activated protein kinase signaling cascade	94	0.258224486	< 0.001	< 0.001
GO:0045494	photoreceptor cell maintenance	13	0.258172458	< 0.001	< 0.001
GO:0030810	positive regulation of nucleotide biosynthetic process	23	0.258116502	0.0006	0.000927725
GO:1900373	positive regulation of purine nucleotide biosynthetic process	23	0.258116502	0.0006	0.000927725
GO:1900745	positive regulation of p38MAPK cascade	7	0.258098915	0.001	0.001450349
GO:0009880	embryonic pattern specification	21	0.258000858	< 0.001	< 0.001
GO:0014706	striated muscle tissue development	131	0.257962215	< 0.001	< 0.001
GO:1903203	regulation of oxidative stress-induced neuron death	11	0.257961858	< 0.001	< 0.001
GO:0010830	regulation of myotube differentiation	13	0.257875458	< 0.001	< 0.001
GO:0032409	regulation of transporter activity	114	0.257874416	0.0012	0.001702047
GO:0045981	positive regulation of nucleotide metabolic process	35	0.257863578	< 0.001	< 0.001
GO:1900544	positive regulation of purine nucleotide metabolic process	35	0.257863578	< 0.001	< 0.001
GO:0060411	cardiac septum morphogenesis	24	0.257797083	< 0.001	< 0.001
GO:1903307	positive regulation of regulated secretory pathway	27	0.257791124	0.0011	0.001576346
GO:0035728	response to hepatocyte growth factor	7	0.257767972	0.0001	0.000192793
GO:0035729	cellular response to hepatocyte growth factor stimulus	7	0.257767972	0.0001	0.000192793
GO:0060706	cell differentiation involved in embryonic placenta development	5	0.257760618	< 0.001	< 0.001
GO:0051403	stress-activated MAPK cascade	124	0.257751069	< 0.001	< 0.001
GO:0031098	stress-activated protein kinase signaling cascade	126	0.257725072	< 0.001	< 0.001
GO:0002052	positive regulation of neuroblast proliferation	7	0.257694429	0.0381	0.040181967
GO:0070542	response to fatty acid	36	0.257693408	< 0.001	< 0.001
GO:2001222	regulation of neuron migration	20	0.257619048	< 0.001	< 0.001
GO:0060537	muscle tissue development	137	0.257580625	< 0.001	< 0.001
GO:0051092	positive regulation of NF-kappaB transcription factor activity	60	0.257546118	< 0.001	< 0.001
GO:0032873	negative regulation of stress-activated MAPK cascade	22	0.257528958	0.0004	0.000648934
GO:0070303	negative regulation of stress-activated protein kinase signaling cascade	22	0.257528958	0.0004	0.000648934
GO:0006732	coenzyme metabolic process	132	0.257513358	< 0.001	< 0.001
GO:0032602	chemokine production	30	0.257365937	< 0.001	< 0.001
GO:1905207	regulation of cardiocyte differentiation	19	0.25733252	< 0.001	< 0.001
GO:0044272	sulfur compound biosynthetic process	75	0.257273273	< 0.001	< 0.001
GO:0097191	extrinsic apoptotic signaling pathway	75	0.257273273	< 0.001	< 0.001
GO:0007051	spindle organization	67	0.257265795	0.0001	0.000192793
GO:0019674	NAD metabolic process	34	0.257248845	< 0.001	< 0.001
GO:0045841	negative regulation of mitotic metaphase/anaphase transition	15	0.257211497	0.0027	0.003470695

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1902100	negative regulation of metaphase/anaphase transition of cell cycle	15	0.257211497	0.0027	0.003470695
GO:2000816	negative regulation of mitotic sister chromatid separation	15	0.257211497	0.0027	0.003470695
GO:0016202	regulation of striated muscle tissue development	45	0.257205777	< 0.001	< 0.001
GO:0048634	regulation of muscle organ development	45	0.257205777	< 0.001	< 0.001
GO:0000387	spliceosomal snRNP assembly	24	0.257175032	0.0004	0.000648934
GO:0034764	positive regulation of transmembrane transport	57	0.257151889	< 0.001	< 0.001
GO:2000377	regulation of reactive oxygen species metabolic process	65	0.257075537	< 0.001	< 0.001
GO:0007095	mitotic G2 DNA damage checkpoint	7	0.257069314	0.0106	0.012082345
GO:0044818	mitotic G2/M transition checkpoint	7	0.257069314	0.0106	0.012082345
GO:0009247	glycolipid biosynthetic process	23	0.257064518	0.0004	0.000648934
GO:0051251	positive regulation of lymphocyte activation	84	0.25702335	< 0.001	< 0.001
GO:0050803	regulation of synapse structure or activity	95	0.257007383	0.0003	0.000505993
GO:0009913	epidermal cell differentiation	74	0.2570072	< 0.001	< 0.001
GO:0048754	branching morphogenesis of an epithelial tube	44	0.256973207	< 0.001	< 0.001
GO:0090129	positive regulation of synapse maturation	6	0.256885457	0.0132	0.014787065
GO:1901861	regulation of muscle tissue development	46	0.256879861	< 0.001	< 0.001
GO:0002088	lens development in camera-type eye	29	0.256876581	0.0004	0.000648934
GO:0070169	positive regulation of biomineral tissue development	19	0.256844815	< 0.001	< 0.001
GO:0032872	regulation of stress-activated MAPK cascade	93	0.25680796	< 0.001	< 0.001
GO:0061351	neural precursor cell proliferation	55	0.256801217	< 0.001	< 0.001
GO:0030879	mammary gland development	55	0.256796537	< 0.001	< 0.001
GO:0072593	reactive oxygen species metabolic process	89	0.256784232	< 0.001	< 0.001
GO:0050884	neuromuscular process controlling posture	8	0.256756757	< 0.001	< 0.001
GO:0060291	long-term synaptic potentiation	44	0.256745057	0.0036	0.004505419
GO:0035994	response to muscle stretch	7	0.256738371	0.0005	0.000791911
GO:0051651	maintenance of location in cell	44	0.256709957	< 0.001	< 0.001
GO:0032986	protein-DNA complex disassembly	8	0.256692407	0.0341	0.036153894
GO:0045662	negative regulation of myoblast differentiation	8	0.256660232	< 0.001	< 0.001
GO:0014033	neural crest cell differentiation	28	0.256637249	< 0.001	< 0.001
GO:0031669	cellular response to nutrient levels	80	0.256618404	< 0.001	< 0.001
GO:0009260	ribonucleotide biosynthetic process	73	0.256585744	< 0.001	< 0.001
GO:0022898	regulation of transmembrane transporter activity	108	0.256556557	0.0015	0.002069969
GO:0070482	response to oxygen levels	157	0.256551001	0.0001	0.000192793
GO:0002190	cap-independent translational initiation	7	0.256517742	0.0001	0.000192793
GO:0015810	aspartate transport	6	0.256499356	0.013	0.014581154
GO:0060337	type I interferon signaling pathway	23	0.25648257	0.0002	0.000356582
GO:0071357	cellular response to type I interferon	23	0.25648257	0.0002	0.000356582
GO:1902115	regulation of organelle assembly	74	0.256481965	< 0.001	< 0.001
GO:0043647	inositol phosphate metabolic process	31	0.256461992	< 0.001	< 0.001
GO:0090305	nucleic acid phosphodiester bond hydrolysis	104	0.256390456	0.0001	0.000192793
GO:0008543	fibroblast growth factor receptor signaling pathway	45	0.256387816	< 0.001	< 0.001
GO:0048169	regulation of long-term neuronal synaptic plasticity	17	0.256370656	0.0147	0.016362266
GO:1902017	regulation of cilium assembly	23	0.256370656	< 0.001	< 0.001
GO:0045646	regulation of erythrocyte differentiation	21	0.256358399	< 0.001	< 0.001
GO:2000463	positive regulation of excitatory postsynaptic potential	19	0.256357109	0.0234	0.025351564
GO:0044264	cellular polysaccharide metabolic process	37	0.256328916	< 0.001	< 0.001
GO:0002755	MyD88-dependent toll-like receptor signaling pathway	12	0.256284856	0.0023	0.003013139
GO:0031330	negative regulation of cellular catabolic process	41	0.256263929	0.0002	0.000356582
GO:0002312	B cell activation involved in immune response	21	0.256260342	0.0014	0.00194839
GO:0031346	positive regulation of cell projection organization	171	0.256227656	< 0.001	< 0.001
GO:0032239	regulation of nucleobase-containing compound transport	5	0.256216216	0.0048	0.005840847
GO:0042982	amyloid precursor protein metabolic process	23	0.256202787	< 0.001	< 0.001
GO:0045685	regulation of glial cell differentiation	21	0.256199056	< 0.001	< 0.001
GO:0050864	regulation of B cell activation	36	0.256184756	< 0.001	< 0.001
GO:2001257	regulation of cation channel activity	70	0.256131642	0.0028	0.003584743
GO:1905268	negative regulation of chromatin organization	23	0.256113256	< 0.001	< 0.001
GO:1903557	positive regulation of tumor necrosis factor superfamily cytokine production	25	0.256072072	< 0.001	< 0.001
GO:0009581	detection of external stimulus	37	0.256057602	< 0.001	< 0.001
GO:0097484	dendrite extension	21	0.256027456	0.0081	0.00945
GO:0010459	negative regulation of heart rate	6	0.256027456	0.0003	0.000505993
GO:0009142	nucleoside triphosphate biosynthetic process	28	0.256012135	0.0001	0.000192793
GO:0031058	positive regulation of histone modification	34	0.256007268	0.0005	0.000791911
GO:0007016	cytoskeletal anchoring at plasma membrane	5	0.255958816	< 0.001	< 0.001
GO:0031648	protein destabilization	21	0.255941656	< 0.001	< 0.001
GO:0009190	cyclic nucleotide biosynthetic process	29	0.255926863	0.0008	0.001193265
GO:0052652	cyclic purine nucleotide metabolic process	29	0.255926863	0.0008	0.001193265
GO:0050769	positive regulation of neurogenesis	194	0.255886372	< 0.001	< 0.001
GO:1904427	positive regulation of calcium ion transmembrane transport	28	0.255874242	0.0043	0.005276385
GO:0030317	flagellated sperm motility	23	0.255867047	0.001	0.001450349
GO:0097722	sperm motility	23	0.255867047	0.001	0.001450349
GO:0006171	cAMP biosynthetic process	24	0.255845131	0.0018	0.002428764
GO:0030814	regulation of cAMP metabolic process	24	0.255845131	0.0018	0.002428764
GO:0030817	regulation of cAMP biosynthetic process	24	0.255845131	0.0018	0.002428764
GO:0045761	regulation of adenylate cyclase activity	24	0.255845131	0.0018	0.002428764
GO:0023058	adaptation of signaling pathway	10	0.255830116	0.0001	0.000192793
GO:0071385	cellular response to glucocorticoid stimulus	17	0.255810432	< 0.001	< 0.001
GO:1900038	negative regulation of cellular response to hypoxia	5	0.255804376	0.0006	0.000927725
GO:1903297	regulation of hypoxia-induced intrinsic apoptotic signaling pathway	5	0.255804376	0.0006	0.000927725
GO:1903298	negative regulation of hypoxia-induced intrinsic apoptotic signaling pathway	5	0.255804376	0.0006	0.000927725
GO:1990144	intrinsic apoptotic signaling pathway in response to hypoxia	5	0.255804376	0.0006	0.000927725
GO:0035360	positive regulation of peroxisome proliferator activated receptor signaling pathway	5	0.255752896	< 0.001	< 0.001
GO:0002066	columnar/cuboidal epithelial cell development	21	0.255733284	< 0.001	< 0.001
GO:0055074	calcium ion homeostasis	150	0.255730588	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0051186	cofactor metabolic process	153	0.255721267	< 0.001	< 0.001
GO:0002431	Fc receptor mediated stimulatory signaling pathway	45	0.255707136	0.0001	0.000192793
GO:0000717	nucleotide-excision repair, DNA duplex unwinding	12	0.255705706	0.0005	0.000791911
GO:0006778	porphyrin-containing compound metabolic process	11	0.255692056	0.0084	0.009757868
GO:0042168	heme metabolic process	11	0.255692056	0.0084	0.009757868
GO:0009648	photoperiodism	10	0.255598456	0.0111	0.012593827
GO:0048592	eye morphogenesis	44	0.255580906	< 0.001	< 0.001
GO:0051972	regulation of telomerase activity	21	0.255549427	< 0.001	< 0.001
GO:0001942	hair follicle development	27	0.255541256	< 0.001	< 0.001
GO:0022404	molting cycle process	27	0.255541256	< 0.001	< 0.001
GO:0022405	hair cycle process	27	0.255541256	< 0.001	< 0.001
GO:0090307	mitotic spindle assembly	21	0.255475884	0.0001	0.000192793
GO:0045058	T cell selection	13	0.255459855	0.0024	0.003116943
GO:0031398	positive regulation of protein ubiquitination	62	0.255448997	0.0001	0.000192793
GO:0010656	negative regulation of muscle cell apoptotic process	16	0.255405405	< 0.001	< 0.001
GO:0046622	positive regulation of organ growth	17	0.255356197	< 0.001	< 0.001
GO:0006517	protein deglycosylation	14	0.255304284	0.0001	0.000192793
GO:0002696	positive regulation of leukocyte activation	97	0.25528533	< 0.001	< 0.001
GO:0055017	cardiac muscle tissue growth	32	0.255252574	< 0.001	< 0.001
GO:1903706	regulation of hemopoiesis	156	0.255192555	< 0.001	< 0.001
GO:0008652	cellular amino acid biosynthetic process	33	0.255114855	< 0.001	< 0.001
GO:0022618	ribonucleoprotein complex assembly	87	0.255110283	0.0008	0.001193265
GO:0032799	low-density lipoprotein receptor particle metabolic process	12	0.255062205	0.0079	0.009236608
GO:0050710	negative regulation of cytokine secretion	21	0.255059141	< 0.001	< 0.001
GO:0032753	positive regulation of interleukin-4 production	5	0.255032175	0.0014	0.00194839
GO:0002028	regulation of sodium ion transport	33	0.255029055	< 0.001	< 0.001
GO:0051569	regulation of histone H3-K4 methylation	10	0.255006435	< 0.001	< 0.001
GO:0048524	positive regulation of viral process	53	0.255001093	0.0009	0.001319479
GO:0019751	polyol metabolic process	42	0.254985598	< 0.001	< 0.001
GO:0007517	muscle organ development	138	0.254964281	< 0.001	< 0.001
GO:0098869	cellular oxidant detoxification	32	0.254946911	0.0001	0.000192793
GO:0006275	regulation of DNA replication	44	0.254931555	0.0005	0.000791911
GO:0009582	detection of abiotic stimulus	39	0.254885655	0.0001	0.000192793
GO:0000280	nuclear division	146	0.254882671	< 0.001	< 0.001
GO:0050807	regulation of synapse organization	92	0.254882211	0.0002	0.000356582
GO:0019692	deoxyribose phosphate metabolic process	13	0.254865855	0.0001	0.000192793
GO:0051928	positive regulation of calcium ion transport	46	0.254854233	0.0007	0.001063182
GO:0007492	endoderm development	20	0.254851995	< 0.001	< 0.001
GO:0035239	tube morphogenesis	122	0.254811486	< 0.001	< 0.001
GO:0032496	response to lipopolysaccharide	103	0.254808762	< 0.001	< 0.001
GO:0000963	mitochondrial RNA processing	6	0.254783355	0.0027	0.003470695
GO:0071560	cellular response to transforming growth factor beta stimulus	88	0.25477068	< 0.001	< 0.001
GO:0044723	single-organism carbohydrate metabolic process	179	0.254762983	< 0.001	< 0.001
GO:0007215	glutamate receptor signaling pathway	49	0.254736953	0.0147	0.016362266
GO:0045823	positive regulation of heart contraction	15	0.254688975	0.0011	0.001576346
GO:0046320	regulation of fatty acid oxidation	15	0.254671815	< 0.001	< 0.001
GO:0034502	protein localization to chromosome	33	0.254639055	0.0005	0.000791911
GO:0006536	glutamate metabolic process	17	0.254614278	< 0.001	< 0.001
GO:0034063	stress granule assembly	10	0.254594595	0.0006	0.000927725
GO:0045638	negative regulation of myeloid cell differentiation	26	0.254509455	< 0.001	< 0.001
GO:0034121	regulation of toll-like receptor signaling pathway	27	0.254492588	0.0004	0.000648934
GO:0007033	vacuole organization	82	0.254490379	0.0002	0.000356582
GO:0033189	response to vitamin A	5	0.254465894	0.0102	0.011688041
GO:0001782	B cell homeostasis	11	0.254451854	0.0003	0.000505993
GO:0031055	chromatin remodeling at centromere	15	0.254448734	0.0153	0.01697069
GO:1901998	toxin transport	15	0.254448734	0.0001	0.000192793
GO:0003151	outflow tract morphogenesis	27	0.254406788	< 0.001	< 0.001
GO:0006584	catecholamine metabolic process	22	0.254381654	< 0.001	< 0.001
GO:0009712	catechol-containing compound metabolic process	22	0.254381654	< 0.001	< 0.001
GO:0009156	ribonucleoside monophosphate biosynthetic process	37	0.254381022	0.0002	0.000356582
GO:0045682	regulation of epidermis development	23	0.254345028	< 0.001	< 0.001
GO:0045666	positive regulation of neuron differentiation	165	0.254342654	0.0001	0.000192793
GO:1901881	positive regulation of protein depolymerization	13	0.254331254	0.0001	0.000192793
GO:0060074	synapse maturation	18	0.254325754	0.0011	0.001576346
GO:0002040	sprouting angiogenesis	37	0.254269714	0.0007	0.001063182
GO:0032653	regulation of interleukin-10 production	12	0.254268554	0.0015	0.002069969
GO:0035270	endocrine system development	36	0.254254254	< 0.001	< 0.001
GO:1903829	positive regulation of cellular protein localization	152	0.254216623	< 0.001	< 0.001
GO:0044088	regulation of vacuole organization	25	0.254198198	< 0.001	< 0.001
GO:0009062	fatty acid catabolic process	27	0.254177988	< 0.001	< 0.001
GO:0071826	ribonucleoprotein complex subunit organization	92	0.254177159	0.0003	0.000505993
GO:0031929	TOR signaling	48	0.254166667	< 0.001	< 0.001
GO:0098813	nuclear chromosome segregation	91	0.254130426	< 0.001	< 0.001
GO:0060688	regulation of morphogenesis of a branching structure	16	0.254118404	< 0.001	< 0.001
GO:1905477	positive regulation of protein localization to membrane	64	0.25411036	< 0.001	< 0.001
GO:0046661	male sex differentiation	43	0.254107929	< 0.001	< 0.001
GO:0009416	response to light stimulus	119	0.254023772	< 0.001	< 0.001
GO:0034249	negative regulation of cellular amide metabolic process	97	0.253916066	< 0.001	< 0.001
GO:0010824	regulation of centrosome duplication	20	0.253912484	< 0.001	< 0.001
GO:0007339	binding of sperm to zona pellucida	14	0.253906968	< 0.001	< 0.001
GO:0035036	sperm-egg recognition	14	0.253906968	< 0.001	< 0.001
GO:0071622	regulation of granulocyte chemotaxis	17	0.253902642	< 0.001	< 0.001
GO:0072522	purine-containing compound biosynthetic process	70	0.253855488	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0002224	toll-like receptor signaling pathway	57	0.253846328	< 0.001	< 0.001
GO:0008277	regulation of G-protein coupled receptor protein signaling pathway	56	0.253838022	< 0.001	< 0.001
GO:0043588	skin development	101	0.253783911	< 0.001	< 0.001
GO:0046718	viral entry into host cell	33	0.253773254	< 0.001	< 0.001
GO:0006890	retrograde vesicle-mediated transport, Golgi to ER	38	0.253749238	0.0003	0.000505993
GO:1901342	regulation of vasculature development	95	0.253688275	< 0.001	< 0.001
GO:0043153	entrainment of circadian clock by photoperiod	8	0.253667954	0.041	0.043030491
GO:0019371	cyclooxygenase pathway	6	0.253667954	< 0.001	< 0.001
GO:1903051	negative regulation of proteolysis involved in cellular protein catabolic process	24	0.253657229	0.0005	0.000791911
GO:0009112	nucleobase metabolic process	12	0.253603604	< 0.001	< 0.001
GO:1901028	regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	19	0.253593443	0.002	0.002664694
GO:0046605	regulation of centrosome cycle	24	0.253592879	< 0.001	< 0.001
GO:0090646	mitochondrial tRNA processing	5	0.253590734	0.0009	0.001319479
GO:0070723	response to cholesterol	12	0.253582154	< 0.001	< 0.001
GO:0034508	centromere complex assembly	18	0.253567854	0.0088	0.010185307
GO:2000826	regulation of heart morphogenesis	11	0.253492453	< 0.001	< 0.001
GO:1901605	alpha-amino acid metabolic process	76	0.253457969	< 0.001	< 0.001
GO:0060249	anatomical structure homeostasis	161	0.253454519	< 0.001	< 0.001
GO:0030316	osteoclast differentiation	31	0.253364886	< 0.001	< 0.001
GO:0016331	morphogenesis of embryonic epithelium	59	0.253356019	< 0.001	< 0.001
GO:0006874	cellular calcium ion homeostasis	146	0.253340033	< 0.001	< 0.001
GO:0036293	response to decreased oxygen levels	147	0.253329131	0.0002	0.000356582
GO:0072503	cellular divalent inorganic cation homeostasis	149	0.253316404	< 0.001	< 0.001
GO:0050871	positive regulation of B cell activation	28	0.253309432	< 0.001	< 0.001
GO:1903707	negative regulation of hemopoiesis	44	0.253305253	< 0.001	< 0.001
GO:0006942	regulation of striated muscle contraction	40	0.253236808	< 0.001	< 0.001
GO:0061307	cardiac neural crest cell differentiation involved in heart development	5	0.253230373	0.0032	0.004042263
GO:0061308	cardiac neural crest cell development involved in heart development	5	0.253230373	0.0032	0.004042263
GO:0070585	protein localization to mitochondrion	71	0.253223848	0.0002	0.000356582
GO:0001502	cartilage condensation	7	0.25320831	0.0358	0.037852319
GO:0072132	mesenchyme morphogenesis	15	0.253196053	< 0.001	< 0.001
GO:0046390	ribose phosphate biosynthetic process	75	0.253178893	< 0.001	< 0.001
GO:0032606	type I interferon production	51	0.253175865	0.0002	0.000356582
GO:1903039	positive regulation of leukocyte cell-cell adhesion	64	0.253157175	< 0.001	< 0.001
GO:0006790	sulfur compound metabolic process	133	0.253107673	< 0.001	< 0.001
GO:0006457	protein folding	90	0.253095953	0.0001	0.000192793
GO:1902692	regulation of neuroblast proliferation	8	0.253088803	0.0148	0.01645324
GO:0002688	regulation of leukocyte chemotaxis	36	0.253010153	< 0.001	< 0.001
GO:0051606	detection of stimulus	88	0.253006903	< 0.001	< 0.001
GO:0007249	I-kappaB kinase/NF-kappaB signaling	103	0.253001962	< 0.001	< 0.001
GO:0098773	skin epidermis development	28	0.252996874	< 0.001	< 0.001
GO:0015985	energy coupled proton transport, down electrochemical gradient	8	0.252960103	0.0196	0.021436632
GO:0015986	ATP synthesis coupled proton transport	8	0.252960103	0.0196	0.021436632
GO:0042776	mitochondrial ATP synthesis coupled proton transport	8	0.252960103	0.0196	0.021436632
GO:0042157	lipoprotein metabolic process	41	0.252942838	0.0001	0.000192793
GO:0086001	cardiac muscle cell action potential	24	0.252895753	0.0033	0.004153051
GO:0071604	transforming growth factor beta production	15	0.252887173	< 0.001	< 0.001
GO:0071634	regulation of transforming growth factor beta production	15	0.252887173	< 0.001	< 0.001
GO:0071559	response to transforming growth factor beta	90	0.252829973	< 0.001	< 0.001
GO:0000491	small nucleolar ribonucleoprotein complex assembly	5	0.252818533	0.0143	0.015940017
GO:0045737	positive regulation of cyclin-dependent protein serine/threonine kinase activity	15	0.252801373	0.0005	0.000791911
GO:0032609	interferon-gamma production	30	0.252767053	< 0.001	< 0.001
GO:0021782	glial cell development	28	0.252711896	< 0.001	< 0.001
GO:0042632	cholesterol homeostasis	21	0.25269351	0.0001	0.000192793
GO:0055092	sterol homeostasis	21	0.25269351	0.0001	0.000192793
GO:0009124	nucleoside monophosphate biosynthetic process	39	0.252681253	0.0002	0.000356582
GO:0002237	response to molecule of bacterial origin	106	0.252655351	< 0.001	< 0.001
GO:0005976	polysaccharide metabolic process	43	0.252647332	< 0.001	< 0.001
GO:0070373	negative regulation of ERK1 and ERK2 cascade	30	0.252646933	0.0024	0.003116943
GO:0010976	positive regulation of neuron projection development	133	0.252616096	0.0001	0.000192793
GO:2001235	positive regulation of apoptotic signaling pathway	73	0.252615433	< 0.001	< 0.001
GO:0042058	regulation of epidermal growth factor receptor signaling pathway	36	0.252609753	0.0001	0.000192793
GO:1902110	positive regulation of mitochondrial membrane permeability involved in apoptotic process	26	0.252588853	0.0007	0.001063182
GO:0050687	negative regulation of defense response to virus	6	0.252552553	0.0214	0.023282786
GO:0048708	astrocyte differentiation	23	0.252532035	0.0011	0.001576346
GO:0035335	peptidyl-tyrosine dephosphorylation	59	0.252527103	< 0.001	< 0.001
GO:0010821	regulation of mitochondrion organization	99	0.252525253	0.0002	0.000356582
GO:1902230	negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage	17	0.252524794	0.0021	0.002780108
GO:0006979	response to oxidative stress	160	0.252524131	< 0.001	< 0.001
GO:0018126	protein hydroxylation	16	0.252493565	0.0002	0.000356582
GO:0045727	positive regulation of translation	60	0.252475332	0.0001	0.000192793
GO:0010038	response to metal ion	126	0.252411595	< 0.001	< 0.001
GO:0030511	positive regulation of transforming growth factor beta receptor signaling pathway	10	0.252406692	0.0002	0.000356582
GO:1903846	positive regulation of cellular response to transforming growth factor beta stimulus	10	0.252406692	0.0002	0.000356582
GO:0050921	positive regulation of chemotaxis	51	0.252378429	< 0.001	< 0.001
GO:0001553	luteinization	5	0.252355212	0.0002	0.000356582
GO:0032412	regulation of ion transmembrane transporter activity	104	0.252319077	0.0018	0.002428764
GO:0033151	V(D)J recombination	6	0.252295152	0.0386	0.040653752
GO:0010632	regulation of epithelial cell migration	93	0.252291001	< 0.001	< 0.001
GO:0001666	response to hypoxia	142	0.25228488	0.0002	0.000356582
GO:0043467	regulation of generation of precursor metabolites and energy	55	0.252275652	0.0002	0.000356582
GO:0019320	hexose catabolic process	23	0.252263444	0.0017	0.00231289
GO:0045924	regulation of female receptivity	5	0.252252252	0.0169	0.018649704

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0044794	positive regulation by host of viral process	6	0.252252252	0.0015	0.002069969
GO:2001224	positive regulation of neuron migration	7	0.252215481	0.0003	0.000505993
GO:0031667	response to nutrient levels	156	0.252211002	< 0.001	< 0.001
GO:0045922	negative regulation of fatty acid metabolic process	12	0.252187902	< 0.001	< 0.001
GO:0033692	cellular polysaccharide biosynthetic process	26	0.252133452	< 0.001	< 0.001
GO:0030098	lymphocyte differentiation	94	0.252115337	< 0.001	< 0.001
GO:0098815	modulation of excitatory postsynaptic potential	26	0.252054252	0.0145	0.016156289
GO:0050679	positive regulation of epithelial cell proliferation	59	0.252003577	< 0.001	< 0.001
GO:0021545	cranial nerve development	14	0.251994852	0.0014	0.00194839
GO:0071706	tumor necrosis factor superfamily cytokine production	50	0.251953668	< 0.001	< 0.001
GO:0060562	epithelial tube morphogenesis	109	0.251949984	< 0.001	< 0.001
GO:0061337	cardiac conduction	52	0.251940402	0.0017	0.00231289
GO:2000310	regulation of N-methyl-D-aspartate selective glutamate receptor activity	23	0.251927704	0.0128	0.014368758
GO:0002029	desensitization of G-protein coupled receptor protein signaling pathway	9	0.251909052	0.0001	0.000192793
GO:0022401	negative adaptation of signaling pathway	9	0.251909052	0.0001	0.000192793
GO:0031290	retinal ganglion cell axon guidance	11	0.251901252	0.0366	0.038652804
GO:0072655	establishment of protein localization to mitochondrion	70	0.251866152	0.0002	0.000356582
GO:0032649	regulation of interferon-gamma production	26	0.251856252	< 0.001	< 0.001
GO:0050996	positive regulation of lipid catabolic process	9	0.251851852	0.0007	0.001063182
GO:0040017	positive regulation of locomotion	192	0.251836658	< 0.001	< 0.001
GO:1902668	negative regulation of axon guidance	6	0.251823252	0.003	0.003811001
GO:0071470	cellular response to osmotic stress	12	0.251780352	0.0013	0.001826625
GO:0007498	mesoderm development	46	0.251776621	< 0.001	< 0.001
GO:0070670	response to interleukin-4	15	0.251771772	< 0.001	< 0.001
GO:0010042	response to manganese ion	8	0.251769627	0.001	0.001450349
GO:0006936	muscle contraction	128	0.251767616	< 0.001	< 0.001
GO:0043406	positive regulation of MAP kinase activity	101	0.251719612	< 0.001	< 0.001
GO:0001558	regulation of cell growth	180	0.251608752	< 0.001	< 0.001
GO:0030816	positive regulation of cAMP metabolic process	16	0.251608752	0.0058	0.006954338
GO:0030819	positive regulation of cAMP biosynthetic process	16	0.251608752	0.0058	0.006954338
GO:0045762	positive regulation of adenylate cyclase activity	16	0.251608752	0.0058	0.006954338
GO:0072507	divalent inorganic cation homeostasis	156	0.251574102	< 0.001	< 0.001
GO:0044262	cellular carbohydrate metabolic process	107	0.251501702	< 0.001	< 0.001
GO:0034694	response to prostaglandin	15	0.251497211	< 0.001	< 0.001
GO:0042113	B cell activation	67	0.251483893	< 0.001	< 0.001
GO:0010837	regulation of keratinocyte proliferation	14	0.251480051	< 0.001	< 0.001
GO:0071360	cellular response to exogenous dsRNA	6	0.251437151	0.0148	0.01645324
GO:0034976	response to endoplasmic reticulum stress	118	0.251408067	0.0002	0.000356582
GO:1990748	cellular detoxification	34	0.25132864	< 0.001	< 0.001
GO:0055094	response to lipoprotein particle	7	0.251296194	0.0053	0.006400268
GO:0071402	cellular response to lipoprotein particle stimulus	7	0.251296194	0.0053	0.006400268
GO:0030071	regulation of mitotic metaphase/anaphase transition	22	0.251269451	0.0058	0.006954338
GO:1902099	regulation of metaphase/anaphase transition of cell cycle	22	0.251269451	0.0058	0.006954338
GO:0014009	glial cell proliferation	22	0.251222651	0.0004	0.000648934
GO:2000249	regulation of actin cytoskeleton reorganization	16	0.251206564	0.0013	0.001826625
GO:0046685	response to arsenic-containing substance	11	0.251175851	< 0.001	< 0.001
GO:0034243	regulation of transcription elongation from RNA polymerase II promoter	8	0.251158301	0.0022	0.002896881
GO:0035794	positive regulation of mitochondrial membrane permeability	27	0.251098718	0.0007	0.001063182
GO:1902686	mitochondrial outer membrane permeabilization involved in programmed cell death	27	0.251098718	0.0007	0.001063182
GO:1905710	positive regulation of membrane permeability	27	0.251098718	0.0007	0.001063182
GO:0046710	GDP metabolic process	6	0.251093951	< 0.001	< 0.001
GO:0006720	isoprenoid metabolic process	36	0.251051051	< 0.001	< 0.001
GO:0032414	positive regulation of ion transmembrane transporter activity	40	0.251029601	0.0003	0.000505993
GO:0086009	membrane repolarization	17	0.250919827	0.0008	0.001193265
GO:1902893	regulation of pri-miRNA transcription from RNA polymerase II promoter	20	0.250875161	< 0.001	< 0.001
GO:0006909	phagocytosis	100	0.250870013	< 0.001	< 0.001
GO:0007589	body fluid secretion	34	0.250866833	< 0.001	< 0.001
GO:0044724	single-organism carbohydrate catabolic process	63	0.250842679	< 0.001	< 0.001
GO:1901099	negative regulation of signal transduction in absence of ligand	7	0.250744622	0.0003	0.000505993
GO:2001240	negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	7	0.250744622	0.0003	0.000505993
GO:0071478	cellular response to radiation	65	0.250739531	< 0.001	< 0.001
GO:0031214	biomineral tissue development	49	0.250734116	< 0.001	< 0.001
GO:0032148	activation of protein kinase B activity	15	0.250725011	< 0.001	< 0.001
GO:0051235	maintenance of location	115	0.250685468	< 0.001	< 0.001
GO:0060538	skeletal muscle organ development	59	0.250668586	< 0.001	< 0.001
GO:0001523	retinoid metabolic process	24	0.250654226	< 0.001	< 0.001
GO:0009267	cellular response to starvation	58	0.250650158	< 0.001	< 0.001
GO:0016052	carbohydrate catabolic process	65	0.250604891	< 0.001	< 0.001
GO:0048662	negative regulation of smooth muscle cell proliferation	15	0.250604891	< 0.001	< 0.001
GO:0006855	drug transmembrane transport	5	0.250604891	0.0254	0.027370209
GO:0045834	positive regulation of lipid metabolic process	46	0.250590342	< 0.001	< 0.001
GO:0008038	neuron recognition	24	0.250589876	0.0017	0.00231289
GO:0021602	cranial nerve morphogenesis	10	0.250579151	0.0002	0.000356582
GO:0014902	myotube differentiation	36	0.25047905	0.0016	0.002186748
GO:1902742	apoptotic process involved in development	11	0.25047385	< 0.001	< 0.001
GO:0007099	centriole replication	14	0.25045045	< 0.001	< 0.001
GO:0098534	centriole assembly	14	0.25045045	< 0.001	< 0.001
GO:1901021	positive regulation of calcium ion transmembrane transporter activity	18	0.25043615	0.0042	0.005168936
GO:1901379	regulation of potassium ion transmembrane transport	33	0.25043485	0.0003	0.000505993
GO:0043030	regulation of macrophage activation	14	0.250413679	< 0.001	< 0.001
GO:0090181	regulation of cholesterol metabolic process	35	0.250406325	0.0005	0.000791911
GO:0071071	regulation of phospholipid biosynthetic process	8	0.250353925	< 0.001	< 0.001
GO:0033077	T cell differentiation in thymus	22	0.25033345	0.002	0.002664694

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0071594	thymocyte aggregation	22	0.25033345	0.002	0.002664694
GO:0048762	mesenchymal cell differentiation	69	0.250327346	< 0.001	< 0.001
GO:0097300	programmed necrotic cell death	10	0.25029601	0.0066	0.007843941
GO:0043266	regulation of potassium ion transport	37	0.250269575	0.0002	0.000356582
GO:0097104	postsynaptic membrane assembly	6	0.25023595	0.0198	0.021642233
GO:0006941	striated muscle contraction	69	0.250234085	< 0.001	< 0.001
GO:0006379	mRNA cleavage	8	0.250225225	0.0031	0.003925117
GO:0021536	diencephalon development	20	0.25020592	< 0.001	< 0.001
GO:0045333	cellular respiration	65	0.25020097	0.0005	0.000791911
GO:2000351	regulation of endothelial cell apoptotic process	10	0.25019305	0.0008	0.001193265
GO:0006999	nuclear pore organization	6	0.25015015	0.0004	0.000648934
GO:0010635	regulation of mitochondrial fusion	5	0.25014157	0.0102	0.011688041
GO:0006301	postreplication repair	21	0.250119507	< 0.001	< 0.001
GO:0035821	modification of morphology or physiology of other organism	57	0.250053061	< 0.001	< 0.001
GO:0010739	positive regulation of protein kinase A signaling	5	0.25003861	0.0002	0.000356582
GO:0007254	JNK cascade	97	0.250028526	< 0.001	< 0.001
GO:0046634	regulation of alpha-beta T cell activation	20	0.25	0.0002	0.000356582
GO:0045637	regulation of myeloid cell differentiation	76	0.249972905	< 0.001	< 0.001
GO:0035561	regulation of chromatin binding	7	0.249972421	0.0063	0.007507211
GO:0019216	regulation of lipid metabolic process	164	0.249954484	< 0.001	< 0.001
GO:0010559	regulation of glycoprotein biosynthetic process	14	0.24993565	< 0.001	< 0.001
GO:0060485	mesenchyme development	83	0.249882929	< 0.001	< 0.001
GO:0099601	regulation of neurotransmitter receptor activity	38	0.249861139	0.0112	0.012688637
GO:0042254	ribosome biogenesis	105	0.249842496	0.0011	0.001576346
GO:0035282	segmentation	26	0.24983665	0.0037	0.004617737
GO:1903367	positive regulation of fear response	5	0.24978121	0.0071	0.008390203
GO:2000987	positive regulation of behavioral fear response	5	0.24978121	0.0071	0.008390203
GO:0009145	purine nucleoside triphosphate biosynthetic process	21	0.24976405	0.0013	0.001826625
GO:0009206	purine ribonucleoside triphosphate biosynthetic process	21	0.24976405	0.0013	0.001826625
GO:0000819	sister chromatid segregation	70	0.249737084	0.0001	0.000192793
GO:1901626	regulation of postsynaptic membrane organization	9	0.24967825	0.0001	0.000192793
GO:0032642	regulation of chemokine production	29	0.249651622	< 0.001	< 0.001
GO:0006766	vitamin metabolic process	42	0.249647607	< 0.001	< 0.001
GO:0031057	negative regulation of histone modification	22	0.24959635	< 0.001	< 0.001
GO:0017148	negative regulation of translation	91	0.249567935	0.0001	0.000192793
GO:1903779	regulation of cardiac conduction	24	0.249517375	0.0001	0.000192793
GO:0010634	positive regulation of epithelial cell migration	54	0.249516183	< 0.001	< 0.001
GO:0043502	regulation of muscle adaptation	36	0.2495138	< 0.001	< 0.001
GO:0032411	positive regulation of transporter activity	43	0.249438808	0.0001	0.000192793
GO:0006837	serotonin transport	6	0.249377949	0.0001	0.000192793
GO:0090128	regulation of synapse maturation	10	0.249369369	0.0053	0.006400268
GO:0055025	positive regulation of cardiac muscle tissue development	19	0.249353113	< 0.001	< 0.001
GO:0034767	positive regulation of ion transmembrane transport	54	0.249335049	0.0003	0.000505993
GO:0030216	keratinocyte differentiation	59	0.249303056	< 0.001	< 0.001
GO:0043518	negative regulation of DNA damage response, signal transduction by p53 class mediator	9	0.249249249	< 0.001	< 0.001
GO:0019042	viral latency	8	0.249227799	0.0001	0.000192793
GO:0060135	maternal process involved in female pregnancy	24	0.249184899	< 0.001	< 0.001
GO:0046328	regulation of JNK cascade	76	0.249163449	< 0.001	< 0.001
GO:0050685	positive regulation of mRNA processing	8	0.249163449	0.0002	0.000356582
GO:0034470	ncRNA processing	141	0.249145194	0.0007	0.001063182
GO:1900449	regulation of glutamate receptor signaling pathway	38	0.249136354	0.0144	0.016048175
GO:0021756	striatum development	9	0.249134849	0.0041	0.005057384
GO:0006626	protein targeting to mitochondrion	47	0.249125113	0.0003	0.000505993
GO:0001936	regulation of endothelial cell proliferation	42	0.249120549	< 0.001	< 0.001
GO:0051272	positive regulation of cellular component movement	186	0.24910671	< 0.001	< 0.001
GO:1903427	negative regulation of reactive oxygen species biosynthetic process	11	0.249046449	< 0.001	< 0.001
GO:0022409	positive regulation of cell-cell adhesion	75	0.249043329	< 0.001	< 0.001
GO:0046365	monosaccharide catabolic process	24	0.249002574	0.0026	0.003356522
GO:0090501	RNA phosphodiester bond hydrolysis	50	0.248957529	0.002	0.002664694
GO:0051438	regulation of ubiquitin-protein transferase activity	25	0.248957529	0.0002	0.000356582
GO:1901184	regulation of ERBB signaling pathway	40	0.248835264	< 0.001	< 0.001
GO:0051495	positive regulation of cytoskeleton organization	91	0.24880422	0.0002	0.000356582
GO:0032092	positive regulation of protein binding	41	0.248761654	< 0.001	< 0.001
GO:0001947	heart looping	19	0.248757028	< 0.001	< 0.001
GO:0061371	determination of heart left/right asymmetry	19	0.248757028	< 0.001	< 0.001
GO:0006356	regulation of transcription from RNA polymerase I promoter	15	0.248751609	0.0006	0.000927725
GO:0043489	RNA stabilization	17	0.248739496	0.001	0.001450349
GO:0031639	plasminogen activation	5	0.248648649	0.0002	0.000356582
GO:0010743	regulation of macrophage derived foam cell differentiation	5	0.248648649	0.0444	0.046382679
GO:0007052	mitotic spindle organization	41	0.248617258	0.0002	0.000356582
GO:0072678	T cell migration	16	0.248616474	0.0002	0.000356582
GO:0000245	spliceosomal complex assembly	20	0.248610039	0.0037	0.004617737
GO:0018210	peptidyl-threonine modification	59	0.248591933	0.0027	0.003470695
GO:0048864	stem cell development	29	0.248577642	< 0.001	< 0.001
GO:0050854	regulation of antigen receptor-mediated signaling pathway	17	0.248572943	< 0.001	< 0.001
GO:2000147	positive regulation of cell motility	179	0.248558055	< 0.001	< 0.001
GO:0002832	negative regulation of response to biotic stimulus	15	0.248545689	0.0005	0.000791911
GO:0090068	positive regulation of cell cycle process	98	0.248477924	< 0.001	< 0.001
GO:0090102	cochlea development	15	0.248477048	0.0029	0.003693519
GO:0022613	ribonucleoprotein complex biogenesis	176	0.248459986	0.0014	0.00194839
GO:0019318	hexose metabolic process	98	0.248378116	< 0.001	< 0.001
GO:0070050	neuron cellular homeostasis	16	0.248342986	0.0208	0.022657367
GO:0045778	positive regulation of ossification	41	0.2482908	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0045019	negative regulation of nitric oxide biosynthetic process	5	0.248288288	0.0298	0.031844809
GO:1904406	negative regulation of nitric oxide metabolic process	5	0.248288288	0.0298	0.031844809
GO:0086010	membrane depolarization during action potential	6	0.248262548	0.0299	0.031945354
GO:0000271	polysaccharide biosynthetic process	30	0.248228228	< 0.001	< 0.001
GO:0060997	dendritic spine morphogenesis	35	0.248214745	0.0098	0.011263122
GO:0007067	mitotic nuclear division	106	0.248187271	0.0001	0.000192793
GO:0048286	lung alveolus development	16	0.248149936	0.0003	0.000505993
GO:0010659	cardiac muscle cell apoptotic process	20	0.248120978	< 0.001	< 0.001
GO:0010828	positive regulation of glucose transport	18	0.248105248	0.0025	0.003237479
GO:0010257	NADH dehydrogenase complex assembly	26	0.248104148	0.0064	0.007617974
GO:0032981	mitochondrial respiratory chain complex I assembly	26	0.248104148	0.0064	0.007617974
GO:0097031	mitochondrial respiratory chain complex I biogenesis	26	0.248104148	0.0064	0.007617974
GO:0098810	neurotransmitter reuptake	12	0.248005148	0.0058	0.006954338
GO:0050918	positive chemotaxis	26	0.247995248	< 0.001	< 0.001
GO:0050905	neuromuscular process	54	0.247981315	0.0004	0.000648934
GO:0060306	regulation of membrane repolarization	13	0.247935848	0.0007	0.001063182
GO:0097352	autophagosome maturation	18	0.247919348	0.0078	0.009125612
GO:0097576	vacuole fusion	18	0.247919348	0.0078	0.009125612
GO:0071312	cellular response to alkaloid	13	0.247916048	0.0033	0.004153051
GO:0042044	fluid transport	7	0.247913219	0.0001	0.000192793
GO:0007567	parturition	5	0.247876448	< 0.001	< 0.001
GO:0032793	positive regulation of CREB transcription factor activity	8	0.247812098	0.0097	0.01115531
GO:0034599	cellular response to oxidative stress	113	0.247794444	< 0.001	< 0.001
GO:0015701	bicarbonate transport	12	0.247747748	0.0025	0.003237479
GO:0002521	leukocyte differentiation	151	0.247700087	< 0.001	< 0.001
GO:0003170	heart valve development	24	0.247694123	< 0.001	< 0.001
GO:0001525	angiogenesis	157	0.247681348	< 0.001	< 0.001
GO:1902229	regulation of intrinsic apoptotic signaling pathway in response to DNA damage	21	0.247655819	0.0056	0.006732458
GO:0045742	positive regulation of epidermal growth factor receptor signaling pathway	12	0.247597598	0.0001	0.000192793
GO:0071479	cellular response to ionizing radiation	29	0.24759242	0.0022	0.002896881
GO:0032633	interleukin-4 production	7	0.247582276	0.001	0.001450349
GO:0032673	regulation of interleukin-4 production	7	0.247582276	0.001	0.001450349
GO:0007163	establishment or maintenance of cell polarity	87	0.247580586	< 0.001	< 0.001
GO:0061647	histone H3-K9 modification	15	0.247567568	0.0039	0.004841626
GO:0043903	regulation of symbiosis, encompassing mutualism through parasitism	91	0.247556819	0.0003	0.000505993
GO:0043473	pigmentation	33	0.247556648	< 0.001	< 0.001
GO:0098760	response to interleukin-7	11	0.247548848	< 0.001	< 0.001
GO:0098761	cellular response to interleukin-7	11	0.247548848	< 0.001	< 0.001
GO:0022904	respiratory electron transport chain	39	0.247533248	0.0068	0.008063902
GO:0034250	positive regulation of cellular amide metabolic process	68	0.2475282	0.0001	0.000192793
GO:0033059	cellular pigmentation	24	0.247522523	< 0.001	< 0.001
GO:0048871	multicellular organismal homeostasis	122	0.247509336	< 0.001	< 0.001
GO:0007272	ensheathment of neurons	41	0.247499765	< 0.001	< 0.001
GO:0008366	axon ensheathment	41	0.247499765	< 0.001	< 0.001
GO:0030335	positive regulation of cell migration	175	0.247495495	< 0.001	< 0.001
GO:1900363	regulation of mRNA polyadenylation	6	0.247447447	0.0043	0.005276385
GO:0071216	cellular response to biotic stimulus	73	0.247396908	< 0.001	< 0.001
GO:0043484	regulation of RNA splicing	44	0.247390897	< 0.001	< 0.001
GO:0043649	dicarboxylic acid catabolic process	11	0.247361647	0.0003	0.000505993
GO:1901659	glycosyl compound biosynthetic process	44	0.247361647	0.0003	0.000505993
GO:1901264	carbohydrate derivative transport	14	0.247269719	0.0002	0.000356582
GO:0061053	somite development	20	0.247245817	0.0032	0.004042263
GO:0031424	keratinization	36	0.247240097	0.0001	0.000192793
GO:0034329	cell junction assembly	82	0.247239225	< 0.001	< 0.001
GO:0022900	electron transport chain	70	0.247214562	0.0003	0.000505993
GO:0030100	regulation of endocytosis	103	0.247159226	< 0.001	< 0.001
GO:0042177	negative regulation of protein catabolic process	54	0.247137614	< 0.001	< 0.001
GO:0071222	cellular response to lipopolysaccharide	64	0.24708816	< 0.001	< 0.001
GO:0006721	terpenoid metabolic process	30	0.246924067	< 0.001	< 0.001
GO:0034340	response to type I interferon	24	0.246921922	0.0004	0.000648934
GO:0072606	interleukin-8 secretion	9	0.246904047	< 0.001	< 0.001
GO:0046636	negative regulation of alpha-beta T cell activation	7	0.246883618	0.0062	0.00739947
GO:2000515	negative regulation of CD4-positive, alpha-beta T cell activation	7	0.246883618	0.0062	0.00739947
GO:0051156	glucose 6-phosphate metabolic process	8	0.246846847	0.0064	0.007617974
GO:0048168	regulation of neuronal synaptic plasticity	31	0.24683024	0.0122	0.013738029
GO:0010881	regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion	11	0.246823447	0.0001	0.000192793
GO:0043500	muscle adaptation	41	0.246777788	< 0.001	< 0.001
GO:0008037	cell recognition	47	0.246770174	< 0.001	< 0.001
GO:0045987	positive regulation of smooth muscle contraction	11	0.246706447	< 0.001	< 0.001
GO:1903069	regulation of ER-associated ubiquitin-dependent protein catabolic process	5	0.246640927	0.0099	0.011373214
GO:0019985	translesion synthesis	17	0.24663487	< 0.001	< 0.001
GO:0048608	reproductive structure development	145	0.246600098	< 0.001	< 0.001
GO:0002011	morphogenesis of an epithelial sheet	21	0.246589447	0.0004	0.000648934
GO:2000171	negative regulation of dendrite development	14	0.246571061	0.0112	0.012688637
GO:0003179	heart valve morphogenesis	22	0.246566047	< 0.001	< 0.001
GO:0032528	microvillus organization	9	0.246560847	0.0356	0.037648219
GO:0048008	platelet-derived growth factor receptor signaling pathway	24	0.246514372	< 0.001	< 0.001
GO:0007274	neuromuscular synaptic transmission	10	0.246486486	0.0002	0.000356582
GO:0002042	cell migration involved in sprouting angiogenesis	22	0.246484146	0.0103	0.011785137
GO:0045725	positive regulation of glycogen biosynthetic process	7	0.246442361	0.0001	0.000192793
GO:0021683	cerebellar granular layer morphogenesis	5	0.246435006	< 0.001	< 0.001
GO:0006907	pinocytosis	8	0.246396396	0.0003	0.000505993
GO:0009791	post-embryonic development	36	0.246389246	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0042026	protein refolding	6	0.246332046	< 0.001	< 0.001
GO:0090207	regulation of triglyceride metabolic process	11	0.246332046	< 0.001	< 0.001
GO:2001022	positive regulation of response to DNA damage stimulus	38	0.246311725	< 0.001	< 0.001
GO:0045649	regulation of macrophage differentiation	11	0.246308646	< 0.001	< 0.001
GO:2000242	negative regulation of reproductive process	16	0.246299871	0.0002	0.000356582
GO:0003007	heart morphogenesis	91	0.246281132	< 0.001	< 0.001
GO:0009410	response to xenobiotic stimulus	49	0.24625325	< 0.001	< 0.001
GO:1903539	protein localization to postsynaptic membrane	13	0.246153846	0.0068	0.008063902
GO:0042455	ribonucleoside biosynthetic process	41	0.246149983	0.0003	0.000505993
GO:0048255	mRNA stabilization	16	0.246074646	0.0004	0.000648934
GO:0005996	monosaccharide metabolic process	103	0.246049656	< 0.001	< 0.001
GO:0021904	dorsal/ventral neural tube patterning	9	0.246046046	0.0149	0.016557598
GO:0010171	body morphogenesis	14	0.246001103	< 0.001	< 0.001
GO:0045580	regulation of T cell differentiation	37	0.245977251	< 0.001	< 0.001
GO:0048714	positive regulation of oligodendrocyte differentiation	5	0.245920206	0.003	0.003811001
GO:0071868	cellular response to monoamine stimulus	17	0.245892952	0.0005	0.000791911
GO:0071870	cellular response to catecholamine stimulus	17	0.245892952	0.0005	0.000791911
GO:0071346	cellular response to interferon-gamma	53	0.245890095	< 0.001	< 0.001
GO:0009163	nucleoside biosynthetic process	43	0.245889078	0.0003	0.000505993
GO:0070189	kynurenine metabolic process	5	0.245868726	0.0024	0.003116943
GO:0097052	L-kynurenine metabolic process	5	0.245868726	0.0024	0.003116943
GO:0061458	reproductive system development	147	0.245855768	< 0.001	< 0.001
GO:0072178	nephric duct morphogenesis	5	0.245817246	0.0022	0.002896881
GO:0017185	peptidyl-lysine hydroxylation	5	0.245817246	0.0152	0.016877091
GO:0015850	organic hydroxy compound transport	77	0.24581056	< 0.001	< 0.001
GO:0030595	leukocyte chemotaxis	59	0.24580852	< 0.001	< 0.001
GO:0007127	meiosis I	25	0.245776062	0.0015	0.002069969
GO:0030218	erythrocyte differentiation	48	0.245699271	< 0.001	< 0.001
GO:0007030	Golgi organization	50	0.245683398	< 0.001	< 0.001
GO:0061614	pri-miRNA transcription from RNA polymerase II promoter	22	0.245676846	< 0.001	< 0.001
GO:0036151	phosphatidylcholine acyl-chain remodeling	8	0.245624196	0.0027	0.003470695
GO:0071772	response to BMP	43	0.245619706	< 0.001	< 0.001
GO:0071773	cellular response to BMP stimulus	43	0.245619706	< 0.001	< 0.001
GO:0060421	positive regulation of heart growth	15	0.245611326	< 0.001	< 0.001
GO:0007080	mitotic metaphase plate congression	21	0.245608874	0.0039	0.004841626
GO:0010458	exit from mitosis	14	0.245596617	0.0007	0.001063182
GO:0033108	mitochondrial respiratory chain complex assembly	36	0.245588446	0.0041	0.005057384
GO:0006754	ATP biosynthetic process	19	0.245546298	0.0015	0.002069969
GO:0010880	regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	14	0.245394374	< 0.001	< 0.001
GO:0002717	positive regulation of natural killer cell mediated immunity	6	0.245388245	< 0.001	< 0.001
GO:0032543	mitochondrial translation	61	0.245378399	0.004	0.004954389
GO:0006875	cellular metal ion homeostasis	181	0.245377817	< 0.001	< 0.001
GO:0032088	negative regulation of NF-kappaB transcription factor activity	36	0.245323895	< 0.001	< 0.001
GO:0031668	cellular response to extracellular stimulus	95	0.245299736	< 0.001	< 0.001
GO:0046676	negative regulation of insulin secretion	17	0.245287304	0.0021	0.002780108
GO:0015980	energy derivation by oxidation of organic compounds	102	0.24527721	0.0002	0.000356582
GO:1900451	positive regulation of glutamate receptor signaling pathway	9	0.245273845	0.0003	0.000505993
GO:0045776	negative regulation of blood pressure	14	0.245265674	0.0002	0.000356582
GO:0043576	regulation of respiratory gaseous exchange	12	0.245238095	0.0004	0.000648934
GO:0009991	response to extracellular stimulus	171	0.245237719	< 0.001	< 0.001
GO:2000401	regulation of lymphocyte migration	18	0.245216645	< 0.001	< 0.001
GO:0048640	negative regulation of developmental growth	39	0.245203445	0.0013	0.001826625
GO:0030224	monocyte differentiation	12	0.245195195	0.0004	0.000648934
GO:1903131	mononuclear cell differentiation	12	0.245195195	0.0004	0.000648934
GO:0033014	tetrapyrrole biosynthetic process	12	0.245195195	0.0006	0.000927725
GO:0034341	response to interferon-gamma	58	0.245160431	< 0.001	< 0.001
GO:0003416	endochondral bone growth	8	0.24514157	0.0111	0.012593827
GO:0044282	small molecule catabolic process	131	0.245119711	< 0.001	< 0.001
GO:0001510	RNA methylation	20	0.245006435	0.0002	0.000356582
GO:0035973	aggrephagy	6	0.244959245	0.0028	0.003584743
GO:0007194	negative regulation of adenylate cyclase activity	7	0.244897959	< 0.001	< 0.001
GO:0030800	negative regulation of cyclic nucleotide metabolic process	7	0.244897959	< 0.001	< 0.001
GO:0030803	negative regulation of cyclic nucleotide biosynthetic process	7	0.244897959	< 0.001	< 0.001
GO:0030815	negative regulation of cAMP metabolic process	7	0.244897959	< 0.001	< 0.001
GO:0030818	negative regulation of cAMP biosynthetic process	7	0.244897959	< 0.001	< 0.001
GO:0031280	negative regulation of cyclase activity	7	0.244897959	< 0.001	< 0.001
GO:0051350	negative regulation of lyase activity	7	0.244897959	< 0.001	< 0.001
GO:0003012	muscle system process	160	0.244850386	< 0.001	< 0.001
GO:1902108	regulation of mitochondrial membrane permeability involved in apoptotic process	28	0.244833609	0.0007	0.001063182
GO:0000070	mitotic sister chromatid segregation	64	0.244783623	0.0001	0.000192793
GO:0001935	endothelial cell proliferation	44	0.244764245	< 0.001	< 0.001
GO:0016485	protein processing	63	0.244673245	< 0.001	< 0.001
GO:0015949	nucleobase-containing small molecule interconversion	12	0.244637495	< 0.001	< 0.001
GO:0071219	cellular response to molecule of bacterial origin	65	0.244633205	< 0.001	< 0.001
GO:0007029	endoplasmic reticulum organization	24	0.24462677	0.0001	0.000192793
GO:0035872	nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway	12	0.244573145	0.0006	0.000927725
GO:0070423	nucleotide-binding oligomerization domain containing signaling pathway	12	0.244573145	0.0006	0.000927725
GO:0051783	regulation of nuclear division	68	0.244484821	< 0.001	< 0.001
GO:0034260	negative regulation of GTPase activity	21	0.244456702	< 0.001	< 0.001
GO:0046677	response to antibiotic	12	0.244444444	< 0.001	< 0.001
GO:0044319	wound healing, spreading of cells	12	0.244401544	0.0014	0.00194839
GO:0090504	epiboly	12	0.244401544	0.0014	0.00194839
GO:0090505	epiboly involved in wound healing	12	0.244401544	0.0014	0.00194839

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0043393	regulation of protein binding	91	0.244397302	< 0.001	< 0.001
GO:1902475	L-alpha-amino acid transmembrane transport	6	0.244358644	0.0128	0.014368758
GO:0031050	dsRNA fragmentation	19	0.244340581	0.0003	0.000505993
GO:0070918	production of small RNA involved in gene silencing by RNA	19	0.244340581	0.0003	0.000505993
GO:0002714	positive regulation of B cell mediated immunity	12	0.244315744	0.0015	0.002069969
GO:0002891	positive regulation of immunoglobulin mediated immune response	12	0.244315744	0.0015	0.002069969
GO:0042790	transcription of nuclear large rRNA transcript from RNA polymerase I promoter	6	0.244315744	0.033	0.035035756
GO:1901836	regulation of transcription of nuclear large rRNA transcript from RNA polymerase I promoter	6	0.244315744	0.033	0.035035756
GO:2001223	negative regulation of neuron migration	7	0.244309616	< 0.001	< 0.001
GO:0030193	regulation of blood coagulation	29	0.244290596	< 0.001	< 0.001
GO:0050818	regulation of coagulation	29	0.244290596	< 0.001	< 0.001
GO:1900046	regulation of hemostasis	29	0.244290596	< 0.001	< 0.001
GO:0045444	fat cell differentiation	82	0.244247732	< 0.001	< 0.001
GO:0030099	myeloid cell differentiation	136	0.244231206	< 0.001	< 0.001
GO:0007091	metaphase/anaphase transition of mitotic cell cycle	24	0.244176319	0.0012	0.001702047
GO:0010965	regulation of mitotic sister chromatid separation	24	0.244176319	0.0012	0.001702047
GO:0044784	metaphase/anaphase transition of cell cycle	24	0.244176319	0.0012	0.001702047
GO:0006414	translational elongation	55	0.244151164	0.0024	0.003116943
GO:0007565	female pregnancy	66	0.244140244	< 0.001	< 0.001
GO:0009262	deoxyribonucleotide metabolic process	13	0.244114444	0.0001	0.000192793
GO:1903671	negative regulation of sprouting angiogenesis	8	0.244079794	0.0016	0.002186748
GO:0031128	developmental induction	6	0.244058344	0.0102	0.011688041
GO:0090049	regulation of cell migration involved in sprouting angiogenesis	15	0.244049764	0.0018	0.002428764
GO:0010718	positive regulation of epithelial to mesenchymal transition	13	0.243975844	< 0.001	< 0.001
GO:0045540	regulation of cholesterol biosynthetic process	30	0.243963964	0.0011	0.001576346
GO:0042364	water-soluble vitamin biosynthetic process	6	0.243886744	0.0038	0.004725081
GO:1901617	organic hydroxy compound biosynthetic process	105	0.243863455	< 0.001	< 0.001
GO:0043900	regulation of multi-organism process	116	0.243846802	0.0001	0.000192793
GO:0031341	regulation of cell killing	18	0.243843844	< 0.001	< 0.001
GO:0010507	negative regulation of autophagy	35	0.243831587	0.0004	0.000648934
GO:0045740	positive regulation of DNA replication	15	0.243826684	0.0002	0.000356582
GO:0007088	regulation of mitotic nuclear division	64	0.243798263	0.0001	0.000192793
GO:0090559	regulation of membrane permeability	31	0.243749741	0.0004	0.000648934
GO:0010804	negative regulation of tumor necrosis factor-mediated signaling pathway	9	0.243729444	0.0007	0.001063182
GO:0009110	vitamin biosynthetic process	9	0.243700844	0.0018	0.002428764
GO:0018107	peptidyl-threonine phosphorylation	55	0.243687844	0.0038	0.004725081
GO:0001838	embryonic epithelial tube formation	52	0.243663994	< 0.001	< 0.001
GO:0072175	epithelial tube formation	52	0.243663994	< 0.001	< 0.001
GO:2000480	negative regulation of cAMP-dependent protein kinase activity	5	0.243655084	0.0002	0.000356582
GO:0072329	monocarboxylic acid catabolic process	35	0.243647729	< 0.001	< 0.001
GO:0015914	phospholipid transport	27	0.243643644	< 0.001	< 0.001
GO:0045070	positive regulation of viral genome replication	19	0.243636117	0.0014	0.00194839
GO:0048536	spleen development	13	0.243599644	< 0.001	< 0.001
GO:0031116	positive regulation of microtubule polymerization	11	0.243570844	0.0046	0.0056228
GO:0070085	glycosylation	99	0.243557844	< 0.001	< 0.001
GO:0014015	positive regulation of gliogenesis	24	0.243543544	< 0.001	< 0.001
GO:1900271	regulation of long-term synaptic potentiation	23	0.243489452	0.0123	0.013827585
GO:0061029	eyelid development in camera-type eye	5	0.243397683	0.0078	0.009125612
GO:0006869	lipid transport	107	0.243377957	< 0.001	< 0.001
GO:0031065	positive regulation of histone deacetylation	8	0.243307593	0.0117	0.013205263
GO:0046637	regulation of alpha-beta T cell differentiation	16	0.243291506	0.0002	0.000356582
GO:0045606	positive regulation of epidermal cell differentiation	6	0.243243243	0.0003	0.000505993
GO:0021915	neural tube development	65	0.243211563	< 0.001	< 0.001
GO:0000302	response to reactive oxygen species	82	0.243208714	0.0001	0.000192793
GO:0030397	membrane disassembly	7	0.243206472	0.0094	0.010831045
GO:0051081	nuclear envelope disassembly	7	0.243206472	0.0094	0.010831045
GO:0071359	cellular response to dsRNA	27	0.24320511	< 0.001	< 0.001
GO:0007006	mitochondrial membrane organization	57	0.243202601	0.0011	0.001576346
GO:0009072	aromatic amino acid family metabolic process	6	0.243071643	0.0005	0.000791911
GO:0009074	aromatic amino acid family catabolic process	6	0.243071643	0.0005	0.000791911
GO:1903524	positive regulation of blood circulation	26	0.243015543	< 0.001	< 0.001
GO:0070306	lens fiber cell differentiation	14	0.242967457	0.0123	0.013827585
GO:0006006	glucose metabolic process	81	0.242944532	< 0.001	< 0.001
GO:0007256	activation of JNKK activity	6	0.242857143	0.0058	0.006954338
GO:0070167	regulation of biomineral tissue development	29	0.242826077	< 0.001	< 0.001
GO:0034454	microtubule anchoring at centrosome	5	0.242779923	0.0103	0.011785137
GO:0002573	myeloid leukocyte differentiation	67	0.242774544	< 0.001	< 0.001
GO:0071425	hematopoietic stem cell proliferation	8	0.242728443	< 0.001	< 0.001
GO:0046716	muscle cell cellular homeostasis	10	0.242728443	< 0.001	< 0.001
GO:0003229	ventricular cardiac muscle tissue development	24	0.242717718	< 0.001	< 0.001
GO:0007205	protein kinase C-activating G-protein coupled receptor signaling pathway	11	0.242705043	0.0073	0.008600218
GO:0048339	paraxial mesoderm development	8	0.242696268	0.0018	0.002428764
GO:0072376	protein activation cascade	14	0.242691671	< 0.001	< 0.001
GO:0060420	regulation of heart growth	23	0.242683677	< 0.001	< 0.001
GO:0071466	cellular response to xenobiotic stimulus	45	0.242676963	< 0.001	< 0.001
GO:0044236	multicellular organism metabolic process	29	0.242675188	< 0.001	< 0.001
GO:0070734	histone H3-K27 methylation	7	0.2426549	0.0001	0.000192793
GO:0060711	labyrinthine layer development	19	0.242633611	< 0.001	< 0.001
GO:1902652	secondary alcohol metabolic process	63	0.242618128	0.0031	0.003925117
GO:0033013	tetrapyrrole metabolic process	20	0.242612613	0.0002	0.000356582
GO:0071501	cellular response to sterol depletion	5	0.242574003	< 0.001	< 0.001
GO:0006878	cellular copper ion homeostasis	8	0.242535393	0.0041	0.005057384
GO:0046326	positive regulation of glucose import	14	0.2425262	0.0053	0.006400268

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0007032	endosome organization	41	0.242508711	0.0016	0.002186748
GO:1904353	regulation of telomere capping	14	0.242507814	0.0079	0.009236608
GO:1902105	regulation of leukocyte differentiation	76	0.242477816	< 0.001	< 0.001
GO:0042446	hormone biosynthetic process	19	0.242443948	< 0.001	< 0.001
GO:0002693	positive regulation of cellular extravasation	7	0.242434271	< 0.001	< 0.001
GO:0072529	pyrimidine-containing compound catabolic process	11	0.242424242	0.0007	0.001063182
GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling	67	0.24240189	< 0.001	< 0.001
GO:0045687	positive regulation of glial cell differentiation	11	0.242354042	< 0.001	< 0.001
GO:0031279	regulation of cyclase activity	30	0.242256542	0.0011	0.001576346
GO:0035235	ionotropic glutamate receptor signaling pathway	14	0.242250414	0.0222	0.02411918
GO:0050886	endocrine process	20	0.242226512	< 0.001	< 0.001
GO:0010770	positive regulation of cell morphogenesis involved in differentiation	71	0.242217268	< 0.001	< 0.001
GO:0009060	aerobic respiration	17	0.242213642	0.0018	0.002428764
GO:0007613	memory	60	0.242192192	0.0023	0.003013139
GO:0009617	response to bacterium	162	0.242142142	< 0.001	< 0.001
GO:0003143	embryonic heart tube morphogenesis	20	0.242020592	< 0.001	< 0.001
GO:0048854	brain morphogenesis	16	0.241956242	0.0007	0.001063182
GO:0048532	anatomical structure arrangement	6	0.241956242	0.0153	0.01697069
GO:0050856	regulation of T cell receptor signaling pathway	13	0.241936442	0.0018	0.002428764
GO:1905515	non-motile cilium assembly	22	0.241932842	< 0.001	< 0.001
GO:0050773	regulation of dendrite development	78	0.241824242	0.0017	0.00231289
GO:0006323	DNA packaging	57	0.241789158	0.0021	0.002780108
GO:0070920	regulation of production of small RNA involved in gene silencing by RNA	6	0.241784642	0.0003	0.000505993
GO:1903798	regulation of production of miRNAs involved in gene silencing by miRNA	6	0.241784642	0.0003	0.000505993
GO:0006972	hyperosmotic response	10	0.241776062	< 0.001	< 0.001
GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	145	0.241737896	0.0012	0.001702047
GO:0000398	mRNA splicing, via spliceosome	145	0.241737896	0.0012	0.001702047
GO:0097035	regulation of membrane lipid distribution	16	0.241731017	0.0006	0.000927725
GO:0014072	response to isoquinoline alkaloid	20	0.241711712	0.0014	0.00194839
GO:0043278	response to morphine	20	0.241711712	0.0014	0.00194839
GO:0006111	regulation of gluconeogenesis	18	0.241670242	< 0.001	< 0.001
GO:0055065	metal ion homeostasis	198	0.241649442	< 0.001	< 0.001
GO:0001921	positive regulation of receptor recycling	5	0.241647362	0.0003	0.000505993
GO:0010633	negative regulation of epithelial cell migration	35	0.241640007	< 0.001	< 0.001
GO:0045765	regulation of angiogenesis	86	0.241632995	< 0.001	< 0.001
GO:0030520	intracellular estrogen receptor signaling pathway	22	0.241616942	< 0.001	< 0.001
GO:0016051	carbohydrate biosynthetic process	77	0.241611927	< 0.001	< 0.001
GO:0010906	regulation of glucose metabolic process	44	0.241593542	< 0.001	< 0.001
GO:1903115	regulation of actin filament-based movement	14	0.241570142	0.0001	0.000192793
GO:0000281	mitotic cytokinesis	24	0.241516517	0.001	0.001450349
GO:0009411	response to UV	54	0.241493875	0.0001	0.000192793
GO:0048593	camera-type eye morphogenesis	33	0.241449241	< 0.001	< 0.001
GO:0044090	positive regulation of vacuole organization	12	0.241419991	0.0003	0.000505993
GO:0006805	xenobiotic metabolic process	44	0.241400491	< 0.001	< 0.001
GO:1901186	positive regulation of ERBB signaling pathway	13	0.241382041	< 0.001	< 0.001
GO:0034162	toll-like receptor 9 signaling pathway	10	0.241364221	< 0.001	< 0.001
GO:0014037	Schwann cell differentiation	13	0.241342441	0.0002	0.000356582
GO:0002067	glandular epithelial cell differentiation	15	0.241184041	0.0012	0.001702047
GO:0031167	rRNA methylation	5	0.241184041	0.0028	0.003584743
GO:0007519	skeletal muscle tissue development	55	0.241179361	< 0.001	< 0.001
GO:0030799	regulation of cyclic nucleotide metabolic process	26	0.241154341	0.0007	0.001063182
GO:0030802	regulation of cyclic nucleotide biosynthetic process	26	0.241154341	0.0007	0.001063182
GO:0046626	regulation of insulin receptor signaling pathway	21	0.24114727	0.0077	0.00902229
GO:0006695	cholesterol biosynthetic process	41	0.241001978	0.0029	0.003693519
GO:1902653	secondary alcohol biosynthetic process	41	0.241001978	0.0029	0.003693519
GO:0007183	SMAD protein complex assembly	6	0.240883741	< 0.001	< 0.001
GO:0071871	response to epinephrine	6	0.240883741	< 0.001	< 0.001
GO:0043038	amino acid activation	20	0.240836551	0.0027	0.003470695
GO:0043039	tRNA aminoacylation	20	0.240836551	0.0027	0.003470695
GO:0036124	histone H3-K9 trimethylation	6	0.240755041	0.0007	0.001063182
GO:0003016	respiratory system process	15	0.240720721	0.0001	0.000192793
GO:0006486	protein glycosylation	92	0.240652454	< 0.001	< 0.001
GO:0043413	macromolecule glycosylation	92	0.240652454	< 0.001	< 0.001
GO:0061001	regulation of dendritic spine morphogenesis	27	0.240650174	0.0114	0.012893596
GO:0032727	positive regulation of interferon-alpha production	7	0.240632469	0.0084	0.009757868
GO:1901387	positive regulation of voltage-gated calcium channel activity	6	0.240626341	0.0126	0.014156008
GO:0014743	regulation of muscle hypertrophy	28	0.240577312	0.0001	0.000192793
GO:0010664	negative regulation of striated muscle cell apoptotic process	13	0.240570241	< 0.001	< 0.001
GO:0070059	intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	26	0.240550441	0.0002	0.000356582
GO:0010611	regulation of cardiac muscle hypertrophy	27	0.240516707	0.0001	0.000192793
GO:0045773	positive regulation of axon extension	23	0.240512562	0.0015	0.002069969
GO:0046688	response to copper ion	16	0.240444015	0.002	0.002664694
GO:0048679	regulation of axon regeneration	13	0.24043164	0.0168	0.018543137
GO:0000375	RNA splicing, via transesterification reactions	149	0.240287459	0.0014	0.00194839
GO:0006182	cGMP biosynthetic process	6	0.24028314	0.0005	0.000791911
GO:0001707	mesoderm formation	23	0.240255162	< 0.001	< 0.001
GO:0000731	DNA synthesis involved in DNA repair	21	0.24024024	< 0.001	< 0.001
GO:0032091	negative regulation of protein binding	40	0.240160875	< 0.001	< 0.001
GO:0006687	glycosphingolipid metabolic process	25	0.24015444	0.0004	0.000648934
GO:0046058	cAMP metabolic process	26	0.24012474	0.0024	0.003116943
GO:1902253	regulation of intrinsic apoptotic signaling pathway by p53 class mediator	14	0.240117669	0.0304	0.032428267
GO:0048023	positive regulation of melanin biosynthetic process	5	0.24010296	0.0073	0.008600218
GO:1900378	positive regulation of secondary metabolite biosynthetic process	5	0.24010296	0.0073	0.008600218

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0001837	epithelial to mesenchymal transition	49	0.240101909	< 0.001	< 0.001
GO:1902117	positive regulation of organelle assembly	28	0.240080897	0.0001	0.000192793
GO:0072527	pyrimidine-containing compound metabolic process	28	0.240007354	0.0004	0.000648934
GO:1990048	anterograde neuronal dense core vesicle transport	5	0.24	0.0288	0.030849395
GO:0002756	MyD88-independent toll-like receptor signaling pathway	15	0.23998284	0.0004	0.000648934
GO:0086019	cell-cell signaling involved in cardiac conduction	10	0.23994852	0.0348	0.036852675
GO:0031281	positive regulation of cyclase activity	21	0.23989704	0.0025	0.003237479
GO:2001252	positive regulation of chromosome organization	34	0.23989704	0.0001	0.000192793
GO:0002068	glandular epithelial cell development	9	0.23981124	0.01	0.011478335
GO:0045833	negative regulation of lipid metabolic process	26	0.23977824	< 0.001	< 0.001
GO:0030148	sphingolipid biosynthetic process	31	0.239755885	0.0008	0.001193265
GO:1904738	vascular associated smooth muscle cell migration	10	0.23969112	0.0071	0.008390203
GO:1904752	regulation of vascular associated smooth muscle cell migration	10	0.23969112	0.0071	0.008390203
GO:0045619	regulation of lymphocyte differentiation	44	0.23964549	< 0.001	< 0.001
GO:0060395	SMAD protein signal transduction	14	0.239621254	< 0.001	< 0.001
GO:0055003	cardiac myofibril assembly	6	0.23959674	< 0.001	< 0.001
GO:0019227	neuronal action potential propagation	5	0.23958816	0.0315	0.033528856
GO:0098870	action potential propagation	5	0.23958816	0.0315	0.033528856
GO:0045807	positive regulation of endocytosis	59	0.239556748	< 0.001	< 0.001
GO:0090050	positive regulation of cell migration involved in sprouting angiogenesis	7	0.239529325	0.0229	0.024839743
GO:0033045	regulation of sister chromatid segregation	30	0.23950236	0.0001	0.000192793
GO:1904779	regulation of protein localization to centrosome	9	0.239496639	0.0019	0.00254969
GO:0061512	protein localization to cilium	21	0.239455782	< 0.001	< 0.001
GO:2000311	regulation of alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate selective glutamate receptor activity	12	0.239446589	0.0248	0.026750339
GO:0042552	myelination	40	0.239446589	< 0.001	< 0.001
GO:0008203	cholesterol metabolic process	62	0.239432059	0.0032	0.004042263
GO:0051298	centrosome duplication	26	0.239372339	< 0.001	< 0.001
GO:0043902	positive regulation of multi-organism process	72	0.239285714	0.0004	0.000648934
GO:0051497	negative regulation of stress fiber assembly	12	0.239253539	0.0051	0.006185009
GO:0050435	beta-amyloid metabolic process	19	0.239165481	0.0004	0.000648934
GO:0018027	peptidyl-lysine dimethylation	9	0.239153439	0.0021	0.002780108
GO:0032508	DNA duplex unwinding	33	0.239140439	0.0015	0.002069969
GO:0043200	response to amino acid	52	0.239075339	< 0.001	< 0.001
GO:0021532	neural tube patterning	16	0.239044402	0.0082	0.009562538
GO:1903034	regulation of response to wounding	56	0.239028314	< 0.001	< 0.001
GO:0099574	regulation of protein catabolic process at synapse, modulating synaptic transmission	5	0.239021879	0.0002	0.000356582
GO:0006244	pyrimidine nucleotide catabolic process	5	0.239021879	0.01	0.011478335
GO:0060251	regulation of glial cell proliferation	12	0.239017589	0.0122	0.013738029
GO:0046940	nucleoside monophosphate phosphorylation	7	0.239014525	< 0.001	< 0.001
GO:0002761	regulation of myeloid leukocyte differentiation	37	0.239013531	< 0.001	< 0.001
GO:0034728	nucleosome organization	48	0.238969326	0.0035	0.004390436
GO:2001242	regulation of intrinsic apoptotic signaling pathway	65	0.238938719	0.0001	0.000192793
GO:0097205	renal filtration	5	0.238918919	< 0.001	< 0.001
GO:0034248	regulation of cellular amide metabolic process	200	0.238906049	0.0002	0.000356582
GO:0010876	lipid localization	118	0.238893615	< 0.001	< 0.001
GO:0046902	regulation of mitochondrial membrane permeability	30	0.238850279	0.0003	0.000505993
GO:0010658	striated muscle cell apoptotic process	21	0.238708096	< 0.001	< 0.001
GO:0032006	regulation of TOR signaling	41	0.238697931	< 0.001	< 0.001
GO:0035268	protein mannosylation	11	0.238680239	0.0005	0.000791911
GO:0032008	positive regulation of TOR signaling	16	0.238642214	0.0008	0.001193265
GO:0051017	actin filament bundle assembly	65	0.238625879	< 0.001	< 0.001
GO:0010511	regulation of phosphatidylinositol biosynthetic process	5	0.238610039	< 0.001	< 0.001
GO:0031112	positive regulation of microtubule polymerization or depolymerization	14	0.238610039	0.0019	0.00254969
GO:0010934	macrophage cytokine production	6	0.238610039	0.0029	0.003693519
GO:1904030	negative regulation of cyclin-dependent protein kinase activity	12	0.238588589	0.0046	0.0056228
GO:0061051	positive regulation of cell growth involved in cardiac muscle cell development	5	0.238558559	0.005	0.006070546
GO:1904355	positive regulation of telomere capping	9	0.238552839	0.0022	0.002896881
GO:0001974	blood vessel remodeling	14	0.238462953	< 0.001	< 0.001
GO:0046835	carbohydrate phosphorylation	14	0.238462953	0.0006	0.000927725
GO:0019682	glyceraldehyde-3-phosphate metabolic process	8	0.238449163	0.0177	0.019488753
GO:0097062	dendritic spine maintenance	10	0.238352638	0.0011	0.001576346
GO:0003071	renal system process involved in regulation of systemic arterial blood pressure	5	0.238352638	< 0.001	< 0.001
GO:0051306	mitotic sister chromatid separation	25	0.23832175	0.0009	0.001319479
GO:0048512	circadian behavior	14	0.238279095	0.0017	0.00231289
GO:0097345	mitochondrial outer membrane permeabilization	25	0.23827027	0.0013	0.001826625
GO:0043267	negative regulation of potassium ion transport	9	0.238266838	0.0001	0.000192793
GO:0030852	regulation of granulocyte differentiation	6	0.238223938	0.0007	0.001063182
GO:0021675	nerve development	24	0.238191763	0.0049	0.005958506
GO:0071482	cellular response to light stimulus	39	0.238141438	< 0.001	< 0.001
GO:0006418	tRNA aminoacylation for protein translation	18	0.238109538	0.0019	0.00254969
GO:0000154	rRNA modification	10	0.238095238	0.0008	0.001193265
GO:0002262	myeloid cell homeostasis	59	0.238064699	< 0.001	< 0.001
GO:0016197	endosomal transport	138	0.238022495	0.0002	0.000356582
GO:1990089	response to nerve growth factor	24	0.238020163	0.0007	0.001063182
GO:1990090	cellular response to nerve growth factor stimulus	24	0.238020163	0.0007	0.001063182
GO:0060317	cardiac epithelial to mesenchymal transition	10	0.237940798	< 0.001	< 0.001
GO:0016246	RNA interference	5	0.237940798	< 0.001	< 0.001
GO:0036315	cellular response to sterol	10	0.237915058	< 0.001	< 0.001
GO:0006112	energy reserve metabolic process	35	0.237867255	< 0.001	< 0.001
GO:0061099	negative regulation of protein tyrosine kinase activity	9	0.237837838	0.0027	0.003470695
GO:1901615	organic hydroxy compound metabolic process	186	0.237832302	< 0.001	< 0.001
GO:0042059	negative regulation of epidermal growth factor receptor signaling pathway	20	0.237824968	0.0005	0.000791911

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1904018	positive regulation of vasculature development	53	0.237823268	< 0.001	< 0.001
GO:0008535	respiratory chain complex IV assembly	6	0.237666238	0.0201	0.021947949
GO:1903432	regulation of TORC1 signaling	16	0.237660875	< 0.001	< 0.001
GO:0006305	DNA alkylation	18	0.237609038	0.0001	0.000192793
GO:0006306	DNA methylation	18	0.237609038	0.0001	0.000192793
GO:1900739	regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	15	0.237597598	0.0031	0.003925117
GO:1900740	positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	15	0.237597598	0.0031	0.003925117
GO:1900024	regulation of substrate adhesion-dependent cell spreading	20	0.237528958	< 0.001	< 0.001
GO:0044706	multi-multicellular organism process	76	0.237488993	< 0.001	< 0.001
GO:2000352	negative regulation of endothelial cell apoptotic process	7	0.237470123	0.002	0.002664694
GO:0006664	glycolipid metabolic process	41	0.237454876	< 0.001	< 0.001
GO:0032924	activin receptor signaling pathway	14	0.237378195	< 0.001	< 0.001
GO:0045911	positive regulation of DNA recombination	17	0.237338179	0.0009	0.001319479
GO:0035148	tube formation	57	0.237323037	< 0.001	< 0.001
GO:0070168	negative regulation of biomineral tissue development	8	0.237323037	0.0002	0.000356582
GO:0051705	multi-organism behavior	35	0.237264203	0.0009	0.001319479
GO:0051567	histone H3-K9 methylation	14	0.237249494	0.0099	0.011373214
GO:0070304	positive regulation of stress-activated protein kinase signaling cascade	66	0.237248937	< 0.001	< 0.001
GO:0005977	glycogen metabolic process	30	0.237237237	< 0.001	< 0.001
GO:0006073	cellular glucan metabolic process	30	0.237237237	< 0.001	< 0.001
GO:0044042	glucan metabolic process	30	0.237237237	< 0.001	< 0.001
GO:0006631	fatty acid metabolic process	127	0.237221699	< 0.001	< 0.001
GO:0000188	inactivation of MAPK activity	15	0.237220077	0.0081	0.00945
GO:0055022	negative regulation of cardiac muscle tissue growth	8	0.237194337	0.0015	0.002069969
GO:0061117	negative regulation of heart growth	8	0.237194337	0.0015	0.002069969
GO:0006333	chromatin assembly or disassembly	52	0.237120087	0.0033	0.004153051
GO:0043901	negative regulation of multi-organism process	41	0.237103305	0.0001	0.000192793
GO:0034111	negative regulation of homotypic cell-cell adhesion	7	0.237102409	< 0.001	< 0.001
GO:0001773	myeloid dendritic cell activation	8	0.237033462	< 0.001	< 0.001
GO:0072091	regulation of stem cell proliferation	19	0.2369979	< 0.001	< 0.001
GO:0032480	negative regulation of type I interferon production	11	0.236995437	< 0.001	< 0.001
GO:0032438	melanosome organization	13	0.236986437	0.0003	0.000505993
GO:0048753	pigment granule organization	13	0.236986437	0.0003	0.000505993
GO:1901185	negative regulation of ERBB signaling pathway	23	0.23692015	0.0003	0.000505993
GO:0033866	nucleoside bisphosphate biosynthetic process	6	0.236894037	0.0186	0.020421455
GO:0034030	ribonucleoside bisphosphate biosynthetic process	6	0.236894037	0.0186	0.020421455
GO:0034033	purine nucleoside bisphosphate biosynthetic process	6	0.236894037	0.0186	0.020421455
GO:0060603	mammary gland duct morphogenesis	11	0.236878437	< 0.001	< 0.001
GO:0006304	DNA modification	32	0.236832368	0.0008	0.001193265
GO:0006417	regulation of translation	184	0.236806838	0.0002	0.000356582
GO:0055072	iron ion homeostasis	28	0.236780658	0.0003	0.000505993
GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	104	0.236763687	< 0.001	< 0.001
GO:0016064	immunoglobulin mediated immune response	28	0.236743887	< 0.001	< 0.001
GO:0019724	B cell mediated immunity	28	0.236743887	< 0.001	< 0.001
GO:0051875	pigment granule localization	14	0.236716308	< 0.001	< 0.001
GO:0009081	branched-chain amino acid metabolic process	5	0.236705277	0.0019	0.00254969
GO:0009083	branched-chain amino acid catabolic process	5	0.236705277	0.0019	0.00254969
GO:0010714	positive regulation of collagen metabolic process	7	0.236697922	0.0006	0.000927725
GO:0032967	positive regulation of collagen biosynthetic process	7	0.236697922	0.0006	0.000927725
GO:0044253	positive regulation of multicellular organismal metabolic process	7	0.236697922	0.0006	0.000927725
GO:2000404	regulation of T cell migration	12	0.236679537	0.0001	0.000192793
GO:0055088	lipid homeostasis	37	0.236655188	0.0001	0.000192793
GO:0070208	protein heterotrimerization	5	0.236653797	0.0042	0.005168936
GO:1902850	microtubule cytoskeleton organization involved in mitosis	23	0.236651558	0.0004	0.000648934
GO:0009165	nucleotide biosynthetic process	102	0.23663159	< 0.001	< 0.001
GO:0042538	hyperosmotic salinity response	6	0.236593737	0.0003	0.000505993
GO:0034101	erythrocyte homeostasis	53	0.236579976	< 0.001	< 0.001
GO:1903363	negative regulation of cellular protein catabolic process	28	0.236578415	0.0004	0.000648934
GO:0071985	multivesicular body sorting pathway	6	0.236550837	0.0001	0.000192793
GO:1902003	regulation of beta-amyloid formation	13	0.236511237	0.0007	0.001063182
GO:0009151	purine deoxyribonucleotide metabolic process	7	0.236477294	< 0.001	< 0.001
GO:0001961	positive regulation of cytokine-mediated signaling pathway	15	0.236465036	0.0001	0.000192793
GO:0010594	regulation of endothelial cell migration	64	0.236410071	< 0.001	< 0.001
GO:0036035	osteoclast development	6	0.236336336	0.0156	0.0172574
GO:1903859	regulation of dendrite extension	15	0.236327756	0.0187	0.020510412
GO:0006298	mismatch repair	9	0.236322036	0.0212	0.023069835
GO:0046467	membrane lipid biosynthetic process	42	0.236238279	0.0003	0.000505993
GO:1904667	negative regulation of ubiquitin protein ligase activity	6	0.236121836	0.0432	0.045198993
GO:0010663	positive regulation of striated muscle cell apoptotic process	7	0.236109579	0.0095	0.010941603
GO:0010666	positive regulation of cardiac muscle cell apoptotic process	7	0.236109579	0.0095	0.010941603
GO:0006066	alcohol metabolic process	121	0.236070072	< 0.001	< 0.001
GO:0014912	negative regulation of smooth muscle cell migration	11	0.236036036	0.0006	0.000927725
GO:0071867	response to monoamine	18	0.236007436	0.0012	0.001702047
GO:0071869	response to catecholamine	18	0.236007436	0.0012	0.001702047
GO:0060038	cardiac muscle cell proliferation	16	0.235955598	< 0.001	< 0.001
GO:0046135	pyrimidine nucleoside catabolic process	6	0.235950236	0.0045	0.005509289
GO:0046620	regulation of organ growth	35	0.235933076	< 0.001	< 0.001
GO:0098743	cell aggregation	8	0.235907336	0.0182	0.020002603
GO:0045926	negative regulation of growth	100	0.235899614	< 0.001	< 0.001
GO:0051489	regulation of filopodium assembly	24	0.235853711	0.0111	0.012593827
GO:0061041	regulation of wound healing	44	0.235796186	< 0.001	< 0.001
GO:0060976	coronary vasculature development	17	0.235718071	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0051100	negative regulation of binding	66	0.235657736	< 0.001	< 0.001
GO:1900744	regulation of p38MAPK cascade	12	0.235649936	0.0076	0.008916717
GO:1900273	positive regulation of long-term synaptic potentiation	15	0.235624196	0.0173	0.01905998
GO:1901293	nucleoside phosphate biosynthetic process	103	0.2356137	< 0.001	< 0.001
GO:0060081	membrane hyperpolarization	6	0.235607036	0.0012	0.001702047
GO:0001704	formation of primary germ layer	36	0.235542686	< 0.001	< 0.001
GO:0061572	actin filament bundle organization	66	0.235529036	< 0.001	< 0.001
GO:2001238	positive regulation of extrinsic apoptotic signaling pathway	17	0.235521236	< 0.001	< 0.001
GO:0055024	regulation of cardiac muscle tissue development	29	0.235459104	< 0.001	< 0.001
GO:0035094	response to nicotine	15	0.235452595	< 0.001	< 0.001
GO:0071103	DNA conformation change	95	0.235450789	0.0009	0.001319479
GO:0009953	dorsal/ventral pattern formation	27	0.235435435	0.0039	0.004841626
GO:0046697	decidualization	9	0.235435435	0.0163	0.018013333
GO:0051560	mitochondrial calcium ion homeostasis	11	0.235404235	0.0023	0.003013139
GO:0032365	intracellular lipid transport	12	0.235263835	0.0003	0.000505993
GO:0001938	positive regulation of endothelial cell proliferation	34	0.235256265	< 0.001	< 0.001
GO:0022010	central nervous system myelination	6	0.235220935	0.0004	0.000648934
GO:0032291	axon ensheathment in central nervous system	6	0.235220935	0.0004	0.000648934
GO:0090023	positive regulation of neutrophil chemotaxis	8	0.235199485	< 0.001	< 0.001
GO:1902624	positive regulation of neutrophil migration	8	0.235199485	< 0.001	< 0.001
GO:0006839	mitochondrial transport	103	0.235158876	0.0006	0.000927725
GO:0090136	epithelial cell-cell adhesion	6	0.235049335	< 0.001	< 0.001
GO:1903509	liposaccharide metabolic process	42	0.235049335	< 0.001	< 0.001
GO:0000338	protein deneddylation	7	0.235006435	0.0104	0.011884458
GO:0048483	autonomic nervous system development	9	0.234920635	0.0114	0.012893596
GO:0032733	positive regulation of interleukin-10 production	9	0.234920635	0.0032	0.004042263
GO:0031497	chromatin assembly	43	0.234904672	0.0024	0.003116943
GO:0032874	positive regulation of stress-activated MAPK cascade	65	0.234899515	< 0.001	< 0.001
GO:0070301	cellular response to hydrogen peroxide	34	0.234877735	< 0.001	< 0.001
GO:0035357	peroxisome proliferator activated receptor signaling pathway	11	0.234819235	< 0.001	< 0.001
GO:0009451	RNA modification	47	0.234814754	0.0003	0.000505993
GO:0034754	cellular hormone metabolic process	29	0.234811166	< 0.001	< 0.001
GO:0071218	cellular response to misfolded protein	8	0.234749035	< 0.001	< 0.001
GO:1903543	positive regulation of exosomal secretion	6	0.234706135	0.0391	0.041116248
GO:0009201	ribonucleoside triphosphate biosynthetic process	23	0.234681887	0.0033	0.004153051
GO:0051305	chromosome movement towards spindle pole	6	0.234620335	0.0002	0.000356582
GO:0046916	cellular transition metal ion homeostasis	35	0.234601949	0.0006	0.000927725
GO:0070613	regulation of protein processing	27	0.234558368	< 0.001	< 0.001
GO:0008380	RNA splicing	182	0.234555277	0.0014	0.00194839
GO:0036314	response to sterol	14	0.234546792	0.0005	0.000791911
GO:0032007	negative regulation of TOR signaling	18	0.234534535	< 0.001	< 0.001
GO:0042787	protein ubiquitination involved in ubiquitin-dependent protein catabolic process	13	0.234491634	0.0009	0.001319479
GO:2000058	regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process	13	0.234491634	0.0009	0.001319479
GO:0000096	sulfur amino acid metabolic process	15	0.234440154	< 0.001	< 0.001
GO:0045598	regulation of fat cell differentiation	50	0.234419562	< 0.001	< 0.001
GO:0002673	regulation of acute inflammatory response	22	0.234339534	0.0003	0.000505993
GO:0001841	neural tube formation	48	0.234336122	< 0.001	< 0.001
GO:0050953	sensory perception of light stimulus	59	0.2343084	< 0.001	< 0.001
GO:0003014	renal system process	38	0.234288424	< 0.001	< 0.001
GO:0006119	oxidative phosphorylation	42	0.234271006	0.0084	0.009757868
GO:0016125	sterol metabolic process	64	0.234262387	0.0029	0.003693519
GO:0055021	regulation of cardiac muscle tissue growth	22	0.234222534	< 0.001	< 0.001
GO:0061036	positive regulation of cartilage development	16	0.234185972	< 0.001	< 0.001
GO:0008202	steroid metabolic process	100	0.234177606	0.0003	0.000505993
GO:0009068	aspartate family amino acid catabolic process	7	0.234160691	0.0104	0.011884458
GO:0071675	regulation of mononuclear cell migration	18	0.234076934	0.0004	0.000648934
GO:0031665	negative regulation of lipopolysaccharide-mediated signaling pathway	5	0.234028314	0.0033	0.004153051
GO:0051304	chromosome separation	30	0.233959674	0.001	0.001450349
GO:0006767	water-soluble vitamin metabolic process	29	0.233950206	0.0001	0.000192793
GO:0030252	growth hormone secretion	6	0.233933934	0.011	0.012498738
GO:0016024	CDP-diacylglycerol biosynthetic process	5	0.233873874	< 0.001	< 0.001
GO:0046341	CDP-diacylglycerol metabolic process	5	0.233873874	< 0.001	< 0.001
GO:0021511	spinal cord patterning	6	0.233805234	0.0063	0.007507211
GO:0021513	spinal cord dorsal/ventral patterning	6	0.233805234	0.0063	0.007507211
GO:0042147	retrograde transport, endosome to Golgi	32	0.233799871	0.0004	0.000648934
GO:1903204	negative regulation of oxidative stress-induced neuron death	9	0.233748034	0.0001	0.000192793
GO:0032232	negative regulation of actin filament bundle assembly	14	0.233701048	0.0019	0.00254969
GO:0001756	somitogenesis	17	0.233643728	0.0044	0.005395416
GO:0051604	protein maturation	75	0.233616474	< 0.001	< 0.001
GO:0000288	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	32	0.233574646	0.0027	0.003470695
GO:1901725	regulation of histone deacetylase activity	5	0.233513514	0.0038	0.004725081
GO:0035883	enteroendocrine cell differentiation	11	0.233462033	0.0076	0.008916717
GO:0035050	embryonic heart tube development	21	0.233449776	< 0.001	< 0.001
GO:0060343	trabecula formation	11	0.233438633	0.0188	0.020615909
GO:0051187	cofactor catabolic process	8	0.233429858	0.0003	0.000505993
GO:0035924	cellular response to vascular endothelial growth factor stimulus	14	0.233370105	0.0069	0.008171729
GO:0019748	secondary metabolic process	23	0.233305355	< 0.001	< 0.001
GO:0006622	protein targeting to lysosome	9	0.233261833	0.0004	0.000648934
GO:0016126	sterol biosynthetic process	43	0.233234563	0.0022	0.002896881
GO:0016101	diterpenoid metabolic process	26	0.233214533	< 0.001	< 0.001
GO:0050795	regulation of behavior	26	0.233194733	0.0001	0.000192793
GO:0014855	striated muscle cell proliferation	19	0.233028517	< 0.001	< 0.001
GO:0034643	establishment of mitochondrion localization, microtubule-mediated	10	0.232972973	0.0044	0.005395416

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0047497	mitochondrion transport along microtubule	10	0.232972973	0.0044	0.005395416
GO:0048247	lymphocyte chemotaxis	9	0.232890033	0.0008	0.001193265
GO:0060612	adipose tissue development	14	0.232763376	< 0.001	< 0.001
GO:0051988	regulation of attachment of spindle microtubules to kinetochore	6	0.232732733	0.0001	0.000192793
GO:0007007	inner mitochondrial membrane organization	18	0.232718433	0.0131	0.01468722
GO:0007601	visual perception	58	0.232623264	< 0.001	< 0.001
GO:0030225	macrophage differentiation	19	0.232622096	< 0.001	< 0.001
GO:0010155	regulation of proton transport	7	0.232579518	0.0031	0.003925117
GO:0051339	regulation of lyase activity	30	0.232561133	< 0.001	< 0.001
GO:0055023	positive regulation of cardiac muscle tissue growth	14	0.232524361	< 0.001	< 0.001
GO:0033194	response to hydroperoxide	12	0.232518233	0.0008	0.001193265
GO:0048265	response to pain	7	0.232469204	< 0.001	< 0.001
GO:1900076	regulation of cellular response to insulin stimulus	23	0.232466006	0.0085	0.009867669
GO:0035646	endosome to melanosome transport	6	0.232432432	0.0326	0.034638301
GO:0043485	endosome to pigment granule transport	6	0.232432432	0.0326	0.034638301
GO:0048757	pigment granule maturation	6	0.232432432	0.0326	0.034638301
GO:0050869	negative regulation of B cell activation	5	0.232380952	< 0.001	< 0.001
GO:0002687	positive regulation of leukocyte migration	43	0.232372572	0.0001	0.000192793
GO:0046635	positive regulation of alpha-beta T cell activation	11	0.232362232	0.0029	0.003693519
GO:0042445	hormone metabolic process	52	0.232333432	< 0.001	< 0.001
GO:0070932	histone H3 deacetylation	7	0.232322118	0.0082	0.009562538
GO:0000959	mitochondrial RNA metabolic process	12	0.232303732	0.013	0.014581154
GO:0007100	mitotic centrosome separation	5	0.232175032	0.0032	0.004042263
GO:0051299	centrosome separation	5	0.232175032	0.0032	0.004042263
GO:0007631	feeding behavior	43	0.232151088	0.0005	0.000791911
GO:0006623	protein targeting to vacuole	10	0.232149292	0.0003	0.000505993
GO:0072666	establishment of protein localization to vacuole	10	0.232149292	0.0003	0.000505993
GO:0055070	copper ion homeostasis	9	0.232117832	0.0053	0.006400268
GO:0086002	cardiac muscle cell action potential involved in contraction	19	0.231985369	0.0061	0.007291396
GO:0032988	ribonucleoprotein complex disassembly	5	0.231969112	0.0462	0.04815136
GO:0030509	BMP signaling pathway	39	0.231944032	< 0.001	< 0.001
GO:1903909	regulation of receptor clustering	6	0.231917632	< 0.001	< 0.001
GO:0009395	phospholipid catabolic process	9	0.231917632	< 0.001	< 0.001
GO:1901380	negative regulation of potassium ion transmembrane transport	7	0.23188086	0.0001	0.000192793
GO:0000380	alternative mRNA splicing, via spliceosome	26	0.231788932	0.0012	0.001702047
GO:0051043	regulation of membrane protein ectodomain proteolysis	7	0.231697003	0.0014	0.00194839
GO:0042481	regulation of odontogenesis	5	0.231557272	0.0011	0.001576346
GO:0034637	cellular carbohydrate biosynthetic process	30	0.231514372	< 0.001	< 0.001
GO:0061339	establishment or maintenance of monopolar cell polarity	11	0.231402831	0.0001	0.000192793
GO:0048332	mesoderm morphogenesis	24	0.231370656	< 0.001	< 0.001
GO:0043534	blood vessel endothelial cell migration	47	0.231359019	0.0005	0.000791911
GO:0015748	organophosphate ester transport	34	0.231349837	< 0.001	< 0.001
GO:0006334	nucleosome assembly	39	0.231343431	0.0019	0.00254969
GO:0086065	cell communication involved in cardiac conduction	20	0.231299871	0.0008	0.001193265
GO:0010595	positive regulation of endothelial cell migration	37	0.231256739	0.0001	0.000192793
GO:0046890	regulation of lipid biosynthetic process	73	0.23122653	< 0.001	< 0.001
GO:0034067	protein localization to Golgi apparatus	14	0.231163817	< 0.001	< 0.001
GO:0007097	nuclear migration	6	0.231145431	0.0304	0.032428267
GO:0040023	establishment of nucleus localization	6	0.231145431	0.0304	0.032428267
GO:0032755	positive regulation of interleukin-6 production	25	0.231114543	< 0.001	< 0.001
GO:0031468	nuclear envelope reassembly	12	0.231081081	0.0018	0.002428764
GO:0046006	regulation of activated T cell proliferation	9	0.231059631	< 0.001	< 0.001
GO:0033617	mitochondrial respiratory chain complex IV assembly	5	0.230939511	0.0251	0.02705773
GO:0097034	mitochondrial respiratory chain complex IV biogenesis	5	0.230939511	0.0251	0.02705773
GO:0030801	positive regulation of cyclic nucleotide metabolic process	18	0.230859431	0.0028	0.003584743
GO:0030804	positive regulation of cyclic nucleotide biosynthetic process	18	0.230859431	0.0028	0.003584743
GO:0061462	protein localization to lysosome	16	0.230711068	0.0001	0.000192793
GO:0051297	centrosome organization	47	0.230575865	0.0006	0.000927725
GO:0000715	nucleotide-excision repair, DNA damage recognition	14	0.230557088	0.0063	0.007507211
GO:0007179	transforming growth factor beta receptor signaling pathway	67	0.230434699	< 0.001	< 0.001
GO:0048814	regulation of dendrite morphogenesis	51	0.230433795	0.0025	0.003237479
GO:0051788	response to misfolded protein	9	0.23043043	0.0005	0.000791911
GO:0035176	social behavior	28	0.230281302	0.0021	0.002780108
GO:0051703	intraspecies interaction between organisms	28	0.230281302	0.0021	0.002780108
GO:0007040	lysosome organization	31	0.230240379	< 0.001	< 0.001
GO:0080171	lytic vacuole organization	31	0.230240379	< 0.001	< 0.001
GO:1902187	negative regulation of viral release from host cell	7	0.230226145	0.0008	0.001193265
GO:0072665	protein localization to vacuole	17	0.230206677	0.0002	0.000356582
GO:0006364	rRNA processing	83	0.230072413	0.0036	0.004505419
GO:0006515	misfolded or incompletely synthesized protein catabolic process	8	0.22985843	0.0003	0.000505993
GO:0007252	I-kappaB phosphorylation	8	0.22979408	0.0038	0.004725081
GO:0097006	regulation of plasma lipoprotein particle levels	28	0.229766501	< 0.001	< 0.001
GO:0006879	cellular iron ion homeostasis	24	0.229761905	0.005	0.006070546
GO:0044728	DNA methylation or demethylation	23	0.229757708	0.001	0.001450349
GO:0016053	organic acid biosynthetic process	112	0.229738923	< 0.001	< 0.001
GO:0046394	carboxylic acid biosynthetic process	112	0.229738923	< 0.001	< 0.001
GO:0051668	localization within membrane	50	0.229683398	0.0009	0.001319479
GO:0033047	regulation of mitotic sister chromatid segregation	29	0.229565526	0.0002	0.000356582
GO:0045722	positive regulation of gluconeogenesis	7	0.229564258	0.048	0.049940701
GO:0002467	germinal center formation	6	0.22955813	0.0002	0.000356582
GO:0061035	regulation of cartilage development	23	0.229545073	< 0.001	< 0.001
GO:0001893	maternal placenta development	17	0.229510182	< 0.001	< 0.001
GO:0044060	regulation of endocrine process	13	0.229462429	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0032689	negative regulation of interferon-gamma production	8	0.229440154	0.0081	0.00945
GO:0042454	ribonucleoside catabolic process	7	0.229417172	0.022	0.023906696
GO:0009583	detection of light stimulus	21	0.229343629	0.0001	0.000192793
GO:0001708	cell fate specification	19	0.229330082	0.0038	0.004725081
GO:0046459	short-chain fatty acid metabolic process	7	0.229270086	0.003	0.003811001
GO:0031076	embryonic camera-type eye development	9	0.229229229	< 0.001	< 0.001
GO:0010640	regulation of platelet-derived growth factor receptor signaling pathway	11	0.229179829	0.0003	0.000505993
GO:0060045	positive regulation of cardiac muscle cell proliferation	9	0.229172029	< 0.001	< 0.001
GO:0046426	negative regulation of JAK-STAT cascade	13	0.228987229	0.0009	0.001319479
GO:0048710	regulation of astrocyte differentiation	10	0.228906049	< 0.001	< 0.001
GO:0070227	lymphocyte apoptotic process	19	0.228801734	0.0001	0.000192793
GO:0038066	p38MAPK cascade	15	0.228743029	0.0005	0.000791911
GO:0090085	regulation of protein deubiquitination	5	0.228674389	0.0014	0.00194839
GO:0002183	cytoplasmic translational initiation	13	0.228670429	0.001	0.001450349
GO:0036480	neuron intrinsic apoptotic signaling pathway in response to oxidative stress	5	0.228622909	0.0006	0.000927725
GO:1903376	regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway	5	0.228622909	0.0006	0.000927725
GO:1902306	negative regulation of sodium ion transmembrane transport	5	0.228571429	0.0116	0.013103344
GO:2000650	negative regulation of sodium ion transmembrane transporter activity	5	0.228571429	0.0116	0.013103344
GO:0035196	production of miRNAs involved in gene silencing by miRNA	17	0.22846544	0.0043	0.005276385
GO:0051188	cofactor biosynthetic process	68	0.22840109	0.0001	0.000192793
GO:0045730	respiratory burst	13	0.228393228	< 0.001	< 0.001
GO:0034110	regulation of homotypic cell-cell adhesion	12	0.228378378	< 0.001	< 0.001
GO:0007184	SMAD protein import into nucleus	5	0.228365508	0.0005	0.000791911
GO:0060390	regulation of SMAD protein import into nucleus	5	0.228365508	0.0005	0.000791911
GO:0032392	DNA geometric change	38	0.228347897	0.0003	0.000505993
GO:0034614	cellular response to reactive oxygen species	62	0.228268361	< 0.001	< 0.001
GO:1903317	regulation of protein maturation	28	0.228268064	0.0001	0.000192793
GO:0032647	regulation of interferon-alpha production	9	0.228228228	0.0016	0.002186748
GO:0031023	microtubule organizing center organization	52	0.228210078	0.0003	0.000505993
GO:0055076	transition metal ion homeostasis	42	0.2281792	0.0002	0.000356582
GO:0030575	nuclear body organization	7	0.227983085	< 0.001	< 0.001
GO:0003272	endocardial cushion formation	5	0.227953668	< 0.001	< 0.001
GO:0030301	cholesterol transport	23	0.22789995	0.0012	0.001702047
GO:0032461	positive regulation of protein oligomerization	8	0.227863578	< 0.001	< 0.001
GO:0072386	plus-end-directed organelle transport along microtubule	5	0.227799228	0.0129	0.014478006
GO:0030212	hyaluronan metabolic process	13	0.227759628	< 0.001	< 0.001
GO:0007176	regulation of epidermal growth factor-activated receptor activity	9	0.227742028	0.0028	0.003584743
GO:0098868	bone growth	9	0.227713428	0.0042	0.005168936
GO:1902175	regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	12	0.227606178	0.0007	0.001063182
GO:0045736	negative regulation of cyclin-dependent protein serine/threonine kinase activity	11	0.227588628	0.0113	0.012793882
GO:0071875	adrenergic receptor signaling pathway	8	0.227574003	0.0053	0.006400268
GO:0071674	mononuclear cell migration	24	0.227509653	< 0.001	< 0.001
GO:0043536	positive regulation of blood vessel endothelial cell migration	21	0.227505056	0.0037	0.004617737
GO:0048026	positive regulation of mRNA splicing, via spliceosome	5	0.227490347	0.0089	0.010294435
GO:0097711	ciliary basal body docking	51	0.227466122	< 0.001	< 0.001
GO:0070296	sarcoplasmic reticulum calcium ion transport	17	0.227329851	< 0.001	< 0.001
GO:0030194	positive regulation of blood coagulation	9	0.227227227	< 0.001	< 0.001
GO:0050820	positive regulation of coagulation	9	0.227227227	< 0.001	< 0.001
GO:1900048	positive regulation of hemostasis	9	0.227227227	< 0.001	< 0.001
GO:0006538	glutamate catabolic process	6	0.227198627	0.0079	0.009236608
GO:0006342	chromatin silencing	18	0.227127127	0.0038	0.004725081
GO:0002437	inflammatory response to antigenic stimulus	14	0.22710057	0.0002	0.000356582
GO:0031649	heat generation	8	0.227091377	< 0.001	< 0.001
GO:0048010	vascular endothelial growth factor receptor signaling pathway	35	0.226975547	< 0.001	< 0.001
GO:0010665	regulation of cardiac muscle cell apoptotic process	18	0.226926927	< 0.001	< 0.001
GO:0016072	rRNA metabolic process	86	0.226892341	0.0041	0.005057384
GO:0061298	retina vasculature development in camera-type eye	7	0.226806398	0.0004	0.000648934
GO:0045880	positive regulation of smoothened signaling pathway	8	0.226705277	0.0426	0.044579861
GO:0060443	mammary gland morphogenesis	15	0.226683827	< 0.001	< 0.001
GO:0009235	cobalamin metabolic process	9	0.226626627	< 0.001	< 0.001
GO:0050901	leukocyte tethering or rolling	10	0.226589447	0.0004	0.000648934
GO:0032613	interleukin-10 production	15	0.226529387	0.0016	0.002186748
GO:0007622	rhythmic behavior	15	0.226529387	0.0058	0.006954338
GO:0021781	glial cell fate commitment	6	0.226512227	0.0029	0.003693519
GO:0051654	establishment of mitochondrion localization	13	0.226334026	0.0008	0.001193265
GO:0035264	multicellular organism growth	63	0.226332455	< 0.001	< 0.001
GO:0033144	negative regulation of intracellular steroid hormone receptor signaling pathway	15	0.226306306	0.0027	0.003470695
GO:2000482	regulation of interleukin-8 secretion	8	0.226254826	< 0.001	< 0.001
GO:0048638	regulation of developmental growth	139	0.226147422	< 0.001	< 0.001
GO:0072577	endothelial cell apoptotic process	13	0.226076626	< 0.001	< 0.001
GO:0000038	very long-chain fatty acid metabolic process	8	0.225836551	0.0008	0.001193265
GO:0032735	positive regulation of interleukin-12 production	11	0.225833626	< 0.001	< 0.001
GO:0048144	fibroblast proliferation	37	0.225788723	< 0.001	< 0.001
GO:0072676	lymphocyte migration	25	0.225770914	< 0.001	< 0.001
GO:0002438	acute inflammatory response to antigenic stimulus	5	0.225637066	0.0311	0.033148797
GO:0001890	placenta development	61	0.225621875	< 0.001	< 0.001
GO:0006893	Golgi to plasma membrane transport	17	0.22554319	0.0008	0.001193265
GO:0043631	RNA polyadenylation	16	0.225530888	0.0069	0.008171729
GO:0055010	ventricular cardiac muscle tissue morphogenesis	22	0.225529426	< 0.001	< 0.001
GO:2000781	positive regulation of double-strand break repair	14	0.225501011	0.0003	0.000505993
GO:0045814	negative regulation of gene expression, epigenetic	29	0.225376115	0.0009	0.001319479
GO:0086004	regulation of cardiac muscle cell contraction	11	0.225318825	0.0002	0.000356582
GO:0048066	developmental pigmentation	17	0.225255508	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0001894	tissue homeostasis	75	0.225235521	< 0.001	< 0.001
GO:0014733	regulation of skeletal muscle adaptation	6	0.225225225	< 0.001	< 0.001
GO:1900006	positive regulation of dendrite development	36	0.225203775	0.0008	0.001193265
GO:0032048	cardiolipin metabolic process	5	0.225173745	0.0012	0.001702047
GO:0043535	regulation of blood vessel endothelial cell migration	36	0.225117975	0.0003	0.000505993
GO:0033574	response to testosterone	15	0.225019305	< 0.001	< 0.001
GO:1900272	negative regulation of long-term synaptic potentiation	6	0.225010725	0.0204	0.022253048
GO:0000733	DNA strand renaturation	5	0.224916345	0.0038	0.004725081
GO:0031060	regulation of histone methylation	23	0.224878294	0.0022	0.002896881
GO:0019511	peptidyl-proline hydroxylation	7	0.224783968	0.0123	0.013827585
GO:0018149	peptide cross-linking	5	0.224710425	0.0005	0.000791911
GO:0007098	centrosome cycle	46	0.224654468	0.0008	0.001193265
GO:0032623	interleukin-2 production	18	0.224596025	< 0.001	< 0.001
GO:0032663	regulation of interleukin-2 production	18	0.224596025	< 0.001	< 0.001
GO:0045197	establishment or maintenance of epithelial cell apical/basal polarity	18	0.224453024	< 0.001	< 0.001
GO:1900017	positive regulation of cytokine production involved in inflammatory response	5	0.224401544	0.0185	0.020328182
GO:0030010	establishment of cell polarity	63	0.224379482	< 0.001	< 0.001
GO:0046827	positive regulation of protein export from nucleus	7	0.224379482	0.0024	0.003116943
GO:2000726	negative regulation of cardiac muscle cell differentiation	6	0.224367224	0.0029	0.003693519
GO:0034198	cellular response to amino acid starvation	25	0.224185328	0.0001	0.000192793
GO:0032692	negative regulation of interleukin-1 production	12	0.224174174	0.0016	0.002186748
GO:0014808	release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	16	0.224131274	< 0.001	< 0.001
GO:1903514	calcium ion transport from endoplasmic reticulum to cytosol	16	0.224131274	< 0.001	< 0.001
GO:0071636	positive regulation of transforming growth factor beta production	9	0.224109824	0.0004	0.000648934
GO:0006637	acyl-CoA metabolic process	30	0.224066924	0.0004	0.000648934
GO:0035383	thioester metabolic process	30	0.224066924	0.0004	0.000648934
GO:0032897	negative regulation of viral transcription	9	0.223995424	0.0012	0.001702047
GO:0030307	positive regulation of cell growth	77	0.22399171	< 0.001	< 0.001
GO:0035809	regulation of urine volume	8	0.223970399	0.0001	0.000192793
GO:2000378	negative regulation of reactive oxygen species metabolic process	22	0.223879724	0.0002	0.000356582
GO:1904893	negative regulation of STAT cascade	14	0.223717595	0.0015	0.002069969
GO:0045927	positive regulation of growth	113	0.223623877	< 0.001	< 0.001
GO:0035666	TRIF-dependent toll-like receptor signaling pathway	11	0.223540424	0.0011	0.001576346
GO:0046638	positive regulation of alpha-beta T cell differentiation	10	0.223397683	0.0025	0.003237479
GO:0006101	citrate metabolic process	8	0.223391248	0.0105	0.011988591
GO:0032366	intracellular sterol transport	6	0.223380523	0.0265	0.028498706
GO:0032367	intracellular cholesterol transport	6	0.223380523	0.0265	0.028498706
GO:0070849	response to epidermal growth factor	19	0.223247307	< 0.001	< 0.001
GO:0015918	sterol transport	27	0.22312789	0.0004	0.000648934
GO:0010002	cardioblast differentiation	5	0.223114543	0.0011	0.001576346
GO:1903055	positive regulation of extracellular matrix organization	9	0.223108823	0.0004	0.000648934
GO:0043968	histone H2A acetylation	6	0.223080223	0.0052	0.006299215
GO:0045670	regulation of osteoclast differentiation	18	0.222994423	< 0.001	< 0.001
GO:0044270	cellular nitrogen compound catabolic process	185	0.22293645	0.0042	0.005168936
GO:0010644	cell communication by electrical coupling	10	0.222882883	< 0.001	< 0.001
GO:0086064	cell communication by electrical coupling involved in cardiac conduction	10	0.222882883	< 0.001	< 0.001
GO:0007229	integrin-mediated signaling pathway	30	0.222874303	0.0001	0.000192793
GO:0019730	antimicrobial humoral response	17	0.222863199	< 0.001	< 0.001
GO:0034655	nucleobase-containing compound catabolic process	166	0.222862105	0.0087	0.010084685
GO:0048806	genitalia development	11	0.222861823	0.0002	0.000356582
GO:1904994	regulation of leukocyte adhesion to vascular endothelial cell	8	0.222844273	0.0042	0.005168936
GO:0042733	embryonic digit morphogenesis	17	0.222726929	< 0.001	< 0.001
GO:0010907	positive regulation of glucose metabolic process	15	0.222531103	< 0.001	< 0.001
GO:0046330	positive regulation of JNK cascade	56	0.222274315	< 0.001	< 0.001
GO:0044380	protein localization to cytoskeleton	28	0.222265122	0.0001	0.000192793
GO:0040036	regulation of fibroblast growth factor receptor signaling pathway	7	0.222173194	< 0.001	< 0.001
GO:0060415	muscle tissue morphogenesis	28	0.222164001	< 0.001	< 0.001
GO:2000641	regulation of early endosome to late endosome transport	11	0.222136422	0.0005	0.000791911
GO:0051898	negative regulation of protein kinase B signaling	18	0.221993422	0.0003	0.000505993
GO:0043174	nucleoside salvage	7	0.221989336	0.0024	0.003116943
GO:1902902	negative regulation of autophagosome assembly	7	0.221952565	0.0109	0.012398148
GO:0001843	neural tube closure	40	0.221930502	< 0.001	< 0.001
GO:0060606	tube closure	40	0.221930502	< 0.001	< 0.001
GO:0033619	membrane protein proteolysis	17	0.221894163	0.0017	0.00231289
GO:0038084	vascular endothelial growth factor signaling pathway	10	0.221879022	0.0192	0.02103747
GO:0006998	nuclear envelope organization	27	0.221859955	0.0009	0.001319479
GO:0007064	mitotic sister chromatid cohesion	8	0.221846847	< 0.001	< 0.001
GO:0045724	positive regulation of cilium assembly	11	0.221785422	0.0002	0.000356582
GO:1901862	negative regulation of muscle tissue development	16	0.221750322	< 0.001	< 0.001
GO:0032930	positive regulation of superoxide anion generation	6	0.221750322	0.011	0.012498738
GO:0070664	negative regulation of leukocyte proliferation	14	0.221695165	0.0022	0.002896881
GO:0030510	regulation of BMP signaling pathway	21	0.221682907	< 0.001	< 0.001
GO:0009311	oligosaccharide metabolic process	17	0.221667045	0.0007	0.001063182
GO:0006633	fatty acid biosynthetic process	56	0.2216492	< 0.001	< 0.001
GO:0007585	respiratory gaseous exchange	30	0.221613042	< 0.001	< 0.001
GO:0043567	regulation of insulin-like growth factor receptor signaling pathway	7	0.221400993	0.0331	0.035135023
GO:0021517	ventral spinal cord development	15	0.221381381	0.0003	0.000505993
GO:0034453	microtubule anchoring	15	0.221329901	0.0005	0.000791911
GO:0050906	detection of stimulus involved in sensory perception	37	0.22125987	< 0.001	< 0.001
GO:0071695	anatomical structure maturation	19	0.221255842	0.0008	0.001193265
GO:0003309	type B pancreatic cell differentiation	10	0.221235521	0.0115	0.013001255
GO:0000910	cytokinesis	60	0.221179751	0.0001	0.000192793
GO:0006643	membrane lipid metabolic process	65	0.221158301	0.0002	0.000356582

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0006094	gluconeogenesis	34	0.221152245	0.0001	0.000192793
GO:0019319	hexose biosynthetic process	34	0.221152245	0.0001	0.000192793
GO:0046364	monosaccharide biosynthetic process	34	0.221152245	0.0001	0.000192793
GO:0051646	mitochondrion localization	22	0.221130221	0.0001	0.000192793
GO:0014020	primary neural tube formation	43	0.221112807	< 0.001	< 0.001
GO:0010667	negative regulation of cardiac muscle cell apoptotic process	11	0.221083421	0.0006	0.000927725
GO:0032801	receptor catabolic process	22	0.221024921	0.0008	0.001193265
GO:0010738	regulation of protein kinase A signaling	9	0.221021021	0.0001	0.000192793
GO:0001844	protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	17	0.221015974	0.0024	0.003116943
GO:0051349	positive regulation of lyase activity	22	0.221013221	< 0.001	< 0.001
GO:0006892	post-Golgi vesicle-mediated transport	30	0.221003861	0.0011	0.001576346
GO:0021522	spinal cord motor neuron differentiation	13	0.220908821	0.0022	0.002896881
GO:0061756	leukocyte adhesion to vascular endothelial cell	15	0.220866581	0.001	0.001450349
GO:0060252	positive regulation of glial cell proliferation	8	0.220785071	0.0085	0.009867669
GO:0045739	positive regulation of DNA repair	29	0.220769538	0.0002	0.000356582
GO:0034204	lipid translocation	9	0.220763621	0.0008	0.001193265
GO:0045332	phospholipid translocation	9	0.220763621	0.0008	0.001193265
GO:0071624	positive regulation of granulocyte chemotaxis	9	0.220706421	< 0.001	< 0.001
GO:0010944	negative regulation of transcription by competitive promoter binding	5	0.220694981	0.0267	0.028702367
GO:0036148	phosphatidylglycerol acyl-chain remodeling	5	0.220694981	0.0154	0.017060599
GO:0009108	coenzyme biosynthetic process	53	0.220689153	0.0001	0.000192793
GO:0006446	regulation of translational initiation	29	0.220680779	0.0013	0.001826625
GO:0035358	regulation of peroxisome proliferator activated receptor signaling pathway	9	0.220649221	0.0003	0.000505993
GO:0001892	embryonic placenta development	32	0.220608108	< 0.001	< 0.001
GO:0010996	response to auditory stimulus	9	0.220592021	0.0012	0.001702047
GO:0003323	type B pancreatic cell development	8	0.220592021	0.0124	0.013937105
GO:0007602	phototransduction	16	0.22046332	0.0001	0.000192793
GO:0060644	mammary gland epithelial cell differentiation	6	0.22042042	0.0002	0.000356582
GO:0045843	negative regulation of striated muscle tissue development	15	0.2203861	< 0.001	< 0.001
GO:0048635	negative regulation of muscle organ development	15	0.2203861	< 0.001	< 0.001
GO:0006505	GPI anchor metabolic process	11	0.22033462	0.0043	0.005276385
GO:0001783	B cell apoptotic process	9	0.22022022	0.0012	0.001702047
GO:0061383	trabecula morphogenesis	20	0.22018018	0.0004	0.000648934
GO:1903018	regulation of glycoprotein metabolic process	16	0.22014157	0.0003	0.000505993
GO:0045582	positive regulation of T cell differentiation	18	0.22013442	0.0002	0.000356582
GO:0006690	icosanoid metabolic process	34	0.22007722	< 0.001	< 0.001
GO:1901568	fatty acid derivative metabolic process	34	0.22007722	< 0.001	< 0.001
GO:0044788	modulation by host of viral process	11	0.22005382	< 0.001	< 0.001
GO:0008589	regulation of smoothened signaling pathway	26	0.22004752	0.0026	0.003356522
GO:0009988	cell-cell recognition	20	0.21997426	< 0.001	< 0.001
GO:0006509	membrane protein ectodomain proteolysis	13	0.21993862	0.0033	0.004153051
GO:0006851	mitochondrial calcium ion transport	12	0.21988417	0.0083	0.009660392
GO:0010842	retina layer formation	6	0.21986272	0.0137	0.015318601
GO:0000097	sulfur amino acid biosynthetic process	6	0.21981982	0.0019	0.00254969
GO:1903019	negative regulation of glycoprotein metabolic process	6	0.21964822	0.02	0.021843169
GO:0006220	pyrimidine nucleotide metabolic process	17	0.219638126	0.0009	0.001319479
GO:0072378	blood coagulation, fibrin clot formation	6	0.21960532	< 0.001	< 0.001
GO:1904262	negative regulation of TORC1 signaling	6	0.21956242	0.0001	0.000192793
GO:0006986	response to unfolded protein	67	0.219493267	< 0.001	< 0.001
GO:0008210	estrogen metabolic process	6	0.219476619	0.0098	0.011263122
GO:2000678	negative regulation of transcription regulatory region DNA binding	9	0.219419419	0.0179	0.019692915
GO:0031032	actomyosin structure organization	68	0.219388296	< 0.001	< 0.001
GO:0010596	negative regulation of endothelial cell migration	24	0.219305019	0.0002	0.000356582
GO:0035966	response to topologically incorrect protein	73	0.219255655	< 0.001	< 0.001
GO:0019439	aromatic compound catabolic process	186	0.219206764	0.0042	0.005168936
GO:1901623	regulation of lymphocyte chemotaxis	5	0.219202059	0.0005	0.000791911
GO:0032607	interferon-alpha production	10	0.219124839	0.0052	0.006299215
GO:0061323	cell proliferation involved in heart morphogenesis	5	0.219099099	0.0002	0.000356582
GO:2000136	regulation of cell proliferation involved in heart morphogenesis	5	0.219099099	0.0002	0.000356582
GO:0055008	cardiac muscle tissue morphogenesis	27	0.219066686	< 0.001	< 0.001
GO:1904467	regulation of tumor necrosis factor secretion	7	0.219010848	0.0004	0.000648934
GO:0090630	activation of GTPase activity	17	0.218987054	< 0.001	< 0.001
GO:0006493	protein O-linked glycosylation	34	0.218941631	< 0.001	< 0.001
GO:0000291	nuclear-transcribed mRNA catabolic process, exonucleolytic	19	0.218844408	0.0137	0.015318601
GO:0043928	exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay	19	0.218844408	0.0137	0.015318601
GO:0099024	plasma membrane invagination	17	0.218835642	0.0043	0.005276385
GO:0021561	facial nerve development	5	0.218790219	0.0293	0.031335286
GO:0021604	cranial nerve structural organization	5	0.218790219	0.0293	0.031335286
GO:0021610	facial nerve morphogenesis	5	0.218790219	0.0293	0.031335286
GO:0021612	facial nerve structural organization	5	0.218790219	0.0293	0.031335286
GO:0021783	preganglionic parasympathetic fiber development	5	0.218790219	0.0293	0.031335286
GO:0048486	parasympathetic nervous system development	5	0.218790219	0.0293	0.031335286
GO:0031343	positive regulation of cell killing	11	0.218766819	< 0.001	< 0.001
GO:1901361	organic cyclic compound catabolic process	192	0.218715144	0.0038	0.004725081
GO:0010712	regulation of collagen metabolic process	12	0.218682969	< 0.001	< 0.001
GO:0044246	regulation of multicellular organismal metabolic process	12	0.218682969	< 0.001	< 0.001
GO:0030261	chromosome condensation	11	0.218603019	0.0186	0.020421455
GO:0048145	regulation of fibroblast proliferation	36	0.218454168	< 0.001	< 0.001
GO:0050775	positive regulation of dendrite morphogenesis	19	0.218437987	0.0007	0.001063182
GO:0010717	regulation of epithelial to mesenchymal transition	30	0.218395538	< 0.001	< 0.001
GO:0007625	grooming behavior	9	0.218361218	< 0.001	< 0.001
GO:0046686	response to cadmium ion	23	0.218253036	0.0009	0.001319479
GO:0007350	blastoderm segmentation	5	0.218172458	0.024	0.025944389

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0050885	neuromuscular process controlling balance	25	0.21814157	0.0009	0.001319479
GO:0006694	steroid biosynthetic process	68	0.218108865	0.0011	0.001576346
GO:0006833	water transport	5	0.218069498	< 0.001	< 0.001
GO:0046700	heterocycle catabolic process	183	0.21798848	0.0061	0.007291396
GO:0033962	cytoplasmic mRNA processing body assembly	8	0.217985843	0.0083	0.009660392
GO:0072330	monocarboxylic acid biosynthetic process	80	0.217905405	< 0.001	< 0.001
GO:0048311	mitochondrion distribution	6	0.217803518	0.0062	0.00739947
GO:0090287	regulation of cellular response to growth factor stimulus	80	0.21770592	< 0.001	< 0.001
GO:0035089	establishment of apical/basal cell polarity	10	0.217683398	< 0.001	< 0.001
GO:0061162	establishment of monopolar cell polarity	10	0.217683398	< 0.001	< 0.001
GO:0010662	regulation of striated muscle cell apoptotic process	19	0.217638691	< 0.001	< 0.001
GO:0097435	fibril organization	11	0.217526618	0.0003	0.000505993
GO:0016482	cytosolic transport	72	0.217517518	0.0003	0.000505993
GO:0032368	regulation of lipid transport	32	0.217471042	< 0.001	< 0.001
GO:0010332	response to gamma radiation	23	0.217324156	0.005	0.006070546
GO:0006665	sphingolipid metabolic process	49	0.217214299	0.0001	0.000192793
GO:0090151	establishment of protein localization to mitochondrial membrane	7	0.217209046	0.0153	0.01697069
GO:0043011	myeloid dendritic cell differentiation	6	0.217160017	< 0.001	< 0.001
GO:0071276	cellular response to cadmium ion	18	0.217160017	0.0005	0.000791911
GO:0090140	regulation of mitochondrial fission	9	0.217131417	0.0086	0.009975188
GO:0033559	unsaturated fatty acid metabolic process	40	0.217091377	< 0.001	< 0.001
GO:1901224	positive regulation of NIK/NF-kappaB signaling	23	0.217021991	0.0019	0.00254969
GO:0072698	protein localization to microtubule cytoskeleton	25	0.216936937	0.0002	0.000356582
GO:0048639	positive regulation of developmental growth	75	0.216768769	< 0.001	< 0.001
GO:1903861	positive regulation of dendrite extension	14	0.216749402	0.0269	0.028900119
GO:0099010	modification of postsynaptic structure	9	0.216731017	0.0024	0.003116943
GO:0046847	filopodium assembly	33	0.216731017	0.0072	0.008495371
GO:0071806	protein transmembrane transport	20	0.216589447	0.0149	0.016557598
GO:0006575	cellular modified amino acid metabolic process	59	0.216578322	< 0.001	< 0.001
GO:0051573	negative regulation of histone H3-K9 methylation	5	0.216576577	0.009	0.010394529
GO:0006956	complement activation	10	0.216550837	0.0001	0.000192793
GO:0001759	organ induction	5	0.216525097	0.0106	0.012082345
GO:0070265	necrotic cell death	12	0.216430716	0.0003	0.000505993
GO:0001906	cell killing	42	0.216424588	< 0.001	< 0.001
GO:0051984	positive regulation of chromosome segregation	10	0.216422136	0.0004	0.000648934
GO:0070875	positive regulation of glycogen metabolic process	8	0.216377091	0.0016	0.002186748
GO:0050810	regulation of steroid biosynthetic process	39	0.216374616	0.0047	0.005730776
GO:0035929	steroid hormone secretion	5	0.216370656	0.024	0.025944389
GO:0005978	glycogen biosynthetic process	20	0.216241956	< 0.001	< 0.001
GO:0009250	glucan biosynthetic process	20	0.216241956	< 0.001	< 0.001
GO:0016575	histone deacetylation	22	0.216216216	0.0001	0.000192793
GO:0086091	regulation of heart rate by cardiac conduction	13	0.216196416	0.014	0.015631405
GO:0044546	NLRP3 inflammasome complex assembly	8	0.216055341	0.0059	0.007066401
GO:0006084	acetyl-CoA metabolic process	12	0.216044616	0.008	0.009347459
GO:0090303	positive regulation of wound healing	13	0.215998416	< 0.001	< 0.001
GO:0009200	deoxyribonucleoside triphosphate metabolic process	7	0.215958816	0.0012	0.001702047
GO:0060043	regulation of cardiac muscle cell proliferation	13	0.215919216	< 0.001	< 0.001
GO:0042130	negative regulation of T cell proliferation	12	0.215873016	0.0034	0.00427293
GO:0048009	insulin-like growth factor receptor signaling pathway	13	0.215840016	0.0018	0.002428764
GO:0043506	regulation of JUN kinase activity	40	0.215682111	< 0.001	< 0.001
GO:0032881	regulation of polysaccharide metabolic process	18	0.215644216	0.0013	0.001826625
GO:0002690	positive regulation of leukocyte chemotaxis	28	0.215637066	< 0.001	< 0.001
GO:0032691	negative regulation of interleukin-1 beta production	11	0.215607816	0.0011	0.001576346
GO:0042755	eating behavior	12	0.215572716	< 0.001	< 0.001
GO:0030490	maturation of SSU-rRNA	6	0.215529816	0.0244	0.026339912
GO:0051905	establishment of pigment granule localization	13	0.215483615	< 0.001	< 0.001
GO:0071472	cellular response to salt stress	6	0.215186615	0.0238	0.025753945
GO:0007595	lactation	19	0.21515952	< 0.001	< 0.001
GO:0060389	pathway-restricted SMAD protein phosphorylation	15	0.215083655	0.0037	0.004617737
GO:0048535	lymph node development	8	0.21502574	0.0014	0.00194839
GO:0070231	T cell apoptotic process	12	0.214929215	0.0021	0.002780108
GO:0006884	cell volume homeostasis	10	0.214877735	< 0.001	< 0.001
GO:0061384	heart trabecula morphogenesis	16	0.21483269	< 0.001	< 0.001
GO:0042537	benzene-containing compound metabolic process	12	0.214779065	< 0.001	< 0.001
GO:0031062	positive regulation of histone methylation	14	0.214726972	0.0122	0.013738029
GO:1900026	positive regulation of substrate adhesion-dependent cell spreading	17	0.214717238	< 0.001	< 0.001
GO:0099068	postsynapse assembly	9	0.214614615	0.0173	0.01905998
GO:0030214	hyaluronan catabolic process	7	0.214598272	0.0002	0.000356582
GO:0045943	positive regulation of transcription from RNA polymerase I promoter	12	0.214543115	0.0031	0.003925117
GO:0035088	establishment or maintenance of apical/basal cell polarity	19	0.214482151	< 0.001	< 0.001
GO:0061245	establishment or maintenance of bipolar cell polarity	19	0.214482151	< 0.001	< 0.001
GO:0010766	negative regulation of sodium ion transport	6	0.214371514	0.0004	0.000648934
GO:0060347	heart trabecula formation	9	0.214300014	0.0105	0.011988591
GO:0007603	phototransduction, visible light	11	0.214180414	0.0022	0.002896881
GO:1902004	positive regulation of beta-amyloid formation	6	0.214157014	0.0372	0.039263438
GO:1902993	positive regulation of amyloid precursor protein catabolic process	6	0.214157014	0.0372	0.039263438
GO:0019218	regulation of steroid metabolic process	48	0.214130202	0.0035	0.004390436
GO:0051055	negative regulation of lipid biosynthetic process	16	0.213963964	0.0024	0.003116943
GO:0060571	morphogenesis of an epithelial fold	5	0.213951094	0.0312	0.033235719
GO:0051205	protein insertion into membrane	25	0.213920206	< 0.001	< 0.001
GO:0030038	contractile actin filament bundle assembly	46	0.213843657	< 0.001	< 0.001
GO:0043149	stress fiber assembly	46	0.213843657	< 0.001	< 0.001
GO:0010719	negative regulation of epithelial to mesenchymal transition	13	0.213780814	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0045745	positive regulation of G-protein coupled receptor protein signaling pathway	11	0.213759214	0.0025	0.003237479
GO:0007171	activation of transmembrane receptor protein tyrosine kinase activity	6	0.213728014	0.0304	0.032428267
GO:0045214	sarcomere organization	10	0.213719434	0.0091	0.010505533
GO:0021854	hypothalamus development	5	0.213693694	0.0029	0.003693519
GO:0050919	negative chemotaxis	18	0.213685114	0.0004	0.000648934
GO:0070873	regulation of glycogen metabolic process	14	0.213587056	0.0002	0.000356582
GO:1903670	regulation of sprouting angiogenesis	24	0.213513514	0.0072	0.008495371
GO:0048644	muscle organ morphogenesis	30	0.213359073	< 0.001	< 0.001
GO:0072528	pyrimidine-containing compound biosynthetic process	14	0.21331127	0.0007	0.001063182
GO:0051444	negative regulation of ubiquitin-protein transferase activity	8	0.213223938	0.0236	0.025557996
GO:0042742	defense response to bacterium	51	0.213137507	< 0.001	< 0.001
GO:0046719	regulation by virus of viral protein levels in host cell	5	0.213127413	0.0473	0.049269314
GO:0060760	positive regulation of response to cytokine stimulus	20	0.213050193	0.0007	0.001063182
GO:0032371	regulation of sterol transport	11	0.212987013	0.0006	0.000927725
GO:0032374	regulation of cholesterol transport	11	0.212987013	0.0006	0.000927725
GO:0042116	macrophage activation	23	0.212914778	< 0.001	< 0.001
GO:1903350	response to dopamine	6	0.212870013	0.0346	0.036655244
GO:1903351	cellular response to dopamine	6	0.212870013	0.0346	0.036655244
GO:1900037	regulation of cellular response to hypoxia	8	0.212870013	0.0009	0.001319479
GO:1903649	regulation of cytoplasmic transport	15	0.212801373	0.0001	0.000192793
GO:0086005	ventricular cardiac muscle cell action potential	14	0.212741313	0.0033	0.004153051
GO:1902065	response to L-glutamate	7	0.212722927	0.0052	0.006299215
GO:0006959	humoral immune response	39	0.212711613	< 0.001	< 0.001
GO:1902116	negative regulation of organelle assembly	15	0.212612613	0.0018	0.002428764
GO:0010612	regulation of cardiac muscle adaptation	5	0.212612613	0.0024	0.003116943
GO:1903242	regulation of cardiac muscle hypertrophy in response to stress	5	0.212612613	0.0024	0.003116943
GO:0090150	establishment of protein localization to membrane	153	0.212498212	0.0047	0.005730776
GO:0032231	regulation of actin filament bundle assembly	44	0.212402012	< 0.001	< 0.001
GO:1903844	regulation of cellular response to transforming growth factor beta stimulus	41	0.212399159	< 0.001	< 0.001
GO:0001569	branching involved in blood vessel morphogenesis	10	0.212329472	0.0003	0.000505993
GO:0090100	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	27	0.212298012	0.0032	0.004042263
GO:0007062	sister chromatid cohesion	17	0.212294648	< 0.001	< 0.001
GO:0048070	regulation of developmental pigmentation	6	0.212226512	0.0093	0.010727257
GO:0032456	endocytic recycling	22	0.212214812	0.0013	0.001826625
GO:0032370	positive regulation of lipid transport	23	0.212176151	< 0.001	< 0.001
GO:0070935	3'-UTR-mediated mRNA stabilization	8	0.212033462	0.0007	0.001063182
GO:0031641	regulation of myelination	14	0.211987498	< 0.001	< 0.001
GO:0043931	ossification involved in bone maturation	6	0.211969112	0.0004	0.000648934
GO:0039694	viral RNA genome replication	11	0.211934012	0.0005	0.000791911
GO:0039703	RNA replication	11	0.211934012	0.0005	0.000791911
GO:0061000	negative regulation of dendritic spine development	7	0.211913955	0.0335	0.035545651
GO:0060632	regulation of microtubule-based movement	11	0.211887212	0.0008	0.001193265
GO:0060444	branching involved in mammary gland duct morphogenesis	7	0.211730097	< 0.001	< 0.001
GO:0018208	peptidyl-proline modification	27	0.211697412	0.0059	0.007066401
GO:0019359	nicotinamide nucleotide biosynthetic process	16	0.211615187	0.0003	0.000505993
GO:0019363	pyridine nucleotide biosynthetic process	16	0.211615187	0.0003	0.000505993
GO:0001573	ganglioside metabolic process	7	0.21154624	0.0028	0.003584743
GO:0016226	iron-sulfur cluster assembly	6	0.211540112	0.0376	0.039670129
GO:0031163	metallo-sulfur cluster assembly	6	0.211540112	0.0376	0.039670129
GO:0051085	chaperone mediated protein folding requiring cofactor	9	0.211325611	0.0003	0.000505993
GO:0010225	response to UV-C	9	0.211239811	0.0002	0.000356582
GO:0044275	cellular carbohydrate catabolic process	16	0.211196911	0.0001	0.000192793
GO:1904754	positive regulation of vascular associated smooth muscle cell migration	7	0.211068211	0.0013	0.001826625
GO:0006636	unsaturated fatty acid biosynthetic process	27	0.211039611	< 0.001	< 0.001
GO:0006488	dolichol-linked oligosaccharide biosynthetic process	8	0.210939511	0.0196	0.021436632
GO:0006490	oligosaccharide-lipid intermediate biosynthetic process	8	0.210939511	0.0196	0.021436632
GO:0016558	protein import into peroxisome matrix	5	0.210913771	0.0314	0.033435586
GO:0051385	response to mineralocorticoid	13	0.210890011	< 0.001	< 0.001
GO:1905331	negative regulation of morphogenesis of an epithelium	7	0.210884354	0.0448	0.046773416
GO:0017144	drug metabolic process	9	0.210782211	< 0.001	< 0.001
GO:0009148	pyrimidine nucleoside triphosphate biosynthetic process	5	0.210553411	0.0471	0.049070445
GO:0044065	regulation of respiratory system process	6	0.210553411	0.0106	0.012082345
GO:0045639	positive regulation of myeloid cell differentiation	32	0.210513192	0.0002	0.000356582
GO:0046456	icosanoid biosynthetic process	20	0.210501931	0.0012	0.001702047
GO:1901570	fatty acid derivative biosynthetic process	20	0.210501931	0.0012	0.001702047
GO:0090092	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	66	0.21037011	< 0.001	< 0.001
GO:0010803	regulation of tumor necrosis factor-mediated signaling pathway	24	0.210349635	0.0003	0.000505993
GO:1903365	regulation of fear response	6	0.21033891	0.0154	0.017060599
GO:2000822	regulation of behavioral fear response	6	0.21033891	0.0154	0.017060599
GO:0006825	copper ion transport	5	0.21029601	0.0208	0.022657367
GO:0045472	response to ether	5	0.21024453	0.0014	0.00194839
GO:0032570	response to progesterone	15	0.21010725	< 0.001	< 0.001
GO:0090288	negative regulation of cellular response to growth factor stimulus	48	0.210054698	< 0.001	< 0.001
GO:0006098	pentose-phosphate shunt	5	0.20998713	0.0273	0.029300735
GO:0050779	RNA destabilization	15	0.20990133	0.003	0.003811001
GO:0061157	mRNA destabilization	15	0.20990133	0.003	0.003811001
GO:0051492	regulation of stress fiber assembly	39	0.20966901	< 0.001	< 0.001
GO:0045143	homologous chromosome segregation	13	0.209484209	0.0014	0.00194839
GO:0090394	negative regulation of excitatory postsynaptic potential	5	0.209420849	0.0008	0.001193265
GO:0009584	detection of visible light	18	0.209337909	0.0012	0.001702047
GO:0048771	tissue remodeling	48	0.209239597	0.0001	0.000192793
GO:0045806	negative regulation of endocytosis	25	0.209194337	< 0.001	< 0.001
GO:0051084	'de novo' posttranslational protein folding	11	0.209126009	0.0003	0.000505993

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0042074	cell migration involved in gastrulation	5	0.209111969	0.0004	0.000648934
GO:0072173	metanephric tubule morphogenesis	5	0.209111969	0.003	0.003811001
GO:0072282	metanephric nephron tubule morphogenesis	5	0.209111969	0.003	0.003811001
GO:0055026	negative regulation of cardiac muscle tissue development	10	0.209060489	0.0001	0.000192793
GO:0046889	positive regulation of lipid biosynthetic process	22	0.208880309	0.0004	0.000648934
GO:2001014	regulation of skeletal muscle cell differentiation	6	0.208794509	< 0.001	< 0.001
GO:0018216	peptidyl-arginine methylation	9	0.208780209	0.0024	0.003116943
GO:0002192	IRES-dependent translational initiation	6	0.208751609	0.0015	0.002069969
GO:0001774	microglial cell activation	11	0.208751609	0.0003	0.000505993
GO:0032945	negative regulation of mononuclear cell proliferation	13	0.208751609	0.0021	0.002780108
GO:0050672	negative regulation of lymphocyte proliferation	13	0.208751609	0.0021	0.002780108
GO:0051781	positive regulation of cell division	25	0.208720721	< 0.001	< 0.001
GO:2001239	regulation of extrinsic apoptotic signaling pathway in absence of ligand	9	0.208379808	0.0008	0.001193265
GO:0000002	mitochondrial genome maintenance	12	0.208344058	0.0015	0.002069969
GO:0043501	skeletal muscle adaptation	7	0.20827358	0.0001	0.000192793
GO:0007077	mitotic nuclear envelope disassembly	6	0.208193908	0.0399	0.041924869
GO:0032885	regulation of polysaccharide biosynthetic process	16	0.208188546	0.0015	0.002069969
GO:0045217	cell-cell junction maintenance	5	0.208185328	0.0256	0.027580223
GO:0014823	response to activity	23	0.208113704	0.0002	0.000356582
GO:0060575	intestinal epithelial cell differentiation	5	0.208082368	0.0003	0.000505993
GO:0016242	negative regulation of macroautophagy	15	0.208013728	0.0023	0.003013139
GO:0070584	mitochondrion morphogenesis	14	0.207997794	0.007	0.008288344
GO:0006085	acetyl-CoA biosynthetic process	7	0.207979408	0.0138	0.015427224
GO:0007257	activation of JUN kinase activity	19	0.207843934	0.0001	0.000192793
GO:0006213	pyrimidine nucleoside metabolic process	14	0.207758779	0.0117	0.013205263
GO:0007129	synapsis	10	0.207670528	0.0006	0.000927725
GO:0010669	epithelial structure maintenance	14	0.20753815	< 0.001	< 0.001
GO:1902895	positive regulation of pri-miRNA transcription from RNA polymerase II promoter	15	0.207481767	< 0.001	< 0.001
GO:0065002	intracellular protein transmembrane transport	18	0.207478907	0.0148	0.01645324
GO:0085029	extracellular matrix assembly	8	0.207464607	0.0048	0.005840847
GO:0045453	bone resorption	17	0.207358619	0.0069	0.008171729
GO:0042532	negative regulation of tyrosine phosphorylation of STAT protein	6	0.207335907	0.0347	0.036753979
GO:0000413	protein peptidyl-prolyl isomerization	20	0.207117117	0.0063	0.007507211
GO:1903708	positive regulation of hemopoiesis	54	0.206911674	0.0001	0.000192793
GO:0030183	B cell differentiation	33	0.206895207	0.0003	0.000505993
GO:0051775	response to redox state	9	0.206492206	0.005	0.006070546
GO:0051204	protein insertion into mitochondrial membrane	19	0.206394364	0.0041	0.005057384
GO:0070601	centromeric sister chromatid cohesion	5	0.206383526	0.0027	0.003470695
GO:0090051	negative regulation of cell migration involved in sprouting angiogenesis	6	0.206263406	0.0109	0.012398148
GO:0048873	homeostasis of number of cells within a tissue	9	0.206120406	0.0016	0.002186748
GO:0010613	positive regulation of cardiac muscle hypertrophy	17	0.206086759	0.0001	0.000192793
GO:0014742	positive regulation of muscle hypertrophy	17	0.206086759	0.0001	0.000192793
GO:0048799	animal organ maturation	8	0.206081081	0.0003	0.000505993
GO:0070977	bone maturation	8	0.206081081	0.0003	0.000505993
GO:0046621	negative regulation of organ growth	12	0.206027456	0.0002	0.000356582
GO:0010677	negative regulation of cellular carbohydrate metabolic process	13	0.205979606	0.0027	0.003470695
GO:0043276	anoikis	13	0.205979606	0.0036	0.004505419
GO:0090101	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	37	0.205913249	0.0001	0.000192793
GO:0050879	multicellular organismal movement	19	0.205879564	0.0001	0.000192793
GO:0050881	musculoskeletal movement	19	0.205879564	0.0001	0.000192793
GO:0070098	chemokine-mediated signaling pathway	11	0.205639406	0.0003	0.000505993
GO:0036499	PERK-mediated unfolded protein response	6	0.205577006	0.0045	0.005509289
GO:0051180	vitamin transport	8	0.205148005	0.026	0.028
GO:0002407	dendritic cell chemotaxis	5	0.205148005	0.0324	0.034446114
GO:0045132	meiotic chromosome segregation	23	0.205069666	0.0001	0.000192793
GO:0009147	pyrimidine nucleoside triphosphate metabolic process	6	0.205019305	0.0411	0.043118695
GO:0045912	negative regulation of carbohydrate metabolic process	16	0.205003218	0.0034	0.00427293
GO:0098901	regulation of cardiac muscle cell action potential	10	0.204942085	0.0043	0.005276385
GO:0003197	endocardial cushion development	14	0.204927376	0.0001	0.000192793
GO:0007039	protein catabolic process in the vacuole	7	0.204706748	0.0413	0.043311702
GO:0051785	positive regulation of nuclear division	18	0.204561705	0.0001	0.000192793
GO:0007043	cell-cell junction assembly	33	0.204469404	< 0.001	< 0.001
GO:0071364	cellular response to epidermal growth factor stimulus	17	0.204436369	< 0.001	< 0.001
GO:0032400	melanosome localization	13	0.204395604	0.0003	0.000505993
GO:0010862	positive regulation of pathway-restricted SMAD protein phosphorylation	8	0.204375804	0.0206	0.022453086
GO:0048671	negative regulation of collateral sprouting	5	0.204272844	0.042	0.043994573
GO:0003203	endocardial cushion morphogenesis	10	0.204118404	< 0.001	< 0.001
GO:0042104	positive regulation of activated T cell proliferation	7	0.204044861	0.0002	0.000356582
GO:0046856	phosphatidylinositol dephosphorylation	12	0.204011154	0.0272	0.029199205
GO:0016254	preassembly of GPI anchor in ER membrane	6	0.203989704	0.0132	0.014787065
GO:0006506	GPI anchor biosynthetic process	10	0.203963964	0.0059	0.007066401
GO:0017015	regulation of transforming growth factor beta receptor signaling pathway	40	0.203925354	< 0.001	< 0.001
GO:0030239	myofibril assembly	14	0.203897775	0.0006	0.000927725
GO:0097009	energy homeostasis	10	0.203758044	0.0047	0.005730776
GO:0044458	motile cilium assembly	5	0.203758044	0.0022	0.002896881
GO:0002763	positive regulation of myeloid leukocyte differentiation	21	0.203701661	0.0005	0.000791911
GO:0032604	granulocyte macrophage colony-stimulating factor production	6	0.203603604	0.0008	0.001193265
GO:0032645	regulation of granulocyte macrophage colony-stimulating factor production	6	0.203603604	0.0008	0.001193265
GO:0010324	membrane invagination	21	0.203591346	0.0087	0.010084685
GO:0021846	cell proliferation in forebrain	12	0.203582154	0.0006	0.000927725
GO:0010869	regulation of receptor biosynthetic process	6	0.203517804	0.0029	0.003693519
GO:0032800	receptor biosynthetic process	6	0.203517804	0.0029	0.003693519
GO:0035970	peptidyl-threonine dephosphorylation	9	0.203517804	0.0018	0.002428764

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0099563	modification of synaptic structure	11	0.203439803	0.0112	0.012688637
GO:0051290	protein heterotetramerization	13	0.203425403	0.0011	0.001576346
GO:0005979	regulation of glycogen biosynthetic process	12	0.203303303	0.0004	0.000648934
GO:0010962	regulation of glucan biosynthetic process	12	0.203303303	0.0004	0.000648934
GO:0032459	regulation of protein oligomerization	16	0.203265766	0.0004	0.000648934
GO:0022011	myelination in peripheral nervous system	9	0.203060203	0.0009	0.001319479
GO:0032292	peripheral nervous system axon ensheathment	9	0.203060203	0.0009	0.001319479
GO:0045109	intermediate filament organization	5	0.203037323	0.0096	0.011052066
GO:0045577	regulation of B cell differentiation	9	0.203003003	0.0002	0.000356582
GO:0010259	multicellular organism aging	13	0.202910603	0.017	0.018752398
GO:0072584	caveolin-mediated endocytosis	6	0.202831403	0.0237	0.02566115
GO:0009215	purine deoxyribonucleoside triphosphate metabolic process	5	0.202779923	0.002	0.002664694
GO:0045992	negative regulation of embryonic development	11	0.202550603	< 0.001	< 0.001
GO:0071677	positive regulation of mononuclear cell migration	9	0.202545403	0.0035	0.004390436
GO:0045604	regulation of epidermal cell differentiation	15	0.202436722	< 0.001	< 0.001
GO:0006672	ceramide metabolic process	23	0.202428515	0.0001	0.000192793
GO:0032964	collagen biosynthetic process	13	0.202356202	< 0.001	< 0.001
GO:0030968	endoplasmic reticulum unfolded protein response	48	0.202295152	0.0003	0.000505993
GO:0014044	Schwann cell development	10	0.202239382	0.0009	0.001319479
GO:0045621	positive regulation of lymphocyte differentiation	21	0.202059202	0.0015	0.002069969
GO:0045780	positive regulation of bone resorption	5	0.201750322	0.0342	0.036245695
GO:0046852	positive regulation of bone remodeling	5	0.201750322	0.0342	0.036245695
GO:0008206	bile acid metabolic process	14	0.201654716	0.0006	0.000927725
GO:0008207	C21-steroid hormone metabolic process	10	0.201647362	0.0022	0.002896881
GO:0050926	regulation of positive chemotaxis	7	0.201617944	0.0015	0.002069969
GO:0050927	positive regulation of positive chemotaxis	7	0.201617944	0.0015	0.002069969
GO:0035967	cellular response to topologically incorrect protein	60	0.201613042	0.0002	0.000356582
GO:0070131	positive regulation of mitochondrial translation	12	0.201587302	0.0154	0.017060599
GO:1903541	regulation of exosomal secretion	7	0.201544402	0.0252	0.027160112
GO:0003009	skeletal muscle contraction	15	0.201389961	< 0.001	< 0.001
GO:0035246	peptidyl-arginine N-methylation	6	0.201244101	0.0055	0.006618125
GO:0042398	cellular modified amino acid biosynthetic process	15	0.201201201	0.004	0.004954389
GO:0051645	Golgi localization	11	0.201170001	0.0006	0.000927725
GO:0002861	regulation of inflammatory response to antigenic stimulus	7	0.201139915	0.0029	0.003693519
GO:0043113	receptor clustering	28	0.200726236	0.0088	0.010185307
GO:0018195	peptidyl-arginine modification	10	0.200720721	0.003	0.003811001
GO:0045766	positive regulation of angiogenesis	45	0.200720721	0.0011	0.001576346
GO:1990774	tumor necrosis factor secretion	8	0.200611326	0.0053	0.006400268
GO:0022600	digestive system process	30	0.200600601	< 0.001	< 0.001
GO:0032637	interleukin-8 production	23	0.200503609	0.0011	0.001576346
GO:0034035	purine ribonucleoside bisphosphate metabolic process	7	0.200441258	0.004	0.004954389
GO:0050427	3'-phosphoadenosine 5'-phosphosulfate metabolic process	7	0.200441258	0.004	0.004954389
GO:0051302	regulation of cell division	58	0.200412728	< 0.001	< 0.001
GO:0006071	glycerol metabolic process	5	0.2002574	0.0009	0.001319479
GO:1901222	regulation of NIK/NF-kappaB signaling	31	0.200166065	0.0039	0.004841626
GO:0036498	IRE1-mediated unfolded protein response	29	0.200062131	0.0003	0.000505993
GO:0045954	positive regulation of natural killer cell mediated cytotoxicity	5	0.2	< 0.001	< 0.001
GO:0034620	cellular response to unfolded protein	55	0.19987364	0.0003	0.000505993
GO:0072525	pyridine-containing compound biosynthetic process	19	0.199674863	0.0001	0.000192793
GO:0042036	negative regulation of cytokine biosynthetic process	11	0.199649	0.0001	0.000192793
GO:0044058	regulation of digestive system process	9	0.1996282	0.0001	0.000192793
GO:0035584	calcium-mediated signaling using intracellular calcium source	10	0.19956242	0.0063	0.007507211
GO:0048670	regulation of collateral sprouting	7	0.199558742	0.0086	0.009975188
GO:0035810	positive regulation of urine volume	5	0.19953668	0.0011	0.001576346
GO:0030970	retrograde protein transport, ER to cytosol	14	0.199466814	0.0084	0.009757868
GO:1903513	endoplasmic reticulum to cytosol transport	14	0.199466814	0.0084	0.009757868
GO:0051647	nucleus localization	10	0.199433719	0.0314	0.033435586
GO:0060312	regulation of blood vessel remodeling	5	0.199382239	0.0033	0.004153051
GO:0031063	regulation of histone deacetylation	12	0.199377949	< 0.001	< 0.001
GO:1904886	beta-catenin destruction complex disassembly	7	0.199374885	0.0017	0.00231289
GO:1902107	positive regulation of leukocyte differentiation	42	0.199331985	0.0008	0.001193265
GO:0006401	RNA catabolic process	128	0.199288127	0.0387	0.04075113
GO:0080154	regulation of fertilization	7	0.199264571	0.0382	0.040279571
GO:0033197	response to vitamin E	5	0.199124839	0.0009	0.001319479
GO:0090025	regulation of monocyte chemotaxis	9	0.198970399	0.0041	0.005057384
GO:0045599	negative regulation of fat cell differentiation	21	0.198933628	< 0.001	< 0.001
GO:0045198	establishment of epithelial cell apical/basal polarity	8	0.198809524	0.0026	0.003356522
GO:0010737	protein kinase A signaling	11	0.198806599	< 0.001	< 0.001
GO:0035269	protein O-linked mannosylation	10	0.198532819	0.0028	0.003584743
GO:0006471	protein ADP-ribosylation	11	0.198525799	0.0012	0.001702047
GO:0098885	modification of postsynaptic actin cytoskeleton	7	0.198418827	0.0032	0.004042263
GO:0061002	negative regulation of dendritic spine morphogenesis	5	0.198404118	0.0316	0.033622052
GO:0032965	regulation of collagen biosynthetic process	10	0.198378378	< 0.001	< 0.001
GO:0051292	nuclear pore complex assembly	5	0.198198198	0.0054	0.006510843
GO:0032527	protein exit from endoplasmic reticulum	19	0.198184651	0.0052	0.006299215
GO:0001941	postsynaptic membrane organization	24	0.198166023	0.0041	0.005057384
GO:0001964	startle response	18	0.198098098	0.0103	0.011785137
GO:0042780	tRNA 3'-end processing	5	0.198095238	0.0009	0.001319479
GO:0043628	ncRNA 3'-end processing	5	0.198095238	0.0009	0.001319479
GO:0046471	phosphatidylglycerol metabolic process	9	0.197997998	0.0024	0.003116943
GO:0032781	positive regulation of ATPase activity	19	0.197696945	0.0005	0.000791911
GO:0006221	pyrimidine nucleotide biosynthetic process	11	0.197683398	0.0009	0.001319479
GO:0010039	response to iron ion	9	0.197683398	0.0277	0.029712346

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0021510	spinal cord development	32	0.197627091	0.0023	0.003013139
GO:0014002	astrocyte development	7	0.197536312	0.0086	0.009975188
GO:1903053	regulation of extracellular matrix organization	17	0.197425997	< 0.001	< 0.001
GO:0010955	negative regulation of protein processing	9	0.197397397	0.0215	0.023377465
GO:1903318	negative regulation of protein maturation	9	0.197397397	0.0215	0.023377465
GO:0032878	regulation of establishment or maintenance of cell polarity	11	0.197379197	< 0.001	< 0.001
GO:0006749	glutathione metabolic process	22	0.197098397	0.0001	0.000192793
GO:0050829	defense response to Gram-negative bacterium	20	0.197001287	0.0002	0.000356582
GO:1901616	organic hydroxy compound catabolic process	20	0.196936937	< 0.001	< 0.001
GO:0050892	intestinal absorption	7	0.196800883	0.016	0.017689034
GO:0048596	embryonic camera-type eye morphogenesis	7	0.196764111	0.0004	0.000648934
GO:0071539	protein localization to centrosome	19	0.196762176	0.0006	0.000927725
GO:1905508	protein localization to microtubule organizing center	19	0.196762176	0.0006	0.000927725
GO:0032464	positive regulation of protein homooligomerization	5	0.196550837	0.001	0.001450349
GO:0001522	pseudouridine synthesis	7	0.196286082	0.0444	0.046382679
GO:1902176	negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	8	0.196171171	0.0028	0.003584743
GO:1905214	regulation of RNA binding	6	0.195967396	0.0041	0.005057384
GO:0006378	mRNA polyadenylation	15	0.195933076	0.0181	0.019900793
GO:0007020	microtubule nucleation	7	0.195808053	0.0367	0.03875084
GO:0090141	positive regulation of mitochondrial fission	5	0.195778636	0.0105	0.011988591
GO:0072531	pyrimidine-containing compound transmembrane transport	5	0.195572716	0.0116	0.013103344
GO:0007606	sensory perception of chemical stimulus	35	0.195418275	< 0.001	< 0.001
GO:0051044	positive regulation of membrane protein ectodomain proteolysis	5	0.195366795	0.0238	0.025753945
GO:1904781	positive regulation of protein localization to centrosome	6	0.195323895	0.0205	0.022357619
GO:0032104	regulation of response to extracellular stimulus	9	0.195252395	0.0021	0.002780108
GO:0032107	regulation of response to nutrient levels	9	0.195252395	0.0021	0.002780108
GO:0055069	zinc ion homeostasis	6	0.194894895	0.0148	0.01645324
GO:0005980	glycogen catabolic process	8	0.19488417	0.0018	0.002428764
GO:0009251	glucan catabolic process	8	0.19488417	0.0018	0.002428764
GO:0052173	response to defenses of other organism involved in symbiotic interaction	5	0.194851995	0.02	0.021843169
GO:0052200	response to host defenses	5	0.194851995	0.02	0.021843169
GO:0075136	response to host	5	0.194851995	0.02	0.021843169
GO:0046839	phospholipid dephosphorylation	13	0.194574795	0.0104	0.011884458
GO:0043032	positive regulation of macrophage activation	6	0.194551695	0.004	0.004954389
GO:0051683	establishment of Golgi localization	6	0.194251394	0.0037	0.004617737
GO:0046655	folic acid metabolic process	6	0.194122694	0.001	0.001450349
GO:0015721	bile acid and bile salt transport	8	0.194111969	0.0065	0.007730194
GO:0061082	myeloid leukocyte cytokine production	9	0.194108394	0.002	0.002664694
GO:0097028	dendritic cell differentiation	12	0.194036894	0.0031	0.003925117
GO:1902914	regulation of protein polyubiquitination	9	0.194022594	0.014	0.015631405
GO:0016486	peptide hormone processing	7	0.194006251	0.0004	0.000648934
GO:0031061	negative regulation of histone methylation	10	0.193976834	0.0005	0.000791911
GO:0061081	positive regulation of myeloid leukocyte cytokine production involved in immune response	7	0.19396948	0.0001	0.000192793
GO:1905208	negative regulation of cardiocyte differentiation	7	0.193712079	0.0096	0.011052066
GO:0033687	osteoblast proliferation	8	0.193564994	0.0101	0.011583277
GO:0007528	neuromuscular junction development	16	0.193436293	0.0005	0.000791911
GO:0070572	positive regulation of neuron projection regeneration	5	0.193256113	0.0053	0.006400268
GO:0046849	bone remodeling	24	0.193114543	0.002	0.002664694
GO:0036514	dopaminergic neuron axon guidance	5	0.193101673	0.009	0.010394529
GO:1904938	planar cell polarity pathway involved in axon guidance	5	0.193101673	0.009	0.010394529
GO:0035384	thioester biosynthetic process	17	0.192717087	0.004	0.004954389
GO:0071616	acyl-CoA biosynthetic process	17	0.192717087	0.004	0.004954389
GO:0015074	DNA integration	6	0.192664093	< 0.001	< 0.001
GO:0045838	positive regulation of membrane potential	6	0.192621193	0.0365	0.038569808
GO:1903036	positive regulation of response to wounding	17	0.192520251	0.0002	0.000356582
GO:0035914	skeletal muscle cell differentiation	20	0.192496782	< 0.001	< 0.001
GO:0034103	regulation of tissue remodeling	22	0.192453492	0.0003	0.000505993
GO:1900221	regulation of beta-amyloid clearance	8	0.192374517	< 0.001	< 0.001
GO:0044793	negative regulation by host of viral process	5	0.192277992	0.0043	0.005276385
GO:1905244	regulation of modification of synaptic structure	5	0.192226512	0.0101	0.011583277
GO:1903845	negative regulation of cellular response to transforming growth factor beta stimulus	29	0.192135978	0.0014	0.00194839
GO:2000403	positive regulation of lymphocyte migration	8	0.191988417	0.0047	0.005730776
GO:0101023	vascular endothelial cell proliferation	11	0.191903592	0.0002	0.000356582
GO:1905562	regulation of vascular endothelial cell proliferation	11	0.191903592	0.0002	0.000356582
GO:0060134	prepulse inhibition	10	0.191763192	0.0111	0.012593827
GO:2001244	positive regulation of intrinsic apoptotic signaling pathway	23	0.191740809	0.0162	0.017906484
GO:0030213	hyaluronan biosynthetic process	5	0.191711712	0.0239	0.025846628
GO:0002548	monocyte chemotaxis	14	0.191487406	< 0.001	< 0.001
GO:0051904	pigment granule transport	12	0.191462891	0.0003	0.000505993
GO:1990542	mitochondrial transmembrane transport	27	0.191410458	0.0244	0.026339912
GO:0048194	Golgi vesicle budding	5	0.191402831	0.0087	0.010084685
GO:0043297	apical junction assembly	25	0.191258687	0.0002	0.000356582
GO:0032462	regulation of protein homooligomerization	10	0.191093951	0.0147	0.016362266
GO:0030865	cortical cytoskeleton organization	16	0.191071429	0.0001	0.000192793
GO:0061077	chaperone-mediated protein folding	24	0.191001716	0.0038	0.004725081
GO:0010883	regulation of lipid storage	10	0.190913771	0.0123	0.013827585
GO:0032677	regulation of interleukin-8 production	22	0.190885691	0.0033	0.004153051
GO:0021515	cell differentiation in spinal cord	17	0.19085472	0.0001	0.000192793
GO:0060512	prostate gland morphogenesis	6	0.190776491	0.0106	0.012082345
GO:0060740	prostate gland epithelium morphogenesis	6	0.190776491	0.0106	0.012082345
GO:0042474	middle ear morphogenesis	6	0.190519091	0.0031	0.003925117
GO:0086014	atrial cardiac muscle cell action potential	6	0.190519091	0.0423	0.044274492
GO:0086026	atrial cardiac muscle cell to AV node cell signaling	6	0.190519091	0.0423	0.044274492

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0086066	atrial cardiac muscle cell to AV node cell communication	6	0.190519091	0.0423	0.044274492
GO:1904861	excitatory synapse assembly	11	0.19049959	0.0238	0.025753945
GO:1905314	semi-lunar valve development	15	0.19032175	0.0003	0.000505993
GO:1901017	negative regulation of potassium ion transmembrane transporter activity	6	0.19017589	0.0002	0.000356582
GO:0090162	establishment of epithelial cell polarity	15	0.18996139	< 0.001	< 0.001
GO:0042089	cytokine biosynthetic process	30	0.18961819	0.0005	0.000791911
GO:0042107	cytokine metabolic process	30	0.18961819	0.0005	0.000791911
GO:0050766	positive regulation of phagocytosis	19	0.189446589	0.0003	0.000505993
GO:0033344	cholesterol efflux	12	0.189253539	0.0071	0.008390203
GO:0034356	NAD biosynthesis via nicotinamide riboside salvage pathway	8	0.189189189	0.0413	0.043311702
GO:0034375	high-density lipoprotein particle remodeling	6	0.189189189	0.0081	0.00945
GO:0043507	positive regulation of JUN kinase activity	34	0.189181619	0.0003	0.000505993
GO:0006081	cellular aldehyde metabolic process	24	0.189167739	0.0022	0.002896881
GO:0017004	cytochrome complex assembly	9	0.189160589	0.0177	0.019488753
GO:0051570	regulation of histone H3-K9 methylation	9	0.188960389	0.0478	0.049742191
GO:0019915	lipid storage	16	0.188674389	0.0289	0.030950377
GO:0035640	exploration behavior	13	0.188397188	0.0156	0.0172574
GO:0000272	polysaccharide catabolic process	9	0.188388388	0.0008	0.001193265
GO:0044247	cellular polysaccharide catabolic process	9	0.188388388	0.0008	0.001193265
GO:0051657	maintenance of organelle location	5	0.188314028	0.0227	0.024637638
GO:0000212	meiotic spindle organization	5	0.188005148	0.0142	0.01584489
GO:0060179	male mating behavior	6	0.187945088	0.0065	0.007730194
GO:0032233	positive regulation of actin filament bundle assembly	24	0.187934363	0.0003	0.000505993
GO:0051412	response to corticosterone	7	0.187828645	< 0.001	< 0.001
GO:0002181	cytoplasmic translation	30	0.187782068	0.0309	0.032948619
GO:0006555	methionine metabolic process	6	0.187430287	0.0241	0.02604728
GO:0090045	positive regulation of deacetylase activity	5	0.187284427	0.0136	0.015222535
GO:0071825	protein-lipid complex subunit organization	15	0.187250107	0.0002	0.000356582
GO:0070262	peptidyl-serine dephosphorylation	10	0.187155727	0.0114	0.012893596
GO:0045124	regulation of bone resorption	9	0.186958387	0.0072	0.008495371
GO:1901223	negative regulation of NIK/NF-kappaB signaling	5	0.186924067	0.0074	0.008712331
GO:0048668	collateral sprouting	11	0.186825787	0.0061	0.007291396
GO:0051291	protein heterooligomerization	46	0.1867271	0.0002	0.000356582
GO:0097734	extracellular exosome biogenesis	8	0.186647362	0.0383	0.040353519
GO:1990182	exosomal secretion	8	0.186647362	0.0383	0.040353519
GO:0009409	response to cold	14	0.186486486	0.0008	0.001193265
GO:0070830	bicellular tight junction assembly	19	0.186452618	< 0.001	< 0.001
GO:0002026	regulation of the force of heart contraction	11	0.186357786	< 0.001	< 0.001
GO:0045955	negative regulation of calcium ion-dependent exocytosis	5	0.186254826	0.0168	0.018543137
GO:0072643	interferon-gamma secretion	6	0.186229086	0.0287	0.030748374
GO:0010642	negative regulation of platelet-derived growth factor receptor signaling pathway	7	0.186173929	0.0025	0.003237479
GO:0051457	maintenance of protein location in nucleus	9	0.186157586	0.0009	0.001319479
GO:0019400	alditol metabolic process	6	0.185928786	0.0026	0.003356522
GO:0003176	aortic valve development	12	0.185757186	< 0.001	< 0.001
GO:0036010	protein localization to endosome	7	0.1854385	< 0.001	< 0.001
GO:0060716	labyrinthine layer blood vessel development	8	0.18523166	0.0009	0.001319479
GO:1902237	positive regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	5	0.185070785	0.0104	0.011884458
GO:0009299	mRNA transcription	5	0.185019305	0.0041	0.005057384
GO:0090110	cargo loading into COPII-coated vesicle	6	0.184984985	0.0437	0.045686748
GO:0061548	ganglion development	6	0.184899185	0.0192	0.02103747
GO:0010715	regulation of extracellular matrix disassembly	9	0.184841985	0.0132	0.014787065
GO:0009220	pyrimidine ribonucleotide biosynthetic process	8	0.18478121	0.0008	0.001193265
GO:0006103	2-oxoglutarate metabolic process	8	0.18465251	0.0086	0.009975188
GO:0014829	vascular smooth muscle contraction	6	0.184384384	0.0001	0.000192793
GO:0045616	regulation of keratinocyte differentiation	9	0.184212784	0.0065	0.007730194
GO:0006700	C21-steroid hormone biosynthetic process	7	0.18418827	0.0017	0.00231289
GO:0043537	negative regulation of blood vessel endothelial cell migration	16	0.184185972	0.0043	0.005276385
GO:2000036	regulation of stem cell population maintenance	8	0.184169884	0.0016	0.002186748
GO:0009593	detection of chemical stimulus	31	0.184157429	0.0007	0.001063182
GO:0044743	intracellular protein transmembrane import	14	0.183986027	0.0393	0.041318521
GO:0045721	negative regulation of gluconeogenesis	5	0.183835264	0.0051	0.006185009
GO:0002920	regulation of humoral immune response	15	0.183766624	0.0014	0.00194839
GO:0050765	negative regulation of phagocytosis	8	0.183719434	0.0137	0.015318601
GO:0006750	glutathione biosynthetic process	7	0.183710241	0.0118	0.013309789
GO:0019184	nonribosomal peptide biosynthetic process	7	0.183710241	0.0118	0.013309789
GO:2000251	positive regulation of actin cytoskeleton reorganization	9	0.183669384	0.008	0.009347459
GO:0051602	response to electrical stimulus	16	0.183478121	< 0.001	< 0.001
GO:0046850	regulation of bone remodeling	12	0.183440583	0.0046	0.0056228
GO:0044033	multi-organism metabolic process	114	0.183399941	0.0403	0.042328707
GO:0046174	polyol catabolic process	9	0.183268983	0.0021	0.002780108
GO:2000209	regulation of anoikis	9	0.183240383	0.004	0.004954389
GO:1904294	positive regulation of ERAD pathway	6	0.183183183	0.0155	0.017160828
GO:0060674	placenta blood vessel development	15	0.182891463	0.0024	0.003116943
GO:0030199	collagen fibril organization	11	0.182566983	< 0.001	< 0.001
GO:0006699	bile acid biosynthetic process	12	0.182561133	0.002	0.002664694
GO:0031122	cytoplasmic microtubule organization	18	0.182282282	0.0007	0.001063182
GO:2001138	regulation of phospholipid transport	6	0.182024882	0.0055	0.006618125
GO:2001140	positive regulation of phospholipid transport	6	0.182024882	0.0055	0.006618125
GO:0060263	regulation of respiratory burst	6	0.181981982	0.0275	0.029503673
GO:0006984	ER-nucleus signaling pathway	16	0.181965894	0.001	0.001450349
GO:0043173	nucleotide salvage	6	0.181810382	0.002	0.002664694
GO:0035902	response to immobilization stress	11	0.181537382	0.0242	0.026144902
GO:0043268	positive regulation of potassium ion transport	13	0.181486981	0.0008	0.001193265

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0003156	regulation of animal organ formation	9	0.181209781	< 0.001	< 0.001
GO:0000303	response to superoxide	6	0.181166881	0.0328	0.034837107
GO:0097709	connective tissue replacement	5	0.181158301	0.0271	0.029103418
GO:0006911	phagocytosis, engulfment	12	0.181145431	0.0239	0.025846628
GO:0032350	regulation of hormone metabolic process	7	0.181136238	0.0067	0.007954042
GO:0030277	maintenance of gastrointestinal epithelium	9	0.181009581	0.0041	0.005057384
GO:0009435	NAD biosynthetic process	14	0.180933995	0.0029	0.003693519
GO:0050830	defense response to Gram-positive bacterium	17	0.180922099	0.0002	0.000356582
GO:0032743	positive regulation of interleukin-2 production	10	0.180540541	0.0103	0.011785137
GO:0045655	regulation of monocyte differentiation	5	0.18043758	0.0154	0.017060599
GO:0045657	positive regulation of monocyte differentiation	5	0.18043758	0.0154	0.017060599
GO:0046931	pore complex assembly	7	0.180069866	0.013	0.014581154
GO:0070129	regulation of mitochondrial translation	14	0.179720537	0.034	0.036054945
GO:1900103	positive regulation of endoplasmic reticulum unfolded protein response	7	0.17966538	0.0139	0.015532589
GO:0038034	signal transduction in absence of ligand	17	0.179453403	0.0019	0.00254969
GO:0097192	extrinsic apoptotic signaling pathway in absence of ligand	17	0.179453403	0.0019	0.00254969
GO:0030512	negative regulation of transforming growth factor beta receptor signaling pathway	28	0.179306858	0.0031	0.003925117
GO:0042572	retinol metabolic process	7	0.179297665	0.0111	0.012593827
GO:0033688	regulation of osteoblast proliferation	6	0.179279279	0.0016	0.002186748
GO:0098927	vesicle-mediated transport between endosomal compartments	25	0.179202059	0.0038	0.004725081
GO:0021983	pituitary gland development	9	0.179064779	0.0268	0.028804137
GO:0032682	negative regulation of chemokine production	7	0.179003493	0.0033	0.004153051
GO:0070192	chromosome organization involved in meiotic cell cycle	16	0.178989704	< 0.001	< 0.001
GO:0046134	pyrimidine nucleoside biosynthetic process	9	0.178978979	0.0204	0.022253048
GO:0032401	establishment of melanosome localization	12	0.178700129	0.0004	0.000648934
GO:0010927	cellular component assembly involved in morphogenesis	24	0.178657229	0.0016	0.002186748
GO:0040015	negative regulation of multicellular organism growth	7	0.178451921	0.0085	0.009867669
GO:0051496	positive regulation of stress fiber assembly	21	0.178219035	0.0009	0.001319479
GO:0019731	antibacterial humoral response	11	0.178191178	0.0027	0.003470695
GO:0032460	negative regulation of protein oligomerization	6	0.177992278	0.0445	0.046469179
GO:2000406	positive regulation of T cell migration	7	0.177606178	0.0434	0.045399458
GO:0042035	regulation of cytokine biosynthetic process	29	0.177464164	0.0019	0.00254969
GO:0042135	neurotransmitter catabolic process	5	0.177451737	0.0028	0.003584743
GO:0046164	alcohol catabolic process	16	0.177059202	0.0006	0.000927725
GO:0006448	regulation of translational elongation	6	0.177005577	0.0234	0.025351564
GO:0048048	embryonic eye morphogenesis	8	0.176930502	0.0021	0.002780108
GO:0030431	sleep	10	0.176499356	< 0.001	< 0.001
GO:0001732	formation of cytoplasmic translation initiation complex	7	0.176355948	0.0239	0.025846628
GO:1901381	positive regulation of potassium ion transmembrane transport	9	0.176233376	0.0167	0.018447833
GO:0090026	positive regulation of monocyte chemotaxis	7	0.176061776	0.0076	0.008916717
GO:0032717	negative regulation of interleukin-8 production	8	0.175675676	0.0069	0.008171729
GO:0055089	fatty acid homeostasis	6	0.175632776	0.0215	0.023377465
GO:1900225	regulation of NLRP3 inflammasome complex assembly	7	0.175583747	0.0172	0.018961404
GO:0098911	regulation of ventricular cardiac muscle cell action potential	6	0.175203775	0.0115	0.013001255
GO:0006760	folic acid-containing compound metabolic process	7	0.17466446	0.0012	0.001702047
GO:0018202	peptidyl-histidine modification	6	0.174603175	0.044	0.045991489
GO:1901201	regulation of extracellular matrix assembly	6	0.174517375	0.0076	0.008916717
GO:1901203	positive regulation of extracellular matrix assembly	6	0.174517375	0.0076	0.008916717
GO:0071168	protein localization to chromatin	11	0.174330174	0.0034	0.004272793
GO:0050764	regulation of phagocytosis	30	0.174294294	0.0011	0.001576346
GO:0033147	negative regulation of intracellular estrogen receptor signaling pathway	6	0.174259974	0.0041	0.005057384
GO:1904292	regulation of ERAD pathway	15	0.173968254	0.0065	0.007730194
GO:0044062	regulation of excretion	7	0.173929031	0.0475	0.049449046
GO:0003044	regulation of systemic arterial blood pressure mediated by a chemical signal	9	0.173888174	0.001	0.001450349
GO:0042228	interleukin-8 biosynthetic process	5	0.173487773	0.0146	0.016261006
GO:0045414	regulation of interleukin-8 biosynthetic process	5	0.173487773	0.0146	0.016261006
GO:1901016	regulation of potassium ion transmembrane transporter activity	23	0.172883442	0.0088	0.010185307
GO:0034138	toll-like receptor 3 signaling pathway	9	0.172858573	0.0327	0.034737724
GO:0034367	macromolecular complex remodeling	7	0.172825887	0.011	0.012498738
GO:0034368	protein-lipid complex remodeling	7	0.172825887	0.011	0.012498738
GO:0034369	plasma lipoprotein particle remodeling	7	0.172825887	0.011	0.012498738
GO:0003180	aortic valve morphogenesis	11	0.172715573	< 0.001	< 0.001
GO:0014819	regulation of skeletal muscle contraction	5	0.172509653	0.0003	0.000505993
GO:0045022	early endosome to late endosome transport	24	0.172415272	0.0106	0.012082345
GO:0045116	protein neddylation	6	0.172372372	0.0475	0.049449046
GO:0050802	circadian sleep/wake cycle, sleep	6	0.172029172	< 0.001	< 0.001
GO:0045647	negative regulation of erythrocyte differentiation	8	0.171428571	0.0009	0.001319479
GO:0030948	negative regulation of vascular endothelial growth factor receptor signaling pathway	6	0.171299871	0.0143	0.015940017
GO:0032928	regulation of superoxide anion generation	8	0.171171171	0.039	0.041027059
GO:0030859	polarized epithelial cell differentiation	10	0.170888031	0.0262	0.028209763
GO:1902235	regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	16	0.170865508	0.0077	0.00902229
GO:0007398	ectoderm development	7	0.170325427	0.0054	0.006510843
GO:0010763	positive regulation of fibroblast migration	6	0.17022737	0.032	0.034034245
GO:0035813	regulation of renal sodium excretion	5	0.17014157	0.0388	0.040832561
GO:0071108	protein K48-linked deubiquitination	21	0.169982227	0.0078	0.009125612
GO:0007588	excretion	20	0.16993565	0.0126	0.014156008
GO:0030513	positive regulation of BMP signaling pathway	8	0.16988417	0.0075	0.008822377
GO:0006206	pyrimidine nucleobase metabolic process	6	0.16979837	0.0366	0.038652804
GO:0061158	3'-UTR-mediated mRNA destabilization	7	0.16962677	< 0.001	< 0.001
GO:0006107	oxaloacetate metabolic process	5	0.16957529	0.0421	0.044090775
GO:0046885	regulation of hormone biosynthetic process	5	0.16952381	0.0035	0.004390436
GO:0071236	cellular response to antibiotic	5	0.169420849	0.0028	0.003584743
GO:0043651	linoleic acid metabolic process	6	0.169412269	0.0218	0.023694127

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1900101	regulation of endoplasmic reticulum unfolded protein response	9	0.169083369	0.0117	0.013205263
GO:0070193	synaptonemal complex organization	6	0.168768769	0.008	0.009347459
GO:1902236	negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	9	0.168625769	0.0211	0.022970266
GO:0003376	sphingosine-1-phosphate signaling pathway	5	0.167876448	0.0097	0.01115531
GO:0090520	sphingolipid mediated signaling pathway	5	0.167876448	0.0097	0.01115531
GO:0008211	glucocorticoid metabolic process	6	0.167782068	0.0168	0.018543137
GO:0042558	pteridine-containing compound metabolic process	12	0.167589018	0.0033	0.004153051
GO:0048261	negative regulation of receptor-mediated endocytosis	10	0.167490347	0.0081	0.00945
GO:0065005	protein-lipid complex assembly	10	0.167052767	0.0014	0.00194839
GO:0009218	pyrimidine ribonucleotide metabolic process	9	0.166394966	0.0108	0.012299937
GO:0035791	platelet-derived growth factor receptor-beta signaling pathway	5	0.166280566	0.0312	0.033235719
GO:0071827	plasma lipoprotein particle organization	14	0.165949623	0.001	0.001450349
GO:0002024	diet induced thermogenesis	6	0.165722866	0.0036	0.004505419
GO:1990845	adaptive thermogenesis	6	0.165722866	0.0036	0.004505419
GO:0097242	beta-amyloid clearance	10	0.165585586	0.0033	0.004153051
GO:0097150	neuronal stem cell population maintenance	7	0.165545137	0.0067	0.007954042
GO:1902074	response to salt	8	0.165411184	0.0456	0.047571892
GO:0034308	primary alcohol metabolic process	17	0.1651904	0.0084	0.009757868
GO:0060049	regulation of protein glycosylation	8	0.16489704	0.0061	0.007291396
GO:0044320	cellular response to leptin stimulus	8	0.164800515	0.0005	0.000791911
GO:0051712	positive regulation of killing of cells of other organism	5	0.164684685	0.0245	0.02644258
GO:0016056	rhodopsin mediated signaling pathway	9	0.164507365	0.003	0.003811001
GO:2000114	regulation of establishment of cell polarity	10	0.164375804	< 0.001	< 0.001
GO:0034123	positive regulation of toll-like receptor signaling pathway	8	0.164285714	0.0054	0.006510843
GO:0022410	circadian sleep/wake cycle process	7	0.163706564	0.0013	0.001826625
GO:0042133	neurotransmitter metabolic process	9	0.163706564	0.0018	0.002428764
GO:0045840	positive regulation of mitotic nuclear division	15	0.163569284	0.005	0.006070546
GO:0034969	histone arginine methylation	5	0.163500644	0.0047	0.005730776
GO:0016338	calcium-independent cell-cell adhesion via plasma membrane cell-adhesion molecules	6	0.163234663	0.0191	0.020936389
GO:0051181	cofactor transport	6	0.163105963	0.0354	0.03746604
GO:0035313	wound healing, spreading of epidermal cells	5	0.163088803	0.0006	0.000927725
GO:0043094	cellular metabolic compound salvage	12	0.162977263	0.0155	0.017160828
GO:0010874	regulation of cholesterol efflux	9	0.162819963	0.0093	0.010727257
GO:0021516	dorsal spinal cord development	6	0.162419562	0.0018	0.002428764
GO:0006801	superoxide metabolic process	17	0.162419562	0.0058	0.006954338
GO:0071447	cellular response to hydroperoxide	6	0.162333762	0.0089	0.010294435
GO:0061311	cell surface receptor signaling pathway involved in heart development	10	0.162239382	0.0172	0.018961404
GO:0032098	regulation of appetite	9	0.162047762	0.0009	0.001319479
GO:0034105	positive regulation of tissue remodeling	9	0.161876162	0.0004	0.000648934
GO:0008655	pyrimidine-containing compound salvage	5	0.161853282	0.0143	0.015940017
GO:0043097	pyrimidine nucleoside salvage	5	0.161853282	0.0143	0.015940017
GO:0002544	chronic inflammatory response	5	0.161801802	0.0156	0.0172574
GO:0046132	pyrimidine ribonucleoside biosynthetic process	7	0.161389961	0.0309	0.032948619
GO:0042745	circadian sleep/wake cycle	8	0.161325611	0.0019	0.00254969
GO:1903651	positive regulation of cytoplasmic transport	9	0.161161161	0.0017	0.00231289
GO:0046653	tetrahydrofolate metabolic process	5	0.161029601	0.012	0.013526909
GO:0048665	neuron fate specification	8	0.160971686	0.0094	0.010831045
GO:0030449	regulation of complement activation	9	0.160503361	0.0034	0.00427293
GO:2000257	regulation of protein activation cascade	9	0.160503361	0.0034	0.00427293
GO:0030947	regulation of vascular endothelial growth factor receptor signaling pathway	8	0.16042471	0.017	0.018752398
GO:0038007	netrin-activated signaling pathway	8	0.159877735	0.002	0.002664694
GO:0016339	calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules	8	0.159813385	0.005	0.006070546
GO:0035247	peptidyl-arginine omega-N-methylation	5	0.15979408	0.0075	0.008822377
GO:0090070	positive regulation of ribosome biogenesis	5	0.15953668	0.0418	0.043793563
GO:2000234	positive regulation of rRNA processing	5	0.15953668	0.0418	0.043793563
GO:0098801	regulation of renal system process	9	0.159445159	0.0004	0.000648934
GO:0032467	positive regulation of cytokinesis	13	0.159429759	0.0007	0.001063182
GO:0040014	regulation of multicellular organism growth	33	0.158714559	0.0007	0.001063182
GO:1903726	negative regulation of phospholipid metabolic process	5	0.158661519	0.0069	0.008171729
GO:0061450	trophoblast cell migration	5	0.158404118	0.0045	0.005509289
GO:1901163	regulation of trophoblast cell migration	5	0.158404118	0.0045	0.005509289
GO:0032095	regulation of response to food	8	0.157657658	0.0016	0.002186748
GO:0055090	acylglycerol homeostasis	8	0.156853282	0.0297	0.031750504
GO:0070328	triglyceride homeostasis	8	0.156853282	0.0297	0.031750504
GO:0000305	response to oxygen radical	7	0.156756757	0.0384	0.040450994
GO:0033145	positive regulation of intracellular steroid hormone receptor signaling pathway	6	0.156713857	0.0437	0.045686748
GO:0032096	negative regulation of response to food	5	0.156653797	0.0013	0.001826625
GO:0032099	negative regulation of appetite	5	0.156653797	0.0013	0.001826625
GO:0032105	negative regulation of response to extracellular stimulus	5	0.156653797	0.0013	0.001826625
GO:0032108	negative regulation of response to nutrient levels	5	0.156653797	0.0013	0.001826625
GO:0032465	regulation of cytokinesis	36	0.156249106	0.0023	0.003013139
GO:2000737	negative regulation of stem cell differentiation	8	0.156241956	0.0049	0.005958506
GO:0010288	response to lead ion	10	0.155984556	0.0226	0.024538959
GO:1905564	positive regulation of vascular endothelial cell proliferation	8	0.15472973	0.0366	0.038652804
GO:2000060	positive regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process	6	0.154440154	0.0177	0.019488753
GO:0060192	negative regulation of lipase activity	5	0.154285714	0.0217	0.023590183
GO:0035627	ceramide transport	6	0.153925354	0.0271	0.029103418
GO:0070861	regulation of protein exit from endoplasmic reticulum	12	0.153839554	0.0269	0.028900119
GO:0001990	regulation of systemic arterial blood pressure by hormone	6	0.152595453	0.0236	0.025557996
GO:0035641	locomotory exploration behavior	7	0.152380952	0.029	0.031051318
GO:0001661	conditioned taste aversion	5	0.152226512	0.0037	0.004617737
GO:0070828	heterochromatin organization	6	0.151737452	0.0398	0.041827927
GO:0002021	response to dietary excess	11	0.151655552	0.0021	0.002780108

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0007608	sensory perception of smell	24	0.151555127	0.0152	0.016877091
GO:0006067	ethanol metabolic process	7	0.151498437	0.0257	0.02768244
GO:1903573	negative regulation of response to endoplasmic reticulum stress	19	0.15125652	0.012	0.013526909
GO:0021527	spinal cord association neuron differentiation	5	0.150733591	0.0465	0.048454686
GO:0042181	ketone biosynthetic process	10	0.14993565	0.036	0.038048895
GO:0009067	aspartate family amino acid biosynthetic process	6	0.14976405	0.0456	0.047571892
GO:0030866	cortical actin cytoskeleton organization	13	0.149391149	0.001	0.001450349
GO:0046460	neutral lipid biosynthetic process	11	0.149268749	0.0071	0.008390203
GO:0046463	acylglycerol biosynthetic process	11	0.149268749	0.0071	0.008390203
GO:0032402	melanosome transport	11	0.149151749	0.0053	0.006400268
GO:0060039	pericardium development	9	0.149006149	0.0041	0.005057384
GO:0071545	inositol phosphate catabolic process	7	0.148850892	0.0198	0.021642233
GO:0019471	4-hydroxyproline metabolic process	5	0.148622909	0.0441	0.046087101
GO:0042554	superoxide anion generation	10	0.148314028	0.0435	0.045495258
GO:0006730	one-carbon metabolic process	7	0.147527119	0.0139	0.015532589
GO:0034498	early endosome to Golgi transport	5	0.147284427	0.046	0.04795216
GO:0007135	meiosis II	5	0.146924067	0.0383	0.040353519
GO:0007635	chemosensory behavior	5	0.146718147	0.0414	0.043408149
GO:0009620	response to fungus	9	0.146575147	0.0106	0.012082345
GO:0010866	regulation of triglyceride biosynthetic process	7	0.146497518	0.0015	0.002069969
GO:0003159	morphogenesis of an endothelium	6	0.145602746	0.0187	0.020510412
GO:0003352	regulation of cilium movement	5	0.145585586	0.009	0.010394529
GO:0019432	triglyceride biosynthetic process	10	0.143552124	0.0043	0.005276385
GO:0044321	response to leptin	10	0.142265122	0.0002	0.000356582
GO:0032094	response to food	11	0.141944542	0.0008	0.001193265
GO:0043555	regulation of translation in response to stress	10	0.141879022	0.0339	0.035955957
GO:0022400	regulation of rhodopsin mediated signaling pathway	7	0.14127597	0.0233	0.025253349
GO:0035336	long-chain fatty-acyl-CoA metabolic process	5	0.140797941	0.0077	0.00902229
GO:0010875	positive regulation of cholesterol efflux	7	0.140209597	0.0355	0.037549814
GO:0032373	positive regulation of sterol transport	7	0.140209597	0.0355	0.037549814
GO:0032376	positive regulation of cholesterol transport	7	0.140209597	0.0355	0.037549814
GO:0036342	post-anal tail morphogenesis	7	0.139841883	0.0051	0.006185009
GO:0051964	negative regulation of synapse assembly	6	0.138567139	0.002	0.002664694
GO:0043496	regulation of protein homodimerization activity	7	0.137672366	0.0118	0.013309789
GO:2000811	negative regulation of anoikis	7	0.134840963	0.0084	0.009757868
GO:0009312	oligosaccharide biosynthetic process	5	0.133899614	0.0383	0.040353519
GO:0035385	Roundabout signaling pathway	5	0.132509653	0.028	0.03002818
GO:1903010	regulation of bone development	8	0.132496782	0.0197	0.021541643
GO:1901522	positive regulation of transcription from RNA polymerase II promoter involved in cellular response to chemical stimulus	8	0.132432432	0.0158	0.017471496
GO:0034377	plasma lipoprotein particle assembly	9	0.131674532	0.012	0.013526909
GO:0061085	regulation of histone H3-K27 methylation	5	0.130965251	0.0359	0.037950626
GO:0007271	synaptic transmission, cholinergic	9	0.12987273	0.0016	0.002186748
GO:0048147	negative regulation of fibroblast proliferation	15	0.128236808	0.005	0.006070546
GO:2000810	regulation of bicellular tight junction assembly	7	0.127964699	0.0067	0.007954042
GO:0042219	cellular modified amino acid catabolic process	6	0.125697126	0.0102	0.011688041
GO:0032725	positive regulation of granulocyte macrophage colony-stimulating factor production	5	0.125508366	0.0284	0.030439032
GO:0035337	fatty-acyl-CoA metabolic process	11	0.125330525	0.0267	0.028702367
GO:0046949	fatty-acyl-CoA biosynthetic process	10	0.122522523	0.0402	0.042231882
GO:0030953	astral microtubule organization	5	0.12020592	0.0226	0.024538959
GO:0055078	sodium ion homeostasis	11	0.11997192	0.0006	0.000927725
GO:0010867	positive regulation of triglyceride biosynthetic process	5	0.11984556	0.023	0.024938202
GO:0090208	positive regulation of triglyceride metabolic process	5	0.11984556	0.023	0.024938202
GO:0006691	leukotriene metabolic process	10	0.116628057	0.0302	0.032240379
GO:1904396	regulation of neuromuscular junction development	5	0.116550837	0.0248	0.026750339
GO:0019081	viral translation	6	0.115658516	0.0156	0.0172574
GO:0014067	negative regulation of phosphatidylinositol 3-kinase signaling	6	0.107164307	0.0391	0.041116248
GO:0071340	skeletal muscle acetylcholine-gated channel clustering	6	0.105448305	0.0016	0.002186748
GO:1903265	positive regulation of tumor necrosis factor-mediated signaling pathway	5	0.102393822	0.0445	0.046469179

Reward COR positive

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0019673	GDP-mannose metabolic process	5	0.427965778	0.0046	0.014132412
GO:0036295	cellular response to increased oxygen levels	7	0.401269407	0.001	0.010787313
GO:1902047	polyamine transmembrane transport	6	0.393502498	0.0021	0.012314604
GO:0045161	neuronal ion channel clustering	5	0.385680142	0.0003	0.007956881
GO:1902267	regulation of polyamine transmembrane transport	5	0.385507543	0.0031	0.013277185
GO:1902414	protein localization to cell junction	5	0.380598847	0.0002	0.006319126
GO:0033182	regulation of histone ubiquitination	5	0.379305912	0.0092	0.017033109
GO:1903365	regulation of fear response	5	0.377964515	0.0028	0.012972436
GO:2000822	regulation of behavioral fear response	5	0.377964515	0.0028	0.012972436
GO:0070669	response to interleukin-2	6	0.376501573	< 0.001	< 0.001
GO:0035815	positive regulation of renal sodium excretion	5	0.37134279	0.0054	0.014720792
GO:0015893	drug transport	8	0.368887536	0.0007	0.010220707
GO:1901725	regulation of histone deacetylase activity	5	0.365805639	0.0007	0.010220707
GO:0002692	negative regulation of cellular extravasation	5	0.364732728	0.0027	0.012827773
GO:0098914	membrane repolarization during atrial cardiac muscle cell action potential	5	0.364561425	0.0046	0.014132412
GO:0097237	cellular response to toxic substance	5	0.361999138	0.0027	0.012827773
GO:2000765	regulation of cytoplasmic translation	6	0.35945983	0.004	0.013824268
GO:0060712	spongiotrophoblast layer development	5	0.359129232	0.0001	0.004220438
GO:1905383	protein localization to presynapse	5	0.356184948	0.0053	0.014634479
GO:0051004	regulation of lipoprotein lipase activity	8	0.354073465	0.0001	0.004220438
GO:0038110	interleukin-2-mediated signaling pathway	5	0.352811758	0.0001	0.004220438
GO:0071352	cellular response to interleukin-2	5	0.352811758	0.0001	0.004220438
GO:0018410	C-terminal protein amino acid modification	6	0.352285712	0.0004	0.008964341
GO:0000097	sulfur amino acid biosynthetic process	6	0.350812188	0.0158	0.021871104
GO:2000848	positive regulation of corticosteroid hormone secretion	5	0.349922933	0.0015	0.011704453
GO:2000108	positive regulation of leukocyte apoptotic process	5	0.345713443	0.0001	0.004220438
GO:0098792	xenophagy	6	0.344722642	0.0039	0.013791927
GO:0001780	neutrophil homeostasis	6	0.344703422	0.0023	0.012498684
GO:0006558	L-phenylalanine metabolic process	5	0.344246355	0.0035	0.01351837
GO:0006559	L-phenylalanine catabolic process	5	0.344246355	0.0035	0.01351837
GO:1902221	erythrose 4-phosphate/phosphoenolpyruvate family amino acid metabolic process	5	0.344246355	0.0035	0.01351837
GO:1902222	erythrose 4-phosphate/phosphoenolpyruvate family amino acid catabolic process	5	0.344246355	0.0035	0.01351837
GO:0042780	tRNA 3'-end processing	5	0.343693832	0.0108	0.018152791
GO:0043628	ncRNA 3'-end processing	5	0.343693832	0.0108	0.018152791
GO:0015846	polyamine transport	7	0.342630473	0.0036	0.01353394
GO:0015695	organic cation transport	6	0.340051767	0.0001	0.004220438
GO:0033523	histone H2B ubiquitination	6	0.339067833	0.0027	0.012827773
GO:0048268	clathrin coat assembly	7	0.338209992	0.0054	0.014720792
GO:0061051	positive regulation of cell growth involved in cardiac muscle cell development	5	0.337659876	0.0005	0.009604651
GO:2001044	regulation of integrin-mediated signaling pathway	8	0.337377913	0.0056	0.014771533
GO:0090050	positive regulation of cell migration involved in sprouting angiogenesis	8	0.337113896	0.0002	0.006319126
GO:0021542	dentate gyrus development	9	0.336348339	0.0065	0.015491756
GO:0007494	midgut development	5	0.335971467	0.0088	0.016916437
GO:0032594	protein transport within lipid bilayer	5	0.335133871	0.0057	0.01480566
GO:0036123	histone H3-K9 dimethylation	5	0.334400456	0.0043	0.014102439
GO:0043252	sodium-independent organic anion transport	5	0.33340607	0.0017	0.012001709
GO:0006489	dolichyl diphosphate biosynthetic process	6	0.333331174	0.0126	0.019370699
GO:0046465	dolichyl diphosphate metabolic process	6	0.333331174	0.0126	0.019370699
GO:0015671	oxygen transport	7	0.333090158	0.0051	0.014547706
GO:0070672	response to interleukin-15	6	0.333065538	0.0003	0.007956881
GO:0099624	atrial cardiac muscle cell membrane repolarization	6	0.332305559	0.0079	0.01629604
GO:0048875	chemical homeostasis within a tissue	6	0.332008392	0.0002	0.006319126
GO:0015721	bile acid and bile salt transport	8	0.331787731	0.0045	0.014132412
GO:0035723	interleukin-15-mediated signaling pathway	5	0.331675159	0.0001	0.004220438
GO:0071350	cellular response to interleukin-15	5	0.331675159	0.0001	0.004220438
GO:0099072	regulation of postsynaptic specialization membrane neurotransmitter receptor levels	11	0.331401395	0.0038	0.01366393
GO:2000251	positive regulation of actin cytoskeleton reorganization	9	0.330098332	0.0077	0.016177834
GO:0043117	positive regulation of vascular permeability	5	0.329010765	0.0132	0.019860109
GO:0001502	cartilage condensation	6	0.328712993	0.0083	0.016559903
GO:0098743	cell aggregation	6	0.328712993	0.0083	0.016559903
GO:0005513	detection of calcium ion	6	0.328692693	0.0125	0.019314538
GO:0018065	protein-cofactor linkage	5	0.328245733	0.0178	0.023348367
GO:0006527	arginine catabolic process	5	0.328207637	0.0049	0.014447629
GO:0006677	glycosylceramide metabolic process	8	0.327160804	0.0038	0.01366393
GO:0090178	regulation of establishment of planar polarity involved in neural tube closure	6	0.32693172	0.0164	0.022306469
GO:0090179	planar cell polarity pathway involved in neural tube closure	6	0.32693172	0.0164	0.022306469
GO:1900087	positive regulation of G1/S transition of mitotic cell cycle	14	0.326385947	0.0008	0.010465158
GO:0070213	protein auto-ADP-ribosylation	5	0.326212386	0.004	0.013824268
GO:0048243	norepinephrine secretion	8	0.326176654	0.0084	0.016633151
GO:0015874	norepinephrine transport	9	0.325787973	0.0114	0.018551872
GO:0033604	negative regulation of catecholamine secretion	6	0.325259076	0.0113	0.018488002
GO:2000727	positive regulation of cardiac muscle cell differentiation	9	0.325036129	0.001	0.010787313
GO:2000311	regulation of alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate selective glutamate receptor activity	10	0.324753072	0.0132	0.019860109
GO:0032042	mitochondrial DNA metabolic process	6	0.324745729	0.0019	0.012288367
GO:0032228	regulation of synaptic transmission, GABAergic	14	0.324092314	0.0001	0.004220438
GO:0031649	heat generation	7	0.323408602	0.0293	0.033401538
GO:0051932	synaptic transmission, GABAergic	16	0.323292721	0.0001	0.004220438
GO:0035307	positive regulation of protein dephosphorylation	25	0.323171021	0.0036	0.01353394
GO:0043476	pigment accumulation	8	0.322682892	< 0.001	< 0.001
GO:0043482	cellular pigment accumulation	8	0.322682892	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0014829	vascular smooth muscle contraction	10	0.322662969	0.0011	0.010890753
GO:0015988	energy coupled proton transmembrane transport, against electrochemical gradient	12	0.322266351	0.0057	0.01480566
GO:0015991	ATP hydrolysis coupled proton transport	12	0.322266351	0.0057	0.01480566
GO:0090662	ATP hydrolysis coupled transmembrane transport	12	0.322266351	0.0057	0.01480566
GO:0035646	endosome to melanosome transport	7	0.322067093	< 0.001	< 0.001
GO:0043485	endosome to pigment granule transport	7	0.322067093	< 0.001	< 0.001
GO:0048757	pigment granule maturation	7	0.322067093	< 0.001	< 0.001
GO:0010447	response to acidic pH	7	0.321878464	0.004	0.013824268
GO:0071447	cellular response to hydroperoxide	7	0.321753143	0.0004	0.008964341
GO:0016556	mRNA modification	5	0.321718082	0.0016	0.011845327
GO:0001696	gastric acid secretion	6	0.321589411	0.0011	0.010890753
GO:0031650	regulation of heat generation	6	0.32132723	0.0283	0.032434212
GO:1903613	regulation of protein tyrosine phosphatase activity	5	0.321124094	0.0239	0.028592965
GO:0045713	low-density lipoprotein particle receptor biosynthetic process	5	0.320622366	0.0004	0.008964341
GO:0071340	skeletal muscle acetylcholine-gated channel clustering	7	0.318416864	0.008	0.016379603
GO:0036296	response to increased oxygen levels	13	0.318300457	0.0027	0.012827773
GO:0021819	layer formation in cerebral cortex	9	0.318084526	0.0031	0.013277185
GO:0044062	regulation of excretion	11	0.317914739	0.0024	0.012603815
GO:0060027	convergent extension involved in gastrulation	5	0.31722663	0.0083	0.016559903
GO:1905146	lysosomal protein catabolic process	6	0.317186763	0.0051	0.014547706
GO:0014049	positive regulation of glutamate secretion	5	0.316917455	0.0022	0.012422266
GO:0032802	low-density lipoprotein particle receptor catabolic process	13	0.316789372	0.0026	0.012805111
GO:0014048	regulation of glutamate secretion	8	0.316504585	0.0013	0.011218806
GO:0038084	vascular endothelial growth factor signaling pathway	14	0.316448103	0.0047	0.014168613
GO:0060368	regulation of Fc receptor mediated stimulatory signaling pathway	5	0.316324244	0.0136	0.020157703
GO:0060369	positive regulation of Fc receptor mediated stimulatory signaling pathway	5	0.316324244	0.0136	0.020157703
GO:0002674	negative regulation of acute inflammatory response	5	0.316200627	0.0019	0.012288367
GO:1905165	regulation of lysosomal protein catabolic process	5	0.315412011	0.0085	0.016693954
GO:0034505	tooth mineralization	6	0.314974208	0.0033	0.013333753
GO:0035970	peptidyl-threonine dephosphorylation	7	0.314837164	0.0073	0.015844069
GO:0035458	cellular response to interferon-beta	8	0.314536935	0.0058	0.014878261
GO:0014061	regulation of norepinephrine secretion	7	0.314508034	0.0091	0.016994897
GO:0000338	protein deneddylation	7	0.31448397	0.0083	0.016559903
GO:0060600	dichotomous subdivision of an epithelial terminal unit	6	0.314009496	0.0028	0.012972436
GO:0007205	protein kinase C-activating G-protein coupled receptor signaling pathway	12	0.313897195	< 0.001	< 0.001
GO:0050432	catecholamine secretion	22	0.313810102	0.0012	0.010961137
GO:0070307	lens fiber cell development	6	0.313805626	0.0051	0.014547706
GO:0021801	cerebral cortex radial glia guided migration	12	0.313727015	0.0087	0.016840777
GO:0022030	telencephalon glial cell migration	12	0.313727015	0.0087	0.016840777
GO:0032799	low-density lipoprotein receptor particle metabolic process	17	0.313631419	0.0021	0.012314604
GO:0031652	positive regulation of heat generation	5	0.313412096	0.0325	0.036312077
GO:0035493	SNARE complex assembly	5	0.313361042	0.0037	0.013609033
GO:0006525	arginine metabolic process	8	0.313024429	0.0003	0.007956881
GO:0002691	regulation of cellular extravasation	10	0.312750467	0.008	0.016379603
GO:0034695	response to prostaglandin E	12	0.311802341	< 0.001	< 0.001
GO:0071380	cellular response to prostaglandin E stimulus	12	0.311802341	< 0.001	< 0.001
GO:0042026	protein refolding	6	0.311221613	0.0125	0.019314538
GO:1904396	regulation of neuromuscular junction development	6	0.311122053	0.0078	0.01620539
GO:0007214	gamma-aminobutyric acid signaling pathway	7	0.311048841	0.0012	0.010961137
GO:0051386	regulation of neurotrophin TRK receptor signaling pathway	9	0.310721727	0.0001	0.004220438
GO:1900746	regulation of vascular endothelial growth factor signaling pathway	7	0.310718601	0.0048	0.014269203
GO:1902547	regulation of cellular response to vascular endothelial growth factor stimulus	7	0.310718601	0.0048	0.014269203
GO:0010888	negative regulation of lipid storage	5	0.310626156	0.0092	0.017033109
GO:0051410	detoxification of nitrogen compound	5	0.310610607	0.0231	0.027930615
GO:0034755	iron ion transmembrane transport	6	0.310584518	0.0035	0.01351837
GO:0030638	polyketide metabolic process	6	0.310220834	0.023	0.027838811
GO:0030647	aminoglycoside antibiotic metabolic process	6	0.310220834	0.023	0.027838811
GO:0044597	daunorubicin metabolic process	6	0.310220834	0.023	0.027838811
GO:0044598	doxorubicin metabolic process	6	0.310220834	0.023	0.027838811
GO:1904886	beta-catenin destruction complex disassembly	8	0.309911303	0.0013	0.011218806
GO:0010043	response to zinc ion	23	0.309827479	0.0076	0.016084627
GO:0086014	atrial cardiac muscle cell action potential	9	0.309793081	0.0022	0.012422266
GO:0086026	atrial cardiac muscle cell to AV node cell signaling	9	0.309793081	0.0022	0.012422266
GO:0086066	atrial cardiac muscle cell to AV node cell communication	9	0.309793081	0.0022	0.012422266
GO:2000402	negative regulation of lymphocyte migration	6	0.309477269	< 0.001	< 0.001
GO:0050433	regulation of catecholamine secretion	21	0.309331678	0.001	0.010787313
GO:0050860	negative regulation of T cell receptor signaling pathway	10	0.309042317	0.0023	0.012498684
GO:0030949	positive regulation of vascular endothelial growth factor receptor signaling pathway	5	0.308942671	< 0.001	< 0.001
GO:0048147	negative regulation of fibroblast proliferation	11	0.308865796	0.0011	0.010890753
GO:1902808	positive regulation of cell cycle G1/S phase transition	19	0.308721747	0.0015	0.011704453
GO:0007213	G-protein coupled acetylcholine receptor signaling pathway	12	0.308465045	< 0.001	< 0.001
GO:0007039	protein catabolic process in the vacuole	8	0.30842277	0.0063	0.015311728
GO:0034694	response to prostaglandin	15	0.308385829	< 0.001	< 0.001
GO:0009268	response to pH	14	0.308310383	0.002	0.012314604
GO:0007191	adenylate cyclase-activating dopamine receptor signaling pathway	6	0.308229643	0.0015	0.011704453
GO:0033227	dsRNA transport	5	0.308156129	0.0007	0.010220707
GO:0034392	negative regulation of smooth muscle cell apoptotic process	5	0.308093932	0.0043	0.014102439
GO:0042249	establishment of planar polarity of embryonic epithelium	9	0.308093874	0.0056	0.014771533
GO:2000833	positive regulation of steroid hormone secretion	6	0.308048018	0.0009	0.010729485
GO:0046951	ketone body biosynthetic process	5	0.307627449	0.0204	0.025564109
GO:0071435	potassium ion export	6	0.307621488	0.0095	0.01725157
GO:0097623	potassium ion export across plasma membrane	6	0.307621488	0.0095	0.01725157
GO:0070106	interleukin-27-mediated signaling pathway	5	0.307022058	0.0001	0.004220438

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:2001032	regulation of double-strand break repair via nonhomologous end joining	9	0.30693141	0.0008	0.010465158
GO:0016578	histone deubiquitination	11	0.306588747	< 0.001	< 0.001
GO:0022417	protein maturation by protein folding	5	0.306345139	0.0116	0.018682786
GO:0021978	telencephalon regionalization	5	0.306342288	0.0108	0.018152791
GO:0046950	cellular ketone body metabolic process	6	0.306217072	0.0188	0.02420971
GO:0009226	nucleotide-sugar biosynthetic process	10	0.306176557	0.0229	0.027770092
GO:0000002	mitochondrial genome maintenance	9	0.305955827	0.0037	0.013609033
GO:1904350	regulation of protein catabolic process in the vacuole	7	0.305903091	0.007	0.015816335
GO:0051957	positive regulation of amino acid transport	6	0.305694655	0.0012	0.010961137
GO:2000052	positive regulation of non-canonical Wnt signaling pathway	5	0.305609651	0.0178	0.023348367
GO:0051443	positive regulation of ubiquitin-protein transferase activity	12	0.305553198	0.0018	0.01210186
GO:0014047	glutamate secretion	24	0.305512165	< 0.001	< 0.001
GO:2001046	positive regulation of integrin-mediated signaling pathway	5	0.305475408	0.013	0.019676963
GO:0006555	methionine metabolic process	6	0.305312614	0.0094	0.017156187
GO:0060192	negative regulation of lipase activity	6	0.305154528	0.0057	0.01480566
GO:0035360	positive regulation of peroxisome proliferator activated receptor signaling pathway	5	0.30502577	0.0189	0.024289798
GO:0071294	cellular response to zinc ion	16	0.30469779	0.0177	0.02329117
GO:0060602	branch elongation of an epithelium	7	0.304449219	0.0219	0.026855949
GO:0042415	norepinephrine metabolic process	5	0.304220828	0.0006	0.009940401
GO:0045117	azole transport	8	0.303801997	0.0053	0.014634479
GO:0060439	trachea morphogenesis	5	0.30350063	0.0244	0.029011063
GO:0051937	catecholamine transport	25	0.303351356	0.0018	0.01210186
GO:0033194	response to hydroperoxide	12	0.303307601	0.0011	0.010890753
GO:0046184	aldehyde biosynthetic process	7	0.302847813	0.0051	0.014547706
GO:1901890	positive regulation of cell junction assembly	16	0.302735971	0.0046	0.014132412
GO:0010225	response to UV-C	6	0.302423227	0.0072	0.015844069
GO:0051901	positive regulation of mitochondrial depolarization	6	0.302241385	0.0141	0.020504577
GO:0045880	positive regulation of smoothened signaling pathway	6	0.302207263	0.0229	0.027770092
GO:1900221	regulation of beta-amyloid clearance	6	0.30204313	0.022	0.026944291
GO:1903727	positive regulation of phospholipid metabolic process	24	0.301087596	0.0041	0.013887639
GO:0035306	positive regulation of dephosphorylation	31	0.300924198	0.0057	0.01480566
GO:0051894	positive regulation of focal adhesion assembly	14	0.300731147	0.0075	0.015990044
GO:0060081	membrane hyperpolarization	7	0.300651827	0.0013	0.011218806
GO:0032509	endosome transport via multivesicular body sorting pathway	6	0.300604808	0.0157	0.021779607
GO:0016188	synaptic vesicle maturation	5	0.300304445	0.0004	0.008964341
GO:0060044	negative regulation of cardiac muscle cell proliferation	6	0.300166616	0.0133	0.019917275
GO:0099560	synaptic membrane adhesion	11	0.29993312	0.009	0.016956012
GO:0010954	positive regulation of protein processing	11	0.299891183	0.0162	0.022196303
GO:1903319	positive regulation of protein maturation	11	0.299891183	0.0162	0.022196303
GO:0022038	corpus callosum development	9	0.299841302	0.0034	0.01347416
GO:0001821	histamine secretion	6	0.299703157	0.0065	0.015491756
GO:0018216	peptidyl-arginine methylation	6	0.299479202	0.0015	0.011704453
GO:0046710	GDP metabolic process	5	0.299210024	0.0273	0.031601321
GO:0031665	negative regulation of lipopolysaccharide-mediated signaling pathway	5	0.299162339	0.003	0.013210967
GO:0071379	cellular response to prostaglandin stimulus	14	0.299040702	< 0.001	< 0.001
GO:0015682	ferric iron transport	18	0.298880189	0.0016	0.011845327
GO:0033572	transferrin transport	18	0.298880189	0.0016	0.011845327
GO:0072512	trivalent inorganic cation transport	18	0.298880189	0.0016	0.011845327
GO:0006703	estrogen biosynthetic process	5	0.298868714	0.0005	0.009604651
GO:0032211	negative regulation of telomere maintenance via telomerase	8	0.2987277	0.0002	0.006319126
GO:0060441	epithelial tube branching involved in lung morphogenesis	11	0.298533436	0.0112	0.018392048
GO:2000345	regulation of hepatocyte proliferation	7	0.298410487	0.0124	0.019242297
GO:0090177	establishment of planar polarity involved in neural tube closure	7	0.29825018	0.0073	0.015844069
GO:0030850	prostate gland development	18	0.298209836	0.0052	0.014616626
GO:0051608	histamine transport	7	0.298196127	0.0085	0.016693954
GO:0043031	negative regulation of macrophage activation	8	0.298036885	0.0086	0.016782045
GO:0008299	isoprenoid biosynthetic process	12	0.297813361	0.0141	0.020504577
GO:1904923	regulation of mitophagy in response to mitochondrial depolarization	5	0.297791139	0.0148	0.020979063
GO:1903012	positive regulation of bone development	5	0.297679183	0.0007	0.010220707
GO:0042574	retinal metabolic process	6	0.297540059	0.0006	0.009940401
GO:0080111	DNA demethylation	5	0.297450865	0.0056	0.014771533
GO:1902224	ketone body metabolic process	7	0.296961799	0.0191	0.02440579
GO:0009309	amine biosynthetic process	11	0.296935614	0.0094	0.017156187
GO:0042401	cellular biogenic amine biosynthetic process	11	0.296935614	0.0094	0.017156187
GO:0009437	carnitine metabolic process	8	0.296816254	0.0167	0.02255007
GO:0072337	modified amino acid transport	11	0.296788601	0.0207	0.025805821
GO:0061469	regulation of type B pancreatic cell proliferation	6	0.296780728	0.0085	0.016693954
GO:0070886	positive regulation of calcineurin-NFAT signaling cascade	6	0.29675978	0.0038	0.01366393
GO:0090218	positive regulation of lipid kinase activity	18	0.296712412	0.0053	0.014634479
GO:0030206	chondroitin sulfate biosynthetic process	17	0.296608071	0.0071	0.01583804
GO:0035864	response to potassium ion	6	0.296568003	0.012	0.018931514
GO:0035865	cellular response to potassium ion	6	0.296568003	0.012	0.018931514
GO:0071549	cellular response to dexamethasone stimulus	8	0.296514822	0.0054	0.014720792
GO:0001835	blastocyst hatching	13	0.296467962	0.012	0.018931514
GO:0035188	hatching	13	0.296467962	0.012	0.018931514
GO:0071684	organism emergence from protective structure	13	0.296467962	0.012	0.018931514
GO:0071548	response to dexamethasone	12	0.296456026	0.0118	0.018836996
GO:2000849	regulation of glucocorticoid secretion	5	0.296430045	0.0002	0.006319126
GO:0009756	carbohydrate mediated signaling	5	0.296331566	0.0056	0.014771533
GO:2000773	negative regulation of cellular senescence	5	0.296329233	< 0.001	< 0.001
GO:1902570	protein localization to nucleolus	5	0.296224793	0.0031	0.013277185
GO:0006826	iron ion transport	30	0.296206522	0.0025	0.012769435
GO:1902473	regulation of protein localization to synapse	6	0.29618769	0.0022	0.012422266

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1902474	positive regulation of protein localization to synapse	6	0.29618769	0.0022	0.012422266
GO:0043555	regulation of translation in response to stress	7	0.296143232	0.0067	0.015576759
GO:0035812	renal sodium excretion	9	0.295734525	0.0037	0.013609033
GO:0035813	regulation of renal sodium excretion	9	0.295734525	0.0037	0.013609033
GO:0007194	negative regulation of adenylate cyclase activity	8	0.295634498	0.0059	0.014942532
GO:0030815	negative regulation of cAMP metabolic process	8	0.295634498	0.0059	0.014942532
GO:0030818	negative regulation of cAMP biosynthetic process	8	0.295634498	0.0059	0.014942532
GO:0009950	dorsal/ventral axis specification	7	0.295587896	0.0023	0.012498684
GO:0043558	regulation of translational initiation in response to stress	6	0.29545298	0.0049	0.014447629
GO:0055093	response to hyperoxia	9	0.295374297	0.0021	0.012314604
GO:0033173	calcineurin-NFAT signaling cascade	19	0.295307431	0.0001	0.004220438
GO:0097720	calcineurin-mediated signaling	19	0.295307431	0.0001	0.004220438
GO:0051450	myoblast proliferation	6	0.295290359	0.0027	0.012827773
GO:0016048	detection of temperature stimulus	8	0.295219198	0.0013	0.011218806
GO:0035510	DNA dealkylation	8	0.295067915	0.0105	0.017924712
GO:0006577	amino-acid betaine metabolic process	11	0.295061436	0.0195	0.02481272
GO:0097242	beta-amyloid clearance	10	0.294807074	0.0179	0.02344231
GO:0030809	negative regulation of nucleotide biosynthetic process	11	0.29467918	0.0107	0.018084595
GO:1900372	negative regulation of purine nucleotide biosynthetic process	11	0.29467918	0.0107	0.018084595
GO:0051561	positive regulation of mitochondrial calcium ion concentration	7	0.294632902	0.0013	0.011218806
GO:0042255	ribosome assembly	11	0.294607676	0.0072	0.015844069
GO:1900451	positive regulation of glutamate receptor signaling pathway	9	0.294592362	0.011	0.018323826
GO:0061045	negative regulation of wound healing	29	0.294543435	0.0138	0.020339434
GO:0021799	cerebral cortex radially oriented cell migration	17	0.294436715	0.0037	0.013609033
GO:0019226	transmission of nerve impulse	21	0.294416937	0.0003	0.007956881
GO:0043586	tongue development	7	0.294183264	0.0002	0.006319126
GO:0055069	zinc ion homeostasis	8	0.293851173	0.003	0.013210967
GO:0048741	skeletal muscle fiber development	12	0.293733472	0.0042	0.013948535
GO:0071467	cellular response to pH	7	0.2937066	< 0.001	< 0.001
GO:0071242	cellular response to ammonium ion	35	0.293403867	0.0016	0.011845327
GO:0048172	regulation of short-term neuronal synaptic plasticity	11	0.293282794	0.0006	0.009940401
GO:0070572	positive regulation of neuron projection regeneration	6	0.2931305	0.0133	0.019917275
GO:0060343	trabecula formation	14	0.292887478	0.0071	0.01583804
GO:0016137	glycoside metabolic process	11	0.292828915	0.0161	0.02211694
GO:1901992	positive regulation of mitotic cell cycle phase transition	29	0.292766466	0.0006	0.009940401
GO:0010869	regulation of receptor biosynthetic process	10	0.292704532	< 0.001	< 0.001
GO:0009642	response to light intensity	6	0.292623631	0.0055	0.01475
GO:0035933	glucocorticoid secretion	6	0.292459931	0.0007	0.010220707
GO:0051969	regulation of transmission of nerve impulse	7	0.292316592	0.0027	0.012827773
GO:0032354	response to follicle-stimulating hormone	5	0.292218223	0.0163	0.022248961
GO:0071372	cellular response to follicle-stimulating hormone stimulus	5	0.292218223	0.0163	0.022248961
GO:1904398	positive regulation of neuromuscular junction development	5	0.292009083	0.0078	0.01620539
GO:0031630	regulation of synaptic vesicle fusion to presynaptic membrane	5	0.291917083	0.0074	0.015911789
GO:0043552	positive regulation of phosphatidylinositol 3-kinase activity	16	0.291898261	0.006	0.015037711
GO:0071371	cellular response to gonadotropin stimulus	6	0.291547697	0.0105	0.017924712
GO:0051481	negative regulation of cytosolic calcium ion concentration	5	0.291534826	0.0071	0.01583804
GO:2000647	negative regulation of stem cell proliferation	5	0.291402397	0.0296	0.033690394
GO:0009071	serine family amino acid catabolic process	5	0.291392808	0.0062	0.015209334
GO:0006188	IMP biosynthetic process	5	0.291307027	0.019	0.024347961
GO:0046040	IMP metabolic process	5	0.291307027	0.019	0.024347961
GO:0032516	positive regulation of phosphoprotein phosphatase activity	12	0.291257333	0.0061	0.015143924
GO:0045780	positive regulation of bone resorption	5	0.291182631	0.0114	0.018551872
GO:0046852	positive regulation of bone remodeling	5	0.291182631	0.0114	0.018551872
GO:0071071	regulation of phospholipid biosynthetic process	6	0.290871729	0.0099	0.017505138
GO:2000846	regulation of corticosteroid hormone secretion	7	0.290857352	0.0001	0.004220438
GO:0032536	regulation of cell projection size	6	0.290819898	0.0024	0.012603815
GO:0060180	female mating behavior	5	0.290779642	0.014	0.020462083
GO:0043046	DNA methylation involved in gamete generation	6	0.290767418	0.0163	0.022248961
GO:0060433	bronchus development	6	0.290597454	0.0067	0.015576759
GO:0006953	acute-phase response	13	0.290406476	0.006	0.015037711
GO:0039694	viral RNA genome replication	9	0.290312094	0.0022	0.012422266
GO:0039703	RNA replication	9	0.290312094	0.0022	0.012422266
GO:0051953	negative regulation of amine transport	12	0.290241977	0.0026	0.012805111
GO:0023019	signal transduction involved in regulation of gene expression	9	0.290134859	0.0175	0.023154462
GO:0015837	amine transport	36	0.290028676	0.0004	0.008964341
GO:0001829	trophectodermal cell differentiation	5	0.289961483	0.0044	0.014132412
GO:0002371	dendritic cell cytokine production	8	0.289950533	0.0006	0.009940401
GO:0002730	regulation of dendritic cell cytokine production	8	0.289950533	0.0006	0.009940401
GO:0001963	synaptic transmission, dopaminergic	12	0.289616329	0.002	0.012314604
GO:0051354	negative regulation of oxidoreductase activity	6	0.289483295	0.0278	0.032045375
GO:0072531	pyrimidine-containing compound transmembrane transport	7	0.289478451	0.0007	0.010220707
GO:0002190	cap-independent translational initiation	6	0.289476816	0.025	0.029554283
GO:0018146	keratan sulfate biosynthetic process	14	0.289471509	0.0013	0.011218806
GO:0070262	peptidyl-serine dephosphorylation	8	0.288741889	0.0121	0.018970228
GO:0035930	corticosteroid hormone secretion	8	0.288576353	0.0004	0.008964341
GO:0032332	positive regulation of chondrocyte differentiation	12	0.288469558	0.0016	0.011845327
GO:0030195	negative regulation of blood coagulation	17	0.288427699	0.0121	0.018970228
GO:1900047	negative regulation of hemostasis	17	0.288427699	0.0121	0.018970228
GO:0051900	regulation of mitochondrial depolarization	11	0.288405692	0.0071	0.01583804
GO:0090313	regulation of protein targeting to membrane	17	0.288343473	0.0037	0.013609033
GO:0018200	peptidyl-glutamic acid modification	10	0.288340455	0.0029	0.013089617
GO:0019359	nicotinamide nucleotide biosynthetic process	14	0.288159248	0.0086	0.016782045
GO:0019363	pyridine nucleotide biosynthetic process	14	0.288159248	0.0086	0.016782045

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0043029	T cell homeostasis	8	0.288048644	0.0005	0.009604651
GO:0045738	negative regulation of DNA repair	13	0.287964019	0.0046	0.014132412
GO:0031063	regulation of histone deacetylation	12	0.287837863	0.0009	0.010729485
GO:0010764	negative regulation of fibroblast migration	6	0.287810219	0.0059	0.014942532
GO:0060312	regulation of blood vessel remodeling	5	0.287378723	0.0173	0.023005658
GO:0090314	positive regulation of protein targeting to membrane	16	0.287317578	0.0037	0.013609033
GO:0021533	cell differentiation in hindbrain	7	0.286951483	0.0024	0.012603815
GO:0060039	pericardium development	7	0.286861704	0.0083	0.016559903
GO:0034067	protein localization to Golgi apparatus	8	0.286805985	0.001	0.010787313
GO:0010752	regulation of cGMP-mediated signaling	6	0.286781365	0.001	0.010787313
GO:1901989	positive regulation of cell cycle phase transition	35	0.286748341	0.0022	0.012422266
GO:0006882	cellular zinc ion homeostasis	6	0.286554603	0.0023	0.012498684
GO:0018027	peptidyl-lysine dimethylation	7	0.286514248	0.0021	0.012314604
GO:0006705	mineralocorticoid biosynthetic process	5	0.286265902	0.0245	0.029070183
GO:0008212	mineralocorticoid metabolic process	5	0.286265902	0.0245	0.029070183
GO:0032341	aldosterone metabolic process	5	0.286265902	0.0245	0.029070183
GO:0032342	aldosterone biosynthetic process	5	0.286265902	0.0245	0.029070183
GO:0002833	positive regulation of response to biotic stimulus	19	0.286100669	0.0169	0.022703485
GO:0050650	chondroitin sulfate proteoglycan biosynthetic process	19	0.286029537	0.0096	0.017302743
GO:0002228	natural killer cell mediated immunity	18	0.285969124	0.0119	0.018881943
GO:0070131	positive regulation of mitochondrial translation	10	0.285911375	0.0032	0.013333753
GO:0090344	negative regulation of cell aging	9	0.285853007	0.0013	0.011218806
GO:0071609	chemokine (C-C motif) ligand 5 production	5	0.285832591	0.0029	0.013089617
GO:0014904	myotube cell development	14	0.28582091	0.0048	0.014269203
GO:0072321	chaperone-mediated protein transport	10	0.285794754	0.014	0.020462083
GO:0090502	RNA phosphodiester bond hydrolysis, endonucleolytic	21	0.285739122	0.0019	0.012288367
GO:1905276	regulation of epithelial tube formation	7	0.285715859	0.0133	0.019917275
GO:0090312	positive regulation of protein deacetylation	11	0.285619399	0.0014	0.011465722
GO:0042267	natural killer cell mediated cytotoxicity	16	0.285530365	0.0134	0.01999969
GO:0021871	forebrain regionalization	9	0.285381197	0.0207	0.025805821
GO:0030201	heparan sulfate proteoglycan metabolic process	13	0.284853834	0.0041	0.013887639
GO:0003401	axis elongation	11	0.284839571	0.0157	0.021779607
GO:0070873	regulation of glycogen metabolic process	12	0.284699685	0.0001	0.004220438
GO:0035900	response to isolation stress	5	0.284444027	0.0015	0.011704453
GO:0035690	cellular response to drug	28	0.284408411	0.0068	0.015633241
GO:0007176	regulation of epidermal growth factor-activated receptor activity	10	0.28434464	< 0.001	< 0.001
GO:0099054	presynapse assembly	30	0.284079566	0.0017	0.012001709
GO:0051590	positive regulation of neurotransmitter transport	17	0.284047486	0.0012	0.010961137
GO:2000249	regulation of actin cytoskeleton reorganization	22	0.284045608	0.01	0.017574468
GO:0046033	AMP metabolic process	9	0.283984916	0.033	0.036785425
GO:0072672	neutrophil extravasation	5	0.283705947	0.0218	0.026744664
GO:0032225	regulation of synaptic transmission, dopaminergic	7	0.283675367	0.0009	0.010729485
GO:0051560	mitochondrial calcium ion homeostasis	13	0.283628619	0.0011	0.010890753
GO:0097711	ciliary basal body docking	38	0.283589947	0.0038	0.01366393
GO:0060347	heart trabecula formation	9	0.283409731	0.0071	0.01583804
GO:0060263	regulation of respiratory burst	6	0.283362003	0.0046	0.014132412
GO:0061179	negative regulation of insulin secretion involved in cellular response to glucose stimulus	5	0.283288445	0.0166	0.02247277
GO:0007614	short-term memory	6	0.283244518	0.0062	0.015209334
GO:0030800	negative regulation of cyclic nucleotide metabolic process	9	0.283238543	0.0102	0.0177
GO:0030803	negative regulation of cyclic nucleotide biosynthetic process	9	0.283238543	0.0102	0.0177
GO:0031280	negative regulation of cyclase activity	9	0.283238543	0.0102	0.0177
GO:0009067	aspartate family amino acid biosynthetic process	6	0.283233936	0.0076	0.016084627
GO:0042762	regulation of sulfur metabolic process	7	0.283197037	0.0132	0.019860109
GO:0051350	negative regulation of lyase activity	10	0.283131655	0.0119	0.018881943
GO:0039532	negative regulation of viral-induced cytoplasmic pattern recognition receptor signaling pathway	6	0.283114076	0.0139	0.020388077
GO:0090383	phagosome acidification	13	0.283002954	0.0046	0.014132412
GO:1905097	regulation of guanyl-nucleotide exchange factor activity	5	0.282908002	0.0065	0.015491756
GO:0039702	viral budding via host ESCRT complex	13	0.282867893	0.0109	0.018225506
GO:0007183	SMAD protein complex assembly	8	0.282846874	0.0143	0.020629391
GO:0031338	regulation of vesicle fusion	10	0.282747973	0.0052	0.014616626
GO:0002922	positive regulation of humoral immune response	6	0.282743049	0.0222	0.027148985
GO:0061299	retina vasculature morphogenesis in camera-type eye	7	0.28266632	0.0088	0.016916437
GO:0003376	sphingosine-1-phosphate signaling pathway	5	0.282587166	0.0032	0.013333753
GO:0008210	estrogen metabolic process	9	0.282494618	0.0038	0.01366393
GO:0002820	negative regulation of adaptive immune response	13	0.282477762	0.0007	0.010220707
GO:0051952	regulation of amine transport	34	0.282351607	0.0005	0.009604651
GO:0048680	positive regulation of axon regeneration	5	0.282312459	0.0121	0.018970228
GO:0071360	cellular response to exogenous dsRNA	10	0.282302352	0.0117	0.018739446
GO:0071377	cellular response to glucagon stimulus	9	0.282268287	< 0.001	< 0.001
GO:1905606	regulation of presynapse assembly	21	0.282260616	0.0022	0.012422266
GO:1900449	regulation of glutamate receptor signaling pathway	35	0.282147154	0.0017	0.012001709
GO:0051954	positive regulation of amine transport	15	0.282079823	0.0001	0.004220438
GO:0014029	neural crest formation	8	0.281941605	0.0008	0.010465158
GO:0010591	regulation of lamellipodium assembly	11	0.281936776	0.0009	0.010729485
GO:0010592	positive regulation of lamellipodium assembly	11	0.281936776	0.0009	0.010729485
GO:1905476	negative regulation of protein localization to membrane	16	0.281784005	0.0023	0.012498684
GO:0016574	histone ubiquitination	18	0.281778336	0.0019	0.012288367
GO:0051489	regulation of filopodium assembly	21	0.281707994	0.002	0.012314604
GO:1900739	regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	10	0.281629451	0.0033	0.013333753
GO:1900740	positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	10	0.281629451	0.0033	0.013333753
GO:0030397	membrane disassembly	8	0.281401749	0.0001	0.004220438
GO:0051081	nuclear envelope disassembly	8	0.281401749	0.0001	0.004220438

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1903035	negative regulation of response to wounding	35	0.281396524	0.0116	0.018682786
GO:0015844	monoamine transport	32	0.281237751	0.0051	0.014547706
GO:0043550	regulation of lipid kinase activity	24	0.281074239	0.0042	0.013948535
GO:0048557	embryonic digestive tract morphogenesis	6	0.281026349	0.0045	0.014132412
GO:0007616	long-term memory	15	0.281016587	0.0059	0.014942532
GO:0089711	L-glutamate transmembrane transport	6	0.280849474	0.0127	0.019457181
GO:0098712	L-glutamate import across plasma membrane	6	0.280849474	0.0127	0.019457181
GO:1903998	regulation of eating behavior	5	0.280807534	< 0.001	< 0.001
GO:0055091	phospholipid homeostasis	5	0.280615757	0.0161	0.02211694
GO:0045540	regulation of cholesterol biosynthetic process	29	0.280569681	0.0102	0.0177
GO:2000780	negative regulation of double-strand break repair	12	0.280393249	0.0104	0.017832977
GO:0001956	positive regulation of neurotransmitter secretion	16	0.280369979	0.0006	0.009940401
GO:0032104	regulation of response to extracellular stimulus	14	0.28026236	0.0177	0.02329117
GO:0032107	regulation of response to nutrient levels	14	0.28026236	0.0177	0.02329117
GO:0035304	regulation of protein dephosphorylation	68	0.280220345	0.0025	0.012769435
GO:0090311	regulation of protein deacetylation	17	0.280175068	0.0011	0.010890753
GO:0021697	cerebellar cortex formation	10	0.279979915	0.0012	0.010961137
GO:0032352	positive regulation of hormone metabolic process	5	0.279972529	0.0133	0.019917275
GO:0042448	progesterone metabolic process	7	0.279937395	0.012	0.018931514
GO:0009072	aromatic amino acid family metabolic process	10	0.279906185	0.0118	0.018836996
GO:2001256	regulation of store-operated calcium entry	6	0.279869212	0.0133	0.019917275
GO:0048845	venous blood vessel morphogenesis	5	0.279863424	0.006	0.015037711
GO:0032881	regulation of polysaccharide metabolic process	17	0.279813163	0.0002	0.006319126
GO:0030239	myofibril assembly	17	0.27973755	0.0083	0.016559903
GO:0048016	inositol phosphate-mediated signaling	25	0.279615359	< 0.001	< 0.001
GO:0042059	negative regulation of epidermal growth factor receptor signaling pathway	20	0.279463674	0.0005	0.009604651
GO:0042753	positive regulation of circadian rhythm	6	0.279297123	0.0001	0.004220438
GO:2000969	positive regulation of alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate selective glutamate receptor activity	5	0.27926218	0.0459	0.048535808
GO:0022010	central nervous system myelination	7	0.278813949	0.0082	0.016514246
GO:0032291	axon ensheathment in central nervous system	7	0.278813949	0.0082	0.016514246
GO:0035924	cellular response to vascular endothelial growth factor stimulus	21	0.278726946	0.0047	0.014168613
GO:2001028	positive regulation of endothelial cell chemotaxis	8	0.278710564	0.0241	0.028760826
GO:0034122	negative regulation of toll-like receptor signaling pathway	15	0.278706374	0.007	0.015816335
GO:0050961	detection of temperature stimulus involved in sensory perception	7	0.278679927	0.0011	0.010890753
GO:0050965	detection of temperature stimulus involved in sensory perception of pain	7	0.278679927	0.0011	0.010890753
GO:0035338	long-chain fatty-acyl-CoA biosynthetic process	5	0.278678558	0.0159	0.021956962
GO:0010753	positive regulation of cGMP-mediated signaling	5	0.278598478	0.0081	0.016514175
GO:0051965	positive regulation of synapse assembly	35	0.278594665	0.0005	0.009604651
GO:1900363	regulation of mRNA polyadenylation	7	0.278542019	0.0093	0.017114131
GO:0034260	negative regulation of GTPase activity	17	0.278493901	0.0038	0.01366393
GO:2001169	regulation of ATP biosynthetic process	9	0.278439384	0.0197	0.024979254
GO:0001662	behavioral fear response	21	0.278413242	0.0105	0.017924712
GO:0002209	behavioral defense response	21	0.278413242	0.0105	0.017924712
GO:0042596	fear response	21	0.278413242	0.0105	0.017924712
GO:0044346	fibroblast apoptotic process	7	0.278348947	0.0071	0.01583804
GO:2000269	regulation of fibroblast apoptotic process	7	0.278348947	0.0071	0.01583804
GO:0031579	membrane raft organization	9	0.278314413	0.013	0.019676963
GO:0046928	regulation of neurotransmitter secretion	52	0.278298877	0.0008	0.010465158
GO:0002063	chondrocyte development	12	0.278298504	0.0071	0.01583804
GO:0072215	regulation of metanephros development	7	0.278292117	0.0076	0.016084627
GO:0010923	negative regulation of phosphatase activity	44	0.27818848	0.0019	0.012288367
GO:0007270	neuron-neuron synaptic transmission	58	0.27815809	0.0001	0.004220438
GO:0051882	mitochondrial depolarization	12	0.278020558	0.0098	0.017418875
GO:2000178	negative regulation of neural precursor cell proliferation	10	0.27795512	0.0083	0.016559903
GO:0032892	positive regulation of organic acid transport	11	0.27788933	0.0016	0.011845327
GO:0032878	regulation of establishment or maintenance of cell polarity	11	0.277877903	0.0055	0.01475
GO:0072497	mesenchymal stem cell differentiation	7	0.277818785	0.0207	0.025805821
GO:0044827	modulation by host of viral genome replication	8	0.277758809	0.0091	0.016994897
GO:2000637	positive regulation of gene silencing by miRNA	8	0.277683167	0.007	0.015816335
GO:0042310	vasoconstriction	25	0.277661832	0.005	0.014547706
GO:0060766	negative regulation of androgen receptor signaling pathway	5	0.27747866	0.0163	0.022248961
GO:0032960	regulation of inositol trisphosphate biosynthetic process	5	0.277428902	0.0012	0.010961137
GO:0045429	positive regulation of nitric oxide biosynthetic process	14	0.277367389	0.013	0.019676963
GO:1904407	positive regulation of nitric oxide metabolic process	14	0.277367389	0.013	0.019676963
GO:0032095	regulation of response to food	12	0.277301612	0.0129	0.019597425
GO:0014046	dopamine secretion	11	0.277257104	0.0033	0.013333753
GO:0014059	regulation of dopamine secretion	11	0.277257104	0.0033	0.013333753
GO:0043011	myeloid dendritic cell differentiation	7	0.277206064	0.0169	0.022703485
GO:0034969	histone arginine methylation	5	0.27716508	0.0026	0.012805111
GO:0043985	histone H4-R3 methylation	5	0.27716508	0.0026	0.012805111
GO:0045663	positive regulation of myoblast differentiation	6	0.277001206	0.0066	0.015525305
GO:0050819	negative regulation of coagulation	18	0.276900567	0.013	0.019676963
GO:0097067	cellular response to thyroid hormone stimulus	5	0.276894001	0.0166	0.02247277
GO:0086064	cell communication by electrical coupling involved in cardiac conduction	7	0.276878045	0.0301	0.034151923
GO:0001990	regulation of systemic arterial blood pressure by hormone	5	0.276855905	0.0012	0.010961137
GO:1905209	positive regulation of cardiocyte differentiation	13	0.276836209	0.0011	0.010890753
GO:1905144	response to acetylcholine	18	0.276829155	0.0008	0.010465158
GO:1905145	cellular response to acetylcholine	18	0.276829155	0.0008	0.010465158
GO:0044546	NLRP3 inflammasome complex assembly	5	0.276814699	0.0139	0.020388077
GO:1900225	regulation of NLRP3 inflammasome complex assembly	5	0.276814699	0.0139	0.020388077
GO:0051764	actin crosslink formation	8	0.276808188	0.0203	0.025471918
GO:0010390	histone monoubiquitination	11	0.276662456	0.0005	0.009604651

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0031065	positive regulation of histone deacetylation	10	0.276635751	0.0011	0.010890753
GO:0033145	positive regulation of intracellular steroid hormone receptor signaling pathway	7	0.276601672	0.0087	0.016840777
GO:0010907	positive regulation of glucose metabolic process	10	0.276391107	0.0129	0.019597425
GO:0044745	amino acid transmembrane import	7	0.276382499	0.0115	0.018599441
GO:0089718	amino acid import across plasma membrane	7	0.276382499	0.0115	0.018599441
GO:0060765	regulation of androgen receptor signaling pathway	11	0.276348405	0.0128	0.019522448
GO:0046755	viral budding	16	0.27625837	0.0082	0.016514246
GO:1902590	multi-organism organelle organization	16	0.27625837	0.0082	0.016514246
GO:1902592	multi-organism membrane budding	16	0.27625837	0.0082	0.016514246
GO:0098962	regulation of postsynaptic neurotransmitter receptor activity	8	0.276192204	0.0052	0.014616626
GO:0032793	positive regulation of CREB transcription factor activity	8	0.276115915	0.0089	0.016916437
GO:0010459	negative regulation of heart rate	5	0.276085431	0.0135	0.020081554
GO:0002115	store-operated calcium entry	7	0.276064291	0.0142	0.020567234
GO:1901524	regulation of macromitophagy	9	0.2758995	0.0055	0.01475
GO:0042481	regulation of odontogenesis	7	0.275862889	0.0033	0.013333753
GO:0035305	negative regulation of dephosphorylation	47	0.275646954	0.0025	0.012769435
GO:0007340	acrosome reaction	12	0.2755861	0.0001	0.004220438
GO:0008631	intrinsic apoptotic signaling pathway in response to oxidative stress	19	0.275583935	0.0061	0.015143924
GO:0030049	muscle filament sliding	24	0.275537076	0.0119	0.018881943
GO:0033275	actin-myosin filament sliding	24	0.275537076	0.0119	0.018881943
GO:0070208	protein heterotrimerization	5	0.275380524	0.0001	0.004220438
GO:0097066	response to thyroid hormone	8	0.275324189	0.0125	0.019314538
GO:0032800	receptor biosynthetic process	11	0.275313543	< 0.001	< 0.001
GO:0051963	regulation of synapse assembly	56	0.275276685	0.0014	0.011465722
GO:0043113	receptor clustering	28	0.275219763	0.0037	0.013609033
GO:1905288	vascular associated smooth muscle cell apoptotic process	6	0.275215613	0.0026	0.012805111
GO:1905459	regulation of vascular associated smooth muscle cell apoptotic process	6	0.275215613	0.0026	0.012805111
GO:0031954	positive regulation of protein autophosphorylation	11	0.275177015	0.0193	0.024606968
GO:0070129	regulation of mitochondrial translation	12	0.275074697	0.0026	0.012805111
GO:0050858	negative regulation of antigen receptor-mediated signaling pathway	14	0.275008133	0.0009	0.010729485
GO:0007223	Wnt signaling pathway, calcium modulating pathway	16	0.274950598	0.002	0.012314604
GO:0046627	negative regulation of insulin receptor signaling pathway	14	0.274931775	0.0004	0.008964341
GO:0061314	Notch signaling involved in heart development	7	0.274914189	0.024	0.028671074
GO:0042058	regulation of epidermal growth factor receptor signaling pathway	36	0.274904589	0.0001	0.004220438
GO:0051668	localization within membrane	50	0.274794543	0.0046	0.014132412
GO:0010829	negative regulation of glucose transport	10	0.274759713	0.004	0.013824268
GO:2000463	positive regulation of excitatory postsynaptic potential	18	0.274625743	< 0.001	< 0.001
GO:0006534	cysteine metabolic process	7	0.274543039	0.0087	0.016840777
GO:1904037	positive regulation of epithelial cell apoptotic process	10	0.274539559	0.0023	0.012498684
GO:0033692	cellular polysaccharide biosynthetic process	23	0.274470386	0.0006	0.009940401
GO:0090181	regulation of cholesterol metabolic process	36	0.274458946	0.0092	0.017033109
GO:0007289	spermatid nucleus differentiation	7	0.274393283	0.0039	0.013791927
GO:0048712	negative regulation of astrocyte differentiation	6	0.274370545	0.0205	0.025639412
GO:0060512	prostate gland morphogenesis	9	0.274350892	0.0101	0.017653628
GO:0042274	ribosomal small subunit biogenesis	9	0.274239455	0.011	0.018323826
GO:1902950	regulation of dendritic spine maintenance	5	0.274191511	0.0047	0.014168613
GO:0032461	positive regulation of protein oligomerization	7	0.274086367	0.0128	0.019522448
GO:0033280	response to vitamin D	11	0.274010925	0.0157	0.021779607
GO:0016056	rhodopsin mediated signaling pathway	13	0.273923582	0.0007	0.010220707
GO:0071498	cellular response to fluid shear stress	6	0.273922419	0.0006	0.009940401
GO:0015732	prostaglandin transport	5	0.273916545	0.0104	0.017832977
GO:0032310	prostaglandin secretion	5	0.273916545	0.0104	0.017832977
GO:0095500	acetylcholine receptor signaling pathway	17	0.273899959	0.0004	0.008964341
GO:1903831	signal transduction involved in cellular response to ammonium ion	17	0.273899959	0.0004	0.008964341
GO:0000188	inactivation of MAPK activity	13	0.27389657	0.0011	0.010890753
GO:0070884	regulation of calcineurin-NFAT signaling cascade	15	0.273886655	< 0.001	< 0.001
GO:0007520	myoblast fusion	13	0.273875638	0.0032	0.013333753
GO:0033540	fatty acid beta-oxidation using acyl-CoA oxidase	10	0.273820527	0.0143	0.020629391
GO:1904357	negative regulation of telomere maintenance via telomere lengthening	11	0.273714544	0.0007	0.010220707
GO:0051491	positive regulation of filopodium assembly	16	0.2736029	0.0069	0.015750415
GO:0000154	rRNA modification	11	0.273574952	0.0029	0.013089617
GO:0033574	response to testosterone	16	0.273476804	0.005	0.014547706
GO:0042940	D-amino acid transport	5	0.273421036	0.0103	0.017772187
GO:0032515	negative regulation of phosphoprotein phosphatase activity	28	0.273392659	0.003	0.013210967
GO:0031629	synaptic vesicle fusion to presynaptic active zone membrane	6	0.273374302	0.0044	0.014132412
GO:0099500	vesicle fusion to plasma membrane	6	0.273374302	0.0044	0.014132412
GO:0000271	polysaccharide biosynthetic process	28	0.27333023	0.0004	0.008964341
GO:0035456	response to interferon-beta	12	0.273236517	0.0011	0.010890753
GO:0006688	glycosphingolipid biosynthetic process	12	0.273227122	0.0005	0.009604651
GO:1903725	regulation of phospholipid metabolic process	35	0.273184241	0.0019	0.012288367
GO:0001967	suckling behavior	7	0.273107308	0.0029	0.013089617
GO:0005976	polysaccharide metabolic process	41	0.273035701	0.0011	0.010890753
GO:0007260	tyrosine phosphorylation of STAT protein	24	0.273032808	0.0017	0.012001709
GO:2000344	positive regulation of acrosome reaction	5	0.27296803	0.0022	0.012422266
GO:0009225	nucleotide-sugar metabolic process	17	0.272810737	0.0094	0.017156187
GO:0021892	cerebral cortex GABAergic interneuron differentiation	6	0.272713451	0.0099	0.017505138
GO:0097154	GABAergic neuron differentiation	6	0.272713451	0.0099	0.017505138
GO:0090151	establishment of protein localization to mitochondrial membrane	9	0.272552054	0.0079	0.01629604
GO:0072525	pyridine-containing compound biosynthetic process	15	0.272466129	0.0127	0.019457181
GO:0021795	cerebral cortex cell migration	23	0.272431665	0.0053	0.014634479
GO:0045737	positive regulation of cyclin-dependent protein serine/threonine kinase activity	9	0.272408653	0.002	0.012314604
GO:0046459	short-chain fatty acid metabolic process	7	0.272402401	0.0172	0.022941269
GO:0036005	response to macrophage colony-stimulating factor	6	0.272396847	0.0359	0.039290895

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0036006	cellular response to macrophage colony-stimulating factor stimulus	6	0.272396847	0.0359	0.039290895
GO:0007635	chemosensory behavior	5	0.272349422	0.0004	0.008964341
GO:0043407	negative regulation of MAP kinase activity	37	0.272260965	0.0016	0.011845327
GO:0034314	Arp2/3 complex-mediated actin nucleation	19	0.272168994	0.0039	0.013791927
GO:1903393	positive regulation of adherens junction organization	17	0.272128391	0.0032	0.013333753
GO:0001844	protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	11	0.272051462	0.0038	0.01366393
GO:0017062	respiratory chain complex III assembly	6	0.271974205	0.02	0.025188412
GO:0034551	mitochondrial respiratory chain complex III assembly	6	0.271974205	0.02	0.025188412
GO:0097033	mitochondrial respiratory chain complex III biogenesis	6	0.271974205	0.02	0.025188412
GO:0016139	glycoside catabolic process	5	0.271958613	0.0139	0.020388077
GO:0001833	inner cell mass cell proliferation	5	0.271815817	0.0106	0.018010344
GO:0090281	negative regulation of calcium ion import	12	0.271779297	0.0178	0.023348367
GO:0009074	aromatic amino acid family catabolic process	8	0.271747821	0.0123	0.019143634
GO:0050856	regulation of T cell receptor signaling pathway	20	0.271726926	0.0012	0.010961137
GO:0006595	polyamine metabolic process	11	0.271662137	0.0138	0.020339434
GO:0035269	protein O-linked mannosylation	11	0.271578618	0.0116	0.018682786
GO:0042730	fibrinolysis	5	0.271473211	0.0031	0.013277185
GO:0035249	synaptic transmission, glutamatergic	34	0.271441548	0.0001	0.004220438
GO:0035774	positive regulation of insulin secretion involved in cellular response to glucose stimulus	17	0.271405038	0.0016	0.011845327
GO:0048521	negative regulation of behavior	8	0.271402818	< 0.001	< 0.001
GO:1901655	cellular response to ketone	31	0.271326486	0.0012	0.010961137
GO:0051683	establishment of Golgi localization	6	0.271127841	0.0106	0.018010344
GO:0061178	regulation of insulin secretion involved in cellular response to glucose stimulus	29	0.270982028	0.0021	0.012314604
GO:0098883	synapse disassembly	7	0.270925205	0.0333	0.037012803
GO:0006596	polyamine biosynthetic process	10	0.27088337	0.0169	0.022703485
GO:1900037	regulation of cellular response to hypoxia	6	0.270832186	0.0124	0.019242297
GO:0032927	positive regulation of activin receptor signaling pathway	5	0.270802253	0.0373	0.040638515
GO:0006398	mRNA 3'-end processing by stem-loop binding and cleavage	5	0.270716732	0.0022	0.012422266
GO:0032785	negative regulation of DNA-templated transcription, elongation	6	0.27068425	0.0078	0.01620539
GO:0008207	C21-steroid hormone metabolic process	19	0.27058793	0.0206	0.025725529
GO:0046717	acid secretion	47	0.27045157	0.0002	0.006319126
GO:1900077	negative regulation of cellular response to insulin stimulus	15	0.270441075	0.0002	0.006319126
GO:0060359	response to ammonium ion	72	0.270409742	0.002	0.012314604
GO:0032925	regulation of activin receptor signaling pathway	7	0.270370238	0.0156	0.021692929
GO:0061041	regulation of wound healing	49	0.270349453	0.0119	0.018881943
GO:0030204	chondroitin sulfate metabolic process	24	0.270268033	0.0088	0.016916437
GO:0035303	regulation of dephosphorylation	96	0.270255251	0.0023	0.012498684
GO:0016081	synaptic vesicle docking	5	0.270240919	< 0.001	< 0.001
GO:1901623	regulation of lymphocyte chemotaxis	5	0.270082833	0.0156	0.021692929
GO:0038179	neurotrophin signaling pathway	20	0.270072013	0.0001	0.004220438
GO:0050728	negative regulation of inflammatory response	53	0.269972065	0.0034	0.01347416
GO:0005979	regulation of glycogen biosynthetic process	10	0.269949238	0.0001	0.004220438
GO:0010962	regulation of glucan biosynthetic process	10	0.269949238	0.0001	0.004220438
GO:0007193	adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway	36	0.26980632	0.0053	0.014634479
GO:0042509	regulation of tyrosine phosphorylation of STAT protein	23	0.269710345	0.0042	0.013948535
GO:0033605	positive regulation of catecholamine secretion	8	0.269687521	< 0.001	< 0.001
GO:0051588	regulation of neurotransmitter transport	57	0.269660693	0.0006	0.009940401
GO:0098801	regulation of renal system process	15	0.269657902	0.0094	0.017156187
GO:0060046	regulation of acrosome reaction	6	0.269622354	0.0015	0.011704453
GO:0071636	positive regulation of transforming growth factor beta production	6	0.269612852	0.0216	0.026572596
GO:0014072	response to isoquinoline alkaloid	23	0.269568034	0.0018	0.01210186
GO:0043278	response to morphine	23	0.269568034	0.0018	0.01210186
GO:0006835	dicarboxylic acid transport	44	0.269529509	0.001	0.010787313
GO:0035336	long-chain fatty-acyl-CoA metabolic process	6	0.269517611	0.021	0.026005997
GO:0045010	actin nucleation	22	0.26951449	0.004	0.013824268
GO:0060438	trachea development	8	0.269482301	0.0166	0.02247277
GO:0032885	regulation of polysaccharide biosynthetic process	15	0.269327995	0.0002	0.006319126
GO:0043551	regulation of phosphatidylinositol 3-kinase activity	20	0.269324604	0.0073	0.015844069
GO:0035810	positive regulation of urine volume	7	0.269322503	0.0014	0.011465722
GO:0035268	protein mannosylation	12	0.269247224	0.0146	0.020879842
GO:0006470	protein dephosphorylation	148	0.269232941	0.0014	0.011465722
GO:0048066	developmental pigmentation	19	0.269218762	0.0017	0.012001709
GO:1902914	regulation of protein polyubiquitination	12	0.269174768	0.004	0.013824268
GO:0010927	cellular component assembly involved in morphogenesis	28	0.269167333	0.0044	0.014132412
GO:0016126	sterol biosynthetic process	44	0.26916289	0.0075	0.015990044
GO:0019317	fucose catabolic process	5	0.269063568	0.0024	0.012603815
GO:0042354	L-fucose metabolic process	5	0.269063568	0.0024	0.012603815
GO:0042355	L-fucose catabolic process	5	0.269063568	0.0024	0.012603815
GO:0006516	glycoprotein catabolic process	9	0.269056312	0.0007	0.010220707
GO:1901071	glucosamine-containing compound metabolic process	5	0.269033247	0.0264	0.030750363
GO:0070542	response to fatty acid	40	0.268990259	0.001	0.010787313
GO:0043666	regulation of phosphoprotein phosphatase activity	56	0.268961812	0.0025	0.012769435
GO:0015669	gas transport	9	0.26885892	0.0152	0.0213213
GO:0032700	negative regulation of interleukin-17 production	8	0.268855303	0.0021	0.012314604
GO:0035308	negative regulation of protein dephosphorylation	30	0.268845012	0.0042	0.013948535
GO:1900006	positive regulation of dendrite development	27	0.268839675	0.0011	0.010890753
GO:0030193	regulation of blood coagulation	25	0.268836546	0.0159	0.021956962
GO:1900046	regulation of hemostasis	25	0.268836546	0.0159	0.021956962
GO:0031214	biomineral tissue development	59	0.268823685	0.0036	0.01353394
GO:0061684	chaperone-mediated autophagy	11	0.268796094	0.0065	0.015491756
GO:0019229	regulation of vasoconstriction	19	0.268686194	0.0028	0.012972436
GO:0090036	regulation of protein kinase C signaling	6	0.268650083	0.0022	0.012422266
GO:0010878	cholesterol storage	7	0.268645733	0.0002	0.006319126

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0050812	regulation of acyl-CoA biosynthetic process	5	0.268641919	0.0091	0.016994897
GO:0009312	oligosaccharide biosynthetic process	6	0.268607538	0.0067	0.015576759
GO:1904385	cellular response to angiotensin	10	0.26860175	0.0008	0.010465158
GO:0043950	positive regulation of cAMP-mediated signaling	8	0.268375538	0.0023	0.012498684
GO:0014866	skeletal myofibril assembly	5	0.26836203	0.0414	0.044386204
GO:0099601	regulation of neurotransmitter receptor activity	38	0.268245423	0.0008	0.010465158
GO:0045453	bone resorption	23	0.26822053	0.0005	0.009604651
GO:0097028	dendritic cell differentiation	14	0.268205443	0.0074	0.015911789
GO:1901184	regulation of ERBB signaling pathway	39	0.268193086	0.0002	0.006319126
GO:2000114	regulation of establishment of cell polarity	10	0.268160405	0.0063	0.015311728
GO:0032024	positive regulation of insulin secretion	34	0.268093543	0.0012	0.010961137
GO:0071312	cellular response to alkaloid	16	0.268088927	0.0045	0.014132412
GO:0030213	hyaluronan biosynthetic process	5	0.268085509	0.0069	0.015750415
GO:1900125	regulation of hyaluronan biosynthetic process	5	0.268085509	0.0069	0.015750415
GO:0033539	fatty acid beta-oxidation using acyl-CoA dehydrogenase	7	0.267988954	0.0266	0.030933467
GO:0015740	C4-dicarboxylate transport	11	0.267948297	0.0022	0.012422266
GO:0046835	carbohydrate phosphorylation	12	0.267928546	0.031	0.034967226
GO:0046173	polyol biosynthetic process	17	0.267888809	0.01	0.017574468
GO:1903429	regulation of cell maturation	7	0.267868446	0.0015	0.011704453
GO:0003351	epithelial cilium movement	7	0.267745347	0.0171	0.022860624
GO:0010921	regulation of phosphatase activity	78	0.267708595	0.0027	0.012827773
GO:0003094	glomerular filtration	9	0.267699912	0.0091	0.016994897
GO:0010893	positive regulation of steroid biosynthetic process	5	0.267675263	0.0213	0.026276211
GO:0006029	proteoglycan metabolic process	46	0.267615905	0.0073	0.015844069
GO:0015012	heparan sulfate proteoglycan biosynthetic process	9	0.267581419	0.0011	0.010890753
GO:0070570	regulation of neuron projection regeneration	18	0.267575084	0.0034	0.01347416
GO:0032692	negative regulation of interleukin-1 production	15	0.267557433	0.0305	0.034510959
GO:1903034	regulation of response to wounding	64	0.267531597	0.0094	0.017156187
GO:0039531	regulation of viral-induced cytoplasmic pattern recognition receptor signaling pathway	9	0.267501513	0.011	0.018323826
GO:0007099	centriole replication	9	0.267500937	0.0141	0.020504577
GO:0098534	centriole assembly	9	0.267500937	0.0141	0.020504577
GO:1901185	negative regulation of ERBB signaling pathway	23	0.267488636	0.001	0.010787313
GO:0060068	vagina development	6	0.267487979	0.0092	0.017033109
GO:0035357	peroxisome proliferator activated receptor signaling pathway	12	0.267477829	0.0016	0.011845327
GO:0035929	steroid hormone secretion	9	0.267476029	0.0003	0.007956881
GO:0016114	terpenoid biosynthetic process	7	0.267472306	0.0275	0.031743861
GO:0010870	positive regulation of receptor biosynthetic process	5	0.267438653	0.0015	0.011704453
GO:0051383	kinetochore organization	9	0.26729721	0.0008	0.010465158
GO:1902930	regulation of alcohol biosynthetic process	39	0.267248558	0.0123	0.019143634
GO:0032703	negative regulation of interleukin-2 production	11	0.267199686	0.0233	0.028125386
GO:0098586	cellular response to virus	21	0.267110412	0.0094	0.017156187
GO:0010676	positive regulation of cellular carbohydrate metabolic process	21	0.266996938	0.0089	0.016916437
GO:0060997	dendritic spine morphogenesis	28	0.266910537	0.0016	0.011845327
GO:0048820	hair follicle maturation	6	0.266862762	0.0315	0.035393121
GO:0035641	locomotory exploration behavior	7	0.266857918	0.0015	0.011704453
GO:2000831	regulation of steroid hormone secretion	8	0.266834363	0.0001	0.004220438
GO:0006851	mitochondrial calcium ion transport	15	0.266813134	0.0074	0.015911789
GO:0015802	basic amino acid transport	5	0.266757588	0.021	0.026005997
GO:0006695	cholesterol biosynthetic process	43	0.266742189	0.0073	0.015844069
GO:1902653	secondary alcohol biosynthetic process	43	0.266742189	0.0073	0.015844069
GO:0015872	dopamine transport	14	0.266413557	0.0051	0.014547706
GO:0001765	membrane raft assembly	6	0.266398223	0.0027	0.012827773
GO:0005980	glycogen catabolic process	10	0.266383753	0.007	0.015816335
GO:0009251	glucan catabolic process	10	0.266383753	0.007	0.015816335
GO:0002715	regulation of natural killer cell mediated immunity	12	0.266373819	0.0164	0.022306469
GO:0036257	multivesicular body organization	19	0.266352143	0.0064	0.015399417
GO:0036258	multivesicular body assembly	19	0.266352143	0.0064	0.015399417
GO:0002717	positive regulation of natural killer cell mediated immunity	8	0.266234738	0.0085	0.016693954
GO:0050803	regulation of synapse structure or activity	88	0.266211119	0.0023	0.012498684
GO:0050807	regulation of synapse organization	88	0.266211119	0.0023	0.012498684
GO:0002089	lens morphogenesis in camera-type eye	9	0.26620803	0.0003	0.007956881
GO:0060999	positive regulation of dendritic spine development	14	0.266152548	0.0027	0.012827773
GO:2001026	regulation of endothelial cell chemotaxis	9	0.266074565	0.0325	0.036312077
GO:0060445	branching involved in salivary gland morphogenesis	12	0.265975689	0.0031	0.013277185
GO:0001961	positive regulation of cytokine-mediated signaling pathway	18	0.265852841	0.0072	0.015844069
GO:0072583	clathrin-dependent endocytosis	38	0.265754718	0.0008	0.010465158
GO:0007215	glutamate receptor signaling pathway	53	0.265712182	0.0047	0.014168613
GO:0009065	glutamine family amino acid catabolic process	15	0.265654615	0.0036	0.01353394
GO:0044264	cellular polysaccharide metabolic process	34	0.265604796	0.0008	0.010465158
GO:0045986	negative regulation of smooth muscle contraction	9	0.265574823	0.004	0.013824268
GO:0042573	retinoic acid metabolic process	8	0.265569028	0.0145	0.020788247
GO:0031290	retinal ganglion cell axon guidance	11	0.26555557	0.003	0.013210967
GO:0006890	retrograde vesicle-mediated transport, Golgi to ER	47	0.265455516	0.0019	0.012288367
GO:0033032	regulation of myeloid cell apoptotic process	11	0.265432588	0.0074	0.015911789
GO:0007076	mitotic chromosome condensation	8	0.265372231	0.0012	0.010961137
GO:0046579	positive regulation of Ras protein signal transduction	27	0.265282791	0.0055	0.01475
GO:0007288	sperm axoneme assembly	6	0.265277368	0.0124	0.019242297
GO:0034244	negative regulation of transcription elongation from RNA polymerase II promoter	5	0.265242814	0.0087	0.016840777
GO:0051412	response to corticosterone	5	0.265193574	0.0263	0.030677143
GO:0032691	negative regulation of interleukin-1 beta production	14	0.265156089	0.0326	0.036409735
GO:0021885	forebrain cell migration	29	0.265020028	0.008	0.016379603
GO:2000242	negative regulation of reproductive process	17	0.265008505	0.0091	0.016994897
GO:0039535	regulation of RIG-I signaling pathway	7	0.264994393	0.0062	0.015209334

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0016075	rRNA catabolic process	5	0.264975364	0.0147	0.02091937
GO:0060231	mesenchymal to epithelial transition	7	0.264867221	0.0006	0.009940401
GO:1990776	response to angiotensin	11	0.264814969	0.0034	0.01347416
GO:0042490	mechanoreceptor differentiation	24	0.264785834	0.0141	0.020504577
GO:0071243	cellular response to arsenic-containing substance	12	0.26473519	0.0042	0.013948535
GO:0090279	regulation of calcium ion import	45	0.264734808	0.0028	0.012972436
GO:0086013	membrane repolarization during cardiac muscle cell action potential	10	0.264714393	0.0036	0.01353394
GO:0097090	presynaptic membrane organization	5	0.264676815	0.0138	0.020339434
GO:0035150	regulation of tube size	38	0.264668713	0.0032	0.013333753
GO:0050880	regulation of blood vessel size	38	0.264668713	0.0032	0.013333753
GO:0072087	renal vesicle development	7	0.264627871	0.004	0.013824268
GO:0050654	chondroitin sulfate proteoglycan metabolic process	26	0.264563723	0.0111	0.018389742
GO:0016233	telomere capping	22	0.264537259	0.0011	0.010890753
GO:0051458	corticotropin secretion	5	0.264532723	0.0279	0.032115827
GO:0051459	regulation of corticotropin secretion	5	0.264532723	0.0279	0.032115827
GO:0044803	multi-organism membrane organization	24	0.264473819	0.0085	0.016693954
GO:0035567	non-canonical Wnt signaling pathway	85	0.264432902	0.0063	0.015311728
GO:0010644	cell communication by electrical coupling	8	0.264411244	0.0311	0.035052671
GO:0009435	NAD biosynthetic process	10	0.264314513	0.0102	0.0177
GO:2001171	positive regulation of ATP biosynthetic process	6	0.264302937	0.0254	0.029880529
GO:0042559	pteridine-containing compound biosynthetic process	9	0.264286812	0.0187	0.024129301
GO:0000291	nuclear-transcribed mRNA catabolic process, exonucleolytic	19	0.264230328	0.0079	0.01629604
GO:0043928	exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay	19	0.264230328	0.0079	0.01629604
GO:0032958	inositol phosphate biosynthetic process	12	0.26411548	0.0127	0.019457181
GO:0051893	regulation of focal adhesion assembly	27	0.264007498	0.0024	0.012603815
GO:0090109	regulation of cell-substrate junction assembly	27	0.264007498	0.0024	0.012603815
GO:0032350	regulation of hormone metabolic process	12	0.263965385	0.0067	0.015576759
GO:0021670	lateral ventricle development	6	0.263937526	0.0466	0.049159132
GO:0035296	regulation of tube diameter	35	0.263896863	0.0045	0.014132412
GO:0097746	regulation of blood vessel diameter	35	0.263896863	0.0045	0.014132412
GO:0090231	regulation of spindle checkpoint	7	0.263895752	0.0002	0.006319126
GO:0090266	regulation of mitotic cell cycle spindle assembly checkpoint	7	0.263895752	0.0002	0.006319126
GO:1903504	regulation of mitotic spindle checkpoint	7	0.263895752	0.0002	0.006319126
GO:0060113	inner ear receptor cell differentiation	22	0.263776927	0.02	0.025188412
GO:0036315	cellular response to sterol	11	0.263754427	0.0055	0.01475
GO:0098815	modulation of excitatory postsynaptic potential	25	0.263753231	< 0.001	< 0.001
GO:0006023	aminoglycan biosynthetic process	60	0.263710699	0.0046	0.014132412
GO:0006024	glycosaminoglycan biosynthetic process	60	0.263710699	0.0046	0.014132412
GO:0050974	detection of mechanical stimulus involved in sensory perception	10	0.263704068	0.0147	0.02091937
GO:0034698	response to gonadotropin	7	0.263668249	0.0057	0.01480566
GO:0019233	sensory perception of pain	51	0.263610937	0.0014	0.011465722
GO:1904181	positive regulation of membrane depolarization	7	0.263599573	0.0101	0.017653628
GO:0021680	cerebellar Purkinje cell layer development	8	0.263597166	0.0021	0.012314604
GO:0010922	positive regulation of phosphatase activity	18	0.263581257	0.0099	0.017505138
GO:0030490	maturation of SSU-rRNA	5	0.263576174	0.0045	0.014132412
GO:0000394	RNA splicing, via endonucleolytic cleavage and ligation	6	0.263545551	0.0021	0.012314604
GO:0006388	tRNA splicing, via endonucleolytic cleavage and ligation	6	0.263545551	0.0021	0.012314604
GO:0000096	sulfur amino acid metabolic process	17	0.263504174	0.0164	0.022306469
GO:0072210	metanephric nephron development	16	0.263473743	0.0116	0.018682786
GO:0021987	cerebral cortex development	49	0.263395896	0.005	0.014547706
GO:0036314	response to sterol	17	0.263364687	0.011	0.018323826
GO:0022406	membrane docking	65	0.26329148	0.0029	0.013089617
GO:0006026	aminoglycan catabolic process	34	0.263258394	0.0091	0.016994897
GO:0006027	glycosaminoglycan catabolic process	34	0.263258394	0.0091	0.016994897
GO:0051044	positive regulation of membrane protein ectodomain proteolysis	5	0.263185625	0.0022	0.012422266
GO:0071499	cellular response to laminar fluid shear stress	5	0.263167743	0.0015	0.011704453
GO:0030730	sequestering of triglyceride	9	0.263145945	0.0021	0.012314604
GO:0050732	negative regulation of peptidyl-tyrosine phosphorylation	20	0.263137162	0.0018	0.01210186
GO:0050931	pigment cell differentiation	18	0.263093033	0.0015	0.011704453
GO:0072224	metanephric glomerulus development	5	0.26303635	0.0378	0.041067193
GO:0008286	insulin receptor signaling pathway	53	0.26296338	0.0029	0.013089617
GO:0050909	sensory perception of taste	15	0.262953506	0.0001	0.004220438
GO:0032330	regulation of chondrocyte differentiation	25	0.26293927	0.0074	0.015911789
GO:0050857	positive regulation of antigen receptor-mediated signaling pathway	12	0.262931132	0.0056	0.014771533
GO:0007175	negative regulation of epidermal growth factor-activated receptor activity	5	0.262865306	0.007	0.015816335
GO:0072173	metanephric tubule morphogenesis	6	0.262844315	0.0322	0.036060507
GO:0031365	N-terminal protein amino acid modification	11	0.262635929	0.004	0.013824268
GO:0032836	glomerular basement membrane development	6	0.262562049	0.013	0.019676963
GO:0003018	vascular process in circulatory system	54	0.262548587	0.0056	0.014771533
GO:2000758	positive regulation of peptidyl-lysine acetylation	13	0.262523857	0.0196	0.0248852
GO:0046165	alcohol biosynthetic process	62	0.262503439	0.0082	0.016514246
GO:0046164	alcohol catabolic process	12	0.262429447	0.0041	0.013887639
GO:0050951	sensory perception of temperature stimulus	9	0.262387046	0.0018	0.01210186
GO:0061517	macrophage proliferation	6	0.262380423	0.0389	0.042009675
GO:0061518	microglial cell proliferation	6	0.262380423	0.0389	0.042009675
GO:1904467	regulation of tumor necrosis factor secretion	8	0.262379775	0.0053	0.014634479
GO:1990774	tumor necrosis factor secretion	8	0.262379775	0.0053	0.014634479
GO:0034105	positive regulation of tissue remodeling	6	0.262359907	0.0208	0.025885837
GO:0007286	spermatid development	42	0.262306378	0.0077	0.016177834
GO:0035329	hippo signaling	14	0.262298326	0.007	0.015816335
GO:0090277	positive regulation of peptide hormone secretion	43	0.262235958	0.0009	0.010729485
GO:0060586	multicellular organismal iron ion homeostasis	5	0.262234777	0.0044	0.014132412
GO:1903077	negative regulation of protein localization to plasma membrane	12	0.262188863	0.0056	0.014771533

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0002097	tRNA wobble base modification	8	0.262161597	0.001	0.010787313
GO:0002098	tRNA wobble uridine modification	8	0.262161597	0.001	0.010787313
GO:0035773	insulin secretion involved in cellular response to glucose stimulus	32	0.262135236	0.0023	0.012498684
GO:0006750	glutathione biosynthetic process	9	0.26209967	0.0072	0.015844069
GO:0060079	excitatory postsynaptic potential	50	0.26208558	0.0006	0.009940401
GO:0051881	regulation of mitochondrial membrane potential	34	0.262072941	0.0073	0.015844069
GO:0060740	prostate gland epithelium morphogenesis	8	0.262060526	0.0134	0.01999969
GO:0010635	regulation of mitochondrial fusion	8	0.26204028	0.0085	0.016693954
GO:0060071	Wnt signaling pathway, planar cell polarity pathway	71	0.261975262	0.0088	0.016916437
GO:0097062	dendritic spine maintenance	9	0.26190559	< 0.001	< 0.001
GO:0007632	visual behavior	23	0.261889997	0.0025	0.012769435
GO:0070670	response to interleukin-4	13	0.261798615	0.0015	0.011704453
GO:0031952	regulation of protein autophosphorylation	19	0.261794728	0.0127	0.019457181
GO:0002793	positive regulation of peptide secretion	44	0.261793315	0.0007	0.010220707
GO:0072574	hepatocyte proliferation	9	0.261752831	0.009	0.016956012
GO:0072575	epithelial cell proliferation involved in liver morphogenesis	9	0.261752831	0.009	0.016956012
GO:0072576	liver morphogenesis	9	0.261752831	0.009	0.016956012
GO:0019218	regulation of steroid metabolic process	56	0.261715986	0.0073	0.015844069
GO:0046949	fatty-acyl-CoA biosynthetic process	10	0.261692879	0.0303	0.034331687
GO:0046425	regulation of JAK-STAT cascade	38	0.261673402	0.0019	0.012288367
GO:0090110	cargo loading into COPII-coated vesicle	8	0.261668227	0.0012	0.010961137
GO:0050818	regulation of coagulation	26	0.26160973	0.0164	0.022306469
GO:0010885	regulation of cholesterol storage	6	0.261535355	0.0027	0.012827773
GO:2000302	positive regulation of synaptic vesicle exocytosis	7	0.261523724	0.0002	0.006319126
GO:0090175	regulation of establishment of planar polarity	72	0.261498533	0.008	0.016379603
GO:0051589	negative regulation of neurotransmitter transport	5	0.261491514	0.0386	0.041834152
GO:0035358	regulation of peroxisome proliferator activated receptor signaling pathway	8	0.26148374	0.0097	0.017363901
GO:0035767	endothelial cell chemotaxis	14	0.261458842	0.0151	0.02121706
GO:0048011	neurotrophin TRK receptor signaling pathway	17	0.261442655	0.0002	0.006319126
GO:0033522	histone H2A ubiquitination	11	0.261309044	0.0042	0.013948535
GO:0002433	immune response-regulating cell surface receptor signaling pathway involved in phagocytosis	43	0.261269453	0.0117	0.018739446
GO:0038094	Fc-gamma receptor signaling pathway	43	0.261269453	0.0117	0.018739446
GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis	43	0.261269453	0.0117	0.018739446
GO:0008343	adult feeding behavior	5	0.261258014	0.0112	0.018392048
GO:0030317	flagellated sperm motility	27	0.261141988	0.0068	0.015633241
GO:0097722	sperm motility	27	0.261141988	0.0068	0.015633241
GO:0002702	positive regulation of production of molecular mediator of immune response	35	0.261137802	0.0072	0.015844069
GO:0042462	eye photoreceptor cell development	12	0.261049435	0.0001	0.004220438
GO:0070050	neuron cellular homeostasis	17	0.260967331	0.0039	0.013791927
GO:0048641	regulation of skeletal muscle tissue development	19	0.260934258	0.0016	0.011845327
GO:0042269	regulation of natural killer cell mediated cytotoxicity	11	0.260915479	0.0228	0.027701114
GO:0000050	urea cycle	6	0.26087688	0.0016	0.011845327
GO:0019627	urea metabolic process	6	0.26087688	0.0016	0.011845327
GO:0039529	RIG-I signaling pathway	8	0.260822403	0.0097	0.017363901
GO:0002693	positive regulation of cellular extravasation	5	0.260768207	0.0221	0.027038129
GO:0050706	regulation of interleukin-1 beta secretion	16	0.260743036	0.0177	0.02329117
GO:0050746	regulation of lipoprotein metabolic process	5	0.260738663	0.0329	0.036702257
GO:0014902	myotube differentiation	36	0.260681468	0.002	0.012314604
GO:0045026	plasma membrane fusion	7	0.260671467	0.0005	0.009604651
GO:0050718	positive regulation of interleukin-1 beta secretion	9	0.260663795	0.0205	0.025639412
GO:0032205	negative regulation of telomere maintenance	13	0.260663507	0.0009	0.010729485
GO:1901387	positive regulation of voltage-gated calcium channel activity	6	0.260588352	0.0037	0.013609033
GO:2000601	positive regulation of Arp2/3 complex-mediated actin nucleation	6	0.260520755	0.0018	0.01210186
GO:0048193	Golgi vesicle transport	159	0.260490442	0.0023	0.012498684
GO:0050810	regulation of steroid biosynthetic process	43	0.26047375	0.0107	0.018084595
GO:2000300	regulation of synaptic vesicle exocytosis	40	0.260394016	0.0008	0.010465158
GO:0043114	regulation of vascular permeability	18	0.26037685	0.0114	0.018551872
GO:0046325	negative regulation of glucose import	7	0.260345669	0.0039	0.013791927
GO:1902992	negative regulation of amyloid precursor protein catabolic process	9	0.260311485	0.0006	0.009940401
GO:0046685	response to arsenic-containing substance	17	0.260304117	0.0021	0.012314604
GO:0098779	mitophagy in response to mitochondrial depolarization	11	0.260264876	0.0078	0.01620539
GO:0045123	cellular extravasation	23	0.260244743	0.0137	0.020264364
GO:0046475	glycerophospholipid catabolic process	9	0.260232442	0.0006	0.009940401
GO:0002431	Fc receptor mediated stimulatory signaling pathway	45	0.26018709	0.0126	0.019370699
GO:0071398	cellular response to fatty acid	31	0.260181182	0.0003	0.007956881
GO:0006576	cellular biogenic amine metabolic process	24	0.260172566	0.0119	0.018881943
GO:0060996	dendritic spine development	43	0.260132627	0.0005	0.009604651
GO:0060425	lung morphogenesis	20	0.260026175	0.0135	0.020081554
GO:0032930	positive regulation of superoxide anion generation	9	0.259977605	0.0315	0.035393121
GO:0060148	positive regulation of posttranscriptional gene silencing	9	0.259941179	0.0031	0.013277185
GO:1901661	quinone metabolic process	18	0.259939739	0.0089	0.016916437
GO:0097106	postsynaptic density organization	10	0.259910785	0.0029	0.013089617
GO:0099084	postsynaptic specialization organization	10	0.259910785	0.0029	0.013089617
GO:0021859	pyramidal neuron differentiation	5	0.259845866	0.0075	0.015990044
GO:0021860	pyramidal neuron development	5	0.259845866	0.0075	0.015990044
GO:0071391	cellular response to estrogen stimulus	7	0.259841238	0.0005	0.009604651
GO:0003338	metanephros morphogenesis	15	0.259827812	0.0066	0.015525305
GO:0010573	vascular endothelial growth factor production	15	0.2597803	0.0168	0.022626974
GO:0051955	regulation of amino acid transport	13	0.259769315	0.0006	0.009940401
GO:0010743	regulation of macrophage derived foam cell differentiation	9	0.259706497	0.0014	0.011465722
GO:0008090	retrograde axonal transport	8	0.259673527	0.0133	0.019917275
GO:0051043	regulation of membrane protein ectodomain proteolysis	8	0.259660731	0.0024	0.012603815
GO:0045745	positive regulation of G-protein coupled receptor protein signaling pathway	13	0.259652994	0.0029	0.013089617

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:2001267	regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway	8	0.259649069	0.0045	0.014132412
GO:0008542	visual learning	22	0.259645785	0.0026	0.012805111
GO:0034637	cellular carbohydrate biosynthetic process	28	0.259624981	0.0007	0.010220707
GO:0051149	positive regulation of muscle cell differentiation	36	0.25960611	0.0008	0.010465158
GO:1904376	negative regulation of protein localization to cell periphery	14	0.25947231	0.0009	0.010729485
GO:0021543	pallium development	73	0.259377484	0.004	0.013824268
GO:0001832	blastocyst growth	9	0.259363258	0.0055	0.01475
GO:0032105	negative regulation of response to extracellular stimulus	9	0.259307971	0.0109	0.018225506
GO:0032108	negative regulation of response to nutrient levels	9	0.259307971	0.0109	0.018225506
GO:0008033	tRNA processing	47	0.259285646	0.0045	0.014132412
GO:0010637	negative regulation of mitochondrial fusion	6	0.25926773	0.0077	0.016177834
GO:0007263	nitric oxide mediated signal transduction	15	0.259183288	0.0118	0.018836996
GO:0070358	actin polymerization-dependent cell motility	5	0.259132147	0.018	0.023514686
GO:0086011	membrane repolarization during action potential	12	0.259119038	0.0049	0.014447629
GO:0022029	telencephalon cell migration	26	0.259111853	0.0092	0.017033109
GO:0019934	cGMP-mediated signaling	15	0.259009048	0.0092	0.017033109
GO:0006885	regulation of pH	37	0.259006092	0.0082	0.016514246
GO:0042531	positive regulation of tyrosine phosphorylation of STAT protein	19	0.258996445	0.0051	0.014547706
GO:0043266	regulation of potassium ion transport	37	0.258974328	0.0004	0.008964341
GO:0034661	ncRNA catabolic process	7	0.258943444	0.0083	0.016559903
GO:0035459	cargo loading into vesicle	9	0.258852431	0.0024	0.012603815
GO:0006112	energy reserve metabolic process	31	0.258784701	0.0006	0.009940401
GO:0045722	positive regulation of gluconeogenesis	5	0.258775547	0.0286	0.032739101
GO:1902803	regulation of synaptic vesicle transport	53	0.258739241	0.0009	0.010729485
GO:0034121	regulation of toll-like receptor signaling pathway	25	0.258645761	0.0115	0.018599441
GO:0070885	negative regulation of calcineurin-NFAT signaling cascade	9	0.258637906	< 0.001	< 0.001
GO:0071361	cellular response to ethanol	9	0.258609975	0.0113	0.018488002
GO:0032102	negative regulation of response to external stimulus	138	0.25855624	0.0064	0.015399417
GO:0071295	cellular response to vitamin	9	0.258518262	0.0287	0.032827577
GO:0060191	regulation of lipase activity	37	0.258517301	0.0059	0.014942532
GO:0061036	positive regulation of cartilage development	18	0.25843094	0.0042	0.013948535
GO:0002686	negative regulation of leukocyte migration	21	0.258407297	0.0058	0.014878261
GO:1905330	regulation of morphogenesis of an epithelium	98	0.258373893	0.0071	0.01583804
GO:2000177	regulation of neural precursor cell proliferation	39	0.258321823	0.0112	0.018392048
GO:0044380	protein localization to cytoskeleton	17	0.258289475	0.0027	0.012827773
GO:0071385	cellular response to glucocorticoid stimulus	16	0.258253346	0.0121	0.018970228
GO:0035337	fatty-acyl-CoA metabolic process	11	0.258240152	0.0314	0.035301342
GO:0051125	regulation of actin nucleation	13	0.258175598	0.0036	0.01353394
GO:0043330	response to exogenous dsRNA	20	0.258166657	0.0046	0.014132412
GO:0002548	monocyte chemotaxis	12	0.258130138	0.0208	0.025885837
GO:0055003	cardiac myofibril assembly	7	0.258100258	0.0302	0.034245225
GO:0010889	regulation of sequestering of triglyceride	8	0.258098013	0.0027	0.012827773
GO:0031943	regulation of glucocorticoid metabolic process	6	0.258084677	0.0107	0.018084595
GO:0001736	establishment of planar polarity	80	0.258041582	0.0073	0.015844069
GO:0007164	establishment of tissue polarity	80	0.258041582	0.0073	0.015844069
GO:0035902	response to immobilization stress	11	0.258031177	0.0063	0.015311728
GO:0006022	aminoglycan metabolic process	82	0.258018097	0.0044	0.014132412
GO:0030203	glycosaminoglycan metabolic process	82	0.258018097	0.0044	0.014132412
GO:0032096	negative regulation of response to food	8	0.257965033	0.0103	0.017772187
GO:0032099	negative regulation of appetite	8	0.257965033	0.0103	0.017772187
GO:0048488	synaptic vesicle endocytosis	25	0.257943601	0.0005	0.009604651
GO:0072170	metanephric tubule development	13	0.257933286	0.0209	0.025971158
GO:0032148	activation of protein kinase B activity	15	0.25791886	0.0062	0.015209334
GO:1905475	regulation of protein localization to membrane	81	0.257875936	0.0045	0.014132412
GO:0034138	toll-like receptor 3 signaling pathway	11	0.257816195	0.0063	0.015311728
GO:0046427	positive regulation of JAK-STAT cascade	26	0.257784171	0.0034	0.01347416
GO:0031348	negative regulation of defense response	82	0.257766588	0.0045	0.014132412
GO:0099565	chemical synaptic transmission, postsynaptic	53	0.257757084	0.0008	0.010465158
GO:0044272	sulfur compound biosynthetic process	98	0.25773162	0.0072	0.015844069
GO:0048169	regulation of long-term neuronal synaptic plasticity	14	0.257717908	0.009	0.016956012
GO:0032232	negative regulation of actin filament bundle assembly	8	0.257709116	0.0188	0.02420971
GO:0060856	establishment of blood-brain barrier	5	0.257698231	0.0065	0.015491756
GO:0001779	natural killer cell differentiation	11	0.25769604	0.0001	0.004220438
GO:0045954	positive regulation of natural killer cell mediated cytotoxicity	7	0.257637477	0.0166	0.02247277
GO:0060078	regulation of postsynaptic membrane potential	68	0.257589332	0.0012	0.010961137
GO:1905477	positive regulation of protein localization to membrane	59	0.257548284	0.0035	0.01351837
GO:0040009	regulation of growth rate	5	0.257546365	0.0054	0.014720792
GO:0048701	embryonic cranial skeleton morphogenesis	18	0.257521515	0.021	0.026005997
GO:0051938	L-glutamate import	8	0.25747474	0.0064	0.015399417
GO:0006891	intra-Golgi vesicle-mediated transport	10	0.257466544	0.0279	0.032115827
GO:0061318	renal filtration cell differentiation	6	0.257451254	0.0095	0.01725157
GO:0072112	glomerular visceral epithelial cell differentiation	6	0.257451254	0.0095	0.01725157
GO:0072311	glomerular epithelial cell differentiation	6	0.257451254	0.0095	0.01725157
GO:0050854	regulation of antigen receptor-mediated signaling pathway	30	0.257442702	0.0022	0.012422266
GO:0015813	L-glutamate transport	11	0.257429108	0.0113	0.018488002
GO:0050806	positive regulation of synaptic transmission	93	0.257373869	0.0005	0.009604651
GO:0010882	regulation of cardiac muscle contraction by calcium ion signaling	10	0.25736936	0.0169	0.022703485
GO:0008211	glucocorticoid metabolic process	11	0.257357015	0.0027	0.012827773
GO:0000041	transition metal ion transport	44	0.257343881	0.0034	0.01347416
GO:0001659	temperature homeostasis	14	0.257342408	0.0032	0.013333753
GO:0034383	low-density lipoprotein particle clearance	17	0.257335777	0.0124	0.019242297
GO:0015780	nucleotide-sugar transport	5	0.257293687	0.0125	0.019314538
GO:0015781	pyrimidine nucleotide-sugar transport	5	0.257293687	0.0125	0.019314538

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0097009	energy homeostasis	13	0.257273233	0.0018	0.01210186
GO:0044848	biological phase	5	0.257168255	0.0401	0.043160499
GO:0044851	hair cycle phase	5	0.257168255	0.0401	0.043160499
GO:0048819	regulation of hair follicle maturation	5	0.257168255	0.0401	0.043160499
GO:0060330	regulation of response to interferon-gamma	7	0.257166922	0.0049	0.014447629
GO:0060334	regulation of interferon-gamma-mediated signaling pathway	7	0.257166922	0.0049	0.014447629
GO:1901096	regulation of autophagosome maturation	5	0.257147263	0.0151	0.02121706
GO:1902751	positive regulation of cell cycle G2/M phase transition	12	0.257046969	0.0147	0.02091937
GO:0045834	positive regulation of lipid metabolic process	61	0.257029062	0.0018	0.01210186
GO:0070527	platelet aggregation	27	0.256978292	0.0187	0.024129301
GO:1901203	positive regulation of extracellular matrix assembly	5	0.256967667	0.0244	0.029011063
GO:0071384	cellular response to corticosteroid stimulus	19	0.256954764	0.0083	0.016559903
GO:0098780	response to mitochondrial depolarisation	14	0.256889994	0.0077	0.016177834
GO:1903510	mucopolysaccharide metabolic process	59	0.256861013	0.0035	0.01351837
GO:0000715	nucleotide-excision repair, DNA damage recognition	15	0.256855106	0.0143	0.020629391
GO:0045191	regulation of isotype switching	13	0.256808146	0.0008	0.010465158
GO:0005978	glycogen biosynthetic process	17	0.256790099	0.0005	0.009604651
GO:0009250	glucan biosynthetic process	17	0.256790099	0.0005	0.009604651
GO:0031663	lipopolysaccharide-mediated signaling pathway	22	0.256736982	0.0191	0.02440579
GO:0060711	labyrinthine layer development	22	0.256653698	0.0088	0.016916437
GO:0072677	eosinophil migration	6	0.256643548	0.0246	0.029170878
GO:0007567	parturition	8	0.256636043	0.0088	0.016916437
GO:1902915	negative regulation of protein polyubiquitination	5	0.256625839	0.0062	0.015209334
GO:0002704	negative regulation of leukocyte mediated immunity	15	0.256612794	0.0198	0.025062084
GO:0051127	positive regulation of actin nucleation	8	0.256585183	0.0113	0.018488002
GO:2000241	regulation of reproductive process	49	0.256579613	0.0061	0.015143924
GO:0044406	adhesion of symbiont to host	7	0.25657808	0.019	0.024347961
GO:0044650	adhesion of symbiont to host cell	7	0.25657808	0.019	0.024347961
GO:0071941	nitrogen cycle metabolic process	7	0.256570675	0.0032	0.01333753
GO:0005977	glycogen metabolic process	27	0.256527023	0.0005	0.009604651
GO:0006073	cellular glucan metabolic process	27	0.256527023	0.0005	0.009604651
GO:0044042	glucan metabolic process	27	0.256527023	0.0005	0.009604651
GO:0007218	neuropeptide signaling pathway	30	0.256524681	0.0053	0.014634479
GO:0030501	positive regulation of bone mineralization	19	0.256517675	0.02	0.025188412
GO:0000272	polysaccharide catabolic process	11	0.256434887	0.0089	0.016916437
GO:0044247	cellular polysaccharide catabolic process	11	0.256434887	0.0089	0.016916437
GO:0060281	regulation of oocyte development	6	0.256423048	0.0036	0.01353394
GO:2000779	regulation of double-strand break repair	27	0.256379399	0.007	0.015816335
GO:0000491	small nucleolar ribonucleoprotein complex assembly	5	0.25637342	0.0275	0.031743861
GO:0048246	macrophage chemotaxis	16	0.256364981	0.0177	0.02329117
GO:0060760	positive regulation of response to cytokine stimulus	21	0.256360326	0.012	0.018931514
GO:0032098	regulation of appetite	13	0.256331596	0.0196	0.0248852
GO:1900272	negative regulation of long-term synaptic potentiation	9	0.256331119	0.0088	0.016916437
GO:0023058	adaptation of signaling pathway	10	0.256319644	0.0202	0.025368462
GO:0031167	rRNA methylation	6	0.256304916	0.0051	0.014547706
GO:0060479	lung cell differentiation	6	0.256269498	0.0165	0.022405589
GO:0060487	lung epithelial cell differentiation	6	0.256269498	0.0165	0.022405589
GO:0009954	proximal/distal pattern formation	11	0.256216842	0.0093	0.017114131
GO:0006998	nuclear envelope organization	23	0.256216145	0.0015	0.011704453
GO:1904668	positive regulation of ubiquitin protein ligase activity	5	0.256178533	0.0067	0.015576759
GO:0071709	membrane assembly	17	0.256136565	0.0013	0.011218806
GO:2001057	reactive nitrogen species metabolic process	32	0.256107038	0.0122	0.019049527
GO:0002192	IRES-dependent translational initiation	5	0.255963692	0.0374	0.040724444
GO:0009133	nucleoside diphosphate biosynthetic process	5	0.255963174	0.0457	0.0483597
GO:0009136	purine nucleoside diphosphate biosynthetic process	5	0.255963174	0.0457	0.0483597
GO:0009180	purine ribonucleoside diphosphate biosynthetic process	5	0.255963174	0.0457	0.0483597
GO:0009188	ribonucleoside diphosphate biosynthetic process	5	0.255963174	0.0457	0.0483597
GO:0006911	phagocytosis, engulfment	18	0.25594188	0.0119	0.018881943
GO:1901616	organic hydroxy compound catabolic process	18	0.255900774	0.0098	0.017418875
GO:0045671	negative regulation of osteoclast differentiation	9	0.255875579	0.0056	0.014771533
GO:1904892	regulation of STAT cascade	39	0.255872622	0.0028	0.012972436
GO:0001539	cilium or flagellum-dependent cell motility	10	0.255806643	0.0281	0.032268957
GO:0060285	cilium-dependent cell motility	10	0.255806643	0.0281	0.032268957
GO:0032400	melanosome localization	11	0.255768971	0.0088	0.016916437
GO:0010523	negative regulation of calcium ion transport into cytosol	9	0.255750463	0.0185	0.023962142
GO:0051280	negative regulation of release of sequestered calcium ion into cytosol	9	0.255750463	0.0185	0.023962142
GO:0051284	positive regulation of sequestering of calcium ion	9	0.255750463	0.0185	0.023962142
GO:0086019	cell-cell signaling involved in cardiac conduction	13	0.255741415	0.01	0.017574468
GO:0048515	spermatid differentiation	44	0.255711573	0.0074	0.015911789
GO:0051057	positive regulation of small GTPase mediated signal transduction	29	0.255703865	0.009	0.016956012
GO:0010971	positive regulation of G2/M transition of mitotic cell cycle	10	0.255701684	0.0094	0.017156187
GO:0086065	cell communication involved in cardiac conduction	20	0.255682831	0.0191	0.02440579
GO:0036017	response to erythropoietin	5	0.255656332	0.0059	0.014942532
GO:0007379	segment specification	5	0.255602168	0.0102	0.0177
GO:0046599	regulation of centriole replication	5	0.255594393	0.0191	0.02440579
GO:0046058	cAMP metabolic process	31	0.255530732	0.0009	0.010729485
GO:1903421	regulation of synaptic vesicle recycling	12	0.255509303	0.0017	0.012001709
GO:0015696	ammonium transport	36	0.255476297	0.0084	0.016633151
GO:0007130	synaptonemal complex assembly	7	0.25544075	0.0049	0.014447629
GO:0006285	base-excision repair, AP site formation	6	0.255377349	0.0013	0.011218806
GO:0070723	response to cholesterol	16	0.255350219	0.0156	0.021692929
GO:1905331	negative regulation of morphogenesis of an epithelium	5	0.255335754	0.004	0.013824268
GO:0048308	organelle inheritance	11	0.255283405	0.0017	0.012001709

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0048313	Golgi inheritance	11	0.255283405	0.0017	0.012001709
GO:0007200	phospholipase C-activating G-protein coupled receptor signaling pathway	35	0.255211359	0.0006	0.009940401
GO:0032025	response to cobalt ion	5	0.255209026	0.0001	0.004220438
GO:0007416	synapse assembly	90	0.255190986	0.0008	0.010465158
GO:0030166	proteoglycan biosynthetic process	33	0.255167451	0.0076	0.016084627
GO:1902259	regulation of delayed rectifier potassium channel activity	7	0.255165673	0.0018	0.01210186
GO:0002823	negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	11	0.255108945	0.0004	0.008964341
GO:0008206	bile acid metabolic process	14	0.255074228	0.0103	0.017772187
GO:0002862	negative regulation of inflammatory response to antigenic stimulus	6	0.255030294	0.017	0.022784886
GO:0060029	convergent extension involved in organogenesis	5	0.254944945	0.0037	0.013609033
GO:0007141	male meiosis I	7	0.25492114	0.0173	0.023005658
GO:0030148	sphingolipid biosynthetic process	41	0.254910471	0.0002	0.006319126
GO:0035809	regulation of urine volume	10	0.254864347	0.0005	0.009604651
GO:0046626	regulation of insulin receptor signaling pathway	25	0.25484885	0.0005	0.009604651
GO:0001909	leukocyte mediated cytotoxicity	30	0.254840548	0.0121	0.018970228
GO:0055081	anion homeostasis	16	0.254828422	0.0037	0.013609033
GO:0017158	regulation of calcium ion-dependent exocytosis	52	0.254808175	0.0007	0.010220707
GO:0031146	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	51	0.254805133	0.0099	0.017505138
GO:0010663	positive regulation of striated muscle cell apoptotic process	8	0.254779344	0.0002	0.006319126
GO:0010666	positive regulation of cardiac muscle cell apoptotic process	8	0.254779344	0.0002	0.006319126
GO:0051279	regulation of release of sequestered calcium ion into cytosol	32	0.254741159	0.0037	0.013609033
GO:0060122	inner ear receptor stereocilium organization	12	0.254732912	0.0162	0.022196303
GO:0006171	cAMP biosynthetic process	28	0.2547314	0.0019	0.012288367
GO:0030814	regulation of cAMP metabolic process	28	0.2547314	0.0019	0.012288367
GO:0030817	regulation of cAMP biosynthetic process	28	0.2547314	0.0019	0.012288367
GO:0045761	regulation of adenylate cyclase activity	28	0.2547314	0.0019	0.012288367
GO:0045740	positive regulation of DNA replication	18	0.254679784	0.0017	0.012001709
GO:0046322	negative regulation of fatty acid oxidation	6	0.254635728	0.0277	0.03194284
GO:0032370	positive regulation of lipid transport	23	0.254612751	0.0127	0.019457181
GO:0045838	positive regulation of membrane potential	5	0.25461141	0.0161	0.02211694
GO:0030282	bone mineralization	45	0.254600842	0.0059	0.014942532
GO:0006694	steroid biosynthetic process	81	0.254599646	0.0097	0.017363901
GO:0045956	positive regulation of calcium ion-dependent exocytosis	15	0.254454015	0.0002	0.006319126
GO:0050711	negative regulation of interleukin-1 secretion	6	0.254445463	0.0266	0.030933467
GO:0050713	negative regulation of interleukin-1 beta secretion	6	0.254445463	0.0266	0.030933467
GO:0031664	regulation of lipopolysaccharide-mediated signaling pathway	11	0.254437492	0.0147	0.02091937
GO:0070200	establishment of protein localization to telomere	8	0.254412798	0.0249	0.029484292
GO:1904888	cranial skeletal system development	25	0.254411704	0.019	0.024347961
GO:0060119	inner ear receptor cell development	19	0.254380242	0.0231	0.027930615
GO:0006303	double-strand break repair via nonhomologous end joining	28	0.254311889	0.0013	0.011218806
GO:0002448	mast cell mediated immunity	23	0.254293931	0.0158	0.021871104
GO:0031468	nuclear envelope reassembly	9	0.254285649	0.0074	0.015911789
GO:0006997	nucleus organization	54	0.25425731	0.0011	0.010890753
GO:0042551	neuron maturation	21	0.25418717	0.0019	0.012288367
GO:1902116	negative regulation of organelle assembly	16	0.254179233	0.0079	0.01629604
GO:0046890	regulation of lipid biosynthetic process	84	0.254169106	0.0062	0.015209334
GO:0097061	dendritic spine organization	39	0.254120254	0.0008	0.010465158
GO:0032401	establishment of melanosome localization	10	0.254004205	0.0069	0.015750415
GO:0032402	melanosome transport	10	0.254004205	0.0069	0.015750415
GO:0007269	neurotransmitter secretion	75	0.253972778	0.0007	0.010220707
GO:0099643	signal release from synapse	75	0.253972778	0.0007	0.010220707
GO:0006904	vesicle docking involved in exocytosis	16	0.253965914	0.0011	0.010890753
GO:0002138	retinoic acid biosynthetic process	5	0.253935528	0.0356	0.03903645
GO:0016102	diterpenoid biosynthetic process	5	0.253935528	0.0356	0.03903645
GO:0042391	regulation of membrane potential	177	0.253930238	0.0017	0.012001709
GO:0060405	regulation of penile erection	5	0.253921534	0.0351	0.038590645
GO:0090049	regulation of cell migration involved in sprouting angiogenesis	20	0.25390417	0.0029	0.013089617
GO:0072077	renal vesicle morphogenesis	6	0.253903393	0.0025	0.012769435
GO:0035563	positive regulation of chromatin binding	6	0.253842275	0.0003	0.007956881
GO:0030207	chondroitin sulfate catabolic process	10	0.253791566	0.0097	0.017363901
GO:0050996	positive regulation of lipid catabolic process	10	0.253749194	0.003	0.013210967
GO:0002042	cell migration involved in sprouting angiogenesis	28	0.253743085	0.0007	0.010220707
GO:0016601	Rac protein signal transduction	14	0.253735403	0.0152	0.0213213
GO:0010800	positive regulation of peptidyl-threonine phosphorylation	14	0.253688477	0.0032	0.013333753
GO:0090183	regulation of kidney development	21	0.253683418	0.0108	0.018152791
GO:0009415	response to water	6	0.25366756	0.0027	0.012827773
GO:0061437	renal system vasculature development	9	0.253659929	0.0402	0.043252028
GO:0061440	kidney vasculature development	9	0.253659929	0.0402	0.043252028
GO:0045931	positive regulation of mitotic cell cycle	58	0.253616488	0.0003	0.007956881
GO:0007173	epidermal growth factor receptor signaling pathway	50	0.253614588	0.0003	0.007956881
GO:0006415	translational termination	58	0.253611662	0.0205	0.025639412
GO:0006901	vesicle coating	40	0.253582653	0.0048	0.014269203
GO:0048199	vesicle targeting, to, from or within Golgi	40	0.253582653	0.0048	0.014269203
GO:0001911	negative regulation of leukocyte mediated cytotoxicity	7	0.25354483	0.0377	0.040981651
GO:0002707	negative regulation of lymphocyte mediated immunity	7	0.25354483	0.0377	0.040981651
GO:0046889	positive regulation of lipid biosynthetic process	27	0.25354302	0.0009	0.010729485
GO:0021537	telencephalon development	110	0.253497659	0.0069	0.015750415
GO:0061001	regulation of dendritic spine morphogenesis	19	0.253468622	0.0064	0.015399417
GO:0003044	regulation of systemic arterial blood pressure mediated by a chemical signal	7	0.253452644	0.0055	0.01475
GO:1901525	negative regulation of macromitophagy	5	0.253444166	0.0121	0.018970228
GO:0006949	syncytium formation	19	0.253440047	0.0128	0.019522448
GO:0007603	phototransduction, visible light	15	0.253427321	0.0001	0.004220438

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0008652	cellular amino acid biosynthetic process	35	0.253414659	0.0066	0.015525305
GO:0006304	DNA modification	31	0.2533865	0.0035	0.01351837
GO:0090394	negative regulation of excitatory postsynaptic potential	6	0.253379463	0.0031	0.013277185
GO:2000739	regulation of mesenchymal stem cell differentiation	6	0.25332612	0.0275	0.031743861
GO:0034754	cellular hormone metabolic process	48	0.253303363	0.0124	0.019242297
GO:0019886	antigen processing and presentation of exogenous peptide antigen via MHC class II	57	0.253264707	0.0088	0.016916437
GO:0009084	glutamine family amino acid biosynthetic process	10	0.253233471	0.0044	0.014132412
GO:0001824	blastocyst development	43	0.253149758	0.0047	0.014168613
GO:0007009	plasma membrane organization	143	0.253149254	0.0014	0.011465722
GO:0043931	ossification involved in bone maturation	5	0.253112445	0.0117	0.018739446
GO:0070296	sarcoplasmic reticulum calcium ion transport	16	0.253069798	0.0093	0.017114131
GO:0090239	regulation of histone H4 acetylation	7	0.253069647	0.0098	0.017418875
GO:1900076	regulation of cellular response to insulin stimulus	26	0.253030482	0.0003	0.007956881
GO:0009713	catechol-containing compound biosynthetic process	9	0.253006421	0.0097	0.017363901
GO:0042423	catecholamine biosynthetic process	9	0.253006421	0.0097	0.017363901
GO:0048643	positive regulation of skeletal muscle tissue development	7	0.252995047	0.0017	0.012001709
GO:1990823	response to leukemia inhibitory factor	35	0.252956692	0.0052	0.014616626
GO:1990830	cellular response to leukemia inhibitory factor	35	0.252956692	0.0052	0.014616626
GO:0099509	regulation of presynaptic cytosolic calcium ion concentration	8	0.252949532	0.0007	0.010220707
GO:0071322	cellular response to carbohydrate stimulus	64	0.252944673	0.0005	0.009604651
GO:0070571	negative regulation of neuron projection regeneration	8	0.252926856	0.0035	0.01351837
GO:1901160	primary amino compound metabolic process	7	0.25291767	0.0013	0.011218806
GO:1900543	negative regulation of purine nucleotide metabolic process	22	0.252891266	0.0057	0.01480566
GO:2000179	positive regulation of neural precursor cell proliferation	26	0.252872147	0.0146	0.020879842
GO:0032091	negative regulation of protein binding	45	0.252848278	0.0038	0.01366393
GO:0021591	ventricular system development	13	0.252832874	0.0357	0.03911643
GO:2000696	regulation of epithelial cell differentiation involved in kidney development	8	0.252799383	0.0037	0.013609033
GO:0048207	vesicle targeting, rough ER to cis-Golgi	38	0.252736469	0.0046	0.014132412
GO:0048208	COPII vesicle coating	38	0.252736469	0.0046	0.014132412
GO:0002495	antigen processing and presentation of peptide antigen via MHC class II	60	0.252729756	0.011	0.018323826
GO:0002504	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	60	0.252729756	0.011	0.018323826
GO:0031532	actin cytoskeleton reorganization	43	0.252698191	0.0126	0.019370699
GO:1901021	positive regulation of calcium ion transmembrane transporter activity	17	0.252697092	0.0046	0.014132412
GO:0090382	phagosome maturation	21	0.252675543	0.0045	0.014132412
GO:0010613	positive regulation of cardiac muscle hypertrophy	13	0.252632526	0.0025	0.012769435
GO:0014742	positive regulation of muscle hypertrophy	13	0.252632526	0.0025	0.012769435
GO:0021766	hippocampus development	40	0.252622832	0.0061	0.015143924
GO:0006888	ER to Golgi vesicle-mediated transport	97	0.252587168	0.0044	0.014132412
GO:0045428	regulation of nitric oxide biosynthetic process	21	0.25257188	0.018	0.023514686
GO:1902916	positive regulation of protein polyubiquitination	5	0.252520271	0.0102	0.0177
GO:0000082	G1/S transition of mitotic cell cycle	89	0.252479513	0.0008	0.010465158
GO:1902745	positive regulation of lamellipodium organization	15	0.252479497	0.0023	0.012498684
GO:0001574	ganglioside biosynthetic process	6	0.252469606	0.0016	0.011845327
GO:0045851	pH reduction	24	0.252468148	0.0094	0.017156187
GO:0030325	adrenal gland development	13	0.252455801	0.0176	0.023223003
GO:0071305	cellular response to vitamin D	6	0.252420582	0.029	0.033098697
GO:0045907	positive regulation of vasoconstriction	7	0.252370293	0.0105	0.017924712
GO:0048599	oocyte development	18	0.252363063	0.0012	0.010961137
GO:0001738	morphogenesis of a polarized epithelium	86	0.252344472	0.0084	0.016633151
GO:0050853	B cell receptor signaling pathway	22	0.252312403	0.013	0.019676963
GO:0034219	carbohydrate transmembrane transport	9	0.252300362	0.012	0.018931514
GO:0007045	cell-substrate adherens junction assembly	36	0.25228474	0.0009	0.010729485
GO:0048041	focal adhesion assembly	36	0.25228474	0.0009	0.010729485
GO:0097484	dendrite extension	21	0.252274096	0.0021	0.012314604
GO:0001522	pseudouridine synthesis	11	0.252263163	0.0101	0.017653628
GO:0034381	plasma lipoprotein particle clearance	25	0.252245357	0.0145	0.020788247
GO:0051865	protein autoubiquitination	31	0.252239646	0.0028	0.012972436
GO:0035637	multicellular organismal signaling	79	0.252221692	0.0012	0.010961137
GO:0046677	response to antibiotic	13	0.252153384	0.0018	0.01210186
GO:0032784	regulation of DNA-templated transcription, elongation	18	0.252139108	0.0043	0.014102439
GO:0002712	regulation of B cell mediated immunity	18	0.252135365	0.0025	0.012769435
GO:0002889	regulation of immunoglobulin mediated immune response	18	0.252135365	0.0025	0.012769435
GO:0006282	regulation of DNA repair	44	0.252110585	0.0024	0.012603815
GO:0030212	hyaluronan metabolic process	14	0.252097808	0.0073	0.015844069
GO:0046887	positive regulation of hormone secretion	60	0.252093115	0.0012	0.010961137
GO:0009108	coenzyme biosynthetic process	65	0.252021473	0.0061	0.015143924
GO:0006862	nucleotide transport	8	0.252014299	0.0008	0.010465158
GO:1900242	regulation of synaptic vesicle endocytosis	9	0.25200521	0.0006	0.009940401
GO:0060706	cell differentiation involved in embryonic placenta development	7	0.252000068	0.0032	0.013333753
GO:0031648	protein destabilization	23	0.251994024	0.0004	0.008964341
GO:0048679	regulation of axon regeneration	15	0.251965415	0.007	0.015816335
GO:0071276	cellular response to cadmium ion	20	0.251939435	0.0162	0.022196303
GO:0050775	positive regulation of dendrite morphogenesis	17	0.251825867	< 0.001	< 0.001
GO:0032305	positive regulation of icosanoid secretion	6	0.251784999	0.01	0.017574468
GO:2000193	positive regulation of fatty acid transport	6	0.251784999	0.01	0.017574468
GO:0060444	branching involved in mammary gland duct morphogenesis	8	0.251760649	0.0183	0.023783007
GO:0048714	positive regulation of oligodendrocyte differentiation	9	0.251759443	0.0304	0.034411276
GO:0072659	protein localization to plasma membrane	113	0.251735921	0.0009	0.010729485
GO:0032481	positive regulation of type I interferon production	36	0.251640159	0.0088	0.016916437
GO:0071482	cellular response to light stimulus	47	0.251627441	0.0035	0.01351837
GO:0045844	positive regulation of striated muscle tissue development	28	0.251606659	0.0062	0.015209334
GO:0048636	positive regulation of muscle organ development	28	0.251606659	0.0062	0.015209334
GO:1901863	positive regulation of muscle tissue development	28	0.251606659	0.0062	0.015209334

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0090195	chemokine secretion	9	0.251605677	0.0235	0.028248857
GO:0090196	regulation of chemokine secretion	9	0.251605677	0.0235	0.028248857
GO:0090197	positive regulation of chemokine secretion	9	0.251605677	0.0235	0.028248857
GO:0006865	amino acid transport	57	0.251605146	0.0005	0.009604651
GO:1903306	negative regulation of regulated secretory pathway	11	0.251574159	0.0397	0.042801678
GO:0043650	dicarboxylic acid biosynthetic process	8	0.251548626	0.0075	0.015990044
GO:0046209	nitric oxide metabolic process	29	0.25154122	0.0125	0.019314538
GO:1901617	organic hydroxy compound biosynthetic process	105	0.251532808	0.009	0.016956012
GO:0032196	transposition	7	0.251515074	0.0071	0.01583804
GO:1901888	regulation of cell junction assembly	36	0.251487148	0.003	0.013210967
GO:1903391	regulation of adherens junction organization	30	0.251471635	0.002	0.012314604
GO:1904263	positive regulation of TORC1 signaling	8	0.251463428	0.0099	0.017505138
GO:0060538	skeletal muscle organ development	66	0.251457558	0.0017	0.012001709
GO:0072234	metanephric nephron tubule development	12	0.25145371	0.0217	0.026655917
GO:0045913	positive regulation of carbohydrate metabolic process	29	0.251447119	0.0094	0.017156187
GO:2000279	negative regulation of DNA biosynthetic process	20	0.251424425	0.0012	0.010961137
GO:1990126	retrograde transport, endosome to plasma membrane	8	0.251423907	0.0025	0.012769435
GO:2000045	regulation of G1/S transition of mitotic cell cycle	52	0.251412394	0.0016	0.011845327
GO:0030168	platelet activation	71	0.251410374	0.0033	0.013333753
GO:0043627	response to estrogen	36	0.251394176	0.0018	0.01210186
GO:0060020	Bergmann glial cell differentiation	5	0.251373241	0.0182	0.023684988
GO:1901607	alpha-amino acid biosynthetic process	28	0.251368188	0.0075	0.015990044
GO:0048144	fibroblast proliferation	39	0.251365447	0.0093	0.017114131
GO:0045070	positive regulation of viral genome replication	15	0.251360024	0.0065	0.015491756
GO:0016051	carbohydrate biosynthetic process	91	0.251347676	0.0033	0.013333753
GO:0072273	metanephric nephron morphogenesis	11	0.251345276	0.0105	0.017924712
GO:0006270	DNA replication initiation	10	0.25133981	0.0003	0.007956881
GO:1905037	autophagosome organization	40	0.251315352	0.0026	0.012805111
GO:0048278	vesicle docking	20	0.251302297	0.001	0.010787313
GO:0071359	cellular response to dsRNA	25	0.251284143	0.0089	0.016916437
GO:0050704	regulation of interleukin-1 secretion	17	0.251280265	0.0121	0.018970228
GO:0050766	positive regulation of phagocytosis	20	0.251277807	0.0102	0.0177
GO:0061311	cell surface receptor signaling pathway involved in heart development	13	0.251276436	0.0228	0.027701114
GO:0001954	positive regulation of cell-matrix adhesion	29	0.251269909	0.0038	0.01366393
GO:0032615	interleukin-12 production	15	0.251265864	0.0014	0.011465722
GO:0048247	lymphocyte chemotaxis	9	0.251259414	0.0154	0.021487162
GO:0010867	positive regulation of triglyceride biosynthetic process	7	0.251054145	0.0074	0.015911789
GO:0090208	positive regulation of triglyceride metabolic process	7	0.251054145	0.0074	0.015911789
GO:0032651	regulation of interleukin-1 beta production	30	0.251048172	0.028	0.032186083
GO:0033059	cellular pigmentation	26	0.251002427	0.0062	0.015209334
GO:0009566	fertilization	50	0.250995857	0.0022	0.012422266
GO:0071453	cellular response to oxygen levels	112	0.2509871	0.0066	0.015525305
GO:0071397	cellular response to cholesterol	10	0.250970252	0.0099	0.017505138
GO:1902991	regulation of amyloid precursor protein catabolic process	15	0.25083359	0.0001	0.004220438
GO:0051204	protein insertion into mitochondrial membrane	12	0.250813591	0.006	0.015037711
GO:0044788	modulation by host of viral process	10	0.250810352	0.0158	0.021871104
GO:0016093	polyprenol metabolic process	5	0.250804651	0.0109	0.018225506
GO:0035335	peptidyl-tyrosine dephosphorylation	48	0.250804467	0.0019	0.012288367
GO:0010863	positive regulation of phospholipase C activity	19	0.250735196	0.0089	0.016916437
GO:1900274	regulation of phospholipase C activity	19	0.250735196	0.0089	0.016916437
GO:0060998	regulation of dendritic spine development	29	0.250730505	0.0007	0.010220707
GO:0006925	inflammatory cell apoptotic process	8	0.250711224	0.0038	0.01366393
GO:0048148	behavioral response to cocaine	7	0.250709651	0.0002	0.006319126
GO:0055025	positive regulation of cardiac muscle tissue development	20	0.250671962	0.0102	0.0177
GO:0044843	cell cycle G1/S phase transition	99	0.250663012	0.001	0.010787313
GO:0016241	regulation of macroautophagy	86	0.250608918	0.0039	0.013791927
GO:0016079	synaptic vesicle exocytosis	55	0.250602956	0.0005	0.009604651
GO:0021544	subpallium development	13	0.250590866	0.0046	0.014132412
GO:0097205	renal filtration	10	0.250569077	0.0062	0.015209334
GO:0035272	exocrine system development	22	0.250542478	0.0056	0.014771533
GO:0060294	cilium movement involved in cell motility	5	0.250530462	0.0227	0.027637692
GO:0001763	morphogenesis of a branching structure	69	0.250521411	0.0068	0.015633241
GO:0017156	calcium ion regulated exocytosis	71	0.250502795	0.0007	0.010220707
GO:0071229	cellular response to acid chemical	102	0.250493405	0.001	0.010787313
GO:0001820	serotonin secretion	5	0.250470338	0.0245	0.029070183
GO:0050912	detection of chemical stimulus involved in sensory perception of taste	5	0.250449346	0.0005	0.009604651
GO:0051875	pigment granule localization	12	0.250361794	0.0057	0.01480566
GO:0051966	regulation of synaptic transmission, glutamatergic	25	0.250311423	< 0.001	< 0.001
GO:1901685	glutathione derivative metabolic process	13	0.250295825	0.0194	0.024690909
GO:1901687	glutathione derivative biosynthetic process	13	0.250295825	0.0194	0.024690909
GO:0006399	tRNA metabolic process	71	0.250248072	0.0057	0.01480566
GO:0003382	epithelial cell morphogenesis	12	0.25022023	0.0112	0.018392048
GO:0060134	prepulse inhibition	10	0.25020509	0.0003	0.007956881
GO:0035115	embryonic forelimb morphogenesis	10	0.250194724	0.0167	0.02255007
GO:0060315	negative regulation of ryanodine-sensitive calcium-release channel activity	7	0.25017986	0.012	0.018931514
GO:0050710	negative regulation of cytokine secretion	29	0.250134399	0.009	0.016956012
GO:1903909	regulation of receptor clustering	9	0.250132512	0.0359	0.039290895
GO:0006521	regulation of cellular amino acid metabolic process	46	0.25013167	0.0155	0.021605834
GO:0061081	positive regulation of myeloid leukocyte cytokine production involved in immune response	11	0.250123703	0.0165	0.022405589
GO:0035066	positive regulation of histone acetylation	11	0.250091898	0.0184	0.023875404
GO:0019184	nonribosomal peptide biosynthetic process	10	0.250077974	0.0128	0.019522448
GO:1902074	response to salt	8	0.250033366	0.0032	0.013333753
GO:0006086	acetyl-CoA biosynthetic process from pyruvate	7	0.250031955	0.0174	0.023064374

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0000423	macromitophagy	17	0.250028155	0.0057	0.01480566
GO:0072207	metanephric epithelium development	14	0.25002742	0.022	0.026944291
GO:0007004	telomere maintenance via telomerase	31	0.250025942	0.0067	0.015576759
GO:0030808	regulation of nucleotide biosynthetic process	39	0.250005005	0.0044	0.014132412
GO:1900371	regulation of purine nucleotide biosynthetic process	39	0.250005005	0.0044	0.014132412
GO:0030574	collagen catabolic process	9	0.249967227	0.0023	0.012498684
GO:0044243	multicellular organism catabolic process	9	0.249967227	0.0023	0.012498684
GO:0032801	receptor catabolic process	28	0.249934123	0.0018	0.01210186
GO:0043486	histone exchange	16	0.249891964	0.0042	0.013948535
GO:0090114	COP1-coated vesicle budding	43	0.249886818	0.0041	0.013887639
GO:0007084	mitotic nuclear envelope reassembly	7	0.249864614	0.0094	0.017156187
GO:0006900	membrane budding	70	0.24986354	0.006	0.015037711
GO:0006378	mRNA polyadenylation	13	0.249825256	0.0089	0.016916437
GO:0043631	RNA polyadenylation	13	0.249825256	0.0089	0.016916437
GO:0050709	negative regulation of protein secretion	60	0.249783809	0.0089	0.016916437
GO:0014819	regulation of skeletal muscle contraction	7	0.249723373	0.0185	0.023962142
GO:0032924	activin receptor signaling pathway	11	0.24972201	0.0062	0.015209334
GO:0099531	presynaptic process involved in chemical synaptic transmission	78	0.249707522	0.0008	0.010465158
GO:0032543	mitochondrial translation	71	0.249633176	0.0172	0.022941269
GO:0030534	adult behavior	69	0.249614755	0.001	0.010787313
GO:0031058	positive regulation of histone modification	36	0.249614486	0.0055	0.01475
GO:0036473	cell death in response to oxidative stress	36	0.24961301	0.0066	0.015525305
GO:0060993	kidney morphogenesis	35	0.249601051	0.0092	0.017033109
GO:0006809	nitric oxide biosynthetic process	27	0.249584059	0.0119	0.018881943
GO:1904894	positive regulation of STAT cascade	27	0.249549313	0.005	0.014547706
GO:0007259	JAK-STAT cascade	47	0.249544204	0.0026	0.012805111
GO:0070528	protein kinase C signaling	12	0.249484979	0.0148	0.020979063
GO:0010453	regulation of cell fate commitment	9	0.249453376	0.0041	0.013887639
GO:0001964	startle response	14	0.249404702	< 0.001	< 0.001
GO:1903010	regulation of bone development	12	0.249386175	0.0024	0.012603815
GO:1903307	positive regulation of regulated secretory pathway	28	0.249355185	0.0011	0.010890753
GO:1903861	positive regulation of dendrite extension	15	0.249340672	0.004	0.013824268
GO:0060314	regulation of ryanodine-sensitive calcium-release channel activity	14	0.24933945	0.0111	0.018389742
GO:0035384	thioester biosynthetic process	21	0.249336858	0.0119	0.018881943
GO:0071616	acyl-CoA biosynthetic process	21	0.249336858	0.0119	0.018881943
GO:0035850	epithelial cell differentiation involved in kidney development	17	0.249310747	0.0066	0.015525305
GO:0006563	L-serine metabolic process	6	0.249246123	0.0068	0.015633241
GO:0010675	regulation of cellular carbohydrate metabolic process	55	0.249230436	0.0011	0.010890753
GO:0031032	actomyosin structure organization	64	0.249211514	0.003	0.013210967
GO:0043403	skeletal muscle tissue regeneration	13	0.249196102	0.0058	0.014878261
GO:0061138	morphogenesis of a branching epithelium	68	0.24915632	0.0066	0.015525305
GO:0031639	plasminogen activation	5	0.249140343	0.0323	0.03615849
GO:0048520	positive regulation of behavior	11	0.249117938	0.0013	0.011218806
GO:0001101	response to acid chemical	158	0.249076394	0.0032	0.013333753
GO:0051307	meiotic chromosome separation	5	0.249046788	0.0153	0.021378589
GO:0030091	protein repair	5	0.249042123	0.0205	0.025639412
GO:0046503	glycerolipid catabolic process	22	0.249036834	0.0075	0.015990044
GO:0010640	regulation of platelet-derived growth factor receptor signaling pathway	8	0.249021844	0.008	0.016379603
GO:0070306	lens fiber cell differentiation	16	0.248990502	0.0082	0.016514246
GO:0051438	regulation of ubiquitin-protein transferase activity	21	0.248956021	0.0045	0.014132412
GO:0070374	positive regulation of ERK1 and ERK2 cascade	81	0.248955299	0.014	0.020462083
GO:0034453	microtubule anchoring	8	0.248918829	0.0032	0.013333753
GO:0001505	regulation of neurotransmitter levels	98	0.248877595	0.0012	0.010961137
GO:0045830	positive regulation of isotype switching	11	0.248864789	0.0035	0.01351837
GO:1903076	regulation of protein localization to plasma membrane	43	0.248801432	0.0033	0.013333753
GO:0045069	regulation of viral genome replication	30	0.24879277	0.0044	0.014132412
GO:0007026	negative regulation of microtubule depolymerization	8	0.24878925	0.0062	0.015209334
GO:0031114	regulation of microtubule depolymerization	8	0.24878925	0.0062	0.015209334
GO:0048715	negative regulation of oligodendrocyte differentiation	8	0.248745517	0.0215	0.026489026
GO:0031440	regulation of mRNA 3'-end processing	12	0.248735583	0.0119	0.018881943
GO:1900151	regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	8	0.248729482	0.0074	0.015911789
GO:1900153	positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	8	0.248729482	0.0074	0.015911789
GO:0051341	regulation of oxidoreductase activity	37	0.248718604	0.0061	0.015143924
GO:0014808	release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	14	0.248718306	0.0127	0.019457181
GO:1903514	calcium ion transport from endoplasmic reticulum to cytosol	14	0.248718306	0.0127	0.019457181
GO:0009069	serine family amino acid metabolic process	20	0.248701007	0.0092	0.017033109
GO:1902806	regulation of cell cycle G1/S phase transition	62	0.248683968	0.0019	0.012288367
GO:0007519	skeletal muscle tissue development	61	0.248673644	0.0018	0.01210186
GO:0071478	cellular response to radiation	78	0.24864119	0.0026	0.012805111
GO:0002183	cytoplasmic translational initiation	11	0.248623419	0.0253	0.029811412
GO:1901800	positive regulation of proteasomal protein catabolic process	48	0.248608596	0.0025	0.012769435
GO:0030858	positive regulation of epithelial cell differentiation	19	0.248504331	0.007	0.015816335
GO:0046580	negative regulation of Ras protein signal transduction	17	0.248484112	0.0046	0.014132412
GO:0046532	regulation of photoreceptor cell differentiation	6	0.2484639	0.0112	0.018392048
GO:0046533	negative regulation of photoreceptor cell differentiation	6	0.2484639	0.0112	0.018392048
GO:2000027	regulation of organ morphogenesis	127	0.248457552	0.0073	0.015844069
GO:0016236	macroautophagy	153	0.248430112	0.0039	0.013791927
GO:0002088	lens development in camera-type eye	29	0.248422442	0.0096	0.017302743
GO:0048168	regulation of neuronal synaptic plasticity	29	0.248415025	0.0031	0.013277185
GO:0046513	ceramide biosynthetic process	22	0.248413973	0.0004	0.008964341
GO:0032486	Rap protein signal transduction	9	0.248401054	0.0029	0.013089617
GO:0002011	morphogenesis of an epithelial sheet	21	0.248390256	0.0101	0.017653628
GO:0040036	regulation of fibroblast growth factor receptor signaling pathway	11	0.248370623	0.0109	0.018225506

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0043954	cellular component maintenance	26	0.24834811	0.0004	0.008964341
GO:0031279	regulation of cyclase activity	31	0.248335903	0.0018	0.01210186
GO:0001510	RNA methylation	20	0.248285578	0.0014	0.011465722
GO:0072282	metanephric nephron tubule morphogenesis	5	0.248275536	0.0337	0.03733539
GO:0051904	pigment granule transport	11	0.2482659	0.0037	0.013609033
GO:0051905	establishment of pigment granule localization	11	0.2482659	0.0037	0.013609033
GO:2000095	regulation of Wnt signaling pathway, planar cell polarity pathway	7	0.248256358	0.0473	0.049788567
GO:0014911	positive regulation of smooth muscle cell migration	15	0.248250138	0.0097	0.017363901
GO:0009636	response to toxic substance	82	0.248211369	0.0094	0.017156187
GO:1903531	negative regulation of secretion by cell	92	0.24818616	0.0103	0.017772187
GO:0048145	regulation of fibroblast proliferation	38	0.248175338	0.0091	0.016994897
GO:0035561	regulation of chromatin binding	9	0.248137146	0.0006	0.009940401
GO:0030032	lamellipodium assembly	27	0.248074564	0.0056	0.014771533
GO:0010742	macrophage derived foam cell differentiation	11	0.248060106	0.0058	0.014878261
GO:0090077	foam cell differentiation	11	0.248060106	0.0058	0.014878261
GO:0032957	inositol trisphosphate metabolic process	6	0.248058319	0.0051	0.014547706
GO:0032959	inositol trisphosphate biosynthetic process	6	0.248058319	0.0051	0.014547706
GO:0015800	acidic amino acid transport	13	0.248028898	0.0054	0.014720792
GO:0051385	response to mineralocorticoid	14	0.24802756	0.0301	0.034151923
GO:0002831	regulation of response to biotic stimulus	77	0.247990487	0.0094	0.017156187
GO:0099068	postsynapse assembly	8	0.247987807	0.0011	0.010890753
GO:0042491	auditory receptor cell differentiation	12	0.247930036	0.0227	0.027637692
GO:0071277	cellular response to calcium ion	31	0.247920833	0.0053	0.014634479
GO:0046461	neutral lipid catabolic process	14	0.247910013	0.0168	0.022626974
GO:0046464	acylglycerol catabolic process	14	0.247910013	0.0168	0.022626974
GO:0031053	primary miRNA processing	5	0.24789302	0.0421	0.045028154
GO:0043200	response to amino acid	53	0.24785288	0.0053	0.014634479
GO:0090075	relaxation of muscle	12	0.247802833	0.0189	0.024289798
GO:0048754	branching morphogenesis of an epithelial tube	51	0.24769635	0.0085	0.016693954
GO:0018197	peptidyl-aspartic acid modification	5	0.247678438	0.0029	0.013089617
GO:0009451	RNA modification	51	0.247677498	0.0021	0.012314604
GO:0019054	modulation by virus of host process	15	0.247612871	0.0024	0.012603815
GO:0044068	modulation by symbiont of host cellular process	15	0.247612871	0.0024	0.012603815
GO:2000021	regulation of ion homeostasis	85	0.24759537	0.0026	0.012805111
GO:0033014	tetrapyrrole biosynthetic process	18	0.247566928	0.015	0.021138192
GO:0061136	regulation of proteasomal protein catabolic process	82	0.247542222	0.0034	0.01347416
GO:0002026	regulation of the force of heart contraction	8	0.24750545	0.0168	0.022626974
GO:0001773	myeloid dendritic cell activation	11	0.247498795	0.0377	0.040981651
GO:0050862	positive regulation of T cell receptor signaling pathway	8	0.247489253	0.0045	0.014132412
GO:0043301	negative regulation of leukocyte degranulation	7	0.247479812	0.0427	0.045577146
GO:0040037	negative regulation of fibroblast growth factor receptor signaling pathway	8	0.247448112	0.0166	0.02247277
GO:0032094	response to food	15	0.247446233	0.0149	0.021043429
GO:0050691	regulation of defense response to virus by host	13	0.247368147	0.0206	0.025725529
GO:0006813	potassium ion transport	75	0.247360936	0.0002	0.006319126
GO:0035987	endodermal cell differentiation	18	0.247343765	0.0044	0.014132412
GO:0010827	regulation of glucose transport	31	0.247339736	0.0091	0.016994897
GO:0045980	negative regulation of nucleotide metabolic process	23	0.247274603	0.0044	0.014132412
GO:0006704	glucocorticoid biosynthetic process	7	0.247241758	0.0083	0.016559903
GO:0060159	regulation of dopamine receptor signaling pathway	6	0.247125353	0.0094	0.017156187
GO:0006754	ATP biosynthetic process	23	0.247108292	0.0236	0.028327839
GO:0010976	positive regulation of neuron projection development	119	0.2471079	0.0012	0.010961137
GO:0046329	negative regulation of JNK cascade	18	0.247104909	0.0002	0.006319126
GO:0002526	acute inflammatory response	57	0.247073533	0.0074	0.015911789
GO:0050999	regulation of nitric-oxide synthase activity	20	0.247063717	0.0061	0.015143924
GO:0051193	regulation of cofactor metabolic process	35	0.247024547	0.0046	0.014132412
GO:0042572	retinol metabolic process	15	0.246999964	0.0098	0.017418875
GO:0044839	cell cycle G2/M phase transition	121	0.246988855	0.0077	0.016177834
GO:0006383	transcription from RNA polymerase III promoter	28	0.246987784	0.0033	0.013333753
GO:0051181	cofactor transport	11	0.246985899	0.0123	0.019143634
GO:0051382	kinetochore assembly	8	0.246966565	0.0023	0.012498684
GO:0050777	negative regulation of immune response	56	0.24694618	0.007	0.015816335
GO:0045824	negative regulation of innate immune response	22	0.246919402	0.01	0.017574468
GO:0000768	syncytium formation by plasma membrane fusion	18	0.246899023	0.0143	0.020629391
GO:0000726	non-recombinational repair	29	0.246875855	0.0009	0.010729485
GO:0046849	bone remodeling	35	0.246875458	0.0018	0.01210186
GO:0001952	regulation of cell-matrix adhesion	44	0.246863447	0.002	0.012314604
GO:0001678	cellular glucose homeostasis	60	0.246851295	0.0007	0.010220707
GO:1905517	macrophage migration	23	0.246833585	0.0312	0.035137982
GO:0047484	regulation of response to osmotic stress	7	0.2468247	0.0046	0.014132412
GO:0001754	eye photoreceptor cell differentiation	17	0.246788995	0.0011	0.010890753
GO:0032011	ARF protein signal transduction	10	0.246784346	0.0015	0.011704453
GO:0032012	regulation of ARF protein signal transduction	10	0.246784346	0.0015	0.011704453
GO:0046847	filopodium assembly	33	0.246767147	0.007	0.015816335
GO:0003341	cilium movement	21	0.246718939	0.0139	0.020388077
GO:1903672	positive regulation of sprouting angiogenesis	15	0.246708067	0.0041	0.013887639
GO:2000310	regulation of N-methyl-D-aspartate selective glutamate receptor activity	23	0.246698148	0.0014	0.011465722
GO:0010866	regulation of triglyceride biosynthetic process	10	0.24668768	0.0076	0.016084627
GO:0036465	synaptic vesicle recycling	29	0.246679744	0.0004	0.008964341
GO:0051897	positive regulation of protein kinase B signaling	58	0.246653158	0.0127	0.019457181
GO:0015810	aspartate transport	8	0.246635006	0.0047	0.014168613
GO:0070371	ERK1 and ERK2 cascade	129	0.246619731	0.0114	0.018551872
GO:0034390	smooth muscle cell apoptotic process	14	0.24658609	0.0039	0.013791927
GO:0034391	regulation of smooth muscle cell apoptotic process	14	0.24658609	0.0039	0.013791927

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0033555	multicellular organismal response to stress	37	0.24657772	0.0187	0.024129301
GO:0006700	C21-steroid hormone biosynthetic process	13	0.246563265	0.0283	0.032434212
GO:0048706	embryonic skeletal system development	41	0.246537451	0.0132	0.019860109
GO:0032890	regulation of organic acid transport	20	0.24653387	0.0007	0.010220707
GO:0050808	synapse organization	174	0.246530848	0.0021	0.012314604
GO:0006699	bile acid biosynthetic process	10	0.246496163	0.0168	0.022626974
GO:0010092	specification of animal organ identity	5	0.246462472	0.0291	0.033199724
GO:0060026	convergent extension	9	0.246428868	0.0053	0.014634479
GO:0001706	endoderm formation	20	0.246408956	0.0026	0.012805111
GO:0060384	innervation	10	0.246359069	0.006	0.015037711
GO:1901215	negative regulation of neuron death	95	0.246347829	0.0012	0.010961137
GO:0071333	cellular response to glucose stimulus	57	0.246335685	0.0008	0.010465158
GO:1903729	regulation of plasma membrane organization	51	0.24632579	0.004	0.013824268
GO:0030521	androgen receptor signaling pathway	20	0.246307043	0.0042	0.013948535
GO:0007030	Golgi organization	47	0.246270249	0.0015	0.011704453
GO:0051775	response to redox state	11	0.246249422	0.001	0.010787313
GO:0070169	positive regulation of biomineral tissue development	21	0.246218828	0.016	0.022026667
GO:0043255	regulation of carbohydrate biosynthetic process	38	0.246205845	0.0031	0.013277185
GO:0007528	neuromuscular junction development	18	0.2461903	0.0038	0.01366393
GO:0048678	response to axon injury	36	0.2461885	0.0118	0.018836996
GO:0034143	regulation of toll-like receptor 4 signaling pathway	6	0.246135589	0.0068	0.015633241
GO:0055089	fatty acid homeostasis	6	0.246116368	0.0014	0.011465722
GO:0001776	leukocyte homeostasis	29	0.246107499	0.0031	0.013277185
GO:0070304	positive regulation of stress-activated protein kinase signaling cascade	51	0.246103169	0.0056	0.014771533
GO:0002714	positive regulation of B cell mediated immunity	16	0.246090209	0.0059	0.014942532
GO:0002891	positive regulation of immunoglobulin mediated immune response	16	0.246090209	0.0059	0.014942532
GO:0039528	cytoplasmic pattern recognition receptor signaling pathway in response to virus	11	0.246066951	0.0132	0.019860109
GO:0003091	renal water homeostasis	15	0.245985537	0.0042	0.013948535
GO:0045820	negative regulation of glycolytic process	6	0.245948996	0.0021	0.012314604
GO:0051195	negative regulation of cofactor metabolic process	6	0.245948996	0.0021	0.012314604
GO:0051198	negative regulation of coenzyme metabolic process	6	0.245948996	0.0021	0.012314604
GO:0030199	collagen fibril organization	19	0.245937652	0.0009	0.010729485
GO:0032261	purine nucleotide salvage	5	0.245921352	0.0169	0.022703485
GO:0010880	regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	12	0.245904075	0.0073	0.015844069
GO:0050920	regulation of chemotaxis	72	0.245853593	0.0179	0.02344231
GO:0002062	chondrocyte differentiation	47	0.245851793	0.0121	0.018970228
GO:0090670	RNA localization to Cajal body	12	0.245842093	0.0228	0.027701114
GO:0090671	telomerase RNA localization to Cajal body	12	0.245842093	0.0228	0.027701114
GO:0090672	telomerase RNA localization	12	0.245842093	0.0228	0.027701114
GO:1904872	regulation of telomerase RNA localization to Cajal body	12	0.245842093	0.0228	0.027701114
GO:0050796	regulation of insulin secretion	75	0.245821179	0.0018	0.01210186
GO:0060563	neuroepithelial cell differentiation	19	0.245803504	0.0309	0.034874839
GO:0002260	lymphocyte homeostasis	17	0.245791697	0.0043	0.014102439
GO:1903859	regulation of dendrite extension	16	0.245759865	0.0038	0.01366393
GO:0010324	membrane invagination	28	0.245728743	0.0084	0.016633151
GO:0007605	sensory perception of sound	46	0.245718167	0.0184	0.023875404
GO:0071326	cellular response to monosaccharide stimulus	58	0.245680939	0.0008	0.010465158
GO:0071331	cellular response to hexose stimulus	58	0.245680939	0.0008	0.010465158
GO:0044321	response to leptin	8	0.245680822	0.0204	0.025564109
GO:0007628	adult walking behavior	11	0.245676449	0.0007	0.010220707
GO:0046467	membrane lipid biosynthetic process	57	0.245675449	0.0027	0.012827773
GO:0045576	mast cell activation	27	0.245673857	0.0179	0.02344231
GO:0007599	hemostasis	125	0.245673111	0.0033	0.013333753
GO:0071287	cellular response to manganese ion	6	0.245645782	0.0095	0.01725157
GO:0010522	regulation of calcium ion transport into cytosol	40	0.245625006	0.0049	0.014447629
GO:0009110	vitamin biosynthetic process	8	0.245525976	0.0344	0.037979912
GO:0016322	neuron remodeling	7	0.245478934	0.0216	0.026572596
GO:0031398	positive regulation of protein ubiquitination	56	0.245456559	0.0058	0.014878261
GO:0060028	convergent extension involved in axis elongation	5	0.24545176	0.0132	0.019860109
GO:0019228	neuronal action potential	8	0.245424256	0.0011	0.010890753
GO:0048873	homeostasis of number of cells within a tissue	9	0.245411245	0.0066	0.015525305
GO:0044728	DNA methylation or demethylation	21	0.245382984	0.0056	0.014771533
GO:2000050	regulation of non-canonical Wnt signaling pathway	8	0.245370319	0.0362	0.03958177
GO:1904375	regulation of protein localization to cell periphery	46	0.245359207	0.002	0.012314604
GO:0048813	dendrite morphogenesis	67	0.245310264	0.0006	0.009940401
GO:0061025	membrane fusion	66	0.245298354	0.0027	0.012827773
GO:0071539	protein localization to centrosome	12	0.245285121	0.0019	0.012288367
GO:1905508	protein localization to microtubule organizing center	12	0.245285121	0.0019	0.012288367
GO:0034308	primary alcohol metabolic process	24	0.245250891	0.0068	0.015633241
GO:1902902	negative regulation of autophagosome assembly	10	0.245243397	0.0153	0.021378589
GO:0022612	gland morphogenesis	51	0.245205215	0.0088	0.016916437
GO:1902749	regulation of cell cycle G2/M phase transition	96	0.245175452	0.0105	0.017924712
GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	35	0.245159578	0.0098	0.017418875
GO:0072028	nephron morphogenesis	25	0.245146732	0.0108	0.018152791
GO:0072078	nephron tubule morphogenesis	25	0.245146732	0.0108	0.018152791
GO:0072088	nephron epithelium morphogenesis	25	0.245146732	0.0108	0.018152791
GO:0006560	proline metabolic process	6	0.245125308	0.014	0.020462083
GO:0010565	regulation of cellular ketone metabolic process	97	0.245121786	0.0099	0.017505138
GO:0042554	superoxide anion generation	15	0.245117965	0.0329	0.036702257
GO:0008209	androgen metabolic process	8	0.245094965	0.0211	0.026113057
GO:0097696	STAT cascade	48	0.245083762	0.0035	0.01351837
GO:0051058	negative regulation of small GTPase mediated signal transduction	20	0.245078314	0.0056	0.014771533
GO:0007596	blood coagulation	122	0.245059963	0.0034	0.01347416

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0070509	calcium ion import	76	0.244998889	0.0035	0.01351837
GO:0007190	activation of adenylate cyclase activity	15	0.244997198	0.0001	0.004220438
GO:0060713	labyrinthine layer morphogenesis	8	0.244933802	0.0126	0.019370699
GO:0060009	Sertoli cell development	6	0.2449331	0.0135	0.020081554
GO:0043536	positive regulation of blood vessel endothelial cell migration	24	0.244922787	0.0015	0.011704453
GO:0048490	anterograde synaptic vesicle transport	15	0.244911676	0.0104	0.017832977
GO:0099514	synaptic vesicle cytoskeletal transport	15	0.244911676	0.0104	0.017832977
GO:0099517	synaptic vesicle transport along microtubule	15	0.244911676	0.0104	0.017832977
GO:0090280	positive regulation of calcium ion import	24	0.244902541	0.0047	0.014168613
GO:0031111	negative regulation of microtubule polymerization or depolymerization	16	0.24489096	0.0052	0.014616626
GO:0051592	response to calcium ion	56	0.244863227	0.0073	0.015844069
GO:0002699	positive regulation of immune effector process	71	0.244856965	0.0109	0.018225506
GO:0006729	tetrahydrobiopterin biosynthetic process	5	0.244842999	0.0272	0.031504487
GO:0046146	tetrahydrobiopterin metabolic process	5	0.244842999	0.0272	0.031504487
GO:0032652	regulation of interleukin-1 production	33	0.244842159	0.0264	0.030750363
GO:1903036	positive regulation of response to wounding	23	0.244833512	0.009	0.016956012
GO:0010906	regulation of glucose metabolic process	40	0.244830916	0.0004	0.008964341
GO:0007281	germ cell development	77	0.24479762	0.0029	0.013089617
GO:0051091	positive regulation of sequence-specific DNA binding transcription factor activity	96	0.244797407	0.0053	0.014634479
GO:0007283	spermatogenesis	168	0.244786406	0.0045	0.014132412
GO:0048232	male gamete generation	168	0.244786406	0.0045	0.014132412
GO:0021696	cerebellar cortex morphogenesis	15	0.244764907	0.0036	0.01353394
GO:0023035	CD40 signaling pathway	5	0.244755404	0.0302	0.034245225
GO:0000086	G2/M transition of mitotic cell cycle	113	0.244654911	0.0073	0.015844069
GO:0097479	synaptic vesicle localization	94	0.24458945	0.0011	0.010890753
GO:0032731	positive regulation of interleukin-1 beta production	14	0.244585027	0.0291	0.033199724
GO:0050716	positive regulation of interleukin-1 secretion	10	0.244585008	0.0089	0.016916437
GO:0002639	positive regulation of immunoglobulin production	18	0.244562145	0.0049	0.014447629
GO:0042339	keratan sulfate metabolic process	19	0.244560914	0.0025	0.012769435
GO:0006958	complement activation, classical pathway	13	0.244543932	0.0329	0.036702257
GO:1901379	regulation of potassium ion transmembrane transport	33	0.244521904	0.0007	0.010220707
GO:0009395	phospholipid catabolic process	16	0.244521661	0.0011	0.010890753
GO:0016125	sterol metabolic process	79	0.244508306	0.0062	0.015209334
GO:0042180	cellular ketone metabolic process	134	0.244496075	0.0103	0.017772187
GO:0048489	synaptic vesicle transport	89	0.244459124	0.0011	0.010890753
GO:0097480	establishment of synaptic vesicle localization	89	0.244459124	0.0011	0.010890753
GO:0006491	N-glycan processing	6	0.244450851	0.0122	0.019049527
GO:0019216	regulation of lipid metabolic process	180	0.244435273	0.0049	0.014447629
GO:0043473	pigmentation	44	0.244428342	0.0044	0.014132412
GO:0070302	regulation of stress-activated protein kinase signaling cascade	84	0.244400948	0.0035	0.01351837
GO:0009127	purine nucleoside monophosphate biosynthetic process	37	0.2444001	0.0229	0.027770092
GO:0009168	purine ribonucleoside monophosphate biosynthetic process	37	0.2444001	0.0229	0.027770092
GO:0034332	adherens junction organization	62	0.244382272	0.0017	0.012001709
GO:1901264	carbohydrate derivative transport	24	0.244366193	0.0031	0.013277185
GO:0010818	T cell chemotaxis	6	0.244356259	0.0191	0.02440579
GO:0010833	telomere maintenance via telomere lengthening	37	0.244337097	0.0072	0.015844069
GO:0070125	mitochondrial translational elongation	53	0.244310935	0.0243	0.028921902
GO:0045471	response to ethanol	62	0.244306385	0.0052	0.014616626
GO:0031098	stress-activated protein kinase signaling cascade	116	0.244302972	0.0029	0.013089617
GO:0072171	mesonephric tubule morphogenesis	23	0.24429655	0.0112	0.018392048
GO:0070372	regulation of ERK1 and ERK2 cascade	118	0.244250788	0.0115	0.018599441
GO:0031345	negative regulation of cell projection organization	75	0.244250618	0.0007	0.010220707
GO:0060124	positive regulation of growth hormone secretion	6	0.244244174	< 0.001	< 0.001
GO:1902475	L-alpha-amino acid transmembrane transport	12	0.244199361	0.0211	0.026113057
GO:0055023	positive regulation of cardiac muscle tissue growth	15	0.244189837	0.0119	0.018881943
GO:0060457	negative regulation of digestive system process	7	0.24418611	0.001	0.010787313
GO:0061013	regulation of mRNA catabolic process	16	0.244182651	0.0025	0.012769435
GO:0010812	negative regulation of cell-substrate adhesion	18	0.244171178	0.0021	0.012314604
GO:0031055	chromatin remodeling at centromere	11	0.244168979	0.0139	0.020388077
GO:0034080	CENP-A containing nucleosome assembly	11	0.244168979	0.0139	0.020388077
GO:0061641	CENP-A containing chromatin organization	11	0.244168979	0.0139	0.020388077
GO:0007613	memory	62	0.244140608	0.0023	0.012498684
GO:0008202	steroid metabolic process	130	0.244025219	0.0068	0.015633241
GO:0043405	regulation of MAP kinase activity	153	0.244013778	0.0064	0.015399417
GO:0051238	sequestering of metal ion	52	0.244006704	0.0044	0.014132412
GO:0031343	positive regulation of cell killing	14	0.243997573	0.0172	0.022941269
GO:0001657	ureteric bud development	40	0.243995588	0.0083	0.016559903
GO:0072163	mesonephric epithelium development	40	0.243995588	0.0083	0.016559903
GO:0072164	mesonephric tubule development	40	0.243995588	0.0083	0.016559903
GO:0035024	negative regulation of Rho protein signal transduction	8	0.243994681	0.0001	0.004220438
GO:0060716	labyrinthine layer blood vessel development	10	0.243982079	0.0148	0.020979063
GO:0006940	regulation of smooth muscle contraction	25	0.243975652	0.0069	0.015750415
GO:0042493	response to drug	122	0.243968391	0.0077	0.016177834
GO:0033239	negative regulation of cellular amine metabolic process	5	0.243961865	0.0234	0.02817551
GO:0009247	glycolipid biosynthetic process	28	0.243960597	0.0126	0.019370699
GO:0006012	galactose metabolic process	9	0.243950894	0.0069	0.015750415
GO:0051092	positive regulation of NF-kappaB transcription factor activity	55	0.243897783	0.0061	0.015143924
GO:1903350	response to dopamine	5	0.243861053	0.0204	0.025564109
GO:0050921	positive regulation of chemotaxis	52	0.243801746	0.0199	0.025133639
GO:0045599	negative regulation of fat cell differentiation	18	0.243747816	0.0033	0.013333753
GO:0090501	RNA phosphodiester bond hydrolysis	47	0.243742447	0.0043	0.014102439
GO:1990778	protein localization to cell periphery	126	0.24373637	0.0008	0.010465158
GO:0050817	coagulation	123	0.24367919	0.0035	0.01351837

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0071300	cellular response to retinoic acid	29	0.243673968	0.0031	0.013277185
GO:0006054	N-acetylneuraminate metabolic process	6	0.243658262	0.0427	0.045577146
GO:0010881	regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion	9	0.243637458	0.0161	0.02211694
GO:1903792	negative regulation of anion transport	8	0.243628783	0.0032	0.013333753
GO:0007143	female meiotic division	7	0.243617075	0.0016	0.011845327
GO:2000781	positive regulation of double-strand break repair	11	0.243616267	0.0058	0.014878261
GO:0009743	response to carbohydrate	104	0.243615028	0.0009	0.010729485
GO:0071248	cellular response to metal ion	89	0.243607501	0.0072	0.015844069
GO:0032526	response to retinoic acid	49	0.24358029	0.0048	0.014269203
GO:0034384	high-density lipoprotein particle clearance	5	0.243563281	0.0057	0.01480566
GO:0061333	renal tubule morphogenesis	26	0.243546576	0.013	0.019676963
GO:1900016	negative regulation of cytokine production involved in inflammatory response	7	0.243526925	0.0051	0.014547706
GO:0032869	cellular response to insulin stimulus	84	0.243503771	0.001	0.010787313
GO:0010842	retina layer formation	9	0.243495353	0.0119	0.018881943
GO:0090207	regulation of triglyceride metabolic process	15	0.243491495	0.0089	0.016916437
GO:0060478	acrosomal vesicle exocytosis	5	0.243470762	< 0.001	< 0.001
GO:0007618	mating	20	0.243441801	0.0088	0.016916437
GO:0072243	metanephric nephron epithelium development	13	0.243438128	0.0232	0.028016374
GO:1901020	negative regulation of calcium ion transmembrane transporter activity	13	0.243428161	0.0037	0.013609033
GO:0010661	positive regulation of muscle cell apoptotic process	16	0.243405989	0.0003	0.007956881
GO:0050690	regulation of defense response to virus by virus	19	0.243405755	0.0087	0.016840777
GO:0051196	regulation of coenzyme metabolic process	34	0.243405013	0.0046	0.014132412
GO:0048013	ephrin receptor signaling pathway	53	0.243382932	0.0011	0.010890753
GO:0060218	hematopoietic stem cell differentiation	42	0.243376984	0.0198	0.025062084
GO:0042445	hormone metabolic process	70	0.243373856	0.0099	0.017505138
GO:0045742	positive regulation of epidermal growth factor receptor signaling pathway	11	0.243326954	< 0.001	< 0.001
GO:1901186	positive regulation of ERBB signaling pathway	11	0.243326954	< 0.001	< 0.001
GO:0043331	response to dsRNA	36	0.243300662	0.007	0.015816335
GO:1904353	regulation of telomere capping	15	0.243297559	0.0023	0.012498684
GO:0006631	fatty acid metabolic process	161	0.243296951	0.0106	0.018010344
GO:0002562	somatic diversification of immune receptors via germline recombination within a single locus	20	0.243280735	0.0003	0.007956881
GO:0016444	somatic cell DNA recombination	20	0.243280735	0.0003	0.007956881
GO:1902837	amino acid import into cell	8	0.243270175	0.0055	0.01475
GO:0045739	positive regulation of DNA repair	25	0.243264007	0.0022	0.012422266
GO:0032210	regulation of telomere maintenance via telomerase	26	0.243230603	0.0051	0.014547706
GO:0046622	positive regulation of organ growth	21	0.243223835	0.0115	0.018599441
GO:1990138	neuron projection extension	80	0.243208398	0.0013	0.011218806
GO:0008203	cholesterol metabolic process	75	0.243180178	0.0064	0.015399417
GO:0010389	regulation of G2/M transition of mitotic cell cycle	90	0.24317839	0.0095	0.01725157
GO:0021587	cerebellum morphogenesis	17	0.243141587	0.0053	0.014634479
GO:0003014	renal system process	48	0.243132389	0.0024	0.012603815
GO:0010544	negative regulation of platelet activation	10	0.243126213	0.0398	0.042885501
GO:0051155	positive regulation of striated muscle cell differentiation	23	0.243113497	0.003	0.013210967
GO:0099558	maintenance of synapse structure	11	0.243090649	0.004	0.013824268
GO:0051926	negative regulation of calcium ion transport	21	0.243085494	0.0087	0.016840777
GO:0060837	blood vessel endothelial cell differentiation	6	0.243078182	0.0193	0.024606968
GO:0006244	pyrimidine nucleotide catabolic process	6	0.243055074	0.0034	0.01347416
GO:0009223	pyrimidine deoxyribonucleotide catabolic process	6	0.243055074	0.0034	0.01347416
GO:0006004	fucose metabolic process	9	0.243042404	0.014	0.020462083
GO:0006771	riboflavin metabolic process	7	0.24299917	0.0126	0.019370699
GO:0048704	embryonic skeletal system morphogenesis	28	0.242992321	0.0133	0.019917275
GO:0070584	mitochondrion morphogenesis	11	0.242939396	0.0175	0.023154462
GO:0001676	long-chain fatty acid metabolic process	48	0.242926926	0.0081	0.016514175
GO:1903305	regulation of regulated secretory pathway	77	0.242925226	0.0024	0.012603815
GO:0008306	associative learning	38	0.242913936	0.0052	0.014616626
GO:0007202	activation of phospholipase C activity	13	0.2428935	0.0037	0.013609033
GO:0072073	kidney epithelium development	57	0.242888418	0.0061	0.015143924
GO:0033238	regulation of cellular amine metabolic process	57	0.242865276	0.0177	0.02329117
GO:0051896	regulation of protein kinase B signaling	82	0.242865194	0.0073	0.015844069
GO:0072507	divalent inorganic cation homeostasis	177	0.242853488	0.0027	0.012827773
GO:0070257	positive regulation of mucus secretion	5	0.242844379	0.0008	0.010465158
GO:0010839	negative regulation of keratinocyte proliferation	7	0.242827941	0.0148	0.020979063
GO:2000379	positive regulation of reactive oxygen species metabolic process	38	0.242801987	0.0181	0.023607986
GO:0019433	triglyceride catabolic process	11	0.2428011	0.0228	0.027701114
GO:0009396	folic acid-containing compound biosynthetic process	5	0.242745381	0.0163	0.022248961
GO:0006909	phagocytosis	118	0.242734169	0.0048	0.014269203
GO:0050954	sensory perception of mechanical stimulus	53	0.24271817	0.0167	0.02255007
GO:0090141	positive regulation of mitochondrial fission	10	0.242713635	0.0135	0.020081554
GO:0050702	interleukin-1 beta secretion	18	0.24270658	0.0278	0.032045375
GO:0071867	response to monoamine	14	0.242692347	0.0078	0.01620539
GO:0071869	response to catecholamine	14	0.242692347	0.0078	0.01620539
GO:0036294	cellular response to decreased oxygen levels	104	0.242657255	0.0078	0.01620539
GO:0061003	positive regulation of dendritic spine morphogenesis	9	0.242629912	0.0022	0.012422266
GO:0072080	nephron tubule development	34	0.242575481	0.0111	0.018389742
GO:0034644	cellular response to UV	33	0.242567859	0.0079	0.016296604
GO:0034315	regulation of Arp2/3 complex-mediated actin nucleation	10	0.242559177	0.0007	0.010220707
GO:0007492	endoderm development	27	0.242531673	0.0045	0.014132412
GO:0001973	adenosine receptor signaling pathway	8	0.242516675	0.01	0.017574468
GO:0032611	interleukin-1 beta production	33	0.242498436	0.0339	0.037513837
GO:0016050	vesicle organization	150	0.242485732	0.0033	0.013333753
GO:0090276	regulation of peptide hormone secretion	87	0.242478554	0.0015	0.011704453
GO:0060326	cell chemotaxis	91	0.24245457	0.0115	0.018599441
GO:0042220	response to cocaine	24	0.24243963	0.0034	0.01347416

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0032872	regulation of stress-activated MAPK cascade	82	0.242438817	0.0035	0.01351837
GO:0071868	cellular response to monoamine stimulus	13	0.242423628	0.0062	0.015209334
GO:0071870	cellular response to catecholamine stimulus	13	0.242423628	0.0062	0.015209334
GO:0002689	negative regulation of leukocyte chemotaxis	5	0.242408477	0.0373	0.040638515
GO:0034470	ncRNA processing	132	0.242394066	0.0062	0.015209334
GO:0050890	cognition	142	0.242387389	0.0043	0.014102439
GO:0071353	cellular response to interleukin-4	12	0.24236928	0.0033	0.013333753
GO:1903802	L-glutamate(1-) import into cell	7	0.242368678	0.0055	0.01475
GO:1990123	L-glutamate import into cell	7	0.242368678	0.0055	0.01475
GO:0006720	isoprenoid metabolic process	58	0.24234228	0.0062	0.015209334
GO:0090201	negative regulation of release of cytochrome c from mitochondria	11	0.242307524	0.0226	0.027544941
GO:0010595	positive regulation of endothelial cell migration	48	0.242302897	0.0042	0.013948535
GO:0070444	oligodendrocyte progenitor proliferation	5	0.242283045	0.0072	0.015844069
GO:0070445	regulation of oligodendrocyte progenitor proliferation	5	0.242283045	0.0072	0.015844069
GO:0050708	regulation of protein secretion	196	0.242268578	0.005	0.014547706
GO:0072503	cellular divalent inorganic cation homeostasis	170	0.242215832	0.0027	0.012827773
GO:0034104	negative regulation of tissue remodeling	12	0.242206766	< 0.001	< 0.001
GO:0051289	protein homotetramerization	44	0.242204744	0.0015	0.011704453
GO:0044106	cellular amine metabolic process	76	0.242164494	0.0153	0.021378589
GO:0051567	histone H3-K9 methylation	12	0.242098568	0.0042	0.013948535
GO:0006836	neurotransmitter transport	92	0.242089263	0.001	0.010787313
GO:0070126	mitochondrial translational termination	54	0.242058231	0.0241	0.028760826
GO:0044262	cellular carbohydrate metabolic process	107	0.242034927	0.0028	0.012972436
GO:0009311	oligosaccharide metabolic process	19	0.242033722	0.004	0.013824268
GO:0099024	plasma membrane invagination	22	0.242030814	0.0085	0.016693954
GO:0042723	thiamine-containing compound metabolic process	5	0.242014299	0.0032	0.013333753
GO:0008088	axo-dendritic transport	36	0.241979968	0.004	0.013824268
GO:0023061	signal release	195	0.241971239	0.001	0.010787313
GO:0051282	regulation of sequestering of calcium ion	45	0.241940295	0.0047	0.014168613
GO:0055074	calcium ion homeostasis	169	0.241934526	0.0027	0.012827773
GO:0007431	salivary gland development	17	0.241928274	0.0098	0.017418875
GO:0051452	intracellular pH reduction	22	0.241918788	0.0104	0.017832977
GO:0031346	positive regulation of cell projection organization	162	0.241897018	0.0013	0.011218806
GO:0008053	mitochondrial fusion	14	0.241896086	0.0084	0.016633151
GO:0051403	stress-activated MAPK cascade	111	0.241866126	0.0033	0.013333753
GO:0006261	DNA-dependent DNA replication	47	0.241861435	0.0018	0.01210186
GO:0045651	positive regulation of macrophage differentiation	5	0.241829002	0.0175	0.023154462
GO:0001913	T cell mediated cytotoxicity	11	0.241797337	0.0112	0.018392048
GO:0061337	cardiac conduction	61	0.241792193	0.0021	0.012314604
GO:0001508	action potential	49	0.241790546	0.0032	0.013333753
GO:0003149	membranous septum morphogenesis	7	0.241784649	0.0053	0.014634479
GO:0045773	positive regulation of axon extension	20	0.241784621	0.0014	0.011465722
GO:0006874	cellular calcium ion homeostasis	165	0.241762673	0.0027	0.012827773
GO:0061154	endothelial tube morphogenesis	7	0.241753735	0.0106	0.018010344
GO:0045920	negative regulation of exocytosis	16	0.241748355	0.0365	0.039857035
GO:0072698	protein localization to microtubule cytoskeleton	16	0.241745683	0.0042	0.013948535
GO:0090102	cochlea development	24	0.241743199	0.0184	0.023875404
GO:1905269	positive regulation of chromatin organization	39	0.241739752	0.0051	0.014547706
GO:0032874	positive regulation of stress-activated MAPK cascade	50	0.241735601	0.006	0.015037711
GO:0051956	negative regulation of amino acid transport	5	0.24173415	0.0117	0.018739446
GO:0072593	reactive oxygen species metabolic process	107	0.241717726	0.0103	0.017772187
GO:0002279	mast cell activation involved in immune response	22	0.241671528	0.0185	0.023962142
GO:0043303	mast cell degranulation	22	0.241671528	0.0185	0.023962142
GO:0060688	regulation of morphogenesis of a branching structure	22	0.241642609	0.01	0.017574468
GO:1901990	regulation of mitotic cell cycle phase transition	181	0.241642009	0.0044	0.014132412
GO:0032436	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	36	0.241638636	0.0014	0.011465722
GO:2000047	regulation of cell-cell adhesion mediated by cadherin	6	0.2416377	0.0175	0.023154462
GO:0042178	xenobiotic catabolic process	7	0.241567882	0.0269	0.031225818
GO:0042116	macrophage activation	35	0.241558368	0.0267	0.031037274
GO:0006779	porphyrin-containing compound biosynthetic process	16	0.241520459	0.0126	0.019370699
GO:0045730	respiratory burst	16	0.241508797	0.0226	0.027544941
GO:0098814	spontaneous synaptic transmission	5	0.241492356	0.0027	0.012827773
GO:0010883	regulation of lipid storage	15	0.241479831	0.0024	0.012603815
GO:0030799	regulation of cyclic nucleotide metabolic process	30	0.241474691	0.0019	0.012288367
GO:0030802	regulation of cyclic nucleotide biosynthetic process	30	0.241474691	0.0019	0.012288367
GO:0071456	cellular response to hypoxia	100	0.241464368	0.0092	0.017033109
GO:0061326	renal tubule development	35	0.241460258	0.0122	0.019049527
GO:0003159	morphogenesis of an endothelium	9	0.241431886	0.018	0.023514686
GO:0071230	cellular response to amino acid stimulus	36	0.241430267	0.0011	0.010890753
GO:0001914	regulation of T cell mediated cytotoxicity	7	0.241426086	0.0147	0.02091937
GO:1901214	regulation of neuron death	145	0.241415941	0.0021	0.012314604
GO:0042987	amyloid precursor protein catabolic process	23	0.241414497	0.0007	0.010220707
GO:0006109	regulation of carbohydrate metabolic process	79	0.241388841	0.0017	0.012001709
GO:0042304	regulation of fatty acid biosynthetic process	18	0.24138675	0.0082	0.016514246
GO:0051607	defense response to virus	105	0.241370417	0.0046	0.014132412
GO:0060539	diaphragm development	5	0.241362	0.0045	0.014132412
GO:2001022	positive regulation of response to DNA damage stimulus	31	0.241344888	0.0028	0.012972436
GO:0007435	salivary gland morphogenesis	16	0.241320665	0.0098	0.017418875
GO:0021549	cerebellum development	42	0.241317179	0.005	0.014547706
GO:1903322	positive regulation of protein modification by small protein conjugation or removal	62	0.241315461	0.005	0.014547706
GO:0035418	protein localization to synapse	30	0.241298637	0.0001	0.004220438
GO:0007188	adenylate cyclase-modulating G-protein coupled receptor signaling pathway	66	0.241295633	0.0026	0.012805111
GO:0009308	amine metabolic process	77	0.241260175	0.0154	0.021487162

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0038127	ERBB signaling pathway	60	0.241248554	0.0005	0.009604651
GO:0002832	negative regulation of response to biotic stimulus	22	0.24124386	0.0072	0.015844069
GO:0000963	mitochondrial RNA processing	6	0.24123903	0.0206	0.025725529
GO:0034333	adherens junction assembly	41	0.241226531	0.0008	0.010465158
GO:0006687	glycosphingolipid metabolic process	37	0.241221607	0.0023	0.012498684
GO:0051048	negative regulation of secretion	102	0.241209583	0.0103	0.017772187
GO:0032844	regulation of homeostatic process	193	0.241205927	0.0036	0.01353394
GO:0043491	protein kinase B signaling	95	0.241149873	0.0054	0.014720792
GO:0046578	regulation of Ras protein signal transduction	101	0.241142405	0.0029	0.013089617
GO:1904837	beta-catenin-TCF complex assembly	11	0.24111328	0.0036	0.01353394
GO:0060193	positive regulation of lipase activity	28	0.241059795	0.01	0.017574468
GO:0000731	DNA synthesis involved in DNA repair	18	0.241019539	0.0213	0.026276211
GO:0031115	negative regulation of microtubule polymerization	8	0.240992669	0.0071	0.01583804
GO:0050688	regulation of defense response to virus	46	0.240990099	0.0097	0.017363901
GO:0007204	positive regulation of cytosolic calcium ion concentration	115	0.240954955	0.0024	0.012603815
GO:0042594	response to starvation	83	0.240948845	0.0016	0.011845327
GO:1904874	positive regulation of telomerase RNA localization to Cajal body	10	0.240936594	0.0362	0.03958177
GO:0071241	cellular response to inorganic substance	99	0.240925404	0.0066	0.015525305
GO:0002637	regulation of immunoglobulin production	27	0.240903302	0.0019	0.012288367
GO:1901987	regulation of cell cycle phase transition	197	0.240895782	0.0047	0.014168613
GO:0030641	regulation of cellular pH	28	0.240884078	0.0084	0.016633151
GO:0031145	anaphase-promoting complex-dependent catabolic process	51	0.240883388	0.0097	0.017363901
GO:0061383	trabecula morphogenesis	20	0.24082872	0.0086	0.016782045
GO:0051346	negative regulation of hydrolase activity	149	0.240826627	0.0047	0.014168613
GO:0032201	telomere maintenance via semi-conservative replication	9	0.240821715	0.0131	0.019786886
GO:1903052	positive regulation of proteolysis involved in cellular protein catabolic process	57	0.240819616	0.0031	0.013277185
GO:0042475	odontogenesis of dentin-containing tooth	28	0.240798	0.0031	0.013277185
GO:1901216	positive regulation of neuron death	46	0.240794829	0.0067	0.015576759
GO:0070202	regulation of establishment of protein localization to chromosome	7	0.240768938	0.0356	0.03903645
GO:0070203	regulation of establishment of protein localization to telomere	7	0.240768938	0.0356	0.03903645
GO:0072009	nephron epithelium development	40	0.240712293	0.0101	0.017653628
GO:0021681	cerebellar granular layer development	7	0.240691746	0.0261	0.030517735
GO:0051100	negative regulation of binding	76	0.240679132	0.0037	0.013609033
GO:0050982	detection of mechanical stimulus	14	0.240641395	0.0281	0.032268957
GO:0008347	glial cell migration	27	0.240592025	0.0173	0.023005658
GO:0010977	negative regulation of neuron projection development	66	0.240588153	0.0006	0.009940401
GO:0042446	hormone biosynthetic process	30	0.24055762	0.0143	0.020629391
GO:0060316	positive regulation of ryanodine-sensitive calcium-release channel activity	5	0.240538399	0.0187	0.024129301
GO:0051650	establishment of vesicle localization	158	0.240528743	0.0019	0.012288367
GO:0051260	protein homooligomerization	160	0.240491718	0.0012	0.010961137
GO:0046697	decidualization	10	0.240489159	0.0007	0.010220707
GO:0050727	regulation of inflammatory response	141	0.240480329	0.0036	0.01353394
GO:0060675	ureteric bud morphogenesis	22	0.240447541	0.0096	0.017302743
GO:0051648	vesicle localization	166	0.240443894	0.0025	0.012769435
GO:0001836	release of cytochrome c from mitochondria	33	0.240443555	0.0088	0.016916437
GO:0009062	fatty acid catabolic process	46	0.240442573	0.017	0.022784886
GO:0043243	positive regulation of protein complex disassembly	14	0.240435828	0.0131	0.019786886
GO:0098930	axonal transport	31	0.240401221	0.0067	0.015576759
GO:0010817	regulation of hormone levels	195	0.240381018	0.0039	0.013791927
GO:0019395	fatty acid oxidation	49	0.24032882	0.0166	0.02247277
GO:0021575	hindbrain morphogenesis	18	0.240328597	0.0083	0.016559903
GO:0030177	positive regulation of Wnt signaling pathway	80	0.240327235	0.0133	0.019917275
GO:1903358	regulation of Golgi organization	10	0.240324724	0.0029	0.013089617
GO:0045746	negative regulation of Notch signaling pathway	20	0.240283518	0.0006	0.009940401
GO:0003071	renal system process involved in regulation of systemic arterial blood pressure	8	0.24025893	0.0103	0.017772187
GO:0000045	autophagosome assembly	38	0.240258768	0.0026	0.012805111
GO:0090263	positive regulation of canonical Wnt signaling pathway	69	0.240245792	0.0117	0.018739446
GO:0033500	carbohydrate homeostasis	87	0.240235474	0.0006	0.009940401
GO:0042593	glucose homeostasis	87	0.240235474	0.0006	0.009940401
GO:0001823	mesonephros development	41	0.240231399	0.0096	0.017302743
GO:0070646	protein modification by small protein removal	128	0.240135061	0.0053	0.014634479
GO:0090184	positive regulation of kidney development	15	0.240125734	0.014	0.020462083
GO:0007216	G-protein coupled glutamate receptor signaling pathway	6	0.240118608	0.0129	0.019597425
GO:0060560	developmental growth involved in morphogenesis	108	0.240111121	0.0016	0.011845327
GO:0032026	response to magnesium ion	8	0.240085781	0.0046	0.014132412
GO:0031669	cellular response to nutrient levels	86	0.240076711	0.0034	0.01347416
GO:1990089	response to nerve growth factor	26	0.240075714	0.0009	0.010729485
GO:0003254	regulation of membrane depolarization	22	0.240072411	0.0025	0.012769435
GO:0046479	glycosphingolipid catabolic process	6	0.240069152	0.0036	0.01353394
GO:0046514	ceramide catabolic process	6	0.240069152	0.0036	0.01353394
GO:0009410	response to xenobiotic stimulus	45	0.240062788	0.009	0.016956012
GO:0051645	Golgi localization	8	0.240058893	0.0147	0.02091937
GO:0030316	osteoclast differentiation	40	0.240058246	0.0066	0.015525305
GO:1902652	secondary alcohol metabolic process	77	0.240057215	0.0073	0.015844069
GO:0071214	cellular response to abiotic stimulus	140	0.240054395	0.0025	0.012769435
GO:0021695	cerebellar cortex development	21	0.240034906	0.0038	0.01366393
GO:0035640	exploration behavior	13	0.240014363	0.0043	0.014102439
GO:0016053	organic acid biosynthetic process	137	0.240007291	0.0074	0.015911789
GO:0046394	carboxylic acid biosynthetic process	137	0.240007291	0.0074	0.015911789
GO:0098876	vesicle-mediated transport to the plasma membrane	30	0.239994212	0.0003	0.007956881
GO:0051388	positive regulation of neurotrophin TRK receptor signaling pathway	5	0.23994778	0.0007	0.010220707
GO:0014066	regulation of phosphatidylinositol 3-kinase signaling	52	0.239919223	0.0053	0.014634479
GO:1904950	negative regulation of establishment of protein localization	98	0.239915517	0.0079	0.01629604

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0015850	organic hydroxy compound transport	86	0.239912221	0.0097	0.017363901
GO:0070920	regulation of production of small RNA involved in gene silencing by RNA	5	0.23990165	0.0073	0.015844069
GO:1903798	regulation of production of miRNAs involved in gene silencing by miRNA	5	0.23990165	0.0073	0.015844069
GO:0090520	sphingolipid mediated signaling pathway	6	0.239901348	0.005	0.014547706
GO:0002791	regulation of peptide secretion	89	0.239880981	0.0014	0.011465722
GO:0090087	regulation of peptide transport	89	0.239880981	0.0014	0.011465722
GO:0002706	regulation of lymphocyte mediated immunity	34	0.239870681	0.0042	0.013948535
GO:0019882	antigen processing and presentation	129	0.239844639	0.0145	0.020788247
GO:0045214	sarcomere organization	12	0.23983591	0.0105	0.017924712
GO:0051928	positive regulation of calcium ion transport	48	0.239828028	0.0044	0.014132412
GO:0030073	insulin secretion	89	0.239815566	0.0015	0.011704453
GO:0001818	negative regulation of cytokine production	122	0.239811818	0.0081	0.016514175
GO:0060216	definitive hemopoiesis	6	0.239756004	0.0311	0.035052671
GO:0032846	positive regulation of homeostatic process	96	0.239747891	0.0049	0.014447629
GO:0070988	demethylation	16	0.239736648	0.0027	0.012827773
GO:0048008	platelet-derived growth factor receptor signaling pathway	25	0.239733353	0.0096	0.017302743
GO:0010656	negative regulation of muscle cell apoptotic process	18	0.23970554	0.0028	0.012972436
GO:0018107	peptidyl-threonine phosphorylation	45	0.239664723	< 0.001	< 0.001
GO:0051054	positive regulation of DNA metabolic process	101	0.239640101	0.0024	0.012603815
GO:0006458	'de novo' protein folding	14	0.239631238	0.0052	0.014616626
GO:0032655	regulation of interleukin-12 production	14	0.239614115	0.0014	0.011465722
GO:0044091	membrane biogenesis	20	0.239610552	0.0031	0.013277185
GO:0061005	cell differentiation involved in kidney development	23	0.239579889	0.0143	0.020629391
GO:0099003	vesicle-mediated transport in synapse	95	0.239577431	0.0008	0.010465158
GO:0003333	amino acid transmembrane transport	20	0.239570771	0.0109	0.018225506
GO:1904031	positive regulation of cyclin-dependent protein kinase activity	12	0.239562931	0.0092	0.017033109
GO:0006939	smooth muscle contraction	47	0.2395406	0.0026	0.012805111
GO:0006782	protoporphyrinogen IX biosynthetic process	5	0.239534683	0.0331	0.03684717
GO:0006085	acetyl-CoA biosynthetic process	9	0.239509948	0.0118	0.018836996
GO:0072595	maintenance of protein localization in organelle	13	0.239478008	0.0023	0.012498684
GO:0007617	mating behavior	12	0.239429574	0.0029	0.013089617
GO:1905516	positive regulation of fertilization	6	0.239426442	0.0033	0.013333753
GO:1904356	regulation of telomere maintenance via telomere lengthening	30	0.23941979	0.0041	0.013887639
GO:0007611	learning or memory	129	0.239405709	0.0036	0.01353394
GO:1902036	regulation of hematopoietic stem cell differentiation	41	0.239397008	0.021	0.026005997
GO:0034199	activation of protein kinase A activity	7	0.239394664	0.0001	0.004220438
GO:0042492	gamma-delta T cell differentiation	5	0.23935742	0.0289	0.033004108
GO:0051208	sequestering of calcium ion	47	0.239330214	0.0058	0.014878261
GO:1901985	positive regulation of protein acetylation	16	0.239323697	0.0141	0.020504577
GO:0045778	positive regulation of ossification	45	0.23930435	0.0111	0.018389742
GO:0009615	response to virus	141	0.239296744	0.0065	0.015491756
GO:0001894	tissue homeostasis	74	0.239259105	0.0035	0.01351837
GO:0051188	cofactor biosynthetic process	88	0.239253857	0.0076	0.016084627
GO:1903170	negative regulation of calcium ion transmembrane transport	16	0.239251295	0.0091	0.016994897
GO:0006278	RNA-dependent DNA biosynthetic process	33	0.239244914	0.0079	0.01629604
GO:0099504	synaptic vesicle cycle	81	0.239234762	0.0009	0.010729485
GO:0006400	tRNA modification	27	0.239229819	0.0082	0.016514246
GO:0097306	cellular response to alcohol	25	0.239218408	0.0147	0.02091937
GO:0019884	antigen processing and presentation of exogenous antigen	106	0.239200869	0.0153	0.021378589
GO:0048546	digestive tract morphogenesis	20	0.239191365	0.0084	0.016633151
GO:0048265	response to pain	14	0.239183729	0.0218	0.026744664
GO:0007140	male meiosis	11	0.239153699	0.0138	0.020339434
GO:0071804	cellular potassium ion transport	59	0.239152167	0.0006	0.009940401
GO:0071805	potassium ion transmembrane transport	59	0.239152167	0.0006	0.009940401
GO:0051224	negative regulation of protein transport	95	0.239141351	0.0081	0.016514175
GO:0051788	response to misfolded protein	11	0.239118006	0.0116	0.018682786
GO:0055094	response to lipoprotein particle	10	0.239076753	0.0066	0.015525305
GO:0055098	response to low-density lipoprotein particle	10	0.239076753	0.0066	0.015525305
GO:0071402	cellular response to lipoprotein particle stimulus	10	0.239076753	0.0066	0.015525305
GO:0071404	cellular response to low-density lipoprotein particle stimulus	10	0.239076753	0.0066	0.015525305
GO:0006739	NADP metabolic process	14	0.239058871	0.0124	0.019242297
GO:0051209	release of sequestered calcium ion into cytosol	44	0.239050419	0.0052	0.014616626
GO:0051283	negative regulation of sequestering of calcium ion	44	0.239050419	0.0052	0.014616626
GO:0051353	positive regulation of oxidoreductase activity	24	0.239021617	0.0043	0.014102439
GO:0070507	regulation of microtubule cytoskeleton organization	62	0.239016507	0.0024	0.012603815
GO:0045666	positive regulation of neuron differentiation	152	0.239003433	0.0013	0.011218806
GO:0032720	negative regulation of tumor necrosis factor production	28	0.23897844	0.0096	0.017302743
GO:1903556	negative regulation of tumor necrosis factor superfamily cytokine production	28	0.23897844	0.0096	0.017302743
GO:1903147	negative regulation of mitophagy	7	0.238960576	0.0163	0.022248961
GO:0014009	glial cell proliferation	27	0.238954584	0.0144	0.020727211
GO:0043279	response to alkaloid	68	0.238948958	0.0055	0.01475
GO:0036124	histone H3-K9 trimethylation	5	0.238937067	0.0316	0.035498582
GO:0090030	regulation of steroid hormone biosynthetic process	6	0.238920654	0.0357	0.03911643
GO:0001701	in utero embryonic development	156	0.238919366	0.0031	0.013277185
GO:0030111	regulation of Wnt signaling pathway	168	0.238895903	0.0063	0.015311728
GO:0060491	regulation of cell projection assembly	68	0.238886912	0.0015	0.011704453
GO:0010719	negative regulation of epithelial to mesenchymal transition	13	0.238885634	0.0091	0.016994897
GO:0042254	ribosome biogenesis	97	0.23887865	0.0052	0.014616626
GO:0042246	tissue regeneration	22	0.238877166	0.0169	0.022703485
GO:0006635	fatty acid beta-oxidation	37	0.238875114	0.0224	0.027324219
GO:0009267	cellular response to starvation	66	0.238870334	0.0014	0.011465722
GO:0045454	cell redox homeostasis	29	0.238860571	0.0089	0.016916437
GO:0032103	positive regulation of response to external stimulus	121	0.238845773	0.01	0.017574468

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0030336	negative regulation of cell migration	123	0.238818097	0.0037	0.013609033
GO:0090659	walking behavior	12	0.238811052	0.0007	0.010220707
GO:0001711	endodermal cell fate commitment	5	0.238797122	0.027	0.031323034
GO:0070987	error-free translesion synthesis	9	0.238731181	0.0369	0.040233038
GO:0014812	muscle cell migration	31	0.238720086	0.007	0.015816335
GO:0015711	organic anion transport	172	0.238684848	0.0031	0.013277185
GO:0030816	positive regulation of cAMP metabolic process	19	0.238683775	0.0007	0.010220707
GO:0030819	positive regulation of cAMP biosynthetic process	19	0.238683775	0.0007	0.010220707
GO:0045762	positive regulation of adenylate cyclase activity	19	0.238683775	0.0007	0.010220707
GO:0048871	multicellular organismal homeostasis	124	0.23866863	0.0018	0.01210186
GO:0044331	cell-cell adhesion mediated by cadherin	7	0.238662545	0.0164	0.022306469
GO:0002093	auditory receptor cell morphogenesis	5	0.238660805	0.0163	0.022248961
GO:0060088	auditory receptor cell stereocilium organization	5	0.238660805	0.0163	0.022248961
GO:0048644	muscle organ morphogenesis	29	0.23859985	0.0164	0.022306469
GO:0002688	regulation of leukocyte chemotaxis	34	0.238597914	0.0139	0.020388077
GO:0071260	cellular response to mechanical stimulus	35	0.238552552	0.0104	0.017832977
GO:0060628	regulation of ER to Golgi vesicle-mediated transport	8	0.23850557	0.0089	0.016916437
GO:0050707	regulation of cytokine secretion	74	0.238493033	0.0162	0.022196303
GO:0032612	interleukin-1 production	37	0.238481931	0.0314	0.035301342
GO:0007032	endosome organization	40	0.238470325	0.0025	0.012769435
GO:2000146	negative regulation of cell motility	129	0.238465732	0.0038	0.01366393
GO:0034103	regulation of tissue remodeling	29	0.238464597	0.0057	0.01480566
GO:2001257	regulation of cation channel activity	73	0.238453224	0.0012	0.010961137
GO:0002478	antigen processing and presentation of exogenous peptide antigen	105	0.238451801	0.0153	0.021378589
GO:0097305	response to alcohol	85	0.238446467	0.0087	0.016840777
GO:0045124	regulation of bone resorption	15	0.238413397	0.0021	0.012314604
GO:0048167	regulation of synaptic plasticity	101	0.238404999	0.0009	0.010729485
GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling	82	0.238402034	0.0041	0.013887639
GO:0019319	hexose biosynthetic process	41	0.238393722	0.0066	0.015525305
GO:0050773	regulation of dendrite development	62	0.23834738	0.0004	0.008964341
GO:0006081	cellular aldehyde metabolic process	39	0.238336188	0.0091	0.016994897
GO:0015849	organic acid transport	122	0.238320719	0.0035	0.01351837
GO:0046942	carboxylic acid transport	122	0.238320719	0.0035	0.01351837
GO:0002673	regulation of acute inflammatory response	38	0.238316079	0.0169	0.022703485
GO:0070979	protein K11-linked ubiquitination	17	0.238301979	0.0025	0.012769435
GO:0031668	cellular response to extracellular stimulus	103	0.238205413	0.0046	0.014132412
GO:0038093	Fc receptor signaling pathway	105	0.238186955	0.0102	0.0177
GO:0051899	membrane depolarization	36	0.238178492	0.0046	0.014132412
GO:0014065	phosphatidylinositol 3-kinase signaling	61	0.238167753	0.0042	0.013948535
GO:0070613	regulation of protein processing	37	0.238131158	0.0253	0.029811412
GO:1903317	regulation of protein maturation	37	0.238131158	0.0253	0.029811412
GO:0045932	negative regulation of muscle contraction	15	0.238107332	0.0078	0.01620539
GO:1903409	reactive oxygen species biosynthetic process	40	0.238071741	0.0141	0.020504577
GO:1902743	regulation of lamellipodium organization	17	0.238069805	0.004	0.013824268
GO:0031047	gene silencing by RNA	53	0.238024369	0.0046	0.014132412
GO:0051216	cartilage development	81	0.238009732	0.0061	0.015143924
GO:0008643	carbohydrate transport	52	0.237986384	0.0082	0.016514246
GO:0021761	limbic system development	52	0.23798449	0.0042	0.013948535
GO:0016239	positive regulation of macroautophagy	34	0.237954175	0.0044	0.014132412
GO:0006937	regulation of muscle contraction	66	0.237951504	0.0107	0.018084595
GO:0055067	monovalent inorganic cation homeostasis	53	0.237941512	0.0083	0.016559903
GO:0002230	positive regulation of defense response to virus by host	12	0.237930781	0.025	0.029554283
GO:0070252	actin-mediated cell contraction	56	0.23791652	0.0056	0.014771533
GO:0007612	learning	76	0.237912134	0.0062	0.015209334
GO:0008089	anterograde axonal transport	25	0.23791153	0.0115	0.018599441
GO:0001658	branching involved in ureteric bud morphogenesis	20	0.237908537	0.0071	0.01583804
GO:0021692	cerebellar Purkinje cell layer morphogenesis	5	0.237877892	0.0046	0.014132412
GO:0032835	glomerulus development	24	0.237874145	0.0245	0.029070183
GO:0014909	smooth muscle cell migration	28	0.237863555	0.0066	0.015525305
GO:0002700	regulation of production of molecular mediator of immune response	54	0.23785439	0.006	0.015037711
GO:0008645	hexose transport	41	0.237803823	0.009	0.016956012
GO:0015749	monosaccharide transport	41	0.237803823	0.009	0.016956012
GO:0015758	glucose transport	41	0.237803823	0.009	0.016956012
GO:2000353	positive regulation of endothelial cell apoptotic process	6	0.237800447	0.0178	0.023348367
GO:0006732	coenzyme metabolic process	162	0.237788553	0.0073	0.015844069
GO:0046324	regulation of glucose import	19	0.237763221	0.0069	0.015750415
GO:0032222	regulation of synaptic transmission, cholinergic	5	0.237752719	0.0095	0.01725157
GO:0035315	hair cell differentiation	13	0.237745343	0.0201	0.025275816
GO:0046328	regulation of JNK cascade	67	0.237744074	0.0023	0.012498684
GO:0000387	spliceosomal snRNP assembly	23	0.237712606	0.0111	0.018389742
GO:0014874	response to stimulus involved in regulation of muscle adaptation	5	0.237677563	0.0005	0.009604651
GO:0046330	positive regulation of JNK cascade	44	0.237643195	0.0057	0.01480566
GO:0048839	inner ear development	74	0.237641316	0.0141	0.020504577
GO:0034123	positive regulation of toll-like receptor signaling pathway	10	0.237639208	0.0228	0.027701114
GO:0030072	peptide hormone secretion	107	0.237619568	0.0016	0.011845327
GO:0009313	oligosaccharide catabolic process	5	0.237613551	0.0013	0.011218806
GO:0072283	metanephric renal vesicle morphogenesis	5	0.23754643	0.0006	0.009940401
GO:0021554	optic nerve development	6	0.237545609	0.0119	0.018881943
GO:0031123	RNA 3'-end processing	46	0.237538999	0.0047	0.014168613
GO:0014075	response to amine	20	0.237482029	0.0051	0.014547706
GO:0046883	regulation of hormone secretion	108	0.23747794	0.002	0.012314604
GO:0072584	caveolin-mediated endocytosis	5	0.237465573	0.0159	0.021956962
GO:0070199	establishment of protein localization to chromosome	12	0.237463111	0.0262	0.030579007

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0010642	negative regulation of platelet-derived growth factor receptor signaling pathway	6	0.237461815	0.0097	0.017363901
GO:0030277	maintenance of gastrointestinal epithelium	7	0.237450986	0.0347	0.038238117
GO:0018212	peptidyl-tyrosine modification	155	0.237445826	0.0006	0.009940401
GO:0034440	lipid oxidation	50	0.237431908	0.0173	0.023005658
GO:0070586	cell-cell adhesion involved in gastrulation	6	0.237422941	0.0143	0.020629391
GO:0060421	positive regulation of heart growth	17	0.237417339	0.0115	0.018599441
GO:0017157	regulation of exocytosis	103	0.237413173	0.0022	0.012422266
GO:0009749	response to glucose	84	0.237395128	0.0011	0.010890753
GO:0010959	regulation of metal ion transport	146	0.237383819	0.0036	0.013533394
GO:0001656	metanephros development	40	0.237369004	0.009	0.016956012
GO:0051271	negative regulation of cellular component movement	138	0.237353758	0.0042	0.013948535
GO:0034762	regulation of transmembrane transport	192	0.237347192	0.0017	0.012001709
GO:0070207	protein homotrimerization	15	0.237309214	0.0046	0.014132412
GO:0060291	long-term synaptic potentiation	49	0.237296867	0.0021	0.012314604
GO:0032768	regulation of monooxygenase activity	24	0.237282834	0.0074	0.015911789
GO:0043583	ear development	84	0.237275037	0.0146	0.020879842
GO:0007584	response to nutrient	74	0.237273856	0.0134	0.01999969
GO:0006783	heme biosynthetic process	15	0.237264121	0.0138	0.020339434
GO:0051480	regulation of cytosolic calcium ion concentration	132	0.237201745	0.0033	0.013333753
GO:1900408	negative regulation of cellular response to oxidative stress	20	0.237196049	0.0084	0.016633151
GO:1902883	negative regulation of response to oxidative stress	20	0.237196049	0.0084	0.016633151
GO:1903202	negative regulation of oxidative stress-induced cell death	20	0.237196049	0.0084	0.016633151
GO:0019318	hexose metabolic process	119	0.237167764	0.0042	0.013948535
GO:0021772	olfactory bulb development	11	0.237144171	0.0283	0.032434212
GO:0021988	olfactory lobe development	11	0.237144171	0.0283	0.032434212
GO:0030500	regulation of bone mineralization	33	0.237126658	0.0077	0.016177834
GO:0090103	cochlea morphogenesis	9	0.237106841	0.0053	0.014634479
GO:1905332	positive regulation of morphogenesis of an epithelium	13	0.237104826	0.0147	0.02091937
GO:0001906	cell killing	40	0.23710191	0.0153	0.021378589
GO:0050701	interleukin-1 secretion	20	0.237081566	0.0201	0.025275816
GO:0019079	viral genome replication	41	0.23707635	0.0043	0.014102439
GO:0009746	response to hexose	85	0.237053543	0.0012	0.010961137
GO:0006471	protein ADP-ribosylation	16	0.237046515	0.0073	0.015844069
GO:0006633	fatty acid biosynthetic process	66	0.237042883	0.0076	0.016084627
GO:0001556	oocyte maturation	10	0.237027079	0.002	0.012314604
GO:0002920	regulation of humoral immune response	25	0.237010441	0.0318	0.035688587
GO:2000738	positive regulation of stem cell differentiation	11	0.237007995	0.0166	0.02247277
GO:0030048	actin filament-based movement	60	0.236983346	0.0032	0.013333753
GO:0097035	regulation of membrane lipid distribution	13	0.236959897	0.0109	0.018225506
GO:0006721	terpenoid metabolic process	49	0.236914425	0.0042	0.013948535
GO:0043116	negative regulation of vascular permeability	6	0.236901603	0.0283	0.032434212
GO:0019730	antimicrobial humoral response	25	0.236874953	0.0071	0.01583804
GO:1902175	regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	12	0.23685258	0.0102	0.0177
GO:0044273	sulfur compound catabolic process	25	0.236847638	0.0112	0.018392048
GO:0032418	lysosome localization	38	0.236773446	0.0173	0.023005658
GO:0006837	serotonin transport	7	0.236723495	0.0357	0.03911643
GO:0046326	positive regulation of glucose import	9	0.23670414	0.0115	0.018599441
GO:0010574	regulation of vascular endothelial growth factor production	13	0.236692766	0.023	0.027838811
GO:0002675	positive regulation of acute inflammatory response	14	0.236668701	0.018	0.023514686
GO:0071280	cellular response to copper ion	11	0.236665083	0.005	0.014547706
GO:0007265	Ras protein signal transduction	152	0.236664813	0.0036	0.013533394
GO:0033363	secretory granule organization	18	0.236662027	0.0212	0.026203164
GO:0015833	peptide transport	113	0.23665794	0.0021	0.012314604
GO:0006805	xenobiotic metabolic process	41	0.23664735	0.0146	0.020879842
GO:0010657	muscle cell apoptotic process	36	0.236582372	0.0008	0.010465158
GO:0042311	vasodilation	12	0.236540403	0.0062	0.015209334
GO:0006903	vesicle targeting	49	0.236533252	0.0048	0.014269203
GO:0043030	regulation of macrophage activation	24	0.236503635	0.0344	0.037979912
GO:0071375	cellular response to peptide hormone stimulus	125	0.23649901	0.001	0.010787313
GO:0009914	hormone transport	132	0.236493912	0.0021	0.012314604
GO:0000098	sulfur amino acid catabolic process	6	0.23648436	0.0324	0.036242368
GO:0002703	regulation of leukocyte mediated immunity	63	0.236481265	0.0072	0.015844069
GO:0001910	regulation of leukocyte mediated cytotoxicity	19	0.236459866	0.0234	0.02817551
GO:0002204	somatic recombination of immunoglobulin genes involved in immune response	18	0.236428138	0.0003	0.007956881
GO:0002208	somatic diversification of immunoglobulins involved in immune response	18	0.236428138	0.0003	0.007956881
GO:0016447	somatic recombination of immunoglobulin gene segments	18	0.236428138	0.0003	0.007956881
GO:0045190	isotype switching	18	0.236428138	0.0003	0.007956881
GO:0043547	positive regulation of GTPase activity	150	0.236406786	0.0022	0.012422266
GO:0007254	JNK cascade	84	0.236395522	0.0028	0.012972436
GO:1901654	response to ketone	79	0.236380924	0.0088	0.016916437
GO:0030866	cortical actin cytoskeleton organization	11	0.236359985	0.0055	0.01475
GO:0060249	anatomical structure homeostasis	163	0.236340861	0.0046	0.014132412
GO:0072089	stem cell proliferation	50	0.236328572	0.0125	0.019314538
GO:0001774	microglial cell activation	17	0.236291453	0.0417	0.044666432
GO:0007229	integrin-mediated signaling pathway	46	0.236280115	0.0101	0.017653628
GO:0048675	axon extension	55	0.23624572	0.0012	0.010961137
GO:0033144	negative regulation of intracellular steroid hormone receptor signaling pathway	12	0.236244964	0.0006	0.009940401
GO:0072386	plus-end-directed organelle transport along microtubule	5	0.236213844	0.0073	0.015844069
GO:0006936	muscle contraction	152	0.236201663	0.0055	0.01475
GO:0042036	negative regulation of cytokine biosynthetic process	16	0.236177205	0.0133	0.019917275
GO:0031341	regulation of cell killing	21	0.236175562	0.0224	0.027324219
GO:0006040	amino sugar metabolic process	16	0.236127965	0.0288	0.032902905
GO:0071466	cellular response to xenobiotic stimulus	42	0.236113704	0.0126	0.019370699

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0019217	regulation of fatty acid metabolic process	41	0.236107166	0.0074	0.015911789
GO:0099566	regulation of postsynaptic cytosolic calcium ion concentration	6	0.236101888	0.0313	0.035223161
GO:1903428	positive regulation of reactive oxygen species biosynthetic process	19	0.236080473	0.0112	0.018392048
GO:0015748	organophosphate ester transport	35	0.236070826	0.0021	0.012314604
GO:0050922	negative regulation of chemotaxis	18	0.236052648	0.0237	0.028436066
GO:0046888	negative regulation of hormone secretion	29	0.236038081	0.0059	0.014942532
GO:0002762	negative regulation of myeloid leukocyte differentiation	17	0.236030001	0.0032	0.013333753
GO:0001974	blood vessel remodeling	17	0.236022311	< 0.001	< 0.001
GO:0042476	odontogenesis	44	0.23601669	0.0071	0.01583804
GO:0000288	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	33	0.236009691	0.0031	0.013277185
GO:0007187	G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	73	0.23598745	0.0033	0.013333753
GO:0038202	TORC1 signaling	21	0.235949664	0.0027	0.012827773
GO:0010659	cardiac muscle cell apoptotic process	18	0.235936099	0.0004	0.008964341
GO:0002931	response to ischemia	24	0.235934893	0.0048	0.014269203
GO:0016202	regulation of striated muscle tissue development	57	0.235931253	0.0024	0.012603815
GO:1903050	regulation of proteolysis involved in cellular protein catabolic process	99	0.235908423	0.003	0.013210967
GO:0060137	maternal process involved in parturition	5	0.235897672	0.0294	0.033482529
GO:0019748	secondary metabolic process	27	0.235888035	0.0131	0.019786886
GO:0016358	dendrite development	104	0.235879536	0.0009	0.010729485
GO:0010586	miRNA metabolic process	9	0.235877429	0.0034	0.01347416
GO:0008277	regulation of G-protein coupled receptor protein signaling pathway	70	0.235849246	0.0032	0.013333753
GO:0070997	neuron death	156	0.235783282	0.0025	0.012769435
GO:1901626	regulation of postsynaptic membrane organization	9	0.235777077	0.019	0.024347961
GO:1903532	positive regulation of secretion by cell	183	0.235772206	0.0039	0.013791927
GO:1903078	positive regulation of protein localization to plasma membrane	25	0.235770426	0.001	0.010787313
GO:0006665	sphingolipid metabolic process	67	0.235767672	0.0012	0.010961137
GO:2000736	regulation of stem cell differentiation	62	0.235724291	0.017	0.022784886
GO:0009070	serine family amino acid biosynthetic process	8	0.235718173	0.0166	0.02247277
GO:0016559	peroxisome fission	7	0.235704822	0.0158	0.021871104
GO:0060041	retina development in camera-type eye	66	0.235675005	0.0039	0.013791927
GO:0097104	postsynaptic membrane assembly	5	0.235671946	0.0083	0.016559903
GO:0031667	response to nutrient levels	183	0.235670497	0.0054	0.014720792
GO:2000737	negative regulation of stem cell differentiation	8	0.235624876	0.0374	0.040724444
GO:1904862	inhibitory synapse assembly	5	0.235613117	0.0385	0.041733596
GO:0030595	leukocyte chemotaxis	65	0.23560295	0.0151	0.02121706
GO:0002790	peptide secretion	109	0.23558777	0.0017	0.012001709
GO:0051262	protein tetramerization	71	0.235580398	0.0047	0.014168613
GO:0007338	single fertilization	37	0.235554471	0.0021	0.012314604
GO:0043507	positive regulation of JUN kinase activity	27	0.235536781	0.002	0.012314604
GO:0006520	cellular amino acid metabolic process	179	0.23553437	0.0103	0.017772187
GO:0010517	regulation of phospholipase activity	25	0.235507588	0.012	0.018931514
GO:0048002	antigen processing and presentation of peptide antigen	112	0.23545676	0.0179	0.02344231
GO:0014910	regulation of smooth muscle cell migration	25	0.23543461	0.0051	0.014547706
GO:0016486	peptide hormone processing	5	0.235434299	0.0057	0.01480566
GO:0071496	cellular response to external stimulus	136	0.235396933	0.0058	0.014878261
GO:0061448	connective tissue development	103	0.235364611	0.0066	0.015525305
GO:1901606	alpha-amino acid catabolic process	48	0.235357027	0.0072	0.015844069
GO:0033028	myeloid cell apoptotic process	14	0.235345519	0.005	0.014547706
GO:0001504	neurotransmitter uptake	13	0.235322223	0.0071	0.01583804
GO:0046777	protein autophosphorylation	97	0.235290766	0.0003	0.007956881
GO:0048771	tissue remodeling	60	0.235279388	0.0011	0.010890753
GO:0035588	G-protein coupled purinergic receptor signaling pathway	14	0.235267402	0.008	0.016379603
GO:1902170	cellular response to reactive nitrogen species	7	0.235266106	0.0052	0.014616626
GO:0034765	regulation of ion transmembrane transport	184	0.235259676	0.0013	0.011218806
GO:0044242	cellular lipid catabolic process	87	0.23524372	0.0082	0.016514246
GO:0032479	regulation of type I interferon production	60	0.23522585	0.0068	0.015633241
GO:0032606	type I interferon production	60	0.23522585	0.0068	0.015633241
GO:0019731	antibacterial humoral response	14	0.235217699	0.0274	0.03166636
GO:0032735	positive regulation of interleukin-12 production	10	0.235201964	0.0068	0.015633241
GO:0007189	adenylate cyclase-activating G-protein coupled receptor signaling pathway	29	0.235150066	0.0003	0.007956881
GO:0002697	regulation of immune effector process	160	0.235131611	0.01	0.017574468
GO:0034284	response to monosaccharide	87	0.235127487	0.0014	0.011465722
GO:0072330	monocarboxylic acid biosynthetic process	98	0.235124363	0.0081	0.016514175
GO:0008593	regulation of Notch signaling pathway	41	0.235122337	0.0047	0.014168613
GO:0031396	regulation of protein ubiquitination	101	0.235119554	0.0048	0.014269203
GO:0043388	positive regulation of DNA binding	20	0.235114693	0.0129	0.019597425
GO:1903426	regulation of reactive oxygen species biosynthetic process	31	0.235109692	0.0156	0.021692929
GO:0009066	aspartate family amino acid metabolic process	23	0.235109259	0.0131	0.019786886
GO:0030178	negative regulation of Wnt signaling pathway	111	0.235084801	0.0048	0.014269203
GO:0018095	protein polyglutamylation	5	0.235081327	0.0044	0.014132412
GO:0033197	response to vitamin E	7	0.235028237	0.0079	0.01629604
GO:0016579	protein deubiquitination	120	0.235027854	0.0052	0.014616626
GO:0060415	muscle tissue morphogenesis	28	0.235024072	0.0174	0.023064374
GO:0051055	negative regulation of lipid biosynthetic process	22	0.234988042	0.0161	0.02211694
GO:0043087	regulation of GTPase activity	189	0.234952039	0.0023	0.012498684
GO:0006790	sulfur compound metabolic process	180	0.234933564	0.0087	0.016840777
GO:0047496	vesicle transport along microtubule	27	0.234930737	0.0099	0.017505138
GO:0001942	hair follicle development	27	0.23492805	0.0112	0.018392048
GO:0022404	molting cycle process	27	0.23492805	0.0112	0.018392048
GO:0022405	hair cycle process	27	0.23492805	0.0112	0.018392048
GO:0098773	skin epidermis development	27	0.23492805	0.0112	0.018392048
GO:1900182	positive regulation of protein localization to nucleus	36	0.234881077	0.0142	0.020567234
GO:0051298	centrosome duplication	21	0.234850097	0.0026	0.012805111

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0035589	G-protein coupled purinergic nucleotide receptor signaling pathway	8	0.23483218	0.0202	0.025368462
GO:0021762	substantia nigra development	23	0.234828975	0.0061	0.015143924
GO:0018108	peptidyl-tyrosine phosphorylation	152	0.234817602	0.0006	0.009940401
GO:0032868	response to insulin	109	0.234801525	0.0007	0.010220707
GO:0090140	regulation of mitochondrial fission	14	0.234792774	0.0078	0.01620539
GO:0015858	nucleoside transport	9	0.234767948	0.0001	0.004220438
GO:0030539	male genitalia development	6	0.234761181	0.0337	0.03733539
GO:0033762	response to glucagon	13	0.23475148	< 0.001	< 0.001
GO:0016072	rRNA metabolic process	79	0.234747513	0.0056	0.014771533
GO:0050714	positive regulation of protein secretion	111	0.234747056	0.0079	0.01629604
GO:0090342	regulation of cell aging	22	0.234742667	0.0029	0.013089617
GO:2001259	positive regulation of cation channel activity	30	0.234725504	0.003	0.013210967
GO:1901532	regulation of hematopoietic progenitor cell differentiation	48	0.234704815	0.0197	0.024979254
GO:0043508	negative regulation of JUN kinase activity	9	0.234648592	0.002	0.012314604
GO:0051924	regulation of calcium ion transport	92	0.234559719	0.0067	0.015576759
GO:0061000	negative regulation of dendritic spine development	6	0.234535283	< 0.001	< 0.001
GO:1903038	negative regulation of leukocyte cell-cell adhesion	41	0.234528108	0.0093	0.017114131
GO:0010038	response to metal ion	158	0.234454222	0.0059	0.014942532
GO:2001021	negative regulation of response to DNA damage stimulus	30	0.23444704	0.0259	0.0303391
GO:0010744	positive regulation of macrophage derived foam cell differentiation	5	0.234435507	0.0006	0.009940401
GO:0034114	regulation of heterotypic cell-cell adhesion	9	0.234430612	0.0157	0.021779607
GO:0008344	adult locomotory behavior	31	0.234410093	0.0007	0.010220707
GO:0097320	membrane tubulation	7	0.234409591	0.0053	0.014634479
GO:0051898	negative regulation of protein kinase B signaling	23	0.234392915	0.0018	0.01210186
GO:0046426	negative regulation of JAK-STAT cascade	7	0.234378863	0.0114	0.018551872
GO:1904893	negative regulation of STAT cascade	7	0.234378863	0.0114	0.018551872
GO:0071480	cellular response to gamma radiation	14	0.234373957	0.005	0.014547706
GO:0034605	cellular response to heat	47	0.234356988	0.0041	0.013887639
GO:0036297	interstrand cross-link repair	20	0.234352188	0.0098	0.017418875
GO:0009994	oocyte differentiation	21	0.234348258	< 0.001	< 0.001
GO:0032048	cardiolipin metabolic process	6	0.234347394	0.0054	0.014720792
GO:0009190	cyclic nucleotide biosynthetic process	36	0.234343254	0.0023	0.012498684
GO:0052652	cyclic purine nucleotide metabolic process	36	0.234343254	0.0023	0.012498684
GO:1901861	regulation of muscle tissue development	58	0.234333967	0.0028	0.012972436
GO:0009187	cyclic nucleotide metabolic process	42	0.234277545	0.0022	0.012422266
GO:0007126	meiotic nuclear division	45	0.234263542	0.0018	0.01210186
GO:0006066	alcohol metabolic process	144	0.234249949	0.0071	0.01583804
GO:0002705	positive regulation of leukocyte mediated immunity	38	0.234249323	0.0073	0.015844069
GO:0001953	negative regulation of cell-matrix adhesion	9	0.234243731	0.003	0.013210967
GO:2000772	regulation of cellular senescence	17	0.234230468	0.0011	0.010890753
GO:0072010	glomerular epithelium development	7	0.234204857	0.0112	0.018392048
GO:0072329	monocarboxylic acid catabolic process	54	0.234193579	0.0147	0.02091937
GO:0010506	regulation of autophagy	149	0.234186047	0.0028	0.012972436
GO:0071677	positive regulation of mononuclear cell migration	8	0.234158047	0.0384	0.04164081
GO:0019048	modulation by virus of host morphology or physiology	24	0.234136289	0.0017	0.012001709
GO:0044003	modification by symbiont of host morphology or physiology	24	0.234136289	0.0017	0.012001709
GO:0021884	forebrain neuron development	15	0.234131084	0.0065	0.015491756
GO:1903046	meiotic cell cycle process	48	0.234113423	0.0018	0.01210186
GO:0060292	long term synaptic depression	12	0.234094176	< 0.001	< 0.001
GO:0009314	response to radiation	181	0.234079452	0.0018	0.01210186
GO:0009156	ribonucleoside monophosphate biosynthetic process	47	0.234072163	0.0171	0.022860624
GO:0007409	axonogenesis	199	0.234066202	0.001	0.010787313
GO:0051705	multi-organism behavior	36	0.234055842	0.0026	0.012805111
GO:0051047	positive regulation of secretion	196	0.234044801	0.0038	0.01366393
GO:0010799	regulation of peptidyl-threonine phosphorylation	21	0.234026779	0.005	0.014547706
GO:0002449	lymphocyte mediated immunity	73	0.234015779	0.0064	0.015399417
GO:0032607	interferon-alpha production	11	0.234010725	0.0415	0.044476923
GO:0071806	protein transmembrane transport	29	0.233971169	0.0054	0.014720792
GO:0042471	ear morphogenesis	40	0.233956714	0.009	0.016956012
GO:0032873	negative regulation of stress-activated MAPK cascade	21	0.233951747	0.0008	0.010465158
GO:0070303	negative regulation of stress-activated protein kinase signaling cascade	21	0.233951747	0.0008	0.010465158
GO:0000244	spliceosomal tri-snRNP complex assembly	7	0.233929966	0.0087	0.016840777
GO:0022412	cellular process involved in reproduction in multicellular organism	90	0.233909447	0.005	0.014547706
GO:0050730	regulation of peptidyl-tyrosine phosphorylation	103	0.233900775	0.001	0.010787313
GO:0042886	amide transport	127	0.233893858	0.0017	0.012001709
GO:0048634	regulation of muscle organ development	58	0.233891188	0.0021	0.012314604
GO:0002683	negative regulation of immune system process	169	0.233883541	0.0071	0.01583804
GO:0016572	histone phosphorylation	18	0.233832175	0.0006	0.009940401
GO:0050849	negative regulation of calcium-mediated signaling	18	0.233824616	0.0011	0.010890753
GO:0002438	acute inflammatory response to antigenic stimulus	11	0.233808818	0.0086	0.016782045
GO:0090305	nucleic acid phosphodiester bond hydrolysis	97	0.233797112	0.0039	0.013791927
GO:0030214	hyaluronan catabolic process	9	0.233791214	0.0167	0.02255007
GO:0097553	calcium ion transmembrane import into cytosol	54	0.233789222	0.0047	0.014168613
GO:1902656	calcium ion import into cytosol	54	0.233789222	0.0047	0.014168613
GO:0060252	positive regulation of glial cell proliferation	5	0.233783727	0.033	0.036785425
GO:0010837	regulation of keratinocyte proliferation	17	0.233763452	0.0141	0.020504577
GO:1903405	protein localization to nuclear body	6	0.2337509	0.0388	0.041925173
GO:1904816	positive regulation of protein localization to chromosome, telomeric region	6	0.2337509	0.0388	0.041925173
GO:1904851	positive regulation of establishment of protein localization to telomere	6	0.2337509	0.0388	0.041925173
GO:1904867	protein localization to Cajal body	6	0.2337509	0.0388	0.041925173
GO:1904869	regulation of protein localization to Cajal body	6	0.2337509	0.0388	0.041925173
GO:1904871	positive regulation of protein localization to Cajal body	6	0.2337509	0.0388	0.041925173
GO:1990173	protein localization to nucleoplasm	6	0.2337509	0.0388	0.041925173

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0043687	post-translational protein modification	187	0.233748463	0.0048	0.014269203
GO:0010875	positive regulation of cholesterol efflux	7	0.233745038	0.025	0.029554283
GO:0035587	purinergic receptor signaling pathway	17	0.233740737	0.0076	0.016084627
GO:0060443	mammary gland morphogenesis	16	0.23374048	0.0123	0.019143634
GO:0006743	ubiquinone metabolic process	9	0.23374039	0.0072	0.015844069
GO:2000369	regulation of clathrin-dependent endocytosis	14	0.233721437	0.001	0.010787313
GO:0009798	axis specification	29	0.233714291	0.0058	0.014878261
GO:0051495	positive regulation of cytoskeleton organization	93	0.233694067	0.0045	0.014132412
GO:0021794	thalamus development	6	0.233683088	0.0176	0.023223003
GO:1903312	negative regulation of mRNA metabolic process	15	0.233675313	0.0061	0.015143924
GO:0071383	cellular response to steroid hormone stimulus	84	0.233670022	0.0041	0.013887639
GO:0061351	neural precursor cell proliferation	64	0.233658461	0.0111	0.018389742
GO:0006414	translational elongation	67	0.233653703	0.0253	0.029811412
GO:0042752	regulation of circadian rhythm	54	0.233652709	0.0001	0.004220438
GO:0014821	phasic smooth muscle contraction	8	0.233642162	0.0123	0.019143634
GO:0016101	diterpenoid metabolic process	44	0.233634682	0.006	0.015037711
GO:1900119	positive regulation of execution phase of apoptosis	5	0.233607241	0.001	0.010787313
GO:0072006	nephron development	56	0.233591974	0.0122	0.019049527
GO:0016558	protein import into peroxisome matrix	6	0.233578345	0.0059	0.014942532
GO:0043409	negative regulation of MAPK cascade	78	0.233558327	0.0053	0.014634479
GO:0007080	mitotic metaphase plate congression	21	0.233531789	0.0024	0.012603815
GO:0070266	necroptotic process	15	0.23349684	0.0179	0.02344231
GO:0005996	monosaccharide metabolic process	130	0.233494318	0.0046	0.014132412
GO:0051310	metaphase plate congression	26	0.233442437	0.0055	0.01475
GO:0007100	mitotic centrosome separation	5	0.233437234	< 0.001	< 0.001
GO:0070206	protein trimerization	25	0.233436093	0.0069	0.015750415
GO:0060271	cilium assembly	140	0.233379247	0.0036	0.01353394
GO:0055088	lipid homeostasis	48	0.233351285	0.0015	0.011704453
GO:1900180	regulation of protein localization to nucleus	65	0.233341166	0.0107	0.018084595
GO:0099623	regulation of cardiac muscle cell membrane repolarization	12	0.233340028	0.0176	0.023223003
GO:0030705	cytoskeleton-dependent intracellular transport	80	0.233339078	0.0045	0.014132412
GO:0046605	regulation of centrosome cycle	22	0.233290386	0.0015	0.011704453
GO:0048588	developmental cell growth	109	0.233282924	0.0012	0.010961137
GO:0018210	peptidyl-threonine modification	50	0.233272384	0.0001	0.004220438
GO:0010810	regulation of cell-substrate adhesion	80	0.233216626	0.0046	0.014132412
GO:0001569	branching involved in blood vessel morphogenesis	12	0.233214337	0.0109	0.018225506
GO:0042558	pteridine-containing compound metabolic process	18	0.233210558	0.01	0.017574468
GO:0050663	cytokine secretion	84	0.23319652	0.0131	0.019786886
GO:0032204	regulation of telomere maintenance	37	0.23319509	0.0049	0.014447629
GO:0006094	gluconeogenesis	39	0.233194178	0.0067	0.015576759
GO:0033143	regulation of intracellular steroid hormone receptor signaling pathway	32	0.233190136	0.0088	0.016916437
GO:0050878	regulation of body fluid levels	191	0.233186173	0.0028	0.012972436
GO:0032331	negative regulation of chondrocyte differentiation	6	0.23318421	0.0068	0.015633241
GO:0097006	regulation of plasma lipoprotein particle levels	34	0.233175432	0.0129	0.019597425
GO:0007530	sex determination	6	0.233161966	0.009	0.016956012
GO:0046879	hormone secretion	129	0.233151183	0.0021	0.012314604
GO:0007411	axon guidance	111	0.233148733	0.002	0.012314604
GO:0006284	base-excision repair	14	0.233113713	0.0009	0.010729485
GO:0051056	regulation of small GTPase mediated signal transduction	152	0.233105895	0.0036	0.01353394
GO:0060021	palate development	31	0.233104735	0.0033	0.013333753
GO:0035036	sperm-egg recognition	11	0.233101908	0.0128	0.019522448
GO:0003073	regulation of systemic arterial blood pressure	28	0.233078495	0.0028	0.012972436
GO:1904355	positive regulation of telomere capping	12	0.233060031	0.0055	0.01475
GO:0007156	homophilic cell adhesion via plasma membrane adhesion molecules	47	0.233011246	0.0005	0.009604651
GO:0043406	positive regulation of MAP kinase activity	103	0.233001513	0.0094	0.017156187
GO:0009145	purine nucleoside triphosphate biosynthetic process	29	0.232987221	0.0189	0.024289798
GO:0098542	defense response to other organism	174	0.232951527	0.0046	0.014132412
GO:0001946	lymphangiogenesis	6	0.232938659	0.0057	0.01480566
GO:0006301	postreplication repair	18	0.232906264	0.0338	0.0374175
GO:0042398	cellular modified amino acid biosynthetic process	22	0.232895584	0.0135	0.020081554
GO:0006140	regulation of nucleotide metabolic process	82	0.232886474	0.0043	0.014102439
GO:0044557	relaxation of smooth muscle	5	0.232883156	0.0176	0.023223003
GO:0060087	relaxation of vascular smooth muscle	5	0.232883156	0.0176	0.023223003
GO:0097091	synaptic vesicle clustering	8	0.232865663	0.0174	0.023064374
GO:0019372	lipoxygenase pathway	10	0.232863201	0.0135	0.020081554
GO:0051817	modification of morphology or physiology of other organism involved in symbiotic interaction	46	0.232844648	0.0075	0.015990044
GO:0032465	regulation of cytokinesis	27	0.232823358	0.0014	0.011465722
GO:0032891	negative regulation of organic acid transport	6	0.23281923	0.0163	0.022248961
GO:0001889	liver development	58	0.232812826	0.003	0.013210967
GO:0061008	hepaticobiliary system development	58	0.232812826	0.003	0.013210967
GO:0050769	positive regulation of neurogenesis	192	0.232790723	0.0027	0.012827773
GO:0070862	negative regulation of protein exit from endoplasmic reticulum	5	0.232782084	0.0254	0.029880529
GO:0006979	response to oxidative stress	197	0.232737962	0.0048	0.014269203
GO:0098661	inorganic anion transmembrane transport	36	0.232725898	0.0159	0.021956962
GO:2000272	negative regulation of receptor activity	26	0.23272183	0.0024	0.012603815
GO:0071695	anatomical structure maturation	22	0.2327213	0.0045	0.014132412
GO:0010212	response to ionizing radiation	63	0.232700121	0.0023	0.012498684
GO:1901028	regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	19	0.232648414	0.0032	0.013333753
GO:0060541	respiratory system development	84	0.232631187	0.0054	0.014720792
GO:0043535	regulation of blood vessel endothelial cell migration	42	0.232620605	0.0036	0.01353394
GO:0032412	regulation of ion transmembrane transporter activity	109	0.232611136	0.0012	0.010961137
GO:0006685	sphingomyelin catabolic process	6	0.23260089	0.0169	0.022703485
GO:0035590	purinergic nucleotide receptor signaling pathway	11	0.232591486	0.0152	0.0213213

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0097300	programmed necrotic cell death	17	0.2325711	0.0148	0.020979063
GO:0006898	receptor-mediated endocytosis	126	0.232564485	0.0067	0.015576759
GO:0048747	muscle fiber development	22	0.232552966	0.0121	0.018970228
GO:0050680	negative regulation of epithelial cell proliferation	56	0.232534451	0.0112	0.018392048
GO:0010634	positive regulation of epithelial cell migration	68	0.2325259	0.0033	0.013333753
GO:0098722	asymmetric stem cell division	5	0.232509192	0.0236	0.028327839
GO:0042307	positive regulation of protein import into nucleus	25	0.23250857	0.0147	0.02091937
GO:0021700	developmental maturation	121	0.23250363	0.0014	0.011465722
GO:0032727	positive regulation of interferon-alpha production	7	0.232479796	0.045	0.047741284
GO:0043001	Golgi to plasma membrane protein transport	12	0.232456842	0.0004	0.008964341
GO:0006361	transcription initiation from RNA polymerase I promoter	20	0.232440645	0.0065	0.015491756
GO:0097485	neuron projection guidance	112	0.23241901	0.0021	0.012314604
GO:0006497	protein lipidation	36	0.23241077	0.0098	0.017418875
GO:0071902	positive regulation of protein serine/threonine kinase activity	137	0.232405994	0.0078	0.01620539
GO:0045862	positive regulation of proteolysis	146	0.232400014	0.0042	0.013948535
GO:0044782	cilium organization	144	0.232394042	0.0035	0.01351837
GO:0045833	negative regulation of lipid metabolic process	32	0.232361076	0.0102	0.0177
GO:0070167	regulation of biomineral tissue development	38	0.232342302	0.008	0.016379603
GO:0034650	cortisol metabolic process	5	0.232333483	0.044	0.046783376
GO:0034651	cortisol biosynthetic process	5	0.232333483	0.044	0.046783376
GO:0010569	regulation of double-strand break repair via homologous recombination	11	0.232318547	0.0257	0.030153693
GO:0070193	synaptonemal complex organization	8	0.232280129	0.0091	0.016994897
GO:0031113	regulation of microtubule polymerization	18	0.232277016	0.0051	0.014547706
GO:0032956	regulation of actin cytoskeleton organization	137	0.232274467	0.0095	0.01725157
GO:0032480	negative regulation of type I interferon production	22	0.232268305	0.0116	0.018682786
GO:0001655	urogenital system development	146	0.232259066	0.0082	0.016514246
GO:0060964	regulation of gene silencing by miRNA	30	0.232254138	0.0063	0.015311728
GO:0000187	activation of MAPK activity	70	0.232243056	0.0074	0.015911789
GO:2000725	regulation of cardiac muscle cell differentiation	17	0.232236406	0.0005	0.009604651
GO:0032620	interleukin-17 production	14	0.232228414	0.004	0.013824268
GO:0099622	cardiac muscle cell membrane repolarization	16	0.232223763	0.0076	0.016084627
GO:0043524	negative regulation of neuron apoptotic process	63	0.232209759	0.0035	0.01351837
GO:0000132	establishment of mitotic spindle orientation	10	0.232207533	0.0013	0.011218806
GO:1904591	positive regulation of protein import	26	0.232200227	0.0151	0.02121706
GO:0032496	response to lipopolysaccharide	121	0.232196678	0.0126	0.019370699
GO:0060259	regulation of feeding behavior	11	0.23218779	0.0007	0.010220707
GO:0032409	regulation of transporter activity	118	0.23218532	0.0016	0.011845327
GO:0010762	regulation of fibroblast migration	14	0.232182784	0.007	0.015816335
GO:0007517	muscle organ development	158	0.232180832	0.0023	0.012498684
GO:0031110	regulation of microtubule polymerization or depolymerization	25	0.23216187	0.0041	0.013887639
GO:0035023	regulation of Rho protein signal transduction	55	0.232152144	0.0012	0.010961137
GO:0050872	white fat cell differentiation	8	0.232148121	0.0003	0.007956881
GO:0071347	cellular response to interleukin-1	73	0.232131689	0.0071	0.01583804
GO:0090025	regulation of monocyte chemotaxis	8	0.232129818	0.0256	0.03006687
GO:0030324	lung development	76	0.232121592	0.0078	0.01620539
GO:0043648	dicarboxylic acid metabolic process	48	0.2321015	0.0061	0.015143924
GO:0009266	response to temperature stimulus	91	0.232098137	0.0027	0.012827773
GO:0034446	substrate adhesion-dependent cell spreading	42	0.232071161	0.0072	0.015844069
GO:0010543	regulation of platelet activation	15	0.232046165	0.0412	0.04417997
GO:0060828	regulation of canonical Wnt signaling pathway	131	0.232033239	0.0064	0.015399417
GO:0034393	positive regulation of smooth muscle cell apoptotic process	8	0.232032634	0.0052	0.014616626
GO:0002768	immune response-regulating cell surface receptor signaling pathway	182	0.232030806	0.0073	0.015844069
GO:0019068	virion assembly	23	0.232029289	0.0147	0.02091937
GO:0007413	axonal fasciculation	11	0.232014508	0.0106	0.018010344
GO:0030513	positive regulation of BMP signaling pathway	15	0.232007809	0.0122	0.019049527
GO:0010758	regulation of macrophage chemotaxis	11	0.231993187	0.0208	0.025885837
GO:0003085	negative regulation of systemic arterial blood pressure	8	0.231991169	0.0033	0.013333753
GO:0072524	pyridine-containing compound metabolic process	79	0.23195452	0.0081	0.016514175
GO:0006364	rRNA processing	75	0.231942208	0.0057	0.01480566
GO:0032715	negative regulation of interleukin-6 production	16	0.231937475	0.0142	0.020567234
GO:0030540	female genitalia development	7	0.231916129	0.0097	0.017363901
GO:0006733	oxidoreduction coenzyme metabolic process	86	0.231886335	0.0073	0.015844069
GO:0045978	negative regulation of nucleoside metabolic process	13	0.231881613	0.0061	0.015143924
GO:1903579	negative regulation of ATP metabolic process	13	0.231881613	0.0061	0.015143924
GO:0010518	positive regulation of phospholipase activity	24	0.231875466	0.0107	0.018084595
GO:0031281	positive regulation of cyclase activity	22	0.231860251	0.001	0.010787313
GO:0009063	cellular amino acid catabolic process	59	0.231847999	0.0123	0.019143634
GO:0043038	amino acid activation	22	0.231808243	0.0104	0.017832977
GO:0043039	tRNA aminoacylation	22	0.231808243	0.0104	0.017832977
GO:0097421	liver regeneration	15	0.231796078	0.0085	0.016693954
GO:0035195	gene silencing by miRNA	45	0.2317824	0.0065	0.015491756
GO:0097581	lamellipodium organization	36	0.231768888	0.0078	0.01620539
GO:0060732	positive regulation of inositol phosphate biosynthetic process	8	0.23175809	0.0347	0.038238117
GO:0030323	respiratory tube development	79	0.231756314	0.0083	0.016559903
GO:0001675	acrosome assembly	7	0.231725834	0.0171	0.022860624
GO:0019362	pyridine nucleotide metabolic process	77	0.231669627	0.0075	0.015990044
GO:0046496	nicotinamide nucleotide metabolic process	77	0.231669627	0.0075	0.015990044
GO:0090646	mitochondrial tRNA processing	5	0.23166123	0.0262	0.030579007
GO:0030210	heparin biosynthetic process	5	0.2316519	0.0239	0.028592965
GO:0015914	phospholipid transport	24	0.231646922	0.0051	0.014547706
GO:0040013	negative regulation of locomotion	146	0.231643497	0.0041	0.013887639
GO:0070373	negative regulation of ERK1 and ERK2 cascade	37	0.231618224	0.008	0.016379603
GO:0046323	glucose import	20	0.231612443	0.0044	0.014132412

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0032928	regulation of superoxide anion generation	13	0.231584978	0.0356	0.03903645
GO:0022400	regulation of rhodopsin mediated signaling pathway	10	0.231563787	0.003	0.013210967
GO:0044342	type B pancreatic cell proliferation	12	0.231560482	0.0148	0.020979063
GO:0098900	regulation of action potential	18	0.231549	0.0213	0.026276211
GO:0006000	fructose metabolic process	7	0.231541647	0.0256	0.03006687
GO:0050772	positive regulation of axonogenesis	34	0.231541636	0.0012	0.010961137
GO:0045995	regulation of embryonic development	47	0.231541494	0.0047	0.014168613
GO:0071479	cellular response to ionizing radiation	33	0.231540408	0.0054	0.014720792
GO:0002381	immunoglobulin production involved in immunoglobulin mediated immune response	20	0.231540268	0.0006	0.009940401
GO:0032803	regulation of low-density lipoprotein particle receptor catabolic process	5	0.231540203	0.0164	0.022306469
GO:0014850	response to muscle activity	10	0.231465048	0.0071	0.01583804
GO:0008584	male gonad development	49	0.231417648	0.0069	0.015750415
GO:0035584	calcium-mediated signaling using intracellular calcium source	11	0.231417386	0.0012	0.010961137
GO:0006547	histidine metabolic process	5	0.231407774	0.0058	0.014878261
GO:0052803	imidazole-containing compound metabolic process	5	0.231407774	0.0058	0.014878261
GO:2000679	positive regulation of transcription regulatory region DNA binding	9	0.23140596	0.0253	0.029811412
GO:0042074	cell migration involved in gastrulation	5	0.231393261	0.0353	0.038781037
GO:0050764	regulation of phagocytosis	34	0.231368954	0.0128	0.019522448
GO:0002819	regulation of adaptive immune response	47	0.231334774	0.002	0.012314604
GO:1902476	chloride transmembrane transport	27	0.231313143	0.0136	0.020157703
GO:0043647	inositol phosphate metabolic process	33	0.231310975	0.0125	0.019314538
GO:0000578	embryonic axis specification	14	0.231277955	0.0087	0.016840777
GO:0045089	positive regulation of innate immune response	151	0.231262694	0.0114	0.018551872
GO:0001960	negative regulation of cytokine-mediated signaling pathway	22	0.231249582	0.0173	0.023005658
GO:0061548	ganglion development	7	0.231219922	0.002	0.012314604
GO:0015807	L-amino acid transport	23	0.231210522	0.0093	0.017114131
GO:1902108	regulation of mitochondrial membrane permeability involved in apoptotic process	26	0.231207406	0.0025	0.012769435
GO:0036109	alpha-linolenic acid metabolic process	6	0.231205761	0.0431	0.045953199
GO:0007569	cell aging	46	0.231199029	0.0019	0.012288367
GO:0046189	phenol-containing compound biosynthetic process	20	0.23118464	0.0085	0.016693954
GO:1903169	regulation of calcium ion transmembrane transport	55	0.231173095	0.0052	0.014616626
GO:0036119	response to platelet-derived growth factor	7	0.231163278	0.0041	0.013887639
GO:0036120	cellular response to platelet-derived growth factor stimulus	7	0.231163278	0.0041	0.013887639
GO:0045132	meiotic chromosome segregation	20	0.231149913	0.0068	0.015633241
GO:0007625	grooming behavior	7	0.231144026	0.0013	0.011218806
GO:0007219	Notch signaling pathway	76	0.231117835	0.0069	0.015750415
GO:0007212	dopamine receptor signaling pathway	23	0.231107817	0.0023	0.012498684
GO:0035278	miRNA mediated inhibition of translation	6	0.231085037	0.0111	0.018389742
GO:0040033	negative regulation of translation, ncRNA-mediated	6	0.231085037	0.0111	0.018389742
GO:0045974	regulation of translation, ncRNA-mediated	6	0.231085037	0.0111	0.018389742
GO:1903825	organic acid transmembrane transport	35	0.231080718	0.0088	0.016916437
GO:1905039	carboxylic acid transmembrane transport	35	0.231080718	0.0088	0.016916437
GO:0072091	regulation of stem cell proliferation	26	0.231079522	0.0188	0.02420971
GO:0015718	monocarboxylic acid transport	54	0.231068696	0.0087	0.016840777
GO:0035082	axoneme assembly	24	0.231058257	0.0098	0.017418875
GO:0032530	regulation of microvillus organization	6	0.231047243	0.001	0.010787313
GO:0042181	ketone biosynthetic process	19	0.231034683	0.0116	0.018682786
GO:0002695	negative regulation of leukocyte activation	65	0.231033571	0.0122	0.019049527
GO:0008217	regulation of blood pressure	64	0.231031903	0.0077	0.016177834
GO:0070588	calcium ion transmembrane transport	108	0.231023331	0.0046	0.014132412
GO:0061035	regulation of cartilage development	34	0.23098422	0.0051	0.014547706
GO:0032438	melanosome organization	15	0.230972995	0.012	0.018931514
GO:0048753	pigment granule organization	15	0.230972995	0.012	0.018931514
GO:0042726	flavin-containing compound metabolic process	8	0.23096766	0.0139	0.020388077
GO:0045216	cell-cell junction organization	93	0.230966354	0.0037	0.013609033
GO:1900542	regulation of purine nucleotide metabolic process	79	0.230927569	0.0045	0.014132412
GO:0050832	defense response to fungus	7	0.230920225	0.008	0.016379603
GO:0051090	regulation of sequence-specific DNA binding transcription factor activity	162	0.230891861	0.0064	0.015399417
GO:1901343	negative regulation of vasculature development	52	0.230886325	0.0073	0.015844069
GO:0002708	positive regulation of lymphocyte mediated immunity	26	0.230877778	0.0055	0.01475
GO:0042219	cellular modified amino acid catabolic process	7	0.230865062	0.002	0.012314604
GO:2000377	regulation of reactive oxygen species metabolic process	79	0.230852725	0.0102	0.0177
GO:0046320	regulation of fatty acid oxidation	18	0.230842941	0.0168	0.022626974
GO:0030810	positive regulation of nucleotide biosynthetic process	27	0.230835958	0.0031	0.013277185
GO:1900373	positive regulation of purine nucleotide biosynthetic process	27	0.230835958	0.0031	0.013277185
GO:1904062	regulation of cation transmembrane transport	133	0.230831976	0.0015	0.011704453
GO:0040019	positive regulation of embryonic development	15	0.23081871	0.0057	0.01480566
GO:0010042	response to manganese ion	10	0.230816248	0.0142	0.020567234
GO:0090129	positive regulation of synapse maturation	6	0.230811194	< 0.001	< 0.001
GO:2000181	negative regulation of blood vessel morphogenesis	48	0.230803393	0.007	0.015816335
GO:0035455	response to interferon-alpha	6	0.230788734	0.011	0.018323826
GO:0021872	forebrain generation of neurons	29	0.230778844	0.0129	0.019597425
GO:0016054	organic acid catabolic process	119	0.23076472	0.0125	0.019314538
GO:0046395	carboxylic acid catabolic process	119	0.23076472	0.0125	0.019314538
GO:0019985	translesion synthesis	15	0.230761609	0.0331	0.03684717
GO:0001708	cell fate specification	21	0.230747454	0.0178	0.023348367
GO:0048010	vascular endothelial growth factor receptor signaling pathway	45	0.230743525	0.0077	0.016177834
GO:0043470	regulation of carbohydrate catabolic process	30	0.230730035	0.0021	0.012314604
GO:0022898	regulation of transmembrane transporter activity	113	0.230696684	0.0015	0.011704453
GO:0000959	mitochondrial RNA metabolic process	12	0.230692846	0.0082	0.016514246
GO:0009612	response to mechanical stimulus	84	0.230669676	0.006	0.015037711
GO:0090493	catecholamine uptake	6	0.230658076	0.0242	0.028862294
GO:0090494	dopamine uptake	6	0.230658076	0.0242	0.028862294

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1903522	regulation of blood circulation	117	0.230645433	0.0035	0.01351837
GO:0042659	regulation of cell fate specification	6	0.230641014	0.009	0.016956012
GO:1904377	positive regulation of protein localization to cell periphery	26	0.230614484	0.001	0.010787313
GO:0050850	positive regulation of calcium-mediated signaling	24	0.230613911	0.0114	0.018551872
GO:2000106	regulation of leukocyte apoptotic process	26	0.23060965	0.0022	0.012422266
GO:0032886	regulation of microtubule-based process	71	0.230600875	0.0031	0.013277185
GO:0009582	detection of abiotic stimulus	46	0.230600657	0.0035	0.01351837
GO:0046655	folic acid metabolic process	10	0.230593114	0.0129	0.019597425
GO:0000209	protein polyubiquitination	154	0.230525524	0.0044	0.014132412
GO:0060339	negative regulation of type I interferon-mediated signaling pathway	5	0.230506425	0.0104	0.017832977
GO:0051146	striated muscle cell differentiation	94	0.230498552	0.0044	0.014132412
GO:0009896	positive regulation of catabolic process	141	0.230492982	0.0031	0.013277185
GO:0032728	positive regulation of interferon-beta production	11	0.23046946	0.0062	0.015209334
GO:0050918	positive chemotaxis	24	0.230439412	0.0295	0.033583186
GO:0060043	regulation of cardiac muscle cell proliferation	17	0.230434883	0.022	0.026944291
GO:0032434	regulation of proteasomal ubiquitin-dependent protein catabolic process	57	0.23041873	0.0031	0.013277185
GO:0090278	negative regulation of peptide hormone secretion	20	0.230372636	0.0115	0.018599441
GO:0002429	immune response-activating cell surface receptor signaling pathway	167	0.230351733	0.0077	0.016177834
GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	99	0.230333023	0.0046	0.014132412
GO:0016441	posttranscriptional gene silencing	47	0.230329686	0.0055	0.01475
GO:0035194	posttranscriptional gene silencing by RNA	47	0.230329686	0.0055	0.01475
GO:0050848	regulation of calcium-mediated signaling	53	0.2303153	0.0049	0.014447629
GO:0070482	response to oxygen levels	186	0.230300996	0.0068	0.015633241
GO:1900024	regulation of substrate adhesion-dependent cell spreading	25	0.230299307	0.012	0.018931514
GO:0043241	protein complex disassembly	116	0.230291439	0.0102	0.0177
GO:1901019	regulation of calcium ion transmembrane transporter activity	35	0.230272629	0.0066	0.015525305
GO:0097529	myeloid leukocyte migration	64	0.23023133	0.0213	0.026276211
GO:0032303	regulation of icosanoid secretion	8	0.23022145	0.018	0.023514686
GO:2000191	regulation of fatty acid transport	8	0.23022145	0.018	0.023514686
GO:0022410	circadian sleep/wake cycle process	10	0.230203471	0.0003	0.007956881
GO:0050802	circadian sleep/wake cycle, sleep	10	0.230203471	0.0003	0.007956881
GO:0002281	macrophage activation involved in immune response	8	0.230184358	0.0183	0.023783007
GO:0022037	metencephalon development	46	0.230182344	0.0042	0.013948535
GO:0006816	calcium ion transport	167	0.230164085	0.0045	0.014132412
GO:0014044	Schwann cell development	10	0.230144124	0.0041	0.013887639
GO:0045911	positive regulation of DNA recombination	16	0.230097783	0.0035	0.01351837
GO:0060074	synapse maturation	17	0.230093939	0.0002	0.006319126
GO:0031050	dsRNA fragmentation	14	0.230067691	0.0082	0.016514246
GO:0070918	production of small RNA involved in gene silencing by RNA	14	0.230067691	0.0082	0.016514246
GO:0010660	regulation of muscle cell apoptotic process	34	0.230034752	0.0009	0.010729485
GO:0061099	negative regulation of protein tyrosine kinase activity	12	0.230033291	0.0042	0.013948535
GO:0002573	myeloid leukocyte differentiation	80	0.230022611	0.0064	0.015399417
GO:0002031	G-protein coupled receptor internalization	5	0.230021024	0.0375	0.040825645
GO:0097151	positive regulation of inhibitory postsynaptic potential	5	0.22998837	0.0006	0.009940401
GO:0098828	modulation of inhibitory postsynaptic potential	5	0.22998837	0.0006	0.009940401
GO:0006879	cellular iron ion homeostasis	30	0.229986729	0.0103	0.017772187
GO:1904948	midbrain dopaminergic neuron differentiation	7	0.229974487	0.0166	0.02247277
GO:0035136	forelimb morphogenesis	11	0.229955858	0.0206	0.025725529
GO:0045922	negative regulation of fatty acid metabolic process	12	0.22995306	0.0284	0.032523034
GO:0006942	regulation of striated muscle contraction	35	0.2299502	0.0139	0.020388077
GO:0008637	apoptotic mitochondrial changes	63	0.229944252	0.0049	0.014447629
GO:0035627	ceramide transport	6	0.229909543	0.0006	0.009940401
GO:0043488	regulation of mRNA stability	86	0.229876978	0.0126	0.019370699
GO:0002690	positive regulation of leukocyte chemotaxis	28	0.229850184	0.0135	0.020081554
GO:0031929	TOR signaling	50	0.229842672	0.0016	0.011845327
GO:0000723	telomere maintenance	63	0.229817121	0.0084	0.016633151
GO:0032200	telomere organization	63	0.229817121	0.0084	0.016633151
GO:0099518	vesicle cytoskeletal trafficking	29	0.229811026	0.0096	0.017302743
GO:0051225	spindle assembly	26	0.229802624	0.0062	0.015209334
GO:0006302	double-strand break repair	75	0.229802071	0.0026	0.012805111
GO:0061450	trophoblast cell migration	5	0.229785191	0.0188	0.02420971
GO:1901163	regulation of trophoblast cell migration	5	0.229785191	0.0188	0.02420971
GO:0010508	positive regulation of autophagy	53	0.229754469	0.0014	0.011465722
GO:0022616	DNA strand elongation	5	0.229751242	0.0451	0.047829824
GO:0001822	kidney development	127	0.229738161	0.0071	0.01583804
GO:0006110	regulation of glycolytic process	27	0.229735404	0.0041	0.013887639
GO:1903829	positive regulation of cellular protein localization	149	0.229734405	0.004	0.013824268
GO:0021514	ventral spinal cord interneuron differentiation	6	0.22969833	0.0229	0.027770092
GO:0036010	protein localization to endosome	10	0.229693449	0.0051	0.014547706
GO:0072395	signal transduction involved in cell cycle checkpoint	24	0.22967641	0.0018	0.01210186
GO:0034243	regulation of transcription elongation from RNA polymerase II promoter	12	0.22967587	0.009	0.016956012
GO:0048814	regulation of dendrite morphogenesis	42	0.229672445	0.0008	0.010465158
GO:2000042	negative regulation of double-strand break repair via homologous recombination	5	0.229666756	0.0397	0.042801678
GO:0050866	negative regulation of cell activation	76	0.229657894	0.016	0.022026667
GO:0006644	phospholipid metabolic process	186	0.229639658	0.0058	0.014878261
GO:0002029	desensitization of G-protein coupled receptor protein signaling pathway	8	0.229621501	0.0317	0.035590175
GO:0022401	negative adaptation of signaling pathway	8	0.229621501	0.0317	0.035590175
GO:0045686	negative regulation of glial cell differentiation	13	0.229614985	0.0183	0.023783007
GO:0032147	activation of protein kinase activity	136	0.229582208	0.0043	0.014102439
GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	86	0.229571881	0.0041	0.013887639
GO:0002534	cytokine production involved in inflammatory response	16	0.229548856	0.0011	0.010890753
GO:0043467	regulation of generation of precursor metabolites and energy	54	0.229548667	0.0017	0.012001709
GO:0048477	oogenesis	31	0.229522347	0.0008	0.010465158

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0019722	calcium-mediated signaling	90	0.229506496	0.0027	0.012827773
GO:0021756	striatum development	10	0.229489234	0.0051	0.014547706
GO:0045806	negative regulation of endocytosis	30	0.229478695	0.002	0.012314604
GO:0032732	positive regulation of interleukin-1 production	16	0.229460014	0.0264	0.030750363
GO:0071222	cellular response to lipopolysaccharide	74	0.229453754	0.0078	0.01620539
GO:0019674	NAD metabolic process	37	0.229449674	0.0097	0.017363901
GO:0055090	acylglycerol homeostasis	10	0.229446214	0.0004	0.008964341
GO:0070328	triglyceride homeostasis	10	0.229446214	0.0004	0.008964341
GO:0010575	positive regulation of vascular endothelial growth factor production	10	0.229445436	0.0308	0.034775552
GO:1903320	regulation of protein modification by small protein conjugation or removal	110	0.229408577	0.0039	0.013791927
GO:0060603	mammary gland duct morphogenesis	11	0.229390188	0.0253	0.029811412
GO:0048146	positive regulation of fibroblast proliferation	25	0.229374323	0.0245	0.029070183
GO:0043506	regulation of JUN kinase activity	39	0.229361974	0.003	0.013210967
GO:0007252	I-kappaB phosphorylation	9	0.22933515	0.033	0.036785425
GO:0031329	regulation of cellular catabolic process	178	0.229333467	0.003	0.013210967
GO:0032970	regulation of actin filament-based process	151	0.229328618	0.0086	0.016782045
GO:0030208	dermatan sulfate biosynthetic process	9	0.229301604	0.0142	0.020567234
GO:0006664	glycolipid metabolic process	56	0.229298711	0.0095	0.01725157
GO:1905521	regulation of macrophage migration	18	0.229292101	0.0377	0.040981651
GO:0090090	negative regulation of canonical Wnt signaling pathway	94	0.229269416	0.0079	0.01629604
GO:0009100	glycoprotein metabolic process	184	0.229262822	0.0032	0.013333753
GO:0042755	eating behavior	16	0.229243213	0.0001	0.004220438
GO:0010770	positive regulation of cell morphogenesis involved in differentiation	68	0.229239044	0.0015	0.011704453
GO:0003413	chondrocyte differentiation involved in endochondral bone morphogenesis	6	0.229237462	0.0093	0.017114131
GO:0006293	nucleotide-excision repair, preincision complex stabilization	11	0.229229864	0.0145	0.020788247
GO:0006295	nucleotide-excision repair, DNA incision, 3'-to lesion	11	0.229229864	0.0145	0.020788247
GO:0031647	regulation of protein stability	134	0.229215879	0.0045	0.014132412
GO:0010421	hydrogen peroxide-mediated programmed cell death	5	0.229199237	0.0143	0.020629391
GO:0097468	programmed cell death in response to reactive oxygen species	5	0.229199237	0.0143	0.020629391
GO:0010594	regulation of endothelial cell migration	80	0.229194507	0.0041	0.013887639
GO:0000018	regulation of DNA recombination	31	0.229194346	0.0033	0.013333753
GO:0042769	DNA damage response, detection of DNA damage	18	0.229194198	0.0248	0.029383934
GO:0042754	negative regulation of circadian rhythm	9	0.229170586	< 0.001	< 0.001
GO:0048639	positive regulation of developmental growth	78	0.229147688	0.0027	0.012827773
GO:0051930	regulation of sensory perception of pain	22	0.229143106	0.0029	0.013089617
GO:0051931	regulation of sensory perception	22	0.229143106	0.0029	0.013089617
GO:0097345	mitochondrial outer membrane permeabilization	25	0.229139371	0.0029	0.013089617
GO:1902110	positive regulation of mitochondrial membrane permeability involved in apoptotic process	25	0.229139371	0.0029	0.013089617
GO:0046785	microtubule polymerization	25	0.229127709	0.0033	0.013333753
GO:0031589	cell-substrate adhesion	127	0.229126591	0.0047	0.014168613
GO:0006643	membrane lipid metabolic process	87	0.229121549	0.0045	0.014132412
GO:0001892	embryonic placenta development	36	0.229107956	0.0022	0.012422266
GO:0044801	single-organism membrane fusion	45	0.229095948	0.0032	0.013333753
GO:0007588	excretion	30	0.22907618	0.0077	0.016177834
GO:0051222	positive regulation of protein transport	193	0.229024923	0.006	0.015037711
GO:0010639	negative regulation of organelle organization	140	0.229022936	0.0033	0.013333753
GO:0070838	divalent metal ion transport	176	0.228952566	0.0047	0.014168613
GO:0072511	divalent inorganic cation transport	176	0.228952566	0.0047	0.014168613
GO:0006260	DNA replication	103	0.228950484	0.0017	0.012001709
GO:1990090	cellular response to nerve growth factor stimulus	24	0.228948502	0.0012	0.010961137
GO:0032663	regulation of interleukin-2 production	20	0.228947271	0.0112	0.018392048
GO:0002237	response to molecule of bacterial origin	127	0.228946222	0.0139	0.020388077
GO:1903670	regulation of sprouting angiogenesis	32	0.22893765	0.0048	0.014269203
GO:0051220	cytoplasmic sequestering of protein	21	0.228921075	0.0051	0.014547706
GO:0007565	female pregnancy	78	0.228900326	0.0031	0.013277185
GO:0051152	positive regulation of smooth muscle cell differentiation	6	0.228899694	0.0164	0.022306469
GO:2001014	regulation of skeletal muscle cell differentiation	8	0.228884523	0.0014	0.011465722
GO:0060070	canonical Wnt signaling pathway	148	0.228883249	0.0068	0.015633241
GO:0015672	monovalent inorganic cation transport	183	0.228878555	0.0016	0.011845327
GO:0009064	glutamine family amino acid metabolic process	35	0.228873143	0.0021	0.012314604
GO:0000226	microtubule cytoskeleton organization	173	0.228868886	0.0023	0.012498684
GO:0007626	locomotory behavior	87	0.228858743	0.0021	0.012314604
GO:0051052	regulation of DNA metabolic process	177	0.228850502	0.0022	0.012422266
GO:0051453	regulation of intracellular pH	25	0.228842896	0.0087	0.016840777
GO:0030900	forebrain development	177	0.228824103	0.0076	0.016084627
GO:0051409	response to nitrosative stress	8	0.228803212	0.0089	0.016916437
GO:1904427	positive regulation of calcium ion transmembrane transport	27	0.228800135	0.0058	0.014878261
GO:0055002	striated muscle cell development	56	0.228797034	0.0042	0.013948535
GO:0032613	interleukin-10 production	16	0.228749761	0.0117	0.018739446
GO:0007623	circadian rhythm	93	0.228743636	0.0004	0.008964341
GO:0031023	microtubule organizing center organization	42	0.228726028	0.002	0.012314604
GO:0001941	postsynaptic membrane organization	19	0.22870145	0.0056	0.014771533
GO:0072189	ureter development	5	0.228678072	0.0332	0.036915846
GO:0032780	negative regulation of ATPase activity	7	0.228669446	0.0126	0.019370699
GO:0006111	regulation of gluconeogenesis	14	0.228630572	0.0059	0.014942532
GO:0006457	protein folding	92	0.228624443	0.0147	0.02091937
GO:0006006	glucose metabolic process	95	0.228622148	0.0036	0.01353394
GO:0010919	regulation of inositol phosphate biosynthetic process	10	0.228617299	0.0247	0.029271449
GO:0038003	opioid receptor signaling pathway	6	0.228609222	0.0002	0.006319126
GO:0045732	positive regulation of protein catabolic process	103	0.228608421	0.0036	0.01353394
GO:0090398	cellular senescence	29	0.22860179	0.0022	0.012422266
GO:2001225	regulation of chloride transport	5	0.228585293	0.0475	0.049962707
GO:1901223	negative regulation of NIK/NF-kappaB signaling	7	0.228577074	0.0249	0.029484292

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0048538	thymus development	16	0.228573048	0.0032	0.013333753
GO:0016525	negative regulation of angiogenesis	47	0.228571801	0.0066	0.015525305
GO:0045088	regulation of innate immune response	173	0.228568953	0.0115	0.018599441
GO:0060147	regulation of posttranscriptional gene silencing	31	0.228568691	0.0054	0.014720792
GO:0060966	regulation of gene silencing by RNA	31	0.228568691	0.0054	0.014720792
GO:0006513	protein monoubiquitination	33	0.22853175	0.0016	0.011845327
GO:2000278	regulation of DNA biosynthetic process	53	0.228518729	0.005	0.014547706
GO:0043534	blood vessel endothelial cell migration	55	0.228469615	0.0019	0.012288367
GO:0050805	negative regulation of synaptic transmission	31	0.228467578	0.0036	0.01353394
GO:0034508	centromere complex assembly	14	0.228466192	0.0134	0.01999969
GO:0009235	cobalamin metabolic process	7	0.228464156	0.015	0.021138192
GO:0007162	negative regulation of cell adhesion	96	0.228435101	0.0122	0.019049527
GO:0098754	detoxification	48	0.228410103	0.0145	0.020788247
GO:0003158	endothelium development	46	0.228405174	0.0059	0.014942532
GO:0050434	positive regulation of viral transcription	20	0.22839734	0.0157	0.021779607
GO:1902882	regulation of response to oxidative stress	39	0.228394155	0.0067	0.015576759
GO:0050821	protein stabilization	82	0.228392326	0.0051	0.014547706
GO:0051851	modification by host of symbiont morphology or physiology	25	0.228351637	0.0243	0.028921902
GO:0016082	synaptic vesicle priming	5	0.2283435	0.013	0.019676963
GO:0002218	activation of innate immune response	136	0.228339645	0.0143	0.020629391
GO:0046364	monosaccharide biosynthetic process	44	0.228289625	0.0085	0.016693954
GO:0060251	regulation of glial cell proliferation	17	0.228267948	0.0139	0.020388077
GO:1901605	alpha-amino acid metabolic process	96	0.228257295	0.007	0.015816335
GO:0051604	protein maturation	96	0.228246362	0.0113	0.018488002
GO:0050651	dermatan sulfate proteoglycan biosynthetic process	11	0.228231756	0.0138	0.020339434
GO:0031331	positive regulation of cellular catabolic process	110	0.228228823	0.0035	0.01351837
GO:0046546	development of primary male sexual characteristics	50	0.228223666	0.0071	0.01583804
GO:0031102	neuron projection regeneration	27	0.228212568	0.0072	0.015844069
GO:0048285	organelle fission	164	0.228165397	0.0016	0.011845327
GO:0017145	stem cell division	17	0.228148583	0.022	0.026944291
GO:0007006	mitochondrial membrane organization	59	0.22812626	0.008	0.016379603
GO:1904321	response to forskolin	5	0.228111813	0.0076	0.016084627
GO:1904322	cellular response to forskolin	5	0.228111813	0.0076	0.016084627
GO:0000212	meiotic spindle organization	6	0.228098899	0.0092	0.017033109
GO:0060401	cytosolic calcium ion transport	66	0.228095051	0.0054	0.014720792
GO:0050000	chromosome localization	32	0.228080285	0.0046	0.014132412
GO:0051303	establishment of chromosome localization	32	0.228080285	0.0046	0.014132412
GO:0090002	establishment of protein localization to plasma membrane	22	0.228061242	< 0.001	< 0.001
GO:0002455	humoral immune response mediated by circulating immunoglobulin	16	0.228056597	0.0365	0.039857035
GO:1903509	liposaccharide metabolic process	57	0.22802937	0.011	0.018323826
GO:0002720	positive regulation of cytokine production involved in immune response	17	0.228013059	0.0096	0.017302743
GO:1903362	regulation of cellular protein catabolic process	117	0.227979969	0.0036	0.01353394
GO:0007015	actin filament organization	158	0.227962746	0.0082	0.016514246
GO:0032275	luteinizing hormone secretion	6	0.227958738	0.0018	0.01210186
GO:0072202	cell differentiation involved in metanephros development	12	0.22790939	0.0149	0.021043429
GO:0014706	striated muscle tissue development	151	0.227887198	0.0038	0.01366393
GO:0051258	protein polymerization	106	0.227880934	0.0051	0.014547706
GO:0098656	anion transmembrane transport	79	0.227858771	0.0089	0.016916437
GO:0060402	calcium ion transport into cytosol	62	0.227857179	0.0053	0.014634479
GO:1901016	regulation of potassium ion transmembrane transporter activity	21	0.227853347	0.0002	0.006319126
GO:0001523	retinoid metabolic process	42	0.22784946	0.0086	0.016782045
GO:0031295	T cell costimulation	24	0.227846274	0.0056	0.014771533
GO:0042474	middle ear morphogenesis	10	0.227838532	0.0301	0.034151923
GO:1903523	negative regulation of blood circulation	14	0.227818855	0.0063	0.015311728
GO:0060135	maternal process involved in female pregnancy	26	0.227807812	0.0033	0.013333753
GO:0090303	positive regulation of wound healing	17	0.227804362	0.0108	0.018152791
GO:1903779	regulation of cardiac conduction	31	0.227761667	0.0056	0.014771533
GO:0051496	positive regulation of stress fiber assembly	26	0.227756678	0.0041	0.013887639
GO:0032469	endoplasmic reticulum calcium ion homeostasis	10	0.227752751	0.005	0.014547706
GO:0010039	response to iron ion	14	0.227673912	0.0125	0.019314538
GO:0043487	regulation of RNA stability	87	0.227654049	0.0132	0.019860109
GO:0022408	negative regulation of cell-cell adhesion	60	0.227651464	0.0134	0.01999969
GO:0010155	regulation of proton transport	10	0.227649477	0.0089	0.016916437
GO:1903902	positive regulation of viral life cycle	48	0.227642917	0.0101	0.017653628
GO:0019432	triglyceride biosynthetic process	17	0.227638577	0.0011	0.010890753
GO:0043434	response to peptide hormone	172	0.2276345	0.0015	0.011704453
GO:0006825	copper ion transport	7	0.227634298	0.0174	0.023064374
GO:0006637	acyl-CoA metabolic process	42	0.227629793	0.0181	0.023607986
GO:0035383	thioester metabolic process	42	0.227629793	0.0181	0.023607986
GO:0018105	peptidyl-serine phosphorylation	94	0.227587886	0.001	0.010787313
GO:0021879	forebrain neuron differentiation	25	0.227547265	0.0112	0.018392048
GO:2000479	regulation of cAMP-dependent protein kinase activity	8	0.227544194	0.0015	0.011704453
GO:0070268	cornification	21	0.227536127	0.0042	0.013948535
GO:0090066	regulation of anatomical structure size	182	0.227522134	0.0022	0.012422266
GO:1900044	regulation of protein K63-linked ubiquitination	6	0.227509748	0.0091	0.016994897
GO:0007339	binding of sperm to zona pellucida	10	0.227502017	0.011	0.018323826
GO:0042542	response to hydrogen peroxide	57	0.227484321	0.0055	0.01475
GO:0055072	iron ion homeostasis	39	0.227455907	0.0084	0.016633151
GO:0060537	muscle tissue development	157	0.227429515	0.0042	0.013948535
GO:0043902	positive regulation of multi-organism process	69	0.227425325	0.0067	0.015576759
GO:1902692	regulation of neuroblast proliferation	13	0.227410654	0.0216	0.026572596
GO:0042088	T-helper 1 type immune response	15	0.227395157	0.0031	0.013277185

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1901030	positive regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	14	0.227386803	0.0008	0.010465158
GO:0048863	stem cell differentiation	109	0.227383781	0.0112	0.018392048
GO:0000186	activation of MAPKK activity	19	0.227363449	0.0009	0.010729485
GO:0045840	positive regulation of mitotic nuclear division	16	0.227355982	0.001	0.010787313
GO:0060253	negative regulation of glial cell proliferation	11	0.227348619	0.0202	0.025368462
GO:0070664	negative regulation of leukocyte proliferation	27	0.227340792	0.0161	0.02211694
GO:0045669	positive regulation of osteoblast differentiation	31	0.227339492	0.0077	0.016177834
GO:1903201	regulation of oxidative stress-induced cell death	29	0.227317398	0.0084	0.016633151
GO:0046916	cellular transition metal ion homeostasis	43	0.227311307	0.005	0.014547706
GO:0010658	striated muscle cell apoptotic process	19	0.227307458	0.001	0.010787313
GO:0015908	fatty acid transport	37	0.227290824	0.0076	0.016084627
GO:0042472	inner ear morphogenesis	30	0.227287694	0.0068	0.015633241
GO:0043523	regulation of neuron apoptotic process	88	0.227266396	0.0028	0.012972436
GO:0006749	glutathione metabolic process	23	0.227252121	0.015	0.021138192
GO:0000038	very long-chain fatty acid metabolic process	9	0.227245768	0.0411	0.044080913
GO:0001501	skeletal system development	199	0.227196323	0.0047	0.014168613
GO:0045926	negative regulation of growth	109	0.227178013	0.0052	0.014616626
GO:0001912	positive regulation of leukocyte mediated cytotoxicity	13	0.227166747	0.0202	0.025368462
GO:0007249	I-kappaB kinase/NF-kappaB signaling	106	0.227144426	0.0061	0.015143924
GO:1905048	regulation of metallopeptidase activity	7	0.227144121	0.0133	0.019917275
GO:0034599	cellular response to oxidative stress	134	0.227143676	0.0059	0.014942532
GO:0000266	mitochondrial fission	18	0.227137642	0.0077	0.016177834
GO:0021895	cerebral cortex neuron differentiation	14	0.227128571	0.0057	0.01480566
GO:0008038	neuron recognition	20	0.227128506	0.0123	0.019143634
GO:0019935	cyclic-nucleotide-mediated signaling	47	0.227116302	0.003	0.013210967
GO:0002250	adaptive immune response	129	0.227098868	0.0064	0.015399417
GO:0043471	regulation of cellular carbohydrate catabolic process	5	0.227092548	0.0021	0.012314604
GO:0002437	inflammatory response to antigenic stimulus	21	0.227007384	0.0243	0.028921902
GO:2000644	regulation of receptor catabolic process	8	0.226996077	0.002	0.012314604
GO:0045921	positive regulation of exocytosis	46	0.226977387	0.0008	0.010465158
GO:0030258	lipid modification	89	0.226909685	0.0045	0.014132412
GO:2000573	positive regulation of DNA biosynthetic process	30	0.226905696	0.0131	0.019786886
GO:0042632	cholesterol homeostasis	31	0.226905403	0.0016	0.011845327
GO:0055092	sterol homeostasis	31	0.226905403	0.0016	0.011845327
GO:0060850	regulation of transcription involved in cell fate commitment	8	0.226901809	0.0035	0.01351837
GO:0097503	sialylation	8	0.226873949	0.0005	0.009604651
GO:0050891	multicellular organismal water homeostasis	21	0.226866082	0.0001	0.004220438
GO:0051000	positive regulation of nitric-oxide synthase activity	10	0.226851662	0.0025	0.012769435
GO:0008654	phospholipid biosynthetic process	122	0.226844709	0.0045	0.014132412
GO:0072348	sulfur compound transport	16	0.226843417	0.0058	0.014878261
GO:0010288	response to lead ion	12	0.226833024	0.0102	0.0177
GO:0000083	regulation of transcription involved in G1/S transition of mitotic cell cycle	12	0.22682255	0.0002	0.006319126
GO:0000280	nuclear division	142	0.226813914	0.0019	0.012288367
GO:0046620	regulation of organ growth	43	0.226808572	0.0071	0.01583804
GO:0038095	Fc-epsilon receptor signaling pathway	71	0.226801102	0.0119	0.018881943
GO:0046718	viral entry into host cell	48	0.226797714	0.0049	0.014447629
GO:0044743	intracellular protein transmembrane import	19	0.226782392	0.0074	0.015911789
GO:0090503	RNA phosphodiester bond hydrolysis, exonucleolytic	12	0.226779681	0.0032	0.013333753
GO:0070555	response to interleukin-1	84	0.226777182	0.0074	0.015911789
GO:0034109	homotypic cell-cell adhesion	35	0.226761864	0.0283	0.032434212
GO:0006310	DNA recombination	83	0.226756431	0.0025	0.012769435
GO:0007568	aging	134	0.226724238	0.0045	0.014132412
GO:0010985	negative regulation of lipoprotein particle clearance	5	0.226717289	0.0263	0.030677143
GO:0001654	eye development	149	0.226708806	0.0068	0.015633241
GO:0030202	heparin metabolic process	6	0.22669729	0.0243	0.028921902
GO:0051304	chromosome separation	27	0.226680997	0.0026	0.012805111
GO:0051702	interaction with symbiont	27	0.226671159	0.023	0.027838811
GO:0031128	developmental induction	10	0.22666779	0.0256	0.03006687
GO:0009152	purine ribonucleotide biosynthetic process	87	0.226652928	0.0079	0.01629604
GO:0050852	T cell receptor signaling pathway	101	0.226639226	0.0087	0.016840777
GO:1903055	positive regulation of extracellular matrix organization	11	0.226637822	0.0016	0.011845327
GO:0046834	lipid phosphorylation	14	0.22663608	< 0.001	< 0.001
GO:0043112	receptor metabolic process	84	0.226634522	0.0026	0.012805111
GO:0003012	muscle system process	188	0.226613999	0.0063	0.015311728
GO:0043101	purine-containing compound salvage	8	0.226611391	0.0308	0.034775552
GO:0042176	regulation of protein catabolic process	188	0.226609471	0.0024	0.012603815
GO:0050851	antigen receptor-mediated signaling pathway	115	0.22660104	0.0093	0.017114131
GO:0002888	positive regulation of myeloid leukocyte mediated immunity	15	0.22658892	0.0166	0.02247277
GO:0071415	cellular response to purine-containing compound	6	0.226586501	0.0283	0.032434212
GO:0033209	tumor necrosis factor-mediated signaling pathway	82	0.226577262	0.008	0.016379603
GO:0045198	establishment of epithelial cell apical/basal polarity	7	0.226576566	0.0466	0.049159132
GO:0016458	gene silencing	68	0.22657649	0.0036	0.01353394
GO:0030205	dermatan sulfate metabolic process	10	0.226563868	0.0136	0.020157703
GO:0045727	positive regulation of translation	57	0.226551787	0.0107	0.018084595
GO:2000785	regulation of autophagosome assembly	19	0.226537693	0.0064	0.015399417
GO:0072676	lymphocyte migration	28	0.226518765	0.012	0.018931514
GO:0048709	oligodendrocyte differentiation	49	0.226489669	0.0135	0.020081554
GO:0009206	purine ribonucleoside triphosphate biosynthetic process	28	0.226479845	0.021	0.026005997
GO:0006584	catecholamine metabolic process	24	0.226474577	0.0073	0.015844069
GO:0009712	catechol-containing compound metabolic process	24	0.226474577	0.0073	0.015844069
GO:0031000	response to caffeine	5	0.226413038	0.0172	0.022941269
GO:1901841	regulation of high voltage-gated calcium channel activity	9	0.226382774	0.013	0.019676963

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0072350	tricarboxylic acid metabolic process	17	0.226382427	0.0238	0.028526451
GO:1903749	positive regulation of establishment of protein localization to mitochondrion	30	0.226378182	0.0034	0.01347416
GO:0006090	pyruvate metabolic process	66	0.226345072	0.0068	0.015633241
GO:0051024	positive regulation of immunoglobulin secretion	7	0.226332033	0.0053	0.014634479
GO:0008016	regulation of heart contraction	103	0.226330367	0.004	0.013824268
GO:0006369	termination of RNA polymerase II transcription	18	0.226328063	0.0025	0.012769435
GO:1904018	positive regulation of vasculature development	83	0.226277849	0.0042	0.013948535
GO:0072001	renal system development	135	0.226271654	0.0086	0.016782045
GO:0033044	regulation of chromosome organization	69	0.226239418	0.0028	0.012972436
GO:0060428	lung epithelium development	11	0.226227764	0.019	0.024347961
GO:0042113	B cell activation	90	0.226210507	0.0028	0.012972436
GO:0030335	positive regulation of cell migration	199	0.226209703	0.0068	0.015633241
GO:0015697	quaternary ammonium group transport	5	0.2262096	0.0069	0.015750415
GO:0061647	histone H3-K9 modification	13	0.22620956	0.0051	0.014547706
GO:0051895	negative regulation of focal adhesion assembly	8	0.226197387	0.0026	0.012805111
GO:1901889	negative regulation of cell junction assembly	8	0.226197387	0.0026	0.012805111
GO:1903392	negative regulation of adherens junction organization	8	0.226197387	0.0026	0.012805111
GO:0051101	regulation of DNA binding	50	0.226192677	0.005	0.014547706
GO:0051783	regulation of nuclear division	75	0.226179088	0.0017	0.012001709
GO:0044088	regulation of vacuole organization	25	0.226165906	0.0099	0.017505138
GO:0003208	cardiac ventricle morphogenesis	31	0.226161622	0.0115	0.018599441
GO:0009409	response to cold	16	0.226155193	0.0011	0.010890753
GO:0031099	regeneration	76	0.226136289	0.009	0.016956012
GO:0045672	positive regulation of osteoclast differentiation	10	0.226131205	0.0272	0.031504487
GO:1903533	regulation of protein targeting	90	0.226113582	0.0078	0.01620539
GO:0016540	protein autoprocessing	8	0.22610814	0.0053	0.014634479
GO:0050655	dermatan sulfate proteoglycan metabolic process	12	0.226039463	0.0136	0.020157703
GO:1901293	nucleoside phosphate biosynthetic process	126	0.226028778	0.0089	0.016916437
GO:0045912	negative regulation of carbohydrate metabolic process	22	0.226022971	0.0012	0.010961137
GO:0045822	negative regulation of heart contraction	10	0.226014714	0.0132	0.019860109
GO:0009581	detection of external stimulus	44	0.226013489	0.0033	0.013333753
GO:0030100	regulation of endocytosis	105	0.226001953	0.0079	0.01629604
GO:0018023	peptidyl-lysine trimethylation	15	0.22599113	0.0055	0.01475
GO:0009408	response to heat	67	0.225968437	0.0052	0.014616626
GO:0007620	copulation	9	0.225960204	0.0338	0.0374175
GO:0010761	fibroblast migration	15	0.225947765	0.0091	0.016994897
GO:0051017	actin filament bundle assembly	67	0.225947259	0.0072	0.015844069
GO:0061572	actin filament bundle organization	67	0.225947259	0.0072	0.015844069
GO:0045638	negative regulation of myeloid cell differentiation	28	0.225920806	0.0052	0.014616626
GO:0071320	cellular response to cAMP	25	0.225895501	0.0173	0.023005658
GO:0045116	protein neddylation	6	0.225893471	0.0189	0.024289798
GO:0007160	cell-matrix adhesion	77	0.225889447	0.0048	0.014269203
GO:2000243	positive regulation of reproductive process	24	0.22588791	0.0075	0.015990044
GO:0010811	positive regulation of cell-substrate adhesion	56	0.225880822	0.0082	0.016514246
GO:0010771	negative regulation of cell morphogenesis involved in differentiation	37	0.225857826	0.0011	0.010890753
GO:0030038	contractile actin filament bundle assembly	41	0.225838253	0.0052	0.014616626
GO:0043149	stress fiber assembly	41	0.225838253	0.0052	0.014616626
GO:0007088	regulation of mitotic nuclear division	66	0.225824206	0.0017	0.012001709
GO:0048732	gland development	178	0.225819609	0.0037	0.013609033
GO:0006919	activation of cysteine-type endopeptidase activity involved in apoptotic process	31	0.225803526	0.01	0.017574468
GO:0051147	regulation of muscle cell differentiation	73	0.225799219	0.001	0.010787313
GO:0009124	nucleoside monophosphate biosynthetic process	51	0.225789923	0.0182	0.023684988
GO:0018195	peptidyl-arginine modification	8	0.2257782	0.0033	0.013333753
GO:0007566	embryo implantation	20	0.225762619	0.0044	0.014132412
GO:0070741	response to interleukin-6	12	0.225761085	0.001	0.010787313
GO:0048806	genitalia development	16	0.225759411	0.0135	0.020081554
GO:0097178	ruffle assembly	20	0.2257253	0.0016	0.011845327
GO:0018904	ether metabolic process	7	0.225723569	0.032	0.035892144
GO:0006766	vitamin metabolic process	61	0.225722898	0.01	0.017574468
GO:0060395	SMAD protein signal transduction	13	0.225698422	0.0332	0.036915846
GO:0090257	regulation of muscle system process	95	0.22567976	0.0077	0.016177834
GO:0033003	regulation of mast cell activation	20	0.225630513	0.0307	0.034703304
GO:0044706	multi-multicellular organism process	93	0.225620917	0.0023	0.012498684
GO:0051281	positive regulation of release of sequestered calcium ion into cytosol	17	0.225617761	0.0056	0.014771533
GO:0030307	positive regulation of cell growth	75	0.225611102	0.0033	0.013333753
GO:0019915	lipid storage	26	0.225602734	0.0028	0.012972436
GO:0048017	inositol lipid-mediated signaling	75	0.225597194	0.0075	0.015990044
GO:0045777	positive regulation of blood pressure	14	0.225586216	0.0016	0.011845327
GO:0030318	melanocyte differentiation	11	0.225564086	0.0117	0.018739446
GO:0032459	regulation of protein oligomerization	17	0.225551905	0.0046	0.014132412
GO:0071219	cellular response to molecule of bacterial origin	79	0.22554207	0.0093	0.017114131
GO:0036293	response to decreased oxygen levels	175	0.225526469	0.0075	0.015990044
GO:0022600	digestive system process	35	0.225522389	0.006	0.015037711
GO:0048535	lymph node development	6	0.225520285	0.0007	0.010220707
GO:0051497	negative regulation of stress fiber assembly	6	0.225515534	0.0168	0.022626974
GO:0044282	small molecule catabolic process	177	0.225508854	0.0101	0.017653628
GO:0061458	reproductive system development	175	0.225507573	0.0034	0.01347416
GO:0003214	cardiac left ventricle morphogenesis	7	0.225489402	0.0187	0.024129301
GO:0034587	piRNA metabolic process	6	0.225481843	0.0102	0.0177
GO:0009165	nucleotide biosynthetic process	124	0.225477427	0.0096	0.017302743
GO:0055076	transition metal ion homeostasis	57	0.225450915	0.0065	0.015491756
GO:0030260	entry into host cell	54	0.225426029	0.0054	0.014720792
GO:0044409	entry into host	54	0.225426029	0.0054	0.014720792

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0051806	entry into cell of other organism involved in symbiotic interaction	54	0.225426029	0.0054	0.014720792
GO:0051828	entry into other organism involved in symbiotic interaction	54	0.225426029	0.0054	0.014720792
GO:0032259	methylation	126	0.225423595	0.0024	0.012603815
GO:0045661	regulation of myoblast differentiation	19	0.225417452	0.0133	0.019917275
GO:0045940	positive regulation of steroid metabolic process	9	0.225406472	0.0207	0.025805821
GO:0019377	glycolipid catabolic process	8	0.225335204	0.0054	0.014720792
GO:0034198	cellular response to amino acid starvation	29	0.225322514	0.0029	0.013089617
GO:0040001	establishment of mitotic spindle localization	11	0.225303987	0.0015	0.011704453
GO:0048608	reproductive structure development	172	0.225275447	0.0038	0.01366393
GO:0022613	ribonucleoprotein complex biogenesis	155	0.22526952	0.0066	0.015525305
GO:0009101	glycoprotein biosynthetic process	164	0.225267475	0.0034	0.01347416
GO:0048284	organelle fusion	63	0.22524203	0.0067	0.015576759
GO:1902600	hydrogen ion transmembrane transport	52	0.225241957	0.0091	0.016994897
GO:0061418	regulation of transcription from RNA polymerase II promoter in response to hypoxia	51	0.225236267	0.0191	0.02440579
GO:0030252	growth hormone secretion	11	0.225220114	< 0.001	< 0.001
GO:0009416	response to light stimulus	123	0.225211893	0.0012	0.010961137
GO:0072678	T cell migration	21	0.225210129	0.0208	0.025885837
GO:0048661	positive regulation of smooth muscle cell proliferation	37	0.22518836	0.0127	0.019457181
GO:0044030	regulation of DNA methylation	6	0.225150122	0.0141	0.020504577
GO:0044829	positive regulation by host of viral genome replication	5	0.225148092	0.0301	0.034151923
GO:0001945	lymph vessel development	10	0.225138762	0.0065	0.015491756
GO:1903432	regulation of TORC1 signaling	18	0.225136516	0.0038	0.01366393
GO:0035601	protein deacylation	34	0.225111299	0.0005	0.009604651
GO:0098732	macromolecule deacylation	34	0.225111299	0.0005	0.009604651
GO:0031646	positive regulation of neurological system process	17	0.225110042	0.0017	0.012001709
GO:0006801	superoxide metabolic process	27	0.225091356	0.016	0.022026667
GO:0007051	spindle organization	56	0.225082872	0.0058	0.014878261
GO:0048305	immunoglobulin secretion	12	0.225037821	0.0006	0.009940401
GO:0007044	cell-substrate junction assembly	45	0.225032105	0.0031	0.013277185
GO:0071625	vocalization behavior	9	0.225021623	0.0052	0.014616626
GO:0055078	sodium ion homeostasis	14	0.225003482	0.0092	0.017033109
GO:1903719	regulation of I-kappaB phosphorylation	5	0.224987156	0.0047	0.014168613
GO:0006164	purine nucleotide biosynthetic process	90	0.224975666	0.0083	0.016559903
GO:0048569	post-embryonic animal organ development	5	0.224959944	0.0156	0.021692929
GO:0016042	lipid catabolic process	127	0.224951937	0.0115	0.018599441
GO:0009135	purine nucleoside diphosphate metabolic process	61	0.224940371	0.0071	0.01583804
GO:0009179	purine ribonucleoside diphosphate metabolic process	61	0.224940371	0.0071	0.01583804
GO:0072401	signal transduction involved in DNA integrity checkpoint	23	0.224934073	0.0016	0.011845327
GO:0072422	signal transduction involved in DNA damage checkpoint	23	0.224934073	0.0016	0.011845327
GO:2001020	regulation of response to DNA damage stimulus	73	0.22492309	0.0058	0.014878261
GO:0006564	L-serine biosynthetic process	5	0.224905521	0.0188	0.02420971
GO:0061028	establishment of endothelial barrier	14	0.224862797	0.006	0.015037711
GO:0060562	epithelial tube morphogenesis	120	0.224857966	0.0067	0.015576759
GO:0042158	lipoprotein biosynthetic process	39	0.224855995	0.0111	0.018389742
GO:0021683	cerebellar granular layer morphogenesis	5	0.224843064	0.0307	0.034703304
GO:0050994	regulation of lipid catabolic process	24	0.224840753	0.0027	0.012827773
GO:0006869	lipid transport	123	0.224775635	0.0052	0.014616626
GO:1903828	negative regulation of cellular protein localization	68	0.224774014	0.0041	0.013887639
GO:0048015	phosphatidylinositol-mediated signaling	74	0.224751189	0.0073	0.015844069
GO:0070254	mucus secretion	8	0.224732501	0.0013	0.011218806
GO:2000134	negative regulation of G1/S transition of mitotic cell cycle	36	0.224727912	0.0035	0.01351837
GO:0034504	protein localization to nucleus	104	0.224721138	0.0086	0.016782045
GO:0001885	endothelial cell development	20	0.224715364	0.0048	0.014269203
GO:0051098	regulation of binding	173	0.224701759	0.0032	0.013333753
GO:0035176	social behavior	28	0.224663755	0.0024	0.012603815
GO:0051703	intraspecies interaction between organisms	28	0.224663755	0.0024	0.012603815
GO:0019932	second-messenger-mediated signaling	145	0.224651476	0.0036	0.01353394
GO:0006418	tRNA aminoacylation for protein translation	20	0.224648502	0.0105	0.017924712
GO:0016197	endosomal transport	132	0.224634429	0.0013	0.011218806
GO:0048864	stem cell development	32	0.224630539	0.0093	0.017114131
GO:0006906	vesicle fusion	30	0.2246106	0.0046	0.014132412
GO:0090174	organelle membrane fusion	30	0.2246106	0.0046	0.014132412
GO:0097502	mannosylation	19	0.224597629	0.0169	0.022703485
GO:0031124	mRNA 3'-end processing	41	0.224593287	0.0043	0.014102439
GO:1900026	positive regulation of substrate adhesion-dependent cell spreading	20	0.224591487	0.0161	0.02211694
GO:0051297	centrosome organization	40	0.224585041	0.0026	0.012805111
GO:0050678	regulation of epithelial cell proliferation	134	0.224576376	0.0116	0.018682786
GO:0045670	regulation of osteoclast differentiation	24	0.22457177	0.0067	0.015576759
GO:0034330	cell junction organization	111	0.22455444	0.0041	0.013887639
GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	57	0.224528475	0.023	0.027838811
GO:0002758	innate immune response-activating signal transduction	127	0.224527868	0.0136	0.020157703
GO:0042692	muscle cell differentiation	147	0.224522358	0.0032	0.013333753
GO:0010876	lipid localization	139	0.224521991	0.0038	0.01366393
GO:0006506	GPI anchor biosynthetic process	14	0.224489055	0.0325	0.036312077
GO:0002360	T cell lineage commitment	6	0.224481281	0.0106	0.018010344
GO:0009118	regulation of nucleoside metabolic process	49	0.224470148	0.0091	0.016994897
GO:1903578	regulation of ATP metabolic process	49	0.224470148	0.0091	0.016994897
GO:0072522	purine-containing compound biosynthetic process	94	0.224466476	0.0095	0.01725157
GO:0045717	negative regulation of fatty acid biosynthetic process	8	0.224420217	0.0269	0.031225818
GO:0051205	protein insertion into membrane	20	0.224413965	0.0051	0.014547706
GO:0051445	regulation of meiotic cell cycle	15	0.22439239	0.0034	0.01347416
GO:0045776	negative regulation of blood pressure	15	0.224389107	0.0089	0.016916437
GO:0001666	response to hypoxia	170	0.224385332	0.008	0.016379603

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0003016	respiratory system process	12	0.224358613	0.001	0.010787313
GO:0007007	inner mitochondrial membrane organization	20	0.224299028	0.0126	0.019370699
GO:0090169	regulation of spindle assembly	7	0.224292281	0.021	0.026005997
GO:1901673	regulation of mitotic spindle assembly	7	0.224292281	0.021	0.026005997
GO:0051348	negative regulation of transferase activity	130	0.224239447	0.0039	0.013791927
GO:0006575	cellular modified amino acid metabolic process	72	0.224211649	0.0058	0.014878261
GO:0051988	regulation of attachment of spindle microtubules to kinetochore	7	0.224201946	0.0056	0.014771533
GO:0019471	4-hydroxyproline metabolic process	7	0.224195838	0.015	0.021138192
GO:0055024	regulation of cardiac muscle tissue development	36	0.224175691	0.0055	0.01475
GO:0002532	production of molecular mediator involved in inflammatory response	27	0.224159302	0.0064	0.015399417
GO:0046688	response to copper ion	15	0.224146709	0.0124	0.019242297
GO:0031670	cellular response to nutrient	14	0.224117998	0.0199	0.025133639
GO:0033673	negative regulation of kinase activity	118	0.22411767	0.0038	0.01366393
GO:1902932	positive regulation of alcohol biosynthetic process	10	0.224117424	0.0461	0.04873838
GO:0051235	maintenance of location	125	0.224110292	0.0036	0.01353394
GO:0014003	oligodendrocyte development	18	0.224106871	0.0046	0.014132412
GO:0032368	regulation of lipid transport	39	0.224104141	0.0121	0.018970228
GO:0032945	negative regulation of mononuclear cell proliferation	25	0.224098039	0.0192	0.02450649
GO:0050672	negative regulation of lymphocyte proliferation	25	0.224098039	0.0192	0.02450649
GO:0071526	semaphorin-plexin signaling pathway	9	0.224094849	0.0141	0.020504577
GO:1901653	cellular response to peptide	158	0.224089773	0.0015	0.011704453
GO:1901342	regulation of vasculature development	141	0.224078209	0.0048	0.014269203
GO:0006625	protein targeting to peroxisome	40	0.224076574	0.0096	0.017302743
GO:0043574	peroxisomal transport	40	0.224076574	0.0096	0.017302743
GO:0072662	protein localization to peroxisome	40	0.224076574	0.0096	0.017302743
GO:0072663	establishment of protein localization to peroxisome	40	0.224076574	0.0096	0.017302743
GO:0006818	hydrogen transport	60	0.224055529	0.0083	0.016559903
GO:0015992	proton transport	60	0.224055529	0.0083	0.016559903
GO:1903364	positive regulation of cellular protein catabolic process	71	0.224035914	0.0048	0.014269203
GO:1904589	regulation of protein import	48	0.224011018	0.0128	0.019522448
GO:0009185	ribonucleoside diphosphate metabolic process	62	0.223984744	0.0076	0.016084627
GO:0046850	regulation of bone remodeling	21	0.223950996	0.0035	0.01351837
GO:0051339	regulation of lyase activity	35	0.223942937	0.0037	0.013609033
GO:0045744	negative regulation of G-protein coupled receptor protein signaling pathway	20	0.223919234	0.0176	0.023223003
GO:0051250	negative regulation of lymphocyte activation	50	0.223917666	0.0112	0.018392048
GO:0048713	regulation of oligodendrocyte differentiation	20	0.223913273	0.0269	0.031225818
GO:0010632	regulation of epithelial cell migration	109	0.2239004	0.0032	0.013333753
GO:2000322	regulation of glucocorticoid receptor signaling pathway	6	0.223889107	0.0002	0.006319126
GO:0051291	protein heterooligomerization	45	0.223884643	0.0096	0.017302743
GO:1904707	positive regulation of vascular smooth muscle cell proliferation	18	0.223879532	0.0115	0.018599441
GO:0002064	epithelial cell development	86	0.223869263	0.0019	0.012288367
GO:0007018	microtubule-based movement	109	0.223858495	0.0081	0.016514175
GO:0032984	macromolecular complex disassembly	132	0.22385417	0.0099	0.017505138
GO:0007033	vacuole organization	89	0.223835397	0.0065	0.015491756
GO:0043401	steroid hormone mediated signaling pathway	63	0.223827937	0.0034	0.01347416
GO:0031397	negative regulation of protein ubiquitination	39	0.223796574	0.0068	0.015633241
GO:0030198	extracellular matrix organization	152	0.223781846	0.0086	0.016782045
GO:0043062	extracellular structure organization	152	0.223781846	0.0086	0.016782045
GO:1990748	cellular detoxification	46	0.223775838	0.0148	0.020979063
GO:0001893	maternal placenta development	15	0.223759096	0.0028	0.012972436
GO:0060080	inhibitory postsynaptic potential	9	0.223754057	0.0103	0.017772187
GO:0098813	nuclear chromosome segregation	91	0.223746827	0.0027	0.012827773
GO:0043280	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	50	0.223690722	0.0084	0.016633151
GO:0050687	negative regulation of defense response to virus	11	0.223679896	0.0075	0.015990044
GO:0010824	regulation of centrosome duplication	17	0.223665622	0.0022	0.012422266
GO:0006476	protein deacetylation	32	0.223664855	0.0004	0.008964341
GO:0043949	regulation of cAMP-mediated signaling	17	0.223657618	0.0007	0.010220707
GO:0050829	defense response to Gram-negative bacterium	21	0.223614647	0.0196	0.0248852
GO:0046686	response to cadmium ion	28	0.223614585	0.021	0.026005997
GO:0006892	post-Golgi vesicle-mediated transport	33	0.223613065	0.0009	0.010729485
GO:0032212	positive regulation of telomere maintenance via telomerase	17	0.223612723	0.018	0.023514686
GO:0044275	cellular carbohydrate catabolic process	18	0.223605114	0.0036	0.01353394
GO:0035239	tube morphogenesis	138	0.223597837	0.0059	0.014942532
GO:0007292	female gamete generation	40	0.22358071	0.0008	0.010465158
GO:1904262	negative regulation of TORC1 signaling	6	0.223580494	0.0037	0.013609033
GO:0010739	positive regulation of protein kinase A signaling	5	0.223565419	0.0098	0.017418875
GO:1901565	organonitrogen compound catabolic process	167	0.223561482	0.0091	0.016994897
GO:0046390	ribose phosphate biosynthetic process	99	0.223556168	0.0073	0.015844069
GO:0014823	response to activity	28	0.22354341	0.0041	0.013887639
GO:0007019	microtubule depolymerization	12	0.22353201	0.0053	0.014634479
GO:2001251	negative regulation of chromosome organization	30	0.22352931	0.0016	0.011845327
GO:0051580	regulation of neurotransmitter uptake	7	0.223526287	0.0011	0.010890753
GO:1904358	positive regulation of telomere maintenance via telomere lengthening	19	0.223523968	0.0175	0.023154462
GO:0065002	intracellular protein transmembrane transport	25	0.223474144	0.0053	0.014634479
GO:0070098	chemokine-mediated signaling pathway	20	0.223442255	0.0144	0.02072711
GO:2001135	regulation of endocytic recycling	5	0.223424956	0.0035	0.01351837
GO:0048857	neural nucleus development	31	0.223421286	0.0057	0.01480566
GO:0032623	interleukin-2 production	24	0.223411934	0.0138	0.020339434
GO:0032007	negative regulation of TOR signaling	17	0.223359054	0.0001	0.004220438
GO:0001819	positive regulation of cytokine production	162	0.223350996	0.0128	0.019522448
GO:0051384	response to glucocorticoid	47	0.223343195	0.018	0.023514686
GO:0021782	glial cell development	41	0.223332266	0.0071	0.01583804
GO:0002440	production of molecular mediator of immune response	70	0.223305207	0.0066	0.015525305

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1903203	regulation of oxidative stress-induced neuron death	16	0.223298309	0.0086	0.016782045
GO:0045665	negative regulation of neuron differentiation	101	0.223292545	0.001	0.010787313
GO:0050886	endocrine process	28	0.223283466	0.007	0.015816335
GO:0046031	ADP metabolic process	54	0.223273009	0.0071	0.01583804
GO:0035821	modification of morphology or physiology of other organism	56	0.223269096	0.0082	0.016514246
GO:0045927	positive regulation of growth	113	0.223251339	0.0046	0.014132412
GO:0018209	peptidyl-serine modification	106	0.223247399	0.0009	0.010729485
GO:0090316	positive regulation of intracellular protein transport	82	0.223235241	0.004	0.013824268
GO:0046661	male sex differentiation	56	0.223206968	0.0082	0.016514246
GO:0018126	protein hydroxylation	14	0.223197435	0.0116	0.018682786
GO:0016266	O-glycan processing	25	0.223192389	0.0046	0.014132412
GO:0010970	transport along microtubule	73	0.223060993	0.0047	0.014168613
GO:0099111	microtubule-based transport	73	0.223060993	0.0047	0.014168613
GO:0001188	RNA polymerase I transcriptional preinitiation complex assembly	5	0.223022485	0.0196	0.0248852
GO:0048524	positive regulation of viral process	51	0.223021819	0.0082	0.016514246
GO:0045598	regulation of fat cell differentiation	56	0.222986638	0.0019	0.012288367
GO:0032387	negative regulation of intracellular transport	43	0.222954785	0.016	0.022026667
GO:0046851	negative regulation of bone remodeling	8	0.22294788	0.0001	0.004220438
GO:0030838	positive regulation of actin filament polymerization	40	0.222931165	0.0026	0.012805111
GO:0051571	positive regulation of histone H3-K4 methylation	6	0.222920507	0.0198	0.025062084
GO:0031294	lymphocyte costimulation	25	0.222901614	0.0033	0.013333753
GO:0032845	negative regulation of homeostatic process	80	0.222894105	0.0033	0.013333753
GO:0035428	hexose transmembrane transport	8	0.222871591	0.0174	0.023064374
GO:1904659	glucose transmembrane transport	8	0.222871591	0.0174	0.023064374
GO:0061162	establishment of monopolar cell polarity	10	0.222846777	0.0239	0.028592965
GO:0033077	T cell differentiation in thymus	26	0.222820382	0.0037	0.013609033
GO:0071594	thymocyte aggregation	26	0.222820382	0.0037	0.013609033
GO:0050771	negative regulation of axonogenesis	26	0.222816894	0.0011	0.010890753
GO:0007067	mitotic nuclear division	103	0.222808736	0.002	0.012314604
GO:0050953	sensory perception of light stimulus	73	0.222792464	0.0021	0.012314604
GO:0044786	cell cycle DNA replication	23	0.222740308	0.0023	0.012498684
GO:0048799	animal organ maturation	7	0.222735117	0.0089	0.016916437
GO:0070977	bone maturation	7	0.222735117	0.0089	0.016916437
GO:0009584	detection of visible light	19	0.222713693	0.0005	0.009604651
GO:0031547	brain-derived neurotrophic factor receptor signaling pathway	6	0.222697632	< 0.001	< 0.001
GO:0046341	CDP-diacylglycerol metabolic process	10	0.222696336	0.0038	0.01366393
GO:1904754	positive regulation of vascular associated smooth muscle cell migration	9	0.222695688	0.0041	0.013887639
GO:0009260	ribonucleotide biosynthetic process	94	0.222690629	0.0072	0.015844069
GO:0015698	inorganic anion transport	61	0.222685683	0.0073	0.015844069
GO:0048681	negative regulation of axon regeneration	7	0.222662183	0.0114	0.018551872
GO:0043501	skeletal muscle adaptation	7	0.222661998	0.0426	0.045512417
GO:0038128	ERBB2 signaling pathway	11	0.222649982	0.0053	0.014634479
GO:0034405	response to fluid shear stress	11	0.222627011	0.0012	0.010961137
GO:0042306	regulation of protein import into nucleus	46	0.222608532	0.0129	0.019597425
GO:0031644	regulation of neurological system process	43	0.222596334	0.002	0.012314604
GO:0090287	regulation of cellular response to growth factor stimulus	115	0.222544904	0.0052	0.014616626
GO:0060968	regulation of gene silencing	34	0.222544691	0.0055	0.01475
GO:0001503	ossification	160	0.222514181	0.0053	0.014634479
GO:0002221	pattern recognition receptor signaling pathway	70	0.222502653	0.0128	0.019522448
GO:0006839	mitochondrial transport	127	0.222470466	0.0075	0.015990044
GO:0010823	negative regulation of mitochondrion organization	33	0.222458755	0.0087	0.016840777
GO:0035794	positive regulation of mitochondrial membrane permeability	27	0.222455296	0.004	0.013824268
GO:1902686	mitochondrial outer membrane permeabilization involved in programmed cell death	27	0.222455296	0.004	0.013824268
GO:1905710	positive regulation of membrane permeability	27	0.222455296	0.004	0.013824268
GO:0051402	neuron apoptotic process	97	0.222453095	0.0032	0.013333753
GO:0008334	histone mRNA metabolic process	16	0.222448355	0.0027	0.012827773
GO:1901201	regulation of extracellular matrix assembly	8	0.222445601	0.0293	0.033401538
GO:0033559	unsaturated fatty acid metabolic process	46	0.222436108	0.0172	0.022941269
GO:0006636	unsaturated fatty acid biosynthetic process	29	0.22243166	0.026	0.030450071
GO:0009755	hormone-mediated signaling pathway	78	0.222413389	0.0037	0.013609033
GO:0006352	DNA-templated transcription, initiation	97	0.222404283	0.0041	0.013887639
GO:0070534	protein K63-linked ubiquitination	26	0.22240284	0.0067	0.015576759
GO:0070498	interleukin-1-mediated signaling pathway	55	0.222396762	0.0186	0.024075487
GO:0007601	visual perception	72	0.222382414	0.0021	0.012314604
GO:0042110	T cell activation	171	0.222382221	0.0121	0.018970228
GO:0070489	T cell aggregation	171	0.222382221	0.0121	0.018970228
GO:0043542	endothelial cell migration	107	0.222374696	0.003	0.013210967
GO:0031342	negative regulation of cell killing	8	0.222370608	0.0427	0.045577146
GO:0010874	regulation of cholesterol efflux	9	0.222341938	0.0205	0.025639412
GO:0002576	platelet degranulation	61	0.222337881	0.0204	0.025564109
GO:1902807	negative regulation of cell cycle G1/S phase transition	38	0.222336721	0.003	0.013210967
GO:0051302	regulation of cell division	59	0.222328783	0.0046	0.014132412
GO:0006757	ATP generation from ADP	48	0.222322502	0.0064	0.015399417
GO:0070168	negative regulation of biomineral tissue development	12	0.222304253	0.0033	0.013333753
GO:0002224	toll-like receptor signaling pathway	55	0.222304196	0.0126	0.019370699
GO:0033273	response to vitamin	36	0.222296262	0.0197	0.024979254
GO:0021781	glial cell fate commitment	9	0.222272398	0.0189	0.024289798
GO:0006959	humoral immune response	60	0.222253112	0.0202	0.025368462
GO:0071901	negative regulation of protein serine/threonine kinase activity	64	0.22225174	0.0031	0.013277185
GO:0048251	elastic fiber assembly	6	0.222251233	0.0331	0.03684717
GO:0016485	protein processing	81	0.222251009	0.0166	0.022472777
GO:0051153	regulation of striated muscle cell differentiation	40	0.222249808	0.0005	0.009604651
GO:0032786	positive regulation of DNA-templated transcription, elongation	13	0.222219836	0.0056	0.014771533

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0043393	regulation of protein binding	102	0.22221485	0.0036	0.01353394
GO:0043616	keratinocyte proliferation	22	0.222183499	0.0138	0.020339434
GO:0050863	regulation of T cell activation	115	0.222181081	0.0107	0.018084595
GO:0060038	cardiac muscle cell proliferation	21	0.222178793	0.0227	0.027637692
GO:0008543	fibroblast growth factor receptor signaling pathway	45	0.222166403	0.0082	0.016514246
GO:0046794	transport of virus	28	0.222165388	0.0093	0.017114131
GO:0075733	intracellular transport of virus	28	0.222165388	0.0093	0.017114131
GO:0009201	ribonucleoside triphosphate biosynthetic process	30	0.222141524	0.0186	0.024075487
GO:0034135	regulation of toll-like receptor 2 signaling pathway	5	0.222136686	0.0424	0.045323868
GO:0030449	regulation of complement activation	20	0.222130725	0.0379	0.041160368
GO:2000257	regulation of protein activation cascade	20	0.222130725	0.0379	0.041160368
GO:0031334	positive regulation of protein complex assembly	100	0.222122873	0.0038	0.01366393
GO:0003231	cardiac ventricle development	55	0.222104951	0.0077	0.016177834
GO:0030104	water homeostasis	24	0.222083807	0.0001	0.004220438
GO:0006469	negative regulation of protein kinase activity	109	0.222075649	0.0042	0.013948535
GO:0009620	response to fungus	11	0.222039431	0.0116	0.018682786
GO:0061014	positive regulation of mRNA catabolic process	13	0.222039123	0.0046	0.014132412
GO:0097164	ammonium ion metabolic process	91	0.221977666	0.0132	0.019860109
GO:2000641	regulation of early endosome to late endosome transport	10	0.22196927	0.0098	0.017418875
GO:0007159	leukocyte cell-cell adhesion	195	0.221944697	0.0118	0.018836996
GO:0010665	regulation of cardiac muscle cell apoptotic process	16	0.221941622	0.0006	0.009940401
GO:0071593	lymphocyte aggregation	172	0.221935845	0.012	0.018931514
GO:0022407	regulation of cell-cell adhesion	158	0.221928173	0.0114	0.018551872
GO:0045165	cell fate commitment	76	0.221922871	0.0054	0.014720792
GO:0034982	mitochondrial protein processing	5	0.221913033	0.0245	0.029070183
GO:1903793	positive regulation of anion transport	18	0.221902955	0.0065	0.015491756
GO:0046337	phosphatidylethanolamine metabolic process	10	0.221900723	0.0028	0.012972436
GO:0045821	positive regulation of glycolytic process	8	0.221891167	0.0133	0.019917275
GO:0090288	negative regulation of cellular response to growth factor stimulus	62	0.221860909	0.0141	0.020504577
GO:0046902	regulation of mitochondrial membrane permeability	32	0.221782807	0.0055	0.01475
GO:0090130	tissue migration	145	0.221779085	0.0031	0.013277185
GO:1903037	regulation of leukocyte cell-cell adhesion	128	0.221771114	0.0093	0.017114131
GO:2000060	positive regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process	9	0.221750916	0.006	0.015037711
GO:0070486	leukocyte aggregation	173	0.221716973	0.0122	0.019049527
GO:0009202	deoxyribonucleoside triphosphate biosynthetic process	5	0.221685234	0.0227	0.027637692
GO:0043094	cellular metabolic compound salvage	18	0.221663523	0.0212	0.026203164
GO:0051249	regulation of lymphocyte activation	166	0.221661565	0.0082	0.016514246
GO:0003015	heart process	121	0.221650888	0.0042	0.013948535
GO:0010507	negative regulation of autophagy	42	0.221634902	0.0051	0.014547706
GO:0002821	positive regulation of adaptive immune response	31	0.221620813	0.0037	0.013609033
GO:0051306	mitotic sister chromatid separation	22	0.221597863	0.0018	0.01210186
GO:0034113	heterotypic cell-cell adhesion	21	0.221585261	0.0274	0.03166636
GO:0002181	cytoplasmic translation	25	0.221573589	0.0287	0.032827577
GO:0042428	serotonin metabolic process	5	0.221571205	0.0007	0.010220707
GO:0032231	regulation of actin filament bundle assembly	43	0.221560037	0.0107	0.018084595
GO:0030516	regulation of axon extension	39	0.221559251	0.0003	0.007956881
GO:0007224	smoothened signaling pathway	55	0.221536266	0.0142	0.020567234
GO:2001234	negative regulation of apoptotic signaling pathway	92	0.221532537	0.01	0.017574468
GO:0008037	cell recognition	51	0.221461617	0.0064	0.015399417
GO:1902430	negative regulation of beta-amyloid formation	8	0.221446388	0.0027	0.012827773
GO:0045446	endothelial cell differentiation	37	0.221433523	0.0075	0.015990044
GO:0031529	ruffle organization	27	0.221421019	0.0038	0.01366393
GO:0007127	meiosis I	26	0.22140967	0.0065	0.015491756
GO:1903845	negative regulation of cellular response to transforming growth factor beta stimulus	32	0.22134799	0.013	0.019676963
GO:0015865	purine nucleotide transport	6	0.221340944	< 0.001	< 0.001
GO:0015867	ATP transport	6	0.221340944	< 0.001	< 0.001
GO:0015868	purine ribonucleotide transport	6	0.221340944	< 0.001	< 0.001
GO:0051503	adenine nucleotide transport	6	0.221340944	< 0.001	< 0.001
GO:0001933	negative regulation of protein phosphorylation	189	0.221305303	0.0056	0.014771533
GO:0043624	cellular protein complex disassembly	100	0.221294594	0.0136	0.020157703
GO:0060306	regulation of membrane repolarization	15	0.221274211	0.0104	0.017832977
GO:0030801	positive regulation of cyclic nucleotide metabolic process	21	0.221273964	0.0008	0.010465158
GO:0030804	positive regulation of cyclic nucleotide biosynthetic process	21	0.221273964	0.0008	0.010465158
GO:0051602	response to electrical stimulus	18	0.221268884	0.0245	0.029070183
GO:0002040	sprouting angiogenesis	50	0.221240624	0.0042	0.013948535
GO:0035116	embryonic hindlimb morphogenesis	7	0.221181099	0.0171	0.022860624
GO:0010769	regulation of cell morphogenesis involved in differentiation	132	0.221178058	0.0009	0.010729485
GO:0019751	polyol metabolic process	43	0.22116434	0.0105	0.017924712
GO:0060236	regulation of mitotic spindle organization	14	0.221160274	0.0114	0.018551872
GO:0090224	regulation of spindle organization	14	0.221160274	0.0114	0.018551872
GO:0033013	tetrapyrrole metabolic process	27	0.221155191	0.0199	0.025133639
GO:0002824	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	28	0.221141995	0.0038	0.01366393
GO:0043900	regulation of multi-organism process	123	0.221141535	0.0099	0.017505138
GO:0071472	cellular response to salt stress	6	0.221113318	0.0292	0.033300671
GO:0002716	negative regulation of natural killer cell mediated immunity	5	0.221092283	0.0435	0.046336957
GO:0045953	negative regulation of natural killer cell mediated cytotoxicity	5	0.221092283	0.0435	0.046336957
GO:0014074	response to purine-containing compound	66	0.221078685	0.0065	0.015491756
GO:0043537	negative regulation of blood vessel endothelial cell migration	19	0.221077183	0.0094	0.017156187
GO:1901976	regulation of cell cycle checkpoint	12	0.221071205	0.0005	0.009604651
GO:0045766	positive regulation of angiogenesis	75	0.221068319	0.0053	0.014634479
GO:0090330	regulation of platelet aggregation	8	0.221063808	0.0356	0.03903645
GO:0072384	organelle transport along microtubule	41	0.22106107	0.0046	0.014132412

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0044058	regulation of digestive system process	16	0.221048906	0.0011	0.010890753
GO:0071356	cellular response to tumor necrosis factor	117	0.221047327	0.0068	0.015633241
GO:0006305	DNA alkylation	17	0.221011243	0.0058	0.014878261
GO:0006306	DNA methylation	17	0.221011243	0.0058	0.014878261
GO:0009988	cell-cell recognition	20	0.221006178	0.0139	0.020388077
GO:0033860	regulation of NAD(P)H oxidase activity	5	0.220993803	0.0208	0.025885837
GO:0033864	positive regulation of NAD(P)H oxidase activity	5	0.220993803	0.0208	0.025885837
GO:0032682	negative regulation of chemokine production	8	0.22098687	0.0152	0.0213213
GO:0009265	2'-deoxyribonucleotide biosynthetic process	6	0.220944865	0.0259	0.0303391
GO:0046385	deoxyribose phosphate biosynthetic process	6	0.220944865	0.0259	0.0303391
GO:0051492	regulation of stress fiber assembly	36	0.220937703	0.0104	0.017832977
GO:0006767	water-soluble vitamin metabolic process	41	0.220936264	0.0077	0.016177834
GO:0043010	camera-type eye development	128	0.220906147	0.0087	0.016840777
GO:0045472	response to ether	5	0.220895064	0.0121	0.018970228
GO:0044724	single-organism carbohydrate catabolic process	79	0.220820965	0.0062	0.015209334
GO:0016242	negative regulation of macroautophagy	18	0.220816151	0.0161	0.02211694
GO:0070936	protein K48-linked ubiquitination	25	0.220811408	0.0016	0.011845327
GO:0002685	regulation of leukocyte migration	72	0.220794284	0.0126	0.019370699
GO:0060042	retina morphogenesis in camera-type eye	24	0.220787805	0.009	0.016956012
GO:0007405	neuroblast proliferation	26	0.220787195	0.0191	0.02440579
GO:0072655	establishment of protein localization to mitochondrion	74	0.22078668	0.0075	0.015990044
GO:0030488	tRNA methylation	8	0.220766263	0.0281	0.032268957
GO:0006359	regulation of transcription from RNA polymerase III promoter	10	0.220754342	0.0061	0.015143924
GO:0072378	blood coagulation, fibrin clot formation	9	0.220751721	0.0078	0.01620539
GO:1903204	negative regulation of oxidative stress-induced neuron death	12	0.220709248	0.0049	0.014447629
GO:0030512	negative regulation of transforming growth factor beta receptor signaling pathway	31	0.220670291	0.0141	0.020504577
GO:0071674	mononuclear cell migration	21	0.220665315	0.0261	0.030517735
GO:1904896	ESCRT complex disassembly	6	0.220632365	0.0145	0.020788247
GO:1904903	ESCRT III complex disassembly	6	0.220632365	0.0145	0.020788247
GO:0043414	macromolecule methylation	100	0.220627808	0.0012	0.010961137
GO:0071887	leukocyte apoptotic process	34	0.220624641	0.0024	0.012603815
GO:0006893	Golgi to plasma membrane transport	17	0.220596286	0.0007	0.010220707
GO:1900407	regulation of cellular response to oxidative stress	34	0.220580966	0.0074	0.015911789
GO:0006907	pinocytosis	8	0.220567198	0.0098	0.017418875
GO:0030902	hindbrain development	57	0.220537545	0.006	0.015037711
GO:0002223	stimulatory C-type lectin receptor signaling pathway	62	0.220536512	0.0129	0.019597425
GO:0090101	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	44	0.220493147	0.0108	0.018152791
GO:0010310	regulation of hydrogen peroxide metabolic process	8	0.220465479	0.0106	0.018010344
GO:0006067	ethanol metabolic process	5	0.220464345	0.0313	0.035223161
GO:0043270	positive regulation of ion transport	112	0.220464345	0.0057	0.01480566
GO:0007059	chromosome segregation	107	0.220448032	0.0026	0.012805111
GO:0030865	cortical cytoskeleton organization	13	0.220438429	0.0067	0.015576759
GO:0002479	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	47	0.220415877	0.0225	0.027440413
GO:0034142	toll-like receptor 4 signaling pathway	14	0.22041057	0.0229	0.027770092
GO:0035019	somatic stem cell population maintenance	36	0.220400347	0.0114	0.018551872
GO:0045445	myoblast differentiation	32	0.22036955	0.0078	0.01620539
GO:0003205	cardiac chamber development	73	0.220346801	0.0045	0.014132412
GO:0098869	cellular oxidant detoxification	44	0.22034098	0.0158	0.021871104
GO:0046148	pigment biosynthetic process	32	0.220337317	0.009	0.016956012
GO:0035196	production of miRNAs involved in gene silencing by miRNA	13	0.220332175	0.0115	0.018599441
GO:0010801	negative regulation of peptidyl-threonine phosphorylation	9	0.220308131	0.024	0.028671074
GO:0072376	protein activation cascade	33	0.220282621	0.0175	0.023154462
GO:1901998	toxin transport	20	0.220273152	0.0108	0.018152791
GO:0048638	regulation of developmental growth	143	0.220252217	0.0017	0.012001709
GO:0045765	regulation of angiogenesis	129	0.220240445	0.0061	0.015143924
GO:0006684	sphingomyelin metabolic process	9	0.220238878	0.0095	0.01725157
GO:0050868	negative regulation of T cell activation	35	0.220223588	0.0136	0.020157703
GO:0090026	positive regulation of monocyte chemotaxis	6	0.22021469	0.0444	0.04718265
GO:0001977	renal system process involved in regulation of blood volume	6	0.220209939	0.0108	0.018152791
GO:0003093	regulation of glomerular filtration	6	0.220209939	0.0108	0.018152791
GO:0032413	negative regulation of ion transmembrane transporter activity	28	0.22018552	0.0009	0.010729485
GO:0042745	circadian sleep/wake cycle	11	0.22016867	0.0007	0.010220707
GO:0030149	sphingolipid catabolic process	11	0.220148173	0.0014	0.011465722
GO:0046716	muscle cell cellular homeostasis	10	0.220105153	0.0183	0.023783007
GO:0021800	cerebral cortex tangential migration	7	0.220085975	0.0123	0.019143634
GO:0070585	protein localization to mitochondrion	77	0.220076619	0.0079	0.01629604
GO:0032273	positive regulation of protein polymerization	49	0.220076323	0.0032	0.013333753
GO:0006817	phosphate ion transport	6	0.220055308	0.0249	0.029484292
GO:0044319	wound healing, spreading of cells	13	0.219998958	0.0084	0.016633151
GO:0090504	epiboly	13	0.219998958	0.0084	0.016633151
GO:0090505	epiboly involved in wound healing	13	0.219998958	0.0084	0.016633151
GO:0060571	morphogenesis of an epithelial fold	5	0.219998121	0.0327	0.036514368
GO:0070255	regulation of mucus secretion	7	0.219968799	0.0026	0.012805111
GO:0000413	protein peptidyl-prolyl isomerization	20	0.219953676	0.0112	0.018392048
GO:2000811	negative regulation of anoikis	8	0.219953319	0.0023	0.012498684
GO:0072529	pyrimidine-containing compound catabolic process	14	0.219933535	0.0147	0.02091937
GO:0002792	negative regulation of peptide secretion	21	0.219926964	0.0166	0.02247277
GO:0016064	immunoglobulin mediated immune response	45	0.219923282	0.0091	0.016994897
GO:0019724	B cell mediated immunity	45	0.219923282	0.0091	0.016994897
GO:0055021	regulation of cardiac muscle tissue growth	29	0.219911178	0.0054	0.014720792
GO:0000422	mitophagy	38	0.219883628	0.0038	0.01366393
GO:0061726	mitochondrion disassembly	38	0.219883628	0.0038	0.01366393
GO:0001764	neuron migration	78	0.219879514	0.0029	0.013089617

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0052312	modulation of transcription in other organism involved in symbiotic interaction	8	0.219870227	0.0211	0.026113057
GO:0060047	heart contraction	118	0.21985974	0.0044	0.014132412
GO:0006941	striated muscle contraction	70	0.219844756	0.0073	0.015844069
GO:0033081	regulation of T cell differentiation in thymus	9	0.21981602	0.0004	0.008964341
GO:2000398	regulation of thymocyte aggregation	9	0.21981602	0.0004	0.008964341
GO:0050855	regulation of B cell receptor signaling pathway	12	0.219813968	0.0106	0.018010344
GO:0006821	chloride transport	41	0.219809025	0.0088	0.016916437
GO:0042590	antigen processing and presentation of exogenous peptide antigen via MHC class I	49	0.219798972	0.0264	0.030750363
GO:1905207	regulation of cardiocyte differentiation	22	0.219781584	0.0011	0.010890753
GO:0030278	regulation of ossification	89	0.219763383	0.0054	0.014720792
GO:0021532	neural tube patterning	12	0.219735141	0.0324	0.036242368
GO:0030518	intracellular steroid hormone receptor signaling pathway	48	0.219724748	0.005	0.014547706
GO:0071500	cellular response to nitrosative stress	5	0.219717972	0.0174	0.023064374
GO:0001890	placenta development	65	0.219705812	0.003	0.013210967
GO:2000678	negative regulation of transcription regulatory region DNA binding	12	0.21970577	0.0026	0.012805111
GO:0045606	positive regulation of epidermal cell differentiation	6	0.21970523	0.0337	0.03733539
GO:0031638	zymogen activation	20	0.219704043	0.0163	0.022248961
GO:0014033	neural crest cell differentiation	33	0.219683654	0.0055	0.01475
GO:0007131	reciprocal meiotic recombination	9	0.219677947	0.0241	0.028760826
GO:0031642	negative regulation of myelination	5	0.219661994	0.0005	0.009604651
GO:0031645	negative regulation of neurological system process	5	0.219661994	0.0005	0.009604651
GO:1903900	regulation of viral life cycle	79	0.219648754	0.008	0.016379603
GO:0010332	response to gamma radiation	26	0.219639976	0.0003	0.007956881
GO:0044344	cellular response to fibroblast growth factor stimulus	56	0.219638675	0.0083	0.016559903
GO:0050870	positive regulation of T cell activation	70	0.219604961	0.0144	0.020727211
GO:0030575	nuclear body organization	8	0.219565231	0.0044	0.014132412
GO:0006672	ceramide metabolic process	34	0.219546052	0.0029	0.013089617
GO:1902275	regulation of chromatin organization	63	0.219534012	0.0029	0.013089617
GO:0007631	feeding behavior	44	0.219518568	0.0006	0.009940401
GO:0022618	ribonucleoprotein complex assembly	72	0.219475786	0.0102	0.0177
GO:0032463	negative regulation of protein homooligomerization	7	0.219473809	0.0205	0.025639412
GO:0070198	protein localization to chromosome, telomeric region	13	0.219456423	0.0146	0.020879842
GO:0045930	negative regulation of mitotic cell cycle	129	0.219416034	0.0097	0.017363901
GO:0031960	response to corticosteroid	56	0.219407632	0.0199	0.025133639
GO:0034329	cell junction assembly	82	0.219401769	0.0034	0.01347416
GO:0033688	regulation of osteoblast proliferation	5	0.219374071	0.0038	0.01366393
GO:1902959	regulation of aspartic-type endopeptidase activity involved in amyloid precursor protein catabolic process	5	0.21937122	0.0002	0.006319126
GO:0090083	regulation of inclusion body assembly	9	0.219367102	0.0105	0.017924712
GO:0010894	negative regulation of steroid biosynthetic process	11	0.219334066	0.0262	0.030579007
GO:0045939	negative regulation of steroid metabolic process	11	0.219334066	0.0262	0.030579007
GO:0050715	positive regulation of cytokine secretion	45	0.219326962	0.0301	0.034151923
GO:0097193	intrinsic apoptotic signaling pathway	117	0.219298547	0.0075	0.015990044
GO:0010828	positive regulation of glucose transport	13	0.219263151	0.0201	0.025275816
GO:2000316	regulation of T-helper 17 type immune response	5	0.219239309	0.0068	0.015633241
GO:0051701	interaction with host	93	0.219235188	0.0047	0.014168613
GO:0045981	positive regulation of nucleotide metabolic process	39	0.219223248	0.0047	0.014168613
GO:1900544	positive regulation of purine nucleotide metabolic process	39	0.219223248	0.0047	0.014168613
GO:0050673	epithelial cell proliferation	161	0.219215191	0.0115	0.018599441
GO:0051494	negative regulation of cytoskeleton organization	57	0.219179676	0.0096	0.017302743
GO:0010631	epithelial cell migration	140	0.219158868	0.0028	0.012972436
GO:0090132	epithelium migration	140	0.219158868	0.0028	0.012972436
GO:0050913	sensory perception of bitter taste	6	0.219153873	0.0091	0.016994897
GO:0033005	positive regulation of mast cell activation	10	0.219126446	0.0324	0.036242368
GO:0033344	cholesterol efflux	15	0.219122084	0.0224	0.027324219
GO:0050768	negative regulation of neurogenesis	131	0.219121753	0.0027	0.012827773
GO:0014031	mesenchymal cell development	32	0.219104782	0.0119	0.018881943
GO:0048368	lateral mesoderm development	6	0.219101826	0.0428	0.045650175
GO:0042147	retrograde transport, endosome to Golgi	38	0.219090676	0.0027	0.012827773
GO:2001239	regulation of extrinsic apoptotic signaling pathway in absence of ligand	14	0.219052123	0.0153	0.021378589
GO:0015936	coenzyme A metabolic process	10	0.219049088	0.0083	0.016559903
GO:0002200	somatic diversification of immune receptors	24	0.219048699	0.0019	0.012288367
GO:0021954	central nervous system neuron development	45	0.219023892	0.002	0.012314604
GO:0101023	vascular endothelial cell proliferation	7	0.21900492	0.0251	0.029642198
GO:1905562	regulation of vascular endothelial cell proliferation	7	0.21900492	0.0251	0.029642198
GO:0010714	positive regulation of collagen metabolic process	9	0.218982974	0.0201	0.025275816
GO:0032967	positive regulation of collagen biosynthetic process	9	0.218982974	0.0201	0.025275816
GO:0044253	positive regulation of multicellular organismal metabolic process	9	0.218982974	0.0201	0.025275816
GO:0055008	cardiac muscle tissue morphogenesis	25	0.218966831	0.0175	0.023154462
GO:0051583	dopamine uptake involved in synaptic transmission	5	0.218958901	0.0235	0.028248857
GO:0051934	catecholamine uptake involved in synaptic transmission	5	0.218958901	0.0235	0.028248857
GO:2000401	regulation of lymphocyte migration	21	0.218947473	0.0066	0.015525305
GO:0006096	glycolytic process	47	0.218939949	0.0067	0.015576759
GO:0014037	Schwann cell differentiation	15	0.218927888	0.0011	0.010890753
GO:0032233	positive regulation of actin filament bundle assembly	31	0.218916717	0.0053	0.014634479
GO:0002244	hematopoietic progenitor cell differentiation	72	0.218906702	0.0153	0.021378589
GO:0033865	nucleoside bisphosphate metabolic process	21	0.218883733	0.0017	0.012001709
GO:0033875	ribonucleoside bisphosphate metabolic process	21	0.218883733	0.0017	0.012001709
GO:0034032	purine nucleoside bisphosphate metabolic process	21	0.218883733	0.0017	0.012001709
GO:0031109	microtubule polymerization or depolymerization	32	0.218871824	0.0037	0.013609033
GO:0009953	dorsal/ventral pattern formation	32	0.21887065	0.0072	0.015844069
GO:0010677	negative regulation of cellular carbohydrate metabolic process	18	0.21886081	0.0026	0.012805111
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	190	0.218850403	0.0038	0.01366393

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1904814	regulation of protein localization to chromosome, telomeric region	8	0.218832789	0.0441	0.046872463
GO:0071897	DNA biosynthetic process	88	0.218827502	0.0066	0.015525305
GO:0018345	protein palmitoylation	12	0.218821828	0.0105	0.017924712
GO:0019371	cyclooxygenase pathway	7	0.218820918	0.0192	0.02450649
GO:0019062	virion attachment to host cell	5	0.218795891	0.025	0.029554283
GO:0034250	positive regulation of cellular amide metabolic process	68	0.218776393	0.0058	0.014878261
GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	78	0.218754855	0.0022	0.012422266
GO:0043525	positive regulation of neuron apoptotic process	25	0.218733849	0.006	0.015037711
GO:0034035	purine ribonucleoside bisphosphate metabolic process	11	0.218733411	0.0008	0.010465158
GO:0050427	3'-phosphoadenosine 5'-phosphosulfate metabolic process	11	0.218733411	0.0008	0.010465158
GO:0032535	regulation of cellular component size	148	0.218696193	0.0023	0.012498684
GO:1900452	regulation of long term synaptic depression	5	0.218674346	0.0004	0.008964341
GO:0006778	porphyrin-containing compound metabolic process	20	0.218597053	0.0236	0.028327839
GO:0008406	gonad development	84	0.218585517	0.0055	0.01475
GO:0002220	innate immune response activating cell surface receptor signaling pathway	63	0.2185726	0.0124	0.019242297
GO:0090068	positive regulation of cell cycle process	101	0.21853551	0.001	0.010787313
GO:0042742	defense response to bacterium	67	0.218492971	0.0082	0.016514246
GO:0060761	negative regulation of response to cytokine stimulus	26	0.21848274	0.0147	0.02091937
GO:0043090	amino acid import	11	0.218442212	0.0055	0.01475
GO:0043092	L-amino acid import	11	0.218442212	0.0055	0.01475
GO:0051785	positive regulation of nuclear division	22	0.218430727	0.0006	0.009940401
GO:0006363	termination of RNA polymerase I transcription	17	0.218418147	0.0042	0.013948535
GO:0043173	nucleotide salvage	9	0.218392959	0.0223	0.027242468
GO:0051983	regulation of chromosome segregation	39	0.218388363	0.0027	0.012827773
GO:1904058	positive regulation of sensory perception of pain	6	0.21837597	0.0051	0.014547706
GO:0045787	positive regulation of cell cycle	138	0.218358702	0.0012	0.010961137
GO:0018958	phenol-containing compound metabolic process	41	0.218344882	0.0103	0.017772187
GO:0043254	regulation of protein complex assembly	168	0.218321107	0.004	0.013824268
GO:0033157	regulation of intracellular protein transport	125	0.218306996	0.0066	0.015525305
GO:0034620	cellular response to unfolded protein	59	0.218291598	0.0005	0.009604651
GO:0071675	regulation of mononuclear cell migration	16	0.218279407	0.0294	0.033482529
GO:0009411	response to UV	55	0.218279061	0.0068	0.015633241
GO:0030041	actin filament polymerization	72	0.218260015	0.0086	0.016782045
GO:0031056	regulation of histone modification	57	0.218236798	0.0036	0.01353394
GO:0032006	regulation of TOR signaling	44	0.218228466	0.0021	0.012314604
GO:0060841	venous blood vessel development	9	0.218195424	0.0018	0.01210186
GO:0032271	regulation of protein polymerization	79	0.218155304	0.0061	0.015143924
GO:0007098	centrosome cycle	38	0.218127941	0.0027	0.012827773
GO:0090596	sensory organ morphogenesis	96	0.218127571	0.0034	0.01347416
GO:0033260	nuclear DNA replication	19	0.218085623	0.0017	0.012001709
GO:0070265	necrotic cell death	21	0.218064673	0.0182	0.023684988
GO:0045785	positive regulation of cell adhesion	158	0.218060129	0.0124	0.019242297
GO:0045137	development of primary sexual characteristics	89	0.218052655	0.0055	0.01475
GO:0044320	cellular response to leptin stimulus	7	0.21803271	0.0279	0.032115827
GO:0014014	negative regulation of gliogenesis	24	0.218012286	0.0119	0.018881943
GO:0006853	carnitine shuttle	7	0.217982545	0.0171	0.022860624
GO:1902001	fatty acid transmembrane transport	7	0.217982545	0.0171	0.022860624
GO:0010596	negative regulation of endothelial cell migration	28	0.217972688	0.0053	0.014634479
GO:0072148	epithelial cell fate commitment	8	0.217971577	0.0129	0.019597425
GO:1902750	negative regulation of cell cycle G2/M phase transition	50	0.217918929	0.0215	0.026489026
GO:0001578	microtubule bundle formation	33	0.217909016	0.0086	0.016782045
GO:0050770	regulation of axonogenesis	76	0.217880002	0.0001	0.004220438
GO:0042749	regulation of circadian sleep/wake cycle	8	0.217873259	< 0.001	< 0.001
GO:0045187	regulation of circadian sleep/wake cycle, sleep	8	0.217873259	< 0.001	< 0.001
GO:1900181	negative regulation of protein localization to nucleus	22	0.21786117	0.0064	0.015399417
GO:0061077	chaperone-mediated protein folding	21	0.217858581	0.0133	0.019917275
GO:0007548	sex differentiation	105	0.217852571	0.005	0.014547706
GO:0033138	positive regulation of peptidyl-serine phosphorylation	38	0.217825545	0.0116	0.018682786
GO:0035967	cellular response to topologically incorrect protein	65	0.217820563	0.001	0.010787313
GO:0061384	heart trabecula morphogenesis	15	0.217789152	0.0099	0.017505138
GO:0045947	negative regulation of translational initiation	7	0.21776837	0.0072	0.015844069
GO:0060420	regulation of heart growth	31	0.217763593	0.0054	0.014720792
GO:0048705	skeletal system morphogenesis	80	0.217734011	0.0072	0.015844069
GO:0051321	meiotic cell cycle	60	0.217725205	0.0033	0.013333753
GO:0030879	mammary gland development	56	0.217698328	0.0053	0.014634479
GO:0051961	negative regulation of nervous system development	139	0.217640539	0.0026	0.012805111
GO:0044070	regulation of anion transport	33	0.217634702	0.0037	0.013609033
GO:0045779	negative regulation of bone resorption	6	0.217626358	0.0009	0.010729485
GO:0034612	response to tumor necrosis factor	124	0.217586979	0.0076	0.016084627
GO:0006047	UDP-N-acetylglucosamine metabolic process	7	0.217540867	0.0451	0.047829824
GO:0030099	myeloid cell differentiation	147	0.217485527	0.0057	0.01480566
GO:2000010	positive regulation of protein localization to cell surface	8	0.217476263	0.0194	0.024690909
GO:0071108	protein K48-linked deubiquitination	16	0.217474562	0.0012	0.010961137
GO:0002521	leukocyte differentiation	189	0.217461296	0.0037	0.013609033
GO:0032277	negative regulation of gonadotropin secretion	5	0.217453716	0.0128	0.019522448
GO:0002377	immunoglobulin production	40	0.217450671	0.0025	0.012769435
GO:0060261	positive regulation of transcription initiation from RNA polymerase II promoter	6	0.217443004	0.0012	0.010961137
GO:0052547	regulation of peptidase activity	150	0.217420052	0.0083	0.016559903
GO:0000910	cytokinesis	52	0.217415261	0.0015	0.011704453
GO:0045987	positive regulation of smooth muscle contraction	11	0.21740523	0.0194	0.024690909
GO:0061298	retina vasculature development in camera-type eye	13	0.217393532	0.0062	0.015209334
GO:0060674	placenta blood vessel development	14	0.217361123	0.0275	0.031743861
GO:0070301	cellular response to hydrogen peroxide	41	0.217326046	0.0023	0.012498684

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0043300	regulation of leukocyte degranulation	23	0.217322797	0.0307	0.034703304
GO:0000070	mitotic sister chromatid segregation	60	0.217291916	0.003	0.013210967
GO:0014032	neural crest cell development	29	0.217216793	0.0082	0.016514246
GO:0016570	histone modification	166	0.217143472	0.0008	0.010465158
GO:0048545	response to steroid hormone	137	0.217107418	0.0115	0.018599441
GO:0071774	response to fibroblast growth factor	57	0.217105623	0.0084	0.016633151
GO:0001837	epithelial to mesenchymal transition	61	0.2170939	0.007	0.015816335
GO:2001233	regulation of apoptotic signaling pathway	173	0.217093639	0.009	0.016956012
GO:0060117	auditory receptor cell development	8	0.217085421	0.0196	0.0248852
GO:0033137	negative regulation of peptidyl-serine phosphorylation	11	0.217074098	0.0074	0.015911789
GO:0030510	regulation of BMP signaling pathway	31	0.217044014	0.006	0.015037711
GO:0055001	muscle cell development	63	0.217039748	0.0054	0.014720792
GO:0042157	lipoprotein metabolic process	53	0.217034204	0.0078	0.01620539
GO:1903054	negative regulation of extracellular matrix organization	8	0.217022252	0.024	0.028671074
GO:1901988	negative regulation of cell cycle phase transition	105	0.216993243	0.0096	0.017302743
GO:0039530	MDA-5 signaling pathway	5	0.216988011	0.0094	0.017156187
GO:0033619	membrane protein proteolysis	25	0.216971528	0.0104	0.017832977
GO:0042982	amyloid precursor protein metabolic process	27	0.21695934	0.0019	0.012288367
GO:1902581	multi-organism cellular localization	29	0.216950084	0.0096	0.017302743
GO:1902583	multi-organism intracellular transport	29	0.216950084	0.0096	0.017302743
GO:0010821	regulation of mitochondrion organization	111	0.216948586	0.0046	0.014132412
GO:0009126	purine nucleoside monophosphate metabolic process	157	0.216930919	0.0182	0.023684988
GO:0009167	purine ribonucleoside monophosphate metabolic process	157	0.216930919	0.0182	0.023684988
GO:0034162	toll-like receptor 9 signaling pathway	8	0.216928469	0.0217	0.026655917
GO:0016569	covalent chromatin modification	168	0.216923618	0.0008	0.010465158
GO:0071218	cellular response to misfolded protein	9	0.216923538	0.013	0.019676963
GO:0010952	positive regulation of peptidase activity	75	0.216901331	0.006	0.015037711
GO:0010830	regulation of myotube differentiation	20	0.216867049	0.0011	0.010890753
GO:0045979	positive regulation of nucleoside metabolic process	18	0.216830746	0.0151	0.02121706
GO:1903580	positive regulation of ATP metabolic process	18	0.216830746	0.0151	0.02121706
GO:0030101	natural killer cell activation	24	0.216796137	0.0063	0.015311728
GO:0072520	seminiferous tubule development	6	0.216779562	0.038	0.041253474
GO:0043618	regulation of transcription from RNA polymerase II promoter in response to stress	66	0.216761323	0.019	0.024347961
GO:2001204	regulation of osteoclast development	6	0.216754726	0.003	0.013210967
GO:0086009	membrane repolarization	20	0.216700994	0.0063	0.015311728
GO:0097435	fibril organization	11	0.21667264	0.0179	0.02344231
GO:1904779	regulation of protein localization to centrosome	7	0.216662139	0.0024	0.012603815
GO:0044387	negative regulation of protein kinase activity by regulation of protein phosphorylation	5	0.216650329	0.0346	0.038164288
GO:0033683	nucleotide-excision repair, DNA incision	18	0.216649767	0.021	0.026005997
GO:0051968	positive regulation of synaptic transmission, glutamatergic	12	0.216646096	0.0021	0.012314604
GO:0006760	folic acid-containing compound metabolic process	14	0.21663826	0.006	0.015037711
GO:0000245	spliceosomal complex assembly	21	0.216635298	0.0117	0.018739446
GO:0048511	rhythmic process	153	0.216625203	0.0008	0.010465158
GO:0035265	organ growth	70	0.216607753	0.0067	0.015576759
GO:0016575	histone deacetylation	27	0.216605687	0.0004	0.008964341
GO:0003206	cardiac chamber morphogenesis	58	0.216594793	0.0064	0.015399417
GO:0019098	reproductive behavior	15	0.216567399	0.001	0.010787313
GO:0070099	regulation of chemokine-mediated signaling pathway	6	0.216537466	0.0376	0.040911404
GO:2001244	positive regulation of intrinsic apoptotic signaling pathway	21	0.216536201	0.0117	0.018739446
GO:0000819	sister chromatid segregation	67	0.216483981	0.0029	0.013089617
GO:0046530	photoreceptor cell differentiation	25	0.216459693	0.0021	0.012314604
GO:0001570	vasculogenesis	37	0.216446603	0.0022	0.012422266
GO:0003009	skeletal muscle contraction	17	0.216426753	0.0202	0.025368462
GO:2000273	positive regulation of receptor activity	30	0.216408838	0.0055	0.01475
GO:2000036	regulation of stem cell population maintenance	9	0.216407384	0.0054	0.014720792
GO:0007266	Rho protein signal transduction	66	0.216406945	0.0033	0.013333753
GO:0001975	response to amphetamine	13	0.216378433	0.0095	0.01725157
GO:0006493	protein O-linked glycosylation	45	0.21637807	0.0039	0.013791927
GO:1990314	cellular response to insulin-like growth factor stimulus	6	0.216375709	0.0128	0.019522448
GO:0009648	photoperiodism	12	0.216365666	0.0025	0.012769435
GO:0060693	regulation of branching involved in salivary gland morphogenesis	6	0.216350441	0.0223	0.027242468
GO:0034341	response to interferon-gamma	71	0.216347652	0.0149	0.021043429
GO:0019369	arachidonic acid metabolic process	19	0.216332766	0.0013	0.011218806
GO:0072079	nephron tubule formation	8	0.216297422	0.0042	0.013948535
GO:0006991	response to sterol depletion	7	0.216260446	0.0007	0.010220707
GO:0016331	morphogenesis of embryonic epithelium	64	0.216236662	0.0068	0.015633241
GO:0007050	cell cycle arrest	100	0.21619959	0.005	0.014547706
GO:0051194	positive regulation of cofactor metabolic process	9	0.216158161	0.0109	0.018225506
GO:0051197	positive regulation of coenzyme metabolic process	9	0.216158161	0.0109	0.018225506
GO:0033684	regulation of luteinizing hormone secretion	5	0.216146787	< 0.001	< 0.001
GO:0007157	heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	15	0.216123635	0.0136	0.020157703
GO:0007031	peroxisome organization	46	0.216107857	0.0093	0.017114131
GO:0055010	ventricular cardiac muscle tissue morphogenesis	19	0.216090113	0.0144	0.02072711
GO:0061097	regulation of protein tyrosine kinase activity	44	0.216072426	0.0001	0.004220438
GO:0006367	transcription initiation from RNA polymerase II promoter	81	0.216029398	0.0045	0.014132412
GO:0014745	negative regulation of muscle adaptation	6	0.216001443	0.0475	0.049962707
GO:0048102	autophagic cell death	6	0.216000795	0.0287	0.032827577
GO:0050830	defense response to Gram-positive bacterium	20	0.215990968	0.0237	0.028436066
GO:0010633	negative regulation of epithelial cell migration	37	0.215989086	0.004	0.013824268
GO:1901032	negative regulation of response to reactive oxygen species	9	0.215987117	0.0215	0.026489026
GO:1903206	negative regulation of hydrogen peroxide-induced cell death	9	0.215987117	0.0215	0.026489026
GO:1900015	regulation of cytokine production involved in inflammatory response	15	0.215984209	0.0019	0.012288367
GO:0002696	positive regulation of leukocyte activation	121	0.215978495	0.0149	0.021043429

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0098703	calcium ion import across plasma membrane	6	0.215961057	0.0031	0.013277185
GO:1990035	calcium ion import into cell	6	0.215961057	0.0031	0.013277185
GO:0010524	positive regulation of calcium ion transport into cytosol	23	0.215933264	0.0063	0.015311728
GO:0010721	negative regulation of cell development	148	0.215931441	0.0017	0.012001709
GO:1990440	positive regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress	6	0.215911601	0.002	0.012314604
GO:0032722	positive regulation of chemokine production	23	0.21590301	0.0275	0.031743861
GO:0035728	response to hepatocyte growth factor	9	0.215897996	0.0064	0.015399417
GO:0060242	contact inhibition	7	0.215892998	0.0101	0.017653628
GO:0071826	ribonucleoprotein complex subunit organization	79	0.215882233	0.0108	0.018152791
GO:0043921	modulation by host of viral transcription	7	0.215876708	0.0238	0.028526451
GO:0052472	modulation by host of symbiont transcription	7	0.215876708	0.0238	0.028526451
GO:0006690	icosanoid metabolic process	40	0.215830874	0.0137	0.020264364
GO:1901568	fatty acid derivative metabolic process	40	0.215830874	0.0137	0.020264364
GO:0017038	protein import	90	0.215804382	0.012	0.018931514
GO:0061082	myeloid leukocyte cytokine production	14	0.21579424	0.0304	0.034411276
GO:0007271	synaptic transmission, cholinergic	13	0.21575536	0.004	0.013824268
GO:0070231	T cell apoptotic process	12	0.215737318	0.002	0.012314604
GO:1901991	negative regulation of mitotic cell cycle phase transition	98	0.215712738	0.0093	0.017114131
GO:0052548	regulation of endopeptidase activity	136	0.215683715	0.0087	0.016840777
GO:0009161	ribonucleoside monophosphate metabolic process	167	0.215669115	0.0165	0.022405589
GO:0046782	regulation of viral transcription	30	0.215653179	0.0149	0.021043429
GO:0046676	negative regulation of insulin secretion	17	0.215615972	0.0235	0.028248857
GO:0050729	positive regulation of inflammatory response	50	0.21561015	0.0035	0.01351837
GO:0006289	nucleotide-excision repair	52	0.215606917	0.0066	0.015525305
GO:0003407	neural retina development	32	0.215592757	0.0204	0.025564109
GO:0006735	NADH regeneration	17	0.215584949	0.0149	0.021043429
GO:0061621	canonical glycolysis	17	0.215584949	0.0149	0.021043429
GO:0061718	glucose catabolic process to pyruvate	17	0.215584949	0.0149	0.021043429
GO:0007091	metaphase/anaphase transition of mitotic cell cycle	21	0.215578492	0.0017	0.012001709
GO:0010965	regulation of mitotic sister chromatid separation	21	0.215578492	0.0017	0.012001709
GO:0006084	acetyl-CoA metabolic process	17	0.215573287	0.0214	0.026388313
GO:0035729	cellular response to hepatocyte growth factor stimulus	8	0.215568056	0.0047	0.014168613
GO:0006568	tryptophan metabolic process	5	0.215566015	0.0469	0.0494125
GO:0006586	indolalkylamine metabolic process	5	0.215566015	0.0469	0.0494125
GO:0070085	glycosylation	136	0.215557747	0.0034	0.01347416
GO:0040020	regulation of meiotic nuclear division	11	0.215556733	0.0022	0.012422266
GO:0032660	regulation of interleukin-17 production	12	0.215509908	0.0102	0.0177
GO:0043271	negative regulation of ion transport	56	0.215507501	0.0019	0.012288367
GO:0051053	negative regulation of DNA metabolic process	60	0.215502738	0.0026	0.012805111
GO:0071732	cellular response to nitric oxide	6	0.215488527	0.016	0.022026667
GO:0009142	nucleoside triphosphate biosynthetic process	38	0.21548181	0.0231	0.027930615
GO:0000012	single strand break repair	5	0.215480753	< 0.001	< 0.001
GO:0007257	activation of JUN kinase activity	14	0.215476125	0.0051	0.014547706
GO:0007422	peripheral nervous system development	28	0.215465481	0.0002	0.006319126
GO:0030431	sleep	12	0.215452893	0.0001	0.004220438
GO:0051251	positive regulation of lymphocyte activation	101	0.215387161	0.0112	0.018392048
GO:0006294	nucleotide-excision repair, preincision complex assembly	17	0.21537709	0.0163	0.022248961
GO:0001825	blastocyst formation	17	0.21536558	0.0045	0.014132412
GO:0042303	molting cycle	33	0.215350507	0.0048	0.014269203
GO:0042633	hair cycle	33	0.215350507	0.0048	0.014269203
GO:0010951	negative regulation of endopeptidase activity	70	0.215342011	0.0101	0.017653628
GO:0006360	transcription from RNA polymerase I promoter	29	0.215280621	0.0076	0.016084627
GO:0043649	dicarboxylic acid catabolic process	13	0.215258775	0.0101	0.017653628
GO:0071800	podosome assembly	7	0.215255286	0.0397	0.042801678
GO:0035966	response to topologically incorrect protein	87	0.215254824	0.0017	0.012001709
GO:0045807	positive regulation of endocytosis	57	0.215235895	0.0112	0.018392048
GO:2000104	negative regulation of DNA-dependent DNA replication	8	0.215230666	0.0007	0.010220707
GO:0006353	DNA-templated transcription, termination	38	0.215229063	0.004	0.013824268
GO:0043620	regulation of DNA-templated transcription in response to stress	69	0.215199455	0.0181	0.023607986
GO:0006486	protein glycosylation	126	0.215193644	0.0034	0.01347416
GO:0043413	macromolecule glycosylation	126	0.215193644	0.0034	0.01347416
GO:0080154	regulation of fertilization	8	0.215188391	0.0043	0.014102439
GO:0006956	complement activation	25	0.215175673	0.0289	0.033004108
GO:0021675	nerve development	24	0.215169008	0.0052	0.014616626
GO:0043903	regulation of symbiosis, encompassing mutualism through parasitism	93	0.215151358	0.0103	0.017772187
GO:0060048	cardiac muscle contraction	57	0.215145622	0.0082	0.016514246
GO:0060348	bone development	85	0.215142431	0.0031	0.013277185
GO:0016052	carbohydrate catabolic process	82	0.215120666	0.0063	0.015311728
GO:0038061	NIK/NF-kappaB signaling	80	0.215117495	0.0156	0.021692929
GO:0032755	positive regulation of interleukin-6 production	29	0.215097513	0.011	0.018323826
GO:0010826	negative regulation of centrosome duplication	5	0.215063251	0.0234	0.02817551
GO:0046034	ATP metabolic process	141	0.215059677	0.0199	0.025133639
GO:0050774	negative regulation of dendrite morphogenesis	8	0.215050066	0.0001	0.004220438
GO:1903747	regulation of establishment of protein localization to mitochondrion	40	0.215044397	0.0068	0.015633241
GO:0046501	protoporphyrinogen IX metabolic process	6	0.215042777	0.0321	0.035976391
GO:1903321	negative regulation of protein modification by small protein conjugation or removal	43	0.214972172	0.0058	0.014878261
GO:0008154	actin polymerization or depolymerization	83	0.214927405	0.01	0.017574468
GO:0006650	glycerophospholipid metabolic process	137	0.214909009	0.0064	0.015399417
GO:0070536	protein K63-linked deubiquitination	11	0.214899416	0.0014	0.011465722
GO:0046006	regulation of activated T cell proliferation	8	0.21488048	0.0104	0.017832977
GO:0030593	neutrophil chemotaxis	24	0.214788695	0.0182	0.023684988
GO:0021877	forebrain neuron fate commitment	6	0.214750146	0.0198	0.025062084

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:2000677	regulation of transcription regulatory region DNA binding	23	0.21470638	0.0036	0.01353394
GO:0046466	membrane lipid catabolic process	14	0.214679217	0.0044	0.014132412
GO:0060419	heart growth	43	0.214671761	0.0097	0.017363901
GO:0042451	purine nucleoside biosynthetic process	51	0.214626322	0.0172	0.022941269
GO:0046129	purine ribonucleoside biosynthetic process	51	0.214626322	0.0172	0.022941269
GO:0033135	regulation of peptidyl-serine phosphorylation	50	0.21459923	0.0083	0.016559903
GO:0006921	cellular component disassembly involved in execution phase of apoptosis	12	0.214597351	0.0002	0.006319126
GO:0030262	apoptotic nuclear changes	12	0.214597351	0.0002	0.006319126
GO:0001667	ameboidal-type cell migration	173	0.214594233	0.0039	0.013791927
GO:0008589	regulation of smoothened signaling pathway	27	0.2145893	0.0107	0.018084595
GO:1904861	excitatory synapse assembly	9	0.214573271	0.0038	0.01366393
GO:0061213	positive regulation of mesonephros development	10	0.214540271	0.0138	0.020339434
GO:0061217	regulation of mesonephros development	10	0.214540271	0.0138	0.020339434
GO:1990542	mitochondrial transmembrane transport	35	0.214534422	0.0121	0.018970228
GO:0031953	negative regulation of protein autophosphorylation	7	0.214532608	0.0088	0.016916437
GO:0046487	glyoxylate metabolic process	5	0.214529905	0.0157	0.021779607
GO:0001558	regulation of cell growth	185	0.214521997	0.0015	0.011704453
GO:0033006	regulation of mast cell activation involved in immune response	14	0.214475963	0.0244	0.029011063
GO:0043304	regulation of mast cell degranulation	14	0.214475963	0.0244	0.029011063
GO:0035635	entry of bacterium into host cell	6	0.214452547	0.024	0.028671074
GO:0048536	spleen development	12	0.214409786	0.0046	0.014132412
GO:0002886	regulation of myeloid leukocyte mediated immunity	28	0.214372624	0.0218	0.026744664
GO:0006283	transcription-coupled nucleotide-excision repair	38	0.214349054	0.0153	0.021378589
GO:0002067	glandular epithelial cell differentiation	23	0.214335898	0.0001	0.004220438
GO:0030968	endoplasmic reticulum unfolded protein response	51	0.214330959	0.0002	0.006319126
GO:1900271	regulation of long-term synaptic potentiation	25	0.214321232	0.0043	0.014102439
GO:0050792	regulation of viral process	84	0.214319096	0.0087	0.016840777
GO:0051342	regulation of cyclic-nucleotide phosphodiesterase activity	6	0.214269841	0.0295	0.033583186
GO:1903025	regulation of RNA polymerase II regulatory region sequence-specific DNA binding	7	0.214257346	0.0046	0.014132412
GO:1905063	regulation of vascular smooth muscle cell differentiation	7	0.214240316	0.0076	0.016084627
GO:0000302	response to reactive oxygen species	96	0.214223341	0.0033	0.013333753
GO:0055017	cardiac muscle tissue growth	40	0.214210494	0.0097	0.017363901
GO:0051131	chaperone-mediated protein complex assembly	9	0.214201236	0.0041	0.013887639
GO:0007220	Notch receptor processing	6	0.214198789	0.0301	0.034151923
GO:0050867	positive regulation of cell activation	123	0.214187896	0.0169	0.022703485
GO:0070911	global genome nucleotide-excision repair	16	0.214182537	0.0111	0.018389742
GO:0048469	cell maturation	69	0.214173324	0.0041	0.013887639
GO:0032653	regulation of interleukin-10 production	14	0.214147204	0.0158	0.021871104
GO:0045143	homologous chromosome segregation	14	0.214073344	0.0092	0.017033109
GO:0046683	response to organophosphorus	60	0.2140504	0.0076	0.016084627
GO:0016254	preassembly of GPI anchor in ER membrane	9	0.214040703	0.0367	0.040037623
GO:0042168	heme metabolic process	19	0.214030291	0.0261	0.030517735
GO:0030901	midbrain development	40	0.214019268	0.013	0.019676963
GO:0046939	nucleotide phosphorylation	61	0.213981953	0.0085	0.016693954
GO:0021953	central nervous system neuron differentiation	88	0.213975315	0.0026	0.012805111
GO:2000648	positive regulation of stem cell proliferation	18	0.213964179	0.0136	0.020157703
GO:0002027	regulation of heart rate	39	0.213953553	0.0112	0.018392048
GO:0071257	cellular response to electrical stimulus	8	0.213947514	0.0338	0.0374175
GO:0045923	positive regulation of fatty acid metabolic process	13	0.213905476	0.0085	0.016693954
GO:0061180	mammary gland epithelium development	30	0.213901319	0.0101	0.017653628
GO:0033235	positive regulation of protein sumoylation	5	0.21384884	0.0006	0.009940401
GO:0022011	myelination in peripheral nervous system	8	0.213846767	0.0036	0.01353394
GO:0032292	peripheral nervous system axon ensheathment	8	0.213846767	0.0036	0.01353394
GO:0030004	cellular monovalent inorganic cation homeostasis	34	0.213843146	0.0111	0.018389742
GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	78	0.213831799	0.0054	0.014720792
GO:0048562	embryonic organ morphogenesis	96	0.213809338	0.0097	0.017363901
GO:0002822	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	40	0.213788716	0.0026	0.012805111
GO:0098727	maintenance of cell number	62	0.213699946	0.0092	0.017033109
GO:0048762	mesenchymal cell differentiation	86	0.213682097	0.0084	0.016633151
GO:0071706	tumor necrosis factor superfamily cytokine production	66	0.213665023	0.0196	0.0248852
GO:1903555	regulation of tumor necrosis factor superfamily cytokine production	66	0.213665023	0.0196	0.0248852
GO:0051180	vitamin transport	13	0.213637747	0.0207	0.025805821
GO:1901017	negative regulation of potassium ion transmembrane transporter activity	7	0.213592608	< 0.001	< 0.001
GO:1903008	organelle disassembly	52	0.213558778	0.0039	0.013791927
GO:0002312	B cell activation involved in immune response	30	0.213547915	0.0016	0.011845327
GO:0031103	axon regeneration	24	0.21353621	0.009	0.016956012
GO:0071621	granulocyte chemotaxis	31	0.213528798	0.0171	0.022860624
GO:0022409	positive regulation of cell-cell adhesion	86	0.213517336	0.0151	0.02121706
GO:0090317	negative regulation of intracellular protein transport	32	0.213517111	0.0141	0.020504577
GO:0032675	regulation of interleukin-6 production	48	0.213512967	0.0102	0.0177
GO:0006409	tRNA export from nucleus	10	0.213502477	0.0056	0.014771533
GO:0051031	tRNA transport	10	0.213502477	0.0056	0.014771533
GO:0071431	tRNA-containing ribonucleoprotein complex export from nucleus	10	0.213502477	0.0056	0.014771533
GO:0051591	response to cAMP	42	0.21341308	0.0081	0.016514175
GO:0043153	entrainment of circadian clock by photoperiod	10	0.213376008	0.0036	0.01353394
GO:0030514	negative regulation of BMP signaling pathway	15	0.213344693	0.0104	0.017832977
GO:0045667	regulation of osteoblast differentiation	56	0.213330674	0.0036	0.01353394
GO:0006582	melanin metabolic process	11	0.213330455	0.0108	0.018152791
GO:0042438	melanin biosynthetic process	11	0.213330455	0.0108	0.018152791
GO:0032642	regulation of chemokine production	34	0.213287712	0.0258	0.030258742
GO:0060391	positive regulation of SMAD protein import into nucleus	6	0.213256968	0.0322	0.036060507

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0090559	regulation of membrane permeability	34	0.213194415	0.006	0.015037711
GO:0042407	cristae formation	16	0.21318049	0.0239	0.028592965
GO:0060155	platelet dense granule organization	5	0.213180215	0.0469	0.0494125
GO:0009123	nucleoside monophosphate metabolic process	175	0.213171248	0.0167	0.02255007
GO:0044784	metaphase/anaphase transition of cell cycle	22	0.213170838	0.0018	0.01210186
GO:0050435	beta-amyloid metabolic process	19	0.213136676	0.0005	0.009604651
GO:0045684	positive regulation of epidermis development	11	0.213123365	0.028	0.032186083
GO:0010662	regulation of striated muscle cell apoptotic process	17	0.213121051	0.0012	0.010961137
GO:2001242	regulation of intrinsic apoptotic signaling pathway	63	0.21310712	0.0141	0.020504577
GO:0090042	tubulin deacetylation	5	0.213105318	0.0055	0.01475
GO:0071346	cellular response to interferon-gamma	62	0.213079453	0.0158	0.021871104
GO:0046823	negative regulation of nucleocytoplasmic transport	22	0.213058988	0.0145	0.020788247
GO:0055117	regulation of cardiac muscle contraction	27	0.213049331	0.0221	0.027038129
GO:0008361	regulation of cell size	70	0.213031495	0.0006	0.009940401
GO:0045747	positive regulation of Notch signaling pathway	20	0.21302336	0.0165	0.022405589
GO:2001056	positive regulation of cysteine-type endopeptidase activity	59	0.213012127	0.008	0.016379603
GO:0050765	negative regulation of phagocytosis	10	0.212983385	0.0101	0.017653628
GO:1903019	negative regulation of glycoprotein metabolic process	9	0.212983054	0.0139	0.020388077
GO:0009303	rRNA transcription	13	0.21296334	0.0221	0.027038129
GO:0042063	gliogenesis	132	0.212960665	0.0111	0.018389742
GO:0032373	positive regulation of sterol transport	8	0.212959478	0.0404	0.043394538
GO:0032376	positive regulation of cholesterol transport	8	0.212959478	0.0404	0.043394538
GO:0034614	cellular response to reactive oxygen species	73	0.212943356	0.0047	0.014168613
GO:1903706	regulation of hemopoiesis	179	0.212940607	0.0107	0.018084595
GO:0036475	neuron death in response to oxidative stress	17	0.212925082	0.0072	0.015844069
GO:0060412	ventricular septum morphogenesis	22	0.212919573	0.0258	0.030258742
GO:0009214	cyclic nucleotide catabolic process	5	0.212864043	0.0013	0.011218806
GO:0086003	cardiac muscle cell contraction	29	0.212853435	0.0031	0.013277185
GO:2001258	negative regulation of cation channel activity	15	0.212805992	0.0018	0.01210186
GO:0060219	camera-type eye photoreceptor cell differentiation	9	0.212792285	0.0127	0.019457181
GO:0010566	regulation of ketone biosynthetic process	7	0.212785889	0.0263	0.030677143
GO:0045649	regulation of macrophage differentiation	7	0.212785703	0.0362	0.03958177
GO:0032640	tumor necrosis factor production	65	0.212780156	0.0193	0.024606968
GO:0032680	regulation of tumor necrosis factor production	65	0.212780156	0.0193	0.024606968
GO:0032456	endocytic recycling	18	0.212773856	0.0028	0.012972436
GO:0046486	glycerolipid metabolic process	172	0.212706174	0.0057	0.01480566
GO:0050879	multicellular organismal movement	20	0.212703884	0.0163	0.022248961
GO:0050881	musculoskeletal movement	20	0.212703884	0.0163	0.022248961
GO:0001959	regulation of cytokine-mediated signaling pathway	62	0.212700435	0.0132	0.019860109
GO:0006775	fat-soluble vitamin metabolic process	17	0.212656168	0.017	0.022784886
GO:0090128	regulation of synapse maturation	9	0.212631896	< 0.001	< 0.001
GO:0006354	DNA-templated transcription, elongation	53	0.212573425	0.0073	0.015844069
GO:0090189	regulation of branching involved in ureteric bud morphogenesis	9	0.212559188	0.0143	0.020629391
GO:0090190	positive regulation of branching involved in ureteric bud morphogenesis	9	0.212559188	0.0143	0.020629391
GO:0030308	negative regulation of cell growth	75	0.212550791	0.002	0.012314604
GO:0030833	regulation of actin filament polymerization	61	0.21255011	0.0073	0.015844069
GO:2001238	positive regulation of extrinsic apoptotic signaling pathway	23	0.212549347	0.0069	0.015750415
GO:0048738	cardiac muscle tissue development	87	0.212504512	0.0058	0.014878261
GO:0001845	phagolysosome assembly	7	0.212469347	0.0081	0.016514175
GO:0010972	negative regulation of G2/M transition of mitotic cell cycle	46	0.212450107	0.0217	0.026655917
GO:0006403	RNA localization	85	0.212424543	0.0086	0.016782045
GO:0032410	negative regulation of transporter activity	32	0.212422293	0.0014	0.011465722
GO:0000281	mitotic cytokinesis	22	0.212318388	0.0043	0.014102439
GO:1903053	regulation of extracellular matrix organization	20	0.212304847	0.0029	0.013089617
GO:0097352	autophagosome maturation	20	0.212302255	0.0196	0.0248852
GO:0097576	vacuole fusion	20	0.212302255	0.0196	0.0248852
GO:0051482	positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G-protein coupled signaling pathway	10	0.212297396	0.0001	0.004220438
GO:0006986	response to unfolded protein	79	0.212279128	0.0012	0.010961137
GO:0030502	negative regulation of bone mineralization	8	0.212272873	0.0002	0.006319126
GO:0046474	glycerophospholipid biosynthetic process	100	0.212236675	0.0055	0.01475
GO:0007602	phototransduction	22	0.212222617	0.001	0.010787313
GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	82	0.212198591	0.0103	0.017772187
GO:1903978	regulation of microglial cell activation	8	0.212181682	0.0407	0.043676206
GO:0042278	purine nucleoside metabolic process	195	0.212117531	0.0146	0.020879842
GO:0031442	positive regulation of mRNA 3'-end processing	6	0.212095512	0.0114	0.018551872
GO:0060350	endochondral bone morphogenesis	23	0.212095484	0.0016	0.011845327
GO:0071875	adrenergic receptor signaling pathway	5	0.212093828	0.0032	0.013333753
GO:0006275	regulation of DNA replication	48	0.212081232	0.0014	0.011465722
GO:1900034	regulation of cellular response to heat	32	0.212072593	0.0037	0.013609033
GO:0043502	regulation of muscle adaptation	36	0.212035186	0.0056	0.014771533
GO:1901136	carbohydrate derivative catabolic process	88	0.212000773	0.0119	0.018881943
GO:0033008	positive regulation of mast cell activation involved in immune response	6	0.212000272	0.0272	0.031504487
GO:0043306	positive regulation of mast cell degranulation	6	0.212000272	0.0272	0.031504487
GO:0045017	glycerolipid biosynthetic process	115	0.211975325	0.0047	0.014168613
GO:0006626	protein targeting to mitochondrion	56	0.211962023	0.0085	0.016693954
GO:0033622	integrin activation	10	0.211932373	0.0434	0.046247475
GO:0046128	purine ribonucleoside metabolic process	193	0.211911205	0.0145	0.020788247
GO:0006266	DNA ligation	8	0.211907785	0.0085	0.016693954
GO:0006336	DNA replication-independent nucleosome assembly	13	0.211889632	0.0177	0.02329117
GO:0034724	DNA replication-independent nucleosome organization	13	0.211889632	0.0177	0.02329117
GO:0032635	interleukin-6 production	49	0.211884656	0.0087	0.016840777
GO:0010948	negative regulation of cell cycle process	142	0.211874289	0.0085	0.016693954

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0045008	depyrimidination	5	0.211874063	0.0038	0.01366393
GO:0071168	protein localization to chromatin	7	0.211849776	0.0161	0.02211694
GO:0042130	negative regulation of T cell proliferation	17	0.211826789	0.017	0.022784886
GO:0070633	transepithelial transport	8	0.211817566	0.0356	0.03903645
GO:0002052	positive regulation of neuroblast proliferation	10	0.21177338	0.0188	0.02420971
GO:0061615	glycolytic process through fructose-6-phosphate	18	0.211750833	0.0126	0.019370699
GO:0061620	glycolytic process through glucose-6-phosphate	18	0.211750833	0.0126	0.019370699
GO:0070232	regulation of T cell apoptotic process	9	0.211730317	0.004	0.013824268
GO:0061462	protein localization to lysosome	17	0.211714056	0.0108	0.018152791
GO:1903039	positive regulation of leukocyte cell-cell adhesion	77	0.211693491	0.0146	0.020879842
GO:0051570	regulation of histone H3-K9 methylation	8	0.211692847	0.0147	0.02091937
GO:0042744	hydrogen peroxide catabolic process	7	0.211679287	0.0266	0.030933467
GO:0032648	regulation of interferon-beta production	17	0.211660166	0.0076	0.016084627
GO:0090100	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	37	0.211608384	0.0114	0.018551872
GO:0055007	cardiac muscle cell differentiation	46	0.211606748	0.004	0.013824268
GO:0050900	leukocyte migration	158	0.211574771	0.0186	0.024075487
GO:0046456	icosanoid biosynthetic process	21	0.211534591	0.0388	0.041925173
GO:1901570	fatty acid derivative biosynthetic process	21	0.211534591	0.0388	0.041925173
GO:0010001	glial cell differentiation	96	0.211492864	0.0118	0.018836996
GO:0019081	viral translation	5	0.211491806	0.0387	0.041895413
GO:0006488	dolichol-linked oligosaccharide biosynthetic process	13	0.211476974	0.0079	0.01629604
GO:0006490	oligosaccharide-lipid intermediate biosynthetic process	13	0.211476974	0.0079	0.01629604
GO:0015909	long-chain fatty acid transport	30	0.21147604	0.0117	0.018739446
GO:0002828	regulation of type 2 immune response	10	0.211473017	0.0038	0.01366393
GO:0042092	type 2 immune response	10	0.211473017	0.0038	0.01366393
GO:0098840	protein transport along microtubule	27	0.21145657	0.0082	0.016514246
GO:0099118	microtubule-based protein transport	27	0.21145657	0.0082	0.016514246
GO:0051023	regulation of immunoglobulin secretion	10	0.211455524	0.001	0.010787313
GO:0006479	protein methylation	68	0.211451202	0.0014	0.011465722
GO:0008213	protein alkylation	68	0.211451202	0.0014	0.011465722
GO:0050679	positive regulation of epithelial cell proliferation	72	0.211450931	0.0101	0.017653628
GO:0061053	somite development	31	0.211443335	0.0149	0.021043429
GO:0032388	positive regulation of intracellular transport	114	0.211388252	0.0051	0.014547706
GO:0044766	multi-organism transport	32	0.211380765	0.0119	0.018881943
GO:1902579	multi-organism localization	32	0.211380765	0.0119	0.018881943
GO:0010528	regulation of transposition	5	0.211320762	0.0332	0.036915846
GO:0010529	negative regulation of transposition	5	0.211320762	0.0332	0.036915846
GO:0043302	positive regulation of leukocyte degranulation	10	0.211317911	0.0305	0.034510959
GO:0034764	positive regulation of transmembrane transport	69	0.211284792	0.0073	0.015844069
GO:0032411	positive regulation of transporter activity	51	0.211284135	0.0093	0.017114131
GO:0016445	somatic diversification of immunoglobulins	22	0.211239116	0.0017	0.012001709
GO:0014854	response to inactivity	5	0.211220727	0.0057	0.01480566
GO:0034763	negative regulation of transmembrane transport	42	0.211203642	0.0033	0.01333753
GO:0009151	purine deoxyribonucleotide metabolic process	10	0.211184445	0.0342	0.037780741
GO:0010466	negative regulation of peptidase activity	74	0.211168255	0.0117	0.018739446
GO:0032414	positive regulation of ion transmembrane transporter activity	47	0.211159996	0.0071	0.01583804
GO:0090162	establishment of epithelial cell polarity	13	0.211020957	0.0387	0.041895413
GO:0061387	regulation of extent of cell growth	45	0.210994195	0.0001	0.004220438
GO:0022617	extracellular matrix disassembly	29	0.21097955	0.0045	0.014132412
GO:0043276	anoikis	15	0.210973405	0.0003	0.007956881
GO:0033628	regulation of cell adhesion mediated by integrin	22	0.210936432	0.0096	0.017302743
GO:0040015	negative regulation of multicellular organism growth	5	0.210922956	0.0376	0.040911404
GO:0010950	positive regulation of endopeptidase activity	64	0.210922077	0.0078	0.01620539
GO:0045444	fat cell differentiation	99	0.210910346	0.0012	0.010961137
GO:0048853	forebrain morphogenesis	5	0.210903001	0.0328	0.036618961
GO:1902305	regulation of sodium ion transmembrane transport	26	0.210834214	0.0023	0.012498684
GO:0097191	extrinsic apoptotic signaling pathway	88	0.210821357	0.0057	0.01480566
GO:0015931	nucleobase-containing compound transport	84	0.210790101	0.0043	0.014102439
GO:0008625	extrinsic apoptotic signaling pathway via death domain receptors	37	0.210789203	0.0058	0.014878261
GO:0006656	phosphatidylcholine biosynthetic process	15	0.210784911	0.0159	0.021956962
GO:0006474	N-terminal protein amino acid acetylation	6	0.210764956	0.0384	0.04164081
GO:2000649	regulation of sodium ion transmembrane transporter activity	21	0.210760575	0.0006	0.009940401
GO:0072132	mesenchyme morphogenesis	28	0.210751135	0.0162	0.022196303
GO:0036303	lymph vessel morphogenesis	7	0.210746137	0.0025	0.012769435
GO:0071985	multivesicular body sorting pathway	6	0.210745736	0.006	0.015037711
GO:0003229	ventricular cardiac muscle tissue development	22	0.210737293	0.0116	0.018682786
GO:0035094	response to nicotine	19	0.210693233	0.0109	0.018225506
GO:0097094	craniofacial suture morphogenesis	8	0.210689423	0.0345	0.038068511
GO:0019827	stem cell population maintenance	61	0.210686579	0.0091	0.016994897
GO:1904646	cellular response to beta-amyloid	17	0.210678418	0.0145	0.020788247
GO:0006509	membrane protein ectodomain proteolysis	18	0.210662157	0.0075	0.015990044
GO:0090092	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	89	0.21064041	0.0079	0.01629604
GO:0071493	cellular response to UV-B	5	0.210630627	0.0318	0.035688587
GO:1902510	regulation of apoptotic DNA fragmentation	6	0.210628251	0.0009	0.010729485
GO:0009263	deoxyribonucleotide biosynthetic process	7	0.210623592	0.0285	0.032631089
GO:1901739	regulation of myoblast fusion	8	0.210607464	0.0035	0.01351837
GO:1901741	positive regulation of myoblast fusion	8	0.210607464	0.0035	0.01351837
GO:0035282	segmentation	29	0.210578616	0.0153	0.021378589
GO:0097194	execution phase of apoptosis	25	0.210565526	0.0014	0.011465722
GO:0009132	nucleoside diphosphate metabolic process	71	0.210541126	0.0102	0.0177
GO:0006362	transcription elongation from RNA polymerase I promoter	16	0.210508013	0.0034	0.01347416
GO:0035025	positive regulation of Rho protein signal transduction	7	0.210503454	0.0109	0.018225506
GO:0045197	establishment or maintenance of epithelial cell apical/basal polarity	15	0.210477119	0.0284	0.032523034

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0046822	regulation of nucleocytoplasmic transport	65	0.210462852	0.0094	0.017156187
GO:2000008	regulation of protein localization to cell surface	17	0.210453256	0.0111	0.018389742
GO:0022900	electron transport chain	95	0.210436736	0.0308	0.034775552
GO:0007163	establishment or maintenance of cell polarity	82	0.210422005	0.0053	0.014634479
GO:0060485	mesenchyme development	109	0.210404577	0.0088	0.016916437
GO:0009205	purine ribonucleoside triphosphate metabolic process	155	0.210352568	0.017	0.022784886
GO:1902946	protein localization to early endosome	5	0.210303311	0.028	0.032186083
GO:0043268	positive regulation of potassium ion transport	18	0.210210144	0.0013	0.011218806
GO:0090329	regulation of DNA-dependent DNA replication	21	0.210172103	0.0013	0.011218806
GO:0030728	ovulation	9	0.210118215	0.0038	0.01366393
GO:0048592	eye morphogenesis	61	0.210111781	0.0013	0.011218806
GO:0002698	negative regulation of immune effector process	43	0.21009387	0.0143	0.020629391
GO:0070192	chromosome organization involved in meiotic cell cycle	15	0.210068169	0.0155	0.021605834
GO:0031112	positive regulation of microtubule polymerization or depolymerization	9	0.21006552	0.0128	0.019522448
GO:0071216	cellular response to biotic stimulus	90	0.21004473	0.0083	0.016559903
GO:0086002	cardiac muscle cell action potential involved in contraction	22	0.210035861	0.0031	0.013277185
GO:0046660	female sex differentiation	50	0.210024406	0.003	0.013210967
GO:0030903	notochord development	9	0.210020311	0.02	0.025188412
GO:0033630	positive regulation of cell adhesion mediated by integrin	10	0.209996728	0.0151	0.02121706
GO:0055123	digestive system development	59	0.209986072	0.01	0.017574468
GO:1902805	positive regulation of synaptic vesicle transport	12	0.209980142	< 0.001	< 0.001
GO:0046321	positive regulation of fatty acid oxidation	9	0.209955954	0.0224	0.027324219
GO:0042440	pigment metabolic process	36	0.209955774	0.0153	0.021378589
GO:0060840	artery development	37	0.20994386	0.0118	0.018836996
GO:0030890	positive regulation of B cell proliferation	19	0.209919513	0.0233	0.028125386
GO:0001958	endochondral ossification	12	0.209904879	0.0062	0.015209334
GO:0036075	replacement ossification	12	0.209904879	0.0062	0.015209334
GO:0042273	ribosomal large subunit biogenesis	11	0.209895916	0.0118	0.018836996
GO:0070471	uterine smooth muscle contraction	5	0.209847454	0.0184	0.023875404
GO:0048565	digestive tract development	57	0.209766519	0.0095	0.01725157
GO:0009199	ribonucleoside triphosphate metabolic process	157	0.209729032	0.0167	0.02255007
GO:0003207	cardiac chamber formation	7	0.2097208	0.0331	0.03684717
GO:0032507	maintenance of protein location in cell	39	0.209712579	0.0063	0.015311728
GO:0032608	interferon-beta production	19	0.209669358	0.0087	0.016840777
GO:0046460	neutral lipid biosynthetic process	19	0.209638941	0.0024	0.012603815
GO:0046463	acylglycerol biosynthetic process	19	0.209638941	0.0024	0.012603815
GO:0008272	sulfate transport	7	0.209600477	0.0457	0.0483597
GO:1902358	sulfate transmembrane transport	7	0.209600477	0.0457	0.0483597
GO:0006505	GPI anchor metabolic process	15	0.209595812	0.0363	0.039683607
GO:0031100	animal organ regeneration	33	0.209585948	0.0098	0.017418875
GO:0045071	negative regulation of viral genome replication	16	0.2095433	0.0107	0.018084595
GO:0010822	positive regulation of mitochondrion organization	73	0.209538048	0.004	0.013824268
GO:0031122	cytoplasmic microtubule organization	17	0.209534392	0.0032	0.013333753
GO:0042308	negative regulation of protein import into nucleus	18	0.209503941	0.0142	0.020567234
GO:1904590	negative regulation of protein import	18	0.209503941	0.0142	0.020567234
GO:0071545	inositol phosphate catabolic process	5	0.209465197	0.0032	0.013333753
GO:2000144	positive regulation of DNA-templated transcription, initiation	8	0.209376144	0.0121	0.018970228
GO:0050905	neuromuscular process	49	0.209375936	0.0005	0.009604651
GO:0070661	leukocyte proliferation	111	0.209343865	0.0183	0.023783007
GO:0009119	ribonucleoside metabolic process	200	0.20934371	0.0141	0.020504577
GO:1901381	positive regulation of potassium ion transmembrane transport	16	0.209297344	0.0027	0.012827773
GO:0010996	response to auditory stimulus	9	0.209272355	0.0002	0.006319126
GO:0055006	cardiac cell development	37	0.209272153	0.0051	0.014547706
GO:0030183	B cell differentiation	41	0.209263952	0.0026	0.012805111
GO:1902115	regulation of organelle assembly	63	0.209261454	0.0079	0.01629604
GO:0035089	establishment of apical/basal cell polarity	9	0.209244856	0.0333	0.037012803
GO:0014855	striated muscle cell proliferation	24	0.209205856	0.024	0.028671074
GO:0007586	digestion	46	0.209197009	0.0115	0.018599441
GO:0051099	positive regulation of binding	80	0.209154937	0.0027	0.012827773
GO:2000209	regulation of anoikis	12	0.209144144	0.0001	0.004220438
GO:0042552	myelination	52	0.209133969	0.0066	0.015525305
GO:0071622	regulation of granulocyte chemotaxis	15	0.209125442	0.0259	0.0303391
GO:0000075	cell cycle checkpoint	76	0.209113943	0.0026	0.012805111
GO:0006606	protein import into nucleus	67	0.209065723	0.017	0.022784886
GO:0044744	protein targeting to nucleus	67	0.209065723	0.017	0.022784886
GO:1902593	single-organism nuclear import	67	0.209065723	0.017	0.022784886
GO:0010944	negative regulation of transcription by competitive promoter binding	5	0.209054951	0.03	0.034118804
GO:0042461	photoreceptor cell development	18	0.209053799	0.0006	0.009940401
GO:0006814	sodium ion transport	64	0.209027659	0.0029	0.013089617
GO:1903707	negative regulation of hemopoiesis	48	0.208985815	0.0118	0.018836996
GO:0046628	positive regulation of insulin receptor signaling pathway	6	0.208932931	0.0125	0.019314538
GO:1900078	positive regulation of cellular response to insulin stimulus	6	0.208932931	0.0125	0.019314538
GO:0048568	embryonic organ development	159	0.208883378	0.0057	0.01480566
GO:0006641	triglyceride metabolic process	40	0.20883172	0.0041	0.013887639
GO:0008356	asymmetric cell division	10	0.208800459	0.028	0.032186083
GO:0010460	positive regulation of heart rate	12	0.208776789	0.004	0.013824268
GO:0048103	somatic stem cell division	11	0.208764224	0.0319	0.035793868
GO:2000404	regulation of T cell migration	14	0.208703053	0.0133	0.019917275
GO:0032941	secretion by tissue	38	0.208685857	0.0014	0.011465722
GO:0071624	positive regulation of granulocyte chemotaxis	11	0.20864725	0.0301	0.034151923
GO:0090022	regulation of neutrophil chemotaxis	11	0.20864725	0.0301	0.034151923
GO:0090023	positive regulation of neutrophil chemotaxis	11	0.20864725	0.0301	0.034151923
GO:1902622	regulation of neutrophil migration	11	0.20864725	0.0301	0.034151923

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1902624	positive regulation of neutrophil migration	11	0.20864725	0.0301	0.034151923
GO:1903311	regulation of mRNA metabolic process	52	0.208609001	0.0035	0.01351837
GO:0033108	mitochondrial respiratory chain complex assembly	51	0.208595125	0.0315	0.035393121
GO:0034767	positive regulation of ion transmembrane transport	65	0.208586315	0.0073	0.015844069
GO:0030194	positive regulation of blood coagulation	8	0.208545707	0.0243	0.028921902
GO:0050820	positive regulation of coagulation	8	0.208545707	0.0243	0.028921902
GO:1900048	positive regulation of hemostasis	8	0.208545707	0.0243	0.028921902
GO:1902106	negative regulation of leukocyte differentiation	35	0.208512868	0.0081	0.016514175
GO:0031570	DNA integrity checkpoint	51	0.208485517	0.0014	0.011465722
GO:0007016	cytoskeletal anchoring at plasma membrane	6	0.208475303	0.0252	0.029736
GO:0009880	embryonic pattern specification	22	0.208455002	0.0164	0.022306469
GO:1903146	regulation of mitophagy	27	0.208451163	0.0036	0.01353394
GO:0046824	positive regulation of nucleocytoplasmic transport	33	0.20842834	0.0142	0.020567234
GO:0032757	positive regulation of interleukin-8 production	19	0.208426086	0.0257	0.030153693
GO:0033262	regulation of nuclear cell cycle DNA replication	11	0.208418367	0.0021	0.012314604
GO:0050995	negative regulation of lipid catabolic process	9	0.208390789	0.0028	0.012972436
GO:0060759	regulation of response to cytokine stimulus	69	0.208387002	0.0142	0.020567234
GO:0019933	cAMP-mediated signaling	33	0.208363001	0.0027	0.012827773
GO:0045793	positive regulation of cell size	5	0.208352376	0.0174	0.023064374
GO:0051145	smooth muscle cell differentiation	27	0.208332287	0.0142	0.020567234
GO:1903115	regulation of actin filament-based movement	14	0.208326627	0.0079	0.01629604
GO:0006296	nucleotide-excision repair, DNA incision, 5'-to lesion	17	0.208324814	0.025	0.029554283
GO:0001649	osteoblast differentiation	91	0.208288487	0.0063	0.015311728
GO:0097186	amelogenesis	7	0.208275999	0.0157	0.021779607
GO:0060008	Sertoli cell differentiation	9	0.208272872	0.0127	0.019457181
GO:0070897	DNA-templated transcriptional preinitiation complex assembly	12	0.208194981	0.0068	0.015633241
GO:0048659	smooth muscle cell proliferation	59	0.208181811	0.0106	0.018010344
GO:0015980	energy derivation by oxidation of organic compounds	127	0.208163899	0.0162	0.022196303
GO:0010561	negative regulation of glycoprotein biosynthetic process	8	0.208149683	0.0129	0.019597425
GO:1904063	negative regulation of cation transmembrane transport	36	0.20814297	0.0021	0.012314604
GO:0003298	physiological muscle hypertrophy	17	0.208132504	0.001	0.010787313
GO:0003301	physiological cardiac muscle hypertrophy	17	0.208132504	0.001	0.010787313
GO:0061049	cell growth involved in cardiac muscle cell development	17	0.208132504	0.001	0.010787313
GO:1900017	positive regulation of cytokine production involved in inflammatory response	5	0.20809581	0.0404	0.043394538
GO:0071318	cellular response to ATP	10	0.20809283	0.0173	0.023005658
GO:0032964	collagen biosynthetic process	17	0.208083874	0.0107	0.018084595
GO:0043277	apoptotic cell clearance	18	0.208051509	0.0005	0.009604651
GO:0007052	mitotic spindle organization	38	0.208042226	0.006	0.015037711
GO:0070849	response to epidermal growth factor	24	0.208020374	0.0018	0.01210186
GO:0002687	positive regulation of leukocyte migration	45	0.208004242	0.0154	0.021487162
GO:0032693	negative regulation of interleukin-10 production	6	0.20795958	0.0203	0.025471918
GO:0046037	GMP metabolic process	6	0.207929561	0.013	0.019676963
GO:0034248	regulation of cellular amide metabolic process	194	0.207898102	0.0048	0.014269203
GO:0051151	negative regulation of smooth muscle cell differentiation	8	0.207897814	0.021	0.026005997
GO:0010611	regulation of cardiac muscle hypertrophy	26	0.207896369	0.0023	0.012498684
GO:0019320	hexose catabolic process	33	0.20789377	0.0094	0.017156187
GO:0030522	intracellular receptor signaling pathway	105	0.207850549	0.0056	0.014771533
GO:0019064	fusion of virus membrane with host plasma membrane	6	0.207849438	0.0336	0.037253154
GO:0039663	membrane fusion involved in viral entry into host cell	6	0.207849438	0.0336	0.037253154
GO:0044800	multi-organism membrane fusion	6	0.207849438	0.0336	0.037253154
GO:0035725	sodium ion transmembrane transport	45	0.207845925	0.0012	0.010961137
GO:0042976	activation of Janus kinase activity	6	0.207844039	0.0024	0.012603815
GO:0086001	cardiac muscle cell action potential	27	0.20784128	0.0101	0.017653628
GO:0006446	regulation of translational initiation	33	0.207789557	0.0059	0.014942532
GO:0070286	axonemal dynein complex assembly	11	0.207750919	0.0134	0.01999969
GO:0002082	regulation of oxidative phosphorylation	15	0.207734113	0.0057	0.01480566
GO:0048660	regulation of smooth muscle cell proliferation	58	0.207709255	0.0099	0.017505138
GO:0098927	vesicle-mediated transport between endosomal compartments	24	0.207707064	0.0018	0.01210186
GO:0036035	osteoclast development	9	0.207685161	0.0021	0.012314604
GO:0032770	positive regulation of monooxygenase activity	13	0.207642445	0.0032	0.013333753
GO:0006165	nucleoside diphosphate phosphorylation	59	0.20763253	0.0087	0.016840777
GO:0010560	positive regulation of glycoprotein biosynthetic process	6	0.207625699	0.0053	0.014634479
GO:0032733	positive regulation of interleukin-10 production	9	0.207616629	0.0353	0.038781037
GO:0070242	thymocyte apoptotic process	5	0.207559873	0.0045	0.014132412
GO:0006744	ubiquinone biosynthetic process	8	0.207521874	0.0133	0.019917275
GO:1901663	quinone biosynthetic process	8	0.207521874	0.0133	0.019917275
GO:0009144	purine nucleoside triphosphate metabolic process	161	0.207516942	0.019	0.024347961
GO:0051170	nuclear import	79	0.207516788	0.0178	0.023348367
GO:0030261	chromosome condensation	12	0.207505623	0.0033	0.013333753
GO:0008064	regulation of actin polymerization or depolymerization	69	0.207496309	0.0106	0.018010344
GO:0030832	regulation of actin filament length	69	0.207496309	0.0106	0.018010344
GO:0009895	negative regulation of catabolic process	87	0.207471039	0.0021	0.012314604
GO:0033002	muscle cell proliferation	78	0.207459041	0.0154	0.021487162
GO:0030851	granulocyte differentiation	14	0.207456322	0.0059	0.014942532
GO:0051606	detection of stimulus	107	0.207426596	0.0085	0.016693954
GO:0044550	secondary metabolite biosynthetic process	12	0.207376477	0.0147	0.02091937
GO:0002679	respiratory burst involved in defense response	7	0.207337665	0.0418	0.044765253
GO:0006417	regulation of translation	174	0.207330201	0.0064	0.015399417
GO:0048645	animal organ formation	22	0.207328022	0.0287	0.032827577
GO:0007585	respiratory gaseous exchange	30	0.207303092	0.0032	0.013333753
GO:0002065	columnar/cuboidal epithelial cell differentiation	47	0.207274293	0.0029	0.013089617
GO:0003002	regionalization	102	0.207273614	0.0089	0.016916437
GO:0072331	signal transduction by p53 class mediator	109	0.207263486	0.0062	0.015209334

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0042733	embryonic digit morphogenesis	25	0.207239503	0.0144	0.02072711
GO:0001756	somitogenesis	21	0.207210924	0.0145	0.020788247
GO:0033045	regulation of sister chromatid segregation	31	0.207207119	0.0035	0.01351837
GO:0007272	ensheathment of neurons	53	0.207188677	0.0056	0.014771533
GO:0008366	axon ensheathment	53	0.207188677	0.0056	0.014771533
GO:0009952	anterior/posterior pattern specification	55	0.207181457	0.0146	0.020879842
GO:0044060	regulation of endocrine process	20	0.20714114	0.0097	0.017363901
GO:0007595	lactation	21	0.207085603	0.0024	0.012603815
GO:0070278	extracellular matrix constituent secretion	7	0.207085357	0.0057	0.01480566
GO:0042033	chemokine biosynthetic process	6	0.207070455	0.0454	0.048095053
GO:0045073	regulation of chemokine biosynthetic process	6	0.207070455	0.0454	0.048095053
GO:0050755	chemokine metabolic process	6	0.207070455	0.0454	0.048095053
GO:0050686	negative regulation of mRNA processing	12	0.207059657	0.0152	0.0213213
GO:0002825	regulation of T-helper 1 type immune response	9	0.207031222	0.0071	0.01583804
GO:2001243	negative regulation of intrinsic apoptotic signaling pathway	38	0.20702084	0.0198	0.025062084
GO:0009791	post-embryonic development	24	0.206999781	0.0078	0.01620539
GO:2001235	positive regulation of apoptotic signaling pathway	79	0.206988616	0.0069	0.015750415
GO:0031623	receptor internalization	43	0.206965873	0.0092	0.017033109
GO:0034389	lipid particle organization	13	0.206905541	0.0134	0.01999969
GO:0016482	cytosolic transport	70	0.20688786	0.0021	0.012314604
GO:0042098	T cell proliferation	68	0.206885863	0.0206	0.025725529
GO:0098781	ncRNA transcription	49	0.20687975	0.0085	0.016693954
GO:0042455	ribonucleoside biosynthetic process	57	0.20687919	0.0164	0.022306469
GO:0006661	phosphatidylinositol biosynthetic process	57	0.206843181	0.0039	0.013791927
GO:0070227	lymphocyte apoptotic process	20	0.206838056	0.0039	0.013791927
GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	40	0.206790501	0.0181	0.023607986
GO:0051150	regulation of smooth muscle cell differentiation	15	0.206785425	0.0114	0.018551872
GO:0097530	granulocyte migration	36	0.206775088	0.0192	0.02450649
GO:0043967	histone H4 acetylation	22	0.206769597	0.0096	0.017302743
GO:0042149	cellular response to glucose starvation	14	0.206745213	0.0158	0.021871104
GO:0043455	regulation of secondary metabolic process	8	0.206738248	0.0019	0.012288367
GO:0034616	response to laminar fluid shear stress	9	0.206735494	0.002	0.012314604
GO:0032460	negative regulation of protein oligomerization	9	0.206706411	0.0121	0.018970228
GO:0017004	cytochrome complex assembly	19	0.206666068	0.0188	0.02420971
GO:0060260	regulation of transcription initiation from RNA polymerase II promoter	10	0.206643882	0.0059	0.014942532
GO:0040014	regulation of multicellular organism growth	31	0.206628571	0.0129	0.019597425
GO:0060544	regulation of necroptotic process	6	0.206564451	0.0326	0.036409735
GO:0002763	positive regulation of myeloid leukocyte differentiation	22	0.206559916	0.0266	0.030933467
GO:0030010	establishment of cell polarity	59	0.206538184	0.0035	0.01351837
GO:0035148	tube formation	62	0.206508293	0.0067	0.015576759
GO:0042743	hydrogen peroxide metabolic process	18	0.20650758	0.0268	0.031128485
GO:0060986	endocrine hormone secretion	23	0.206487323	0.0092	0.017033109
GO:0043392	negative regulation of DNA binding	25	0.206469755	0.0064	0.015399417
GO:0046545	development of primary female sexual characteristics	43	0.206460637	0.003	0.013210967
GO:0015918	sterol transport	33	0.20645266	0.0156	0.021692929
GO:0000717	nucleotide-excision repair, DNA duplex unwinding	14	0.206449218	0.0167	0.02255007
GO:0071474	cellular hyperosmotic response	8	0.206442647	0.0067	0.015576759
GO:0032943	mononuclear cell proliferation	101	0.206406878	0.0191	0.02440579
GO:0006536	glutamate metabolic process	18	0.206380017	0.0063	0.015311728
GO:0055013	cardiac muscle cell development	34	0.206375304	0.0048	0.014269203
GO:0046488	phosphatidylinositol metabolic process	71	0.206318416	0.0056	0.014771533
GO:0006368	transcription elongation from RNA polymerase II promoter	45	0.206292595	0.0107	0.018084595
GO:0046651	lymphocyte proliferation	100	0.206285157	0.0187	0.024129301
GO:1904064	positive regulation of cation transmembrane transport	56	0.206258645	0.0055	0.01475
GO:0048021	regulation of melanin biosynthetic process	6	0.206248063	0.0022	0.012422266
GO:1900376	regulation of secondary metabolite biosynthetic process	6	0.206248063	0.0022	0.012422266
GO:0061640	cytoskeleton-dependent cytokinesis	28	0.20624342	0.0027	0.012827773
GO:0036474	cell death in response to hydrogen peroxide	12	0.206182518	0.0092	0.017033109
GO:0006968	cellular defense response	17	0.206177087	0.0106	0.018010344
GO:0042133	neurotransmitter metabolic process	10	0.206151743	0.0308	0.034775552
GO:0016073	snRNA metabolic process	36	0.206149151	0.0056	0.014771533
GO:0048340	paraxial mesoderm morphogenesis	5	0.20614358	0.0473	0.049788567
GO:1901881	positive regulation of protein depolymerization	11	0.206088426	0.0208	0.025885837
GO:0050864	regulation of B cell activation	51	0.206079598	0.0109	0.018225506
GO:0031062	positive regulation of histone methylation	14	0.206053726	0.0116	0.018682786
GO:0051651	maintenance of location in cell	46	0.206047601	0.0068	0.015633241
GO:0098751	bone cell development	14	0.206033179	0.0008	0.010465158
GO:0003281	ventricular septum development	31	0.206005716	0.0132	0.019860109
GO:0018208	peptidyl-proline modification	25	0.205989226	0.0144	0.02072711
GO:0002761	regulation of myeloid leukocyte differentiation	44	0.205981583	0.009	0.016956012
GO:0006638	neutral lipid metabolic process	51	0.205941381	0.0048	0.014269203
GO:0046174	polyol catabolic process	6	0.205909215	0.0024	0.012603815
GO:0019682	glyceraldehyde-3-phosphate metabolic process	10	0.205865893	0.0232	0.028016374
GO:1990868	response to chemokine	5	0.205792681	0.0121	0.018970228
GO:1990869	cellular response to chemokine	5	0.205792681	0.0121	0.018970228
GO:0015812	gamma-aminobutyric acid transport	5	0.205680207	0.0075	0.015990044
GO:2001224	positive regulation of neuron migration	8	0.205672788	0.0002	0.006319126
GO:1903524	positive regulation of blood circulation	25	0.205661444	0.012	0.018931514
GO:0090656	t-circle formation	9	0.205654377	0.0065	0.015491756
GO:0030071	regulation of mitotic metaphase/anaphase transition	20	0.20565293	0.002	0.012314604
GO:0071425	hematopoietic stem cell proliferation	8	0.205612048	0.0012	0.010961137
GO:1901385	regulation of voltage-gated calcium channel activity	16	0.205592854	0.0164	0.022306469
GO:0046470	phosphatidylcholine metabolic process	32	0.205582772	0.0135	0.020081554

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0048872	homeostasis of number of cells	83	0.205558203	0.0071	0.01583804
GO:0032602	chemokine production	37	0.205554018	0.0229	0.027770092
GO:2000169	regulation of peptidyl-cysteine S-nitrosylation	5	0.205552442	0.012	0.018931514
GO:0048259	regulation of receptor-mediated endocytosis	43	0.205515105	0.0065	0.015491756
GO:0014743	regulation of muscle hypertrophy	27	0.20550349	0.0039	0.013791927
GO:0048745	smooth muscle tissue development	6	0.205502986	0.022	0.026944291
GO:2001236	regulation of extrinsic apoptotic signaling pathway	62	0.205498103	0.008	0.016379603
GO:0048566	embryonic digestive tract development	15	0.205496551	0.0051	0.014547706
GO:0050871	positive regulation of B cell activation	33	0.205424081	0.0149	0.021043429
GO:0032570	response to progesterone	21	0.205418112	0.0324	0.036242368
GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	138	0.205410694	0.0098	0.017418875
GO:0000398	mRNA splicing, via spliceosome	138	0.205410694	0.0098	0.017418875
GO:0033146	regulation of intracellular estrogen receptor signaling pathway	13	0.205404124	0.0239	0.028592965
GO:0032508	DNA duplex unwinding	33	0.205379906	0.0057	0.01480566
GO:0045136	development of secondary sexual characteristics	5	0.205318164	0.0393	0.042425803
GO:0008360	regulation of cell shape	55	0.20530808	0.0145	0.020788247
GO:0019058	viral life cycle	199	0.205287034	0.0135	0.020081554
GO:0046885	regulation of hormone biosynthetic process	7	0.20526015	0.0255	0.029992067
GO:0008585	female gonad development	39	0.205232815	0.0021	0.012314604
GO:0070228	regulation of lymphocyte apoptotic process	14	0.205226274	0.0033	0.013333753
GO:0045685	regulation of glial cell differentiation	31	0.205214451	0.0196	0.0248852
GO:0046838	phosphorylated carbohydrate dephosphorylation	5	0.205154377	0.0113	0.018488002
GO:0010717	regulation of epithelial to mesenchymal transition	36	0.205134299	0.0113	0.018488002
GO:0009141	nucleoside triphosphate metabolic process	169	0.205090606	0.0184	0.023875404
GO:0006929	substrate-dependent cell migration	13	0.205086159	0.0209	0.025971158
GO:0061050	regulation of cell growth involved in cardiac muscle cell development	12	0.205002597	0.0004	0.008964341
GO:0021517	ventral spinal cord development	18	0.204961924	0.0063	0.015311728
GO:0045637	regulation of myeloid cell differentiation	80	0.204961402	0.0067	0.015576759
GO:0035825	reciprocal DNA recombination	10	0.204956769	0.0141	0.020504577
GO:0045022	early endosome to late endosome transport	22	0.204926754	0.0027	0.012827773
GO:0086091	regulation of heart rate by cardiac conduction	15	0.204906622	0.014	0.020462083
GO:0071559	response to transforming growth factor beta	105	0.204897268	0.0085	0.016693954
GO:0007158	neuron cell-cell adhesion	9	0.204826802	0.0308	0.034775552
GO:0031333	negative regulation of protein complex assembly	58	0.204825328	0.0055	0.01475
GO:2000116	regulation of cysteine-type endopeptidase activity	93	0.204791788	0.0097	0.017363901
GO:0071560	cellular response to transforming growth factor beta stimulus	104	0.204735125	0.0078	0.01620539
GO:0048009	insulin-like growth factor receptor signaling pathway	11	0.204734448	0.0044	0.014132412
GO:0030033	microvillus assembly	9	0.204687865	0.0024	0.012603815
GO:1901796	regulation of signal transduction by p53 class mediator	79	0.204682527	0.0089	0.016916437
GO:1902176	negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	7	0.204627806	0.016	0.022026667
GO:0006622	protein targeting to lysosome	10	0.20459693	0.0136	0.020157703
GO:0097120	receptor localization to synapse	7	0.204545802	0.0317	0.035590175
GO:0006007	glucose catabolic process	22	0.204532364	0.0162	0.022196303
GO:0008380	RNA splicing	164	0.204518958	0.0101	0.017653628
GO:0046365	monosaccharide catabolic process	36	0.204508831	0.0129	0.019597425
GO:0006298	mismatch repair	9	0.20449105	0.0168	0.022626974
GO:0000375	RNA splicing, via transesterification reactions	139	0.204483577	0.01	0.017574468
GO:0061158	3'-UTR-mediated mRNA destabilization	9	0.204471613	0.025	0.029554283
GO:0045861	negative regulation of proteolysis	109	0.204462651	0.0092	0.017033109
GO:2000403	positive regulation of lymphocyte migration	11	0.204434061	0.0131	0.019786886
GO:0001516	prostaglandin biosynthetic process	12	0.204394118	0.0274	0.03166636
GO:0046457	prostanoid biosynthetic process	12	0.204394118	0.0274	0.03166636
GO:0035051	cardiocyte differentiation	60	0.204326931	0.007	0.015816335
GO:0009394	2'-deoxyribonucleotide metabolic process	19	0.204321309	0.0208	0.025885837
GO:0042430	indole-containing compound metabolic process	9	0.204305752	0.0091	0.016994897
GO:0070663	regulation of leukocyte proliferation	87	0.204297555	0.019	0.024347961
GO:0030301	cholesterol transport	31	0.204253689	0.0194	0.024690909
GO:0048663	neuron fate commitment	19	0.204252292	0.0205	0.025639412
GO:0060351	cartilage development involved in endochondral bone morphogenesis	10	0.204225169	0.0003	0.007956881
GO:1903624	regulation of DNA catabolic process	7	0.2042213	0.0041	0.013887639
GO:0051315	attachment of mitotic spindle microtubules to kinetochore	7	0.204203159	0.0145	0.020788247
GO:0001573	ganglioside metabolic process	9	0.204194027	0.0044	0.014132412
GO:0042698	ovulation cycle	51	0.204190139	0.002	0.012314604
GO:0010257	NADH dehydrogenase complex assembly	37	0.204156741	0.0403	0.043327371
GO:0032981	mitochondrial respiratory chain complex I assembly	37	0.204156741	0.0403	0.043327371
GO:0097031	mitochondrial respiratory chain complex I biogenesis	37	0.204156741	0.0403	0.043327371
GO:0040029	regulation of gene expression, epigenetic	83	0.204155585	0.0034	0.01347416
GO:1902105	regulation of leukocyte differentiation	98	0.204150693	0.0111	0.018389742
GO:0032944	regulation of mononuclear cell proliferation	82	0.204140446	0.0212	0.026203164
GO:0002285	lymphocyte activation involved in immune response	58	0.20413874	0.0066	0.015525305
GO:0045652	regulation of megakaryocyte differentiation	16	0.204029246	0.0187	0.024129301
GO:0061339	establishment or maintenance of monopolar cell polarity	11	0.204016583	0.0152	0.0213213
GO:0050670	regulation of lymphocyte proliferation	81	0.203962193	0.0209	0.025971158
GO:0010737	protein kinase A signaling	14	0.203917901	0.0182	0.023684988
GO:0030219	megakaryocyte differentiation	22	0.203861736	0.0085	0.016693954
GO:0032922	circadian regulation of gene expression	23	0.203816709	0.0001	0.004220438
GO:0034139	regulation of toll-like receptor 3 signaling pathway	5	0.20381583	0.0104	0.017832977
GO:0034141	positive regulation of toll-like receptor 3 signaling pathway	5	0.20381583	0.0104	0.017832977
GO:0034976	response to endoplasmic reticulum stress	127	0.20381565	0.0018	0.01210186
GO:0016024	CDP-diacylglycerol biosynthetic process	9	0.203753891	0.005	0.014547706
GO:0060416	response to growth hormone	14	0.203680494	0.0008	0.010465158
GO:0033198	response to ATP	16	0.203651281	0.0074	0.015911789
GO:0043966	histone H3 acetylation	19	0.203627791	0.0087	0.016840777

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0006639	acylglycerol metabolic process	50	0.203606638	0.0047	0.014168613
GO:1902099	regulation of metaphase/anaphase transition of cell cycle	21	0.203603272	0.0022	0.012422266
GO:1903313	positive regulation of mRNA metabolic process	23	0.203595242	0.0026	0.012805111
GO:0002456	T cell mediated immunity	21	0.203585501	0.003	0.013210967
GO:0042073	intraciliary transport	22	0.203569713	0.007	0.015816335
GO:0060123	regulation of growth hormone secretion	8	0.203565679	< 0.001	< 0.001
GO:0009650	UV protection	5	0.203476334	0.0166	0.02247277
GO:0033627	cell adhesion mediated by integrin	25	0.203455602	0.0143	0.020629391
GO:0051639	actin filament network formation	5	0.203427353	0.0018	0.01210186
GO:0051294	establishment of spindle orientation	13	0.20341609	0.0027	0.012827773
GO:0035735	intraciliary transport involved in cilium assembly	19	0.203415009	0.007	0.015816335
GO:0014013	regulation of gliogenesis	54	0.203390399	0.0191	0.02440579
GO:0071772	response to BMP	53	0.203389556	0.0059	0.014942532
GO:0071773	cellular response to BMP stimulus	53	0.203389556	0.0059	0.014942532
GO:0072413	signal transduction involved in mitotic cell cycle checkpoint	18	0.20331354	0.002	0.012314604
GO:0072431	signal transduction involved in mitotic G1 DNA damage checkpoint	18	0.20331354	0.002	0.012314604
GO:1902400	intracellular signal transduction involved in G1 DNA damage checkpoint	18	0.20331354	0.002	0.012314604
GO:1902402	signal transduction involved in mitotic DNA damage checkpoint	18	0.20331354	0.002	0.012314604
GO:1902403	signal transduction involved in mitotic DNA integrity checkpoint	18	0.20331354	0.002	0.012314604
GO:0070841	inclusion body assembly	13	0.203266676	0.0054	0.014720792
GO:0072665	protein localization to vacuole	19	0.203250717	0.0148	0.020979063
GO:0035088	establishment or maintenance of apical/basal cell polarity	17	0.20319556	0.0234	0.02817551
GO:0061245	establishment or maintenance of bipolar cell polarity	17	0.20319556	0.0234	0.02817551
GO:0043044	ATP-dependent chromatin remodeling	27	0.203177843	0.0059	0.014942532
GO:0090630	activation of GTPase activity	20	0.203174157	0.0066	0.015525305
GO:0050685	positive regulation of mRNA processing	11	0.203123904	0.0022	0.012422266
GO:0010259	multicellular organism aging	14	0.203112385	0.0004	0.008964341
GO:0002718	regulation of cytokine production involved in immune response	29	0.203111807	0.0143	0.020629391
GO:0045185	maintenance of protein location	42	0.203104024	0.0075	0.015990044
GO:0035855	megakaryocyte development	5	0.203059609	0.0009	0.010729485
GO:0007589	body fluid secretion	43	0.20305474	0.002	0.012314604
GO:0032933	SREBP signaling pathway	5	0.203040432	0.0013	0.011218806
GO:0045724	positive regulation of cilium assembly	9	0.203012414	0.0136	0.020157703
GO:0051236	establishment of RNA localization	68	0.203003955	0.0067	0.015576759
GO:1904019	epithelial cell apoptotic process	37	0.202990113	0.014	0.020462083
GO:0009081	branched-chain amino acid metabolic process	13	0.20295798	0.034	0.037588528
GO:0009083	branched-chain amino acid catabolic process	13	0.20295798	0.034	0.037588528
GO:0002028	regulation of sodium ion transport	32	0.202918676	0.0049	0.014447629
GO:0002367	cytokine production involved in immune response	31	0.20291673	0.0134	0.01999969
GO:0048012	hepatocyte growth factor receptor signaling pathway	8	0.202871623	0.0086	0.016782045
GO:0034766	negative regulation of ion transmembrane transport	37	0.202839907	0.0026	0.012805111
GO:0010664	negative regulation of striated muscle cell apoptotic process	10	0.202831162	0.0148	0.020979063
GO:0006356	regulation of transcription from RNA polymerase I promoter	13	0.202786238	0.0206	0.025725529
GO:0046621	negative regulation of organ growth	17	0.202698131	0.0026	0.012805111
GO:0034249	negative regulation of cellular amide metabolic process	94	0.202695593	0.0077	0.016177834
GO:0035235	ionotropic glutamate receptor signaling pathway	19	0.202670069	0.0053	0.014634479
GO:0006397	mRNA processing	191	0.202669237	0.0084	0.016633151
GO:0097734	extracellular exosome biogenesis	12	0.202631525	0.0073	0.015844069
GO:1990182	exosomal secretion	12	0.202631525	0.0073	0.015844069
GO:0001895	retina homeostasis	18	0.202590852	0.0074	0.015911789
GO:0001838	embryonic epithelial tube formation	57	0.202542468	0.0078	0.01620539
GO:0072175	epithelial tube formation	57	0.202542468	0.0078	0.01620539
GO:0060612	adipose tissue development	18	0.202539524	0.0139	0.020388077
GO:0006734	NADH metabolic process	23	0.202537599	0.0141	0.020504577
GO:1901018	positive regulation of potassium ion transmembrane transporter activity	11	0.202526193	0.0029	0.013089617
GO:0002864	regulation of acute inflammatory response to antigenic stimulus	9	0.202518288	0.0094	0.017156187
GO:0043433	negative regulation of sequence-specific DNA binding transcription factor activity	62	0.202516792	0.0099	0.017505138
GO:1902236	negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	9	0.202506194	0.0128	0.019522448
GO:0034145	positive regulation of toll-like receptor 4 signaling pathway	5	0.202466399	0.0116	0.018682786
GO:0021846	cell proliferation in forebrain	13	0.202464983	0.0302	0.034245225
GO:0032206	positive regulation of telomere maintenance	26	0.202457856	0.0134	0.01999969
GO:0050795	regulation of behavior	29	0.202425934	0.0013	0.011218806
GO:1902306	negative regulation of sodium ion transmembrane transport	9	0.202370856	0.0098	0.017418875
GO:0009301	snRNA transcription	35	0.202368104	0.0067	0.015576759
GO:0042795	snRNA transcription from RNA polymerase II promoter	35	0.202368104	0.0067	0.015576759
GO:0009583	detection of light stimulus	25	0.202314273	0.0024	0.012603815
GO:1902235	regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	12	0.202303475	0.0092	0.017033109
GO:0031330	negative regulation of cellular catabolic process	49	0.202291134	0.0036	0.01353394
GO:0043462	regulation of ATPase activity	36	0.202124765	0.0106	0.018010344
GO:0030098	lymphocyte differentiation	124	0.202078764	0.0033	0.013333753
GO:0043543	protein acylation	87	0.202070412	0.0048	0.014269203
GO:0043267	negative regulation of potassium ion transport	12	0.202066346	0.0006	0.009940401
GO:1904738	vascular associated smooth muscle cell migration	11	0.20204263	0.0128	0.019522448
GO:1904752	regulation of vascular associated smooth muscle cell migration	11	0.20204263	0.0128	0.019522448
GO:0048485	sympathetic nervous system development	9	0.20203208	0.0072	0.015844069
GO:0006323	DNA packaging	46	0.202006524	0.0174	0.023064374
GO:0044849	estrous cycle	9	0.202006308	0.003	0.013210967
GO:0006487	protein N-linked glycosylation	35	0.201964744	0.0111	0.018389742
GO:0030433	ER-associated ubiquitin-dependent protein catabolic process	35	0.201950972	0.0038	0.01366393
GO:0036480	neuron intrinsic apoptotic signaling pathway in response to oxidative stress	6	0.201920139	0.0066	0.015525305
GO:1903376	regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway	6	0.201920139	0.0066	0.015525305
GO:0002320	lymphoid progenitor cell differentiation	9	0.201919059	0.024	0.028671074
GO:0038034	signal transduction in absence of ligand	22	0.20182853	0.0051	0.014547706

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0097192	extrinsic apoptotic signaling pathway in absence of ligand	22	0.20182853	0.0051	0.014547706
GO:0050657	nucleic acid transport	67	0.201811818	0.0065	0.015491756
GO:0050658	RNA transport	67	0.201811818	0.0065	0.015491756
GO:0006913	nucleocytoplasmic transport	152	0.20180988	0.0099	0.017505138
GO:0032988	ribonucleoprotein complex disassembly	7	0.201795589	0.0187	0.024129301
GO:0048593	camera-type eye morphogenesis	50	0.201781757	0.0042	0.013948535
GO:0030279	negative regulation of ossification	32	0.201758138	0.0004	0.008964341
GO:0010712	regulation of collagen metabolic process	16	0.201744452	0.0142	0.020567234
GO:0044246	regulation of multicellular organismal metabolic process	16	0.201744452	0.0142	0.020567234
GO:0035313	wound healing, spreading of epidermal cells	5	0.201730911	0.0159	0.021956962
GO:1902229	regulation of intrinsic apoptotic signaling pathway in response to DNA damage	15	0.201729356	0.0466	0.049159132
GO:0021915	neural tube development	64	0.201720399	0.0137	0.020264364
GO:0044794	positive regulation by host of viral process	7	0.20168193	0.04	0.043076923
GO:0035137	hindlimb morphogenesis	9	0.201668972	0.0123	0.019143634
GO:2000650	negative regulation of sodium ion transmembrane transporter activity	8	0.20160645	0.007	0.015816335
GO:0000077	DNA damage checkpoint	49	0.201581017	0.002	0.012314604
GO:0007043	cell-cell junction assembly	25	0.20157609	0.0063	0.015311728
GO:0090343	positive regulation of cell aging	5	0.201569197	0.0124	0.019242297
GO:0071103	DNA conformation change	85	0.201562169	0.0121	0.018970228
GO:1902043	positive regulation of extrinsic apoptotic signaling pathway via death domain receptors	8	0.201543119	0.0167	0.02255007
GO:0009262	deoxyribonucleotide metabolic process	20	0.201540041	0.0224	0.027324219
GO:0033033	negative regulation of myeloid cell apoptotic process	6	0.201495553	0.0353	0.038781037
GO:0051293	establishment of spindle localization	15	0.201483588	0.0021	0.012314604
GO:0042129	regulation of T cell proliferation	53	0.201477049	0.0224	0.027324219
GO:1902017	regulation of cilium assembly	21	0.201473432	0.0035	0.01351837
GO:0016571	histone methylation	53	0.20142935	0.0017	0.012001709
GO:0032008	positive regulation of TOR signaling	20	0.201379947	0.0082	0.016514246
GO:1903649	regulation of cytoplasmic transport	16	0.2013626	0.0093	0.017114131
GO:0002753	cytoplasmic pattern recognition receptor signaling pathway	21	0.201330093	0.0235	0.028248857
GO:0021955	central nervous system neuron axonogenesis	20	0.201291898	0.001	0.010787313
GO:2000756	regulation of peptidyl-lysine acetylation	25	0.201264635	0.0104	0.017832977
GO:0007094	mitotic spindle assembly checkpoint	14	0.201223037	0.0009	0.010729485
GO:0031577	spindle checkpoint	14	0.201223037	0.0009	0.010729485
GO:0071173	spindle assembly checkpoint	14	0.201223037	0.0009	0.010729485
GO:0071174	mitotic spindle checkpoint	14	0.201223037	0.0009	0.010729485
GO:0006896	Golgi to vacuole transport	5	0.201194196	0.0089	0.016916437
GO:0090160	Golgi to lysosome transport	5	0.201194196	0.0089	0.016916437
GO:0006475	internal protein amino acid acetylation	60	0.201148714	0.0033	0.013333753
GO:1904035	regulation of epithelial cell apoptotic process	27	0.201148306	0.0163	0.022248961
GO:0032392	DNA geometric change	38	0.201146532	0.0071	0.01583804
GO:0086004	regulation of cardiac muscle cell contraction	11	0.201083159	0.0159	0.021956962
GO:0007369	gastrulation	69	0.201067558	0.0112	0.018392048
GO:1901838	positive regulation of transcription of nuclear large rRNA transcript from RNA polymerase I promoter	6	0.201000995	0.0388	0.041925173
GO:0046434	organophosphate catabolic process	55	0.200985575	0.0076	0.016084627
GO:0065004	protein-DNA complex assembly	66	0.200970799	0.0165	0.022405589
GO:0071392	cellular response to estradiol stimulus	10	0.200945535	0.0116	0.018682786
GO:0051784	negative regulation of nuclear division	23	0.200937755	0.002	0.012314604
GO:1903557	positive regulation of tumor necrosis factor superfamily cytokine production	35	0.200936446	0.0364	0.039777887
GO:0030852	regulation of granulocyte differentiation	8	0.200925353	0.012	0.018931514
GO:0010763	positive regulation of fibroblast migration	5	0.200925191	0.0078	0.01620539
GO:2000105	positive regulation of DNA-dependent DNA replication	6	0.200920656	0.0002	0.006319126
GO:0010803	regulation of tumor necrosis factor-mediated signaling pathway	27	0.200901675	0.0127	0.019457181
GO:0045948	positive regulation of translational initiation	11	0.200865938	0.0047	0.014168613
GO:0008608	attachment of spindle microtubules to kinetochore	15	0.200852713	0.0047	0.014168613
GO:0035518	histone H2A monoubiquitination	5	0.200798463	0.0043	0.014102439
GO:0010715	regulation of extracellular matrix disassembly	7	0.200797834	0.0009	0.010729485
GO:0043500	muscle adaptation	45	0.200779861	0.0125	0.019314538
GO:0009649	entrainment of circadian clock	15	0.200770215	0.0017	0.012001709
GO:0036003	positive regulation of transcription from RNA polymerase II promoter in response to stress	10	0.200706462	0.0052	0.014616626
GO:0014912	negative regulation of smooth muscle cell migration	9	0.200686047	0.0325	0.036312077
GO:0017148	negative regulation of translation	85	0.200679403	0.0082	0.016514246
GO:0032355	response to estradiol	48	0.200678101	0.004	0.013824268
GO:0072643	interferon-gamma secretion	6	0.200672513	0.0422	0.045118417
GO:0034502	protein localization to chromosome	27	0.200589774	0.0089	0.016916437
GO:0061512	protein localization to cilium	17	0.200502384	0.0042	0.013948535
GO:0036498	IRE1-mediated unfolded protein response	31	0.200500048	< 0.001	< 0.001
GO:0000380	alternative mRNA splicing, via spliceosome	17	0.200490264	0.0142	0.020567234
GO:0030888	regulation of B cell proliferation	28	0.200395446	0.0174	0.023064374
GO:0071711	basement membrane organization	8	0.200380313	0.0148	0.020979063
GO:0002861	regulation of inflammatory response to antigenic stimulus	13	0.200366707	0.0271	0.031420132
GO:0007129	synapsis	11	0.200349744	0.0164	0.022306469
GO:0010873	positive regulation of cholesterol esterification	5	0.200317986	0.0072	0.015844069
GO:0032088	negative regulation of NF-kappaB transcription factor activity	33	0.200289942	0.027	0.031323034
GO:0051972	regulation of telomerase activity	21	0.200289269	0.0091	0.016994897
GO:0070293	renal absorption	7	0.200288405	0.0085	0.016693954
GO:0032309	icosanoid secretion	14	0.200275725	0.0039	0.013791927
GO:0071715	icosanoid transport	14	0.200275725	0.0039	0.013791927
GO:1901571	fatty acid derivative transport	14	0.200275725	0.0039	0.013791927
GO:0061515	myeloid cell development	27	0.200240104	0.0047	0.014168613
GO:0009163	nucleoside biosynthetic process	62	0.20023205	0.0176	0.023223003
GO:0071731	response to nitric oxide	7	0.200228058	0.0113	0.018488002
GO:1901361	organic cyclic compound catabolic process	199	0.200185349	0.0152	0.0213213
GO:0032968	positive regulation of transcription elongation from RNA polymerase II promoter	8	0.200179952	0.0226	0.027544941

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0098885	modification of postsynaptic actin cytoskeleton	5	0.200168452	0.0012	0.010961137
GO:1904645	response to beta-amyloid	21	0.200114153	0.0087	0.016840777
GO:0048710	regulation of astrocyte differentiation	13	0.200112135	0.019	0.024347961
GO:0008544	epidermis development	126	0.200022892	0.0082	0.016514246
GO:0051169	nuclear transport	154	0.199982633	0.0105	0.017924712
GO:0045061	thymic T cell selection	8	0.199923225	0.0256	0.03006687
GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	128	0.199883096	0.0056	0.014771533
GO:1990416	cellular response to brain-derived neurotrophic factor stimulus	7	0.199847282	0.0336	0.037253154
GO:0042537	benzene-containing compound metabolic process	11	0.199781601	0.0117	0.018739446
GO:1905666	regulation of protein localization to endosome	5	0.19973877	0.0132	0.019860109
GO:1905668	positive regulation of protein localization to endosome	5	0.19973877	0.0132	0.019860109
GO:0042100	B cell proliferation	32	0.199737968	0.0123	0.019143634
GO:0061098	positive regulation of protein tyrosine kinase activity	30	0.199725121	0.0001	0.004220438
GO:0018158	protein oxidation	8	0.199720434	0.014	0.020462083
GO:0060142	regulation of syncytium formation by plasma membrane fusion	11	0.199712571	0.0148	0.020979063
GO:0060143	positive regulation of syncytium formation by plasma membrane fusion	11	0.199712571	0.0148	0.020979063
GO:0090150	establishment of protein localization to membrane	133	0.199697907	0.0119	0.018881943
GO:0033598	mammary gland epithelial cell proliferation	14	0.199667724	0.0023	0.012498684
GO:0006654	phosphatidic acid biosynthetic process	16	0.1996388	0.0059	0.014942532
GO:0046473	phosphatidic acid metabolic process	16	0.1996388	0.0059	0.014942532
GO:0003300	cardiac muscle hypertrophy	35	0.199583016	0.011	0.018323826
GO:0046854	phosphatidylinositol phosphorylation	9	0.199567064	0.001	0.010787313
GO:0048665	neuron fate specification	7	0.199547956	0.0348	0.038319101
GO:0007035	vacuolar acidification	8	0.199520235	0.0342	0.037780741
GO:0032092	positive regulation of protein binding	47	0.199453178	0.0025	0.012769435
GO:0042533	tumor necrosis factor biosynthetic process	11	0.19942738	0.0465	0.049080504
GO:0042534	regulation of tumor necrosis factor biosynthetic process	11	0.19942738	0.0465	0.049080504
GO:0043951	negative regulation of cAMP-mediated signaling	7	0.199413194	0.0084	0.016633151
GO:0046469	platelet activating factor metabolic process	5	0.199359104	0.0383	0.041555752
GO:0070665	positive regulation of leukocyte proliferation	52	0.199357589	0.0212	0.026203164
GO:0035914	skeletal muscle cell differentiation	25	0.199353403	0.0009	0.010729485
GO:0045103	intermediate filament-based process	14	0.199341278	0.0236	0.028327839
GO:0045104	intermediate filament cytoskeleton organization	14	0.199341278	0.0236	0.028327839
GO:0051156	glucose 6-phosphate metabolic process	11	0.19928343	0.0216	0.026572596
GO:0071156	regulation of cell cycle arrest	40	0.199259426	0.0019	0.012288367
GO:0033047	regulation of mitotic sister chromatid segregation	26	0.199205384	0.0043	0.014102439
GO:0003184	pulmonary valve morphogenesis	11	0.199204505	0.0366	0.039958686
GO:0042759	long-chain fatty acid biosynthetic process	13	0.199199802	0.002	0.012314604
GO:1904666	regulation of ubiquitin protein ligase activity	10	0.199095801	0.0234	0.02817551
GO:0071364	cellular response to epidermal growth factor stimulus	22	0.19908276	0.0015	0.011704453
GO:0048708	astrocyte differentiation	35	0.199025384	0.0167	0.02255007
GO:0007389	pattern specification process	145	0.198987509	0.007	0.015816335
GO:0003007	heart morphogenesis	104	0.198977775	0.0047	0.014168613
GO:0007597	blood coagulation, intrinsic pathway	5	0.198943935	0.0051	0.014547706
GO:0032760	positive regulation of tumor necrosis factor production	34	0.198870418	0.0356	0.03903645
GO:0046541	saliva secretion	6	0.19882861	0.0239	0.028592965
GO:1901659	glycosyl compound biosynthetic process	63	0.198826388	0.0197	0.024979254
GO:1902041	regulation of extrinsic apoptotic signaling pathway via death domain receptors	27	0.198820307	0.0046	0.014132412
GO:1904705	regulation of vascular smooth muscle cell proliferation	28	0.198770114	0.0109	0.018225506
GO:1990874	vascular smooth muscle cell proliferation	28	0.198770114	0.0109	0.018225506
GO:1900029	positive regulation of ruffle assembly	8	0.198759933	0.0021	0.012314604
GO:1903955	positive regulation of protein targeting to mitochondrion	20	0.198752547	0.006	0.015037711
GO:0051781	positive regulation of cell division	29	0.198733794	0.0017	0.012001709
GO:0090199	regulation of release of cytochrome c from mitochondria	26	0.198713584	0.0189	0.024289798
GO:0032677	regulation of interleukin-8 production	29	0.198671105	0.0351	0.038590645
GO:0042053	regulation of dopamine metabolic process	12	0.198667284	0.0463	0.048905115
GO:0042069	regulation of catecholamine metabolic process	12	0.198667284	0.0463	0.048905115
GO:0006878	cellular copper ion homeostasis	8	0.198616749	0.003	0.013210967
GO:0019692	deoxyribose phosphate metabolic process	20	0.19860865	0.0243	0.028921902
GO:0071514	genetic imprinting	8	0.198517297	0.0197	0.024979254
GO:0051299	centrosome separation	6	0.198475724	0.0002	0.006319126
GO:0006972	hyperosmotic response	13	0.198431102	0.0153	0.021378589
GO:0035999	tetrahydrofolate interconversion	5	0.198420437	0.0001	0.004220438
GO:0048854	brain morphogenesis	13	0.198364718	0.0162	0.022196303
GO:0051187	cofactor catabolic process	9	0.198347153	0.0321	0.035976391
GO:0042177	negative regulation of protein catabolic process	63	0.198344109	0.0031	0.013277185
GO:0032965	regulation of collagen biosynthetic process	14	0.198339636	0.014	0.020462083
GO:0051349	positive regulation of lyase activity	25	0.198333827	0.004	0.013824268
GO:0071354	cellular response to interleukin-6	10	0.198320921	0.0101	0.017653628
GO:0048640	negative regulation of developmental growth	45	0.198297136	0.0052	0.014616626
GO:0003176	aortic valve development	15	0.198253972	0.0465	0.049080504
GO:0044783	G1 DNA damage checkpoint	22	0.19822548	0.0022	0.012422266
GO:1990266	neutrophil migration	27	0.198216903	0.0205	0.025639412
GO:2000142	regulation of DNA-templated transcription, initiation	13	0.19821341	0.0121	0.018970228
GO:0021545	cranial nerve development	14	0.19819784	0.0045	0.014132412
GO:0018205	peptidyl-lysine modification	148	0.198156701	0.0012	0.010961137
GO:0034367	macromolecular complex remodeling	9	0.198146882	0.0232	0.028016374
GO:0034368	protein-lipid complex remodeling	9	0.198146882	0.0232	0.028016374
GO:0034369	plasma lipoprotein particle remodeling	9	0.198146882	0.0232	0.028016374
GO:0034629	cellular protein complex localization	9	0.198120247	0.0037	0.013609033
GO:0007093	mitotic cell cycle checkpoint	56	0.198052249	0.0067	0.015576759
GO:0014897	striated muscle hypertrophy	36	0.198019283	0.0132	0.019860109
GO:0046636	negative regulation of alpha-beta T cell activation	10	0.197974946	0.0064	0.015399417

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0032528	microvillus organization	12	0.197962701	0.0002	0.006319126
GO:0055022	negative regulation of cardiac muscle tissue growth	13	0.197902422	0.0013	0.011218806
GO:0061117	negative regulation of heart growth	13	0.197902422	0.0013	0.011218806
GO:0045600	positive regulation of fat cell differentiation	34	0.197901208	0.0009	0.010729485
GO:0050779	RNA destabilization	12	0.197870268	0.0276	0.031846578
GO:0061157	mRNA destabilization	12	0.197870268	0.0276	0.031846578
GO:0030217	T cell differentiation	84	0.197858051	0.0067	0.015576759
GO:0002374	cytokine secretion involved in immune response	6	0.197834742	0.0336	0.037253154
GO:0002739	regulation of cytokine secretion involved in immune response	6	0.197834742	0.0336	0.037253154
GO:0006119	oxidative phosphorylation	61	0.197769974	0.035	0.03849534
GO:0043651	linoleic acid metabolic process	9	0.197755843	0.0061	0.015143924
GO:0033687	osteoblast proliferation	6	0.197755699	0.0194	0.024690909
GO:0097113	AMPA glutamate receptor clustering	5	0.197740927	0.0387	0.041895413
GO:0097688	glutamate receptor clustering	5	0.197740927	0.0387	0.041895413
GO:0060976	coronary vasculature development	18	0.197668521	0.0288	0.032902905
GO:0030878	thyroid gland development	8	0.197644099	0.0174	0.023064374
GO:0001841	neural tube formation	48	0.197476106	0.0085	0.016693954
GO:0060045	positive regulation of cardiac muscle cell proliferation	10	0.197454818	0.0447	0.047449128
GO:0031016	pancreas development	29	0.197392522	0.0011	0.010890753
GO:0032462	regulation of protein homooligomerization	11	0.197375091	0.0189	0.024289798
GO:0021522	spinal cord motor neuron differentiation	14	0.197367519	0.0069	0.015750415
GO:0050798	activated T cell proliferation	9	0.19735127	0.0009	0.010729485
GO:0050684	regulation of mRNA processing	38	0.197287784	0.0057	0.01480566
GO:0018394	peptidyl-lysine acetylation	62	0.197276342	0.005	0.014547706
GO:0035107	appendage morphogenesis	46	0.197264653	0.0114	0.018551872
GO:0035108	limb morphogenesis	46	0.197264653	0.0114	0.018551872
GO:0009109	coenzyme catabolic process	5	0.197262005	0.0312	0.035137982
GO:0010884	positive regulation of lipid storage	8	0.197120278	0.0015	0.011704453
GO:0036503	ERAD pathway	46	0.19707851	0.0041	0.013887639
GO:0018393	internal peptidyl-lysine acetylation	57	0.1970497	0.0034	0.01347416
GO:0046839	phospholipid dephosphorylation	15	0.197045695	0.0003	0.007956881
GO:0032276	regulation of gonadotropin secretion	7	0.19698156	0.0003	0.007956881
GO:1903844	regulation of cellular response to transforming growth factor beta stimulus	52	0.196961058	0.0102	0.0177
GO:0001843	neural tube closure	41	0.196957463	0.009	0.016956012
GO:0060606	tube closure	41	0.196957463	0.009	0.016956012
GO:0032609	interferon-gamma production	31	0.196909509	0.0144	0.02072711
GO:0071712	ER-associated misfolded protein catabolic process	7	0.196889374	0.0359	0.039290895
GO:0070830	bicellular tight junction assembly	13	0.19688832	0.0075	0.015990044
GO:1903959	regulation of anion transmembrane transport	7	0.196845502	0.0111	0.018389742
GO:0015985	energy coupled proton transport, down electrochemical gradient	11	0.196829566	0.0428	0.045650175
GO:0015986	ATP synthesis coupled proton transport	11	0.196829566	0.0428	0.045650175
GO:0042776	mitochondrial ATP synthesis coupled proton transport	11	0.196829566	0.0428	0.045650175
GO:0045933	positive regulation of muscle contraction	18	0.196774645	0.0229	0.027770092
GO:0098657	import into cell	35	0.196720144	0.0047	0.014168613
GO:0035065	regulation of histone acetylation	21	0.19670784	0.0063	0.015311728
GO:0006692	prostanoid metabolic process	18	0.19669625	0.0209	0.025971158
GO:0006693	prostaglandin metabolic process	18	0.19669625	0.0209	0.025971158
GO:0009219	pyrimidine deoxyribonucleotide metabolic process	9	0.196695602	0.0125	0.019314538
GO:0031116	positive regulation of microtubule polymerization	8	0.19669526	0.0222	0.027148985
GO:0048483	autonomic nervous system development	17	0.196623563	0.005	0.014547706
GO:0019439	aromatic compound catabolic process	192	0.196616028	0.0156	0.021692929
GO:0031571	mitotic G1 DNA damage checkpoint	21	0.196615346	0.0035	0.01351837
GO:0044819	mitotic G1/S transition checkpoint	21	0.196615346	0.0035	0.01351837
GO:0006401	RNA catabolic process	111	0.196582663	0.0234	0.02817551
GO:0052173	response to defenses of other organism involved in symbiotic interaction	7	0.19655321	0.0071	0.01583804
GO:0052200	response to host defenses	7	0.19655321	0.0071	0.01583804
GO:0075136	response to host	7	0.19655321	0.0071	0.01583804
GO:0009215	purine deoxyribonucleoside triphosphate metabolic process	8	0.19639399	0.0419	0.044864037
GO:1901799	negative regulation of proteasomal protein catabolic process	20	0.196345755	0.0091	0.016994897
GO:0002262	myeloid cell homeostasis	49	0.196319704	0.0093	0.017114131
GO:2001237	negative regulation of extrinsic apoptotic signaling pathway	36	0.196319213	0.0048	0.014269203
GO:0051123	RNA polymerase II transcriptional preinitiation complex assembly	6	0.196288654	0.0111	0.018389742
GO:0031641	regulation of myelination	23	0.196265433	0.0078	0.01620539
GO:1901068	guanosine-containing compound metabolic process	22	0.196214597	0.0059	0.014942532
GO:0031503	protein complex localization	35	0.196195277	0.0061	0.015143924
GO:0017015	regulation of transforming growth factor beta receptor signaling pathway	51	0.196070949	0.01	0.017574468
GO:0003279	cardiac septum development	46	0.196038642	0.0052	0.014616626
GO:0006406	mRNA export from nucleus	41	0.196025003	0.0063	0.015311728
GO:0071427	mRNA-containing ribonucleoprotein complex export from nucleus	41	0.196025003	0.0063	0.015311728
GO:0010165	response to X-ray	12	0.195990083	0.0115	0.018599441
GO:0010890	positive regulation of sequestering of triglyceride	5	0.195953002	0.0191	0.02440579
GO:0002295	T-helper cell lineage commitment	5	0.195943931	0.0274	0.03166636
GO:0002363	alpha-beta T cell lineage commitment	5	0.195943931	0.0274	0.03166636
GO:0043369	CD4-positive or CD8-positive, alpha-beta T cell lineage commitment	5	0.195943931	0.0274	0.03166636
GO:0043373	CD4-positive, alpha-beta T cell lineage commitment	5	0.195943931	0.0274	0.03166636
GO:0051290	protein heterotetramerization	15	0.195941599	0.0403	0.043327371
GO:0072332	intrinsic apoptotic signaling pathway by p53 class mediator	32	0.195940303	0.0262	0.030579007
GO:0032946	positive regulation of mononuclear cell proliferation	49	0.195926711	0.0252	0.029736
GO:0060669	embryonic placenta morphogenesis	11	0.195923576	0.0059	0.014942532
GO:0031018	endocrine pancreas development	21	0.195900874	0.001	0.010787313
GO:0007034	vacuolar transport	51	0.195849624	0.0012	0.010961137
GO:0031958	corticosteroid receptor signaling pathway	11	0.195811903	0.0092	0.017033109
GO:0042921	glucocorticoid receptor signaling pathway	11	0.195811903	0.0092	0.017033109

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1902884	positive regulation of response to oxidative stress	11	0.195799651	0.0275	0.031743861
GO:0048844	artery morphogenesis	25	0.195733133	0.0123	0.019143634
GO:0035264	multicellular organism growth	63	0.19569361	0.0045	0.014132412
GO:0010955	negative regulation of protein processing	8	0.195684871	0.0264	0.030750363
GO:1903318	negative regulation of protein maturation	8	0.195684871	0.0264	0.030750363
GO:0090322	regulation of superoxide metabolic process	17	0.195676268	0.0378	0.041067193
GO:0015701	bicarbonate transport	13	0.195609678	0.0449	0.047643935
GO:0071166	ribonucleoprotein complex localization	46	0.195579624	0.0083	0.016559903
GO:0006658	phosphatidylserine metabolic process	10	0.195565691	0.0125	0.019314538
GO:0003334	keratinocyte development	5	0.195555714	0.0018	0.01210186
GO:0021983	pituitary gland development	19	0.195551567	0.0178	0.023348367
GO:0031998	regulation of fatty acid beta-oxidation	10	0.195542886	0.014	0.020462083
GO:2001212	regulation of vasculogenesis	8	0.195541201	0.0008	0.010465158
GO:0001935	endothelial cell proliferation	51	0.195472956	0.0129	0.019597425
GO:0014896	muscle hypertrophy	37	0.195463909	0.0155	0.021605834
GO:0050671	positive regulation of lymphocyte proliferation	48	0.195454788	0.025	0.029554283
GO:0035904	aorta development	24	0.195422799	0.0113	0.018488002
GO:0036015	response to interleukin-3	6	0.195394345	0.0006	0.009940401
GO:0036016	cellular response to interleukin-3	6	0.195394345	0.0006	0.009940401
GO:0051797	regulation of hair follicle development	9	0.195368286	0.042	0.044946141
GO:0090307	mitotic spindle assembly	20	0.195235137	0.0092	0.017033109
GO:1902850	microtubule cytoskeleton organization involved in mitosis	20	0.195235137	0.0092	0.017033109
GO:0014020	primary neural tube formation	43	0.195213428	0.0081	0.016514175
GO:0051340	regulation of ligase activity	6	0.195205809	0.0228	0.027701114
GO:0071470	cellular response to osmotic stress	18	0.195191843	0.0037	0.013609033
GO:0032729	positive regulation of interferon-gamma production	20	0.195175466	0.0209	0.025971158
GO:0033046	negative regulation of sister chromatid segregation	17	0.195132571	0.0023	0.012498684
GO:0033048	negative regulation of mitotic sister chromatid segregation	17	0.195132571	0.0023	0.012498684
GO:0021536	diencephalon development	36	0.195110568	0.0149	0.021043429
GO:0010872	regulation of cholesterol esterification	6	0.194998699	0.0043	0.014102439
GO:0045058	T cell selection	16	0.194989925	0.0213	0.026276211
GO:0043588	skin development	109	0.194979757	0.006	0.015037711
GO:0071824	protein-DNA complex subunit organization	76	0.194967407	0.0149	0.021043429
GO:0072070	loop of Henle development	5	0.194945399	0.0252	0.029736
GO:0032637	interleukin-8 production	32	0.194940564	0.0243	0.028921902
GO:0003416	endochondral bone growth	10	0.194913911	0.0028	0.012972436
GO:0030856	regulation of epithelial cell differentiation	48	0.194858322	0.0036	0.01353394
GO:0006473	protein acetylation	73	0.194725477	0.0048	0.014269203
GO:0035270	endocrine system development	54	0.194722241	0.0073	0.015844069
GO:0045836	positive regulation of meiotic nuclear division	6	0.194630048	0.0046	0.014132412
GO:0050873	brown fat cell differentiation	14	0.194618602	0.0092	0.017033109
GO:0043244	regulation of protein complex disassembly	37	0.194564809	0.0168	0.022626974
GO:0097201	negative regulation of transcription from RNA polymerase II promoter in response to stress	6	0.194451229	0.0371	0.040443477
GO:0034115	negative regulation of heterotypic cell-cell adhesion	5	0.194438228	0.0261	0.030517735
GO:0070587	regulation of cell-cell adhesion involved in gastrulation	5	0.194438228	0.0261	0.030517735
GO:0021510	spinal cord development	42	0.194399552	0.0117	0.018739446
GO:0009060	aerobic respiration	31	0.19439326	0.0271	0.031420132
GO:0055026	negative regulation of cardiac muscle tissue development	15	0.194336034	0.0014	0.011465722
GO:1905245	regulation of aspartic-type peptidase activity	6	0.194246279	0.0002	0.006319126
GO:0043154	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	32	0.194071011	0.0149	0.021043429
GO:0046640	regulation of alpha-beta T cell proliferation	14	0.19402578	0.0254	0.029880529
GO:0006910	phagocytosis, recognition	6	0.193993385	0.0021	0.012314604
GO:0030225	macrophage differentiation	18	0.193977332	0.0259	0.0303391
GO:0001759	organ induction	6	0.193945873	0.0415	0.044476923
GO:0048821	erythrocyte development	12	0.193906999	0.0101	0.017653628
GO:0040034	regulation of development, heterochronic	5	0.19386886	0.0437	0.046498601
GO:0048505	regulation of timing of cell differentiation	5	0.19386886	0.0437	0.046498601
GO:0044270	cellular nitrogen compound catabolic process	186	0.193836706	0.0167	0.02255007
GO:0090153	regulation of sphingolipid biosynthetic process	7	0.193825396	0.0056	0.014771533
GO:1905038	regulation of membrane lipid metabolic process	7	0.193825396	0.0056	0.014771533
GO:2000303	regulation of ceramide biosynthetic process	7	0.193825396	0.0056	0.014771533
GO:0071426	ribonucleoprotein complex export from nucleus	45	0.193775333	0.0073	0.015844069
GO:0050885	neuromuscular process controlling balance	26	0.193749129	0.0053	0.014634479
GO:0098760	response to interleukin-7	10	0.19369963	0.0174	0.023064374
GO:0098761	cellular response to interleukin-7	10	0.19369963	0.0174	0.023064374
GO:0048596	embryonic camera-type eye morphogenesis	10	0.193679546	0.0079	0.01629604
GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	17	0.193675041	0.0026	0.012805111
GO:0007368	determination of left/right symmetry	49	0.19359382	0.0092	0.017033109
GO:0045333	cellular respiration	94	0.193591967	0.0339	0.037513837
GO:0014002	astrocyte development	11	0.193582562	0.02	0.025188412
GO:0014015	positive regulation of gliogenesis	29	0.193577147	0.0436	0.046426372
GO:0042990	regulation of transcription factor import into nucleus	8	0.193564966	0.0094	0.017156187
GO:0042991	transcription factor import into nucleus	8	0.193564966	0.0094	0.017156187
GO:0042992	negative regulation of transcription factor import into nucleus	8	0.193564966	0.0094	0.017156187
GO:0042994	cytoplasmic sequestering of transcription factor	8	0.193564966	0.0094	0.017156187
GO:1902742	apoptotic process involved in development	11	0.193561947	0.0355	0.038985945
GO:0045839	negative regulation of mitotic nuclear division	21	0.193545691	0.0026	0.012805111
GO:0002328	pro-B cell differentiation	7	0.193496451	0.0314	0.035301342
GO:0046700	heterocycle catabolic process	184	0.193356049	0.0156	0.021692929
GO:0086010	membrane depolarization during action potential	10	0.193335644	0.0003	0.007956881
GO:0051985	negative regulation of chromosome segregation	18	0.193325767	0.0024	0.012603815
GO:0001936	regulation of endothelial cell proliferation	47	0.193234647	0.0126	0.019370699
GO:0051305	chromosome movement towards spindle pole	5	0.19315566	0.0155	0.021605834

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0072578	neurotransmitter-gated ion channel clustering	6	0.193140758	0.0462	0.048826247
GO:0030509	BMP signaling pathway	50	0.193018228	0.0058	0.014878261
GO:0036445	neuronal stem cell division	6	0.192998006	0.0446	0.047360367
GO:0055057	neuroblast division	6	0.192998006	0.0446	0.047360367
GO:0030520	intracellular estrogen receptor signaling pathway	18	0.192988719	0.0187	0.024129301
GO:0006405	RNA export from nucleus	45	0.192983666	0.0081	0.016514175
GO:1901099	negative regulation of signal transduction in absence of ligand	10	0.192853612	0.0147	0.02091937
GO:2001240	negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	10	0.192853612	0.0147	0.02091937
GO:0080182	histone H3-K4 trimethylation	5	0.192819014	0.0082	0.016514246
GO:0042102	positive regulation of T cell proliferation	30	0.19272196	0.0313	0.035223161
GO:0046471	phosphatidylglycerol metabolic process	8	0.19269436	0.0089	0.016916437
GO:0007501	mesodermal cell fate specification	6	0.192650951	0.0422	0.045118417
GO:1902107	positive regulation of leukocyte differentiation	53	0.19260341	0.0217	0.026655917
GO:0003156	regulation of animal organ formation	10	0.192585514	0.0459	0.048535808
GO:0003309	type B pancreatic cell differentiation	15	0.192567027	0.0002	0.006319126
GO:0035883	enteroendocrine cell differentiation	16	0.192563323	0.0005	0.009604651
GO:1900120	regulation of receptor binding	12	0.192546208	0.0015	0.011704453
GO:0007184	SMAD protein import into nucleus	12	0.192537462	0.023	0.027838811
GO:0060390	regulation of SMAD protein import into nucleus	12	0.192537462	0.023	0.027838811
GO:0071827	plasma lipoprotein particle organization	12	0.192532495	0.0279	0.032115827
GO:0045841	negative regulation of mitotic metaphase/anaphase transition	15	0.192511395	0.0014	0.011465722
GO:2000816	negative regulation of mitotic sister chromatid separation	15	0.192511395	0.0014	0.011465722
GO:0032371	regulation of sterol transport	17	0.19247339	0.0254	0.029880529
GO:0032374	regulation of cholesterol transport	17	0.19247339	0.0254	0.029880529
GO:1902003	regulation of beta-amyloid formation	12	0.192403456	0.0008	0.010465158
GO:0034110	regulation of homotypic cell-cell adhesion	11	0.192392324	0.0303	0.034331687
GO:0007041	lysosomal transport	46	0.192322244	0.0012	0.010961137
GO:0046633	alpha-beta T cell proliferation	15	0.192320569	0.0311	0.035052671
GO:0060397	JAK-STAT cascade involved in growth hormone signaling pathway	7	0.192291185	< 0.001	< 0.001
GO:0031223	auditory behavior	6	0.192265887	0.0001	0.004220438
GO:0070391	response to lipoteichoic acid	6	0.192225933	0.0367	0.040037623
GO:0071223	cellular response to lipoteichoic acid	6	0.192225933	0.0367	0.040037623
GO:0007179	transforming growth factor beta receptor signaling pathway	79	0.192207062	0.0045	0.014132412
GO:0032488	Cdc42 protein signal transduction	5	0.192173713	0.0257	0.030153693
GO:0032489	regulation of Cdc42 protein signal transduction	5	0.192173713	0.0257	0.030153693
GO:0045687	positive regulation of glial cell differentiation	18	0.192120111	0.0372	0.040544844
GO:0060349	bone morphogenesis	40	0.191977628	0.005	0.014547706
GO:0010458	exit from mitosis	16	0.191977304	0.001	0.010787313
GO:1900424	regulation of defense response to bacterium	10	0.191932826	0.0369	0.040233038
GO:0032649	regulation of interferon-gamma production	28	0.191830024	0.0164	0.022306469
GO:0006309	apoptotic DNA fragmentation	9	0.191788318	0.0003	0.007956881
GO:0048512	circadian behavior	22	0.191770406	0.0004	0.008964341
GO:009563	modification of synaptic structure	9	0.191765281	0.0014	0.011465722
GO:0036158	outer dynein arm assembly	8	0.191718957	0.0045	0.014132412
GO:1905314	semi-lunar valve development	19	0.191714609	0.0417	0.044666432
GO:0051028	mRNA transport	52	0.191694586	0.0065	0.015491756
GO:0009310	amine catabolic process	12	0.191660431	0.0427	0.045577146
GO:0006970	response to osmotic stress	34	0.191540539	0.0013	0.011218806
GO:0000724	double-strand break repair via homologous recombination	34	0.191511345	0.0138	0.020339434
GO:0000725	recombinational repair	34	0.191511345	0.0138	0.020339434
GO:0016925	protein sumoylation	28	0.191431107	0.0013	0.011218806
GO:0050869	negative regulation of B cell activation	11	0.191428259	0.004	0.013824268
GO:0000381	regulation of alternative mRNA splicing, via spliceosome	14	0.191370529	0.0176	0.023223003
GO:0009162	deoxyribonucleoside monophosphate metabolic process	6	0.191313916	0.038	0.041253474
GO:0034655	nucleobase-containing compound catabolic process	164	0.191200256	0.0171	0.022860624
GO:0030517	negative regulation of axon extension	13	0.191145198	0.0136	0.020157703
GO:0001938	positive regulation of endothelial cell proliferation	37	0.190932476	0.0089	0.016916437
GO:2000171	negative regulation of dendrite development	14	0.19083972	< 0.001	< 0.001
GO:0042748	circadian sleep/wake cycle, non-REM sleep	6	0.190817846	0.0018	0.01210186
GO:1900117	regulation of execution phase of apoptosis	12	0.190754568	0.0051	0.014547706
GO:0045582	positive regulation of T cell differentiation	28	0.190692741	0.0314	0.035301342
GO:1902100	negative regulation of metaphase/anaphase transition of cell cycle	16	0.190642564	0.0019	0.012288367
GO:0051168	nuclear export	71	0.190619515	0.0051	0.014547706
GO:0048260	positive regulation of receptor-mediated endocytosis	22	0.190614682	0.0151	0.02121706
GO:1902117	positive regulation of organelle assembly	24	0.190549834	0.0107	0.018084595
GO:0010831	positive regulation of myotube differentiation	12	0.19052759	0.0037	0.013609033
GO:0051654	establishment of mitochondrion localization	10	0.190460036	0.0005	0.009604651
GO:0060393	regulation of pathway-restricted SMAD protein phosphorylation	18	0.190435229	0.0058	0.014878261
GO:0048736	appendage development	61	0.190428158	0.0103	0.017772187
GO:0060173	limb development	61	0.190428158	0.0103	0.017772187
GO:0060317	cardiac epithelial to mesenchymal transition	14	0.190411185	0.0078	0.01620539
GO:0006308	DNA catabolic process	13	0.190405603	0.0007	0.010220707
GO:0040018	positive regulation of multicellular organism growth	14	0.190368054	0.0178	0.023348367
GO:0098739	import across plasma membrane	24	0.190326419	0.004	0.013824268
GO:0072538	T-helper 17 type immune response	6	0.190318968	0.0122	0.019049527
GO:0032274	gonadotropin secretion	9	0.190294133	0.0013	0.011218806
GO:0045580	regulation of T cell differentiation	48	0.190233555	0.017	0.022784886
GO:0031268	pseudopodium organization	5	0.190194012	0.02	0.025188412
GO:0031269	pseudopodium assembly	5	0.190194012	0.02	0.025188412
GO:0031272	regulation of pseudopodium assembly	5	0.190194012	0.02	0.025188412
GO:0031274	positive regulation of pseudopodium assembly	5	0.190194012	0.02	0.025188412
GO:0007040	lysosome organization	33	0.190155366	0.0117	0.018739446
GO:0080171	lytic vacuole organization	33	0.190155366	0.0117	0.018739446

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0046135	pyrimidine nucleoside catabolic process	7	0.190150732	0.0425	0.045422366
GO:0051084	'de novo' posttranslational protein folding	11	0.190123992	0.0082	0.016514246
GO:0046415	urate metabolic process	7	0.19007243	0.0407	0.043676206
GO:1902188	positive regulation of viral release from host cell	7	0.190052808	0.0452	0.047918298
GO:0042787	protein ubiquitination involved in ubiquitin-dependent protein catabolic process	17	0.189908268	0.0028	0.012972436
GO:2000058	regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process	17	0.189908268	0.0028	0.012972436
GO:2000351	regulation of endothelial cell apoptotic process	17	0.189853464	0.0177	0.02329117
GO:0045494	photoreceptor cell maintenance	11	0.189852584	0.0053	0.014634479
GO:0022602	ovulation cycle process	37	0.189805073	0.003	0.013210967
GO:0007096	regulation of exit from mitosis	10	0.189753704	0.0019	0.012288367
GO:0003417	growth plate cartilage development	7	0.189498952	0.0012	0.010961137
GO:0034205	beta-amyloid formation	15	0.189496792	0.0013	0.011218806
GO:0006370	7-methylguanosine mRNA capping	22	0.18949424	0.0182	0.023684988
GO:0034433	steroid esterification	7	0.189481551	0.0078	0.01620539
GO:0034434	sterol esterification	7	0.189481551	0.0078	0.01620539
GO:0034435	cholesterol esterification	7	0.189481551	0.0078	0.01620539
GO:0009651	response to salt stress	9	0.189457919	0.0173	0.023005658
GO:0035333	Notch receptor processing, ligand-dependent	5	0.189448676	0.0462	0.048826247
GO:0051457	maintenance of protein location in nucleus	5	0.18942872	0.0069	0.015750415
GO:0002313	mature B cell differentiation involved in immune response	9	0.189398601	0.0138	0.020339434
GO:0002021	response to dietary excess	8	0.189386381	0.0009	0.010729485
GO:0006611	protein export from nucleus	25	0.189385182	0.0051	0.014547706
GO:0042771	intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	20	0.189369438	0.04	0.043076923
GO:0000737	DNA catabolic process, endonucleolytic	10	0.189249254	0.0007	0.010220707
GO:0046598	positive regulation of viral entry into host cell	6	0.189216903	0.0075	0.015990044
GO:1901798	positive regulation of signal transduction by p53 class mediator	5	0.189151941	0.0221	0.027038129
GO:0044236	multicellular organism metabolic process	36	0.189133252	0.0057	0.01480566
GO:0070059	intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	24	0.189125712	0.0074	0.015911789
GO:0009452	7-methylguanosine RNA capping	24	0.189110648	0.0187	0.024129301
GO:0036260	RNA capping	24	0.189110648	0.0187	0.024129301
GO:0010667	negative regulation of cardiac muscle cell apoptotic process	8	0.189103899	0.008	0.016379603
GO:1903541	regulation of exosomal secretion	11	0.189075819	0.0073	0.015844069
GO:0006623	protein targeting to vacuole	11	0.189064157	0.0213	0.026276211
GO:0072666	establishment of protein localization to vacuole	11	0.189064157	0.0213	0.026276211
GO:0032272	negative regulation of protein polymerization	30	0.188968069	0.0187	0.024129301
GO:0034968	histone lysine methylation	42	0.188967186	0.0016	0.011845327
GO:0006541	glutamine metabolic process	8	0.188938039	0.0126	0.019370699
GO:0042089	cytokine biosynthetic process	43	0.188908134	0.0238	0.028526451
GO:0042107	cytokine metabolic process	43	0.188908134	0.0238	0.028526451
GO:0001709	cell fate determination	15	0.18888043	0.0187	0.024129301
GO:2000378	negative regulation of reactive oxygen species metabolic process	24	0.188861425	0.0177	0.02329117
GO:0071786	endoplasmic reticulum tubular network organization	6	0.188842852	0.0367	0.040037623
GO:0051646	mitochondrion localization	17	0.188820875	0.0014	0.011465722
GO:0090154	positive regulation of sphingolipid biosynthetic process	6	0.188785406	0.002	0.012314604
GO:2000304	positive regulation of ceramide biosynthetic process	6	0.188785406	0.002	0.012314604
GO:0015937	coenzyme A biosynthetic process	6	0.188698372	0.0066	0.015525305
GO:0032963	collagen metabolic process	34	0.188611834	0.0051	0.014547706
GO:0044259	multicellular organismal macromolecule metabolic process	34	0.188611834	0.0051	0.014547706
GO:0060333	interferon-gamma-mediated signaling pathway	35	0.188540478	0.0381	0.041354271
GO:0032781	positive regulation of ATPase activity	25	0.188478236	0.0142	0.020567234
GO:0016573	histone acetylation	54	0.18844447	0.0033	0.013333753
GO:0043901	negative regulation of multi-organism process	45	0.188442311	0.014	0.020462083
GO:0043489	RNA stabilization	19	0.188420926	0.0028	0.012972436
GO:1903214	regulation of protein targeting to mitochondrion	28	0.18839522	0.0134	0.01999969
GO:0002826	negative regulation of T-helper 1 type immune response	5	0.188384835	0.0134	0.01999969
GO:0051569	regulation of histone H3-K4 methylation	12	0.188249167	0.015	0.021138192
GO:0042340	keratan sulfate catabolic process	6	0.188240096	0.0182	0.023684988
GO:0070102	interleukin-6-mediated signaling pathway	5	0.188194355	0.0112	0.018392048
GO:0045668	negative regulation of osteoblast differentiation	21	0.18811388	0.0002	0.006319126
GO:0045943	positive regulation of transcription from RNA polymerase I promoter	8	0.188092215	0.0391	0.042217778
GO:0014067	negative regulation of phosphatidylinositol 3-kinase signaling	6	0.188003183	0.0191	0.02440579
GO:0097202	activation of cysteine-type endopeptidase activity	9	0.187989362	0.0266	0.030933467
GO:0043171	peptide catabolic process	5	0.187976922	0.0227	0.027637692
GO:0099010	modification of postsynaptic structure	6	0.187943577	0.003	0.013210967
GO:0009799	specification of symmetry	52	0.187822729	0.008	0.016379603
GO:0009855	determination of bilateral symmetry	52	0.187822729	0.008	0.016379603
GO:0042770	signal transduction in response to DNA damage	45	0.187818059	0.0098	0.017418875
GO:0001955	blood vessel maturation	5	0.187772447	0.0217	0.026655917
GO:2000117	negative regulation of cysteine-type endopeptidase activity	34	0.187754253	0.0157	0.021779607
GO:2001252	positive regulation of chromosome organization	33	0.187705781	0.0089	0.016916437
GO:2000778	positive regulation of interleukin-6 secretion	7	0.187603773	0.0329	0.036702257
GO:0006338	chromatin remodeling	52	0.187587568	0.0022	0.012422266
GO:1904177	regulation of adipose tissue development	5	0.187583781	0.0168	0.022626974
GO:0043383	negative T cell selection	6	0.187566504	0.0304	0.034411276
GO:0045060	negative thymic T cell selection	6	0.187566504	0.0304	0.034411276
GO:0018196	peptidyl-asparagine modification	24	0.18756456	0.0133	0.019917275
GO:0006402	mRNA catabolic process	98	0.187550447	0.0234	0.02817551
GO:0055070	copper ion homeostasis	11	0.187508154	0.0137	0.020264364
GO:0051653	spindle localization	17	0.187495134	0.0045	0.014132412
GO:0098810	neurotransmitter reuptake	8	0.187446913	0.015	0.021138192
GO:0046634	regulation of alpha-beta T cell activation	31	0.187333652	0.0213	0.026276211
GO:0046631	alpha-beta T cell activation	47	0.18733204	0.0187	0.024129301
GO:0006334	nucleosome assembly	30	0.187318533	0.0395	0.042617839

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0006515	misfolded or incompletely synthesized protein catabolic process	12	0.187191374	0.0176	0.023223003
GO:1901222	regulation of NIK/NF-kappaB signaling	38	0.187140315	0.0158	0.021871104
GO:0032365	intracellular lipid transport	19	0.187118457	0.0097	0.017363901
GO:0001916	positive regulation of T cell mediated cytotoxicity	5	0.187075055	0.0335	0.0372227945
GO:1903708	positive regulation of hemopoiesis	67	0.187037752	0.0181	0.023607986
GO:0030947	regulation of vascular endothelial growth factor receptor signaling pathway	14	0.187026685	0.0176	0.023223003
GO:0018206	peptidyl-methionine modification	5	0.187001195	0.003	0.013210967
GO:1903818	positive regulation of voltage-gated potassium channel activity	8	0.186992578	0.0041	0.013887639
GO:1903573	negative regulation of response to endoplasmic reticulum stress	20	0.186984415	0.0154	0.021487162
GO:0010470	regulation of gastrulation	15	0.186927681	0.0136	0.020157703
GO:0003177	pulmonary valve development	13	0.186927515	0.0309	0.034874839
GO:0000460	maturation of 5.8S rRNA	6	0.186900254	0.0055	0.01475
GO:0007029	endoplasmic reticulum organization	22	0.186854666	0.0036	0.01353394
GO:1903671	negative regulation of sprouting angiogenesis	14	0.186831207	0.0148	0.020979063
GO:0000956	nuclear-transcribed mRNA catabolic process	91	0.186750804	0.0246	0.029170878
GO:0045992	negative regulation of embryonic development	12	0.186708585	0.0108	0.018152791
GO:0010559	regulation of glycoprotein biosynthetic process	18	0.18669408	0.0069	0.015750415
GO:0098877	neurotransmitter receptor transport to plasma membrane	6	0.18668105	0.0043	0.014102439
GO:0098969	neurotransmitter receptor transport to postsynaptic membrane	6	0.18668105	0.0043	0.014102439
GO:0099637	neurotransmitter receptor transport	6	0.18668105	0.0043	0.014102439
GO:0048026	positive regulation of mRNA splicing, via spliceosome	6	0.186659669	0.0041	0.013887639
GO:0042044	fluid transport	13	0.186629086	0.0185	0.023962142
GO:0060795	cell fate commitment involved in formation of primary germ layer	13	0.186585029	0.0244	0.029011063
GO:0010862	positive regulation of pathway-restricted SMAD protein phosphorylation	12	0.186567777	0.011	0.018323826
GO:0061577	calcium ion transmembrane transport via high voltage-gated calcium channel	9	0.186541105	0.0194	0.024690909
GO:0044241	lipid digestion	8	0.186533708	0.0281	0.032268957
GO:0043484	regulation of RNA splicing	36	0.186500684	0.0097	0.017363901
GO:0090148	membrane fission	6	0.186405911	0.0239	0.028592965
GO:0006884	cell volume homeostasis	8	0.186402348	0.0194	0.024690909
GO:0046856	phosphatidylinositol dephosphorylation	11	0.186364328	0.0003	0.007956881
GO:0051546	keratinocyte migration	7	0.18634575	0.0032	0.013333753
GO:0007062	sister chromatid cohesion	16	0.186307027	0.0134	0.01999969
GO:0006376	mRNA splice site selection	8	0.18626953	0.0277	0.03194284
GO:0010738	regulation of protein kinase A signaling	8	0.186145458	0.0027	0.012827773
GO:0050906	detection of stimulus involved in sensory perception	49	0.186082414	0.0153	0.021378589
GO:0045619	regulation of lymphocyte differentiation	63	0.186029002	0.0145	0.020788247
GO:0035886	vascular smooth muscle cell differentiation	12	0.185996227	0.0246	0.029170878
GO:0007622	rhythmic behavior	23	0.185969457	0.0004	0.008964341
GO:1904714	regulation of chaperone-mediated autophagy	5	0.18595446	0.0396	0.042717761
GO:0031497	chromatin assembly	32	0.185941737	0.0395	0.042617839
GO:0010766	negative regulation of sodium ion transport	10	0.18592984	0.018	0.023514686
GO:0060632	regulation of microtubule-based movement	8	0.185919668	0.031	0.034967226
GO:0030326	embryonic limb morphogenesis	37	0.185741523	0.0148	0.020979063
GO:0035113	embryonic appendage morphogenesis	37	0.185741523	0.0148	0.020979063
GO:0072577	endothelial cell apoptotic process	18	0.185698556	0.0153	0.021378589
GO:0046637	regulation of alpha-beta T cell differentiation	21	0.185689033	0.0177	0.02329117
GO:0002286	T cell activation involved in immune response	29	0.18563617	0.0223	0.027242468
GO:0060307	regulation of ventricular cardiac muscle cell membrane repolarization	9	0.185611595	0.0298	0.033898013
GO:0051642	centrosome localization	7	0.185605856	0.0115	0.018599441
GO:0018149	peptide cross-linking	10	0.18558244	0.0229	0.027770092
GO:0032743	positive regulation of interleukin-2 production	10	0.18556702	0.0117	0.018739446
GO:0045719	negative regulation of glycogen biosynthetic process	5	0.185484349	0.0018	0.01210186
GO:0070874	negative regulation of glycogen metabolic process	5	0.185484349	0.0018	0.01210186
GO:0045639	positive regulation of myeloid cell differentiation	33	0.185437213	0.0185	0.023962142
GO:0008045	motor neuron axon guidance	11	0.18542724	0.0031	0.013277185
GO:0010804	negative regulation of tumor necrosis factor-mediated signaling pathway	8	0.185416741	0.0331	0.03684717
GO:0051647	nucleus localization	10	0.185399863	0.025	0.029554283
GO:0043174	nucleoside salvage	10	0.18534259	0.0178	0.023348367
GO:0043297	apical junction assembly	17	0.18529992	0.0115	0.018599441
GO:0031297	replication fork processing	10	0.185258234	0.021	0.026005997
GO:0045005	DNA-dependent DNA replication maintenance of fidelity	10	0.185258234	0.021	0.026005997
GO:0006379	mRNA cleavage	8	0.185257359	0.0294	0.033482529
GO:0034728	nucleosome organization	41	0.185245899	0.0262	0.030579007
GO:1901658	glycosyl compound catabolic process	20	0.185157292	0.0406	0.043585072
GO:1900027	regulation of ruffle assembly	11	0.185111068	0.0018	0.01210186
GO:0042035	regulation of cytokine biosynthetic process	42	0.1850433	0.0242	0.028862294
GO:0045815	positive regulation of gene expression, epigenetic	14	0.185037469	0.0039	0.013791927
GO:0032506	cytokinetic process	9	0.184977667	0.0082	0.016514246
GO:0007250	activation of NF-kappaB-inducing kinase activity	10	0.18492729	0.0182	0.023684988
GO:0071158	positive regulation of cell cycle arrest	27	0.18483182	0.0004	0.008964341
GO:1903363	negative regulation of cellular protein catabolic process	32	0.18482238	0.0045	0.014132412
GO:0008333	endosome to lysosome transport	24	0.184789689	0.0001	0.004220438
GO:0060389	pathway-restricted SMAD protein phosphorylation	20	0.184755663	0.0098	0.017418875
GO:0018022	peptidyl-lysine methylation	48	0.184750734	0.0016	0.011845327
GO:0070292	N-acylphosphatidylethanolamine metabolic process	5	0.184743159	0.016	0.022026667
GO:0030889	negative regulation of B cell proliferation	7	0.184720094	0.0124	0.019242297
GO:0001541	ovarian follicle development	27	0.184691827	0.0039	0.013791927
GO:0042094	interleukin-2 biosynthetic process	7	0.184618467	0.0234	0.02817551
GO:0045076	regulation of interleukin-2 biosynthetic process	7	0.184618467	0.0234	0.02817551
GO:0031640	killing of cells of other organism	12	0.184365049	0.0092	0.017033109
GO:0044364	disruption of cells of other organism	12	0.184365049	0.0092	0.017033109
GO:0045577	regulation of B cell differentiation	12	0.184302635	0.0201	0.025275816
GO:0010226	response to lithium ion	11	0.184175628	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:2000786	positive regulation of autophagosome assembly	6	0.184100277	0.0128	0.019522448
GO:1901983	regulation of protein acetylation	30	0.184089133	0.0077	0.016177834
GO:0061635	regulation of protein complex stability	6	0.18401713	0.0145	0.020788247
GO:0001937	negative regulation of endothelial cell proliferation	13	0.183985683	0.0279	0.032115827
GO:1903205	regulation of hydrogen peroxide-induced cell death	11	0.183898801	0.0138	0.020339434
GO:0072527	pyrimidine-containing compound metabolic process	42	0.183898597	0.0133	0.019917275
GO:0021602	cranial nerve morphogenesis	9	0.183878121	0.0002	0.006319126
GO:0060055	angiogenesis involved in wound healing	7	0.183867097	0.0033	0.013333753
GO:0009948	anterior/posterior axis specification	13	0.183725828	0.0173	0.023005658
GO:0035020	regulation of Rac protein signal transduction	5	0.183612197	0.0337	0.03733539
GO:0045910	negative regulation of DNA recombination	10	0.183534839	0.0368	0.040139144
GO:1902895	positive regulation of pri-miRNA transcription from RNA polymerase II promoter	16	0.183431921	0.0271	0.031420132
GO:0007350	blastoderm segmentation	6	0.183384355	0.0421	0.045028154
GO:0003323	type B pancreatic cell development	13	0.183378756	0.0001	0.004220438
GO:0021952	central nervous system projection neuron axonogenesis	14	0.183289084	0.0018	0.01210186
GO:0002066	columnar/cuboidal epithelial cell development	33	0.18322142	0.0004	0.008964341
GO:0043567	regulation of insulin-like growth factor receptor signaling pathway	7	0.183189586	0.0048	0.014269203
GO:0046606	negative regulation of centrosome cycle	6	0.183100794	0.0134	0.01999969
GO:2001214	positive regulation of vasculogenesis	5	0.1830703	0.0039	0.013791927
GO:0003283	atrial septum development	8	0.183021481	0.02	0.025188412
GO:0060413	atrial septum morphogenesis	8	0.183021481	0.02	0.025188412
GO:0046597	negative regulation of viral entry into host cell	9	0.18297755	0.0032	0.013333753
GO:0033189	response to vitamin A	8	0.182915712	0.002	0.012314604
GO:0007606	sensory perception of chemical stimulus	48	0.182909287	0.0146	0.020879842
GO:0046653	tetrahydrofolate metabolic process	10	0.18290405	0.0058	0.014878261
GO:0015949	nucleobase-containing small molecule interconversion	14	0.182837595	0.0436	0.046426372
GO:0010224	response to UV-B	8	0.182689922	0.0066	0.015525305
GO:0048255	mRNA stabilization	17	0.182666731	0.0028	0.012972436
GO:0048048	embryonic eye morphogenesis	13	0.182643248	0.0017	0.012001709
GO:0046039	GTP metabolic process	14	0.182504115	0.0021	0.012314604
GO:0045292	mRNA cis splicing, via spliceosome	5	0.182449618	0.0346	0.038164288
GO:0072553	terminal button organization	5	0.182408931	0.0207	0.025805821
GO:0008156	negative regulation of DNA replication	17	0.182252842	0.0041	0.013887639
GO:0018198	peptidyl-cysteine modification	15	0.182140271	0.0004	0.008964341
GO:0021515	cell differentiation in spinal cord	18	0.182130826	0.0112	0.018392048
GO:0006220	pyrimidine nucleotide metabolic process	26	0.18200632	0.0147	0.02091937
GO:1902893	regulation of pri-miRNA transcription from RNA polymerase II promoter	21	0.181952357	0.0398	0.042885501
GO:0061614	pri-miRNA transcription from RNA polymerase II promoter	24	0.18193923	0.0239	0.028592965
GO:0046632	alpha-beta T cell differentiation	34	0.181928057	0.0139	0.020388077
GO:0035909	aorta morphogenesis	13	0.18184654	0.009	0.016956012
GO:0006538	glutamate catabolic process	7	0.181829381	0.0241	0.028760826
GO:0031060	regulation of histone methylation	24	0.181792968	0.0108	0.018152791
GO:0046825	regulation of protein export from nucleus	11	0.18177277	0.0091	0.016994897
GO:0051446	positive regulation of meiotic cell cycle	7	0.181736085	0.0132	0.019860109
GO:0006333	chromatin assembly or disassembly	42	0.181695576	0.032	0.035892144
GO:0006730	one-carbon metabolic process	12	0.181677697	0.0034	0.01347416
GO:0032467	positive regulation of cytokinesis	10	0.181553842	0.0022	0.012422266
GO:0002701	negative regulation of production of molecular mediator of immune response	12	0.181544123	0.024	0.028671074
GO:0086012	membrane depolarization during cardiac muscle cell action potential	7	0.181519318	0.0002	0.006319126
GO:0060411	cardiac septum morphogenesis	35	0.181457046	0.0104	0.017832977
GO:0071825	protein-lipid complex subunit organization	14	0.181448698	0.0344	0.037979912
GO:0001704	formation of primary germ layer	47	0.181447242	0.0102	0.0177
GO:0035067	negative regulation of histone acetylation	8	0.18138134	0.0154	0.021487162
GO:0045682	regulation of epidermis development	28	0.181363592	0.0236	0.028327839
GO:0085029	extracellular matrix assembly	19	0.181320634	0.0307	0.034703304
GO:0001783	B cell apoptotic process	9	0.181190374	0.0193	0.024606968
GO:0009913	epidermal cell differentiation	86	0.181183156	0.0123	0.019143634
GO:0045843	negative regulation of striated muscle tissue development	24	0.181048053	0.0042	0.013948535
GO:0030836	positive regulation of actin filament depolymerization	8	0.181015119	0.034	0.037588528
GO:0043457	regulation of cellular respiration	16	0.180990742	0.0072	0.015844069
GO:0090324	negative regulation of oxidative phosphorylation	5	0.180832996	0.021	0.026005997
GO:0090051	negative regulation of cell migration involved in sprouting angiogenesis	10	0.180791272	0.0283	0.032434212
GO:0035973	aggrephagy	5	0.180693569	0.0115	0.018599441
GO:2001222	regulation of neuron migration	19	0.180686722	0.0018	0.01210186
GO:0009264	deoxyribonucleotide catabolic process	11	0.180678538	0.021	0.026005997
GO:0033599	regulation of mammary gland epithelial cell proliferation	8	0.18063189	0.0119	0.018881943
GO:0010759	positive regulation of macrophage chemotaxis	6	0.180575955	0.0452	0.047918298
GO:0046639	negative regulation of alpha-beta T cell differentiation	7	0.180470842	0.0065	0.015491756
GO:0071157	negative regulation of cell cycle arrest	12	0.180434175	0.021	0.026005997
GO:0017014	protein nitrosylation	7	0.18041716	0.0025	0.012769435
GO:0018119	peptidyl-cysteine S-nitrosylation	7	0.18041716	0.0025	0.012769435
GO:0061756	leukocyte adhesion to vascular endothelial cell	13	0.180254318	0.0387	0.041895413
GO:0048261	negative regulation of receptor-mediated endocytosis	14	0.180246023	0.0026	0.012805111
GO:0046596	regulation of viral entry into host cell	16	0.180181199	0.0064	0.015399417
GO:0045589	regulation of regulatory T cell differentiation	10	0.180111891	0.044	0.046783376
GO:0051568	histone H3-K4 methylation	18	0.180095363	0.0122	0.019049527
GO:0033127	regulation of histone phosphorylation	8	0.180082315	0.0139	0.020388077
GO:0018279	protein N-linked glycosylation via asparagine	23	0.180074533	0.0184	0.023875404
GO:0044773	mitotic DNA damage checkpoint	29	0.180034577	0.0077	0.016177834
GO:0044774	mitotic DNA integrity checkpoint	29	0.180034577	0.0077	0.016177834
GO:0044033	multi-organism metabolic process	92	0.179953025	0.0338	0.0374175
GO:0003198	epithelial to mesenchymal transition involved in endocardial cushion formation	9	0.179801003	0.0383	0.041555752
GO:0032816	positive regulation of natural killer cell activation	9	0.179600013	0.0151	0.02121706

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0070932	histone H3 deacetylation	7	0.179588782	0.0146	0.020879842
GO:2000826	regulation of heart morphogenesis	14	0.179569068	0.0268	0.031128485
GO:1901862	negative regulation of muscle tissue development	25	0.179537677	0.0057	0.01480566
GO:1903599	positive regulation of mitophagy	11	0.179472279	0.0033	0.013333753
GO:0003170	heart valve development	28	0.179274323	0.027	0.031323034
GO:0071634	regulation of transforming growth factor beta production	14	0.179252711	0.0234	0.02817551
GO:0035710	CD4-positive, alpha-beta T cell activation	31	0.179251502	0.0108	0.018152791
GO:0035722	interleukin-12-mediated signaling pathway	25	0.17924711	0.0361	0.039494834
GO:0010939	regulation of necrotic cell death	9	0.179156566	0.0325	0.036312077
GO:0008535	respiratory chain complex IV assembly	13	0.179135855	0.0256	0.03006687
GO:1903018	regulation of glycoprotein metabolic process	21	0.179091509	0.0107	0.018084595
GO:0033561	regulation of water loss via skin	6	0.179067445	0.0023	0.012498684
GO:0043576	regulation of respiratory gaseous exchange	9	0.179047432	0.0051	0.014547706
GO:0009166	nucleotide catabolic process	27	0.17892678	0.0189	0.024289798
GO:0003151	outflow tract morphogenesis	36	0.178918069	0.0168	0.022626974
GO:0002068	glandular epithelial cell development	17	0.178836007	< 0.001	< 0.001
GO:1901224	positive regulation of NIK/NF-kappaB signaling	28	0.178817235	0.0129	0.019597425
GO:0009154	purine ribonucleotide catabolic process	13	0.178792971	0.0121	0.018970228
GO:0009261	ribonucleotide catabolic process	13	0.178792971	0.0121	0.018970228
GO:0072606	interleukin-8 secretion	16	0.178631116	0.0282	0.032370935
GO:0000079	regulation of cyclin-dependent protein serine/threonine kinase activity	36	0.178625258	0.0058	0.014878261
GO:0061037	negative regulation of cartilage development	8	0.178559766	0.0009	0.010729485
GO:0007638	mechanosensory behavior	7	0.178554745	< 0.001	< 0.001
GO:0048635	negative regulation of muscle organ development	25	0.178510429	0.0029	0.013089617
GO:2000370	positive regulation of clathrin-dependent endocytosis	6	0.17850421	0.0012	0.010961137
GO:0043242	negative regulation of protein complex disassembly	24	0.178199214	0.0197	0.024979254
GO:0045621	positive regulation of lymphocyte differentiation	34	0.178097714	0.0256	0.03006687
GO:1901292	nucleoside phosphate catabolic process	31	0.178066401	0.0236	0.028327839
GO:0048286	lung alveolus development	18	0.17801865	< 0.001	< 0.001
GO:0001702	gastrulation with mouth forming second	9	0.178004036	0.0147	0.02091937
GO:1904029	regulation of cyclin-dependent protein kinase activity	39	0.177897948	0.007	0.015816335
GO:0048525	negative regulation of viral process	32	0.177884014	0.0113	0.018488002
GO:1903901	negative regulation of viral life cycle	32	0.177884014	0.0113	0.018488002
GO:0060004	reflex	6	0.177876833	0.0267	0.031037274
GO:0090084	negative regulation of inclusion body assembly	6	0.177875754	0.0184	0.023875404
GO:1900273	positive regulation of long-term synaptic potentiation	12	0.17787435	0.0068	0.015633241
GO:0002709	regulation of T cell mediated immunity	12	0.177802542	0.0053	0.014634479
GO:0070671	response to interleukin-12	27	0.177797718	0.0365	0.039857035
GO:0043248	proteasome assembly	7	0.177720074	0.0205	0.025639412
GO:1904380	endoplasmic reticulum mannose trimming	8	0.177606392	0.0031	0.013277185
GO:0045604	regulation of epidermal cell differentiation	18	0.177544032	0.0336	0.037253154
GO:0030299	intestinal cholesterol absorption	6	0.177524596	0.0322	0.036060507
GO:0098856	intestinal lipid absorption	6	0.177524596	0.0322	0.036060507
GO:1903051	negative regulation of proteolysis involved in cellular protein catabolic process	27	0.177440801	0.0072	0.015844069
GO:0006482	protein demethylation	8	0.177363432	0.0038	0.01366393
GO:0008214	protein dealkylation	8	0.177363432	0.0038	0.01366393
GO:0009200	deoxyribonucleoside triphosphate metabolic process	13	0.177280689	0.0321	0.035976391
GO:0034394	protein localization to cell surface	28	0.177150391	0.0137	0.020264364
GO:0021854	hypothalamus development	11	0.177055992	0.003	0.013210967
GO:0032897	negative regulation of viral transcription	10	0.177054485	0.0301	0.034151923
GO:0000289	nuclear-transcribed mRNA poly(A) tail shortening	10	0.176983216	0.0007	0.010220707
GO:0070317	negative regulation of G0 to G1 transition	13	0.17678221	0.004	0.013824268
GO:0033120	positive regulation of RNA splicing	10	0.176631799	0.0106	0.018010344
GO:0090237	regulation of arachidonic acid secretion	6	0.176526409	0.0331	0.03684717
GO:0031293	membrane protein intracellular domain proteolysis	10	0.176517252	0.0472	0.049710455
GO:0030218	erythrocyte differentiation	37	0.176466149	0.0113	0.018488002
GO:0060749	mammary gland alveolus development	5	0.176391301	0.0044	0.014132412
GO:0061377	mammary gland lobule development	5	0.176391301	0.0044	0.014132412
GO:0002287	alpha-beta T cell activation involved in immune response	19	0.176374415	0.0089	0.016916437
GO:0002292	T cell differentiation involved in immune response	19	0.176374415	0.0089	0.016916437
GO:0002293	alpha-beta T cell differentiation involved in immune response	19	0.176374415	0.0089	0.016916437
GO:0002294	CD4-positive, alpha-beta T cell differentiation involved in immune response	19	0.176374415	0.0089	0.016916437
GO:0042093	T-helper cell differentiation	19	0.176374415	0.0089	0.016916437
GO:0045879	negative regulation of smoothened signaling pathway	14	0.176314239	0.0176	0.023223003
GO:0006612	protein targeting to membrane	79	0.176291483	0.0331	0.03684717
GO:0034101	erythrocyte homeostasis	40	0.176286958	0.0162	0.022196303
GO:0071450	cellular response to oxygen radical	9	0.176273011	0.0458	0.048447786
GO:0071451	cellular response to superoxide	9	0.176273011	0.0458	0.048447786
GO:0010713	negative regulation of collagen metabolic process	6	0.176259693	0.0109	0.018225506
GO:0044252	negative regulation of multicellular organismal metabolic process	6	0.176259693	0.0109	0.018225506
GO:0031057	negative regulation of histone modification	18	0.176144872	0.0045	0.014132412
GO:1905268	negative regulation of chromatin organization	18	0.176144872	0.0045	0.014132412
GO:0042417	dopamine metabolic process	17	0.176061653	0.0203	0.025471918
GO:0071349	cellular response to interleukin-12	26	0.176038678	0.0349	0.038392656
GO:0018243	protein O-linked glycosylation via threonine	5	0.175741335	0.0341	0.037691875
GO:1902042	negative regulation of extrinsic apoptotic signaling pathway via death domain receptors	14	0.175667827	0.0052	0.014616626
GO:0098868	bone growth	12	0.175662767	0.0002	0.006319126
GO:0045662	negative regulation of myoblast differentiation	11	0.175607539	0.0308	0.034775552
GO:0007498	mesoderm development	45	0.175573113	0.0294	0.033482529
GO:0019835	cytolysis	10	0.175463648	0.0429	0.045748395
GO:0021548	pons development	5	0.175382403	0.0163	0.022248961
GO:0048668	collateral sprouting	9	0.175288645	0.0004	0.008964341
GO:0046339	diacylglycerol metabolic process	8	0.175192343	0.0177	0.02329117

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0003197	endocardial cushion development	22	0.17515531	0.0113	0.018488002
GO:0006829	zinc II ion transport	6	0.175098453	0.0131	0.019786886
GO:0002902	regulation of B cell apoptotic process	6	0.175065842	0.018	0.023514686
GO:0043367	CD4-positive, alpha-beta T cell differentiation	25	0.17502404	0.0094	0.017156187
GO:0043568	positive regulation of insulin-like growth factor receptor signaling pathway	5	0.174974489	0.022	0.026944291
GO:0003143	embryonic heart tube morphogenesis	24	0.17496828	0.0183	0.023783007
GO:0010835	regulation of protein ADP-ribosylation	7	0.17491007	0.0262	0.030579007
GO:0071501	cellular response to sterol depletion	6	0.174890263	0.0006	0.009940401
GO:1901879	regulation of protein depolymerization	32	0.174725415	0.0273	0.031601321
GO:0048024	regulation of mRNA splicing, via spliceosome	24	0.174723107	0.0102	0.0177
GO:0007063	regulation of sister chromatid cohesion	8	0.174597092	0.0216	0.026572596
GO:2000107	negative regulation of leukocyte apoptotic process	16	0.174578465	0.0082	0.016514246
GO:0031076	embryonic camera-type eye development	15	0.174506711	0.0117	0.018739446
GO:1903020	positive regulation of glycoprotein metabolic process	8	0.174316554	0.0047	0.014168613
GO:0021783	preganglionic parasympathetic fiber development	6	0.174133308	0.0264	0.030750363
GO:0035404	histone-serine phosphorylation	5	0.174038154	0.0041	0.013887639
GO:0003203	endocardial cushion morphogenesis	18	0.17395557	0.0142	0.020567234
GO:0045823	positive regulation of heart contraction	18	0.173952546	0.012	0.018931514
GO:0046638	positive regulation of alpha-beta T cell differentiation	16	0.173885138	0.0439	0.046702815
GO:0003179	heart valve morphogenesis	26	0.173874666	0.0303	0.034331687
GO:1903543	positive regulation of exosomal secretion	10	0.173694642	0.0128	0.019522448
GO:1900744	regulation of p38MAPK cascade	10	0.173441186	0.015	0.021138192
GO:0051261	protein depolymerization	41	0.173404155	0.011	0.018323826
GO:0045066	regulatory T cell differentiation	11	0.173399756	0.0468	0.049334111
GO:0061626	pharyngeal arch artery morphogenesis	6	0.1733878	0.0384	0.04164081
GO:0060561	apoptotic process involved in morphogenesis	7	0.17338419	0.0357	0.03911643
GO:0006413	translational initiation	83	0.173358925	0.033	0.036785425
GO:0043368	positive T cell selection	10	0.173315365	0.0468	0.049334111
GO:0036037	CD8-positive, alpha-beta T cell activation	7	0.173197597	0.0261	0.030517735
GO:0046386	deoxyribose phosphate catabolic process	12	0.173127671	0.029	0.033098697
GO:0006544	glycine metabolic process	8	0.173092846	0.0218	0.026744664
GO:0009593	detection of chemical stimulus	42	0.172938069	0.0297	0.03379756
GO:0045814	negative regulation of gene expression, epigenetic	17	0.172670506	0.0164	0.022306469
GO:0060972	left/right pattern formation	7	0.172517864	0.0051	0.014547706
GO:0002090	regulation of receptor internalization	22	0.172408127	0.0169	0.022703485
GO:0001782	B cell homeostasis	9	0.172370968	0.0151	0.02121706
GO:0042297	vocal learning	5	0.17236996	0.001	0.010787313
GO:0098596	imitative learning	5	0.17236996	0.001	0.010787313
GO:0098597	observational learning	5	0.17236996	0.001	0.010787313
GO:0098598	learned vocalization behavior or vocal learning	5	0.17236996	0.001	0.010787313
GO:1905515	non-motile cilium assembly	21	0.172343365	0.015	0.021138192
GO:0060338	regulation of type I interferon-mediated signaling pathway	11	0.172226834	0.0298	0.033898013
GO:0010463	mesenchymal cell proliferation	18	0.172157523	0.034	0.037588528
GO:0030853	negative regulation of granulocyte differentiation	6	0.172137366	0.0067	0.015576759
GO:0051148	negative regulation of muscle cell differentiation	31	0.172030422	0.0104	0.017832977
GO:0030216	keratinocyte differentiation	66	0.171868353	0.0157	0.021779607
GO:0045023	G0 to G1 transition	14	0.171819251	0.0078	0.01620539
GO:0070316	regulation of G0 to G1 transition	14	0.171819251	0.0078	0.01620539
GO:0015804	neutral amino acid transport	11	0.171770011	0.0097	0.017363901
GO:0019080	viral gene expression	84	0.171766787	0.042	0.044946141
GO:1903540	establishment of protein localization to postsynaptic membrane	7	0.171658573	0.0063	0.015311728
GO:0050482	arachidonic acid secretion	11	0.171592842	0.0112	0.018392048
GO:1903963	arachidonate transport	11	0.171592842	0.0112	0.018392048
GO:1990709	presynaptic active zone organization	5	0.171549727	0.0332	0.036915846
GO:0030220	platelet formation	6	0.171508478	0.0103	0.017772187
GO:0036344	platelet morphogenesis	6	0.171508478	0.0103	0.017772187
GO:0045063	T-helper 1 cell differentiation	9	0.171491849	0.0172	0.022941269
GO:0021984	adenohypophysis development	5	0.171470425	0.0475	0.049962707
GO:1901380	negative regulation of potassium ion transmembrane transport	10	0.171448527	0.004	0.013824268
GO:0050892	intestinal absorption	11	0.171421327	0.0254	0.029880529
GO:0003209	cardiac atrium morphogenesis	13	0.171361739	0.0198	0.025062084
GO:0003230	cardiac atrium development	13	0.171361739	0.0198	0.025062084
GO:2000514	regulation of CD4-positive, alpha-beta T cell activation	19	0.171063535	0.0199	0.025133639
GO:0090385	phagosome-lysosome fusion	5	0.171053701	0.0257	0.030153693
GO:0010718	positive regulation of epithelial to mesenchymal transition	19	0.171001542	0.0245	0.029070183
GO:0051547	regulation of keratinocyte migration	6	0.170984981	0.0009	0.010729485
GO:0030857	negative regulation of epithelial cell differentiation	14	0.170892024	< 0.001	< 0.001
GO:0051973	positive regulation of telomerase activity	17	0.170754267	0.0179	0.02344231
GO:0033629	negative regulation of cell adhesion mediated by integrin	5	0.170500918	0.0034	0.01347416
GO:1902947	regulation of tau-protein kinase activity	5	0.170456603	0.0342	0.037780741
GO:0099625	ventricular cardiac muscle cell membrane repolarization	12	0.170442155	0.0216	0.026572596
GO:0070861	regulation of protein exit from endoplasmic reticulum	10	0.170419154	0.0118	0.018836996
GO:0032689	negative regulation of interferon-gamma production	9	0.170397342	0.0232	0.028016374
GO:0048642	negative regulation of skeletal muscle tissue development	8	0.170391781	0.0279	0.032115827
GO:1904526	regulation of microtubule binding	5	0.170299294	0.0251	0.029642198
GO:0032369	negative regulation of lipid transport	7	0.170106222	0.0086	0.016782045
GO:0051085	chaperone mediated protein folding requiring cofactor	9	0.170090529	0.008	0.016379603
GO:0030837	negative regulation of actin filament polymerization	22	0.170050032	0.0304	0.034411276
GO:0098659	inorganic cation import into cell	9	0.170046616	0.008	0.016379603
GO:0099587	inorganic ion import into cell	9	0.170046616	0.008	0.016379603
GO:1900101	regulation of endoplasmic reticulum unfolded protein response	5	0.169960835	0.0086	0.016782045
GO:0031069	hair follicle morphogenesis	7	0.169917037	0.0471	0.049614174
GO:0071604	transforming growth factor beta production	15	0.169685956	0.0265	0.03085441

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0006984	ER-nucleus signaling pathway	17	0.169505435	0.0098	0.017418875
GO:0021527	spinal cord association neuron differentiation	5	0.169462994	0.0389	0.042009675
GO:0035050	embryonic heart tube development	26	0.169404753	0.0148	0.020979063
GO:1901880	negative regulation of protein depolymerization	23	0.169345032	0.0235	0.028248857
GO:0043370	regulation of CD4-positive, alpha-beta T cell differentiation	14	0.169281269	0.0157	0.021779607
GO:0071542	dopaminergic neuron differentiation	11	0.169232038	0.0016	0.011845327
GO:0021511	spinal cord patterning	11	0.169102106	0.0365	0.039857035
GO:2000757	negative regulation of peptidyl-lysine acetylation	10	0.169000269	0.0259	0.0303391
GO:0021513	spinal cord dorsal/ventral patterning	9	0.168868315	0.0345	0.038068511
GO:0048532	anatomical structure arrangement	6	0.168551279	0.0447	0.047449128
GO:0072673	lamellipodium morphogenesis	8	0.168463166	0.0358	0.039211138
GO:0006103	2-oxoglutarate metabolic process	11	0.168215553	0.0284	0.032523034
GO:0070935	3'-UTR-mediated mRNA stabilization	8	0.16814667	0.0173	0.023005658
GO:0090166	Golgi disassembly	5	0.168114858	0.0311	0.035052671
GO:0045616	regulation of keratinocyte differentiation	10	0.168089202	0.029	0.033098697
GO:0033233	regulation of protein sumoylation	8	0.168067141	0.0028	0.012972436
GO:0051984	positive regulation of chromosome segregation	10	0.168050847	0.0023	0.012498684
GO:0097011	cellular response to granulocyte macrophage colony-stimulating factor stimulus	5	0.167992536	0.0437	0.046498601
GO:0097012	response to granulocyte macrophage colony-stimulating factor	5	0.167992536	0.0437	0.046498601
GO:1904152	regulation of retrograde protein transport, ER to cytosol	6	0.167869264	0.0314	0.035301342
GO:0031061	negative regulation of histone methylation	8	0.167669173	0.0217	0.026655917
GO:0045188	regulation of circadian sleep/wake cycle, non-REM sleep	5	0.167501693	0.0033	0.013333753
GO:0045988	negative regulation of striated muscle contraction	5	0.167376779	0.0426	0.045512417
GO:0060037	pharyngeal system development	10	0.167369393	0.0273	0.031601321
GO:0000729	DNA double-strand break processing	5	0.167343866	0.0313	0.035223161
GO:0002091	negative regulation of receptor internalization	8	0.167308297	0.0056	0.014771533
GO:0033866	nucleoside bisphosphate biosynthetic process	10	0.167065531	0.0036	0.01353394
GO:0034030	ribonucleoside bisphosphate biosynthetic process	10	0.167065531	0.0036	0.01353394
GO:0034033	purine nucleoside bisphosphate biosynthetic process	10	0.167065531	0.0036	0.01353394
GO:0001947	heart looping	22	0.16685539	0.016	0.022026667
GO:0060396	growth hormone receptor signaling pathway	11	0.166780176	0.0007	0.010220707
GO:0071378	cellular response to growth hormone stimulus	11	0.166780176	0.0007	0.010220707
GO:0003188	heart valve formation	8	0.166758721	0.0213	0.026276211
GO:0031498	chromatin disassembly	8	0.166758721	0.0078	0.01620539
GO:0006182	cGMP biosynthetic process	9	0.16668218	0.0159	0.021956962
GO:0032435	negative regulation of proteasomal ubiquitin-dependent protein catabolic process	14	0.166465897	0.0093	0.017114131
GO:0046635	positive regulation of alpha-beta T cell activation	22	0.166453991	0.042	0.044946141
GO:0019083	viral transcription	78	0.166427071	0.0463	0.048905115
GO:0072567	chemokine (C-X-C motif) ligand 2 production	6	0.166387533	0.0178	0.023348367
GO:2000341	regulation of chemokine (C-X-C motif) ligand 2 production	6	0.166387533	0.0178	0.023348367
GO:0048662	negative regulation of smooth muscle cell proliferation	20	0.166387382	0.0394	0.042525817
GO:0045601	regulation of endothelial cell differentiation	8	0.166379542	0.0053	0.014634479
GO:0030330	DNA damage response, signal transduction by p53 class mediator	37	0.166192494	0.0137	0.020264364
GO:0045475	locomotor rhythm	8	0.166190681	0.0031	0.013277185
GO:0045579	positive regulation of B cell differentiation	5	0.166165997	0.0374	0.040724444
GO:1902004	positive regulation of beta-amyloid formation	5	0.166126086	0.0011	0.010890753
GO:1902993	positive regulation of amyloid precursor protein catabolic process	5	0.166126086	0.0011	0.010890753
GO:0043124	negative regulation of I-kappaB kinase/NF-kappaB signaling	11	0.165871594	0.0105	0.017924712
GO:1901031	regulation of response to reactive oxygen species	15	0.165797043	0.0156	0.021692929
GO:1903539	protein localization to postsynaptic membrane	11	0.165709974	0.0004	0.008964341
GO:0045620	negative regulation of lymphocyte differentiation	18	0.165498696	0.0172	0.022941269
GO:0046068	cGMP metabolic process	13	0.165175857	0.0112	0.018392048
GO:0043249	erythrocyte maturation	7	0.16489957	0.0188	0.02420971
GO:0048384	retinoic acid receptor signaling pathway	13	0.16478443	0.0016	0.011845327
GO:0032814	regulation of natural killer cell activation	11	0.164693725	0.0239	0.028592965
GO:0046689	response to mercury ion	6	0.164493958	0.0144	0.02072711
GO:1902514	regulation of calcium ion transmembrane transport via high voltage-gated calcium channel	8	0.164385328	0.0282	0.032370935
GO:0006206	pyrimidine nucleobase metabolic process	11	0.16433491	0.015	0.021138192
GO:1902186	regulation of viral release from host cell	16	0.164209911	0.018	0.023514686
GO:0001302	replicative cell aging	5	0.164102847	0.0044	0.014132412
GO:0032527	protein exit from endoplasmic reticulum	24	0.164012196	0.0135	0.020081554
GO:0098915	membrane repolarization during ventricular cardiac muscle cell action potential	7	0.163985115	0.0354	0.038883511
GO:0051016	barbed-end actin filament capping	7	0.163936431	0.028	0.032186083
GO:0060324	face development	20	0.16387116	0.0292	0.033300671
GO:0043162	ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway	6	0.163819717	0.0445	0.047271541
GO:2000352	negative regulation of endothelial cell apoptotic process	11	0.163700564	0.0473	0.049788567
GO:0033119	negative regulation of RNA splicing	11	0.163656625	0.0352	0.038693232
GO:2000074	regulation of type B pancreatic cell development	6	0.163521687	< 0.001	< 0.001
GO:0000303	response to superoxide	11	0.163488055	0.0268	0.031128485
GO:0000305	response to oxygen radical	11	0.163488055	0.0268	0.031128485
GO:0002335	mature B cell differentiation	12	0.16347493	0.0162	0.022196303
GO:0046641	positive regulation of alpha-beta T cell proliferation	10	0.163333279	0.0399	0.042985243
GO:0032634	interleukin-5 production	5	0.163270693	0.0349	0.038392656
GO:0032674	regulation of interleukin-5 production	5	0.163270693	0.0349	0.038392656
GO:0010614	negative regulation of cardiac muscle hypertrophy	13	0.163160212	0.0059	0.014942532
GO:0048387	negative regulation of retinoic acid receptor signaling pathway	5	0.163087469	0.0029	0.013089617
GO:0007274	neuromuscular synaptic transmission	9	0.162805333	0.002	0.012314604
GO:0090200	positive regulation of release of cytochrome c from mitochondria	16	0.162769159	0.0377	0.040981651
GO:2000406	positive regulation of T cell migration	9	0.162700662	0.0358	0.039211138
GO:0002507	tolerance induction	8	0.162626299	0.0167	0.02255007
GO:1903862	positive regulation of oxidative phosphorylation	5	0.162278121	0.019	0.024347961
GO:0019388	galactose catabolic process	5	0.16221074	0.0231	0.027930615
GO:0086005	ventricular cardiac muscle cell action potential	13	0.162088996	0.0294	0.033482529

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1904994	regulation of leukocyte adhesion to vascular endothelial cell	7	0.162055875	0.0262	0.030579007
GO:0070229	negative regulation of lymphocyte apoptotic process	10	0.162039956	0.0085	0.016693954
GO:0006144	purine nucleobase metabolic process	9	0.161985964	0.0218	0.026744664
GO:0038066	p38MAPK cascade	13	0.161838012	0.0231	0.027930615
GO:0014741	negative regulation of muscle hypertrophy	14	0.161740814	0.0096	0.017302743
GO:1902187	negative regulation of viral release from host cell	8	0.161676326	0.0065	0.015491756
GO:1904292	regulation of ERAD pathway	12	0.161586754	0.0051	0.014547706
GO:0002467	germinal center formation	5	0.161509461	0.0073	0.015844069
GO:0002634	regulation of germinal center formation	5	0.161509461	0.0073	0.015844069
GO:0060337	type I interferon signaling pathway	31	0.161421657	0.0072	0.015844069
GO:0071357	cellular response to type I interferon	31	0.161421657	0.0072	0.015844069
GO:0044090	positive regulation of vacuole organization	11	0.161404785	0.0454	0.048095053
GO:0048385	regulation of retinoic acid receptor signaling pathway	9	0.161269827	< 0.001	< 0.001
GO:0032966	negative regulation of collagen biosynthetic process	5	0.161181627	0.0218	0.026744664
GO:2000001	regulation of DNA damage checkpoint	5	0.161116838	0.0159	0.021956962
GO:0032616	interleukin-13 production	7	0.161059231	0.0141	0.020504577
GO:0032656	regulation of interleukin-13 production	7	0.161059231	0.0141	0.020504577
GO:0006195	purine nucleotide catabolic process	19	0.161000599	0.0312	0.035137982
GO:0070734	histone H3-K27 methylation	6	0.160935514	0.0243	0.028921902
GO:0007064	mitotic sister chromatid cohesion	8	0.160457963	0.0203	0.025471918
GO:0061371	determination of heart left/right asymmetry	23	0.160338138	0.0178	0.023348367
GO:0060049	regulation of protein glycosylation	12	0.160213114	0.0149	0.021043429
GO:0031424	keratinization	42	0.159927146	0.0277	0.03194284
GO:0003272	endocardial cushion formation	13	0.159787788	0.0449	0.047643935
GO:0002903	negative regulation of B cell apoptotic process	5	0.159775699	0.0312	0.035137982
GO:0010749	regulation of nitric oxide mediated signal transduction	5	0.159700285	0.0467	0.049255637
GO:0009299	mRNA transcription	6	0.159692424	0.0041	0.013887639
GO:0060575	intestinal epithelial cell differentiation	9	0.15930196	0.0083	0.016559903
GO:0017144	drug metabolic process	7	0.159283819	0.0106	0.018010344
GO:0006833	water transport	10	0.159187024	0.0385	0.041733596
GO:2000515	negative regulation of CD4-positive, alpha-beta T cell activation	8	0.159162663	0.0165	0.022405589
GO:0045623	negative regulation of T-helper cell differentiation	5	0.159078048	0.0406	0.043585072
GO:0001707	mesoderm formation	26	0.159056409	0.0349	0.038392656
GO:0048332	mesoderm morphogenesis	26	0.159056409	0.0349	0.038392656
GO:0045581	negative regulation of T cell differentiation	13	0.159026058	0.0348	0.038319101
GO:0010832	negative regulation of myotube differentiation	5	0.158912188	0.0214	0.026388313
GO:0072523	purine-containing compound catabolic process	22	0.15868334	0.0348	0.038319101
GO:0060576	intestinal epithelial cell development	8	0.15867642	0.0033	0.013333753
GO:0001881	receptor recycling	14	0.158218776	0.0174	0.023064374
GO:0048333	mesodermal cell differentiation	13	0.158104654	0.0323	0.03615849
GO:0031643	positive regulation of myelination	8	0.157955315	0.0387	0.041895413
GO:1900118	negative regulation of execution phase of apoptosis	6	0.157396507	0.0364	0.039777887
GO:0019076	viral release from host cell	20	0.15732187	0.0122	0.019049527
GO:0035890	exit from host	20	0.15732187	0.0122	0.019049527
GO:0035891	exit from host cell	20	0.15732187	0.0122	0.019049527
GO:0052126	movement in host environment	20	0.15732187	0.0122	0.019049527
GO:0052192	movement in environment of other organism involved in symbiotic interaction	20	0.15732187	0.0122	0.019049527
GO:0071285	cellular response to lithium ion	8	0.157134597	0.0018	0.01210186
GO:0036499	PERK-mediated unfolded protein response	5	0.156924193	0.0204	0.025564109
GO:0030511	positive regulation of transforming growth factor beta receptor signaling pathway	12	0.156838887	0.0199	0.025133639
GO:1903846	positive regulation of cellular response to transforming growth factor beta stimulus	12	0.156838887	0.0199	0.025133639
GO:0009147	pyrimidine nucleoside triphosphate metabolic process	12	0.156798502	0.019	0.024347961
GO:0008655	pyrimidine-containing compound salvage	7	0.156720755	0.0207	0.025805821
GO:0043097	pyrimidine nucleoside salvage	7	0.156720755	0.0207	0.025805821
GO:0009112	nucleobase metabolic process	19	0.156626367	0.0144	0.02072711
GO:0060065	uterus development	8	0.156443619	0.0217	0.026655917
GO:0036507	protein demannosylation	12	0.156212591	0.0011	0.010890753
GO:0036508	protein alpha-1,2-demannosylation	12	0.156212591	0.0011	0.010890753
GO:0003190	atrioventricular valve formation	5	0.156165122	0.0234	0.02817551
GO:0060973	cell migration involved in heart development	8	0.156114651	0.0433	0.046157928
GO:1903651	positive regulation of cytoplasmic transport	9	0.15568643	0.021	0.026005997
GO:0042772	DNA damage response, signal transduction resulting in transcription	9	0.155417626	0.0321	0.035976391
GO:0034340	response to type I interferon	33	0.155279566	0.0086	0.016782045
GO:0030970	retrograde protein transport, ER to cytosol	17	0.155190965	0.0212	0.026203164
GO:1903513	endoplasmic reticulum to cytosol transport	17	0.155190965	0.0212	0.026203164
GO:0006517	protein deglycosylation	14	0.155155816	0.002	0.012314604
GO:0051549	positive regulation of keratinocyte migration	5	0.154878666	0.0027	0.012827773
GO:0071888	macrophage apoptotic process	5	0.154875815	0.0411	0.044080913
GO:0048486	parasympathetic nervous system development	7	0.154745792	0.0135	0.020081554
GO:0045622	regulation of T-helper cell differentiation	11	0.154612747	0.0111	0.018389742
GO:0055012	ventricular cardiac muscle cell differentiation	8	0.15415105	0.0085	0.016693954
GO:0045086	positive regulation of interleukin-2 biosynthetic process	5	0.154108969	0.0445	0.047271541
GO:0021516	dorsal spinal cord development	7	0.154027187	0.012	0.018931514
GO:0044458	motile cilium assembly	5	0.153939739	0.0398	0.042885501
GO:0035907	dorsal aorta development	5	0.153690171	0.0057	0.01480566
GO:0035912	dorsal aorta morphogenesis	5	0.153690171	0.0057	0.01480566
GO:1904706	negative regulation of vascular smooth muscle cell proliferation	10	0.153573162	0.0475	0.049962707
GO:0009113	purine nucleobase biosynthetic process	5	0.15314309	0.0198	0.025062084
GO:0071816	tail-anchored membrane protein insertion into ER membrane	6	0.152859529	0.0175	0.023154462
GO:0003084	positive regulation of systemic arterial blood pressure	5	0.15283573	0.028	0.032186083
GO:0019400	alditol metabolic process	7	0.152768423	0.0306	0.034617335
GO:0001867	complement activation, lectin pathway	5	0.152701227	0.0151	0.02121706
GO:0072528	pyrimidine-containing compound biosynthetic process	22	0.152609992	0.0143	0.020629391

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1902667	regulation of axon guidance	10	0.152563745	0.0405	0.043493871
GO:0003171	atrioventricular valve development	14	0.152258531	0.0191	0.02440579
GO:0003181	atrioventricular valve morphogenesis	14	0.152258531	0.0191	0.02440579
GO:1903423	positive regulation of synaptic vesicle recycling	5	0.152096614	0.0059	0.014942532
GO:1901070	guanosine-containing compound biosynthetic process	7	0.151924867	0.0172	0.022941269
GO:0046112	nucleobase biosynthetic process	7	0.15168274	0.0137	0.020264364
GO:0001919	regulation of receptor recycling	11	0.151565412	0.0251	0.029642198
GO:0042634	regulation of hair cycle	12	0.151196604	0.0224	0.027324219
GO:0006342	chromatin silencing	10	0.15104923	0.014	0.020462083
GO:0009048	dosage compensation by inactivation of X chromosome	5	0.150964097	0.007	0.015816335
GO:0045048	protein insertion into ER membrane	7	0.150787537	0.0117	0.018739446
GO:0070233	negative regulation of T cell apoptotic process	6	0.150720187	0.0112	0.018392048
GO:0016339	calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules	13	0.150502578	0.0004	0.008964341
GO:0060644	mammary gland epithelial cell differentiation	9	0.149942356	0.0107	0.018084595
GO:0002711	positive regulation of T cell mediated immunity	9	0.149697164	0.0163	0.022248961
GO:0008298	intracellular mRNA localization	5	0.149685675	0.0376	0.040911404
GO:0052564	response to immune response of other organism involved in symbiotic interaction	5	0.149274392	0.0288	0.032902905
GO:0052572	response to host immune response	5	0.149274392	0.0288	0.032902905
GO:0016577	histone demethylation	7	0.149113937	0.0096	0.017302743
GO:0070076	histone lysine demethylation	7	0.149113937	0.0096	0.017302743
GO:1903715	regulation of aerobic respiration	6	0.148541107	0.0061	0.015143924
GO:0006312	mitotic recombination	7	0.148519542	0.01	0.017574468
GO:0033483	gas homeostasis	5	0.148423839	0.0262	0.030579007
GO:0006978	DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator	8	0.148341232	0.0345	0.038068511
GO:0006337	nucleosome disassembly	7	0.148119329	0.0209	0.025971158
GO:0002866	positive regulation of acute inflammatory response to antigenic stimulus	6	0.147823242	0.0434	0.046247475
GO:0010765	positive regulation of sodium ion transport	12	0.147801321	0.0094	0.017156187
GO:1901388	regulation of transforming growth factor beta activation	5	0.147734999	0.034	0.037588528
GO:0043371	negative regulation of CD4-positive, alpha-beta T cell differentiation	6	0.14770187	0.0265	0.03085441
GO:1901984	negative regulation of protein acetylation	12	0.147057648	0.0254	0.029880529
GO:0060325	face morphogenesis	11	0.146987401	0.0336	0.037253154
GO:0009218	pyrimidine ribonucleotide metabolic process	13	0.146794537	0.0189	0.024289798
GO:2000009	negative regulation of protein localization to cell surface	7	0.146350766	0.0228	0.027701114
GO:0009208	pyrimidine ribonucleoside triphosphate metabolic process	8	0.14633649	0.0176	0.023223003
GO:0007256	activation of JNKK activity	6	0.14624044	0.003	0.013210967
GO:0051154	negative regulation of striated muscle cell differentiation	14	0.145852352	0.0102	0.0177
GO:0006089	lactate metabolic process	7	0.145744524	0.0347	0.038238117
GO:0006213	pyrimidine nucleoside metabolic process	23	0.145334066	0.0284	0.032523034
GO:0060323	head morphogenesis	12	0.144597059	0.0427	0.045577146
GO:0098976	excitatory chemical synaptic transmission	7	0.144374878	0.0025	0.012769435
GO:0046827	positive regulation of protein export from nucleus	5	0.143518512	0.0216	0.026572596
GO:0030042	actin filament depolymerization	22	0.143323331	0.0411	0.044080913
GO:0009220	pyrimidine ribonucleotide biosynthetic process	12	0.143199338	0.0153	0.021378589
GO:0006221	pyrimidine nucleotide biosynthetic process	17	0.142896321	0.0288	0.032902905
GO:0048670	regulation of collateral sprouting	6	0.142321335	0.0001	0.004220438
GO:0045646	regulation of erythrocyte differentiation	16	0.142080076	0.0139	0.020388077
GO:0036150	phosphatidylserine acyl-chain remodeling	6	0.141673874	0.0347	0.038238117
GO:0071679	commissural neuron axon guidance	8	0.141605576	0.0421	0.045028154
GO:0046051	UTP metabolic process	6	0.141313646	0.0254	0.029880529
GO:0099022	vesicle tethering	6	0.141307599	0.0153	0.021378589
GO:0006222	UMP biosynthetic process	6	0.141028573	0.0336	0.037253154
GO:0009173	pyrimidine ribonucleoside monophosphate metabolic process	6	0.141028573	0.0336	0.037253154
GO:0009174	pyrimidine ribonucleoside monophosphate biosynthetic process	6	0.141028573	0.0336	0.037253154
GO:0046049	UMP metabolic process	6	0.141028573	0.0336	0.037253154
GO:0045625	regulation of T-helper 1 cell differentiation	5	0.140951042	0.0468	0.049334111
GO:0035162	embryonic hemopoiesis	8	0.140238036	0.0178	0.023348367
GO:0006241	CTP biosynthetic process	7	0.140107856	0.016	0.022026667
GO:0009209	pyrimidine ribonucleoside triphosphate biosynthetic process	7	0.140107856	0.016	0.022026667
GO:0046036	CTP metabolic process	7	0.140107856	0.016	0.022026667
GO:0046131	pyrimidine ribonucleoside metabolic process	13	0.139827795	0.014	0.020462083
GO:0060394	negative regulation of pathway-restricted SMAD protein phosphorylation	5	0.139610163	0.0441	0.046872463
GO:0055075	potassium ion homeostasis	6	0.138862235	0.0348	0.038319101
GO:0002070	epithelial cell maturation	9	0.138830705	0.0052	0.014616626
GO:0001755	neural crest cell migration	15	0.138152145	0.0178	0.023348367
GO:1905208	negative regulation of cardiocyte differentiation	9	0.137369346	0.0118	0.018836996
GO:0010107	potassium ion import	8	0.136822668	0.0261	0.030517735
GO:1990573	potassium ion import across plasma membrane	8	0.136822668	0.0261	0.030517735
GO:0046132	pyrimidine ribonucleoside biosynthetic process	11	0.136737853	0.0173	0.023005658
GO:1904996	positive regulation of leukocyte adhesion to vascular endothelial cell	5	0.136684019	0.0332	0.036915846
GO:0007549	dosage compensation	6	0.136683372	0.0181	0.023607986
GO:0036152	phosphatidylethanolamine acyl-chain remodeling	9	0.135673594	0.0288	0.032902905
GO:0014832	urinary bladder smooth muscle contraction	5	0.135516257	0.0199	0.025133639
GO:0014848	urinary tract smooth muscle contraction	5	0.135516257	0.0199	0.025133639
GO:0072396	response to cell cycle checkpoint signaling	5	0.135061436	0.0013	0.011218806
GO:0072402	response to DNA integrity checkpoint signaling	5	0.135061436	0.0013	0.011218806
GO:0072423	response to DNA damage checkpoint signaling	5	0.135061436	0.0013	0.011218806
GO:0032736	positive regulation of interleukin-13 production	5	0.134840635	0.0192	0.02450649
GO:1904294	positive regulation of ERAD pathway	5	0.134491032	0.0171	0.022860624
GO:0036151	phosphatidylcholine acyl-chain remodeling	10	0.134485201	0.0325	0.036312077
GO:0034643	establishment of mitochondrion localization, microtubule-mediated	8	0.13439631	0.0095	0.01725157
GO:0047497	mitochondrion transport along microtubule	8	0.13439631	0.0095	0.01725157
GO:0033631	cell-cell adhesion mediated by integrin	6	0.133246948	0.0378	0.041067193

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0046134	pyrimidine nucleoside biosynthetic process	16	0.132899353	0.0219	0.026855949
GO:0006071	glycerol metabolic process	5	0.132289751	0.0404	0.043394538
GO:0018242	protein O-linked glycosylation via serine	5	0.132140994	0.0173	0.023005658
GO:0006183	GTP biosynthetic process	5	0.13158899	0.0223	0.027242468
GO:0006228	UTP biosynthetic process	5	0.13158899	0.0223	0.027242468
GO:0042789	mRNA transcription from RNA polymerase II promoter	5	0.13131843	0.0303	0.034331687
GO:0019042	viral latency	5	0.131111363	0.0098	0.017418875
GO:0019043	establishment of viral latency	5	0.131111363	0.0098	0.017418875
GO:0075713	establishment of integrated proviral latency	5	0.131111363	0.0098	0.017418875
GO:1900122	positive regulation of receptor binding	6	0.130389308	0.0032	0.013333753
GO:0032986	protein-DNA complex disassembly	8	0.129834334	0.0404	0.043394538
GO:0009148	pyrimidine nucleoside triphosphate biosynthetic process	10	0.129268497	0.0252	0.029736
GO:0036363	transforming growth factor beta activation	6	0.129071062	0.0361	0.039494834
GO:0045648	positive regulation of erythrocyte differentiation	10	0.128230831	0.0087	0.016840777
GO:0008340	determination of adult lifespan	6	0.128190576	0.0347	0.038238117
GO:2000726	negative regulation of cardiac muscle cell differentiation	8	0.127836718	0.0256	0.03006687
GO:0010171	body morphogenesis	18	0.127740794	0.0251	0.029642198
GO:0009129	pyrimidine nucleoside monophosphate metabolic process	7	0.126184267	0.0247	0.029271449
GO:0009130	pyrimidine nucleoside monophosphate biosynthetic process	7	0.126184267	0.0247	0.029271449
GO:0003148	outflow tract septum morphogenesis	16	0.123506121	0.0106	0.018010344
GO:0030011	maintenance of cell polarity	7	0.12241242	0.0206	0.025725529
GO:1902307	positive regulation of sodium ion transmembrane transport	8	0.122267431	0.028	0.032186083
GO:0032633	interleukin-4 production	13	0.121902194	0.0171	0.022860624
GO:0032673	regulation of interleukin-4 production	13	0.121902194	0.0171	0.022860624
GO:0032239	regulation of nucleobase-containing compound transport	6	0.121841441	0.0417	0.044666432
GO:2000059	negative regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process	7	0.119100391	0.031	0.034967226
GO:0003174	mitral valve development	7	0.119074661	0.016	0.022026667
GO:0003183	mitral valve morphogenesis	7	0.119074661	0.016	0.022026667
GO:0045736	negative regulation of cyclin-dependent protein serine/threonine kinase activity	16	0.116446194	0.0253	0.029811412
GO:0032753	positive regulation of interleukin-4 production	12	0.115891301	0.0149	0.021043429
GO:1904030	negative regulation of cyclin-dependent protein kinase activity	17	0.115847555	0.0241	0.028760826
GO:0048070	regulation of developmental pigmentation	5	0.111384839	0.0221	0.027038129
GO:0061052	negative regulation of cell growth involved in cardiac muscle cell development	7	0.110247398	0.0465	0.049080504
GO:0002069	columnar/cuboidal epithelial cell maturation	6	0.101164372	0.0074	0.015911789

Reward SUBC positive

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0006729	tetrahydrobiopterin biosynthetic process	5	0.535186615	< 0.001	< 0.001
GO:0046146	tetrahydrobiopterin metabolic process	5	0.535186615	< 0.001	< 0.001
GO:0000054	ribosomal subunit export from nucleus	5	0.516808237	0.0001	0.000877824
GO:0033750	ribosome localization	5	0.516808237	0.0001	0.000877824
GO:0033753	establishment of ribosome localization	5	0.516808237	0.0001	0.000877824
GO:0001514	selenocysteine incorporation	5	0.514028314	0.0002	0.001341684
GO:0006451	translational readthrough	5	0.514028314	0.0002	0.001341684
GO:0034975	protein folding in endoplasmic reticulum	6	0.497039897	< 0.001	< 0.001
GO:0060456	positive regulation of digestive system process	5	0.495444015	< 0.001	< 0.001
GO:0032817	regulation of natural killer cell proliferation	5	0.48993565	0.0005	0.002177563
GO:0032819	positive regulation of natural killer cell proliferation	5	0.48993565	0.0005	0.002177563
GO:0032525	somite rostral/caudal axis specification	5	0.488597169	< 0.001	< 0.001
GO:0002579	positive regulation of antigen processing and presentation	5	0.487052767	< 0.001	< 0.001
GO:0071428	rRNA-containing ribonucleoprotein complex export from nucleus	6	0.485971686	0.0001	0.000877824
GO:0051096	positive regulation of helicase activity	5	0.483294723	< 0.001	< 0.001
GO:0009263	deoxyribonucleotide biosynthetic process	6	0.47979408	0.0008	0.002313249
GO:0043508	negative regulation of JUN kinase activity	8	0.475933076	0.0001	0.000877824
GO:0045329	carnitine biosynthetic process	5	0.475881596	< 0.001	< 0.001
GO:0046689	response to mercury ion	5	0.475881596	0.0001	0.000877824
GO:0001787	natural killer cell proliferation	6	0.475203775	0.0009	0.002399874
GO:0010421	hydrogen peroxide-mediated programmed cell death	5	0.474337194	0.0001	0.000877824
GO:0097468	programmed cell death in response to reactive oxygen species	5	0.474337194	0.0001	0.000877824
GO:0008105	asymmetric protein localization	7	0.472145615	0.0001	0.000877824
GO:0051095	regulation of helicase activity	7	0.468284611	< 0.001	< 0.001
GO:0070424	regulation of nucleotide-binding oligomerization domain containing signaling pathway	5	0.467644788	0.0001	0.000877824
GO:0035434	copper ion transmembrane transport	5	0.465637066	0.0006	0.002177563
GO:0051764	actin crosslink formation	5	0.464247104	< 0.001	< 0.001
GO:0042559	pteridine-containing compound biosynthetic process	11	0.45971686	< 0.001	< 0.001
GO:0051280	negative regulation of release of sequestered calcium ion into cytosol	5	0.458584299	< 0.001	< 0.001
GO:0051284	positive regulation of sequestering of calcium ion	5	0.458584299	< 0.001	< 0.001
GO:0051974	negative regulation of telomerase activity	5	0.458275418	0.0002	0.001341684
GO:0045955	negative regulation of calcium ion-dependent exocytosis	6	0.457014157	0.0009	0.002399874
GO:0071236	cellular response to antibiotic	9	0.455998856	0.0002	0.001341684
GO:0031573	intra-S DNA damage checkpoint	5	0.454723295	0.0004	0.002007244
GO:0042711	maternal behavior	5	0.454517375	< 0.001	< 0.001
GO:0060746	parental behavior	5	0.454517375	< 0.001	< 0.001
GO:0034063	stress granule assembly	9	0.452595453	0.0001	0.000877824
GO:0009265	2'-deoxyribonucleotide biosynthetic process	5	0.45045045	0.0009	0.002399874
GO:0046385	deoxyribose phosphate biosynthetic process	5	0.45045045	0.0009	0.002399874
GO:1904667	negative regulation of ubiquitin protein ligase activity	7	0.447104247	0.0002	0.001341684
GO:0001866	NK T cell proliferation	5	0.446229086	0.0005	0.002177563
GO:0036480	neuron intrinsic apoptotic signaling pathway in response to oxidative stress	5	0.444015444	0.0008	0.002313249
GO:1903376	regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway	5	0.444015444	0.0008	0.002313249
GO:0048642	negative regulation of skeletal muscle tissue development	5	0.443912484	0.0018	0.003459409
GO:0033194	response to hydroperoxide	13	0.443758044	< 0.001	< 0.001
GO:2000669	negative regulation of dendritic cell apoptotic process	5	0.443140283	0.0005	0.002177563
GO:0009597	detection of virus	6	0.442642643	0.0001	0.000877824
GO:0002480	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent	9	0.441841842	0.0012	0.002741075
GO:0051315	attachment of mitotic spindle microtubules to kinetochore	8	0.441537967	0.0001	0.000877824
GO:0071671	regulation of smooth muscle cell chemotaxis	6	0.441441441	< 0.001	< 0.001
GO:1903862	positive regulation of oxidative phosphorylation	5	0.441235521	0.0001	0.000877824
GO:0045351	type I interferon biosynthetic process	5	0.441235521	< 0.001	< 0.001
GO:0032928	regulation of superoxide anion generation	16	0.441071429	0.0005	0.002177563
GO:0035520	monoubiquitinated protein deubiquitination	5	0.440772201	0.0025	0.004279479
GO:0071638	negative regulation of monocyte chemotactic protein-1 production	5	0.44020592	0.0014	0.002975058
GO:0048532	anatomical structure arrangement	5	0.439073359	< 0.001	< 0.001
GO:0033864	positive regulation of NAD(P)H oxidase activity	6	0.438009438	< 0.001	< 0.001
GO:0045579	positive regulation of B cell differentiation	8	0.437612613	< 0.001	< 0.001
GO:0019511	peptidyl-proline hydroxylation	7	0.437065637	< 0.001	< 0.001
GO:0072641	type I interferon secretion	6	0.437022737	0.0005	0.002177563
GO:0072642	interferon-alpha secretion	6	0.437022737	0.0005	0.002177563
GO:1902739	regulation of interferon-alpha secretion	6	0.437022737	0.0005	0.002177563
GO:1902741	positive regulation of interferon-alpha secretion	6	0.437022737	0.0005	0.002177563
GO:0097201	negative regulation of transcription from RNA polymerase II promoter in response to stress	8	0.436840412	0.0015	0.003088691
GO:0010869	regulation of receptor biosynthetic process	11	0.436784837	0.0007	0.002248538
GO:1901739	regulation of myoblast fusion	8	0.436454311	0.0019	0.003579279
GO:0045176	apical protein localization	5	0.436241956	0.0001	0.000877824
GO:0010944	negative regulation of transcription by competitive promoter binding	7	0.435999265	< 0.001	< 0.001
GO:0032056	positive regulation of translation in response to stress	5	0.434954955	< 0.001	< 0.001
GO:0010870	positive regulation of receptor biosynthetic process	8	0.434073359	0.0007	0.002248538
GO:0006825	copper ion transport	12	0.433998284	0.0006	0.002177563
GO:0061469	regulation of type B pancreatic cell proliferation	5	0.433925354	0.0013	0.002859821
GO:1903897	regulation of PERK-mediated unfolded protein response	6	0.432947233	0.0021	0.003804235
GO:0032930	positive regulation of superoxide anion generation	12	0.432882883	0.0011	0.002610912
GO:0032800	receptor biosynthetic process	13	0.432531433	0.0008	0.002313249
GO:0051132	NK T cell activation	6	0.432303732	0.0013	0.002859821
GO:0032875	regulation of DNA endoreduplication	5	0.43021879	0.0008	0.002313249
GO:0043102	amino acid salvage	6	0.429343629	0.0002	0.001341684
GO:0071265	L-methionine biosynthetic process	6	0.429343629	0.0002	0.001341684
GO:0071267	L-methionine salvage	6	0.429343629	0.0002	0.001341684
GO:1903209	positive regulation of oxidative stress-induced cell death	11	0.429203229	0.0001	0.000877824

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0003174	mitral valve development	6	0.428528529	< 0.001	< 0.001
GO:0003183	mitral valve morphogenesis	6	0.428528529	< 0.001	< 0.001
GO:0071763	nuclear membrane organization	5	0.428365508	0.0004	0.002007244
GO:0070525	tRNA threonylcarbamoyladenosine metabolic process	8	0.427767053	0.0034	0.005263104
GO:0042554	superoxide anion generation	17	0.426572791	0.0005	0.002177563
GO:0070208	protein heterotrimerization	7	0.426034197	0.0006	0.002177563
GO:0021542	dentate gyrus development	6	0.425053625	< 0.001	< 0.001
GO:1901033	positive regulation of response to reactive oxygen species	7	0.424416253	0.0001	0.000877824
GO:0033860	regulation of NAD(P)H oxidase activity	7	0.424195624	0.0001	0.000877824
GO:0035795	negative regulation of mitochondrial membrane permeability	5	0.424092664	0.0009	0.002399874
GO:1901741	positive regulation of myoblast fusion	7	0.424048538	0.0028	0.004605006
GO:0042023	DNA endoreduplication	6	0.423509224	< 0.001	< 0.001
GO:0009086	methionine biosynthetic process	9	0.423223223	0.0002	0.001341684
GO:0070933	histone H4 deacetylation	6	0.422779923	0.0008	0.002313249
GO:0044342	type B pancreatic cell proliferation	7	0.421879022	0.0017	0.003334595
GO:1901678	iron coordination entity transport	6	0.420592021	< 0.001	< 0.001
GO:0090343	positive regulation of cell aging	7	0.419599191	0.0006	0.002177563
GO:0051451	myoblast migration	7	0.419047619	0.0006	0.002177563
GO:0030889	negative regulation of B cell proliferation	9	0.418761619	0.0062	0.008281828
GO:1902884	positive regulation of response to oxidative stress	14	0.418293804	0.0001	0.000877824
GO:0060700	regulation of ribonuclease activity	6	0.417932218	0.0006	0.002177563
GO:0090169	regulation of spindle assembly	15	0.417915058	0.0003	0.001720882
GO:0045876	positive regulation of sister chromatid cohesion	7	0.417613532	0.0007	0.002248538
GO:0002082	regulation of oxidative phosphorylation	13	0.417285417	0.0002	0.001341684
GO:0072321	chaperone-mediated protein transport	9	0.417217217	0.0001	0.000877824
GO:0090646	mitochondrial tRNA processing	6	0.417117117	0.0012	0.002741075
GO:0036336	dendritic cell migration	16	0.416618404	0.0008	0.002313249
GO:1902931	negative regulation of alcohol biosynthetic process	5	0.416370656	0.0002	0.001341684
GO:1905063	regulation of vascular smooth muscle cell differentiation	7	0.415922044	0.0003	0.001720882
GO:2001034	positive regulation of double-strand break repair via nonhomologous end joining	7	0.415333701	0.0013	0.002859821
GO:0031340	positive regulation of vesicle fusion	5	0.414826255	< 0.001	< 0.001
GO:0017062	respiratory chain complex III assembly	6	0.414714715	0.0006	0.002177563
GO:0034551	mitochondrial respiratory chain complex III assembly	6	0.414714715	0.0006	0.002177563
GO:0097033	mitochondrial respiratory chain complex III biogenesis	6	0.414714715	0.0006	0.002177563
GO:2000774	positive regulation of cellular senescence	6	0.414586015	0.0005	0.002177563
GO:0002385	mucosal immune response	6	0.414500215	0.0005	0.002177563
GO:0042532	negative regulation of tyrosine phosphorylation of STAT protein	6	0.414242814	0.0003	0.001720882
GO:0006999	nuclear pore organization	8	0.414157014	0.0005	0.002177563
GO:0060287	epithelial cilium movement involved in determination of left/right asymmetry	5	0.413899614	0.0007	0.002248538
GO:0045820	negative regulation of glycolytic process	5	0.413230373	0.0042	0.006097175
GO:0051195	negative regulation of cofactor metabolic process	5	0.413230373	0.0042	0.006097175
GO:0051198	negative regulation of coenzyme metabolic process	5	0.413230373	0.0042	0.006097175
GO:1900409	positive regulation of cellular response to oxidative stress	13	0.413186813	0.0001	0.000877824
GO:0090322	regulation of superoxide metabolic process	24	0.412172887	0.0006	0.002177563
GO:0002604	regulation of dendritic cell antigen processing and presentation	6	0.411840412	0.0022	0.003910907
GO:0048102	autophagic cell death	7	0.411619783	0.0021	0.003804235
GO:0002921	negative regulation of humoral immune response	5	0.411531532	0.002	0.003693422
GO:0045916	negative regulation of complement activation	5	0.411531532	0.002	0.003693422
GO:2000258	negative regulation of protein activation cascade	5	0.411531532	0.002	0.003693422
GO:0009120	deoxyribonucleoside metabolic process	7	0.411104983	0.0009	0.002399874
GO:0002475	antigen processing and presentation via MHC class Ib	6	0.411068211	0.0036	0.005475609
GO:0009130	pyrimidine nucleoside monophosphate biosynthetic process	10	0.411016731	0.0015	0.003088691
GO:0002834	regulation of response to tumor cell	7	0.410884354	< 0.001	< 0.001
GO:0002837	regulation of immune response to tumor cell	7	0.410884354	< 0.001	< 0.001
GO:0046498	S-adenosylhomocysteine metabolic process	6	0.41042471	0.0014	0.002975058
GO:0035994	response to muscle stretch	5	0.41024453	0.0018	0.003459409
GO:0051292	nuclear pore complex assembly	6	0.40956671	0.0002	0.001341684
GO:0080182	histone H3-K4 trimethylation	8	0.409427284	0.0006	0.002177563
GO:0000076	DNA replication checkpoint	6	0.409395109	0.0037	0.005561344
GO:0017004	cytochrome complex assembly	19	0.409225767	0.0009	0.002399874
GO:0046007	negative regulation of activated T cell proliferation	5	0.408906049	0.0028	0.004605006
GO:0072050	S-shaped body morphogenesis	5	0.408442728	0.0002	0.001341684
GO:0071712	ER-associated misfolded protein catabolic process	5	0.407824968	< 0.001	< 0.001
GO:0002251	organ or tissue specific immune response	7	0.40728075	0.001	0.002498236
GO:0003180	aortic valve morphogenesis	16	0.40719112	0.0001	0.000877824
GO:0051151	negative regulation of smooth muscle cell differentiation	10	0.406924067	0.0012	0.002741075
GO:0036363	transforming growth factor beta activation	6	0.406778207	0.0006	0.002177563
GO:0032486	Rap protein signal transduction	7	0.40676595	0.0009	0.002399874
GO:0001911	negative regulation of leukocyte mediated cytotoxicity	8	0.406306306	0.0009	0.002399874
GO:0031342	negative regulation of cell killing	8	0.406306306	0.0009	0.002399874
GO:0051409	response to nitrosative stress	7	0.406251149	0.0001	0.000877824
GO:0003084	positive regulation of systemic arterial blood pressure	6	0.405619906	0.0001	0.000877824
GO:1904026	regulation of collagen fibril organization	5	0.405559846	0.002	0.003693422
GO:0032823	regulation of natural killer cell differentiation	7	0.405552491	0.0004	0.002007244
GO:0070900	mitochondrial tRNA modification	5	0.405199485	0.0057	0.007745437
GO:0070901	mitochondrial tRNA methylation	5	0.405199485	0.0057	0.007745437
GO:1900864	mitochondrial RNA modification	5	0.405199485	0.0057	0.007745437
GO:0045047	protein targeting to ER	95	0.404077762	0.0009	0.002399874
GO:0036302	atrioventricular canal development	5	0.404066924	0.0048	0.006748379
GO:0003176	aortic valve development	18	0.403918204	0.0005	0.002177563
GO:1900122	positive regulation of receptor binding	5	0.403861004	0.0021	0.003804235
GO:2000508	regulation of dendritic cell chemotaxis	5	0.403861004	0.0045	0.006417207
GO:1901673	regulation of mitotic spindle assembly	14	0.403842618	0.0005	0.002177563

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:2000973	regulation of pro-B cell differentiation	5	0.403655084	0.0002	0.001341684
GO:0034091	regulation of maintenance of sister chromatid cohesion	6	0.403389103	0.0001	0.000877824
GO:0034182	regulation of maintenance of mitotic sister chromatid cohesion	6	0.403389103	0.0001	0.000877824
GO:0060405	regulation of penile erection	5	0.403294723	< 0.001	< 0.001
GO:0002115	store-operated calcium entry	5	0.402831403	< 0.001	< 0.001
GO:0061419	positive regulation of transcription from RNA polymerase II promoter in response to hypoxia	5	0.402676963	0.0073	0.009463568
GO:0032060	bleb assembly	10	0.402548263	0.0012	0.002741075
GO:0071731	response to nitric oxide	10	0.402419562	0.0006	0.002177563
GO:0006614	SRP-dependent cotranslational protein targeting to membrane	90	0.402379522	0.001	0.002498236
GO:0071394	cellular response to testosterone stimulus	5	0.402007722	0.0021	0.003804235
GO:0010560	positive regulation of glycoprotein biosynthetic process	12	0.401951952	0.0002	0.001341684
GO:0006222	UMP biosynthetic process	7	0.401581173	0.0017	0.003334595
GO:0009173	pyrimidine ribonucleoside monophosphate metabolic process	7	0.401581173	0.0017	0.003334595
GO:0009174	pyrimidine ribonucleoside monophosphate biosynthetic process	7	0.401581173	0.0017	0.003334595
GO:0046049	UMP metabolic process	7	0.401581173	0.0017	0.003334595
GO:0022417	protein maturation by protein folding	6	0.401415701	0.0005	0.002177563
GO:1904732	regulation of electron carrier activity	6	0.401287001	0.0025	0.004279479
GO:0002327	immature B cell differentiation	5	0.401184041	0.0015	0.003088691
GO:0042276	error-prone translesion synthesis	15	0.401029601	0.0002	0.001341684
GO:0021783	preganglionic parasympathetic fiber development	5	0.400823681	< 0.001	< 0.001
GO:0035456	response to interferon-beta	17	0.400166553	0.0007	0.002248538
GO:1901533	negative regulation of hematopoietic progenitor cell differentiation	7	0.399705828	0.0007	0.002248538
GO:0051444	negative regulation of ubiquitin-protein transferase activity	12	0.39963535	0.0001	0.000877824
GO:0032825	positive regulation of natural killer cell differentiation	6	0.3996139	0.0008	0.002313249
GO:0006613	cotranslational protein targeting to membrane	93	0.399316367	0.0009	0.002399874
GO:0072599	establishment of protein localization to endoplasmic reticulum	97	0.399307408	0.0006	0.002177563
GO:0043101	purine-containing compound salvage	13	0.399267399	0.0002	0.001341684
GO:0000578	embryonic axis specification	17	0.399212658	< 0.001	< 0.001
GO:0006369	termination of RNA polymerase II transcription	26	0.398920899	< 0.001	< 0.001
GO:0060019	radial glial cell differentiation	6	0.398670099	0.0004	0.002007244
GO:2001198	regulation of dendritic cell differentiation	6	0.398627199	0.0001	0.000877824
GO:0044829	positive regulation by host of viral genome replication	6	0.398627199	0.0002	0.001341684
GO:0019755	one-carbon compound transport	5	0.398558559	0.0009	0.002399874
GO:0018023	peptidyl-lysine trimethylation	25	0.398496782	0.0008	0.002313249
GO:0060009	Sertoli cell development	8	0.398487773	0.0003	0.001720882
GO:0045777	positive regulation of blood pressure	15	0.398438438	< 0.001	< 0.001
GO:0032740	positive regulation of interleukin-17 production	6	0.398326898	0.0022	0.003910907
GO:0071360	cellular response to exogenous dsRNA	14	0.397756941	0.0021	0.003804235
GO:0001768	establishment of T cell polarity	5	0.397683398	0.001	0.002498236
GO:0008334	histone mRNA metabolic process	18	0.397154297	< 0.001	< 0.001
GO:1902459	positive regulation of stem cell population maintenance	7	0.397131826	0.0002	0.001341684
GO:0032196	transposition	6	0.396954097	0.0006	0.002177563
GO:0071732	cellular response to nitric oxide	7	0.39672734	0.0012	0.002741075
GO:0070474	positive regulation of uterine smooth muscle contraction	5	0.396705277	0.0001	0.000877824
GO:0009396	folic acid-containing compound biosynthetic process	7	0.396396396	0.0005	0.002177563
GO:0070431	nucleotide-binding oligomerization domain containing 2 signaling pathway	6	0.396353496	0.0007	0.002248538
GO:0034661	ncRNA catabolic process	13	0.395921196	< 0.001	< 0.001
GO:0043616	keratinocyte proliferation	15	0.395555556	< 0.001	< 0.001
GO:0031392	regulation of prostaglandin biosynthetic process	5	0.395469755	< 0.001	< 0.001
GO:2001279	regulation of unsaturated fatty acid biosynthetic process	5	0.395469755	< 0.001	< 0.001
GO:1902358	sulfate transmembrane transport	6	0.395066495	< 0.001	< 0.001
GO:0009067	aspartate family amino acid biosynthetic process	14	0.394962309	0.0001	0.000877824
GO:0043628	ncRNA 3'-end processing	9	0.394737595	< 0.001	< 0.001
GO:0014889	muscle atrophy	6	0.394551695	0.0035	0.005358035
GO:0035356	cellular triglyceride homeostasis	5	0.394543115	0.0001	0.000877824
GO:0006616	SRP-dependent cotranslational protein targeting to membrane, translocation	5	0.393925354	0.002	0.003693422
GO:0043094	cellular metabolic compound salvage	27	0.393393393	0.0001	0.000877824
GO:0048539	bone marrow development	5	0.392998713	0.0013	0.002859821
GO:0002407	dendritic cell chemotaxis	14	0.39297665	0.0019	0.003579279
GO:0000183	chromatin silencing at rDNA	10	0.392818533	0.0026	0.004377754
GO:0006206	pyrimidine nucleobase metabolic process	11	0.392675793	0.0004	0.002007244
GO:2000059	negative regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process	12	0.392492492	0.0008	0.002313249
GO:1904385	cellular response to angiotensin	10	0.392406692	0.001	0.002498236
GO:0033617	mitochondrial respiratory chain complex IV assembly	12	0.392342342	0.0009	0.002399874
GO:0097034	mitochondrial respiratory chain complex IV biogenesis	12	0.392342342	0.0009	0.002399874
GO:0090070	positive regulation of ribosome biogenesis	9	0.392106392	< 0.001	< 0.001
GO:2000234	positive regulation of rRNA processing	9	0.392106392	< 0.001	< 0.001
GO:0070972	protein localization to endoplasmic reticulum	104	0.392065142	0.0004	0.002007244
GO:0032735	positive regulation of interleukin-12 production	19	0.392061234	0.0001	0.000877824
GO:0008340	determination of adult lifespan	7	0.391873506	0.0012	0.002741075
GO:0002396	MHC protein complex assembly	6	0.391720292	0.0025	0.004279479
GO:1990776	response to angiotensin	13	0.391584992	0.0007	0.002248538
GO:0010523	negative regulation of calcium ion transport into cytosol	8	0.390830116	< 0.001	< 0.001
GO:0072257	metanephric nephron tubule epithelial cell differentiation	5	0.390785071	0.0001	0.000877824
GO:0072307	regulation of metanephric nephron tubule epithelial cell differentiation	5	0.390785071	0.0001	0.000877824
GO:0050798	activated T cell proliferation	16	0.390749678	0.0007	0.002248538
GO:0005984	disaccharide metabolic process	5	0.390733591	0.0024	0.004156304
GO:0002176	male germ cell proliferation	5	0.390579151	0.0008	0.002313249
GO:0036093	germ cell proliferation	5	0.390579151	0.0008	0.002313249
GO:0008535	respiratory chain complex IV assembly	13	0.390555391	0.0014	0.002975058
GO:2000371	regulation of DNA topoisomerase (ATP-hydrolyzing) activity	6	0.39021879	0.0012	0.002741075
GO:2000373	positive regulation of DNA topoisomerase (ATP-hydrolyzing) activity	6	0.39021879	0.0012	0.002741075
GO:0009129	pyrimidine nucleoside monophosphate metabolic process	11	0.38970399	0.0028	0.004605006

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1903799	negative regulation of production of miRNAs involved in gene silencing by miRNA	5	0.389292149	0.0108	0.013015961
GO:2000271	positive regulation of fibroblast apoptotic process	5	0.389240669	0.0001	0.000877824
GO:0035458	cellular response to interferon-beta	10	0.389034749	0.0002	0.001341684
GO:2000347	positive regulation of hepatocyte proliferation	6	0.388888889	0.0007	0.002248538
GO:0019614	catechol-containing compound catabolic process	5	0.388777349	0.0001	0.000877824
GO:0042424	catecholamine catabolic process	5	0.388777349	0.0001	0.000877824
GO:0032968	positive regulation of transcription elongation from RNA polymerase II promoter	7	0.388674389	0.0022	0.003910907
GO:0002428	antigen processing and presentation of peptide antigen via MHC class Ib	5	0.388622909	0.0056	0.007655255
GO:0019509	L-methionine biosynthetic process from methylthioadenosine	5	0.388571429	0.0014	0.002975058
GO:0060576	intestinal epithelial cell development	7	0.388564074	0.0031	0.004916949
GO:0032816	positive regulation of natural killer cell activation	13	0.388278388	0.0015	0.003088691
GO:0071157	negative regulation of cell cycle arrest	15	0.388211068	0.0007	0.002248538
GO:0033240	positive regulation of cellular amine metabolic process	7	0.388122817	0.0004	0.002007244
GO:0097048	dendritic cell apoptotic process	6	0.388030888	< 0.001	< 0.001
GO:2000668	regulation of dendritic cell apoptotic process	6	0.388030888	< 0.001	< 0.001
GO:0097435	fibril organization	10	0.387696268	0.001	0.002498236
GO:0048308	organelle inheritance	5	0.387593308	0.0001	0.000877824
GO:0048313	Golgi inheritance	5	0.387593308	0.0001	0.000877824
GO:0034433	steroid esterification	8	0.387580438	0.0009	0.002399874
GO:0034434	sterol esterification	8	0.387580438	0.0009	0.002399874
GO:0034435	cholesterol esterification	8	0.387580438	0.0009	0.002399874
GO:0010745	negative regulation of macrophage derived foam cell differentiation	8	0.387580438	0.0011	0.002610912
GO:1902916	positive regulation of protein polyubiquitination	7	0.387313844	0.0011	0.002610912
GO:0060142	regulation of syncytium formation by plasma membrane fusion	12	0.387087087	0.003	0.004825593
GO:0034471	ncRNA 5'-end processing	6	0.387001287	0.0066	0.008731949
GO:0035965	cardiolipin acyl-chain remodeling	5	0.386975547	0.0019	0.003579279
GO:0060100	positive regulation of phagocytosis, engulfment	7	0.386762272	0.0048	0.006748379
GO:1905155	positive regulation of membrane invagination	7	0.386762272	0.0048	0.006748379
GO:0060368	regulation of Fc receptor mediated stimulatory signaling pathway	6	0.386615187	0.0001	0.000877824
GO:1903306	negative regulation of regulated secretory pathway	13	0.386179586	0.0003	0.001720882
GO:0033962	cytoplasmic mRNA processing body assembly	12	0.386014586	< 0.001	< 0.001
GO:0090023	positive regulation of neutrophil chemotaxis	14	0.385806214	0.0005	0.002177563
GO:0045292	mRNA cis splicing, via spliceosome	10	0.385740026	0.0004	0.002007244
GO:1900102	negative regulation of endoplasmic reticulum unfolded protein response	9	0.385585586	0.0011	0.002610912
GO:0051085	chaperone mediated protein folding requiring cofactor	8	0.385553411	0.0001	0.000877824
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	111	0.385437175	0.0015	0.003088691
GO:0045915	positive regulation of catecholamine metabolic process	5	0.385276705	0.0004	0.002007244
GO:0045964	positive regulation of dopamine metabolic process	5	0.385276705	0.0004	0.002007244
GO:0035812	renal sodium excretion	12	0.385135135	< 0.001	< 0.001
GO:0035813	regulation of renal sodium excretion	12	0.385135135	< 0.001	< 0.001
GO:0055070	copper ion homeostasis	9	0.384841985	0.0001	0.000877824
GO:0031167	rRNA methylation	12	0.384620335	0.002	0.003693422
GO:2001032	regulation of double-strand break repair via nonhomologous end joining	12	0.384598885	< 0.001	< 0.001
GO:0072173	metanephric tubule morphogenesis	5	0.384350064	0.0001	0.000877824
GO:0072282	metanephric nephron tubule morphogenesis	5	0.384350064	0.0001	0.000877824
GO:0060099	regulation of phagocytosis, engulfment	8	0.383751609	0.0062	0.008281828
GO:0006515	misfolded or incompletely synthesized protein catabolic process	12	0.383569284	0.0004	0.002007244
GO:0060333	interferon-gamma-mediated signaling pathway	52	0.383209583	0.0022	0.003910907
GO:0046543	development of secondary female sexual characteristics	5	0.382857143	0.0001	0.000877824
GO:0006983	ER overload response	11	0.382754183	0.0002	0.001341684
GO:0048490	anterograde synaptic vesicle transport	8	0.382625483	0.0002	0.001341684
GO:0099514	synaptic vesicle cytoskeletal transport	8	0.382625483	0.0002	0.001341684
GO:0099517	synaptic vesicle transport along microtubule	8	0.382625483	0.0002	0.001341684
GO:0007131	reciprocal meiotic recombination	16	0.382593308	< 0.001	< 0.001
GO:0035825	reciprocal DNA recombination	16	0.382593308	< 0.001	< 0.001
GO:0061085	regulation of histone H3-K27 methylation	6	0.382453882	< 0.001	< 0.001
GO:0035666	TRIF-dependent toll-like receptor signaling pathway	19	0.382361309	0.0004	0.002007244
GO:0014824	artery smooth muscle contraction	5	0.382187902	0.0008	0.002313249
GO:0006555	methionine metabolic process	10	0.381981982	0.0006	0.002177563
GO:0090162	establishment of epithelial cell polarity	17	0.381966841	0.0024	0.004156304
GO:0006409	tRNA export from nucleus	24	0.381724582	0.0006	0.002177563
GO:0051031	tRNA transport	24	0.381724582	0.0006	0.002177563
GO:0071431	tRNA-containing ribonucleoprotein complex export from nucleus	24	0.381724582	0.0006	0.002177563
GO:0043518	negative regulation of DNA damage response, signal transduction by p53 class mediator	9	0.381695982	0.0001	0.000877824
GO:0006568	tryptophan metabolic process	6	0.381681682	0.0023	0.004032435
GO:0017182	peptidyl-diphthamide metabolic process	6	0.381467181	0.0008	0.002313249
GO:0017183	peptidyl-diphthamide biosynthetic process from peptidyl-histidine	6	0.381467181	0.0008	0.002313249
GO:0018202	peptidyl-histidine modification	6	0.381467181	0.0008	0.002313249
GO:0043084	penile erection	7	0.38143041	< 0.001	< 0.001
GO:0008272	sulfate transport	7	0.381393639	< 0.001	< 0.001
GO:0070986	left/right axis specification	8	0.381048906	< 0.001	< 0.001
GO:0060340	positive regulation of type I interferon-mediated signaling pathway	5	0.380694981	0.008	0.010168329
GO:0045621	positive regulation of lymphocyte differentiation	49	0.380679221	0.0014	0.002975058
GO:0036474	cell death in response to hydrogen peroxide	16	0.38043758	0.0005	0.002177563
GO:1903020	positive regulation of glycoprotein metabolic process	13	0.38037818	0.0003	0.001720882
GO:0007183	SMAD protein complex assembly	10	0.38030888	0.0001	0.000877824
GO:0006349	regulation of gene expression by genetic imprinting	9	0.37995138	< 0.001	< 0.001
GO:0034086	maintenance of sister chromatid cohesion	10	0.37981982	0.0008	0.002313249
GO:0034088	maintenance of mitotic sister chromatid cohesion	10	0.37981982	0.0008	0.002313249
GO:0045683	negative regulation of epidermis development	7	0.379812466	0.0009	0.002399874
GO:0044794	positive regulation by host of viral process	11	0.37964198	0.0006	0.002177563
GO:0090026	positive regulation of monocyte chemotaxis	9	0.37960818	0.0002	0.001341684
GO:0032069	regulation of nuclease activity	14	0.379591837	0.0008	0.002313249

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0035933	glucocorticoid secretion	7	0.379555065	< 0.001	< 0.001
GO:1903054	negative regulation of extracellular matrix organization	8	0.379472329	0.0001	0.000877824
GO:0044849	estrous cycle	8	0.379472329	0.0003	0.001720882
GO:0032727	positive regulation of interferon-alpha production	16	0.379198842	0.0001	0.000877824
GO:0097340	inhibition of cysteine-type endopeptidase activity	5	0.378790219	0.0063	0.008390784
GO:0097341	zymogen inhibition	5	0.378790219	0.0063	0.008390784
GO:0038155	interleukin-23-mediated signaling pathway	5	0.378481338	< 0.001	< 0.001
GO:1904959	regulation of cytochrome-c oxidase activity	5	0.378275418	0.0031	0.004916949
GO:0000966	RNA 5'-end processing	7	0.378231293	0.008	0.010168329
GO:0014842	regulation of skeletal muscle satellite cell proliferation	6	0.378206778	< 0.001	< 0.001
GO:0014857	regulation of skeletal muscle cell proliferation	6	0.378206778	< 0.001	< 0.001
GO:0010887	negative regulation of cholesterol storage	6	0.378035178	0.002	0.003693422
GO:0071494	cellular response to UV-C	6	0.377863578	< 0.001	< 0.001
GO:0006612	protein targeting to membrane	127	0.377853444	0.0008	0.002313249
GO:0034508	centromere complex assembly	23	0.377751665	< 0.001	< 0.001
GO:0006586	indolalkylamine metabolic process	8	0.377702703	0.0002	0.001341684
GO:0042430	indole-containing compound metabolic process	8	0.377702703	0.0002	0.001341684
GO:0032071	regulation of endodeoxyribonuclease activity	6	0.377691978	0.001	0.002498236
GO:0002716	negative regulation of natural killer cell mediated immunity	6	0.377691978	0.0038	0.005666214
GO:0045953	negative regulation of natural killer cell mediated cytotoxicity	6	0.377691978	0.0038	0.005666214
GO:0045582	positive regulation of T cell differentiation	41	0.377668958	0.0028	0.004605006
GO:0035886	vascular smooth muscle cell differentiation	16	0.37733269	0.0006	0.002177563
GO:0016254	preassembly of GPI anchor in ER membrane	13	0.377269577	0.0002	0.001341684
GO:0051571	positive regulation of histone H3-K4 methylation	11	0.377231777	0.0005	0.002177563
GO:0001835	blastocyst hatching	13	0.377170577	0.0003	0.001720882
GO:0035188	hatching	13	0.377170577	0.0003	0.001720882
GO:0071684	organism emergence from protective structure	13	0.377170577	0.0003	0.001720882
GO:0007035	vacuolar acidification	11	0.376974377	0.0077	0.009887588
GO:0051006	positive regulation of lipoprotein lipase activity	5	0.376885457	0.003	0.004825593
GO:0061365	positive regulation of triglyceride lipase activity	5	0.376885457	0.003	0.004825593
GO:0000185	activation of MAPKKK activity	6	0.376662377	0.0031	0.004916949
GO:0006458	'de novo' protein folding	14	0.376558191	0.0002	0.001341684
GO:1901841	regulation of high voltage-gated calcium channel activity	6	0.376447876	< 0.001	< 0.001
GO:0048641	regulation of skeletal muscle tissue development	19	0.376278534	0.0033	0.005149584
GO:0060575	intestinal epithelial cell differentiation	8	0.376254826	0.0033	0.005149584
GO:0045662	negative regulation of myoblast differentiation	14	0.376080162	0.0005	0.002177563
GO:2001014	regulation of skeletal muscle cell differentiation	7	0.375988233	0.0068	0.008946408
GO:0045672	positive regulation of osteoclast differentiation	13	0.375487575	0.0021	0.003804235
GO:0002483	antigen processing and presentation of endogenous peptide antigen	9	0.375403975	0.0079	0.010077402
GO:0036089	cleavage furrow formation	5	0.375341055	0.0068	0.008946408
GO:1905456	regulation of lymphoid progenitor cell differentiation	6	0.375289575	0.0012	0.002741075
GO:0001302	replicative cell aging	5	0.375186615	0.0001	0.000877824
GO:0006578	amino-acid betaine biosynthetic process	7	0.375179261	0.0003	0.001720882
GO:0090281	negative regulation of calcium ion import	8	0.375160875	< 0.001	< 0.001
GO:0010911	regulation of isomerase activity	8	0.375	0.0031	0.004916949
GO:0010912	positive regulation of isomerase activity	8	0.375	0.0031	0.004916949
GO:0045472	response to ether	7	0.374958632	0.0013	0.002859821
GO:0035739	CD4-positive, alpha-beta T cell proliferation	7	0.374848318	0.0051	0.007095023
GO:2000561	regulation of CD4-positive, alpha-beta T cell proliferation	7	0.374848318	0.0051	0.007095023
GO:0060143	positive regulation of syncytium formation by plasma membrane fusion	11	0.374704575	0.004	0.005880507
GO:0060602	branch elongation of an epithelium	9	0.374660375	0.0004	0.002007244
GO:0002864	regulation of acute inflammatory response to antigenic stimulus	7	0.374480603	0.0004	0.002007244
GO:0010837	regulation of keratinocyte proliferation	13	0.374457974	< 0.001	< 0.001
GO:0031293	membrane protein intracellular domain proteolysis	15	0.374414414	0.001	0.002498236
GO:0097186	amelogenesis	7	0.374370289	0.0007	0.002248538
GO:0032814	regulation of natural killer cell activation	17	0.374214551	0.0011	0.002610912
GO:0031062	positive regulation of histone methylation	26	0.374200574	0.0007	0.002248538
GO:0060842	arterial endothelial cell differentiation	6	0.374088374	0.0002	0.001341684
GO:2000737	negative regulation of stem cell differentiation	16	0.374034749	0.0002	0.001341684
GO:0008156	negative regulation of DNA replication	21	0.374014831	0.0001	0.000877824
GO:0010878	cholesterol storage	10	0.374002574	0.0009	0.002399874
GO:0001955	blood vessel maturation	5	0.374002574	0.0023	0.004032435
GO:0002830	positive regulation of type 2 immune response	8	0.373552124	0.0003	0.001720882
GO:0060122	inner ear receptor stereocilium organization	18	0.373516374	0.0001	0.000877824
GO:0045628	regulation of T-helper 2 cell differentiation	7	0.373377459	0.0014	0.002975058
GO:0042492	gamma-delta T cell differentiation	6	0.373359073	0.0003	0.001720882
GO:0036124	histone H3-K9 trimethylation	9	0.373316173	0.0016	0.003223775
GO:0000245	spliceosomal complex assembly	37	0.373160806	< 0.001	< 0.001
GO:0090022	regulation of neutrophil chemotaxis	16	0.373133848	0.0014	0.002975058
GO:0010934	macrophage cytokine production	10	0.373101673	0.0002	0.001341684
GO:0036499	PERK-mediated unfolded protein response	13	0.372992773	0.0072	0.009362497
GO:0033539	fatty acid beta-oxidation using acyl-CoA dehydrogenase	10	0.372895753	0.0006	0.002177563
GO:0001921	positive regulation of receptor recycling	11	0.372809173	0.01	0.012232246
GO:0051412	response to corticosterone	9	0.372744173	0.0005	0.002177563
GO:0071426	ribonucleoprotein complex export from nucleus	88	0.372698023	0.0006	0.002177563
GO:0000956	nuclear-transcribed mRNA catabolic process	172	0.372682649	0.0004	0.002007244
GO:0003190	atrioventricular valve formation	5	0.372664093	0.0009	0.002399874
GO:0000338	protein deneddylation	6	0.372586873	0.0007	0.002248538
GO:0097084	vascular smooth muscle cell development	9	0.372400972	0.0069	0.009046225
GO:0050869	negative regulation of B cell activation	15	0.372389532	0.0011	0.002610912
GO:0032075	positive regulation of nuclease activity	7	0.372347858	0.0033	0.005149584
GO:0050862	positive regulation of T cell receptor signaling pathway	8	0.372297297	0.0003	0.001720882
GO:0071166	ribonucleoprotein complex localization	89	0.372249939	0.0006	0.002177563

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0070098	chemokine-mediated signaling pathway	26	0.372210672	0.0038	0.005666214
GO:0032025	response to cobalt ion	8	0.372039897	0.0034	0.005263104
GO:1903332	regulation of protein folding	7	0.371833058	0.0043	0.006204188
GO:0043174	nucleoside salvage	12	0.371707422	0.0003	0.001720882
GO:0006801	superoxide metabolic process	38	0.371672424	0.0007	0.002248538
GO:1902074	response to salt	10	0.371660232	0.0001	0.000877824
GO:1900246	positive regulation of RIG-I signaling pathway	6	0.371643072	< 0.001	< 0.001
GO:0014841	skeletal muscle satellite cell proliferation	7	0.371538886	0.0001	0.000877824
GO:0014856	skeletal muscle cell proliferation	7	0.371538886	0.0001	0.000877824
GO:0050691	regulation of defense response to virus by host	24	0.371503647	0.0001	0.000877824
GO:0006044	N-acetylglucosamine metabolic process	8	0.371428571	0.0003	0.001720882
GO:0014820	tonic smooth muscle contraction	6	0.371128271	0.0018	0.003459409
GO:0007567	parturition	5	0.370604891	0.0002	0.001341684
GO:0071624	positive regulation of granulocyte chemotaxis	15	0.370570571	0.0011	0.002610912
GO:0060330	regulation of response to interferon-gamma	10	0.37047619	0.0007	0.002248538
GO:0060334	regulation of interferon-gamma-mediated signaling pathway	10	0.37047619	0.0007	0.002248538
GO:0002707	negative regulation of lymphocyte mediated immunity	14	0.370435742	0.0002	0.001341684
GO:0010742	macrophage derived foam cell differentiation	18	0.37039897	0.0005	0.002177563
GO:0090077	foam cell differentiation	18	0.37039897	0.0005	0.002177563
GO:0097421	liver regeneration	21	0.370325427	0.0005	0.002177563
GO:0051574	positive regulation of histone H3-K9 methylation	7	0.370251885	0.0037	0.005561344
GO:0060453	regulation of gastric acid secretion	8	0.370173745	0.0031	0.004916949
GO:0042538	hyperosmotic salinity response	7	0.370031256	< 0.001	< 0.001
GO:1902667	regulation of axon guidance	7	0.369994484	< 0.001	< 0.001
GO:0051084	'de novo' posttranslational protein folding	13	0.36996337	0.0001	0.000877824
GO:0045048	protein insertion into ER membrane	5	0.36993565	0.0015	0.003088691
GO:2000781	positive regulation of double-strand break repair	18	0.36992707	0.0007	0.002248538
GO:0001767	establishment of lymphocyte polarity	6	0.36988417	0.0007	0.002248538
GO:0033033	negative regulation of myeloid cell apoptotic process	8	0.369851995	0.0218	0.023945433
GO:0002866	positive regulation of acute inflammatory response to antigenic stimulus	6	0.36984127	0.0002	0.001341684
GO:0010888	negative regulation of lipid storage	11	0.36974377	0.0051	0.007095023
GO:0060281	regulation of oocyte development	5	0.36962677	0.0006	0.002177563
GO:0045005	DNA-dependent DNA replication maintenance of fidelity	22	0.369392769	0.0001	0.000877824
GO:0071670	smooth muscle cell chemotaxis	8	0.369369369	< 0.001	< 0.001
GO:1904177	regulation of adipose tissue development	6	0.369197769	0.0008	0.002313249
GO:0010224	response to UV-B	9	0.369197769	0.0004	0.002007244
GO:1903204	negative regulation of oxidative stress-induced neuron death	9	0.369169169	0.0004	0.002007244
GO:0006376	mRNA splice site selection	16	0.369160232	0.0003	0.001720882
GO:0006406	mRNA export from nucleus	80	0.369137709	0.0008	0.002313249
GO:0071427	mRNA-containing ribonucleoprotein complex export from nucleus	80	0.369137709	0.0008	0.002313249
GO:0000097	sulfur amino acid biosynthetic process	12	0.369047619	< 0.001	< 0.001
GO:2000678	negative regulation of transcription regulatory region DNA binding	12	0.369047619	< 0.001	< 0.001
GO:0039528	cytoplasmic pattern recognition receptor signaling pathway in response to virus	22	0.369041769	0.0001	0.000877824
GO:0046006	regulation of activated T cell proliferation	14	0.368946498	0.0009	0.002399874
GO:0097709	connective tissue replacement	6	0.368897469	0.001	0.002498236
GO:0035735	intraciliary transport involved in cilium assembly	29	0.368854569	< 0.001	< 0.001
GO:2000104	negative regulation of DNA-dependent DNA replication	13	0.368795169	0.0001	0.000877824
GO:0032607	interferon-alpha production	21	0.36863394	0.0002	0.001341684
GO:0016075	rRNA catabolic process	7	0.368523626	0.001	0.002498236
GO:0010259	multicellular organism aging	19	0.36848879	0.0004	0.002007244
GO:0006402	mRNA catabolic process	190	0.368437309	0.0001	0.000877824
GO:0010528	regulation of transposition	5	0.368391248	0.0017	0.003334595
GO:0010529	negative regulation of transposition	5	0.368391248	0.0017	0.003334595
GO:1902176	negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	12	0.368382668	0.0006	0.002177563
GO:0001696	gastric acid secretion	9	0.368339768	0.0044	0.006304227
GO:2000810	regulation of bicellular tight junction assembly	13	0.368220968	0.0003	0.001720882
GO:0035584	calcium-mediated signaling using intracellular calcium source	5	0.368133848	0.0007	0.002248538
GO:0045542	positive regulation of cholesterol biosynthetic process	5	0.368030888	0.0003	0.001720882
GO:0042149	cellular response to glucose starvation	25	0.367907336	0.0016	0.003223775
GO:0046600	negative regulation of centriole replication	7	0.367677882	0.0015	0.003088691
GO:0010225	response to UV-C	11	0.367614368	< 0.001	< 0.001
GO:1990314	cellular response to insulin-like growth factor stimulus	6	0.367567568	0.0115	0.013693853
GO:0097150	neuronal stem cell population maintenance	17	0.367537285	0.0005	0.002177563
GO:0010955	negative regulation of protein processing	19	0.367391452	0.0045	0.006417207
GO:1903318	negative regulation of protein maturation	19	0.367391452	0.0045	0.006417207
GO:0071027	nuclear RNA surveillance	5	0.367361647	0.0022	0.003910907
GO:0071028	nuclear mRNA surveillance	5	0.367361647	0.0022	0.003910907
GO:0038065	collagen-activated signaling pathway	5	0.367361647	0.0129	0.015093024
GO:0018158	protein oxidation	8	0.367342342	0.0001	0.000877824
GO:2000615	regulation of histone H3-K9 acetylation	6	0.367310167	0.0026	0.004377754
GO:0015949	nucleobase-containing small molecule interconversion	16	0.367181467	0.0003	0.001720882
GO:1901213	regulation of transcription from RNA polymerase II promoter involved in heart development	6	0.367181467	0.0033	0.005149584
GO:0032647	regulation of interferon-alpha production	20	0.367129987	0.0002	0.001341684
GO:0006620	posttranslational protein targeting to membrane	6	0.367095667	0.0004	0.002007244
GO:0009950	dorsal/ventral axis specification	8	0.367052767	< 0.001	< 0.001
GO:0051969	regulation of transmission of nerve impulse	9	0.367024167	0.0003	0.001720882
GO:0031297	replication fork processing	18	0.366966967	< 0.001	< 0.001
GO:0071346	cellular response to interferon-gamma	87	0.366922588	0.0006	0.002177563
GO:0090713	immunological memory process	6	0.366881167	0.0117	0.013882722
GO:1904714	regulation of chaperone-mediated autophagy	6	0.366838267	0.0004	0.002007244
GO:0042274	ribosomal small subunit biogenesis	23	0.366828941	0.0003	0.001720882
GO:0046599	regulation of centriole replication	13	0.366815167	0.0004	0.002007244
GO:0046716	muscle cell cellular homeostasis	12	0.366709567	0.0007	0.002248538

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0070071	proton-transporting two-sector ATPase complex assembly	7	0.366648281	0.0006	0.002177563
GO:0060969	negative regulation of gene silencing	12	0.366645217	0.0044	0.006304227
GO:2001185	regulation of CD8-positive, alpha-beta T cell activation	6	0.366623767	0.0099	0.012121556
GO:0002468	dendritic cell antigen processing and presentation	7	0.366611509	0.0038	0.005666214
GO:0010044	response to aluminum ion	5	0.366537967	0.0036	0.005475609
GO:0051602	response to electrical stimulus	20	0.366396396	0.0002	0.001341684
GO:0060337	type I interferon signaling pathway	53	0.366387412	0.0012	0.002741075
GO:0071357	cellular response to type I interferon	53	0.366387412	0.0012	0.002741075
GO:0045059	positive thymic T cell selection	5	0.366383526	0.0154	0.017651835
GO:0006266	DNA ligation	13	0.366359766	< 0.001	< 0.001
GO:0050847	progesterone receptor signaling pathway	5	0.366332046	< 0.001	< 0.001
GO:0031643	positive regulation of myelination	9	0.366251966	0.0033	0.005149584
GO:0071801	regulation of podosome assembly	7	0.366059937	0.0117	0.013882722
GO:0032007	negative regulation of TOR signaling	21	0.365814794	0.0004	0.002007244
GO:0019083	viral transcription	149	0.365553281	0.0006	0.002177563
GO:0071481	cellular response to X-ray	6	0.365551266	0.0002	0.001341684
GO:0045687	positive regulation of glial cell differentiation	25	0.365456885	0.0014	0.002975058
GO:0039529	RIG-I signaling pathway	17	0.365387236	< 0.001	< 0.001
GO:0044062	regulation of excretion	13	0.365310365	< 0.001	< 0.001
GO:0042756	drinking behavior	5	0.365302445	0.0007	0.002248538
GO:1905564	positive regulation of vascular endothelial cell proliferation	11	0.365297765	0.0001	0.000877824
GO:0006405	RNA export from nucleus	89	0.365262534	0.0008	0.002313249
GO:0060027	convergent extension involved in gastrulation	5	0.365199485	0.0002	0.001341684
GO:0033540	fatty acid beta-oxidation using acyl-CoA oxidase	10	0.365173745	< 0.001	< 0.001
GO:0051385	response to mineralocorticoid	16	0.365074003	0.0003	0.001720882
GO:0001731	formation of translation preinitiation complex	5	0.364993565	0.0001	0.000877824
GO:0002418	immune response to tumor cell	9	0.364879165	0.0002	0.001341684
GO:0051123	RNA polymerase II transcriptional preinitiation complex assembly	11	0.364665965	0.0004	0.002007244
GO:1902415	regulation of mRNA binding	5	0.364633205	0.004	0.005880507
GO:0002756	MyD88-independent toll-like receptor signaling pathway	20	0.364620335	0.0002	0.001341684
GO:0098586	cellular response to virus	32	0.364422458	0.0001	0.000877824
GO:0001561	fatty acid alpha-oxidation	5	0.364324324	0.0011	0.002610912
GO:0043558	regulation of translational initiation in response to stress	9	0.364307164	0.0002	0.001341684
GO:0048670	regulation of collateral sprouting	9	0.364164164	0.0008	0.002313249
GO:0090502	RNA phosphodiester bond hydrolysis, endonucleolytic	44	0.364110214	< 0.001	< 0.001
GO:0006298	mismatch repair	20	0.363899614	0.0007	0.002248538
GO:0033483	gas homeostasis	7	0.363816878	0.0076	0.009790742
GO:1902170	cellular response to reactive nitrogen species	8	0.363803089	0.0028	0.004605006
GO:0061684	chaperone-mediated autophagy	12	0.363728014	0.0009	0.002399874
GO:0010998	regulation of translational initiation by eIF2 alpha phosphorylation	6	0.363706564	0.0001	0.000877824
GO:0046654	tetrahydrofolate biosynthetic process	6	0.363577864	0.0006	0.002177563
GO:0036500	ATF6-mediated unfolded protein response	10	0.363552124	0.0006	0.002177563
GO:0019388	galactose catabolic process	5	0.363397683	0.003	0.004825593
GO:0098659	inorganic cation import into cell	8	0.363320463	0.0098	0.012008345
GO:0099587	inorganic ion import into cell	8	0.363320463	0.0098	0.012008345
GO:0051028	mRNA transport	105	0.363311883	0.0007	0.002248538
GO:1903203	regulation of oxidative stress-induced neuron death	14	0.363283692	0.001	0.002498236
GO:0002828	regulation of type 2 immune response	13	0.363251163	0.0003	0.001720882
GO:0071514	genetic imprinting	16	0.363111326	< 0.001	< 0.001
GO:0071479	cellular response to ionizing radiation	46	0.363012702	0.0004	0.002007244
GO:0002753	cytoplasmic pattern recognition receptor signaling pathway	40	0.362985843	0.0001	0.000877824
GO:0019883	antigen processing and presentation of endogenous antigen	11	0.362864163	0.0027	0.004491543
GO:0046485	ether lipid metabolic process	5	0.362728443	0.0124	0.014577606
GO:0098801	regulation of renal system process	19	0.36269051	< 0.001	< 0.001
GO:0010883	regulation of lipid storage	24	0.362666238	0.0013	0.002859821
GO:0090136	epithelial cell-cell adhesion	9	0.362648363	0.0015	0.003088691
GO:0010935	regulation of macrophage cytokine production	8	0.362580438	0.0003	0.001720882
GO:0098869	cellular oxidant detoxification	57	0.36251891	0.0003	0.001720882
GO:0009157	deoxyribonucleoside monophosphate biosynthetic process	7	0.362456334	0.0023	0.004032435
GO:0001916	positive regulation of T cell mediated cytotoxicity	10	0.362445302	0.0024	0.004156304
GO:0071218	cellular response to misfolded protein	10	0.362342342	0.0002	0.001341684
GO:0009880	embryonic pattern specification	26	0.362320562	< 0.001	< 0.001
GO:0033605	positive regulation of catecholamine secretion	6	0.362290862	< 0.001	< 0.001
GO:0021591	ventricular system development	15	0.362265122	0.0001	0.000877824
GO:0060008	Sertoli cell differentiation	12	0.362226512	0.0007	0.002248538
GO:0061311	cell surface receptor signaling pathway involved in heart development	14	0.362180548	< 0.001	< 0.001
GO:0051569	regulation of histone H3-K4 methylation	15	0.362076362	< 0.001	< 0.001
GO:0032781	positive regulation of ATPase activity	36	0.362004862	0.0011	0.002610912
GO:0051290	protein heterotetramerization	22	0.361939862	0.0002	0.001341684
GO:1903051	negative regulation of proteolysis involved in cellular protein catabolic process	37	0.361821281	0.0008	0.002313249
GO:0051103	DNA ligation involved in DNA repair	8	0.361808237	0.0001	0.000877824
GO:0045723	positive regulation of fatty acid biosynthetic process	9	0.361790362	0.0023	0.004032435
GO:0048711	positive regulation of astrocyte differentiation	9	0.361733162	0.0017	0.003334595
GO:1904706	negative regulation of vascular smooth muscle cell proliferation	9	0.361733162	0.0081	0.010256567
GO:0060674	placenta blood vessel development	16	0.361727799	0.0006	0.002177563
GO:0014807	regulation of somitogenesis	5	0.361544402	0.0157	0.017969846
GO:0046500	S-adenosylmethionine metabolic process	11	0.361460161	0.0016	0.003223775
GO:1905522	negative regulation of macrophage migration	6	0.361432861	< 0.001	< 0.001
GO:0070987	error-free translesion synthesis	16	0.361422136	0.0005	0.002177563
GO:0032070	regulation of deoxyribonuclease activity	8	0.361293436	0.0022	0.003910907
GO:0043970	histone H3-K9 acetylation	8	0.361164736	0.0035	0.005358035
GO:0043330	response to exogenous dsRNA	23	0.361143752	0.0045	0.006417207
GO:0030279	negative regulation of ossification	35	0.36099283	0.0005	0.002177563

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0070269	pyroptosis	5	0.360978121	0.0001	0.000877824
GO:0071472	cellular response to salt stress	9	0.360960961	0.0005	0.002177563
GO:0044789	modulation by host of viral release from host cell	5	0.360926641	0.001	0.002498236
GO:0044791	positive regulation by host of viral release from host cell	5	0.360926641	0.001	0.002498236
GO:0045197	establishment or maintenance of epithelial cell apical/basal polarity	18	0.360918061	0.0032	0.005044175
GO:0021904	dorsal/ventral neural tube patterning	12	0.360918061	< 0.001	< 0.001
GO:0006353	DNA-templated transcription, termination	53	0.360850878	< 0.001	< 0.001
GO:0042090	interleukin-12 biosynthetic process	5	0.360823681	0.0002	0.001341684
GO:0045075	regulation of interleukin-12 biosynthetic process	5	0.360823681	0.0002	0.001341684
GO:1903205	regulation of hydrogen peroxide-induced cell death	14	0.360654532	0.0012	0.002741075
GO:0098840	protein transport along microtubule	37	0.360541236	< 0.001	< 0.001
GO:0099118	microtubule-based protein transport	37	0.360541236	< 0.001	< 0.001
GO:1905214	regulation of RNA binding	8	0.360456885	0.0012	0.002741075
GO:0060379	cardiac muscle cell myoblast differentiation	7	0.360397132	0.0088	0.010992238
GO:0022616	DNA strand elongation	12	0.36033891	0.0005	0.002177563
GO:0043171	peptide catabolic process	10	0.3602574	0.0008	0.002313249
GO:0008210	estrogen metabolic process	14	0.360250046	0.0028	0.004605006
GO:0072710	response to hydroxyurea	6	0.36023166	0.0034	0.005263104
GO:0060253	negative regulation of glial cell proliferation	10	0.36020592	0.0025	0.004279479
GO:0051150	regulation of smooth muscle cell differentiation	20	0.36019305	0.0006	0.002177563
GO:0034340	response to type I interferon	56	0.360093767	0.0012	0.002741075
GO:0031053	primary miRNA processing	6	0.36001716	0.0028	0.004605006
GO:0035457	cellular response to interferon-alpha	8	0.35997426	0.001	0.002498236
GO:0044827	modulation by host of viral genome replication	10	0.3598713	0.0003	0.001720882
GO:1903613	regulation of protein tyrosine phosphatase activity	5	0.35953668	0.008	0.010168329
GO:0046184	aldehyde biosynthetic process	7	0.359514617	0.0013	0.002859821
GO:0002230	positive regulation of defense response to virus by host	17	0.359497312	< 0.001	< 0.001
GO:0050966	detection of mechanical stimulus involved in sensory perception of pain	6	0.359073359	0.0065	0.008621124
GO:0033574	response to testosterone	28	0.359018202	0.0009	0.002399874
GO:0001840	neural plate development	5	0.358970399	0.0001	0.000877824
GO:0034341	response to interferon-gamma	99	0.358914759	0.0009	0.002399874
GO:0034123	positive regulation of toll-like receptor signaling pathway	14	0.35885273	0.0002	0.001341684
GO:0051148	negative regulation of muscle cell differentiation	41	0.358841071	0.0007	0.002248538
GO:0046134	pyrimidine nucleoside biosynthetic process	22	0.358734059	0.0005	0.002177563
GO:0048668	collateral sprouting	12	0.358494208	0.0014	0.002975058
GO:0048368	lateral mesoderm development	7	0.358411473	< 0.001	< 0.001
GO:0003081	regulation of systemic arterial blood pressure by renin-angiotensin	8	0.358365508	0.0017	0.003334595
GO:0071604	transforming growth factor beta production	18	0.358229658	0.0006	0.002177563
GO:0030223	neutrophil differentiation	7	0.358227615	0.002	0.003693422
GO:0035455	response to interferon-alpha	17	0.358180029	0.0015	0.003088691
GO:0071459	protein localization to chromosome, centromeric region	13	0.358142758	0.0007	0.002248538
GO:0042073	intraciliary transport	33	0.358137358	< 0.001	< 0.001
GO:0048087	positive regulation of developmental pigmentation	6	0.358129558	0.0002	0.001341684
GO:0045779	negative regulation of bone resorption	6	0.357957958	0.0047	0.006644432
GO:0010826	negative regulation of centrosome duplication	10	0.357940798	0.0005	0.002177563
GO:0007549	dosage compensation	12	0.357936508	0.0006	0.002177563
GO:1903363	negative regulation of cellular protein catabolic process	43	0.357852204	0.0008	0.002313249
GO:0061756	leukocyte adhesion to vascular endothelial cell	20	0.357773488	0.0016	0.003223775
GO:0043379	memory T cell differentiation	5	0.357683398	0.0109	0.013101792
GO:0090715	immunological memory formation process	5	0.357683398	0.0109	0.013101792
GO:0019080	viral gene expression	161	0.357679241	0.0007	0.002248538
GO:0019915	lipid storage	37	0.357556785	0.0008	0.002313249
GO:0070168	negative regulation of biomineral tissue development	16	0.35751287	0.0006	0.002177563
GO:0071025	RNA surveillance	7	0.357418643	0.0029	0.004714719
GO:0019062	virion attachment to host cell	5	0.357323037	0.0067	0.008845888
GO:0032905	transforming growth factor beta1 production	5	0.357323037	0.0148	0.017062301
GO:0090201	negative regulation of release of cytochrome c from mitochondria	11	0.357294957	0.0001	0.000877824
GO:0045978	negative regulation of nucleoside metabolic process	12	0.357293007	0.0029	0.004714719
GO:1903579	negative regulation of ATP metabolic process	12	0.357293007	0.0029	0.004714719
GO:0007140	male meiosis	13	0.357212157	0.0008	0.002313249
GO:0090205	positive regulation of cholesterol metabolic process	6	0.357142857	0.0009	0.002399874
GO:0035914	skeletal muscle cell differentiation	33	0.357099957	0.0021	0.003804235
GO:0003093	regulation of glomerular filtration	6	0.357099957	0.0176	0.019838132
GO:0061314	Notch signaling involved in heart development	7	0.3570877	< 0.001	< 0.001
GO:0042053	regulation of dopamine metabolic process	10	0.356988417	0.002	0.003693422
GO:0042069	regulation of catecholamine metabolic process	10	0.356988417	0.002	0.003693422
GO:0031646	positive regulation of neurological system process	15	0.356911197	0.0022	0.003910907
GO:0036462	TRAIL-activated apoptotic signaling pathway	6	0.356670957	0.0041	0.005981983
GO:1900034	regulation of cellular response to heat	50	0.356607465	0.0008	0.002313249
GO:0045136	development of secondary sexual characteristics	7	0.356499356	0.0014	0.002975058
GO:0035872	nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway	20	0.356486486	0.0007	0.002248538
GO:0045589	regulation of regulatory T cell differentiation	16	0.356483269	0.0027	0.004491543
GO:0072528	pyrimidine-containing compound biosynthetic process	28	0.356379849	0.0005	0.002177563
GO:0030970	retrograde protein transport, ER to cytosol	23	0.356230765	0.001	0.002498236
GO:1903513	endoplasmic reticulum to cytosol transport	23	0.356230765	0.001	0.002498236
GO:2000849	regulation of glucocorticoid secretion	6	0.356156156	< 0.001	< 0.001
GO:0002861	regulation of inflammatory response to antigenic stimulus	12	0.356070356	0.001	0.002498236
GO:0009048	dosage compensation by inactivation of X chromosome	10	0.355984556	0.0023	0.004032435
GO:0040015	negative regulation of multicellular organism growth	6	0.355984556	< 0.001	< 0.001
GO:0034501	protein localization to kinetochore	10	0.355958816	0.0006	0.002177563
GO:0006346	methylation-dependent chromatin silencing	12	0.355920206	0.0009	0.002399874
GO:1903427	negative regulation of reactive oxygen species biosynthetic process	16	0.355904118	0.0006	0.002177563
GO:0019372	lipoxygenase pathway	9	0.355870156	0.0008	0.002313249

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0051788	response to misfolded protein	11	0.355820756	0.0002	0.001341684
GO:0002755	MyD88-dependent toll-like receptor signaling pathway	22	0.355785656	0.0003	0.001720882
GO:0039530	MDA-5 signaling pathway	7	0.355763927	0.0091	0.011322589
GO:0045019	negative regulation of nitric oxide biosynthetic process	8	0.355759331	0.0021	0.003804235
GO:1904406	negative regulation of nitric oxide metabolic process	8	0.355759331	0.0021	0.003804235
GO:0060765	regulation of androgen receptor signaling pathway	19	0.35575425	0.0029	0.004714719
GO:0006891	intra-Golgi vesicle-mediated transport	13	0.355746956	0.0015	0.003088691
GO:0009651	response to salt stress	15	0.355744316	0.0001	0.000877824
GO:0009218	pyrimidine ribonucleotide metabolic process	15	0.355675676	0.0033	0.005149584
GO:0101023	vascular endothelial cell proliferation	13	0.355667756	0.0001	0.000877824
GO:1905562	regulation of vascular endothelial cell proliferation	13	0.355667756	0.0001	0.000877824
GO:0000731	DNA synthesis involved in DNA repair	36	0.355648506	0.0005	0.002177563
GO:0042558	pteridine-containing compound metabolic process	25	0.355583012	0.0008	0.002313249
GO:0007221	positive regulation of transcription of Notch receptor target	14	0.355469755	0.0022	0.003910907
GO:1902107	positive regulation of leukocyte differentiation	78	0.355436755	0.0019	0.003579279
GO:2000001	regulation of DNA damage checkpoint	12	0.355426855	0.0002	0.001341684
GO:0018208	peptidyl-proline modification	28	0.355414598	< 0.001	< 0.001
GO:0042769	DNA damage response, detection of DNA damage	28	0.355405405	< 0.001	< 0.001
GO:1990748	cellular detoxification	60	0.355272415	0.0002	0.001341684
GO:0060628	regulation of ER to Golgi vesicle-mediated transport	10	0.355238095	0.0058	0.007856196
GO:0070206	protein trimerization	31	0.355220658	0.0006	0.002177563
GO:0042953	lipoprotein transport	5	0.355109395	< 0.001	< 0.001
GO:0044872	lipoprotein localization	5	0.355109395	< 0.001	< 0.001
GO:0001914	regulation of T cell mediated cytotoxicity	14	0.355028498	0.0012	0.002741075
GO:0050665	hydrogen peroxide biosynthetic process	8	0.355019305	0.0004	0.002007244
GO:0035088	establishment or maintenance of apical/basal cell polarity	20	0.354980695	0.0042	0.006097175
GO:0061245	establishment or maintenance of bipolar cell polarity	20	0.354980695	0.0042	0.006097175
GO:1905314	semi-lunar valve development	21	0.354893669	< 0.001	< 0.001
GO:1902894	negative regulation of pri-miRNA transcription from RNA polymerase II promoter	5	0.354851995	0.0009	0.002399874
GO:0051894	positive regulation of focal adhesion assembly	15	0.354800515	0.0019	0.003579279
GO:0045661	regulation of myoblast differentiation	23	0.354787085	0.0005	0.002177563
GO:0071634	regulation of transforming growth factor beta production	16	0.354777992	0.0007	0.002248538
GO:0046426	negative regulation of JAK-STAT cascade	10	0.354671815	0.0006	0.002177563
GO:1904893	negative regulation of STAT cascade	10	0.354671815	0.0006	0.002177563
GO:1905709	negative regulation of membrane permeability	7	0.354660783	0.0034	0.005263104
GO:0035722	interleukin-12-mediated signaling pathway	30	0.354628915	0.0002	0.001341684
GO:0071349	cellular response to interleukin-12	30	0.354628915	0.0002	0.001341684
GO:0045604	regulation of epidermal cell differentiation	27	0.354602221	0.0008	0.002313249
GO:1903800	positive regulation of production of miRNAs involved in gene silencing by miRNA	5	0.354440154	0.0109	0.013101792
GO:0000154	rRNA modification	20	0.354427284	0.0007	0.002248538
GO:0090084	negative regulation of inclusion body assembly	8	0.354375804	0.0012	0.002741075
GO:2000121	regulation of removal of superoxide radicals	8	0.354375804	0.0014	0.002975058
GO:0000387	spliceosomal snRNP assembly	27	0.354325754	0.0001	0.000877824
GO:0007099	centriole replication	18	0.354225654	0.0005	0.002177563
GO:0090069	regulation of ribosome biogenesis	12	0.354225654	0.0003	0.001720882
GO:2000232	regulation of rRNA processing	12	0.354225654	0.0003	0.001720882
GO:0003188	heart valve formation	8	0.354214929	0.0001	0.000877824
GO:0045624	positive regulation of T-helper cell differentiation	10	0.354157014	0.0019	0.003579279
GO:0043615	astrocyte cell migration	5	0.354131274	0.0016	0.003223775
GO:0090239	regulation of histone H4 acetylation	9	0.353982554	0.0001	0.000877824
GO:0000715	nucleotide-excision repair, DNA damage recognition	17	0.353940495	0.0002	0.001341684
GO:0044806	G-quadruplex DNA unwinding	7	0.353851811	0.0022	0.003910907
GO:0006413	translational initiation	157	0.353815508	0.0008	0.002313249
GO:0034755	iron ion transmembrane transport	8	0.353796654	0.0001	0.000877824
GO:0046642	negative regulation of alpha-beta T cell proliferation	6	0.353796654	0.005	0.006974174
GO:0002507	tolerance induction	14	0.353778268	0.0013	0.002859821
GO:0043313	regulation of neutrophil degranulation	5	0.353770914	0.0111	0.013284563
GO:0032988	ribonucleoprotein complex disassembly	11	0.353667954	0.0006	0.002177563
GO:0003085	negative regulation of systemic arterial blood pressure	6	0.353667954	0.0014	0.002975058
GO:0071605	monocyte chemotactic protein-1 production	8	0.353635779	0.0049	0.006860215
GO:0071637	regulation of monocyte chemotactic protein-1 production	8	0.353635779	0.0049	0.006860215
GO:0070423	nucleotide-binding oligomerization domain containing signaling pathway	19	0.353559575	0.0005	0.002177563
GO:0090557	establishment of endothelial intestinal barrier	5	0.353513514	0.0006	0.002177563
GO:0050657	nucleic acid transport	121	0.353485008	0.0007	0.002248538
GO:0050658	RNA transport	121	0.353485008	0.0007	0.002248538
GO:0033077	T cell differentiation in thymus	32	0.353410553	0.0007	0.002248538
GO:0071594	thymocyte aggregation	32	0.353410553	0.0007	0.002248538
GO:0046606	negative regulation of centrosome cycle	11	0.353363753	0.0006	0.002177563
GO:0036109	alpha-linolenic acid metabolic process	10	0.353333333	0.0049	0.006860215
GO:0060603	mammary gland duct morphogenesis	15	0.353324753	0.0005	0.002177563
GO:0002717	positive regulation of natural killer cell mediated immunity	10	0.353178893	0.0003	0.001720882
GO:0045652	regulation of megakaryocyte differentiation	33	0.353168753	0.0001	0.000877824
GO:0060457	negative regulation of digestive system process	9	0.353124553	< 0.001	< 0.001
GO:0070670	response to interleukin-4	19	0.353085416	0.0002	0.001341684
GO:1904380	endoplasmic reticulum mannose trimming	13	0.352875953	0.0004	0.002007244
GO:0010592	positive regulation of lamellipodium assembly	7	0.352858981	0.0012	0.002741075
GO:0043383	negative T cell selection	6	0.352767053	0.0005	0.002177563
GO:0045060	negative thymic T cell selection	6	0.352767053	0.0005	0.002177563
GO:0050849	negative regulation of calcium-mediated signaling	10	0.352741313	0.001	0.002498236
GO:0098754	detoxification	62	0.35273384	< 0.001	< 0.001
GO:0072643	interferon-gamma secretion	9	0.352724153	0.009	0.011215682
GO:2000483	negative regulation of interleukin-8 secretion	5	0.352689833	0.0018	0.003459409
GO:0071478	cellular response to radiation	105	0.352648158	0.0005	0.002177563

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1902624	positive regulation of neutrophil migration	16	0.352606178	0.003	0.004825593
GO:1904886	beta-catenin destruction complex disassembly	10	0.352561133	0.0018	0.003459409
GO:0099022	vesicle tethering	7	0.352491267	0.0001	0.000877824
GO:0034036	purine ribonucleoside bisphosphate biosynthetic process	5	0.352483912	0.0015	0.003088691
GO:0050428	3'-phosphoadenosine 5'-phosphosulfate biosynthetic process	5	0.352483912	0.0015	0.003088691
GO:0006297	nucleotide-excision repair, DNA gap filling	18	0.352180752	0.0011	0.002610912
GO:0045064	T-helper 2 cell differentiation	8	0.352123552	0.0024	0.004156304
GO:0060837	blood vessel endothelial cell differentiation	7	0.352086781	0.0006	0.002177563
GO:0006221	pyrimidine nucleotide biosynthetic process	20	0.352007722	0.0016	0.003223775
GO:0042092	type 2 immune response	15	0.351986272	0.0004	0.002007244
GO:0009948	anterior/posterior axis specification	19	0.351960984	< 0.001	< 0.001
GO:1904036	negative regulation of epithelial cell apoptotic process	23	0.351944491	0.0006	0.002177563
GO:0007143	female meiotic division	13	0.351866152	0.0009	0.002399874
GO:0016973	poly(A)+ mRNA export from nucleus	6	0.351823252	0.001	0.002498236
GO:0071359	cellular response to dsRNA	50	0.351619048	0.001	0.002498236
GO:0007492	endoderm development	40	0.351544402	0.0002	0.001341684
GO:0030214	hyaluronan catabolic process	8	0.351480051	< 0.001	< 0.001
GO:0006957	complement activation, alternative pathway	6	0.351480051	0.0003	0.001720882
GO:0002710	negative regulation of T cell mediated immunity	7	0.351461666	0.0002	0.001341684
GO:1901798	positive regulation of signal transduction by p53 class mediator	9	0.351437151	0.0022	0.003910907
GO:0045591	positive regulation of regulatory T cell differentiation	9	0.351408551	0.0107	0.012912536
GO:0051168	nuclear export	131	0.351365106	0.0007	0.002248538
GO:2000403	positive regulation of lymphocyte migration	15	0.351334191	0.0031	0.004916949
GO:2000406	positive regulation of T cell migration	15	0.351334191	0.0031	0.004916949
GO:1904996	positive regulation of leukocyte adhesion to vascular endothelial cell	9	0.351236951	0.0019	0.003579279
GO:0035437	maintenance of protein localization in endoplasmic reticulum	5	0.351145431	0.0059	0.007964563
GO:0035728	response to hepatocyte growth factor	9	0.351093951	0.0039	0.005778819
GO:0048662	negative regulation of smooth muscle cell proliferation	22	0.351093951	0.0026	0.004377754
GO:0060766	negative regulation of androgen receptor signaling pathway	8	0.351061776	0.0018	0.003459409
GO:0051236	establishment of RNA localization	122	0.350948372	0.0007	0.002248538
GO:0051665	membrane raft localization	5	0.350888031	0.0043	0.006204188
GO:0045793	positive regulation of cell size	6	0.350879451	< 0.001	< 0.001
GO:0007042	lysosomal lumen acidification	8	0.350868726	0.0136	0.015813319
GO:0060716	labyrinthine layer blood vessel development	13	0.350836551	0.0001	0.000877824
GO:0015074	DNA integration	9	0.350836551	0.0001	0.000877824
GO:0031055	chromatin remodeling at centromere	17	0.350730562	< 0.001	< 0.001
GO:1900037	regulation of cellular response to hypoxia	6	0.350707851	0.0003	0.001720882
GO:0010830	regulation of myotube differentiation	23	0.350512003	0.0118	0.013977955
GO:0000027	ribosomal large subunit assembly	7	0.350432065	0.0068	0.008946408
GO:0002479	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	59	0.350426456	0.0005	0.002177563
GO:0043922	negative regulation by host of viral transcription	6	0.35040755	0.0031	0.004916949
GO:0060242	contact inhibition	7	0.350284979	< 0.001	< 0.001
GO:0034105	positive regulation of tissue remodeling	12	0.35027885	0.0072	0.009362497
GO:1903573	negative regulation of response to endoplasmic reticulum stress	32	0.350176963	0.0013	0.002859821
GO:0071826	ribonucleoprotein complex subunit organization	139	0.350042128	0.0001	0.000877824
GO:0072182	regulation of nephron tubule epithelial cell differentiation	7	0.349843721	< 0.001	< 0.001
GO:0036342	post-anal tail morphogenesis	6	0.34980695	0.0002	0.001341684
GO:1901031	regulation of response to reactive oxygen species	20	0.34970399	0.001	0.002498236
GO:0015669	gas transport	9	0.34952095	0.0033	0.005149584
GO:0070671	response to interleukin-12	31	0.349516337	0.0003	0.001720882
GO:0043368	positive T cell selection	11	0.34950275	0.0042	0.006097175
GO:0009650	UV protection	8	0.349420849	0.0004	0.002007244
GO:0044033	multi-organism metabolic process	174	0.349388305	0.0006	0.002177563
GO:0046719	regulation by virus of viral protein levels in host cell	7	0.349292149	0.0012	0.002741075
GO:0046951	ketone body biosynthetic process	5	0.349292149	0.0118	0.013977955
GO:0051984	positive regulation of chromosome segregation	17	0.349125596	0.0023	0.004032435
GO:0030853	negative regulation of granulocyte differentiation	5	0.349086229	< 0.001	< 0.001
GO:0061512	protein localization to cilium	25	0.349045045	< 0.001	< 0.001
GO:0022618	ribonucleoprotein complex assembly	130	0.349044649	< 0.001	< 0.001
GO:0032790	ribosome disassembly	6	0.348991849	0.0006	0.002177563
GO:2000114	regulation of establishment of cell polarity	13	0.348658549	0.0018	0.003459409
GO:0043928	exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay	31	0.3486528	< 0.001	< 0.001
GO:0071353	cellular response to interleukin-4	17	0.348565372	0.0007	0.002248538
GO:0030219	megakaryocyte differentiation	43	0.348424172	0.0007	0.002248538
GO:0000288	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	56	0.348400441	< 0.001	< 0.001
GO:0002833	positive regulation of response to biotic stimulus	21	0.348397377	0.0001	0.000877824
GO:0072160	nephron tubule epithelial cell differentiation	8	0.348391248	0.0001	0.000877824
GO:0048681	negative regulation of axon regeneration	5	0.348365508	0.0208	0.022969745
GO:0046638	positive regulation of alpha-beta T cell differentiation	23	0.348307314	0.0058	0.007856196
GO:0009219	pyrimidine deoxyribonucleotide metabolic process	11	0.348262548	0.0016	0.003223775
GO:0019430	removal of superoxide radicals	15	0.348228228	0.0012	0.002741075
GO:0034505	tooth mineralization	5	0.348211068	0.0091	0.011322589
GO:0045580	regulation of T cell differentiation	66	0.348204048	0.0007	0.002248538
GO:0007253	cytoplasmic sequestering of NF-kappaB	5	0.348108108	0.0008	0.002313249
GO:0042345	regulation of NF-kappaB import into nucleus	5	0.348108108	0.0008	0.002313249
GO:0042347	negative regulation of NF-kappaB import into nucleus	5	0.348108108	0.0008	0.002313249
GO:0042348	NF-kappaB import into nucleus	5	0.348108108	0.0008	0.002313249
GO:0031100	animal organ regeneration	46	0.348049913	0.0011	0.002610912
GO:0039531	regulation of viral-induced cytoplasmic pattern recognition receptor signaling pathway	17	0.347990007	< 0.001	< 0.001
GO:0030157	pancreatic juice secretion	9	0.347919348	0.0007	0.002248538
GO:0000291	nuclear-transcribed mRNA catabolic process, exonucleolytic	32	0.347779923	< 0.001	< 0.001
GO:0072074	kidney mesenchyme development	9	0.347776348	0.0001	0.000877824
GO:0006972	hyperosmotic response	18	0.347747748	0.0002	0.001341684

GOLabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:003234	negative regulation of protein sumoylation	5	0.347644788	0.0021	0.003804235
GO:0045577	regulation of B cell differentiation	16	0.347619048	0.0002	0.001341684
GO:1902563	regulation of neutrophil activation	7	0.347600662	0.0148	0.017062301
GO:0060831	smoothened signaling pathway involved in dorsal/ventral neural tube patterning	9	0.347518948	< 0.001	< 0.001
GO:0048535	lymph node development	11	0.347513748	0.0002	0.001341684
GO:0001771	immunological synapse formation	10	0.347464607	0.0041	0.005981983
GO:1903798	regulation of production of miRNAs involved in gene silencing by miRNA	10	0.347413127	0.0144	0.016652368
GO:0051383	kinetochore organization	14	0.347398419	0.0001	0.000877824
GO:1902175	regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	18	0.347361647	0.0008	0.002313249
GO:0031123	RNA 3'-end processing	85	0.347281399	0.0001	0.000877824
GO:0035729	cellular response to hepatocyte growth factor stimulus	8	0.347265122	0.0033	0.005149584
GO:1904994	regulation of leukocyte adhesion to vascular endothelial cell	12	0.347211497	0.002	0.003693422
GO:1902475	L-alpha-amino acid transmembrane transport	16	0.347136422	0.001	0.002498236
GO:0035563	positive regulation of chromatin binding	11	0.347045747	0.0001	0.000877824
GO:0034770	histone H4-K20 methylation	7	0.347012318	0.0042	0.006097175
GO:0060760	positive regulation of response to cytokine stimulus	35	0.34694613	0.001	0.002498236
GO:0007220	Notch receptor processing	9	0.346861147	0.0088	0.010992238
GO:0072678	T cell migration	30	0.346761047	0.0013	0.002859821
GO:0010889	regulation of sequestering of triglyceride	8	0.346750322	0.0011	0.002610912
GO:0042104	positive regulation of activated T cell proliferation	9	0.346746747	0.0004	0.002007244
GO:0003401	axis elongation	16	0.346685972	0.0008	0.002313249
GO:0009220	pyrimidine ribonucleotide biosynthetic process	14	0.346644604	0.0031	0.004916949
GO:0046132	pyrimidine ribonucleoside biosynthetic process	14	0.346644604	0.0031	0.004916949
GO:0010885	regulation of cholesterol storage	9	0.346603747	0.0013	0.002859821
GO:0045910	negative regulation of DNA recombination	19	0.346582673	< 0.001	< 0.001
GO:0008089	anterograde axonal transport	20	0.346550837	0.0009	0.002399874
GO:0046835	carbohydrate phosphorylation	14	0.346534289	0.0002	0.001341684
GO:0007100	mitotic centrosome separation	7	0.346534289	0.0019	0.003579279
GO:0051299	centrosome separation	7	0.346534289	0.0019	0.003579279
GO:0019934	cGMP-mediated signaling	10	0.346486486	0.0005	0.002177563
GO:0048714	positive regulation of oligodendrocyte differentiation	12	0.346460746	0.0016	0.003223775
GO:0002501	peptide antigen assembly with MHC protein complex	5	0.346409266	0.008	0.010168329
GO:0098543	detection of other organism	5	0.346306306	0.0001	0.000877824
GO:1905153	regulation of membrane invagination	9	0.346289146	0.0101	0.012328539
GO:0048194	Golgi vesicle budding	5	0.346254826	0.0014	0.002975058
GO:0036475	neuron death in response to oxidative stress	15	0.346151866	0.0008	0.002313249
GO:0009642	response to light intensity	5	0.346100386	0.0006	0.002177563
GO:1901522	positive regulation of transcription from RNA polymerase II promoter involved in cellular response to chemical stimulus	20	0.346036036	0.0008	0.002313249
GO:0048486	parasympathetic nervous system development	6	0.346031746	0.0001	0.000877824
GO:0042990	regulation of transcription factor import into nucleus	9	0.346031746	0.0006	0.002177563
GO:0042991	transcription factor import into nucleus	9	0.346031746	0.0006	0.002177563
GO:0042992	negative regulation of transcription factor import into nucleus	9	0.346031746	0.0006	0.002177563
GO:0042994	cytoplasmic sequestering of transcription factor	9	0.346031746	0.0006	0.002177563
GO:1903894	regulation of IRE1-mediated unfolded protein response	9	0.345974546	0.0086	0.010769857
GO:0006342	chromatin silencing	38	0.345973041	0.0021	0.003804235
GO:0033523	histone H2B ubiquitination	9	0.345917346	0.0078	0.009981807
GO:0033344	cholesterol efflux	22	0.345899146	< 0.001	< 0.001
GO:0002360	T cell lineage commitment	7	0.345872403	0.0007	0.002248538
GO:0002363	alpha-beta T cell lineage commitment	7	0.345872403	0.0007	0.002248538
GO:0035333	Notch receptor processing, ligand-dependent	7	0.345762089	0.0167	0.018954426
GO:0042590	antigen processing and presentation of exogenous peptide antigen via MHC class I	62	0.345613817	0.0008	0.002313249
GO:0044058	regulation of digestive system process	20	0.345611326	< 0.001	< 0.001
GO:0050766	positive regulation of phagocytosis	30	0.345602746	0.0007	0.002248538
GO:0009404	toxin metabolic process	11	0.345594946	0.004	0.005880507
GO:0071364	cellular response to epidermal growth factor stimulus	32	0.345551802	0.001	0.002498236
GO:0046688	response to copper ion	18	0.345545546	0.0002	0.001341684
GO:0038113	interleukin-9-mediated signaling pathway	5	0.345534106	0.0001	0.000877824
GO:0071355	cellular response to interleukin-9	5	0.345534106	0.0001	0.000877824
GO:0008655	pyrimidine-containing compound salvage	8	0.345495495	0.0005	0.002177563
GO:0043097	pyrimidine nucleoside salvage	8	0.345495495	0.0005	0.002177563
GO:0045721	negative regulation of gluconeogenesis	10	0.345353925	0.0005	0.002177563
GO:0006635	fatty acid beta-oxidation	46	0.345336019	0.0007	0.002248538
GO:0035809	regulation of urine volume	11	0.345243945	0.0003	0.001720882
GO:1901620	regulation of smoothened signaling pathway involved in dorsal/ventral neural tube patterning	6	0.345216645	< 0.001	< 0.001
GO:0032239	regulation of nucleobase-containing compound transport	10	0.345173745	0.0009	0.002399874
GO:0060947	cardiac vascular smooth muscle cell differentiation	5	0.345173745	0.0008	0.002313249
GO:2000107	negative regulation of leukocyte apoptotic process	28	0.345136974	0.0009	0.002399874
GO:0032728	positive regulation of interferon-beta production	23	0.345106597	0.0012	0.002741075
GO:0090224	regulation of spindle organization	25	0.345019305	0.0015	0.003088691
GO:0031122	cytoplasmic microtubule organization	16	0.34494852	0.0001	0.000877824
GO:0002524	hypersensitivity	5	0.344916345	0.0006	0.002177563
GO:0002883	regulation of hypersensitivity	5	0.344916345	0.0006	0.002177563
GO:0002885	positive regulation of hypersensitivity	5	0.344916345	0.0006	0.002177563
GO:0031124	mRNA 3'-end processing	75	0.344902617	0.0003	0.001720882
GO:0003348	cardiac endothelial cell differentiation	5	0.344864865	0.0036	0.005475609
GO:0060956	endocardial cell differentiation	5	0.344864865	0.0036	0.005475609
GO:1902622	regulation of neutrophil migration	19	0.344835061	0.0049	0.006860215
GO:0006370	7-methylguanosine mRNA capping	21	0.344830545	0.0001	0.000877824
GO:0014829	vascular smooth muscle contraction	14	0.344732488	0.0039	0.005778819
GO:0006054	N-acetylneuraminate metabolic process	6	0.344530245	0.0127	0.014886353
GO:0034644	cellular response to UV	51	0.344522674	0.0006	0.002177563
GO:0006853	carnitine shuttle	8	0.344465894	0.0012	0.002741075

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1902882	regulation of response to oxidative stress	47	0.34445631	0.0006	0.002177563
GO:0007064	mitotic sister chromatid cohesion	14	0.34441993	0.001	0.002498236
GO:1904469	positive regulation of tumor necrosis factor secretion	10	0.344401544	0.0014	0.002975058
GO:0009798	axis specification	42	0.344364773	< 0.001	< 0.001
GO:0010664	negative regulation of striated muscle cell apoptotic process	19	0.344279618	0.001	0.002498236
GO:0014061	regulation of norepinephrine secretion	7	0.344254459	< 0.001	< 0.001
GO:1902065	response to L-glutamate	5	0.344247104	0.0086	0.010769857
GO:0090150	establishment of protein localization to membrane	191	0.344214222	0.0002	0.001341684
GO:0055078	sodium ion homeostasis	18	0.344172744	0.0003	0.001720882
GO:0010743	regulation of macrophage derived foam cell differentiation	13	0.344104544	0.0016	0.003223775
GO:0046635	positive regulation of alpha-beta T cell activation	31	0.344102628	0.0102	0.012424427
GO:0006457	protein folding	126	0.344017487	0.0002	0.001341684
GO:0007184	SMAD protein import into nucleus	13	0.343965944	0.0037	0.005561344
GO:0060390	regulation of SMAD protein import into nucleus	13	0.343965944	0.0037	0.005561344
GO:2000249	regulation of actin cytoskeleton reorganization	20	0.343951094	< 0.001	< 0.001
GO:0015791	polyol transport	5	0.343886744	< 0.001	< 0.001
GO:0051225	spindle assembly	57	0.343864165	0.0009	0.002399874
GO:0042983	amyloid precursor protein biosynthetic process	9	0.343858144	0.0103	0.012519912
GO:0042984	regulation of amyloid precursor protein biosynthetic process	9	0.343858144	0.0103	0.012519912
GO:0015802	basic amino acid transport	8	0.343822394	0.0058	0.007856196
GO:0002437	inflammatory response to antigenic stimulus	22	0.343804844	0.0004	0.002007244
GO:0072676	lymphocyte migration	42	0.343794815	0.0008	0.002313249
GO:0045814	negative regulation of gene expression, epigenetic	54	0.343786644	0.0006	0.002177563
GO:0050961	detection of temperature stimulus involved in sensory perception	6	0.343758044	< 0.001	< 0.001
GO:0050965	detection of temperature stimulus involved in sensory perception of pain	6	0.343758044	< 0.001	< 0.001
GO:0075733	intracellular transport of virus	51	0.343715144	0.0009	0.002399874
GO:0019985	translesion synthesis	32	0.343709781	0.0005	0.002177563
GO:1901890	positive regulation of cell junction assembly	18	0.343700844	0.0015	0.003088691
GO:0015936	coenzyme A metabolic process	8	0.343661519	0.0001	0.000877824
GO:0051193	regulation of cofactor metabolic process	52	0.343634294	0.001	0.002498236
GO:0039535	regulation of RIG-I signaling pathway	15	0.343595024	< 0.001	< 0.001
GO:0031077	post-embryonic camera-type eye development	6	0.343586444	0.0064	0.008500875
GO:0043691	reverse cholesterol transport	8	0.343500644	< 0.001	< 0.001
GO:0001780	neutrophil homeostasis	8	0.343500644	0.0028	0.004605006
GO:0010501	RNA secondary structure unwinding	7	0.343482258	0.0044	0.006304227
GO:0070571	negative regulation of neuron projection regeneration	6	0.343457743	0.0217	0.023852035
GO:0048672	positive regulation of collateral sprouting	6	0.343457743	0.0013	0.002859821
GO:0060260	regulation of transcription initiation from RNA polymerase II promoter	15	0.343440583	0.0006	0.002177563
GO:0010155	regulation of proton transport	14	0.343390329	0.0013	0.002859821
GO:0009452	7-methylguanosine RNA capping	24	0.343382668	0.0001	0.000877824
GO:0036260	RNA capping	24	0.343382668	0.0001	0.000877824
GO:1901998	toxin transport	26	0.343282843	0.0002	0.001341684
GO:0032373	positive regulation of sterol transport	15	0.343148863	0.0002	0.001341684
GO:0032376	positive regulation of cholesterol transport	15	0.343148863	0.0002	0.001341684
GO:0035815	positive regulation of renal sodium excretion	9	0.343143143	0.0001	0.000877824
GO:0098534	centriole assembly	19	0.343141638	0.0006	0.002177563
GO:0046931	pore complex assembly	10	0.343140283	0.0002	0.001341684
GO:0048548	regulation of pinocytosis	9	0.343114543	0.0021	0.003804235
GO:0009262	deoxyribonucleotide metabolic process	20	0.343037323	0.0004	0.002007244
GO:2000345	regulation of hepatocyte proliferation	9	0.343028743	0.0003	0.001720882
GO:0000038	very long-chain fatty acid metabolic process	16	0.343018018	0.0007	0.002248538
GO:2001224	positive regulation of neuron migration	6	0.342942943	0.0012	0.002741075
GO:0010603	regulation of cytoplasmic mRNA processing body assembly	6	0.342857143	0.0006	0.002177563
GO:0046598	positive regulation of viral entry into host cell	6	0.342814243	0.0079	0.010077402
GO:1902946	protein localization to early endosome	5	0.342805663	0.002	0.003693422
GO:1902965	regulation of protein localization to early endosome	5	0.342805663	0.002	0.003693422
GO:1902966	positive regulation of protein localization to early endosome	5	0.342805663	0.002	0.003693422
GO:0006403	RNA localization	145	0.342784361	0.0007	0.002248538
GO:1903707	negative regulation of hemopoiesis	76	0.342755537	0.0002	0.001341684
GO:0090307	mitotic spindle assembly	35	0.342636514	0.0007	0.002248538
GO:0051350	negative regulation of lyase activity	11	0.342623143	0.001	0.002498236
GO:0031047	gene silencing by RNA	95	0.342621418	0.0002	0.001341684
GO:1990403	embryonic brain development	8	0.342599743	0.0008	0.002313249
GO:0042509	regulation of tyrosine phosphorylation of STAT protein	33	0.342521743	< 0.001	< 0.001
GO:0042135	neurotransmitter catabolic process	11	0.342506143	< 0.001	< 0.001
GO:0006984	ER-nucleus signaling pathway	32	0.342495174	0.0034	0.005263104
GO:2000404	regulation of T cell migration	21	0.342464914	0.0013	0.002859821
GO:2000811	negative regulation of anoikis	9	0.342399542	0.008	0.010168329
GO:0045454	cell redox homeostasis	46	0.342370321	0.0002	0.001341684
GO:0001833	inner cell mass cell proliferation	8	0.342342342	0.0023	0.004032435
GO:0018126	protein hydroxylation	17	0.342296919	0.0001	0.000877824
GO:0001919	regulation of receptor recycling	19	0.342288153	0.0038	0.005666214
GO:0045039	protein import into mitochondrial inner membrane	5	0.342239382	0.004	0.005880507
GO:1901799	negative regulation of proteasomal protein catabolic process	26	0.342193842	0.0013	0.002859821
GO:0015727	lactate transport	5	0.342136422	0.0018	0.003459409
GO:0035873	lactate transmembrane transport	5	0.342136422	0.0018	0.003459409
GO:0071482	cellular response to light stimulus	64	0.342105051	0.0006	0.002177563
GO:0042177	negative regulation of protein catabolic process	69	0.342099864	0.0011	0.002610912
GO:0048266	behavioral response to pain	9	0.342027742	0.0026	0.004377754
GO:0017148	negative regulation of translation	147	0.341808281	0.0005	0.002177563
GO:0055094	response to lipoprotein particle	13	0.341807742	0.0016	0.003223775
GO:0071402	cellular response to lipoprotein particle stimulus	13	0.341807742	0.0016	0.003223775
GO:0061014	positive regulation of mRNA catabolic process	21	0.341778513	0.0001	0.000877824

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0032786	positive regulation of DNA-templated transcription, elongation	15	0.341776062	0.0009	0.002399874
GO:0044818	mitotic G2/M transition checkpoint	16	0.341763192	0.0011	0.002610912
GO:0006220	pyrimidine nucleotide metabolic process	30	0.341758902	0.0007	0.002248538
GO:0035195	gene silencing by miRNA	80	0.341753539	0.0005	0.002177563
GO:0033689	negative regulation of osteoblast proliferation	6	0.341741742	0.0057	0.007745437
GO:0035930	corticosteroid hormone secretion	9	0.341741742	< 0.001	< 0.001
GO:0061099	negative regulation of protein tyrosine kinase activity	18	0.341727442	0.0043	0.006204188
GO:0050821	protein stabilization	105	0.341719679	0.0005	0.002177563
GO:0000289	nuclear-transcribed mRNA poly(A) tail shortening	22	0.341698842	0.0001	0.000877824
GO:0060479	lung cell differentiation	10	0.341698842	0.0008	0.002313249
GO:0060487	lung epithelial cell differentiation	10	0.341698842	0.0008	0.002313249
GO:0071385	cellular response to glucocorticoid stimulus	31	0.341678084	0.0001	0.000877824
GO:0010831	positive regulation of myotube differentiation	12	0.341677392	0.0125	0.014684332
GO:0030490	maturation of SSU-rRNA	12	0.341634492	0.0002	0.001341684
GO:0071450	cellular response to oxygen radical	17	0.341615565	0.0016	0.003223775
GO:0071451	cellular response to superoxide	17	0.341615565	0.0016	0.003223775
GO:0045671	negative regulation of osteoclast differentiation	13	0.341589942	0.0028	0.004605006
GO:1902902	negative regulation of autophagosome assembly	11	0.341570142	0.0009	0.002399874
GO:0032570	response to progesterone	23	0.34155895	0.0001	0.000877824
GO:0045581	negative regulation of T cell differentiation	20	0.341544402	0.0001	0.000877824
GO:0021575	hindbrain morphogenesis	22	0.341511642	0.0017	0.003334595
GO:0006301	postreplication repair	37	0.341500574	0.0005	0.002177563
GO:0072665	protein localization to vacuole	25	0.341498069	0.0012	0.002741075
GO:0051170	nuclear import	101	0.341399391	0.0005	0.002177563
GO:0016925	protein sumoylation	46	0.341357507	0.0018	0.003459409
GO:0051196	regulation of coenzyme metabolic process	51	0.341348071	0.001	0.002498236
GO:0006833	water transport	10	0.341338481	< 0.001	< 0.001
GO:0006662	glycerol ether metabolic process	7	0.341312741	0.0053	0.007330056
GO:0000281	mitotic cytokinesis	30	0.341252681	0.0022	0.003910907
GO:2000378	negative regulation of reactive oxygen species metabolic process	31	0.341238012	0.0006	0.002177563
GO:2000279	negative regulation of DNA biosynthetic process	21	0.341165655	0.0007	0.002248538
GO:0014911	positive regulation of smooth muscle cell migration	20	0.341158301	0.0006	0.002177563
GO:1903867	extraembryonic membrane development	5	0.341158301	0.0056	0.007655255
GO:1905208	negative regulation of cardiocyte differentiation	12	0.341119691	0.0008	0.002313249
GO:0006471	protein ADP-ribosylation	20	0.341093951	0.0011	0.002610912
GO:0031503	protein complex localization	48	0.341092879	< 0.001	< 0.001
GO:0035194	posttranscriptional gene silencing by RNA	83	0.341021228	0.0005	0.002177563
GO:0008631	intrinsic apoptotic signaling pathway in response to oxidative stress	26	0.341015741	0.0002	0.001341684
GO:1904357	negative regulation of telomere maintenance via telomere lengthening	17	0.340994776	0.0005	0.002177563
GO:0045619	regulation of lymphocyte differentiation	82	0.340989421	0.0007	0.002248538
GO:0032435	negative regulation of proteasomal ubiquitin-dependent protein catabolic process	20	0.340978121	0.0012	0.002741075
GO:0010872	regulation of cholesterol esterification	5	0.340900901	0.004	0.005880507
GO:0003071	renal system process involved in regulation of systemic arterial blood pressure	9	0.340855141	0.0203	0.022456501
GO:0033866	nucleoside bisphosphate biosynthetic process	9	0.340740741	0.0017	0.003334595
GO:0034030	ribonucleoside bisphosphate biosynthetic process	9	0.340740741	0.0017	0.003334595
GO:0034033	purine nucleoside bisphosphate biosynthetic process	9	0.340740741	0.0017	0.003334595
GO:0060972	left/right pattern formation	11	0.340727741	< 0.001	< 0.001
GO:0030422	production of siRNA involved in RNA interference	6	0.340626341	0.0031	0.004916949
GO:0050870	positive regulation of T cell activation	98	0.340558926	0.0014	0.002975058
GO:0070471	uterine smooth muscle contraction	7	0.340540541	< 0.001	< 0.001
GO:0007340	acrosome reaction	7	0.340503769	0.0003	0.001720882
GO:0042026	protein refolding	13	0.34046134	0.0049	0.006860215
GO:0016458	gene silencing	135	0.34045474	0.0007	0.002248538
GO:0036120	cellular response to platelet-derived growth factor stimulus	12	0.34041184	0.0007	0.002248538
GO:1903053	regulation of extracellular matrix organization	27	0.34036894	0.0022	0.003910907
GO:0002577	regulation of antigen processing and presentation	12	0.34036894	0.0089	0.011106266
GO:0033211	adiponectin-activated signaling pathway	6	0.34032604	0.0028	0.004605006
GO:0032287	peripheral nervous system myelin maintenance	7	0.34028314	0.0047	0.006644432
GO:0043462	regulation of ATPase activity	49	0.340193838	0.0008	0.002313249
GO:0043470	regulation of carbohydrate catabolic process	48	0.340149078	0.0019	0.003579279
GO:0030513	positive regulation of BMP signaling pathway	19	0.340147666	0.0021	0.003804235
GO:0097202	activation of cysteine-type endopeptidase activity	8	0.34009009	0.0012	0.002741075
GO:0032211	negative regulation of telomere maintenance via telomerase	13	0.34006534	0.0004	0.002007244
GO:0048569	post-embryonic animal organ development	12	0.34004719	0.0008	0.002313249
GO:2001046	positive regulation of integrin-mediated signaling pathway	5	0.33997426	0.0007	0.002248538
GO:0006517	protein deglycosylation	17	0.339965175	0.0005	0.002177563
GO:0045668	negative regulation of osteoblast differentiation	21	0.339890911	0.0019	0.003579279
GO:0010667	negative regulation of cardiac muscle cell apoptotic process	17	0.339844046	0.0006	0.002177563
GO:0009112	nucleobase metabolic process	20	0.33972973	0.0025	0.004279479
GO:1902581	multi-organism cellular localization	52	0.33972874	0.0009	0.002399874
GO:1902583	multi-organism intracellular transport	52	0.33972874	0.0009	0.002399874
GO:0036503	ERAD pathway	62	0.339726824	0.0001	0.000877824
GO:0006930	substrate-dependent cell migration, cell extension	7	0.339694797	0.001	0.002498236
GO:0042178	xenobiotic catabolic process	8	0.339607465	0.0005	0.002177563
GO:0090025	regulation of monocyte chemotaxis	13	0.33959014	0.0003	0.001720882
GO:0006188	IMP biosynthetic process	5	0.33956242	0.0031	0.004916949
GO:0046040	IMP metabolic process	5	0.33956242	0.0031	0.004916949
GO:0071622	regulation of granulocyte chemotaxis	23	0.339555705	0.0022	0.003910907
GO:0044319	wound healing, spreading of cells	16	0.339430502	0.0024	0.004156304
GO:0090504	epiboly	16	0.339430502	0.0024	0.004156304
GO:0090505	epiboly involved in wound healing	16	0.339430502	0.0024	0.004156304
GO:0071480	cellular response to gamma radiation	22	0.339429039	0.0004	0.002007244
GO:0007635	chemosensory behavior	5	0.339407979	0.0004	0.002007244

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0016246	RNA interference	9	0.339396539	0.0043	0.006204188
GO:0016441	posttranscriptional gene silencing	84	0.339388368	0.0005	0.002177563
GO:0070841	inclusion body assembly	14	0.339290311	0.0007	0.002248538
GO:0060612	adipose tissue development	26	0.339263439	0.0011	0.002610912
GO:0051382	kinetochore assembly	11	0.339253539	0.0001	0.000877824
GO:0006084	acetyl-CoA metabolic process	25	0.339222651	0.0013	0.002859821
GO:0032096	negative regulation of response to food	10	0.339202059	0.0008	0.002313249
GO:0032099	negative regulation of appetite	10	0.339202059	0.0008	0.002313249
GO:0032105	negative regulation of response to extracellular stimulus	10	0.339202059	0.0008	0.002313249
GO:0032108	negative regulation of response to nutrient levels	10	0.339202059	0.0008	0.002313249
GO:0036473	cell death in response to oxidative stress	47	0.339160437	0.0005	0.002177563
GO:0002328	pro-B cell differentiation	7	0.339106453	0.0001	0.000877824
GO:0048710	regulation of astrocyte differentiation	13	0.339015939	0.0039	0.005778819
GO:1903708	positive regulation of hemopoiesis	105	0.338978979	0.0023	0.004032435
GO:0018344	protein geranylgeranylation	5	0.338944659	0.0083	0.010468217
GO:0016072	rRNA metabolic process	137	0.338941653	0.0001	0.000877824
GO:0060965	negative regulation of gene silencing by miRNA	6	0.338867439	0.0209	0.023072181
GO:0021680	cerebellar Purkinje cell layer development	15	0.338807379	0.0017	0.003334595
GO:0031935	regulation of chromatin silencing	13	0.338778339	0.001	0.002498236
GO:0009595	detection of biotic stimulus	8	0.338706564	< 0.001	< 0.001
GO:0060964	regulation of gene silencing by miRNA	54	0.338629105	0.0006	0.002177563
GO:0070920	regulation of production of small RNA involved in gene silencing by RNA	11	0.338621739	0.0132	0.015415723
GO:0060050	positive regulation of protein glycosylation	6	0.338610039	0.0001	0.000877824
GO:0021681	cerebellar granular layer development	7	0.338554881	0.0014	0.002975058
GO:0009081	branched-chain amino acid metabolic process	19	0.338549075	0.0022	0.003910907
GO:0009083	branched-chain amino acid catabolic process	19	0.338549075	0.0022	0.003910907
GO:0006506	GPI anchor biosynthetic process	23	0.338537295	0.0011	0.002610912
GO:0045898	regulation of RNA polymerase II transcriptional preinitiation complex assembly	6	0.338524239	0.0003	0.001720882
GO:0035307	positive regulation of protein dephosphorylation	17	0.338420774	0.001	0.002498236
GO:1905521	regulation of macrophage migration	21	0.338407796	0.0004	0.002007244
GO:0046950	cellular ketone body metabolic process	6	0.338395538	0.0033	0.005149584
GO:1902224	ketone body metabolic process	6	0.338395538	0.0033	0.005149584
GO:0045954	positive regulation of natural killer cell mediated cytotoxicity	9	0.338395538	0.0001	0.000877824
GO:0006364	rRNA processing	132	0.338317538	0.0001	0.000877824
GO:1900543	negative regulation of purine nucleotide metabolic process	21	0.338272967	0.0027	0.004491543
GO:0001975	response to amphetamine	14	0.338242324	0.0001	0.000877824
GO:0090501	RNA phosphodiester bond hydrolysis	95	0.338194134	< 0.001	< 0.001
GO:0061614	pri-miRNA transcription from RNA polymerase II promoter	27	0.338166738	0.0004	0.002007244
GO:0048563	post-embryonic animal organ morphogenesis	7	0.338113624	0.0003	0.001720882
GO:0030903	notochord development	9	0.338109538	0.0031	0.004916949
GO:0043162	ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway	12	0.338095238	0.0042	0.006097175
GO:0046839	phospholipid dephosphorylation	20	0.338082368	0.0037	0.005561344
GO:0042531	positive regulation of tyrosine phosphorylation of STAT protein	28	0.338076852	< 0.001	< 0.001
GO:0009411	response to UV	86	0.338059322	0.0006	0.002177563
GO:0034249	negative regulation of cellular amide metabolic process	158	0.33801867	0.0005	0.002177563
GO:0007595	lactation	30	0.338009438	0.001	0.002498236
GO:1903025	regulation of RNA polymerase II regulatory region sequence-specific DNA binding	8	0.337934363	0.0061	0.008182551
GO:0010758	regulation of macrophage chemotaxis	12	0.337837838	0.0001	0.000877824
GO:0002098	tRNA wobble uridine modification	8	0.337773488	0.0031	0.004916949
GO:0000272	polysaccharide catabolic process	15	0.337726298	0.002	0.003693422
GO:0044247	cellular polysaccharide catabolic process	15	0.337726298	0.002	0.003693422
GO:0046794	transport of virus	53	0.337694568	0.001	0.002498236
GO:0001954	positive regulation of cell-matrix adhesion	31	0.337675925	0.0012	0.002741075
GO:0009062	fatty acid catabolic process	63	0.337631509	0.0011	0.002610912
GO:0043331	response to dsRNA	61	0.337586767	0.0012	0.002741075
GO:0002792	negative regulation of peptide secretion	23	0.337563651	0.0008	0.002313249
GO:0050856	regulation of T cell receptor signaling pathway	21	0.33752528	0.0001	0.000877824
GO:1901797	negative regulation of signal transduction by p53 class mediator	21	0.337500766	< 0.001	< 0.001
GO:0070849	response to epidermal growth factor	34	0.337459308	0.0012	0.002741075
GO:1903201	regulation of oxidative stress-induced cell death	38	0.337458511	0.0009	0.002399874
GO:1900112	regulation of histone H3-K9 trimethylation	7	0.337451737	0.0043	0.006204188
GO:0045824	negative regulation of innate immune response	28	0.337433352	0.0014	0.002975058
GO:0046633	alpha-beta T cell proliferation	20	0.337413127	0.0119	0.014078095
GO:1902993	positive regulation of amyloid precursor protein catabolic process	6	0.337408837	0.0038	0.005666214
GO:0060119	inner ear receptor cell development	24	0.337387387	0.0001	0.000877824
GO:0006379	mRNA cleavage	16	0.337387387	< 0.001	< 0.001
GO:1902188	positive regulation of viral release from host cell	12	0.337323037	0.001	0.002498236
GO:0035912	dorsal aorta morphogenesis	6	0.337237237	0.0021	0.003804235
GO:0000717	nucleotide-excision repair, DNA duplex unwinding	15	0.337211497	0.0004	0.002007244
GO:0046676	negative regulation of insulin secretion	21	0.337206594	0.0013	0.002859821
GO:0002315	marginal zone B cell differentiation	6	0.337194337	0.0048	0.006748379
GO:0061462	protein localization to lysosome	23	0.337104807	0.0017	0.003334595
GO:0002704	negative regulation of leukocyte mediated immunity	21	0.33709628	0.0001	0.000877824
GO:1901385	regulation of voltage-gated calcium channel activity	11	0.337030537	0.0001	0.000877824
GO:0006400	tRNA modification	47	0.337024563	0.0006	0.002177563
GO:0071384	cellular response to corticosteroid stimulus	35	0.33701048	0.0003	0.001720882
GO:0060968	regulation of gene silencing	69	0.336992894	0.0007	0.002248538
GO:0006110	regulation of glycolytic process	43	0.336960881	0.0019	0.003579279
GO:0070472	regulation of uterine smooth muscle contraction	6	0.336936937	< 0.001	< 0.001
GO:0002763	positive regulation of myeloid leukocyte differentiation	30	0.336936937	0.0018	0.003459409
GO:0048147	negative regulation of fibroblast proliferation	22	0.336878437	0.0002	0.001341684
GO:0035690	cellular response to drug	34	0.336868802	0.0009	0.002399874
GO:0021695	cerebellar cortex development	26	0.336847837	0.0011	0.002610912

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0030449	regulation of complement activation	26	0.336837937	0.0048	0.006748379
GO:2000257	regulation of protein activation cascade	26	0.336837937	0.0048	0.006748379
GO:0031647	regulation of protein stability	170	0.336723446	0.0008	0.002313249
GO:0001895	retina homeostasis	34	0.336634113	0.0001	0.000877824
GO:0060147	regulation of posttranscriptional gene silencing	56	0.336578415	0.0006	0.002177563
GO:0060966	regulation of gene silencing by RNA	56	0.336578415	0.0006	0.002177563
GO:0006336	DNA replication-independent nucleosome assembly	20	0.336576577	< 0.001	< 0.001
GO:0034724	DNA replication-independent nucleosome organization	20	0.336576577	< 0.001	< 0.001
GO:1901977	negative regulation of cell cycle checkpoint	5	0.336576577	0.0007	0.002248538
GO:0051145	smooth muscle cell differentiation	34	0.336558407	0.0003	0.001720882
GO:2000401	regulation of lymphocyte migration	28	0.336541644	0.001	0.002498236
GO:1901550	regulation of endothelial cell development	8	0.336486486	0.0041	0.005981983
GO:1903140	regulation of establishment of endothelial barrier	8	0.336486486	0.0041	0.005981983
GO:0070120	ciliary neurotrophic factor-mediated signaling pathway	5	0.336473616	0.0044	0.006304227
GO:0006004	fucose metabolic process	10	0.336396396	0.0001	0.000877824
GO:0097306	cellular response to alcohol	28	0.336376172	< 0.001	< 0.001
GO:1900115	extracellular regulation of signal transduction	5	0.336267696	0.0003	0.001720882
GO:1900116	extracellular negative regulation of signal transduction	5	0.336267696	0.0003	0.001720882
GO:0009118	regulation of nucleoside metabolic process	65	0.336208296	0.0009	0.002399874
GO:1903578	regulation of ATP metabolic process	65	0.336208296	0.0009	0.002399874
GO:0030433	ER-associated ubiquitin-dependent protein catabolic process	48	0.336159374	0.0002	0.001341684
GO:1903039	positive regulation of leukocyte cell-cell adhesion	106	0.336096744	0.0014	0.002975058
GO:1900407	regulation of cellular response to oxidative stress	45	0.336096096	0.0011	0.002610912
GO:0090503	RNA phosphodiester bond hydrolysis, exonucleolytic	29	0.336084853	0.0015	0.003088691
GO:0010824	regulation of centrosome duplication	24	0.336078936	0.0001	0.000877824
GO:0046677	response to antibiotic	21	0.336042165	0.0007	0.002248538
GO:0014044	Schwann cell development	20	0.336036036	0.0026	0.004377754
GO:0010656	negative regulation of muscle cell apoptotic process	22	0.335942436	0.0017	0.003334595
GO:0007569	cell aging	59	0.335929149	0.0007	0.002248538
GO:1902004	positive regulation of beta-amyloid formation	5	0.335907336	0.0015	0.003088691
GO:0031581	hemidesmosome assembly	6	0.335864436	0.002	0.003693422
GO:0051568	histone H3-K4 methylation	27	0.335821536	< 0.001	< 0.001
GO:0019852	L-ascorbic acid metabolic process	6	0.335692836	0.0177	0.019919142
GO:0033865	nucleoside bisphosphate metabolic process	20	0.335688546	0.0001	0.000877824
GO:0033875	ribonucleoside bisphosphate metabolic process	20	0.335688546	0.0001	0.000877824
GO:0034032	purine nucleoside bisphosphate metabolic process	20	0.335688546	0.0001	0.000877824
GO:0002715	regulation of natural killer cell mediated immunity	13	0.335649936	0.0005	0.002177563
GO:0042269	regulation of natural killer cell mediated cytotoxicity	13	0.335649936	0.0005	0.002177563
GO:0014037	Schwann cell differentiation	23	0.335627553	0.0024	0.004156304
GO:0046940	nucleoside monophosphate phosphorylation	10	0.335624196	0.0004	0.002007244
GO:0007062	sister chromatid cohesion	28	0.335613164	0.0006	0.002177563
GO:0070932	histone H3 deacetylation	14	0.335558007	0.0015	0.003088691
GO:0045920	negative regulation of exocytosis	19	0.335487367	0.0013	0.002859821
GO:0043369	CD4-positive or CD8-positive, alpha-beta T cell lineage commitment	6	0.335435435	0.0004	0.002007244
GO:0060216	definitive hemopoiesis	12	0.335371085	0.001	0.002498236
GO:0010606	positive regulation of cytoplasmic mRNA processing body assembly	5	0.335341055	0.0051	0.007095023
GO:0009147	pyrimidine nucleoside triphosphate metabolic process	12	0.335328185	0.0037	0.005561344
GO:0070102	interleukin-6-mediated signaling pathway	13	0.335313335	0.0003	0.001720882
GO:0090394	negative regulation of excitatory postsynaptic potential	5	0.335289575	0.0001	0.000877824
GO:0045616	regulation of keratinocyte differentiation	18	0.335235235	0.0047	0.006644432
GO:0009451	RNA modification	90	0.335132275	0.0009	0.002399874
GO:0007141	male meiosis I	7	0.335098364	0.0026	0.004377754
GO:0001967	suckling behavior	6	0.335092235	0.001	0.002498236
GO:0040029	regulation of gene expression, epigenetic	182	0.334944206	0.0006	0.002177563
GO:0010832	negative regulation of myotube differentiation	8	0.334942085	0.0115	0.013693853
GO:0043201	response to leucine	5	0.334929215	0.0035	0.005358035
GO:0051972	regulation of telomerase activity	32	0.33490991	0.0001	0.000877824
GO:0014075	response to amine	20	0.334787645	< 0.001	< 0.001
GO:0010332	response to gamma radiation	37	0.334773383	0.0004	0.002007244
GO:0042306	regulation of protein import into nucleus	54	0.334768101	0.0006	0.002177563
GO:0045066	regulatory T cell differentiation	18	0.334720435	0.0039	0.005778819
GO:2000515	negative regulation of CD4-positive, alpha-beta T cell activation	17	0.334711182	0.0001	0.000877824
GO:1902236	negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	12	0.334620335	0.0036	0.005475609
GO:0043486	histone exchange	23	0.334575569	0.0001	0.000877824
GO:0051053	negative regulation of DNA metabolic process	83	0.334564513	0.0004	0.002007244
GO:0000726	non-recombinational repair	48	0.334539897	0.0002	0.001341684
GO:0002069	columnar/cuboidal epithelial cell maturation	6	0.334534535	0.0167	0.018954426
GO:0001682	tRNA 5'-leader removal	6	0.334491634	0.0002	0.001341684
GO:1902893	regulation of pri-miRNA transcription from RNA polymerase II promoter	23	0.334486039	0.0003	0.001720882
GO:0002863	positive regulation of inflammatory response to antigenic stimulus	9	0.334477334	0.0012	0.002741075
GO:0071549	cellular response to dexamethasone stimulus	18	0.334477334	< 0.001	< 0.001
GO:0032527	protein exit from endoplasmic reticulum	32	0.334467503	0.002	0.003693422
GO:1903393	positive regulation of adherens junction organization	18	0.334463034	0.0016	0.003223775
GO:0061042	vascular wound healing	8	0.334459459	0.0106	0.012825859
GO:0032469	endoplasmic reticulum calcium ion homeostasis	14	0.334436477	0.0136	0.015813319
GO:0090085	regulation of protein deubiquitination	9	0.334248534	0.0011	0.002610912
GO:0036037	CD8-positive, alpha-beta T cell activation	8	0.334202059	0.0134	0.015626386
GO:0007519	skeletal muscle tissue development	74	0.334161188	0.0035	0.005358035
GO:1903557	positive regulation of tumor necrosis factor superfamily cytokine production	48	0.334148434	0.001	0.002498236
GO:0050732	negative regulation of peptidyl-tyrosine phosphorylation	27	0.334076934	0.0039	0.005778819
GO:0050974	detection of mechanical stimulus involved in sensory perception	13	0.334065934	0.004	0.005880507
GO:0048024	regulation of mRNA splicing, via spliceosome	52	0.334031284	0.0015	0.003088691
GO:0051865	protein autoubiquitination	42	0.334001348	0.0041	0.005981983

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1902237	positive regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	7	0.333884905	0.0026	0.004377754
GO:0060236	regulation of mitotic spindle organization	24	0.333773059	0.0023	0.004032435
GO:1904262	negative regulation of TORC1 signaling	5	0.333745174	0.0019	0.003579279
GO:0010662	regulation of striated muscle cell apoptotic process	22	0.333742834	0.0018	0.003459409
GO:0071280	cellular response to copper ion	11	0.333684334	0.0009	0.002399874
GO:0002291	T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell	6	0.333633634	0.01	0.012232246
GO:0031060	regulation of histone methylation	40	0.333603604	0.001	0.002498236
GO:0006368	transcription elongation from RNA polymerase II promoter	56	0.333549366	0.0003	0.001720882
GO:0061028	establishment of endothelial barrier	22	0.333497133	0.0022	0.003910907
GO:0043516	regulation of DNA damage response, signal transduction by p53 class mediator	16	0.333381596	0.0009	0.002399874
GO:0009886	post-embryonic animal morphogenesis	8	0.333365508	0.0001	0.000877824
GO:0051298	centrosome duplication	34	0.333348475	0.0005	0.002177563
GO:1904589	regulation of protein import	56	0.33327358	0.0006	0.002177563
GO:0008033	tRNA processing	80	0.333272201	0.0006	0.002177563
GO:0018195	peptidyl-arginine modification	9	0.333247533	0.0014	0.002975058
GO:0051291	protein heterooligomerization	66	0.333247533	0.0007	0.002248538
GO:0042490	mechanoreceptor differentiation	30	0.333221793	0.0001	0.000877824
GO:0060113	inner ear receptor cell differentiation	30	0.333221793	0.0001	0.000877824
GO:0036119	response to platelet-derived growth factor	13	0.333194733	0.0005	0.002177563
GO:0035019	somatic stem cell population maintenance	37	0.333131587	0.0001	0.000877824
GO:0046607	positive regulation of centrosome cycle	5	0.333127413	0.0102	0.012424427
GO:1902850	microtubule cytoskeleton organization involved in mitosis	37	0.333117674	0.0008	0.002313249
GO:0043589	skin morphogenesis	5	0.333075933	0.012	0.014185865
GO:0070922	small RNA loading onto RISC	9	0.333047333	0.0062	0.008281828
GO:1903313	positive regulation of mRNA metabolic process	41	0.333038265	0.0005	0.002177563
GO:0042254	ribosome biogenesis	169	0.333019579	0.0001	0.000877824
GO:0006703	estrogen biosynthetic process	8	0.332979408	0.0272	0.02926158
GO:0042273	ribosomal large subunit biogenesis	20	0.332960103	0.0014	0.002975058
GO:0006152	purine nucleoside catabolic process	9	0.332932933	0.0006	0.002177563
GO:0046130	purine ribonucleoside catabolic process	9	0.332932933	0.0006	0.002177563
GO:0003073	regulation of systemic arterial blood pressure	30	0.332921493	0.0024	0.004156304
GO:0007289	spermatid nucleus differentiation	10	0.332921493	0.0054	0.007432873
GO:0051251	positive regulation of lymphocyte activation	137	0.332856109	0.0006	0.002177563
GO:0015931	nucleobase-containing compound transport	150	0.332844273	0.0009	0.002399874
GO:0001779	natural killer cell differentiation	11	0.332818533	0.0035	0.005358035
GO:0071824	protein-DNA complex subunit organization	134	0.332808928	0.0001	0.000877824
GO:1903845	negative regulation of cellular response to transforming growth factor beta stimulus	46	0.332784959	0.0009	0.002399874
GO:0032660	regulation of interleukin-17 production	11	0.332748333	0.0019	0.003579279
GO:0046637	regulation of alpha-beta T cell differentiation	31	0.332727197	0.0013	0.002859821
GO:0032760	positive regulation of tumor necrosis factor production	46	0.332717811	0.001	0.002498236
GO:0061640	cytoskeleton-dependent cytokinesis	37	0.332658527	0.0017	0.003334595
GO:0002689	negative regulation of leukocyte chemotaxis	8	0.332561133	0.0006	0.002177563
GO:0070613	regulation of protein processing	59	0.332521868	0.0026	0.004377754
GO:0010875	positive regulation of cholesterol efflux	12	0.332475332	< 0.001	< 0.001
GO:0045980	negative regulation of nucleotide metabolic process	22	0.332444132	0.0034	0.005263104
GO:0031330	negative regulation of cellular catabolic process	66	0.332409032	0.0008	0.002313249
GO:0042787	protein ubiquitination involved in ubiquitin-dependent protein catabolic process	20	0.332406692	0.0009	0.002399874
GO:2000058	regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process	20	0.332406692	0.0009	0.002399874
GO:0010586	miRNA metabolic process	18	0.332403832	0.0029	0.004714719
GO:0032516	positive regulation of phosphoprotein phosphatase activity	9	0.332389532	0.0005	0.002177563
GO:0032945	negative regulation of mononuclear cell proliferation	37	0.332387213	0.0008	0.002313249
GO:0050672	negative regulation of lymphocyte proliferation	37	0.332387213	0.0008	0.002313249
GO:2000767	positive regulation of cytoplasmic translation	7	0.332377275	0.0011	0.002610912
GO:1901068	guanosine-containing compound metabolic process	26	0.332283932	0.001	0.002498236
GO:1990868	response to chemokine	10	0.332277992	0.0203	0.022456501
GO:1990869	cellular response to chemokine	10	0.332277992	0.0203	0.022456501
GO:0001510	RNA methylation	46	0.332230989	0.0012	0.002741075
GO:0034103	regulation of tissue remodeling	36	0.332210782	0.0022	0.003910907
GO:0006971	hypotonic response	8	0.332207207	0.0098	0.012008345
GO:0018216	peptidyl-arginine methylation	5	0.332200772	0.0008	0.002313249
GO:0030852	regulation of granulocyte differentiation	9	0.332160732	0.0001	0.000877824
GO:0032464	positive regulation of protein homooligomerization	6	0.332132132	0.0006	0.002177563
GO:0050764	regulation of phagocytosis	47	0.332112051	0.0011	0.002610912
GO:1901623	regulation of lymphocyte chemotaxis	8	0.332110682	0.0079	0.010077402
GO:0000462	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	7	0.332046332	0.001	0.002498236
GO:0019692	deoxyribose phosphate metabolic process	20	0.332033462	0.0005	0.002177563
GO:0006855	drug transmembrane transport	7	0.332009561	0.0048	0.006748379
GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	76	0.331917632	0.0009	0.002399874
GO:0070314	G1 to G0 transition	6	0.331917632	0.0088	0.010992238
GO:1905666	regulation of protein localization to endosome	7	0.331899246	0.0025	0.004279479
GO:1900101	regulation of endoplasmic reticulum unfolded protein response	19	0.331856669	0.0082	0.010366713
GO:1901796	regulation of signal transduction by p53 class mediator	109	0.331722811	0.0003	0.001720882
GO:0043983	histone H4-K12 acetylation	6	0.331703132	0.0001	0.000877824
GO:0051125	regulation of actin nucleation	12	0.331638782	0.0015	0.003088691
GO:0006692	prostanoid metabolic process	21	0.331556046	< 0.001	< 0.001
GO:0006693	prostaglandin metabolic process	21	0.331556046	< 0.001	< 0.001
GO:0060338	regulation of type I interferon-mediated signaling pathway	15	0.331531532	0.0002	0.001341684
GO:0042780	tRNA 3'-end processing	6	0.331531532	0.0003	0.001720882
GO:0034135	regulation of toll-like receptor 2 signaling pathway	6	0.331488631	0.0023	0.004032435
GO:0006606	protein import into nucleus	84	0.331482503	0.0006	0.002177563
GO:0044744	protein targeting to nucleus	84	0.331482503	0.0006	0.002177563
GO:1902593	single-organism nuclear import	84	0.331482503	0.0006	0.002177563
GO:0031440	regulation of mRNA 3'-end processing	21	0.331482503	0.0006	0.002177563

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0031050	dsRNA fragmentation	31	0.331456802	0.0009	0.002399874
GO:0070918	production of small RNA involved in gene silencing by RNA	31	0.331456802	0.0009	0.002399874
GO:0006516	glycoprotein catabolic process	10	0.331402831	0.0001	0.000877824
GO:0050684	regulation of mRNA processing	79	0.331388169	0.0008	0.002313249
GO:0007129	synapsis	15	0.331359931	0.0004	0.002007244
GO:0006968	cellular defense response	23	0.331285323	0.0084	0.010571327
GO:0048144	fibroblast proliferation	50	0.331284427	0.0007	0.002248538
GO:0048145	regulation of fibroblast proliferation	50	0.331284427	0.0007	0.002248538
GO:0007260	tyrosine phosphorylation of STAT protein	35	0.331266777	< 0.001	< 0.001
GO:0006213	pyrimidine nucleoside metabolic process	32	0.331258044	0.0007	0.002248538
GO:0045682	regulation of epidermis development	39	0.331221331	0.0004	0.002007244
GO:0046634	regulation of alpha-beta T cell activation	47	0.331175552	0.0039	0.005778819
GO:0019395	fatty acid oxidation	61	0.33116442	0.0006	0.002177563
GO:0061081	positive regulation of myeloid leukocyte cytokine production involved in immune response	11	0.331157131	0.0041	0.005981983
GO:0031099	regeneration	103	0.331134186	0.0028	0.004605006
GO:1905332	positive regulation of morphogenesis of an epithelium	18	0.331131131	0.001	0.002498236
GO:0021587	cerebellum morphogenesis	20	0.331119691	0.0029	0.004714719
GO:0006851	mitochondrial calcium ion transport	15	0.331119691	0.0007	0.002248538
GO:0002645	positive regulation of tolerance induction	5	0.331119691	0.0265	0.028585731
GO:0072711	cellular response to hydroxyurea	5	0.331068211	0.0073	0.009463568
GO:0019336	phenol-containing compound catabolic process	6	0.331059631	0.0008	0.002313249
GO:1905668	positive regulation of protein localization to endosome	6	0.330973831	0.0037	0.005561344
GO:0042102	positive regulation of T cell proliferation	48	0.330941656	0.0013	0.002859821
GO:0071276	cellular response to cadmium ion	23	0.330893627	0.001	0.002498236
GO:0045639	positive regulation of myeloid cell differentiation	53	0.330890459	0.0019	0.003579279
GO:0043489	RNA stabilization	23	0.330882435	0.0007	0.002248538
GO:0042733	embryonic digit morphogenesis	33	0.330868531	0.0001	0.000877824
GO:0050919	negative chemotaxis	12	0.330866581	0.0003	0.001720882
GO:0042743	hydrogen peroxide metabolic process	23	0.330860053	0.0001	0.000877824
GO:0051127	positive regulation of actin nucleation	8	0.330855856	0.0007	0.002248538
GO:0019827	stem cell population maintenance	99	0.330754131	0.0003	0.001720882
GO:0021532	neural tube patterning	20	0.330746461	< 0.001	< 0.001
GO:0006657	CDP-choline pathway	5	0.330707851	0.0025	0.004279479
GO:0051782	negative regulation of cell division	8	0.330630631	0.0002	0.001341684
GO:0061179	negative regulation of insulin secretion involved in cellular response to glucose stimulus	7	0.330612245	0.0026	0.004377754
GO:0002246	wound healing involved in inflammatory response	6	0.330587731	0.0072	0.009362497
GO:0090594	inflammatory response to wounding	6	0.330587731	0.0072	0.009362497
GO:0044766	multi-organism transport	56	0.330575473	0.0009	0.002399874
GO:1902579	multi-organism localization	56	0.330575473	0.0009	0.002399874
GO:0046850	regulation of bone remodeling	24	0.330566281	0.0022	0.003910907
GO:0061626	pharyngeal arch artery morphogenesis	5	0.330553411	0.0004	0.002007244
GO:0050688	regulation of defense response to virus	69	0.330550426	0.0005	0.002177563
GO:0007252	I-kappaB phosphorylation	12	0.330544831	0.0001	0.000877824
GO:0065004	protein-DNA complex assembly	116	0.330513025	< 0.001	< 0.001
GO:1902003	regulation of beta-amyloid formation	13	0.33048213	0.0027	0.004491543
GO:1902991	regulation of amyloid precursor protein catabolic process	13	0.33048213	0.0027	0.004491543
GO:0000460	maturation of 5.8S rRNA	9	0.33041613	0.0008	0.002313249
GO:0001910	regulation of leukocyte mediated cytotoxicity	26	0.33040293	0.0022	0.003910907
GO:0009208	pyrimidine ribonucleoside triphosphate metabolic process	9	0.33038753	0.0055	0.007544447
GO:0055090	acylglycerol homeostasis	13	0.33038313	0.0018	0.003459409
GO:0070328	triglyceride homeostasis	13	0.33038313	0.0018	0.003459409
GO:0034035	purine ribonucleoside bisphosphate metabolic process	12	0.33037323	0.0008	0.002313249
GO:0050427	3'-phosphoadenosine 5'-phosphosulfate metabolic process	12	0.33037323	0.0008	0.002313249
GO:0072203	cell proliferation involved in metanephros development	6	0.33028743	0.0001	0.000877824
GO:0016558	protein import into peroxisome matrix	10	0.33016731	0.0027	0.004491543
GO:1900151	regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	14	0.330152602	< 0.001	< 0.001
GO:1900153	positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	14	0.330152602	< 0.001	< 0.001
GO:0006896	Golgi to vacuole transport	6	0.33011583	0.0047	0.006644432
GO:0090160	Golgi to lysosome transport	6	0.33011583	0.0047	0.006644432
GO:0072329	monocarboxylic acid catabolic process	74	0.330035827	0.0012	0.002741075
GO:0043302	positive regulation of leukocyte degranulation	15	0.33000429	0.0098	0.012008345
GO:0000466	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	5	0.32993565	0.0143	0.016557758
GO:0018196	peptidyl-asparagine modification	27	0.32992993	0.0002	0.001341684
GO:0018279	protein N-linked glycosylation via asparagine	27	0.32992993	0.0002	0.001341684
GO:0010884	positive regulation of lipid storage	10	0.32990991	0.0009	0.002399874
GO:1904293	negative regulation of ERAD pathway	10	0.32990991	0.0026	0.004377754
GO:0043696	dedifferentiation	5	0.32988417	0.0001	0.000877824
GO:0043697	cell dedifferentiation	5	0.32988417	0.0001	0.000877824
GO:0033047	regulation of mitotic sister chromatid segregation	37	0.329868865	0.0001	0.000877824
GO:0050864	regulation of B cell activation	63	0.329868644	0.0002	0.001341684
GO:0030517	negative regulation of axon extension	8	0.32985843	0.0001	0.000877824
GO:0072525	pyridine-containing compound biosynthetic process	22	0.32979993	0.0003	0.001720882
GO:0045494	photoreceptor cell maintenance	20	0.32979408	0.0001	0.000877824
GO:0006479	protein methylation	105	0.329788564	0.0003	0.001720882
GO:0008213	protein alkylation	105	0.329788564	0.0003	0.001720882
GO:0046831	regulation of RNA export from nucleus	9	0.32978693	0.0022	0.003910907
GO:0050901	leukocyte tethering or rolling	13	0.32974953	0.0038	0.005666214
GO:0098727	maintenance of cell number	100	0.329740026	0.0003	0.001720882
GO:0006699	bile acid biosynthetic process	17	0.329638883	0.0012	0.002741075
GO:0002690	positive regulation of leukocyte chemotaxis	43	0.329550148	0.0021	0.003804235
GO:0045727	positive regulation of translation	89	0.32943184	0.0005	0.002177563
GO:0006303	double-strand break repair via nonhomologous end joining	44	0.329413829	0.0002	0.001341684
GO:0032878	regulation of establishment or maintenance of cell polarity	15	0.329403689	0.0019	0.003579279

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0065002	intracellular protein transmembrane transport	35	0.329376724	0.001	0.002498236
GO:1900408	negative regulation of cellular response to oxidative stress	24	0.329365079	0.0014	0.002975058
GO:1902883	negative regulation of response to oxidative stress	24	0.329365079	0.0014	0.002975058
GO:1903202	negative regulation of oxidative stress-induced cell death	24	0.329365079	0.0014	0.002975058
GO:1901607	alpha-amino acid biosynthetic process	39	0.329327129	0.0001	0.000877824
GO:0001912	positive regulation of leukocyte mediated cytotoxicity	19	0.329269119	0.0017	0.003334595
GO:0003351	epithelial cilium movement	10	0.329240669	< 0.001	< 0.001
GO:0006294	nucleotide-excision repair, preincision complex assembly	21	0.329202672	0.0001	0.000877824
GO:0010874	regulation of cholesterol efflux	14	0.329086229	< 0.001	< 0.001
GO:0032941	secretion by tissue	47	0.329078014	0.0002	0.001341684
GO:0022011	myelination in peripheral nervous system	18	0.329043329	0.0027	0.004491543
GO:0032292	peripheral nervous system axon ensheathment	18	0.329043329	0.0027	0.004491543
GO:0006260	DNA replication	162	0.329009962	0.0005	0.002177563
GO:0042771	intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	33	0.329004329	< 0.001	< 0.001
GO:0045342	MHC class II biosynthetic process	6	0.329000429	0.0001	0.000877824
GO:0045346	regulation of MHC class II biosynthetic process	6	0.329000429	0.0001	0.000877824
GO:2000035	regulation of stem cell division	6	0.329000429	0.0192	0.021362011
GO:0070664	negative regulation of leukocyte proliferation	40	0.328944659	0.0006	0.002177563
GO:0010665	regulation of cardiac muscle cell apoptotic process	20	0.328918919	0.0016	0.003223775
GO:0043568	positive regulation of insulin-like growth factor receptor signaling pathway	5	0.328906049	0.0141	0.016361854
GO:0071806	protein transmembrane transport	43	0.328891682	0.0013	0.002859821
GO:1902895	positive regulation of pri-miRNA transcription from RNA polymerase II promoter	18	0.328828829	0.0002	0.001341684
GO:1902106	negative regulation of leukocyte differentiation	49	0.328794684	0.0001	0.000877824
GO:0007520	myoblast fusion	16	0.328780566	0.0036	0.005475609
GO:0051930	regulation of sensory perception of pain	14	0.328773672	< 0.001	< 0.001
GO:0051931	regulation of sensory perception	14	0.328773672	< 0.001	< 0.001
GO:0019064	fusion of virus membrane with host plasma membrane	7	0.328773672	0.0086	0.010769857
GO:0039663	membrane fusion involved in viral entry into host cell	7	0.328773672	0.0086	0.010769857
GO:0044800	multi-organism membrane fusion	7	0.328773672	0.0086	0.010769857
GO:0021522	spinal cord motor neuron differentiation	16	0.328764479	< 0.001	< 0.001
GO:0009409	response to cold	29	0.328744508	0.0002	0.001341684
GO:0001516	prostaglandin biosynthetic process	15	0.328717289	< 0.001	< 0.001
GO:0046457	prostanoid biosynthetic process	15	0.328717289	< 0.001	< 0.001
GO:1901032	negative regulation of response to reactive oxygen species	9	0.328700129	0.0051	0.007095023
GO:1903206	negative regulation of hydrogen peroxide-induced cell death	9	0.328700129	0.0051	0.007095023
GO:0036005	response to macrophage colony-stimulating factor	6	0.328700129	0.0011	0.002610912
GO:0036006	cellular response to macrophage colony-stimulating factor stimulus	6	0.328700129	0.0011	0.002610912
GO:0006958	complement activation, classical pathway	17	0.328669846	0.0078	0.009981807
GO:0032615	interleukin-12 production	29	0.328655749	0.0001	0.000877824
GO:0032655	regulation of interleukin-12 production	29	0.328655749	0.0001	0.000877824
GO:0043414	macromolecule methylation	173	0.32857366	0.0007	0.002248538
GO:0030512	negative regulation of transforming growth factor beta receptor signaling pathway	45	0.328551409	0.0009	0.002399874
GO:0010212	response to ionizing radiation	95	0.328548398	0.0006	0.002177563
GO:0048549	positive regulation of pinocytosis	6	0.328485628	0.0022	0.003910907
GO:0072527	pyrimidine-containing compound metabolic process	50	0.328468468	0.0004	0.002007244
GO:0046131	pyrimidine ribonucleoside metabolic process	17	0.328412446	0.0076	0.009790742
GO:0055098	response to low-density lipoprotein particle	11	0.328395928	0.004	0.005880507
GO:0071404	cellular response to low-density lipoprotein particle stimulus	11	0.328395928	0.004	0.005880507
GO:0043044	ATP-dependent chromatin remodeling	39	0.328389928	0.0006	0.002177563
GO:0070126	mitochondrial translational termination	76	0.328385152	0.003	0.004825593
GO:0035280	miRNA loading onto RISC involved in gene silencing by miRNA	7	0.328332414	0.0079	0.010077402
GO:0060759	regulation of response to cytokine stimulus	99	0.328317928	0.0005	0.002177563
GO:0009108	coenzyme biosynthetic process	91	0.328312614	0.001	0.002498236
GO:0006730	one-carbon metabolic process	17	0.328261034	0.0006	0.002177563
GO:0009148	pyrimidine nucleoside triphosphate biosynthetic process	10	0.328236808	0.0042	0.006097175
GO:0072189	ureter development	8	0.328217503	0.0001	0.000877824
GO:0000413	protein peptidyl-prolyl isomerization	21	0.328197585	0.0001	0.000877824
GO:0048247	lymphocyte chemotaxis	17	0.328185328	0.0045	0.006417207
GO:0050871	positive regulation of B cell activation	42	0.328160814	< 0.001	< 0.001
GO:0050746	regulation of lipoprotein metabolic process	9	0.328156728	0.0007	0.002248538
GO:0001977	renal system process involved in regulation of blood volume	7	0.328148557	0.0272	0.02926158
GO:0009394	2'-deoxyribonucleotide metabolic process	19	0.328117591	0.0005	0.002177563
GO:0006625	protein targeting to peroxisome	52	0.328116028	0.0004	0.002007244
GO:0043574	peroxisomal transport	52	0.328116028	0.0004	0.002007244
GO:0072662	protein localization to peroxisome	52	0.328116028	0.0004	0.002007244
GO:0072663	establishment of protein localization to peroxisome	52	0.328116028	0.0004	0.002007244
GO:0048291	isotype switching to IgG isotypes	7	0.328111785	0.0006	0.002177563
GO:0007589	body fluid secretion	51	0.328104575	0.0003	0.001720882
GO:0045116	protein neddylation	10	0.328082368	0.001	0.002498236
GO:1902235	regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	21	0.328050499	0.0045	0.006417207
GO:1901201	regulation of extracellular matrix assembly	11	0.328021528	0.0047	0.006644432
GO:0001961	positive regulation of cytokine-mediated signaling pathway	28	0.327927928	0.002	0.003693422
GO:0060351	cartilage development involved in endochondral bone morphogenesis	8	0.327895753	0.0006	0.002177563
GO:0031648	protein destabilization	27	0.327889795	0.0009	0.002399874
GO:0009162	deoxyribonucleoside monophosphate metabolic process	9	0.327813528	0.0019	0.003579279
GO:0006289	nucleotide-excision repair	72	0.327788503	0.0001	0.000877824
GO:1901685	glutathione derivative metabolic process	17	0.327746234	< 0.001	< 0.001
GO:1901687	glutathione derivative biosynthetic process	17	0.327746234	< 0.001	< 0.001
GO:0006783	heme biosynthetic process	17	0.327731092	0.0064	0.008500875
GO:0003094	glomerular filtration	12	0.327670528	0.0222	0.024321919
GO:0045776	negative regulation of blood pressure	20	0.327657658	0.0004	0.002007244
GO:0002011	morphogenesis of an epithelial sheet	29	0.327581769	0.0014	0.002975058
GO:0043001	Golgi to plasma membrane protein transport	21	0.32757247	0.0017	0.003334595

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1903055	positive regulation of extracellular matrix organization	15	0.327550408	0.006	0.00807902
GO:0006307	DNA dealkylation involved in DNA repair	10	0.327516088	0.0035	0.005358035
GO:0042340	keratan sulfate catabolic process	8	0.327509653	0.0008	0.002313249
GO:0048243	norepinephrine secretion	8	0.327413127	< 0.001	< 0.001
GO:0002688	regulation of leukocyte chemotaxis	55	0.327394407	0.0013	0.002859821
GO:0035196	production of miRNAs involved in gene silencing by miRNA	29	0.327324369	0.0009	0.002399874
GO:1902570	protein localization to nucleolus	13	0.327314127	0.0004	0.002007244
GO:0032392	DNA geometric change	58	0.327306617	0.0008	0.002313249
GO:0001832	blastocyst growth	11	0.327272727	0.0006	0.002177563
GO:2000377	regulation of reactive oxygen species metabolic process	97	0.32721676	0.0006	0.002177563
GO:0035864	response to potassium ion	6	0.327155727	0.0004	0.002007244
GO:0021545	cranial nerve development	18	0.327141427	0.0004	0.002007244
GO:0003171	atrioventricular valve development	17	0.327080021	0.0001	0.000877824
GO:0003181	atrioventricular valve morphogenesis	17	0.327080021	0.0001	0.000877824
GO:0034080	CENP-A containing nucleosome assembly	16	0.327043115	0.0001	0.000877824
GO:0061641	CENP-A containing chromatin organization	16	0.327043115	0.0001	0.000877824
GO:0070125	mitochondrial translational elongation	75	0.327035607	0.003	0.004825593
GO:1903317	regulation of protein maturation	60	0.327031317	0.0028	0.004605006
GO:0055076	transition metal ion homeostasis	69	0.32700651	0.0008	0.002313249
GO:0002097	tRNA wobble base modification	10	0.326975547	0.0044	0.006304227
GO:0002281	macrophage activation involved in immune response	6	0.326898327	0.0014	0.002975058
GO:0007098	centrosome cycle	64	0.326874196	0.0007	0.002248538
GO:0051147	regulation of muscle cell differentiation	96	0.326836658	0.0009	0.002399874
GO:0033144	negative regulation of intracellular steroid hormone receptor signaling pathway	22	0.326816427	0.0009	0.002399874
GO:1903311	regulation of mRNA metabolic process	102	0.326812527	0.0008	0.002313249
GO:0002295	T-helper cell lineage commitment	5	0.326795367	0.0003	0.001720882
GO:0043373	CD4-positive, alpha-beta T cell lineage commitment	5	0.326795367	0.0003	0.001720882
GO:0000303	response to superoxide	20	0.326769627	0.0007	0.002248538
GO:0000305	response to oxygen radical	20	0.326769627	0.0007	0.002248538
GO:0017038	protein import	114	0.326742532	0.0006	0.002177563
GO:0046851	negative regulation of bone remodeling	8	0.326673102	0.0066	0.008731949
GO:0001990	regulation of systemic arterial blood pressure by hormone	10	0.326666667	0.0058	0.007856196
GO:0006553	lysine metabolic process	9	0.326640927	0.0013	0.002859821
GO:0006554	lysine catabolic process	9	0.326640927	0.0013	0.002859821
GO:0046949	fatty-acyl-CoA biosynthetic process	20	0.326615187	0.0039	0.005778819
GO:0061077	chaperone-mediated protein folding	27	0.326612327	0.0005	0.002177563
GO:0046112	nucleobase biosynthetic process	8	0.326576577	0.0071	0.009268394
GO:0014896	muscle hypertrophy	40	0.326544402	0.0007	0.002248538
GO:0014823	response to activity	37	0.326508748	0.0014	0.002975058
GO:0070193	synaptonemal complex organization	10	0.326486486	0.0005	0.002177563
GO:2000482	regulation of interleukin-8 secretion	15	0.326435006	0.0019	0.003579279
GO:0009299	mRNA transcription	17	0.32642895	0.0068	0.008946408
GO:0001885	endothelial cell development	35	0.326412944	0.0016	0.003223775
GO:0061154	endothelial tube morphogenesis	11	0.326336726	0.0035	0.005358035
GO:0035561	regulation of chromatin binding	17	0.326277538	< 0.001	< 0.001
GO:2000142	regulation of DNA-templated transcription, initiation	20	0.326241956	0.0003	0.001720882
GO:0034243	regulation of transcription elongation from RNA polymerase II promoter	16	0.326190476	0.0047	0.006644432
GO:0050860	negative regulation of T cell receptor signaling pathway	10	0.326151866	0.0004	0.002007244
GO:0007063	regulation of sister chromatid cohesion	14	0.326144512	0.0043	0.006204188
GO:0008298	intracellular mRNA localization	6	0.326126126	0.0135	0.015731487
GO:0015697	quaternary ammonium group transport	6	0.326126126	0.0102	0.012424427
GO:0072606	interleukin-8 secretion	16	0.326093951	0.0019	0.003579279
GO:0007320	insemination	6	0.326083226	< 0.001	< 0.001
GO:0006505	GPI anchor metabolic process	24	0.326061776	0.0012	0.002741075
GO:0007084	mitotic nuclear envelope reassembly	7	0.326052583	0.0003	0.001720882
GO:2001243	negative regulation of intrinsic apoptotic signaling pathway	59	0.326030146	0.0006	0.002177563
GO:0002438	acute inflammatory response to antigenic stimulus	10	0.326023166	0.0009	0.002399874
GO:0061052	negative regulation of cell growth involved in cardiac muscle cell development	5	0.326023166	0.0026	0.004377754
GO:0046477	glycosylceramide catabolic process	5	0.325971686	0.0083	0.010468217
GO:0036010	protein localization to endosome	14	0.325960655	0.0085	0.010671887
GO:0071281	cellular response to iron ion	8	0.325933076	0.0041	0.005981983
GO:0060443	mammary gland morphogenesis	19	0.325922915	0.0031	0.004916949
GO:0030217	T cell differentiation	116	0.325908667	0.0007	0.002248538
GO:0003256	regulation of transcription from RNA polymerase II promoter involved in myocardial precursor cell differentiation	5	0.325868726	0.0153	0.017559319
GO:0009895	negative regulation of catabolic process	99	0.325853126	0.0011	0.002610912
GO:2000042	negative regulation of double-strand break repair via homologous recombination	11	0.325845326	< 0.001	< 0.001
GO:0035418	protein localization to synapse	8	0.325836551	0.0007	0.002248538
GO:0003170	heart valve development	37	0.325833942	< 0.001	< 0.001
GO:0006414	translational elongation	102	0.325777879	0.0024	0.004156304
GO:0006296	nucleotide-excision repair, DNA incision, 5'-to lesion	28	0.325776797	0.0016	0.003223775
GO:0033683	nucleotide-excision repair, DNA incision	29	0.325717836	0.0019	0.003579279
GO:0008608	attachment of spindle microtubules to kinetochore	20	0.325701416	0.0027	0.004491543
GO:0034440	lipid oxidation	63	0.325701211	0.0006	0.002177563
GO:0090278	negative regulation of peptide hormone secretion	22	0.325681526	0.0009	0.002399874
GO:0021766	hippocampus development	36	0.325675676	0.0002	0.001341684
GO:0090305	nucleic acid phosphodiester bond hydrolysis	183	0.325647896	0.0005	0.002177563
GO:0043618	regulation of transcription from RNA polymerase II promoter in response to stress	85	0.325626467	0.0011	0.002610912
GO:0098930	axonal transport	25	0.325621622	0.001	0.002498236
GO:0051013	microtubule severing	7	0.325611326	0.0097	0.011922488
GO:0051898	negative regulation of protein kinase B signaling	28	0.325602133	0.0037	0.005561344
GO:2000379	positive regulation of reactive oxygen species metabolic process	46	0.325588943	0.0008	0.002313249
GO:0044786	cell cycle DNA replication	37	0.325576542	0.0008	0.002313249

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0046628	positive regulation of insulin receptor signaling pathway	11	0.325564526	0.0006	0.002177563
GO:0030953	astral microtubule organization	5	0.325559846	0.0005	0.002177563
GO:0045739	positive regulation of DNA repair	39	0.325545326	0.0008	0.002313249
GO:0006261	DNA-dependent DNA replication	86	0.325542486	0.0008	0.002313249
GO:0046039	GTP metabolic process	18	0.325539826	0.0013	0.002859821
GO:0071677	positive regulation of mononuclear cell migration	14	0.325537783	0.0002	0.001341684
GO:0060538	skeletal muscle organ development	79	0.325520095	0.003	0.004825593
GO:0032733	positive regulation of interleukin-10 production	18	0.325496925	0.0006	0.002177563
GO:0043301	negative regulation of leukocyte degranulation	7	0.32546424	0.0003	0.001720882
GO:0051342	regulation of cyclic-nucleotide phosphodiesterase activity	5	0.325456885	0.017	0.019243517
GO:0030316	osteoclast differentiation	50	0.325410553	0.0037	0.005561344
GO:0032006	regulation of TOR signaling	51	0.325404396	0.0011	0.002610912
GO:2000773	negative regulation of cellular senescence	12	0.325396825	0.0007	0.002248538
GO:0010970	transport along microtubule	83	0.32539114	0.0001	0.000877824
GO:0099111	microtubule-based transport	83	0.32539114	0.0001	0.000877824
GO:0002696	positive regulation of leukocyte activation	160	0.325379665	0.0006	0.002177563
GO:0001711	endodermal cell fate commitment	8	0.32532175	0.0007	0.002248538
GO:2000209	regulation of anoikis	12	0.325311025	0.0078	0.009981807
GO:0030888	regulation of B cell proliferation	32	0.325265444	0.0006	0.002177563
GO:0046653	tetrahydrofolate metabolic process	14	0.325243611	0.0015	0.003088691
GO:0070339	response to bacterial lipopeptide	5	0.325199485	0.042	0.043800687
GO:0071220	cellular response to bacterial lipoprotein	5	0.325199485	0.042	0.043800687
GO:0071221	cellular response to bacterial lipopeptide	5	0.325199485	0.042	0.043800687
GO:0007031	peroxisome organization	60	0.325186615	0.0005	0.002177563
GO:0019377	glycolipid catabolic process	11	0.325143325	0.0035	0.005358035
GO:0000380	alternative mRNA splicing, via spliceosome	38	0.325110072	0.0017	0.003334595
GO:0050779	RNA destabilization	21	0.325084268	< 0.001	< 0.001
GO:0034599	cellular response to oxidative stress	167	0.325074947	0.0006	0.002177563
GO:0032481	positive regulation of type I interferon production	52	0.325056925	0.0002	0.001341684
GO:0042304	regulation of fatty acid biosynthetic process	26	0.325056925	0.0001	0.000877824
GO:0051923	sulfation	5	0.325045045	0.0036	0.005475609
GO:0000381	regulation of alternative mRNA splicing, via spliceosome	27	0.325029792	0.0014	0.002975058
GO:0060688	regulation of morphogenesis of a branching structure	27	0.325010725	0.0028	0.004605006
GO:0006878	cellular copper ion homeostasis	6	0.324924925	0.0002	0.001341684
GO:1901071	glucosamine-containing compound metabolic process	11	0.324909325	0.0002	0.001341684
GO:0050922	negative regulation of chemotaxis	19	0.324852672	0.0003	0.001720882
GO:1903350	response to dopamine	9	0.324839125	0.002	0.003693422
GO:0003044	regulation of systemic arterial blood pressure mediated by a chemical signal	13	0.324839125	0.0043	0.006204188
GO:0022409	positive regulation of cell-cell adhesion	121	0.324828488	0.0021	0.003804235
GO:0061157	mRNA destabilization	20	0.324800515	< 0.001	< 0.001
GO:0010890	positive regulation of sequestering of triglyceride	5	0.324736165	0.0004	0.002007244
GO:0051154	negative regulation of striated muscle cell differentiation	20	0.324723295	0.0014	0.002975058
GO:0043217	myelin maintenance	11	0.324698725	0.0041	0.005981983
GO:0070911	global genome nucleotide-excision repair	19	0.324690104	0.0011	0.002610912
GO:0045620	negative regulation of lymphocyte differentiation	24	0.324688975	0.0001	0.000877824
GO:0002221	pattern recognition receptor signaling pathway	110	0.324675325	0.0003	0.001720882
GO:0030850	prostate gland development	24	0.324667525	0.0006	0.002177563
GO:0006686	sphingomyelin biosynthetic process	5	0.324633205	0.0102	0.012424427
GO:0016024	CDP-diacylglycerol biosynthetic process	10	0.324607465	0.0002	0.001341684
GO:0010042	response to manganese ion	12	0.324560275	0.0078	0.009981807
GO:0046629	gamma-delta T cell activation	7	0.324544953	0.0029	0.004714719
GO:0034205	beta-amyloid formation	18	0.324538825	0.0063	0.008390784
GO:0050765	negative regulation of phagocytosis	11	0.324534925	0.0014	0.002975058
GO:0010803	regulation of tumor necrosis factor-mediated signaling pathway	38	0.324473346	0.001	0.002498236
GO:0060149	negative regulation of posttranscriptional gene silencing	8	0.324453024	0.0101	0.012328539
GO:0060967	negative regulation of gene silencing by RNA	8	0.324453024	0.0101	0.012328539
GO:0045685	regulation of glial cell differentiation	37	0.324449546	0.0028	0.004605006
GO:0008088	axo-dendritic transport	30	0.324444444	0.0017	0.003334595
GO:0006283	transcription-coupled nucleotide-excision repair	54	0.324419658	0.0004	0.002007244
GO:0045880	positive regulation of smoothened signaling pathway	17	0.32440003	< 0.001	< 0.001
GO:0070723	response to cholesterol	17	0.324339466	0.0001	0.000877824
GO:0045670	regulation of osteoclast differentiation	32	0.324332368	0.0058	0.007856196
GO:1901654	response to ketone	109	0.324319601	0.0004	0.002007244
GO:1904666	regulation of ubiquitin protein ligase activity	14	0.324305939	0.0008	0.002313249
GO:0046686	response to cadmium ion	39	0.324198924	0.0024	0.004156304
GO:0010677	negative regulation of cellular carbohydrate metabolic process	23	0.324111689	0.004	0.005880507
GO:0045667	regulation of osteoblast differentiation	64	0.324066924	0.0003	0.001720882
GO:0019885	antigen processing and presentation of endogenous peptide antigen via MHC class I	6	0.324024024	0.0197	0.021861066
GO:0046037	GMP metabolic process	7	0.323993381	0.0071	0.009268394
GO:0001959	regulation of cytokine-mediated signaling pathway	89	0.323983052	0.0005	0.002177563
GO:0043471	regulation of cellular carbohydrate catabolic process	6	0.323981124	0.0043	0.006204188
GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	78	0.323974524	0.0005	0.002177563
GO:0045638	negative regulation of myeloid cell differentiation	45	0.323969684	0.0004	0.002007244
GO:0032715	negative regulation of interleukin-6 production	19	0.32393145	0.0006	0.002177563
GO:0030488	tRNA methylation	20	0.323912484	0.0006	0.002177563
GO:0018022	peptidyl-lysine methylation	76	0.323870487	0.0006	0.002177563
GO:0006415	translational termination	87	0.323850945	0.003	0.004825593
GO:0042982	amyloid precursor protein metabolic process	35	0.323728627	0.005	0.006974174
GO:0003299	muscle hypertrophy in response to stress	9	0.323580724	0.0006	0.002177563
GO:0014887	cardiac muscle adaptation	9	0.323580724	0.0006	0.002177563
GO:0014898	cardiac muscle hypertrophy in response to stress	9	0.323580724	0.0006	0.002177563
GO:0043619	regulation of transcription from RNA polymerase II promoter in response to oxidative stress	9	0.323580724	0.0087	0.010877987
GO:0006390	transcription from mitochondrial promoter	10	0.323552124	0.0187	0.020874952

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0001881	receptor recycling	21	0.323527609	0.0041	0.005981983
GO:0051297	centrosome organization	67	0.323486813	0.0007	0.002248538
GO:0006335	DNA replication-dependent nucleosome assembly	8	0.323455598	0.0009	0.002399874
GO:0034723	DNA replication-dependent nucleosome organization	8	0.323455598	0.0009	0.002399874
GO:0032095	regulation of response to food	12	0.323337623	0.0007	0.002248538
GO:0034377	plasma lipoprotein particle assembly	13	0.323274923	< 0.001	< 0.001
GO:0060444	branching involved in mammary gland duct morphogenesis	10	0.323268983	0.0022	0.003910907
GO:0071214	cellular response to abiotic stimulus	188	0.323257756	0.0015	0.003088691
GO:0035020	regulation of Rac protein signal transduction	5	0.323243243	0.0259	0.02799537
GO:0045625	regulation of T-helper 1 cell differentiation	8	0.323198198	0.0004	0.002007244
GO:0032986	protein-DNA complex disassembly	13	0.323195723	0.0006	0.002177563
GO:0045058	T cell selection	19	0.323186344	0.0003	0.001720882
GO:0051188	cofactor biosynthetic process	121	0.323167087	0.001	0.002498236
GO:0045648	positive regulation of erythrocyte differentiation	18	0.323151723	0.0031	0.004916949
GO:0002347	response to tumor cell	14	0.323147637	0.0002	0.001341684
GO:0060601	lateral sprouting from an epithelium	5	0.323140283	0.014	0.01625173
GO:0042256	mature ribosome assembly	6	0.323123123	0.0015	0.003088691
GO:0042044	fluid transport	14	0.323110866	< 0.001	< 0.001
GO:0071243	cellular response to arsenic-containing substance	15	0.323071643	0.0019	0.003579279
GO:0010658	striated muscle cell apoptotic process	23	0.323026132	0.0014	0.002975058
GO:0060512	prostate gland morphogenesis	15	0.323003003	0.0055	0.007544447
GO:0010559	regulation of glycoprotein biosynthetic process	31	0.322995807	0.0018	0.003459409
GO:0007130	synaptonemal complex assembly	9	0.322980123	0.0002	0.001341684
GO:0000244	spliceosomal tri-snRNP complex assembly	8	0.322940798	0.0035	0.005358035
GO:0034250	positive regulation of cellular amide metabolic process	101	0.322930285	0.0005	0.002177563
GO:0006487	protein N-linked glycosylation	43	0.322881686	0.001	0.002498236
GO:0014912	negative regulation of smooth muscle cell migration	12	0.322865723	0.001	0.002498236
GO:0006354	DNA-templated transcription, elongation	79	0.322864637	< 0.001	< 0.001
GO:0070317	negative regulation of G0 to G1 transition	28	0.322816694	0.0006	0.002177563
GO:0051607	defense response to virus	165	0.322769003	0.0006	0.002177563
GO:0040014	regulation of multicellular organism growth	45	0.322734163	0.0002	0.001341684
GO:0050982	detection of mechanical stimulus	17	0.322719358	0.0036	0.005475609
GO:0045879	negative regulation of smoothened signaling pathway	15	0.322676963	0.0037	0.005561344
GO:0034605	cellular response to heat	75	0.322639211	0.0008	0.002313249
GO:0000768	syncytium formation by plasma membrane fusion	23	0.32258967	0.0037	0.005561344
GO:0071168	protein localization to chromatin	19	0.32253607	0.0023	0.004032435
GO:0019884	antigen processing and presentation of exogenous antigen	124	0.322530826	0.0013	0.002859821
GO:0030521	androgen receptor signaling pathway	39	0.322456522	0.0034	0.005263104
GO:0043467	regulation of generation of precursor metabolites and energy	82	0.322440908	0.0014	0.002975058
GO:0051220	cytoplasmic sequestering of protein	21	0.322412208	0.0002	0.001341684
GO:0071156	regulation of cell cycle arrest	68	0.322393822	0.0008	0.002313249
GO:0006566	threonine metabolic process	5	0.322368082	0.0022	0.003910907
GO:0014067	negative regulation of phosphatidylinositol 3-kinase signaling	9	0.322350922	0.0038	0.005666214
GO:0034504	protein localization to nucleus	160	0.322321429	0.0006	0.002177563
GO:0048050	post-embryonic eye morphogenesis	5	0.322316602	0.0055	0.007544447
GO:1903426	regulation of reactive oxygen species biosynthetic process	44	0.322306072	0.0007	0.002248538
GO:1902253	regulation of intrinsic apoptotic signaling pathway by p53 class mediator	22	0.322218322	0.0001	0.000877824
GO:1990173	protein localization to nucleoplasm	10	0.322213642	< 0.001	< 0.001
GO:0031069	hair follicle morphogenesis	13	0.322205722	0.0001	0.000877824
GO:0002827	positive regulation of T-helper 1 type immune response	6	0.322179322	0.0021	0.003804235
GO:0046651	lymphocyte proliferation	134	0.322142185	0.0009	0.002399874
GO:0043496	regulation of protein homodimerization activity	18	0.322079222	0.0107	0.012912536
GO:1902116	negative regulation of organelle assembly	27	0.322074455	0.0008	0.002313249
GO:0000083	regulation of transcription involved in G1/S transition of mitotic cell cycle	18	0.322064922	0.0012	0.002741075
GO:0003016	respiratory system process	14	0.322062879	< 0.001	< 0.001
GO:0007127	meiosis I	37	0.322049463	0.0006	0.002177563
GO:0030502	negative regulation of bone mineralization	9	0.321979122	0.0024	0.004156304
GO:0046033	AMP metabolic process	10	0.321930502	0.0031	0.004916949
GO:0097066	response to thyroid hormone	15	0.321870442	0.0041	0.005981983
GO:0097205	renal filtration	13	0.321869122	0.0197	0.021861066
GO:0006547	histidine metabolic process	5	0.321853282	< 0.001	< 0.001
GO:0052803	imidazole-containing compound metabolic process	5	0.321853282	< 0.001	< 0.001
GO:1904152	regulation of retrograde protein transport, ER to cytosol	9	0.321836122	0.0041	0.005981983
GO:0006690	icosanoid metabolic process	53	0.321803744	0.0005	0.002177563
GO:1901568	fatty acid derivative metabolic process	53	0.321803744	0.0005	0.002177563
GO:0050671	positive regulation of lymphocyte proliferation	68	0.321773034	0.0005	0.002177563
GO:0000963	mitochondrial RNA processing	10	0.321750322	0.0072	0.009362497
GO:2000134	negative regulation of G1/S transition of mitotic cell cycle	70	0.32173929	0.0024	0.004156304
GO:0045912	negative regulation of carbohydrate metabolic process	25	0.32172973	0.0044	0.006304227
GO:0032461	positive regulation of protein oligomerization	14	0.321695165	0.0019	0.003579279
GO:0071548	response to dexamethasone	23	0.321683174	0.0001	0.000877824
GO:0051131	chaperone-mediated protein complex assembly	11	0.321680122	0.0005	0.002177563
GO:0090398	cellular senescence	41	0.321668707	0.0006	0.002177563
GO:0006334	nucleosome assembly	62	0.321638228	0.0001	0.000877824
GO:0050730	regulation of peptidyl-tyrosine phosphorylation	109	0.321481114	0.0006	0.002177563
GO:0007398	ectoderm development	11	0.321446121	0.0029	0.004714719
GO:0097305	response to alcohol	98	0.321435138	0.0002	0.001341684
GO:0050867	positive regulation of cell activation	167	0.32143281	0.0006	0.002177563
GO:0061097	regulation of protein tyrosine kinase activity	40	0.321428571	0.0007	0.002248538
GO:0071476	cellular hypotonic response	7	0.321382607	0.0097	0.011922488
GO:0031054	pre-miRNA processing	9	0.321321321	0.0057	0.007745437
GO:0008217	regulation of blood pressure	79	0.321313719	0.0027	0.004491543
GO:1904153	negative regulation of retrograde protein transport, ER to cytosol	8	0.321299871	0.0054	0.007432873

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0043173	nucleotide salvage	9	0.321292721	0.0018	0.003459409
GO:0032943	mononuclear cell proliferation	135	0.321290815	0.0009	0.002399874
GO:1902105	regulation of leukocyte differentiation	139	0.321261446	0.0013	0.002859821
GO:0061734	parkin-mediated mitophagy in response to mitochondrial depolarization	5	0.321235521	0.002	0.003693422
GO:0061418	regulation of transcription from RNA polymerase II promoter in response to hypoxia	57	0.321212942	0.0017	0.003334595
GO:0030318	melanocyte differentiation	13	0.321195921	< 0.001	< 0.001
GO:0072673	lamellipodium morphogenesis	10	0.321184041	0.0195	0.021665533
GO:0061158	3'-UTR-mediated mRNA destabilization	10	0.321132561	0.0028	0.004605006
GO:0044650	adhesion of symbiont to host cell	7	0.321125207	0.0032	0.005044175
GO:0035723	interleukin-15-mediated signaling pathway	6	0.321106821	0.0006	0.002177563
GO:0070672	response to interleukin-15	6	0.321106821	0.0006	0.002177563
GO:0071350	cellular response to interleukin-15	6	0.321106821	0.0006	0.002177563
GO:0008354	germ cell migration	6	0.321106821	0.0094	0.011616482
GO:0070661	leukocyte proliferation	145	0.32107398	0.0005	0.002177563
GO:2000726	negative regulation of cardiac muscle cell differentiation	10	0.321055341	0.0008	0.002313249
GO:0010759	positive regulation of macrophage chemotaxis	8	0.321042471	0.0011	0.002610912
GO:0060669	embryonic placenta morphogenesis	13	0.320978121	0.0007	0.002248538
GO:0048002	antigen processing and presentation of peptide antigen	134	0.320966596	0.0013	0.002859821
GO:0033688	regulation of osteoblast proliferation	14	0.32094135	0.0069	0.009046225
GO:0007224	smoothened signaling pathway	77	0.32094135	< 0.001	< 0.001
GO:2000138	positive regulation of cell proliferation involved in heart morphogenesis	5	0.320926641	0.0001	0.000877824
GO:2000778	positive regulation of interleukin-6 secretion	18	0.320920921	0.0007	0.002248538
GO:0031532	actin cytoskeleton reorganization	48	0.320913771	0.0002	0.001341684
GO:0002478	antigen processing and presentation of exogenous peptide antigen	123	0.320898599	0.0015	0.003088691
GO:0002888	positive regulation of myeloid leukocyte mediated immunity	19	0.320856195	0.0146	0.016871405
GO:0008589	regulation of smoothened signaling pathway	44	0.320855271	0.0001	0.000877824
GO:0050857	positive regulation of antigen receptor-mediated signaling pathway	12	0.320849421	0.0002	0.001341684
GO:0031570	DNA integrity checkpoint	94	0.32080287	0.0007	0.002248538
GO:0002920	regulation of humoral immune response	33	0.320751921	0.0041	0.005981983
GO:0021675	nerve development	29	0.320711845	0.0007	0.002248538
GO:0048538	thymus development	18	0.320706421	0.0034	0.005263104
GO:0019098	reproductive behavior	12	0.320699271	< 0.001	< 0.001
GO:0034375	high-density lipoprotein particle remodeling	9	0.320692121	0.0003	0.001720882
GO:0042100	B cell proliferation	39	0.320667921	0.0019	0.003579279
GO:0090329	regulation of DNA-dependent DNA replication	26	0.320661321	0.0005	0.002177563
GO:0045069	regulation of viral genome replication	60	0.320660661	0.0006	0.002177563
GO:2001252	positive regulation of chromosome organization	50	0.320653797	0.0001	0.000877824
GO:0030101	natural killer cell activation	32	0.320632239	0.0024	0.004156304
GO:0042772	DNA damage response, signal transduction resulting in transcription	12	0.320613471	0.0005	0.002177563
GO:0001706	endoderm formation	27	0.320577721	0.0006	0.002177563
GO:0039532	negative regulation of viral-induced cytoplasmic pattern recognition receptor signaling pathway	9	0.320549121	0.003	0.004825593
GO:0031341	regulation of cell killing	33	0.320502321	0.005	0.006974174
GO:0010972	negative regulation of G2/M transition of mitotic cell cycle	61	0.320484419	0.0009	0.002399874
GO:0009066	aspartate family amino acid metabolic process	36	0.32046332	0.0005	0.002177563
GO:0001824	blastocyst development	55	0.32040716	0.0005	0.002177563
GO:0051900	regulation of mitochondrial depolarization	13	0.32038412	0.0097	0.011922488
GO:0010823	negative regulation of mitochondrion organization	35	0.320382423	0.0021	0.003804235
GO:0006551	leucine metabolic process	5	0.32036036	0.0103	0.012519912
GO:0006552	leucine catabolic process	5	0.32036036	0.0103	0.012519912
GO:0061178	regulation of insulin secretion involved in cellular response to glucose stimulus	26	0.32031482	0.0002	0.001341684
GO:0035773	insulin secretion involved in cellular response to glucose stimulus	28	0.320297849	0.0003	0.001720882
GO:0044774	mitotic DNA integrity checkpoint	65	0.32027324	0.0011	0.002610912
GO:0000722	telomere maintenance via recombination	5	0.3202574	0.0007	0.002248538
GO:0043488	regulation of mRNA stability	116	0.320252519	0.0003	0.001720882
GO:0097696	STAT cascade	72	0.320180895	0.0002	0.001341684
GO:0071397	cellular response to cholesterol	10	0.32018018	< 0.001	< 0.001
GO:0048255	mRNA stabilization	19	0.320178825	0.0017	0.003334595
GO:0033137	negative regulation of peptidyl-serine phosphorylation	13	0.32014652	0.0101	0.012328539
GO:0034284	response to monosaccharide	100	0.320133848	0.0012	0.002741075
GO:0032946	positive regulation of mononuclear cell proliferation	69	0.320112659	0.0005	0.002177563
GO:0032627	interleukin-23 production	5	0.32010296	0.0018	0.003459409
GO:0032667	regulation of interleukin-23 production	5	0.32010296	0.0018	0.003459409
GO:0050711	negative regulation of interleukin-1 secretion	6	0.32007722	0.01	0.012232246
GO:0060441	epithelial tube branching involved in lung morphogenesis	15	0.32006864	0.0005	0.002177563
GO:0030071	regulation of mitotic metaphase/anaphase transition	27	0.32003432	< 0.001	< 0.001
GO:1905523	positive regulation of macrophage migration	12	0.32003432	0.001	0.002498236
GO:0014745	negative regulation of muscle adaptation	6	0.31999142	0.0124	0.014577606
GO:0036507	protein demannosylation	15	0.31998284	0.0006	0.002177563
GO:0036508	protein alpha-1,2-demannosylation	15	0.31998284	0.0006	0.002177563
GO:0019724	B cell mediated immunity	63	0.319973034	0.0003	0.001720882
GO:0019433	triglyceride catabolic process	12	0.31996997	< 0.001	< 0.001
GO:0048265	response to pain	14	0.319966906	0.0018	0.003459409
GO:0070233	negative regulation of T cell apoptotic process	12	0.31992707	0.0006	0.002177563
GO:0014897	striated muscle hypertrophy	39	0.31990892	0.0009	0.002399874
GO:0006356	regulation of transcription from RNA polymerase I promoter	25	0.319907336	0.0005	0.002177563
GO:0003413	chondrocyte differentiation involved in endochondral bone morphogenesis	5	0.31984556	0.0049	0.006860215
GO:0051250	negative regulation of lymphocyte activation	69	0.319795572	0.0003	0.001720882
GO:0009267	cellular response to starvation	81	0.319729253	0.0014	0.002975058
GO:0000077	DNA damage checkpoint	89	0.319717149	0.0006	0.002177563
GO:0045669	positive regulation of osteoblast differentiation	35	0.31969112	< 0.001	< 0.001
GO:0034085	establishment of sister chromatid cohesion	5	0.31969112	0.0147	0.016962357
GO:0071921	cohesin loading	5	0.31969112	0.0147	0.016962357
GO:1901991	negative regulation of mitotic cell cycle phase transition	150	0.319684256	0.001	0.002498236

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0035384	thioester biosynthetic process	35	0.319669057	0.0047	0.006644432
GO:0071616	acyl-CoA biosynthetic process	35	0.319669057	0.0047	0.006644432
GO:0031644	regulation of neurological system process	40	0.319658945	0.0002	0.001341684
GO:1902807	negative regulation of cell cycle G1/S phase transition	71	0.319658491	0.0024	0.004156304
GO:0043487	regulation of RNA stability	119	0.319595946	0.0003	0.001720882
GO:0001732	formation of cytoplasmic translation initiation complex	12	0.31954097	0.0009	0.002399874
GO:0034728	nucleosome organization	80	0.319520592	0.0004	0.002007244
GO:2000047	regulation of cell-cell adhesion mediated by cadherin	6	0.319476619	0.0011	0.002610912
GO:2000846	regulation of corticosteroid hormone secretion	8	0.319465894	0.0002	0.001341684
GO:0048715	negative regulation of oligodendrocyte differentiation	9	0.319462319	0.0009	0.002399874
GO:0006521	regulation of cellular amino acid metabolic process	43	0.319457664	0.0007	0.002248538
GO:0009437	carnitine metabolic process	11	0.319363519	< 0.001	< 0.001
GO:1990090	cellular response to nerve growth factor stimulus	26	0.319344619	0.0012	0.002741075
GO:0046602	regulation of mitotic centrosome separation	5	0.319330759	0.0029	0.004714719
GO:0001553	luteinization	7	0.319323405	< 0.001	< 0.001
GO:0009743	response to carbohydrate	115	0.319194225	0.0009	0.002399874
GO:0048713	regulation of oligodendrocyte differentiation	24	0.319176319	0.0011	0.002610912
GO:0034614	cellular response to reactive oxygen species	88	0.319123669	0.0014	0.002975058
GO:2000677	regulation of transcription regulatory region DNA binding	29	0.31908756	0.0007	0.002248538
GO:1904894	positive regulation of STAT cascade	42	0.319072133	0.0002	0.001341684
GO:0021535	cell migration in hindbrain	5	0.319021879	0.0044	0.006304227
GO:0009953	dorsal/ventral pattern formation	47	0.318990115	< 0.001	< 0.001
GO:0071425	hematopoietic stem cell proliferation	10	0.318970399	0.0061	0.008182551
GO:0060428	lung epithelium development	18	0.318961819	0.0046	0.006532041
GO:0070734	histone H3-K27 methylation	14	0.31895569	0.0014	0.002975058
GO:0006890	retrograde vesicle-mediated transport, Golgi to ER	51	0.318944154	0.0013	0.002859821
GO:0019229	regulation of vasoconstriction	21	0.318918919	0.0023	0.004032435
GO:1901532	regulation of hematopoietic progenitor cell differentiation	64	0.318910875	0.001	0.002498236
GO:0010591	regulation of lamellipodium assembly	10	0.318893179	0.0027	0.004491543
GO:0048070	regulation of developmental pigmentation	9	0.318890319	0.0031	0.004916949
GO:0031929	TOR signaling	60	0.318880309	0.0016	0.003223775
GO:0046605	regulation of centrosome cycle	32	0.318822394	0.0001	0.000877824
GO:0045023	G0 to G1 transition	31	0.31881928	0.0008	0.002313249
GO:1903321	negative regulation of protein modification by small protein conjugation or removal	56	0.318794815	0.0008	0.002313249
GO:0048846	axon extension involved in axon guidance	7	0.318771833	< 0.001	< 0.001
GO:1902284	neuron projection extension involved in neuron projection guidance	7	0.318771833	< 0.001	< 0.001
GO:0071871	response to epinephrine	7	0.318771833	0.004	0.005880507
GO:0014812	muscle cell migration	43	0.318727365	0.0006	0.002177563
GO:0033143	regulation of intracellular steroid hormone receptor signaling pathway	51	0.318717036	0.0012	0.002741075
GO:2000785	regulation of autophagosome assembly	24	0.318715144	0.0006	0.002177563
GO:0090263	positive regulation of canonical Wnt signaling pathway	83	0.31866462	0.0006	0.002177563
GO:0051348	negative regulation of transferase activity	145	0.318654418	0.0006	0.002177563
GO:0050910	detection of mechanical stimulus involved in sensory perception of sound	5	0.318610039	0.0057	0.007745437
GO:0010614	negative regulation of cardiac muscle hypertrophy	15	0.318610039	0.0028	0.004605006
GO:0014741	negative regulation of muscle hypertrophy	15	0.318610039	0.0028	0.004605006
GO:0045943	positive regulation of transcription from RNA polymerase I promoter	16	0.318581081	0.0007	0.002248538
GO:0006892	post-Golgi vesicle-mediated transport	53	0.318578956	0.0037	0.005561344
GO:0031145	anaphase-promoting complex-dependent catabolic process	60	0.318567139	0.0009	0.002399874
GO:0031960	response to corticosteroid	89	0.318557402	0.0005	0.002177563
GO:0044788	modulation by host of viral process	17	0.318525248	0.0006	0.002177563
GO:0003300	cardiac muscle hypertrophy	38	0.318512497	0.0009	0.002399874
GO:0016559	peroxisome fission	5	0.318507079	0.0009	0.002399874
GO:0016485	protein processing	125	0.318492664	0.0028	0.004605006
GO:0010833	telomere maintenance via telomere lengthening	52	0.318453618	< 0.001	< 0.001
GO:0035966	response to topologically incorrect protein	130	0.318439758	0.0019	0.003579279
GO:0006310	DNA recombination	142	0.318424058	< 0.001	< 0.001
GO:0051604	protein maturation	144	0.318420206	0.0027	0.004491543
GO:0000050	urea cycle	6	0.318404118	0.0001	0.000877824
GO:0019627	urea metabolic process	6	0.318404118	0.0001	0.000877824
GO:0071941	nitrogen cycle metabolic process	6	0.318404118	0.0001	0.000877824
GO:0075525	viral translational termination-reinitiation	5	0.318404118	0.002	0.003693422
GO:0046325	negative regulation of glucose import	8	0.318371943	0.0001	0.000877824
GO:0034067	protein localization to Golgi apparatus	12	0.318318318	0.0013	0.002859821
GO:0031497	chromatin assembly	71	0.318306234	0.0002	0.001341684
GO:0032330	regulation of chondrocyte differentiation	20	0.318223938	0.0001	0.000877824
GO:0045198	establishment of epithelial cell apical/basal polarity	7	0.318220261	0.0184	0.020586938
GO:0042094	interleukin-2 biosynthetic process	12	0.318211068	0.0047	0.006644432
GO:0007223	Wnt signaling pathway, calcium modulating pathway	19	0.318200908	0.0004	0.002007244
GO:0043620	regulation of DNA-templated transcription in response to stress	89	0.318158287	0.0011	0.002610912
GO:0043372	positive regulation of CD4-positive, alpha-beta T cell differentiation	13	0.318126918	0.0091	0.011322589
GO:0043407	negative regulation of MAP kinase activity	32	0.318122587	0.0005	0.002177563
GO:0022038	corpus callosum development	7	0.318109947	0.0017	0.00334595
GO:0072331	signal transduction by p53 class mediator	165	0.318098358	0.0007	0.002248538
GO:0032508	DNA duplex unwinding	51	0.318096248	0.0008	0.002313249
GO:0031023	microtubule organizing center organization	71	0.318085087	0.0006	0.002177563
GO:0046640	regulation of alpha-beta T cell proliferation	18	0.318075218	0.0183	0.020489441
GO:0046636	negative regulation of alpha-beta T cell activation	20	0.318056628	0.0004	0.002007244
GO:0045637	regulation of myeloid cell differentiation	131	0.31803472	0.0006	0.002177563
GO:0072273	metanephric nephron morphogenesis	16	0.318034106	0.0001	0.000877824
GO:0051384	response to glucocorticoid	79	0.318029422	0.0004	0.002007244
GO:0045861	negative regulation of proteolysis	159	0.317983212	0.0006	0.002177563
GO:2001238	positive regulation of extrinsic apoptotic signaling pathway	39	0.317975118	0.0021	0.003804235
GO:0045851	pH reduction	27	0.317975118	0.0034	0.005263104

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0051452	intracellular pH reduction	27	0.317975118	0.0034	0.005263104
GO:0045071	negative regulation of viral genome replication	35	0.317962861	0.0007	0.002248538
GO:0042795	snRNA transcription from RNA polymerase II promoter	51	0.317934741	0.0002	0.001341684
GO:0035774	positive regulation of insulin secretion involved in cellular response to glucose stimulus	13	0.317928918	0.0001	0.000877824
GO:0045923	positive regulation of fatty acid metabolic process	18	0.317903618	0.0029	0.004714719
GO:0071044	histone mRNA catabolic process	8	0.317889318	< 0.001	< 0.001
GO:0002931	response to ischemia	30	0.317889318	0.0024	0.004156304
GO:0002070	epithelial cell maturation	11	0.317865918	0.0151	0.01736105
GO:1903409	reactive oxygen species biosynthetic process	54	0.317855951	0.0006	0.002177563
GO:0042255	ribosome assembly	19	0.317848676	0.0011	0.002610912
GO:1902036	regulation of hematopoietic stem cell differentiation	54	0.317813051	0.0011	0.002610912
GO:0009636	response to toxic substance	117	0.317792518	0.0002	0.001341684
GO:0042398	cellular modified amino acid biosynthetic process	32	0.317784749	0.0025	0.004279479
GO:0001826	inner cell mass cell differentiation	5	0.317734878	0.0001	0.000877824
GO:0048841	regulation of axon extension involved in axon guidance	6	0.317717718	< 0.001	< 0.001
GO:0086069	bundle of His cell to Purkinje myocyte communication	5	0.317683398	0.0075	0.00968541
GO:0048026	positive regulation of mRNA splicing, via spliceosome	12	0.317674818	0.0043	0.006204188
GO:0006978	DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator	11	0.317655318	0.0007	0.002248538
GO:0070417	cellular response to cold	7	0.317631918	0.0023	0.004032435
GO:1902806	regulation of cell cycle G1/S phase transition	102	0.317591541	0.0023	0.004032435
GO:0002053	positive regulation of mesenchymal cell proliferation	16	0.317583655	0.0062	0.008281828
GO:0090344	negative regulation of cell aging	13	0.317552718	0.0011	0.002610912
GO:0007617	mating behavior	9	0.317517518	< 0.001	< 0.001
GO:0000018	regulation of DNA recombination	49	0.317505844	< 0.001	< 0.001
GO:0050920	regulation of chemotaxis	93	0.317499066	0.0004	0.002007244
GO:0090183	regulation of kidney development	30	0.317494637	0.0001	0.000877824
GO:0035306	positive regulation of dephosphorylation	24	0.317492492	0.0008	0.002313249
GO:0000729	DNA double-strand break processing	16	0.317471042	0.0005	0.002177563
GO:0010660	regulation of muscle cell apoptotic process	33	0.317468117	0.0021	0.003804235
GO:0010659	cardiac muscle cell apoptotic process	21	0.317411289	0.0011	0.002610912
GO:0003179	heart valve morphogenesis	32	0.317398649	< 0.001	< 0.001
GO:0046461	neutral lipid catabolic process	15	0.317374517	0.0005	0.002177563
GO:0046464	acylglycerol catabolic process	15	0.317374517	0.0005	0.002177563
GO:0006348	chromatin silencing at telomere	5	0.317374517	0.0123	0.014492124
GO:0001836	release of cytochrome c from mitochondria	35	0.317337746	0.0015	0.003088691
GO:0044773	mitotic DNA damage checkpoint	62	0.317337153	0.001	0.002498236
GO:0045191	regulation of isotype switching	19	0.31730678	< 0.001	< 0.001
GO:0090184	positive regulation of kidney development	22	0.317304317	0.0004	0.002007244
GO:0016064	immunoglobulin mediated immune response	62	0.317291485	0.0003	0.001720882
GO:0043484	regulation of RNA splicing	83	0.317284582	0.0015	0.003088691
GO:0002021	response to dietary excess	14	0.317227432	0.0011	0.002610912
GO:0042116	macrophage activation	43	0.317200922	0.0035	0.005358035
GO:0015693	magnesium ion transport	5	0.317168597	0.0176	0.019838132
GO:0043353	enucleate erythrocyte differentiation	5	0.317168597	0.0257	0.027793331
GO:1902231	positive regulation of intrinsic apoptotic signaling pathway in response to DNA damage	5	0.317168597	0.0084	0.010571327
GO:0048146	positive regulation of fibroblast proliferation	27	0.317164784	0.0016	0.003223775
GO:0048570	notochord morphogenesis	6	0.317117117	0.0251	0.027199847
GO:0007052	mitotic spindle organization	61	0.317104458	0.0009	0.002399874
GO:0001649	osteoblast differentiation	120	0.317042042	0.0006	0.002177563
GO:0070862	negative regulation of protein exit from endoplasmic reticulum	9	0.317031317	0.0078	0.009981807
GO:0005980	glycogen catabolic process	14	0.317025188	0.0037	0.005561344
GO:0009251	glucan catabolic process	14	0.317025188	0.0037	0.005561344
GO:1901679	nucleotide transmembrane transport	5	0.317014157	0.0298	0.031859654
GO:0031397	negative regulation of protein ubiquitination	52	0.317013167	0.0008	0.002313249
GO:0071378	cellular response to growth hormone stimulus	14	0.316988417	0.0001	0.000877824
GO:0007259	JAK-STAT cascade	69	0.316964169	0.0002	0.001341684
GO:0006338	chromatin remodeling	80	0.316936937	0.0009	0.002399874
GO:1902750	negative regulation of cell cycle G2/M phase transition	67	0.316936553	0.0008	0.002313249
GO:0006399	tRNA metabolic process	117	0.316923517	0.0014	0.002975058
GO:0072593	reactive oxygen species metabolic process	143	0.316920917	0.0005	0.002177563
GO:0032722	positive regulation of chemokine production	30	0.316911197	0.0001	0.000877824
GO:0061136	regulation of proteasomal protein catabolic process	91	0.316890831	0.0006	0.002177563
GO:0016054	organic acid catabolic process	149	0.316842442	0.0009	0.002399874
GO:0046395	carboxylic acid catabolic process	149	0.316842442	0.0009	0.002399874
GO:0090002	establishment of protein localization to plasma membrane	27	0.31684065	0.001	0.002498236
GO:0045103	intermediate filament-based process	25	0.316839125	0.0022	0.003910907
GO:0045104	intermediate filament cytoskeleton organization	25	0.316839125	0.0022	0.003910907
GO:0031442	positive regulation of mRNA 3'-end processing	11	0.316789517	0.0032	0.005044175
GO:0045686	negative regulation of glial cell differentiation	12	0.316773917	0.0024	0.004156304
GO:0070391	response to lipoteichoic acid	6	0.316731017	0.0038	0.005666214
GO:0071223	cellular response to lipoteichoic acid	6	0.316731017	0.0038	0.005666214
GO:0043031	negative regulation of macrophage activation	6	0.316731017	0.0048	0.006748379
GO:0033687	osteoblast proliferation	16	0.316682754	0.0055	0.007544447
GO:0055072	iron ion homeostasis	53	0.316670309	0.0012	0.002741075
GO:2000117	negative regulation of cysteine-type endopeptidase activity	54	0.316664283	0.0006	0.002177563
GO:0045738	negative regulation of DNA repair	17	0.31664774	< 0.001	< 0.001
GO:0002371	dendritic cell cytokine production	9	0.316630917	0.0004	0.002007244
GO:0002730	regulation of dendritic cell cytokine production	9	0.316630917	0.0004	0.002007244
GO:0050701	interleukin-1 secretion	29	0.316620068	0.0001	0.000877824
GO:1902042	negative regulation of extrinsic apoptotic signaling pathway via death domain receptors	22	0.316614017	0.0061	0.008182551
GO:0045766	positive regulation of angiogenesis	95	0.316607736	0.0028	0.004605006
GO:0021554	optic nerve development	8	0.316570142	0.0049	0.006860215

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0044843	cell cycle G1/S phase transition	163	0.31655968	0.0008	0.002313249
GO:0009301	snRNA transcription	52	0.316513217	0.0003	0.001720882
GO:0044275	cellular carbohydrate catabolic process	24	0.316505792	0.0013	0.002859821
GO:0045086	positive regulation of interleukin-2 biosynthetic process	7	0.316492002	0.0199	0.022056122
GO:0032371	regulation of sterol transport	24	0.316462891	0.001	0.002498236
GO:0032374	regulation of cholesterol transport	24	0.316462891	0.001	0.002498236
GO:0070665	positive regulation of leukocyte proliferation	71	0.316439176	0.0005	0.002177563
GO:0016073	snRNA metabolic process	55	0.316438516	0.0003	0.001720882
GO:0070192	chromosome organization involved in meiotic cell cycle	20	0.316435006	0.0002	0.001341684
GO:0035510	DNA dealkylation	17	0.316405481	0.0023	0.004032435
GO:0009408	response to heat	102	0.316387816	0.0008	0.002313249
GO:0033238	regulation of cellular amine metabolic process	52	0.316384516	0.0004	0.002007244
GO:0050852	T cell receptor signaling pathway	116	0.316338259	0.0007	0.002248538
GO:0002887	negative regulation of myeloid leukocyte mediated immunity	5	0.316293436	0.0002	0.001341684
GO:0043305	negative regulation of mast cell degranulation	5	0.316293436	0.0002	0.001341684
GO:0010459	negative regulation of heart rate	8	0.316248391	0.0002	0.001341684
GO:0010390	histone monoubiquitination	21	0.316246859	0.0009	0.002399874
GO:0048753	pigment granule organization	19	0.316195895	0.0002	0.001341684
GO:1903362	regulation of cellular protein catabolic process	134	0.316189324	0.0004	0.002007244
GO:1903307	positive regulation of regulated secretory pathway	18	0.316187616	0.002	0.003693422
GO:1902166	negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	13	0.316127116	0.0001	0.000877824
GO:0032488	Cdc42 protein signal transduction	7	0.316087516	0.0007	0.002248538
GO:0021696	cerebellar cortex morphogenesis	16	0.316055341	0.0018	0.003459409
GO:0060740	prostate gland epithelium morphogenesis	14	0.316032359	0.0057	0.007745437
GO:0042417	dopamine metabolic process	18	0.316016016	0.0003	0.001720882
GO:0002320	lymphoid progenitor cell differentiation	10	0.316010296	0.0009	0.002399874
GO:0072332	intrinsic apoptotic signaling pathway by p53 class mediator	52	0.315998416	0.0006	0.002177563
GO:0046916	cellular transition metal ion homeostasis	55	0.315947116	0.0004	0.002007244
GO:0006879	cellular iron ion homeostasis	43	0.315943851	0.0005	0.002177563
GO:2001268	negative regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway	5	0.315933076	0.0003	0.001720882
GO:0035337	fatty-acyl-CoA metabolic process	23	0.315919646	0.0032	0.005044175
GO:0002523	leukocyte migration involved in inflammatory response	8	0.315894466	0.0007	0.002248538
GO:0097320	membrane tubulation	12	0.315851566	0.0055	0.007544447
GO:1902165	regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	15	0.315830116	0.0002	0.001341684
GO:0071294	cellular response to zinc ion	17	0.315814975	0.0016	0.003223775
GO:0050851	antigen receptor-mediated signaling pathway	136	0.315799833	0.0007	0.002248538
GO:0002643	regulation of tolerance induction	10	0.315778636	0.0144	0.016652368
GO:0006622	protein targeting to lysosome	16	0.315765766	0.0073	0.009463568
GO:1903428	positive regulation of reactive oxygen species biosynthetic process	24	0.315744316	0.0006	0.002177563
GO:0090197	positive regulation of chemokine secretion	12	0.315744316	< 0.001	< 0.001
GO:0044803	multi-organism membrane organization	28	0.315710609	0.0016	0.003223775
GO:0061082	myeloid leukocyte cytokine production	20	0.315688546	0.0019	0.003579279
GO:0002724	regulation of T cell cytokine production	12	0.315679966	0.0049	0.006860215
GO:2000045	regulation of G1/S transition of mitotic cell cycle	94	0.315622005	0.0027	0.004491543
GO:0051775	response to redox state	7	0.315609487	0.0003	0.001720882
GO:0032642	regulation of chemokine production	46	0.315583907	0.0002	0.001341684
GO:0050858	negative regulation of antigen receptor-mediated signaling pathway	14	0.315572716	0.0014	0.002975058
GO:0070584	mitochondrion morphogenesis	15	0.315572716	0.0011	0.002610912
GO:0051262	protein tetramerization	94	0.315515211	0.0005	0.002177563
GO:0002695	negative regulation of leukocyte activation	83	0.315495185	0.0003	0.001720882
GO:0060675	ureteric bud morphogenesis	36	0.315486915	0.0001	0.000877824
GO:0014015	positive regulation of gliogenesis	44	0.315484965	0.0033	0.005149584
GO:0060632	regulation of microtubule-based movement	14	0.315480787	< 0.001	< 0.001
GO:0070229	negative regulation of lymphocyte apoptotic process	16	0.31547619	0.0005	0.002177563
GO:0006275	regulation of DNA replication	58	0.315475081	0.0005	0.002177563
GO:0050667	homocysteine metabolic process	5	0.315469755	0.001	0.002498236
GO:0099024	plasma membrane invagination	32	0.315444015	0.0048	0.006748379
GO:1904356	regulation of telomere maintenance via telomere lengthening	41	0.315434598	0.0001	0.000877824
GO:1903050	regulation of proteolysis involved in cellular protein catabolic process	110	0.315420615	0.0006	0.002177563
GO:0006302	double-strand break repair	124	0.315365135	0.0003	0.001720882
GO:1901988	negative regulation of cell cycle phase transition	158	0.31534301	0.0009	0.002399874
GO:0002548	monocyte chemotaxis	20	0.315341055	0.0005	0.002177563
GO:0048298	positive regulation of isotype switching to IgA isotypes	5	0.315315315	0.0014	0.002975058
GO:0000082	G1/S transition of mitotic cell cycle	155	0.315311994	0.0008	0.002313249
GO:0006970	response to osmotic stress	49	0.315278544	0.0028	0.004605006
GO:0048290	isotype switching to IgA isotypes	6	0.315272415	0.0011	0.002610912
GO:0048296	regulation of isotype switching to IgA isotypes	6	0.315272415	0.0011	0.002610912
GO:0051965	positive regulation of synapse assembly	23	0.315248167	< 0.001	< 0.001
GO:1903672	positive regulation of sprouting angiogenesis	22	0.315233415	0.0011	0.002610912
GO:0010839	negative regulation of keratinocyte proliferation	5	0.315212355	0.0002	0.001341684
GO:0071897	DNA biosynthetic process	122	0.315199274	0.0004	0.002007244
GO:0006760	folic acid-containing compound metabolic process	20	0.315173745	0.0038	0.005666214
GO:2000514	regulation of CD4-positive, alpha-beta T cell activation	31	0.315149251	0.0024	0.004156304
GO:1903555	regulation of tumor necrosis factor superfamily cytokine production	81	0.315140537	0.0014	0.002975058
GO:0007406	negative regulation of neuroblast proliferation	5	0.315109395	0.0041	0.005981983
GO:0072111	cell proliferation involved in kidney development	10	0.315006435	0.0001	0.000877824
GO:0030278	regulation of ossification	102	0.314992303	0.0002	0.001341684
GO:0042976	activation of Janus kinase activity	7	0.314984372	< 0.001	< 0.001
GO:1902115	regulation of organelle assembly	106	0.314972924	0.0005	0.002177563
GO:0006893	Golgi to plasma membrane transport	28	0.314947601	0.0032	0.005044175
GO:0070498	interleukin-1-mediated signaling pathway	67	0.314927294	0.0011	0.002610912
GO:0061213	positive regulation of mesonephros development	13	0.314919315	0.0009	0.002399874

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0061217	regulation of mesonephros development	13	0.314919315	0.0009	0.002399874
GO:0090189	regulation of branching involved in ureteric bud morphogenesis	13	0.314919315	0.0009	0.002399874
GO:0090190	positive regulation of branching involved in ureteric bud morphogenesis	13	0.314919315	0.0009	0.002399874
GO:0090083	regulation of inclusion body assembly	11	0.314917515	0.0013	0.002859821
GO:0071467	cellular response to pH	9	0.314914915	0.0135	0.015731487
GO:0007077	mitotic nuclear envelope disassembly	7	0.314910829	< 0.001	< 0.001
GO:0009164	nucleoside catabolic process	19	0.314868252	0.0033	0.005149584
GO:0042113	B cell activation	121	0.314849442	0.0008	0.002313249
GO:0050777	negative regulation of immune response	71	0.314822267	0.0001	0.000877824
GO:0009749	response to glucose	93	0.314808818	0.001	0.002498236
GO:0006596	polyamine biosynthetic process	6	0.314800515	0.0023	0.004032435
GO:0036490	regulation of translation in response to endoplasmic reticulum stress	5	0.314800515	0.0002	0.001341684
GO:0001913	T cell mediated cytotoxicity	18	0.314771915	0.0069	0.009046225
GO:0045840	positive regulation of mitotic nuclear division	27	0.314667048	0.0023	0.004032435
GO:0030857	negative regulation of epithelial cell differentiation	22	0.314636715	0.0004	0.002007244
GO:0009266	response to temperature stimulus	134	0.314625713	0.0005	0.002177563
GO:0043153	entrainment of circadian clock by photoperiod	9	0.314600315	0.0015	0.003088691
GO:0036065	fucosylation	5	0.314594595	0.0382	0.040087041
GO:0036066	protein O-linked fucosylation	5	0.314594595	0.0382	0.040087041
GO:0046822	regulation of nucleocytoplasmic transport	89	0.314557575	0.0008	0.002313249
GO:0051785	positive regulation of nuclear division	28	0.314524729	0.0029	0.004714719
GO:1905517	macrophage migration	27	0.314514515	0.0004	0.002007244
GO:2000516	positive regulation of CD4-positive, alpha-beta T cell activation	17	0.314512832	0.0153	0.017559319
GO:1903909	regulation of receptor clustering	7	0.314506343	0.0003	0.001720882
GO:0014888	striated muscle adaptation	18	0.314485914	0.003	0.004825593
GO:0030705	cytoskeleton-dependent intracellular transport	89	0.314467919	0.0001	0.000877824
GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	63	0.314465486	0.0004	0.002007244
GO:1900180	regulation of protein localization to nucleus	92	0.314431201	0.0006	0.002177563
GO:0042308	negative regulation of protein import into nucleus	18	0.314428714	0.0003	0.001720882
GO:1904590	negative regulation of protein import	18	0.314428714	0.0003	0.001720882
GO:0045807	positive regulation of endocytosis	73	0.314416177	0.0015	0.003088691
GO:0000096	sulfur amino acid metabolic process	26	0.314404514	0.0001	0.000877824
GO:0032543	mitochondrial translation	104	0.314369864	0.0045	0.006417207
GO:1905268	negative regulation of chromatin organization	30	0.314362934	0.0001	0.000877824
GO:0042790	transcription of nuclear large rRNA transcript from RNA polymerase I promoter	10	0.314362934	0.0011	0.002610912
GO:1901836	regulation of transcription of nuclear large rRNA transcript from RNA polymerase I promoter	10	0.314362934	0.0011	0.002610912
GO:0050921	positive regulation of chemotaxis	69	0.314326749	0.0005	0.002177563
GO:0048025	negative regulation of mRNA splicing, via spliceosome	13	0.314325314	0.003	0.004825593
GO:0032490	detection of molecule of bacterial origin	7	0.314285714	0.0002	0.001341684
GO:0098581	detection of external biotic stimulus	7	0.314285714	0.0002	0.001341684
GO:0071887	leukocyte apoptotic process	58	0.3142724	0.0017	0.003334595
GO:0006493	protein O-linked glycosylation	60	0.314199914	0.0006	0.002177563
GO:2001242	regulation of intrinsic apoptotic signaling pathway	106	0.314132731	0.0011	0.002610912
GO:0071470	cellular response to osmotic stress	27	0.314123647	0.01	0.012232246
GO:0030183	B cell differentiation	64	0.314108752	0.0027	0.004491543
GO:0051310	metaphase plate congression	37	0.314042228	0.0001	0.000877824
GO:0045117	azole transport	11	0.314004914	0.0042	0.006097175
GO:0051004	regulation of lipoprotein lipase activity	10	0.314002574	0.0039	0.005778819
GO:0034198	cellular response to amino acid starvation	25	0.313966538	0.0006	0.002177563
GO:2001044	regulation of integrin-mediated signaling pathway	10	0.313951094	0.0041	0.005981983
GO:0051016	barbed-end actin filament capping	9	0.313942514	0.0009	0.002399874
GO:0045446	endothelial cell differentiation	59	0.313927972	0.0008	0.002313249
GO:0071435	potassium ion export	7	0.313918	0.0028	0.004605006
GO:0097623	potassium ion export across plasma membrane	7	0.313918	0.0028	0.004605006
GO:0006986	response to unfolded protein	121	0.313904932	0.0025	0.004279479
GO:0070663	regulation of leukocyte proliferation	115	0.313902971	0.0008	0.002313249
GO:0051973	positive regulation of telomerase activity	26	0.313899614	0.0001	0.000877824
GO:0002720	positive regulation of cytokine production involved in immune response	26	0.313830314	0.0021	0.003804235
GO:0002224	toll-like receptor signaling pathway	82	0.31381486	0.0006	0.002177563
GO:0042246	tissue regeneration	36	0.313799514	0.0076	0.009790742
GO:0032480	negative regulation of type I interferon production	31	0.313795823	0.0029	0.004714719
GO:0060788	ectodermal placode formation	8	0.313738739	0.0121	0.014285532
GO:0071696	ectodermal placode development	8	0.313738739	0.0121	0.014285532
GO:0071697	ectodermal placode morphogenesis	8	0.313738739	0.0121	0.014285532
GO:0032104	regulation of response to extracellular stimulus	15	0.313736594	0.0008	0.002313249
GO:0032107	regulation of response to nutrient levels	15	0.313736594	0.0008	0.002313249
GO:1901658	glycosyl compound catabolic process	24	0.313728014	0.0023	0.004032435
GO:1903830	magnesium ion transmembrane transport	8	0.313706564	0.022	0.024152627
GO:0032648	regulation of interferon-beta production	35	0.313645891	0.0006	0.002177563
GO:0032230	positive regulation of synaptic transmission, GABAergic	6	0.313642214	< 0.001	< 0.001
GO:0016556	mRNA modification	13	0.313632314	0.0027	0.004491543
GO:0080009	mRNA methylation	13	0.313632314	0.0027	0.004491543
GO:0016126	sterol biosynthetic process	48	0.313626126	0.0016	0.003223775
GO:0045601	regulation of endothelial cell differentiation	19	0.313567703	0.0012	0.002741075
GO:0019079	viral genome replication	78	0.313563014	0.0007	0.002248538
GO:0042307	positive regulation of protein import into nucleus	31	0.313538423	0.0012	0.002741075
GO:0035751	regulation of lysosomal lumen pH	10	0.313487773	0.025	0.027100697
GO:0016571	histone methylation	80	0.313481338	0.0011	0.002610912
GO:0031668	cellular response to extracellular stimulus	122	0.313454438	0.0011	0.002610912
GO:0043371	negative regulation of CD4-positive, alpha-beta T cell differentiation	12	0.313449163	0.0001	0.000877824
GO:0009072	aromatic amino acid family metabolic process	15	0.313427713	0.0015	0.003088691
GO:0043968	histone H2A acetylation	12	0.313427713	0.0001	0.000877824
GO:0045471	response to ethanol	70	0.313417908	0.0002	0.001341684

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0050854	regulation of antigen receptor-mediated signaling pathway	32	0.313416988	0.0004	0.002007244
GO:0071706	tumor necrosis factor superfamily cytokine production	85	0.313410553	0.0014	0.002975058
GO:0006623	protein targeting to vacuole	17	0.313407525	0.0045	0.006417207
GO:0072666	establishment of protein localization to vacuole	17	0.313407525	0.0045	0.006417207
GO:0009746	response to hexose	96	0.313392857	0.0014	0.002975058
GO:1902254	negative regulation of intrinsic apoptotic signaling pathway by p53 class mediator	17	0.313362102	< 0.001	< 0.001
GO:0034138	toll-like receptor 3 signaling pathway	14	0.313348042	0.0124	0.014577606
GO:0006388	tRNA splicing, via endonucleolytic cleavage and ligation	15	0.313324753	0.0026	0.004377754
GO:1903902	positive regulation of viral life cycle	75	0.313317889	0.0008	0.002313249
GO:2000484	positive regulation of interleukin-8 secretion	10	0.313307593	0.0187	0.020874952
GO:0046427	positive regulation of JAK-STAT cascade	39	0.313295713	0.0002	0.001341684
GO:1903533	regulation of protein targeting	103	0.3132911	0.0005	0.002177563
GO:0006085	acetyl-CoA biosynthetic process	15	0.313290433	0.0058	0.007856196
GO:0032984	macromolecular complex disassembly	184	0.31326031	0.0018	0.003459409
GO:0070316	regulation of G0 to G1 transition	30	0.313256113	0.0008	0.002313249
GO:2000106	regulation of leukocyte apoptotic process	42	0.313243856	0.0007	0.002248538
GO:0032606	type I interferon production	86	0.313241148	0.0006	0.002177563
GO:0072524	pyridine-containing compound metabolic process	111	0.313230605	0.0018	0.003459409
GO:0000188	inactivation of MAPK activity	9	0.313198913	0.004	0.005880507
GO:0032691	negative regulation of interleukin-1 beta production	14	0.313164185	0.011	0.013192134
GO:0042594	response to starvation	100	0.313142857	0.0014	0.002975058
GO:0030851	granulocyte differentiation	18	0.313141713	0.0013	0.002859821
GO:0060148	positive regulation of posttranscriptional gene silencing	15	0.313135993	0.0014	0.002975058
GO:2000637	positive regulation of gene silencing by miRNA	15	0.313135993	0.0014	0.002975058
GO:0002637	regulation of immunoglobulin production	34	0.313134984	< 0.001	< 0.001
GO:0002312	B cell activation involved in immune response	42	0.313133542	0.0006	0.002177563
GO:0032602	chemokine production	51	0.313109748	0.0001	0.000877824
GO:0050670	regulation of lymphocyte proliferation	109	0.313083726	0.0009	0.002399874
GO:2000780	negative regulation of double-strand break repair	16	0.313079151	< 0.001	< 0.001
GO:2001020	regulation of response to DNA damage stimulus	123	0.31305103	0.0006	0.002177563
GO:0045428	regulation of nitric oxide biosynthetic process	32	0.313014801	0.0007	0.002248538
GO:0046349	amino sugar biosynthetic process	9	0.312998713	0.0001	0.000877824
GO:2000696	regulation of epithelial cell differentiation involved in kidney development	11	0.312928513	0.0001	0.000877824
GO:0002831	regulation of response to biotic stimulus	102	0.312925531	0.0005	0.002177563
GO:0007194	negative regulation of adenylate cyclase activity	9	0.312912913	0.0037	0.005561344
GO:0030800	negative regulation of cyclic nucleotide metabolic process	9	0.312912913	0.0037	0.005561344
GO:0030803	negative regulation of cyclic nucleotide biosynthetic process	9	0.312912913	0.0037	0.005561344
GO:0030815	negative regulation of cAMP metabolic process	9	0.312912913	0.0037	0.005561344
GO:0030818	negative regulation of cAMP biosynthetic process	9	0.312912913	0.0037	0.005561344
GO:0031280	negative regulation of cyclase activity	9	0.312912913	0.0037	0.005561344
GO:0035726	common myeloid progenitor cell proliferation	5	0.312895753	0.0011	0.002610912
GO:0050435	beta-amyloid metabolic process	22	0.312893413	0.0083	0.010468217
GO:0071901	negative regulation of protein serine/threonine kinase activity	64	0.312890122	0.0008	0.002313249
GO:2000779	regulation of double-strand break repair	41	0.312860596	0.0001	0.000877824
GO:0022400	regulation of rhodopsin mediated signaling pathway	10	0.312844273	0.0071	0.009268394
GO:0090196	regulation of chemokine secretion	13	0.312820513	< 0.001	< 0.001
GO:0050866	negative regulation of cell activation	93	0.3127939	0.0004	0.002007244
GO:0002063	chondrocyte development	15	0.312792793	0.0002	0.001341684
GO:0006739	NADP metabolic process	22	0.312764713	0.0022	0.003910907
GO:0007093	mitotic cell cycle checkpoint	100	0.312759331	0.0007	0.002248538
GO:0072170	metanephric tubule development	14	0.312741313	0.0001	0.000877824
GO:0072234	metanephric nephron tubule development	14	0.312741313	0.0001	0.000877824
GO:0032438	melanosome organization	18	0.312727013	0.0002	0.001341684
GO:1901888	regulation of cell junction assembly	54	0.312717479	0.0016	0.003223775
GO:0009435	NAD biosynthetic process	17	0.31271103	0.0009	0.002399874
GO:0048730	epidermis morphogenesis	16	0.31269305	0.0001	0.000877824
GO:0032675	regulation of interleukin-6 production	67	0.312614534	0.0012	0.002741075
GO:0070373	negative regulation of ERK1 and ERK2 cascade	33	0.312561913	0.0014	0.002975058
GO:0006695	cholesterol biosynthetic process	45	0.312558273	0.0022	0.003910907
GO:1902653	secondary alcohol biosynthetic process	45	0.312558273	0.0022	0.003910907
GO:0070131	positive regulation of mitochondrial translation	11	0.312554113	0.0044	0.006304227
GO:0044344	cellular response to fibroblast growth factor stimulus	62	0.312533732	0.0003	0.001720882
GO:0006140	regulation of nucleotide metabolic process	92	0.312517486	0.0018	0.003459409
GO:0071675	regulation of mononuclear cell migration	26	0.312464112	0.0003	0.001720882
GO:0010001	glial cell differentiation	125	0.312424196	0.0015	0.003088691
GO:0010640	regulation of platelet-derived growth factor receptor signaling pathway	13	0.312404712	0.004	0.005880507
GO:0003159	morphogenesis of an endothelium	15	0.312398112	0.0044	0.006304227
GO:2000425	regulation of apoptotic cell clearance	5	0.312380952	0.0121	0.014285532
GO:0030098	lymphocyte differentiation	168	0.312376662	0.0014	0.002975058
GO:0048339	paraxial mesoderm development	11	0.312366912	< 0.001	< 0.001
GO:0070301	cellular response to hydrogen peroxide	54	0.312340912	0.0014	0.002975058
GO:0046661	male sex differentiation	91	0.312319855	0.0006	0.002177563
GO:0002369	T cell cytokine production	16	0.31230695	0.0037	0.005561344
GO:0061326	renal tubule development	52	0.312305712	0.0002	0.001341684
GO:0032434	regulation of proteasomal ubiquitin-dependent protein catabolic process	64	0.312298906	0.0013	0.002859821
GO:1900026	positive regulation of substrate adhesion-dependent cell spreading	22	0.312261612	0.0015	0.003088691
GO:0000302	response to reactive oxygen species	127	0.3122407	0.0014	0.002975058
GO:0050931	pigment cell differentiation	20	0.312175032	0.0004	0.002007244
GO:0045602	negative regulation of endothelial cell differentiation	5	0.312175032	0.0201	0.022258436
GO:0006271	DNA strand elongation involved in DNA replication	5	0.312123552	0.0045	0.006417207
GO:0032944	regulation of mononuclear cell proliferation	110	0.312121212	0.001	0.002498236
GO:0014819	regulation of skeletal muscle contraction	6	0.312097812	0.0003	0.001720882
GO:0043129	surfactant homeostasis	6	0.312097812	0.0008	0.002313249

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0048875	chemical homeostasis within a tissue	6	0.312097812	0.0008	0.002313249
GO:0051156	glucose 6-phosphate metabolic process	17	0.3120751	0.0014	0.002975058
GO:0042133	neurotransmitter metabolic process	18	0.312054912	< 0.001	< 0.001
GO:0016052	carbohydrate catabolic process	114	0.31204588	0.0018	0.003459409
GO:0002181	cytoplasmic translation	52	0.312003762	0.0006	0.002177563
GO:1904892	regulation of STAT cascade	56	0.312001287	0.0002	0.001341684
GO:0070189	kynurenine metabolic process	5	0.311969112	0.0029	0.004714719
GO:0001765	membrane raft assembly	6	0.311969112	0.0181	0.020286898
GO:0006883	cellular sodium ion homeostasis	5	0.311917632	0.0391	0.040970783
GO:1904018	positive regulation of vasculature development	105	0.311885763	0.0021	0.003804235
GO:0032732	positive regulation of interleukin-1 production	24	0.311883312	0.0001	0.000877824
GO:0007051	spindle organization	91	0.311870112	0.0009	0.002399874
GO:0001562	response to protozoan	7	0.311822026	< 0.001	< 0.001
GO:0042832	defense response to protozoan	7	0.311822026	< 0.001	< 0.001
GO:0071774	response to fibroblast growth factor	65	0.311806752	0.0004	0.002007244
GO:0034154	toll-like receptor 7 signaling pathway	5	0.311763192	0.0003	0.001720882
GO:0048515	spermatid differentiation	55	0.311758512	0.0001	0.000877824
GO:0072425	signal transduction involved in G2 DNA damage checkpoint	6	0.311754612	0.0005	0.002177563
GO:0014910	regulation of smooth muscle cell migration	32	0.311743887	0.0008	0.002313249
GO:0019682	glyceraldehyde-3-phosphate metabolic process	13	0.311711712	0.0078	0.009981807
GO:0034134	toll-like receptor 2 signaling pathway	11	0.311711712	0.0014	0.002975058
GO:0002517	T cell tolerance induction	6	0.311668812	0.0185	0.020677043
GO:0032526	response to retinoic acid	47	0.311640516	0.0002	0.001341684
GO:0006656	phosphatidylcholine biosynthetic process	27	0.311625912	0.0019	0.003579279
GO:0070757	interleukin-35-mediated signaling pathway	6	0.311625912	< 0.001	< 0.001
GO:0006333	chromatin assembly or disassembly	86	0.311621921	0.0004	0.002007244
GO:0002313	mature B cell differentiation involved in immune response	13	0.311592912	0.016	0.018267288
GO:0010464	regulation of mesenchymal cell proliferation	20	0.311570142	0.0061	0.008182551
GO:0002248	connective tissue replacement involved in inflammatory response wound healing	5	0.311557272	0.0091	0.011322589
GO:0045979	positive regulation of nucleoside metabolic process	23	0.311543842	0.0013	0.002859821
GO:1903580	positive regulation of ATP metabolic process	23	0.311543842	0.0013	0.002859821
GO:0046888	negative regulation of hormone secretion	29	0.311534194	0.0008	0.002313249
GO:0018212	peptidyl-tyrosine modification	157	0.311514973	0.0006	0.002177563
GO:0035608	protein deglutamylation	5	0.311505792	0.0031	0.004916949
GO:0009416	response to light stimulus	144	0.311500787	0.0007	0.002248538
GO:0043500	muscle adaptation	56	0.311463504	0.0035	0.005358035
GO:0031572	G2 DNA damage checkpoint	18	0.311454311	0.0011	0.002610912
GO:0006241	CTP biosynthetic process	8	0.311422136	0.0057	0.007745437
GO:0009209	pyrimidine ribonucleoside triphosphate biosynthetic process	8	0.311422136	0.0057	0.007745437
GO:0046036	CTP metabolic process	8	0.311422136	0.0057	0.007745437
GO:2001021	negative regulation of response to DNA damage stimulus	46	0.311415142	< 0.001	< 0.001
GO:0034502	protein localization to chromosome	56	0.311376172	0.0003	0.001720882
GO:0060033	anatomical structure regression	8	0.311357786	0.0064	0.008500875
GO:0045717	negative regulation of fatty acid biosynthetic process	10	0.311351351	< 0.001	< 0.001
GO:0009109	coenzyme catabolic process	7	0.311343997	< 0.001	< 0.001
GO:0060218	hematopoietic stem cell differentiation	58	0.311338925	0.001	0.002498236
GO:0050863	regulation of T cell activation	153	0.311321405	0.0013	0.002859821
GO:0048524	positive regulation of viral process	77	0.311290511	0.0008	0.002313249
GO:0002576	platelet degranulation	75	0.311282711	0.0007	0.002248538
GO:0030277	maintenance of gastrointestinal epithelium	12	0.311239811	0.0001	0.000877824
GO:0035810	positive regulation of urine volume	6	0.311239811	0.0035	0.005358035
GO:0071158	positive regulation of cell cycle arrest	53	0.311172628	0.0013	0.002859821
GO:1902914	regulation of protein polyubiquitination	14	0.31116014	0.0027	0.004491543
GO:0044743	intracellular protein transmembrane import	24	0.311132561	0.003	0.004825593
GO:1990542	mitochondrial transmembrane transport	39	0.311130911	0.0044	0.006304227
GO:1902389	ceramide 1-phosphate transport	6	0.311111111	0.0043	0.006204188
GO:0043555	regulation of translation in response to stress	13	0.311097911	0.0003	0.001720882
GO:0003014	renal system process	58	0.311072649	0.002	0.003693422
GO:0051153	regulation of striated muscle cell differentiation	48	0.311062849	0.0056	0.007655255
GO:0071356	cellular response to tumor necrosis factor	157	0.31103788	0.0003	0.001720882
GO:1904292	regulation of ERAD pathway	20	0.311029601	0.0035	0.005358035
GO:0032088	negative regulation of NF-kappaB transcription factor activity	47	0.31102166	0.0001	0.000877824
GO:1903779	regulation of cardiac conduction	21	0.311013054	0.0009	0.002399874
GO:0045070	positive regulation of viral genome replication	24	0.311003861	0.0007	0.002248538
GO:0035067	negative regulation of histone acetylation	7	0.310976282	0.0001	0.000877824
GO:0070278	extracellular matrix constituent secretion	7	0.310976282	0.0143	0.016557758
GO:0046856	phosphatidylinositol dephosphorylation	15	0.310905191	0.0071	0.009268394
GO:0033209	tumor necrosis factor-mediated signaling pathway	107	0.31089621	0.0003	0.001720882
GO:0007179	transforming growth factor beta receptor signaling pathway	105	0.310875774	0.0012	0.002741075
GO:0033673	negative regulation of kinase activity	127	0.310830065	0.0007	0.002248538
GO:0019882	antigen processing and presentation	152	0.310805731	0.0015	0.003088691
GO:0072401	signal transduction involved in DNA integrity checkpoint	45	0.310762191	0.0011	0.002610912
GO:0072422	signal transduction involved in DNA damage checkpoint	45	0.310762191	0.0011	0.002610912
GO:0030111	regulation of Wnt signaling pathway	191	0.310733321	0.0005	0.002177563
GO:0007097	nuclear migration	7	0.310718882	0.002	0.003693422
GO:0040023	establishment of nucleus localization	7	0.310718882	0.002	0.003693422
GO:0033262	regulation of nuclear cell cycle DNA replication	10	0.310707851	0.0064	0.008500875
GO:0010657	muscle cell apoptotic process	34	0.310697252	0.0018	0.003459409
GO:2001234	negative regulation of apoptotic signaling pathway	133	0.310691787	0.0019	0.003579279
GO:0007080	mitotic metaphase plate congression	29	0.310682111	0.0008	0.002313249
GO:0006949	syncytium formation	24	0.310628486	0.0037	0.005561344
GO:0046031	ADP metabolic process	71	0.310613229	0.003	0.004825593
GO:0001709	cell fate determination	18	0.310610611	0.0001	0.000877824

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0018108	peptidyl-tyrosine phosphorylation	156	0.310560011	0.0006	0.002177563
GO:0021782	glial cell development	70	0.310557088	0.0026	0.004377754
GO:0032210	regulation of telomere maintenance via telomerase	37	0.310549932	0.0001	0.000877824
GO:0071496	cellular response to external stimulus	172	0.310508515	0.0013	0.002859821
GO:0009163	nucleoside biosynthetic process	75	0.310489918	0.002	0.003693422
GO:0014012	peripheral nervous system axon regeneration	5	0.31047619	0.0352	0.037152965
GO:1902808	positive regulation of cell cycle G1/S phase transition	29	0.31046909	0.0018	0.003459409
GO:0007040	lysosome organization	40	0.31045045	0.0005	0.002177563
GO:0080171	lytic vacuole organization	40	0.31045045	0.0005	0.002177563
GO:0042168	heme metabolic process	22	0.31043641	0.0136	0.015813319
GO:0007625	grooming behavior	9	0.31042471	0.0055	0.007544447
GO:0060856	establishment of blood-brain barrier	6	0.31042471	0.0031	0.004916949
GO:0003158	endothelium development	72	0.31042471	0.0009	0.002399874
GO:0002285	lymphocyte activation involved in immune response	88	0.31041886	0.0006	0.002177563
GO:0006611	protein export from nucleus	37	0.310396883	0.0015	0.003088691
GO:0007095	mitotic G2 DNA damage checkpoint	13	0.31036531	0.0033	0.005149584
GO:0072080	nephron tubule development	51	0.310354052	0.0002	0.001341684
GO:0043241	protein complex disassembly	158	0.310344884	0.0022	0.003910907
GO:0046456	icosanoid biosynthetic process	33	0.31029991	0.0005	0.002177563
GO:1901570	fatty acid derivative biosynthetic process	33	0.31029991	0.0005	0.002177563
GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	38	0.310275689	0.0015	0.003088691
GO:0072431	signal transduction involved in mitotic G1 DNA damage checkpoint	38	0.310275689	0.0015	0.003088691
GO:1902400	intracellular signal transduction involved in G1 DNA damage checkpoint	38	0.310275689	0.0015	0.003088691
GO:0006446	regulation of translational initiation	55	0.31026091	0.0016	0.003223775
GO:0055003	cardiac myofibril assembly	9	0.31025311	0.0003	0.001720882
GO:0043370	regulation of CD4-positive, alpha-beta T cell differentiation	21	0.31025311	0.0006	0.002177563
GO:1903037	regulation of leukocyte cell-cell adhesion	168	0.310233192	0.0012	0.002741075
GO:0006360	transcription from RNA polymerase I promoter	47	0.310222076	< 0.001	< 0.001
GO:0006367	transcription initiation from RNA polymerase II promoter	109	0.310155503	0.0012	0.002741075
GO:0032731	positive regulation of interleukin-1 beta production	19	0.310140215	0.0001	0.000877824
GO:0061008	hepaticobiliary system development	81	0.310100577	0.0015	0.003088691
GO:0006119	oxidative phosphorylation	80	0.309990347	0.0065	0.008621124
GO:0072413	signal transduction involved in mitotic cell cycle checkpoint	39	0.30998911	0.0017	0.003334595
GO:1902402	signal transduction involved in mitotic DNA damage checkpoint	39	0.30998911	0.0017	0.003334595
GO:1902403	signal transduction involved in mitotic DNA integrity checkpoint	39	0.30998911	0.0017	0.003334595
GO:0002712	regulation of B cell mediated immunity	27	0.30996711	0.0002	0.001341684
GO:0002889	regulation of immunoglobulin mediated immune response	27	0.30996711	0.0002	0.001341684
GO:0071474	cellular hyperosmotic response	10	0.30996139	0.0028	0.004605006
GO:0045445	myoblast differentiation	45	0.30994423	0.0022	0.003910907
GO:0070232	regulation of T cell apoptotic process	17	0.30990991	0.0029	0.004714719
GO:0045603	positive regulation of endothelial cell differentiation	9	0.30988131	0.0014	0.002975058
GO:0006363	termination of RNA polymerase I transcription	23	0.309876336	< 0.001	< 0.001
GO:0007286	spermatid development	50	0.309863578	0.0001	0.000877824
GO:0072395	signal transduction involved in cell cycle checkpoint	46	0.309853953	0.0009	0.002399874
GO:0050796	regulation of insulin secretion	76	0.309838786	0.0008	0.002313249
GO:0060993	kidney morphogenesis	49	0.309820608	0.0001	0.000877824
GO:0032755	positive regulation of interleukin-6 production	46	0.309814784	0.0014	0.002975058
GO:0070507	regulation of microtubule cytoskeleton organization	90	0.30980981	0.0009	0.002399874
GO:0071800	podosome assembly	10	0.30980695	0.0211	0.023264758
GO:2001022	positive regulation of response to DNA damage stimulus	54	0.30978121	0.0017	0.003334595
GO:0042136	neurotransmitter biosynthetic process	6	0.30978121	< 0.001	< 0.001
GO:0002244	hematopoietic progenitor cell differentiation	101	0.309746805	0.0007	0.002248538
GO:2000036	regulation of stem cell population maintenance	18	0.30972401	0.0015	0.003088691
GO:0000394	RNA splicing, via endonucleolytic cleavage and ligation	16	0.30971686	0.0018	0.003459409
GO:0032769	negative regulation of monooxygenase activity	5	0.30970399	0.0156	0.017858595
GO:0043248	proteasome assembly	9	0.30968111	0.0044	0.006304227
GO:0071559	response to transforming growth factor beta	133	0.309658316	0.0011	0.002610912
GO:0048251	elastic fiber assembly	7	0.309615738	0.0025	0.004279479
GO:0060644	mammary gland epithelial cell differentiation	13	0.30961291	< 0.001	< 0.001
GO:0060055	angiogenesis involved in wound healing	13	0.30961291	0.016	0.018267288
GO:0050685	positive regulation of mRNA processing	22	0.30952381	0.0035	0.005358035
GO:0006282	regulation of DNA repair	66	0.30952381	0.0005	0.002177563
GO:0018230	peptidyl-L-cysteine S-palmitoylation	5	0.309498069	0.0117	0.013882722
GO:0018231	peptidyl-S-diacylglycerol-L-cysteine biosynthetic process from peptidyl-cysteine	5	0.309498069	0.0117	0.013882722
GO:0071456	cellular response to hypoxia	122	0.309496382	0.0011	0.002610912
GO:0048305	immunoglobulin secretion	14	0.309450267	0.0001	0.000877824
GO:0010827	regulation of glucose transport	38	0.309422204	0.0006	0.002177563
GO:0001658	branching involved in ureteric bud morphogenesis	32	0.309395109	< 0.001	< 0.001
GO:0033197	response to vitamin E	6	0.309395109	0.0164	0.018653793
GO:0016139	glycoside catabolic process	5	0.309395109	0.0017	0.003334595
GO:0035967	cellular response to topologically incorrect protein	99	0.309392509	0.0019	0.003579279
GO:0071322	cellular response to carbohydrate stimulus	63	0.309391024	0.0005	0.002177563
GO:0032493	response to bacterial lipoprotein	6	0.309352209	0.0101	0.012328539
GO:0002335	mature B cell differentiation	16	0.309330759	0.0192	0.021362011
GO:0045576	mast cell activation	31	0.309303774	0.0004	0.002007244
GO:1902804	negative regulation of synaptic vesicle transport	5	0.309292149	0.0223	0.024414688
GO:0030879	mammary gland development	70	0.309277441	0.0006	0.002177563
GO:0044724	single-organism carbohydrate catabolic process	110	0.309273429	0.002	0.003693422
GO:0048708	astrocyte differentiation	44	0.309266409	0.0036	0.005475609
GO:0002711	positive regulation of T cell mediated immunity	23	0.30922724	0.0028	0.004605006
GO:0060828	regulation of canonical Wnt signaling pathway	146	0.309213519	0.0006	0.002177563
GO:0000959	mitochondrial RNA metabolic process	24	0.309212784	0.0113	0.013488462
GO:0015804	neutral amino acid transport	18	0.309209209	0.0078	0.009981807

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0031953	negative regulation of protein autophosphorylation	9	0.309194909	0.0133	0.015521132
GO:0070227	lymphocyte apoptotic process	36	0.309187759	0.0025	0.004279479
GO:0071498	cellular response to fluid shear stress	10	0.309163449	0.0039	0.005778819
GO:0000075	cell cycle checkpoint	127	0.309137709	0.0006	0.002177563
GO:0006779	porphyrin-containing compound biosynthetic process	20	0.309099099	0.0035	0.005358035
GO:0030866	cortical actin cytoskeleton organization	21	0.309076423	0.0042	0.006097175
GO:1990089	response to nerve growth factor	27	0.309051909	0.0012	0.002741075
GO:1902099	regulation of metaphase/anaphase transition of cell cycle	28	0.30904578	< 0.001	< 0.001
GO:0061333	renal tubule morphogenesis	41	0.309043538	0.0002	0.001341684
GO:0046631	alpha-beta T cell activation	73	0.309031928	0.0042	0.006097175
GO:0006352	DNA-templated transcription, initiation	139	0.309022898	0.0008	0.002313249
GO:0045143	homologous chromosome segregation	17	0.30901658	0.0001	0.000877824
GO:0034104	negative regulation of tissue remodeling	10	0.309009009	0.0119	0.014078095
GO:0090101	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	61	0.308947824	0.0016	0.003223775
GO:0035987	endodermal cell differentiation	25	0.308942085	0.0008	0.002313249
GO:0007088	regulation of mitotic nuclear division	91	0.30893688	0.0009	0.002399874
GO:0033559	unsaturated fatty acid metabolic process	65	0.308919909	0.002	0.003693422
GO:0050951	sensory perception of temperature stimulus	7	0.30891708	0.0001	0.000877824
GO:0051152	positive regulation of smooth muscle cell differentiation	7	0.30891708	0.0001	0.000877824
GO:0032640	tumor necrosis factor production	81	0.308912087	0.0019	0.003579279
GO:0033005	positive regulation of mast cell activation	9	0.308908909	0.0129	0.015093024
GO:0050868	negative regulation of T cell activation	52	0.308885259	0.0004	0.002007244
GO:0032608	interferon-beta production	37	0.308852482	0.0006	0.002177563
GO:0070813	hydrogen sulfide metabolic process	5	0.308828829	0.0071	0.009268394
GO:0035907	dorsal aorta development	7	0.308806766	0.0054	0.007432873
GO:0032886	regulation of microtubule-based process	106	0.308805031	0.0005	0.002177563
GO:0016601	Rac protein signal transduction	17	0.308774321	0.0053	0.007330056
GO:0031669	cellular response to nutrient levels	106	0.308758894	0.0014	0.002975058
GO:0060028	convergent extension involved in axis elongation	5	0.308725869	0.003	0.004825593
GO:0019068	virion assembly	30	0.308691549	0.0017	0.003334595
GO:0001676	long-chain fatty acid metabolic process	54	0.308689642	0.0017	0.003334595
GO:0034612	response to tumor necrosis factor	166	0.308680281	0.0003	0.001720882
GO:0019362	pyridine nucleotide metabolic process	109	0.308670138	0.0019	0.003579279
GO:0046496	nicotinamide nucleotide metabolic process	109	0.308670138	0.0019	0.003579279
GO:0043032	positive regulation of macrophage activation	17	0.308653191	0.0049	0.006860215
GO:0042130	negative regulation of T cell proliferation	29	0.308649536	0.0007	0.002248538
GO:0010453	regulation of cell fate commitment	11	0.308622909	< 0.001	< 0.001
GO:0050884	neuromuscular process controlling posture	6	0.308580009	0.0009	0.002399874
GO:0010324	membrane invagination	39	0.308523909	0.0024	0.004156304
GO:0007004	telomere maintenance via telomerase	47	0.308518853	< 0.001	< 0.001
GO:0048643	positive regulation of skeletal muscle tissue development	7	0.308512594	0.0071	0.009268394
GO:0051321	meiotic cell cycle	88	0.308497133	0.0008	0.002313249
GO:0044106	cellular amine metabolic process	78	0.308494208	0.0004	0.002007244
GO:0042098	T cell proliferation	96	0.308472758	0.0008	0.002313249
GO:1990823	response to leukemia inhibitory factor	65	0.308468468	< 0.001	< 0.001
GO:1990830	cellular response to leukemia inhibitory factor	65	0.308468468	< 0.001	< 0.001
GO:0051882	mitochondrial depolarization	15	0.308468468	0.008	0.010168329
GO:0002381	immunoglobulin production involved in immunoglobulin mediated immune response	27	0.308460842	0.0001	0.000877824
GO:0014014	negative regulation of gliogenesis	22	0.308459108	0.0041	0.005981983
GO:0009132	nucleoside diphosphate metabolic process	91	0.308458851	0.0023	0.004032435
GO:0032479	regulation of type I interferon production	84	0.308451308	0.0006	0.002177563
GO:0060396	growth hormone receptor signaling pathway	13	0.308444708	< 0.001	< 0.001
GO:0097028	dendritic cell differentiation	26	0.308424908	0.0005	0.002177563
GO:0006837	serotonin transport	6	0.308408408	0.0003	0.001720882
GO:0046341	CDP-diacylglycerol metabolic process	11	0.308388908	0.0004	0.002007244
GO:0002687	positive regulation of leukocyte migration	69	0.308354317	0.0016	0.003223775
GO:1903146	regulation of mitophagy	23	0.308331934	0.0034	0.005263104
GO:2000756	regulation of peptidyl-lysine acetylation	34	0.308327655	0.0006	0.002177563
GO:0001678	cellular glucose homeostasis	64	0.308309202	0.0006	0.002177563
GO:1900221	regulation of beta-amyloid clearance	9	0.308308308	< 0.001	< 0.001
GO:0006469	negative regulation of protein kinase activity	118	0.308300068	0.0006	0.002177563
GO:0030730	sequestering of triglyceride	11	0.308295308	0.0053	0.007330056
GO:0033233	regulation of protein sumoylation	10	0.308262548	0.0044	0.006304227
GO:0030178	negative regulation of Wnt signaling pathway	115	0.30826031	0.0004	0.002007244
GO:1903509	liposaccharide metabolic process	74	0.308257679	0.0023	0.004032435
GO:0043154	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	50	0.30823166	0.0006	0.002177563
GO:0007173	epidermal growth factor receptor signaling pathway	69	0.308231213	0.0027	0.004491543
GO:0032635	interleukin-6 production	70	0.308214745	0.0014	0.002975058
GO:0033135	regulation of peptidyl-serine phosphorylation	59	0.308186637	0.0004	0.002007244
GO:0032680	regulation of tumor necrosis factor production	78	0.308180708	0.0018	0.003459409
GO:0030258	lipid modification	115	0.308179733	0.0009	0.002399874
GO:0071888	macrophage apoptotic process	9	0.308165308	0.0121	0.014285532
GO:0043624	cellular protein complex disassembly	134	0.308152289	0.0023	0.004032435
GO:0090050	positive regulation of cell migration involved in sprouting angiogenesis	13	0.308127908	0.0014	0.002975058
GO:0042552	myelination	78	0.308124608	0.0044	0.006304227
GO:0007603	phototransduction, visible light	11	0.308061308	0.0112	0.013379119
GO:0016056	rhodopsin mediated signaling pathway	11	0.308061308	0.0112	0.013379119
GO:0009309	amine biosynthetic process	9	0.308050908	0.0001	0.000877824
GO:0042401	cellular biogenic amine biosynthetic process	9	0.308050908	0.0001	0.000877824
GO:0009135	purine nucleoside diphosphate metabolic process	77	0.308044594	0.0033	0.005149584
GO:0009179	purine ribonucleoside diphosphate metabolic process	77	0.308044594	0.0033	0.005149584
GO:1904035	regulation of epithelial cell apoptotic process	46	0.30804096	0.0044	0.006304227
GO:0035024	negative regulation of Rho protein signal transduction	11	0.308037908	0.0014	0.002975058

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0009649	entrainment of circadian clock	10	0.308005148	0.0026	0.004377754
GO:0002820	negative regulation of adaptive immune response	21	0.307997794	0.0001	0.000877824
GO:0071560	cellular response to transforming growth factor beta stimulus	131	0.307970566	0.0011	0.002610912
GO:1901659	glycosyl compound biosynthetic process	76	0.307959087	0.0022	0.003910907
GO:0034162	toll-like receptor 9 signaling pathway	16	0.307947233	0.0008	0.002313249
GO:0044088	regulation of vacuole organization	34	0.307941555	0.0025	0.004279479
GO:0034968	histone lysine methylation	67	0.307935227	0.0011	0.002610912
GO:0002886	regulation of myeloid leukocyte mediated immunity	31	0.307925437	0.007	0.009166016
GO:0071103	DNA conformation change	151	0.307860936	0.0008	0.002313249
GO:2000109	regulation of macrophage apoptotic process	7	0.307850708	0.0094	0.011616482
GO:0010039	response to iron ion	28	0.307841515	0.0056	0.007655255
GO:0071326	cellular response to monosaccharide stimulus	60	0.307790648	0.0005	0.002177563
GO:0071331	cellular response to hexose stimulus	60	0.307790648	0.0005	0.002177563
GO:1903351	cellular response to dopamine	8	0.307786358	0.0038	0.005666214
GO:0000724	double-strand break repair via homologous recombination	71	0.30777095	< 0.001	< 0.001
GO:0000725	recombinational repair	71	0.30777095	< 0.001	< 0.001
GO:0008625	extrinsic apoptotic signaling pathway via death domain receptors	54	0.307764908	0.0028	0.004605006
GO:0034367	macromolecular complex remodeling	13	0.307751708	0.0006	0.002177563
GO:0034368	protein-lipid complex remodeling	13	0.307751708	0.0006	0.002177563
GO:0034369	plasma lipoprotein particle remodeling	13	0.307751708	0.0006	0.002177563
GO:0030510	regulation of BMP signaling pathway	38	0.307749102	0.0046	0.006532041
GO:1900182	positive regulation of protein localization to nucleus	55	0.307738388	0.0009	0.002399874
GO:0090199	regulation of release of cytochrome c from mitochondria	28	0.307712815	0.0019	0.003579279
GO:0097193	intrinsic apoptotic signaling pathway	175	0.307697739	0.0006	0.002177563
GO:0046824	positive regulation of nucleocytoplasmic transport	49	0.307656344	0.0011	0.002610912
GO:0071347	cellular response to interleukin-1	91	0.30762725	0.0011	0.002610912
GO:0032692	negative regulation of interleukin-1 production	16	0.307625483	0.0116	0.013792313
GO:0050434	positive regulation of viral transcription	34	0.307616019	0.0012	0.002741075
GO:0033619	membrane protein proteolysis	43	0.307593308	0.0043	0.006204188
GO:0016575	histone deacetylation	41	0.307593308	0.002	0.003693422
GO:0070555	response to interleukin-1	100	0.307570142	0.0007	0.002248538
GO:0051306	mitotic sister chromatid separation	30	0.307533248	< 0.001	< 0.001
GO:0098739	import across plasma membrane	22	0.307523108	0.0063	0.008390784
GO:0036314	response to sterol	20	0.307516088	0.0005	0.002177563
GO:0034389	lipid particle organization	12	0.307507508	0.002	0.003693422
GO:0006488	dolichol-linked oligosaccharide biosynthetic process	17	0.307487319	0.0018	0.003459409
GO:0006490	oligosaccharide-lipid intermediate biosynthetic process	17	0.307487319	0.0018	0.003459409
GO:0010389	regulation of G2/M transition of mitotic cell cycle	123	0.307467746	0.0005	0.002177563
GO:0055006	cardiac cell development	38	0.307464607	0.0006	0.002177563
GO:0097067	cellular response to thyroid hormone stimulus	10	0.307464607	0.0152	0.017453982
GO:0035264	multicellular organism growth	92	0.307450618	0.0007	0.002248538
GO:0090317	negative regulation of intracellular protein transport	36	0.307428857	0.0007	0.002248538
GO:0072088	nephron epithelium morphogenesis	41	0.307404966	0.0001	0.000877824
GO:0051702	interaction with symbiont	52	0.307355707	0.001	0.002498236
GO:0046425	regulation of JAK-STAT cascade	53	0.307350477	0.0002	0.001341684
GO:0070970	interleukin-2 secretion	5	0.307335907	0.0013	0.002859821
GO:0030520	intracellular estrogen receptor signaling pathway	34	0.307313196	0.001	0.002498236
GO:0015918	sterol transport	48	0.307303732	0.001	0.002498236
GO:0000910	cytokinesis	68	0.30730184	0.002	0.003693422
GO:0072171	mesonephric tubule morphogenesis	37	0.30728721	0.0001	0.000877824
GO:0006012	galactose metabolic process	8	0.307239382	0.0094	0.011616482
GO:0030593	neutrophil chemotaxis	31	0.307227965	0.0029	0.004714719
GO:0043506	regulation of JUN kinase activity	46	0.307212803	0.0006	0.002177563
GO:0006637	acyl-CoA metabolic process	62	0.307211359	0.0033	0.005149584
GO:0035383	thioester metabolic process	62	0.307211359	0.0033	0.005149584
GO:1903214	regulation of protein targeting to mitochondrion	31	0.307211359	0.0002	0.001341684
GO:0031579	membrane raft organization	15	0.307181467	0.018	0.020203241
GO:0060231	mesenchymal to epithelial transition	9	0.307164307	0.0011	0.002610912
GO:0035304	regulation of protein dephosphorylation	67	0.307147659	0.0005	0.002177563
GO:0001783	B cell apoptotic process	13	0.307137907	0.0024	0.004156304
GO:1901342	regulation of vasculature development	176	0.307131157	0.0018	0.003459409
GO:0007018	microtubule-based movement	130	0.307120087	< 0.001	< 0.001
GO:0060394	negative regulation of pathway-restricted SMAD protein phosphorylation	8	0.307110682	0.0103	0.012519912
GO:1904591	positive regulation of protein import	32	0.307102638	0.0012	0.002741075
GO:0055007	cardiac muscle cell differentiation	52	0.307088407	0.0006	0.002177563
GO:0007091	metaphase/anaphase transition of mitotic cell cycle	29	0.307078507	< 0.001	< 0.001
GO:0010965	regulation of mitotic sister chromatid separation	29	0.307078507	< 0.001	< 0.001
GO:0060736	prostate gland growth	5	0.307078507	0.0032	0.005044175
GO:0035065	regulation of histone acetylation	29	0.307051879	0.0007	0.002248538
GO:0033500	carbohydrate homeostasis	104	0.307048807	0.0005	0.002177563
GO:0042593	glucose homeostasis	104	0.307048807	0.0005	0.002177563
GO:0045815	positive regulation of gene expression, epigenetic	37	0.307022853	0.0003	0.001720882
GO:0034121	regulation of toll-like receptor signaling pathway	32	0.306973938	0.0002	0.001341684
GO:0007351	tripartite regional subdivision	7	0.306968193	0.0015	0.003088691
GO:0008595	anterior/posterior axis specification, embryo	7	0.306968193	0.0015	0.003088691
GO:0045930	negative regulation of mitotic cell cycle	200	0.306931789	0.001	0.002498236
GO:2000009	negative regulation of protein localization to cell surface	7	0.306931421	0.0081	0.010256567
GO:0014003	oligodendrocyte development	30	0.306898327	0.0036	0.005475609
GO:0002758	innate immune response-activating signal transduction	173	0.306891036	0.0007	0.002248538
GO:0032024	positive regulation of insulin secretion	29	0.306883238	< 0.001	< 0.001
GO:0032933	SREBP signaling pathway	5	0.306872587	0.0342	0.036175369
GO:0071501	cellular response to sterol depletion	5	0.306872587	0.0342	0.036175369
GO:0031116	positive regulation of microtubule polymerization	15	0.306855427	0.0061	0.008182551

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0014743	regulation of muscle hypertrophy	30	0.306838267	0.0038	0.005666214
GO:0051101	regulation of DNA binding	70	0.306810075	0.0008	0.002313249
GO:0001889	liver development	78	0.306781507	0.0012	0.002741075
GO:0036353	histone H2A-K119 monoubiquitination	5	0.306769627	0.0004	0.002007244
GO:0002702	positive regulation of production of molecular mediator of immune response	46	0.306748363	0.0003	0.001720882
GO:0055089	fatty acid homeostasis	7	0.306747564	0.0013	0.002859821
GO:0002218	activation of innate immune response	187	0.306738519	0.0006	0.002177563
GO:0002823	negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	20	0.306731017	0.0001	0.000877824
GO:1904044	response to aldosterone	5	0.306718147	0.0028	0.004605006
GO:0050713	negative regulation of interleukin-1 beta secretion	5	0.306718147	0.0114	0.01358747
GO:0006700	C21-steroid hormone biosynthetic process	15	0.306683827	0.0095	0.011730963
GO:0045651	positive regulation of macrophage differentiation	9	0.306678107	0.0023	0.004032435
GO:0033260	nuclear DNA replication	31	0.306621829	0.0017	0.003334595
GO:0046329	negative regulation of JNK cascade	18	0.306620907	0.0008	0.002313249
GO:0030073	insulin secretion	90	0.306603747	0.0008	0.002313249
GO:0033145	positive regulation of intracellular steroid hormone receptor signaling pathway	13	0.306603307	0.0064	0.008500875
GO:0019359	nicotinamide nucleotide biosynthetic process	20	0.306602317	0.0004	0.002007244
GO:0019363	pyridine nucleotide biosynthetic process	20	0.306602317	0.0004	0.002007244
GO:0010818	T cell chemotaxis	9	0.306592307	0.0069	0.009046225
GO:0085029	extracellular matrix assembly	25	0.306574003	0.0029	0.004714719
GO:0002286	T cell activation involved in immune response	46	0.306541324	0.0009	0.002399874
GO:0051092	positive regulation of NF-kappaB transcription factor activity	84	0.306490164	0.0007	0.002248538
GO:0045922	negative regulation of fatty acid metabolic process	16	0.306467181	< 0.001	< 0.001
GO:0010819	regulation of T cell chemotaxis	5	0.306460746	0.0192	0.021362011
GO:0010820	positive regulation of T cell chemotaxis	5	0.306460746	0.0192	0.021362011
GO:0090342	regulation of cell aging	29	0.306421693	0.0003	0.001720882
GO:0048678	response to axon injury	39	0.306418506	0.0013	0.002859821
GO:0097191	extrinsic apoptotic signaling pathway	134	0.306410035	0.0017	0.003334595
GO:2000278	regulation of DNA biosynthetic process	66	0.306376506	0.0004	0.002007244
GO:0002573	myeloid leukocyte differentiation	112	0.306354569	0.003	0.004825593
GO:0071333	cellular response to glucose stimulus	58	0.306350686	0.0005	0.002177563
GO:0006907	pinocytosis	17	0.306336589	0.0023	0.004032435
GO:0044242	cellular lipid catabolic process	121	0.306331834	0.003	0.004825593
GO:0045408	regulation of interleukin-6 biosynthetic process	15	0.306306306	0.0048	0.006748379
GO:1900542	regulation of purine nucleotide metabolic process	89	0.30629763	0.0022	0.003910907
GO:0072207	metanephric epithelium development	16	0.306290219	0.0001	0.000877824
GO:0072243	metanephric nephron epithelium development	16	0.306290219	0.0001	0.000877824
GO:1901722	regulation of cell proliferation involved in kidney development	5	0.306254826	0.0002	0.001341684
GO:0009312	oligosaccharide biosynthetic process	9	0.306249106	0.0218	0.023945433
GO:0050830	defense response to Gram-positive bacterium	27	0.306210973	0.0023	0.004032435
GO:0036294	cellular response to decreased oxygen levels	128	0.306177606	0.0012	0.002741075
GO:0006925	inflammatory cell apoptotic process	12	0.306156156	0.0041	0.005981983
GO:0000012	single strand break repair	5	0.306151866	0.0075	0.00968541
GO:0046546	development of primary male sexual characteristics	78	0.306105006	0.0006	0.002177563
GO:0016226	iron-sulfur cluster assembly	11	0.306095706	0.0056	0.007655255
GO:0031163	metallo-sulfur cluster assembly	11	0.306095706	0.0056	0.007655255
GO:0000469	cleavage involved in rRNA processing	6	0.306091806	0.0092	0.011424708
GO:0038095	Fc-epsilon receptor signaling pathway	70	0.306085678	0.0009	0.002399874
GO:0002228	natural killer cell mediated immunity	22	0.306084006	0.0004	0.002007244
GO:2000243	positive regulation of reproductive process	25	0.306079794	< 0.001	< 0.001
GO:1904705	regulation of vascular smooth muscle cell proliferation	30	0.306074646	0.0026	0.004377754
GO:1990874	vascular smooth muscle cell proliferation	30	0.306074646	0.0026	0.004377754
GO:0002685	regulation of leukocyte migration	102	0.306071618	0.001	0.002498236
GO:0001886	endothelial cell morphogenesis	8	0.305952381	0.0118	0.013977955
GO:0032094	response to food	21	0.305950849	0.0008	0.002313249
GO:0043576	regulation of respiratory gaseous exchange	10	0.305945946	0.0007	0.002248538
GO:1902749	regulation of cell cycle G2/M phase transition	132	0.305920206	0.0003	0.001720882
GO:0043537	negative regulation of blood vessel endothelial cell migration	24	0.305877306	0.0013	0.002859821
GO:0009185	ribonucleoside diphosphate metabolic process	78	0.305864106	0.0037	0.005561344
GO:0030177	positive regulation of Wnt signaling pathway	102	0.305829359	0.0007	0.002248538
GO:0050853	B cell receptor signaling pathway	26	0.305821206	0.0058	0.007856196
GO:0055088	lipid homeostasis	55	0.305814906	0.0016	0.003223775
GO:0009308	amine metabolic process	79	0.305814313	0.0004	0.002007244
GO:0034976	response to endoplasmic reticulum stress	174	0.30580482	0.0006	0.002177563
GO:0031061	negative regulation of histone methylation	14	0.305791506	0.0003	0.001720882
GO:0002204	somatic recombination of immunoglobulin genes involved in immune response	26	0.305761806	0.0001	0.000877824
GO:0002208	somatic diversification of immunoglobulins involved in immune response	26	0.305761806	0.0001	0.000877824
GO:0045190	isotype switching	26	0.305761806	0.0001	0.000877824
GO:0051304	chromosome separation	39	0.305751906	< 0.001	< 0.001
GO:0048302	regulation of isotype switching to IgG isotypes	6	0.305748606	0.0026	0.004377754
GO:0048304	positive regulation of isotype switching to IgG isotypes	6	0.305748606	0.0026	0.004377754
GO:0045911	positive regulation of DNA recombination	22	0.305744706	< 0.001	< 0.001
GO:0033146	regulation of intracellular estrogen receptor signaling pathway	25	0.305709138	0.0008	0.002313249
GO:0070085	glycosylation	170	0.305705201	0.0009	0.002399874
GO:0036003	positive regulation of transcription from RNA polymerase II promoter in response to stress	21	0.305693449	0.0091	0.011322589
GO:0002718	regulation of cytokine production involved in immune response	40	0.305682111	0.0007	0.002248538
GO:0006486	protein glycosylation	158	0.305667693	0.001	0.002498236
GO:0043413	macromolecule glycosylation	158	0.305667693	0.001	0.002498236
GO:0072078	nephron tubule morphogenesis	39	0.305659506	0.0001	0.000877824
GO:0021936	regulation of cerebellar granule cell precursor proliferation	5	0.305637066	0.0394	0.041258002
GO:0006165	nucleoside diphosphate phosphorylation	78	0.305583606	0.0027	0.004491543
GO:0060546	negative regulation of necroptotic process	9	0.305562706	0.0107	0.012912536

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0045124	regulation of bone resorption	18	0.305519806	0.0108	0.013015961
GO:0034244	negative regulation of transcription elongation from RNA polymerase II promoter	9	0.305476905	0.0083	0.010468217
GO:0045948	positive regulation of translational initiation	18	0.305462605	0.0027	0.004491543
GO:0050792	regulation of viral process	141	0.305428225	0.0007	0.002248538
GO:0044458	motile cilium assembly	12	0.305426855	< 0.001	< 0.001
GO:1903038	negative regulation of leukocyte cell-cell adhesion	60	0.305413985	0.0004	0.002007244
GO:0070059	intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	37	0.305408884	0.002	0.003693422
GO:0007272	ensheathment of neurons	81	0.305394283	0.0043	0.006204188
GO:0008366	axon ensheathment	81	0.305394283	0.0043	0.006204188
GO:0043651	linoleic acid metabolic process	11	0.305393705	0.0021	0.003804235
GO:0046685	response to arsenic-containing substance	21	0.30538702	0.0035	0.005358035
GO:0033120	positive regulation of RNA splicing	20	0.305379665	0.0038	0.005666214
GO:0006098	pentose-phosphate shunt	12	0.305341055	0.0089	0.011106266
GO:0097284	hepatocyte apoptotic process	10	0.305328185	0.0013	0.002859821
GO:0000070	mitotic sister chromatid segregation	82	0.305304957	0.0008	0.002313249
GO:0043300	regulation of leukocyte degranulation	27	0.305286239	0.0037	0.005561344
GO:1901203	positive regulation of extracellular matrix assembly	8	0.305276705	0.0062	0.008281828
GO:0071867	response to monoamine	18	0.305248105	0.0016	0.003223775
GO:0071869	response to catecholamine	18	0.305248105	0.0016	0.003223775
GO:0030301	cholesterol transport	45	0.305242385	0.0009	0.002399874
GO:0071104	response to interleukin-9	6	0.305190905	0.0004	0.002007244
GO:0032682	negative regulation of chemokine production	13	0.305138105	0.0016	0.003223775
GO:0000209	protein polyubiquitination	195	0.305113025	0.0007	0.002248538
GO:0032609	interferon-gamma production	50	0.305111969	0.0022	0.003910907
GO:0043030	regulation of macrophage activation	29	0.305108064	0.0069	0.009046225
GO:0032700	negative regulation of interleukin-17 production	6	0.305105105	0.0012	0.002741075
GO:0045765	regulation of angiogenesis	161	0.305100842	0.0021	0.003804235
GO:1901800	positive regulation of proteasomal protein catabolic process	53	0.305063014	0.0006	0.002177563
GO:1901984	negative regulation of protein acetylation	12	0.305062205	0.0001	0.000877824
GO:0045655	regulation of monocyte differentiation	13	0.305039105	0.0031	0.004916949
GO:0032784	regulation of DNA-templated transcription, elongation	28	0.305028498	0.0022	0.003910907
GO:2000757	negative regulation of peptidyl-lysine acetylation	10	0.305019305	0.0002	0.001341684
GO:0002583	regulation of antigen processing and presentation of peptide antigen	5	0.305019305	0.0249	0.02700148
GO:0046755	viral budding	20	0.305006435	0.0015	0.003088691
GO:1902590	multi-organism organelle organization	20	0.305006435	0.0015	0.003088691
GO:1902592	multi-organism membrane budding	20	0.305006435	0.0015	0.003088691
GO:0003177	pulmonary valve development	13	0.304999505	0.0006	0.002177563
GO:0042789	mRNA transcription from RNA polymerase II promoter	14	0.304982534	0.0211	0.023264758
GO:0042089	cytokine biosynthetic process	65	0.304975745	0.001	0.002498236
GO:0042107	cytokine metabolic process	65	0.304975745	0.001	0.002498236
GO:0006096	glycolytic process	65	0.304951985	0.0034	0.005263104
GO:0060544	regulation of necroptotic process	11	0.304925705	0.0122	0.014387602
GO:0002698	negative regulation of immune effector process	71	0.30492142	0.0007	0.002248538
GO:0032873	negative regulation of stress-activated MAPK cascade	25	0.304916345	0.0008	0.002313249
GO:0070303	negative regulation of stress-activated protein kinase signaling cascade	25	0.304916345	0.0008	0.002313249
GO:0002761	regulation of myeloid leukocyte differentiation	62	0.304890605	0.0029	0.004714719
GO:0002699	positive regulation of immune effector process	103	0.304884357	0.0002	0.001341684
GO:0030522	intracellular receptor signaling pathway	165	0.304836785	0.0008	0.002313249
GO:0003091	renal water homeostasis	14	0.304835448	< 0.001	< 0.001
GO:0044272	sulfur compound biosynthetic process	128	0.304830277	0.0007	0.002248538
GO:0045986	negative regulation of smooth muscle contraction	6	0.304804805	0.0001	0.000877824
GO:0002700	regulation of production of molecular mediator of immune response	67	0.304800323	0.0002	0.001341684
GO:0060307	regulation of ventricular cardiac muscle cell membrane repolarization	9	0.304790505	0.0003	0.001720882
GO:1902275	regulation of chromatin organization	95	0.304775452	0.001	0.002498236
GO:0071453	cellular response to oxygen levels	137	0.304771299	0.0012	0.002741075
GO:0001894	tissue homeostasis	114	0.304750615	0.001	0.002498236
GO:0043902	positive regulation of multi-organism process	102	0.304749287	0.0004	0.002007244
GO:0032637	interleukin-8 production	43	0.304725988	0.0011	0.002610912
GO:0006081	cellular aldehyde metabolic process	41	0.304724236	0.0024	0.004156304
GO:0050686	negative regulation of mRNA processing	19	0.304721263	0.0029	0.004714719
GO:0006111	regulation of gluconeogenesis	25	0.304720721	0.0002	0.001341684
GO:0006278	RNA-dependent DNA biosynthetic process	49	0.304714627	< 0.001	< 0.001
GO:0038127	ERBB signaling pathway	82	0.304705402	0.0022	0.003910907
GO:0048754	branching morphogenesis of an epithelial tube	74	0.304699294	0.002	0.003693422
GO:0033007	negative regulation of mast cell activation involved in immune response	6	0.304676105	0.0003	0.001720882
GO:1904896	ESCRT complex disassembly	8	0.30466538	0.002	0.003693422
GO:1904903	ESCRT III complex disassembly	8	0.30466538	0.002	0.003693422
GO:0006884	cell volume homeostasis	16	0.304633205	0.0021	0.003804235
GO:0010611	regulation of cardiac muscle hypertrophy	29	0.30455776	0.0038	0.005666214
GO:0072497	mesenchymal stem cell differentiation	5	0.304555985	0.0034	0.005263104
GO:2000739	regulation of mesenchymal stem cell differentiation	5	0.304555985	0.0034	0.005263104
GO:0003223	ventricular compact myocardium morphogenesis	5	0.304555985	0.0119	0.014078095
GO:0003254	regulation of membrane depolarization	19	0.304531599	0.0094	0.011616482
GO:0002562	somatic diversification of immune receptors via germline recombination within a single locus	34	0.304489363	0.0001	0.000877824
GO:0016444	somatic cell DNA recombination	34	0.304489363	0.0001	0.000877824
GO:0001892	embryonic placenta development	49	0.304472986	0.0008	0.002313249
GO:0019217	regulation of fatty acid metabolic process	49	0.30446248	0.0004	0.002007244
GO:0042744	hydrogen peroxide catabolic process	10	0.304453024	0.0001	0.000877824
GO:0051353	positive regulation of oxidoreductase activity	27	0.304447304	0.0007	0.002248538
GO:0006378	mRNA polyadenylation	28	0.304412576	0.0007	0.002248538
GO:0072028	nephron morphogenesis	43	0.304384783	0.0001	0.000877824
GO:0042310	vasoconstriction	29	0.304380242	0.0037	0.005561344
GO:1904467	regulation of tumor necrosis factor secretion	14	0.304375804	0.0021	0.003804235

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1903844	regulation of cellular response to transforming growth factor beta stimulus	65	0.304373824	0.0012	0.002741075
GO:0090630	activation of GTPase activity	22	0.304352404	0.0039	0.005778819
GO:0006911	phagocytosis, engulfment	27	0.304351971	0.0048	0.006748379
GO:0060502	epithelial cell proliferation involved in lung morphogenesis	5	0.304350064	0.0066	0.008731949
GO:2000794	regulation of epithelial cell proliferation involved in lung morphogenesis	5	0.304350064	0.0066	0.008731949
GO:0032677	regulation of interleukin-8 production	42	0.304339033	0.001	0.002498236
GO:0044273	sulfur compound catabolic process	31	0.30433844	0.0011	0.002610912
GO:0009313	oligosaccharide catabolic process	9	0.304332904	0.0027	0.004491543
GO:0006109	regulation of carbohydrate metabolic process	112	0.30430456	0.0009	0.002399874
GO:1903405	protein localization to nuclear body	9	0.304247104	< 0.001	< 0.001
GO:1904851	positive regulation of establishment of protein localization to telomere	9	0.304247104	< 0.001	< 0.001
GO:1904867	protein localization to Cajal body	9	0.304247104	< 0.001	< 0.001
GO:1904869	regulation of protein localization to Cajal body	9	0.304247104	< 0.001	< 0.001
GO:1904871	positive regulation of protein localization to Cajal body	9	0.304247104	< 0.001	< 0.001
GO:0050848	regulation of calcium-mediated signaling	39	0.304240504	0.0003	0.001720882
GO:2000273	positive regulation of receptor activity	25	0.304236808	0.001	0.002498236
GO:0042129	regulation of T cell proliferation	80	0.304231017	0.0013	0.002859821
GO:0031112	positive regulation of microtubule polymerization or depolymerization	16	0.304198842	0.005	0.006974174
GO:2000772	regulation of cellular senescence	27	0.304189904	< 0.001	< 0.001
GO:0060292	long term synaptic depression	6	0.304161304	0.0001	0.000877824
GO:0000723	telomere maintenance	97	0.304159535	0.0004	0.002007244
GO:0044030	regulation of DNA methylation	13	0.304148104	0.0007	0.002248538
GO:0032703	negative regulation of interleukin-2 production	11	0.304130104	0.0017	0.003334595
GO:0032200	telomere organization	99	0.304124904	0.0005	0.002177563
GO:0002027	regulation of heart rate	40	0.304124839	0.001	0.002498236
GO:0042493	response to drug	158	0.304111888	0.0007	0.002248538
GO:0043900	regulation of multi-organism process	192	0.304099635	0.0007	0.002248538
GO:0045540	regulation of cholesterol biosynthetic process	33	0.304091104	0.0014	0.002975058
GO:0030856	regulation of epithelial cell differentiation	76	0.304087923	0.0015	0.003088691
GO:0060560	developmental growth involved in morphogenesis	99	0.304057304	0.0006	0.002177563
GO:0031056	regulation of histone modification	79	0.304045094	0.0008	0.002313249
GO:0008652	cellular amino acid biosynthetic process	54	0.304027837	0.0002	0.001341684
GO:0010988	regulation of low-density lipoprotein particle clearance	7	0.304026475	0.0087	0.010877987
GO:0042921	glucocorticoid receptor signaling pathway	9	0.304018304	0.001	0.002498236
GO:0002089	lens morphogenesis in camera-type eye	12	0.304011154	0.0015	0.003088691
GO:1900078	positive regulation of cellular response to insulin stimulus	13	0.304009504	0.0008	0.002313249
GO:0002377	immunoglobulin production	53	0.303975134	< 0.001	< 0.001
GO:0044783	G1 DNA damage checkpoint	45	0.303926784	0.0017	0.003334595
GO:0098760	response to interleukin-7	20	0.303925354	0.0008	0.002313249
GO:0098761	cellular response to interleukin-7	20	0.303925354	0.0008	0.002313249
GO:0021697	cerebellar cortex formation	12	0.303925354	0.0028	0.004605006
GO:0018904	ether metabolic process	10	0.303912484	0.0152	0.017453982
GO:0051341	regulation of oxidoreductase activity	51	0.303888763	0.0011	0.002610912
GO:0061448	connective tissue development	126	0.303887561	0.0007	0.002248538
GO:0006664	glycolipid metabolic process	73	0.303883923	0.0024	0.004156304
GO:1901605	alpha-amino acid metabolic process	130	0.303868924	0.0005	0.002177563
GO:2000535	regulation of entry of bacterium into host cell	5	0.303835264	0.0104	0.012619802
GO:0043092	L-amino acid import	9	0.303818104	0.001	0.002498236
GO:0007602	phototransduction	14	0.303787461	0.0147	0.016962357
GO:0071260	cellular response to mechanical stimulus	52	0.303776854	0.0048	0.006748379
GO:0006733	oxidoreduction coenzyme metabolic process	121	0.303753576	0.002	0.003693422
GO:0031058	positive regulation of histone modification	53	0.30375173	0.001	0.002498236
GO:0098781	ncRNA transcription	74	0.303746217	0.0004	0.002007244
GO:0055013	cardiac muscle cell development	34	0.303709592	0.0006	0.002177563
GO:0031571	mitotic G1 DNA damage checkpoint	44	0.303708904	0.0017	0.003334595
GO:0044819	mitotic G1/S transition checkpoint	44	0.303708904	0.0017	0.003334595
GO:0072523	purine-containing compound catabolic process	29	0.3036968	0.0009	0.002399874
GO:0032418	lysosome localization	41	0.303694635	0.0006	0.002177563
GO:0034142	toll-like receptor 4 signaling pathway	19	0.303691662	0.0001	0.000877824
GO:0043303	mast cell degranulation	24	0.303657229	0.0005	0.002177563
GO:0043666	regulation of phosphoprotein phosphatase activity	59	0.303649412	0.0004	0.002007244
GO:0061005	cell differentiation involved in kidney development	32	0.303643822	0.0021	0.003804235
GO:0010922	positive regulation of phosphatase activity	16	0.303635779	0.0003	0.001720882
GO:0032506	cytokinetic process	12	0.303603604	0.0079	0.010077402
GO:1901989	positive regulation of cell cycle phase transition	51	0.303580892	0.0013	0.002859821
GO:0070228	regulation of lymphocyte apoptotic process	24	0.303549979	0.0018	0.003459409
GO:0051904	pigment granule transport	12	0.303539254	0.0001	0.000877824
GO:0051905	establishment of pigment granule localization	12	0.303539254	0.0001	0.000877824
GO:0006304	DNA modification	62	0.303524723	0.0008	0.002313249
GO:0033138	positive regulation of peptidyl-serine phosphorylation	42	0.303523932	< 0.001	< 0.001
GO:0033157	regulation of intracellular protein transport	155	0.303519741	0.0007	0.002248538
GO:0006000	fructose metabolic process	6	0.303517804	0.0002	0.001341684
GO:0007176	regulation of epidermal growth factor-activated receptor activity	10	0.303500644	0.0077	0.009887588
GO:0060976	coronary vasculature development	28	0.303493289	0.0015	0.003088691
GO:0030539	male genitalia development	10	0.303474903	0.0006	0.002177563
GO:0008584	male gonad development	77	0.303458189	0.0006	0.002177563
GO:0017144	drug metabolic process	15	0.303457743	< 0.001	< 0.001
GO:0048546	digestive tract morphogenesis	20	0.303449163	0.0125	0.014684332
GO:0061013	regulation of mRNA catabolic process	27	0.303446303	0.0001	0.000877824
GO:0051048	negative regulation of secretion	120	0.303438438	0.0006	0.002177563
GO:0031076	embryonic camera-type eye development	25	0.303423423	0.002	0.003693422
GO:0043903	regulation of symbiosis, encompassing mutualism through parasitism	157	0.303406045	0.0008	0.002313249
GO:0017185	peptidyl-lysine hydroxylation	6	0.303389103	0.001	0.002498236

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0003160	endocardium morphogenesis	5	0.303371943	0.0315	0.033525301
GO:0072176	nephric duct development	6	0.303346203	0.0002	0.001341684
GO:2000050	regulation of non-canonical Wnt signaling pathway	7	0.303327818	0.0342	0.036175369
GO:0000819	sister chromatid segregation	95	0.303325882	0.0009	0.002399874
GO:0045841	negative regulation of mitotic metaphase/anaphase transition	19	0.303325882	< 0.001	< 0.001
GO:2000816	negative regulation of mitotic sister chromatid separation	19	0.303325882	< 0.001	< 0.001
GO:0039536	negative regulation of RIG-I signaling pathway	7	0.303291046	0.0065	0.008621124
GO:0030330	DNA damage response, signal transduction by p53 class mediator	65	0.303276903	0.0008	0.002313249
GO:0060049	regulation of protein glycosylation	16	0.303265766	0.0011	0.002610912
GO:0016447	somatic recombination of immunoglobulin gene segments	28	0.303263468	0.0001	0.000877824
GO:0022010	central nervous system myelination	13	0.303197703	0.0059	0.007964563
GO:0032291	axon ensheathment in central nervous system	13	0.303197703	0.0059	0.007964563
GO:0070646	protein modification by small protein removal	179	0.303190181	0.0006	0.002177563
GO:0071868	cellular response to monoamine stimulus	14	0.303180732	0.003	0.004825593
GO:0071870	cellular response to catecholamine stimulus	14	0.303180732	0.003	0.004825593
GO:0009791	post-embryonic development	61	0.303154208	0.0003	0.001720882
GO:1902041	regulation of extrinsic apoptotic signaling pathway via death domain receptors	36	0.303153153	0.0023	0.004032435
GO:0006090	pyruvate metabolic process	84	0.30314396	0.003	0.004825593
GO:0006809	nitric oxide biosynthetic process	39	0.303092103	0.0008	0.002313249
GO:0016180	snRNA processing	13	0.303059103	0.001	0.002498236
GO:0010828	positive regulation of glucose transport	19	0.30302784	0.0022	0.003910907
GO:0097300	programmed necrotic cell death	24	0.303024453	0.0085	0.010671887
GO:0032623	interleukin-2 production	33	0.303022503	0.0014	0.002975058
GO:0072719	cellular response to cisplatin	5	0.303011583	0.0142	0.016456919
GO:0006284	base-excision repair	22	0.303006903	0.0012	0.002741075
GO:0046939	nucleotide phosphorylation	79	0.302995944	0.0031	0.004916949
GO:0060070	canonical Wnt signaling pathway	168	0.302989214	0.0007	0.002248538
GO:2001258	negative regulation of cation channel activity	15	0.302942943	0.0002	0.001341684
GO:0050718	positive regulation of interleukin-1 beta secretion	14	0.302941717	< 0.001	< 0.001
GO:1990774	tumor necrosis factor secretion	16	0.302895753	0.0023	0.004032435
GO:0006195	purine nucleotide catabolic process	24	0.302874303	0.0007	0.002248538
GO:0006654	phosphatidic acid biosynthetic process	21	0.302874303	0.0033	0.005149584
GO:0046473	phosphatidic acid metabolic process	21	0.302874303	0.0033	0.005149584
GO:0030224	monocyte differentiation	22	0.302831403	0.0031	0.004916949
GO:1903131	mononuclear cell differentiation	22	0.302831403	0.0031	0.004916949
GO:0008543	fibroblast growth factor receptor signaling pathway	48	0.302809953	0.0002	0.001341684
GO:0035567	non-canonical Wnt signaling pathway	81	0.302807569	0.0004	0.002007244
GO:2000831	regulation of steroid hormone secretion	10	0.302805663	< 0.001	< 0.001
GO:0090090	negative regulation of canonical Wnt signaling pathway	97	0.302798233	0.0006	0.002177563
GO:0060547	negative regulation of necrotic cell death	11	0.302796303	0.0132	0.015415723
GO:0007620	copulation	12	0.302745603	< 0.001	< 0.001
GO:0006757	ATP generation from ADP	66	0.302726103	0.0035	0.005358035
GO:0045649	regulation of macrophage differentiation	11	0.302726103	0.0019	0.003579279
GO:0097502	mannosylation	26	0.302702703	< 0.001	< 0.001
GO:0007517	muscle organ development	197	0.302650439	0.002	0.003693422
GO:0046324	regulation of glucose import	30	0.302642643	0.0006	0.002177563
GO:0035089	establishment of apical/basal cell polarity	8	0.302638353	0.0224	0.024519959
GO:2000725	regulation of cardiac muscle cell differentiation	17	0.302596714	0.0042	0.006097175
GO:0042692	muscle cell differentiation	191	0.302596239	0.0013	0.002859821
GO:0043409	negative regulation of MAPK cascade	82	0.302595976	0.0008	0.002313249
GO:0006997	nucleus organization	80	0.302583655	0.0006	0.002177563
GO:0032288	myelin assembly	12	0.302574003	0.0233	0.025417819
GO:0014013	regulation of gliogenesis	66	0.302566203	0.0043	0.006204188
GO:0033108	mitochondrial respiratory chain complex assembly	67	0.302560556	0.007	0.009166016
GO:1901029	negative regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	7	0.302555617	0.0136	0.015813319
GO:0002448	mast cell mediated immunity	25	0.302527671	0.0005	0.002177563
GO:0045830	positive regulation of isotype switching	15	0.302513943	< 0.001	< 0.001
GO:0046051	UTP metabolic process	7	0.302482074	0.0254	0.027496891
GO:0007568	aging	175	0.30245854	0.0008	0.002313249
GO:0009205	purine ribonucleoside triphosphate metabolic process	199	0.302419433	0.0037	0.005561344
GO:0009247	glycolipid biosynthetic process	39	0.302418902	0.0021	0.003804235
GO:0006305	DNA alkylation	37	0.302410519	0.0006	0.002177563
GO:0006306	DNA methylation	37	0.302410519	0.0006	0.002177563
GO:0008045	motor neuron axon guidance	7	0.302408531	< 0.001	< 0.001
GO:0006595	polyamine metabolic process	9	0.302388102	0.004	0.005880507
GO:0040018	positive regulation of multicellular organism growth	24	0.302359502	0.0012	0.002741075
GO:0060425	lung morphogenesis	25	0.302352638	0.0068	0.008946408
GO:0007029	endoplasmic reticulum organization	29	0.302329916	0.0008	0.002313249
GO:0060071	Wnt signaling pathway, planar cell polarity pathway	63	0.302322731	0.0008	0.002313249
GO:0034620	cellular response to unfolded protein	91	0.302261445	0.0026	0.004377754
GO:0010565	regulation of cellular ketone metabolic process	104	0.302257202	0.0002	0.001341684
GO:0046849	bone remodeling	42	0.302249188	0.0028	0.004605006
GO:0072177	mesonephric duct development	5	0.302239382	< 0.001	< 0.001
GO:0046034	ATP metabolic process	182	0.302228917	0.0045	0.006417207
GO:0070266	necroptotic process	21	0.302224674	0.0088	0.010992238
GO:0042455	ribonucleoside biosynthetic process	67	0.302203269	0.003	0.004825593
GO:0048246	macrophage chemotaxis	18	0.302187902	0.0002	0.001341684
GO:0070633	transepithelial transport	10	0.302162162	0.0058	0.007856196
GO:0071383	cellular response to steroid hormone stimulus	138	0.302158059	0.0016	0.003223775
GO:0008206	bile acid metabolic process	22	0.302129402	0.0045	0.006417207
GO:0032459	regulation of protein oligomerization	27	0.302083035	0.002	0.003693422
GO:0032205	negative regulation of telomere maintenance	23	0.302075989	0.0001	0.000877824

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0031638	zymogen activation	22	0.302070902	0.008	0.010168329
GO:0046632	alpha-beta T cell differentiation	51	0.302061726	0.0022	0.003910907
GO:0009124	nucleoside monophosphate biosynthetic process	63	0.302028559	0.0027	0.004491543
GO:0006638	neutral lipid metabolic process	61	0.302010676	0.0007	0.002248538
GO:0006639	acylglycerol metabolic process	61	0.302010676	0.0007	0.002248538
GO:0010977	negative regulation of neuron projection development	58	0.301974881	0.0012	0.002741075
GO:0032743	positive regulation of interleukin-2 production	17	0.301960784	0.0015	0.003088691
GO:0048066	developmental pigmentation	24	0.301951952	0.0006	0.002177563
GO:0015701	bicarbonate transport	20	0.301943372	0.0016	0.003223775
GO:0033045	regulation of sister chromatid segregation	43	0.301942474	0.0003	0.001720882
GO:0032652	regulation of interleukin-1 production	45	0.301924782	0.0003	0.001720882
GO:0033048	negative regulation of mitotic sister chromatid segregation	21	0.30189373	< 0.001	< 0.001
GO:0006641	triglyceride metabolic process	53	0.301881936	0.0006	0.002177563
GO:0001704	formation of primary germ layer	60	0.301848992	0.0011	0.002610912
GO:0002703	regulation of leukocyte mediated immunity	95	0.301757095	0.0006	0.002177563
GO:0032612	interleukin-1 production	51	0.301708431	0.0002	0.001341684
GO:0003338	metanephros morphogenesis	17	0.301703384	0.0002	0.001341684
GO:0050702	interleukin-1 beta secretion	24	0.301694552	0.0001	0.000877824
GO:0045987	positive regulation of smooth muscle contraction	18	0.301673102	0.0009	0.002399874
GO:0006888	ER to Golgi vesicle-mediated transport	122	0.301595038	0.0009	0.002399874
GO:0045646	regulation of erythrocyte differentiation	30	0.301578722	0.0012	0.002741075
GO:0033148	positive regulation of intracellular estrogen receptor signaling pathway	8	0.301576577	0.0053	0.007330056
GO:0043029	T cell homeostasis	17	0.301536831	0.004	0.005880507
GO:0001580	detection of chemical stimulus involved in sensory perception of bitter taste	11	0.301532702	0.0152	0.017453982
GO:0008361	regulation of cell size	87	0.301492626	0.0007	0.002248538
GO:0033008	positive regulation of mast cell activation involved in immune response	7	0.301489244	0.0279	0.029969105
GO:0043306	positive regulation of mast cell degranulation	7	0.301489244	0.0279	0.029969105
GO:0071300	cellular response to retinoic acid	28	0.301452473	0.0005	0.002177563
GO:1903900	regulation of viral life cycle	136	0.301421379	0.0009	0.002399874
GO:0002495	antigen processing and presentation of peptide antigen via MHC class II	65	0.301384021	0.0027	0.004491543
GO:0002279	mast cell activation involved in immune response	25	0.301374517	0.0004	0.002007244
GO:0002449	lymphocyte mediated immunity	116	0.3013336	0.0005	0.002177563
GO:1903077	negative regulation of protein localization to plasma membrane	16	0.301303089	0.0042	0.006097175
GO:0048588	developmental cell growth	89	0.301294232	0.0005	0.002177563
GO:0042036	negative regulation of cytokine biosynthetic process	23	0.301281406	0.0002	0.001341684
GO:0002262	myeloid cell homeostasis	93	0.301271779	0.0006	0.002177563
GO:0044546	NLRP3 inflammasome complex assembly	7	0.301268616	0.0031	0.004916949
GO:1900225	regulation of NLRP3 inflammasome complex assembly	7	0.301268616	0.0031	0.004916949
GO:0060586	multicellular organismal iron ion homeostasis	5	0.301261261	0.0161	0.018371585
GO:0002456	T cell mediated immunity	46	0.301259023	0.0021	0.003804235
GO:0070886	positive regulation of calcineurin-NFAT signaling cascade	8	0.301254826	0.0052	0.007215241
GO:0016053	organic acid biosynthetic process	194	0.301249851	0.001	0.002498236
GO:0046394	carboxylic acid biosynthetic process	194	0.301249851	0.001	0.002498236
GO:0070296	sarcoplasmic reticulum calcium ion transport	15	0.301244101	0.0015	0.003088691
GO:0007548	sex differentiation	151	0.301214554	0.0006	0.002177563
GO:0002705	positive regulation of leukocyte mediated immunity	64	0.301202542	0.0013	0.002859821
GO:0002726	positive regulation of T cell cytokine production	10	0.301184041	0.0061	0.008182551
GO:0045737	positive regulation of cyclin-dependent protein serine/threonine kinase activity	16	0.301174389	0.0024	0.004156304
GO:0043392	negative regulation of DNA binding	32	0.301174389	0.0006	0.002177563
GO:0070213	protein auto-ADP-ribosylation	8	0.301158301	0.001	0.002498236
GO:0006312	mitotic recombination	11	0.301134901	< 0.001	< 0.001
GO:0051302	regulation of cell division	89	0.301094674	0.0007	0.002248538
GO:0002719	negative regulation of cytokine production involved in immune response	11	0.301088101	0.0001	0.000877824
GO:0090288	negative regulation of cellular response to growth factor stimulus	72	0.301083226	0.0034	0.005263104
GO:0050709	negative regulation of protein secretion	67	0.301081465	0.0008	0.002313249
GO:0042987	amyloid precursor protein catabolic process	23	0.301068771	0.0069	0.009046225
GO:0050680	negative regulation of epithelial cell proliferation	74	0.301015688	0.0006	0.002177563
GO:0030518	intracellular steroid hormone receptor signaling pathway	80	0.300984556	0.0017	0.003334595
GO:0017015	regulation of transforming growth factor beta receptor signaling pathway	64	0.300953185	0.0012	0.002741075
GO:0061647	histone H3-K9 modification	30	0.300943801	0.0025	0.004279479
GO:0070914	UV-damage excision repair	6	0.300943801	0.0024	0.004156304
GO:0060251	regulation of glial cell proliferation	19	0.300887354	0.0032	0.005044175
GO:0051783	regulation of nuclear division	97	0.300884979	0.0012	0.002741075
GO:0055067	monovalent inorganic cation homeostasis	57	0.300873806	0.0029	0.004714719
GO:0042537	benzene-containing compound metabolic process	14	0.300864129	< 0.001	< 0.001
GO:0046479	glycosphingolipid catabolic process	9	0.300843701	0.0079	0.010077402
GO:0060026	convergent extension	9	0.300843701	0.0006	0.002177563
GO:0021549	cerebellum development	53	0.300842622	0.0022	0.003910907
GO:0045453	bone resorption	27	0.300815101	0.0105	0.012724187
GO:0051224	negative regulation of protein transport	105	0.300731752	0.0008	0.002313249
GO:0051646	mitochondrion localization	25	0.300715573	0.0011	0.002610912
GO:0000086	G2/M transition of mitotic cell cycle	152	0.300699384	0.0004	0.002007244
GO:0051235	maintenance of location	155	0.300688338	0.0009	0.002399874
GO:0018342	protein prenylation	6	0.300686401	0.0221	0.024229021
GO:0097354	prenylation	6	0.300686401	0.0221	0.024229021
GO:0070371	ERK1 and ERK2 cascade	135	0.300670194	0.0004	0.002007244
GO:0006633	fatty acid biosynthetic process	96	0.300664951	0.0007	0.002248538
GO:0033059	cellular pigmentation	32	0.300651544	0.0009	0.002399874
GO:0048739	cardiac muscle fiber development	5	0.300643501	0.0098	0.012008345
GO:0046823	negative regulation of nucleocytoplasmic transport	24	0.300643501	0.0005	0.002177563
GO:0045932	negative regulation of muscle contraction	11	0.300643501	0.0001	0.000877824
GO:0060317	cardiac epithelial to mesenchymal transition	18	0.300600601	0.0009	0.002399874
GO:0031343	positive regulation of cell killing	23	0.300576353	0.006	0.00807902

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0021983	pituitary gland development	22	0.300573301	0.0003	0.001720882
GO:1905269	positive regulation of chromatin organization	62	0.300523104	0.0013	0.002859821
GO:0007050	cell cycle arrest	148	0.300485234	0.0009	0.002399874
GO:0072009	nephron epithelium development	62	0.300464981	0.0012	0.002741075
GO:0051851	modification by host of symbiont morphology or physiology	48	0.300445088	0.0011	0.002610912
GO:0022600	digestive system process	49	0.300443884	0.0003	0.001720882
GO:0009151	purine deoxyribonucleotide metabolic process	8	0.300418275	< 0.001	< 0.001
GO:0009215	purine deoxyribonucleoside triphosphate metabolic process	8	0.300418275	< 0.001	< 0.001
GO:0071674	mononuclear cell migration	34	0.300416383	0.0008	0.002313249
GO:0006541	glutamine metabolic process	13	0.3003861	< 0.001	< 0.001
GO:0090314	positive regulation of protein targeting to membrane	17	0.3003861	0.0027	0.004491543
GO:2000573	positive regulation of DNA biosynthetic process	42	0.300367715	< 0.001	< 0.001
GO:0033151	V(D)J recombination	8	0.300353925	0.0015	0.003088691
GO:1903531	negative regulation of secretion by cell	104	0.300339075	0.0006	0.002177563
GO:0045622	regulation of T-helper cell differentiation	17	0.300310394	0.0006	0.002177563
GO:0043457	regulation of cellular respiration	16	0.300305663	0.0024	0.004156304
GO:0070897	DNA-templated transcriptional preinitiation complex assembly	20	0.30029601	0.0003	0.001720882
GO:0034356	NAD biosynthesis via nicotinamide riboside salvage pathway	11	0.3002457	0.0002	0.001341684
GO:0019184	nonribosomal peptide biosynthetic process	14	0.300220629	0.0112	0.013379119
GO:0036297	interstrand cross-link repair	37	0.300219138	0.001	0.002498236
GO:0046641	positive regulation of alpha-beta T cell proliferation	12	0.3002145	0.0356	0.037550281
GO:2001244	positive regulation of intrinsic apoptotic signaling pathway	40	0.30020592	0.0045	0.006417207
GO:0090175	regulation of establishment of planar polarity	65	0.30010494	0.0009	0.002399874
GO:1904950	negative regulation of establishment of protein localization	107	0.300080588	0.0007	0.002248538
GO:0042632	cholesterol homeostasis	39	0.3000627	0.0027	0.004491543
GO:0055092	sterol homeostasis	39	0.3000627	0.0027	0.004491543
GO:0007249	I-kappaB kinase/NF-kappaB signaling	166	0.300049619	0.0015	0.003088691
GO:0007597	blood coagulation, intrinsic pathway	8	0.300032175	0.0312	0.033261559
GO:0032663	regulation of interleukin-2 production	28	0.300009193	0.0009	0.002399874
GO:0060211	regulation of nuclear-transcribed mRNA poly(A) tail shortening	10	0.29997426	0.0001	0.000877824
GO:0060213	positive regulation of nuclear-transcribed mRNA poly(A) tail shortening	10	0.29997426	0.0001	0.000877824
GO:0071216	cellular response to biotic stimulus	111	0.299971013	0.0009	0.002399874
GO:0050000	chromosome localization	41	0.299959193	0.0004	0.002007244
GO:0051303	establishment of chromosome localization	41	0.299959193	0.0004	0.002007244
GO:1901655	cellular response to ketone	46	0.299921661	0.0006	0.002177563
GO:0009063	cellular amino acid catabolic process	75	0.299898756	0.0014	0.002975058
GO:0010596	negative regulation of endothelial cell migration	33	0.2998557	0.0009	0.002399874
GO:0045747	positive regulation of Notch signaling pathway	28	0.299834528	0.0007	0.002248538
GO:2000116	regulation of cysteine-type endopeptidase activity	137	0.299824329	0.0013	0.002859821
GO:0032757	positive regulation of interleukin-8 production	31	0.299813177	0.0027	0.004491543
GO:0072574	hepatocyte proliferation	12	0.2997426	0.0012	0.002741075
GO:0072575	epithelial cell proliferation involved in liver morphogenesis	12	0.2997426	0.0012	0.002741075
GO:0072576	liver morphogenesis	12	0.2997426	0.0012	0.002741075
GO:0010880	regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	10	0.2997426	0.0024	0.004156304
GO:0006998	nuclear envelope organization	35	0.299731568	0.0013	0.002859821
GO:0048565	digestive tract development	62	0.299725993	0.0081	0.010256567
GO:0035051	cardiocyte differentiation	70	0.299724214	0.0013	0.002859821
GO:0071636	positive regulation of transforming growth factor beta production	6	0.2996997	0.0108	0.013015961
GO:0070265	necrotic cell death	31	0.299672022	0.0121	0.014285532
GO:1903008	organelle disassembly	57	0.299654542	0.0029	0.004714719
GO:0009799	specification of symmetry	65	0.29958618	0.0001	0.000877824
GO:0009855	determination of bilateral symmetry	65	0.29958618	0.0001	0.000877824
GO:0030431	sleep	16	0.299565637	0.0002	0.001341684
GO:0006448	regulation of translational elongation	11	0.2995437	0.009	0.011215682
GO:0016266	O-glycan processing	29	0.299542893	0.0012	0.002741075
GO:2001241	positive regulation of extrinsic apoptotic signaling pathway in absense of ligand	8	0.299517375	0.0202	0.02235752
GO:0038093	Fc receptor signaling pathway	102	0.299497817	0.0011	0.002610912
GO:0043473	pigmentation	57	0.299496489	0.0015	0.003088691
GO:0006677	glycosylceramide metabolic process	13	0.299495099	0.0052	0.007215241
GO:0042267	natural killer cell mediated cytotoxicity	21	0.299466814	0.0008	0.002313249
GO:1901343	negative regulation of vasculature development	63	0.299401442	0.0013	0.002859821
GO:0046545	development of primary female sexual characteristics	58	0.299392003	0.0008	0.002313249
GO:0050654	chondroitin sulfate proteoglycan metabolic process	20	0.299369369	0.004	0.005880507
GO:0043124	negative regulation of I-kappaB kinase/NF-kappaB signaling	31	0.299314983	0.0009	0.002399874
GO:0051901	positive regulation of mitochondrial depolarization	6	0.299313599	0.025	0.027100697
GO:0086004	regulation of cardiac muscle cell contraction	13	0.299297099	0.0117	0.013882722
GO:0006067	ethanol metabolic process	8	0.299259974	0.0026	0.004377754
GO:0003214	cardiac left ventricle morphogenesis	8	0.299259974	0.0009	0.002399874
GO:1904358	positive regulation of telomere maintenance via telomere lengthening	27	0.299242099	0.0001	0.000877824
GO:0032620	interleukin-17 production	13	0.299237699	0.0019	0.003579279
GO:0051023	regulation of immunoglobulin secretion	12	0.299227799	0.0007	0.002248538
GO:0014909	smooth muscle cell migration	36	0.299220649	0.0007	0.002248538
GO:0097384	cellular lipid biosynthetic process	5	0.299202059	0.0253	0.027397944
GO:0035865	cellular response to potassium ion	5	0.299202059	0.0025	0.004279479
GO:0034380	high-density lipoprotein particle assembly	8	0.299195624	< 0.001	< 0.001
GO:0006244	pyrimidine nucleotide catabolic process	7	0.299172642	0.0025	0.004279479
GO:0009223	pyrimidine deoxyribonucleotide catabolic process	7	0.299172642	0.0025	0.004279479
GO:0042770	signal transduction in response to DNA damage	76	0.299149902	0.0008	0.002313249
GO:1905330	regulation of morphogenesis of an epithelium	101	0.299147521	0.0007	0.002248538
GO:0090087	regulation of peptide transport	96	0.299109824	0.0007	0.002248538
GO:0072520	seminiferous tubule development	7	0.299099099	< 0.001	< 0.001
GO:0060693	regulation of branching involved in salivary gland morphogenesis	5	0.299099099	0.0195	0.021665533
GO:1901186	positive regulation of ERBB signaling pathway	20	0.299073359	0.0051	0.007095023

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0002791	regulation of peptide secretion	94	0.299071716	0.0007	0.002248538
GO:0043631	RNA polyadenylation	29	0.29905472	0.0007	0.002248538
GO:0038202	TORC1 signaling	16	0.299050837	0.0007	0.002248538
GO:0010721	negative regulation of cell development	155	0.299045958	0.0007	0.002248538
GO:0050704	regulation of interleukin-1 secretion	25	0.299037323	0.0001	0.000877824
GO:0032388	positive regulation of intracellular transport	133	0.299035233	0.0007	0.002248538
GO:0030595	leukocyte chemotaxis	94	0.299027903	0.0011	0.002610912
GO:0072073	kidney epithelium development	77	0.299022213	0.0008	0.002313249
GO:0035929	steroid hormone secretion	13	0.299019899	< 0.001	< 0.001
GO:1903018	regulation of glycoprotein metabolic process	34	0.299008252	0.0034	0.005263104
GO:0072577	endothelial cell apoptotic process	30	0.298987559	0.0053	0.007330056
GO:2000194	regulation of female gonad development	6	0.298970399	0.0003	0.001720882
GO:0030968	endoplasmic reticulum unfolded protein response	82	0.298910757	0.004	0.005880507
GO:0032651	regulation of interleukin-1 beta production	37	0.298876483	0.0002	0.001341684
GO:0061035	regulation of cartilage development	31	0.298833396	0.0006	0.002177563
GO:0001522	pseudouridine synthesis	9	0.298784499	0.0147	0.016962357
GO:0090659	walking behavior	18	0.298770199	0.0083	0.010468217
GO:0015874	norepinephrine transport	9	0.298755899	< 0.001	< 0.001
GO:1905461	positive regulation of vascular associated smooth muscle cell apoptotic process	5	0.298738739	0.0026	0.004377754
GO:0072215	regulation of metanephros development	11	0.298701299	0.0013	0.002859821
GO:0038114	interleukin-21-mediated signaling pathway	5	0.298687259	0.0001	0.000877824
GO:0098756	response to interleukin-21	5	0.298687259	0.0001	0.000877824
GO:0098757	cellular response to interleukin-21	5	0.298687259	0.0001	0.000877824
GO:0072210	metanephric nephron development	23	0.298629064	0.0004	0.002007244
GO:0030100	regulation of endocytosis	129	0.298616224	0.0019	0.003579279
GO:0050716	positive regulation of interleukin-1 secretion	17	0.298614581	< 0.001	< 0.001
GO:0001701	in utero embryonic development	200	0.298595882	0.0007	0.002248538
GO:0050770	regulation of axonogenesis	62	0.29858845	0.0021	0.003804235
GO:0048660	regulation of smooth muscle cell proliferation	72	0.298577149	0.0019	0.003579279
GO:0046639	negative regulation of alpha-beta T cell differentiation	13	0.298544699	0.0001	0.000877824
GO:0002709	regulation of T cell mediated immunity	32	0.29854408	0.0025	0.004279479
GO:0007368	determination of left/right symmetry	63	0.298490327	< 0.001	< 0.001
GO:0007044	cell-substrate junction assembly	57	0.298489467	0.0027	0.004491543
GO:0035358	regulation of peroxisome proliferator activated receptor signaling pathway	9	0.298469898	< 0.001	< 0.001
GO:0048008	platelet-derived growth factor receptor signaling pathway	31	0.298468053	0.0031	0.004916949
GO:0038061	NIK/NF-kappaB signaling	116	0.298466693	0.0016	0.003223775
GO:0001776	leukocyte homeostasis	47	0.29845286	0.001	0.002498236
GO:1901223	negative regulation of NIK/NF-kappaB signaling	13	0.298445698	0.0033	0.005149584
GO:1903078	positive regulation of protein localization to plasma membrane	26	0.298435798	0.0008	0.002313249
GO:0071772	response to BMP	72	0.298423423	0.0015	0.003088691
GO:0071773	cellular response to BMP stimulus	72	0.298423423	0.0015	0.003088691
GO:0071679	commissural neuron axon guidance	8	0.298391248	0.0009	0.002399874
GO:0006694	steroid biosynthetic process	98	0.298368923	0.0038	0.005666214
GO:0014808	release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	13	0.298346698	0.0012	0.002741075
GO:1903514	calcium ion transport from endoplasmic reticulum to cytosol	13	0.298346698	0.0012	0.002741075
GO:0090276	regulation of peptide hormone secretion	91	0.298281641	0.0007	0.002248538
GO:0050678	regulation of epithelial cell proliferation	173	0.298279287	0.0006	0.002177563
GO:0045410	positive regulation of interleukin-6 biosynthetic process	10	0.298275418	0.0194	0.021561946
GO:0002639	positive regulation of immunoglobulin production	22	0.298233298	< 0.001	< 0.001
GO:0032845	negative regulation of homeostatic process	102	0.298170439	0.0006	0.002177563
GO:0045787	positive regulation of cell cycle	195	0.298168498	0.0009	0.002399874
GO:0048709	oligodendrocyte differentiation	63	0.298167555	0.0024	0.004156304
GO:0040034	regulation of development, heterochronic	8	0.298166023	0.0004	0.002007244
GO:0071361	cellular response to ethanol	9	0.298126698	0.0006	0.002177563
GO:0019321	pentose metabolic process	8	0.298101673	0.021	0.023166522
GO:0022037	metencephalon development	59	0.298100037	0.0029	0.004714719
GO:0034143	regulation of toll-like receptor 4 signaling pathway	9	0.298098098	0.0004	0.002007244
GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	126	0.29809197	0.0016	0.003223775
GO:0032212	positive regulation of telomere maintenance via telomerase	25	0.29809009	0.0001	0.000877824
GO:0003143	embryonic heart tube morphogenesis	37	0.298076455	0.0029	0.004714719
GO:0032507	maintenance of protein location in cell	53	0.298064641	0.0014	0.002975058
GO:0035050	embryonic heart tube development	41	0.298050664	0.0035	0.005358035
GO:0009165	nucleotide biosynthetic process	133	0.298042403	0.001	0.002498236
GO:0035601	protein deacylation	53	0.298040358	0.0026	0.004377754
GO:0045778	positive regulation of ossification	50	0.298033462	< 0.001	< 0.001
GO:1905216	positive regulation of RNA binding	6	0.298026598	0.005	0.006974174
GO:0034587	piRNA metabolic process	6	0.298026598	< 0.001	< 0.001
GO:0031345	negative regulation of cell projection organization	68	0.298008933	0.0015	0.003088691
GO:0044839	cell cycle G2/M phase transition	162	0.298002765	0.0003	0.001720882
GO:1990266	neutrophil migration	38	0.297994987	0.0076	0.009790742
GO:1901184	regulation of ERBB signaling pathway	51	0.29796351	0.0056	0.007655255
GO:2000736	regulation of stem cell differentiation	84	0.297949991	0.0005	0.002177563
GO:0043535	regulation of blood vessel endothelial cell migration	60	0.297949378	0.0013	0.002859821
GO:0050768	negative regulation of neurogenesis	136	0.297940798	0.0008	0.002313249
GO:0048340	paraxial mesoderm morphogenesis	6	0.297940798	0.0004	0.002007244
GO:0034446	substrate adhesion-dependent cell spreading	51	0.297933227	0.0014	0.002975058
GO:0002638	negative regulation of immunoglobulin production	7	0.297885641	< 0.001	< 0.001
GO:0033044	regulation of chromosome organization	101	0.297880908	0.0001	0.000877824
GO:0051100	negative regulation of binding	94	0.297880555	0.0008	0.002313249
GO:0016242	negative regulation of macroautophagy	25	0.297873874	0.0049	0.006860215
GO:0050650	chondroitin sulfate proteoglycan biosynthetic process	14	0.297830484	0.0083	0.010468217
GO:0042063	gliogenesis	166	0.297829154	0.0009	0.002399874
GO:0046209	nitric oxide metabolic process	42	0.297824355	0.0007	0.002248538

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0097711	ciliary basal body docking	66	0.297812098	< 0.001	< 0.001
GO:0050706	regulation of interleukin-1 beta secretion	21	0.297799841	0.0001	0.000877824
GO:0002504	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	66	0.297788698	0.0029	0.004714719
GO:0003382	epithelial cell morphogenesis	19	0.297785003	0.001	0.002498236
GO:0042761	very long-chain fatty acid biosynthetic process	7	0.297775326	0.0017	0.003334595
GO:0051146	striated muscle cell differentiation	119	0.297753696	0.0017	0.003334595
GO:0032204	regulation of telomere maintenance	55	0.297751258	0.0001	0.000877824
GO:0019886	antigen processing and presentation of exogenous peptide antigen via MHC class II	62	0.297724914	0.0043	0.006204188
GO:0048659	smooth muscle cell proliferation	73	0.297709843	0.0016	0.003223775
GO:0010804	negative regulation of tumor necrosis factor-mediated signaling pathway	12	0.297704848	0.001	0.002498236
GO:0045137	development of primary sexual characteristics	128	0.297689431	0.0006	0.002177563
GO:0030574	collagen catabolic process	17	0.297660686	0.0084	0.010571327
GO:0044243	multicellular organism catabolic process	17	0.297660686	0.0084	0.010571327
GO:0050663	cytokine secretion	117	0.297620698	0.0005	0.002177563
GO:0051289	protein homotetramerization	60	0.297619048	0.0012	0.002741075
GO:0001655	urogenital system development	190	0.297617016	0.0009	0.002399874
GO:0051216	cartilage development	88	0.297601498	0.0005	0.002177563
GO:0046782	regulation of viral transcription	49	0.297591469	0.0018	0.003459409
GO:0032963	collagen metabolic process	50	0.297585586	0.004	0.005880507
GO:0044259	multicellular organismal macromolecule metabolic process	50	0.297585586	0.004	0.005880507
GO:1903364	positive regulation of cellular protein catabolic process	80	0.297580438	0.0007	0.002248538
GO:0010990	regulation of SMAD protein complex assembly	5	0.297554698	0.0279	0.029969105
GO:1902117	positive regulation of organelle assembly	39	0.297548098	0.0035	0.005358035
GO:0019722	calcium-mediated signaling	72	0.297540398	0.0007	0.002248538
GO:0001818	negative regulation of cytokine production	153	0.297472262	0.0006	0.002177563
GO:0033028	myeloid cell apoptotic process	17	0.29746385	0.0017	0.003334595
GO:0010506	regulation of autophagy	197	0.297458009	0.0029	0.004714719
GO:1901293	nucleoside phosphate biosynthetic process	136	0.29745628	0.001	0.002498236
GO:0071577	zinc II ion transmembrane transport	5	0.297451737	0.0245	0.026594873
GO:0043297	apical junction assembly	41	0.297441693	0.0012	0.002741075
GO:0009200	deoxyribonucleoside triphosphate metabolic process	13	0.297435897	0.0011	0.002610912
GO:0044728	DNA methylation or demethylation	47	0.297434212	0.0009	0.002399874
GO:0008406	gonad development	124	0.297382405	0.0006	0.002177563
GO:0090068	positive regulation of cell cycle process	147	0.297374342	0.0016	0.003223775
GO:0099637	neurotransmitter receptor transport	5	0.297348777	0.0006	0.002177563
GO:0065005	protein-lipid complex assembly	16	0.29734556	0.0006	0.002177563
GO:0031146	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	49	0.297339322	0.001	0.002498236
GO:0002673	regulation of acute inflammatory response	46	0.297336467	0.0055	0.007544447
GO:0010719	negative regulation of epithelial to mesenchymal transition	14	0.297334069	0.0021	0.003804235
GO:0045821	positive regulation of glycolytic process	11	0.297297297	0.024	0.026109935
GO:0051194	positive regulation of cofactor metabolic process	11	0.297297297	0.024	0.026109935
GO:0051197	positive regulation of coenzyme metabolic process	11	0.297297297	0.024	0.026109935
GO:0002825	regulation of T-helper 1 type immune response	12	0.297275847	0.0003	0.001720882
GO:0030509	BMP signaling pathway	68	0.2972708	0.0028	0.004605006
GO:0044784	metaphase/anaphase transition of cell cycle	30	0.297254397	0.0001	0.000877824
GO:0045185	maintenance of protein location	58	0.297252918	0.0013	0.002859821
GO:0030641	regulation of cellular pH	32	0.297240991	0.0087	0.010877987
GO:0051453	regulation of intracellular pH	32	0.297240991	0.0087	0.010877987
GO:0043388	positive regulation of DNA binding	31	0.297239175	0.0009	0.002399874
GO:1903670	regulation of sprouting angiogenesis	40	0.297200772	0.0013	0.002859821
GO:0030004	cellular monovalent inorganic cation homeostasis	39	0.297191697	0.0114	0.01358747
GO:0019370	leukotriene biosynthetic process	14	0.297186983	0.0066	0.008731949
GO:2000269	regulation of fibroblast apoptotic process	12	0.297168597	0.001	0.002498236
GO:1901976	regulation of cell cycle checkpoint	23	0.29715181	0.0001	0.000877824
GO:0000079	regulation of cyclin-dependent protein serine/threonine kinase activity	46	0.297095854	0.0011	0.002610912
GO:0042542	response to hydrogen peroxide	81	0.297093919	0.0027	0.004491543
GO:0002455	humoral immune response mediated by circulating immunoglobulin	24	0.297093522	0.0114	0.01358747
GO:0046883	regulation of hormone secretion	116	0.297066525	0.0006	0.002177563
GO:0002200	somatic diversification of immune receptors	37	0.297053811	0.0001	0.000877824
GO:0055123	digestive system development	70	0.297043574	0.0077	0.009887588
GO:0042762	regulation of sulfur metabolic process	10	0.297014157	0.0005	0.002177563
GO:0070231	T cell apoptotic process	27	0.297001764	0.0044	0.006304227
GO:0000002	mitochondrial genome maintenance	18	0.296996997	0.0096	0.01183839
GO:0090195	chemokine secretion	14	0.29698474	< 0.001	< 0.001
GO:0007039	protein catabolic process in the vacuole	13	0.296980497	0.0102	0.012424427
GO:0008585	female gonad development	55	0.296950977	0.0009	0.002399874
GO:0006476	protein deacetylation	49	0.296945342	0.0024	0.004156304
GO:1901185	negative regulation of ERBB signaling pathway	26	0.296911197	0.0101	0.012328539
GO:0007213	G-protein coupled acetylcholine receptor signaling pathway	7	0.296892811	0.0229	0.025020007
GO:0002706	regulation of lymphocyte mediated immunity	63	0.296851954	0.0008	0.002313249
GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	170	0.296832463	0.0016	0.003223775
GO:0071219	cellular response to molecule of bacterial origin	94	0.296749637	0.0012	0.002741075
GO:0002367	cytokine production involved in immune response	51	0.296747167	0.0007	0.002248538
GO:0070230	positive regulation of lymphocyte apoptotic process	6	0.296739597	0.0167	0.018954426
GO:0072001	renal system development	170	0.296678023	0.0008	0.002313249
GO:0046660	female sex differentiation	65	0.296675577	0.001	0.002498236
GO:0022900	electron transport chain	121	0.296661242	0.0037	0.005561344
GO:0000041	transition metal ion transport	51	0.296626038	0.0025	0.004279479
GO:0007126	meiotic nuclear division	59	0.296625439	0.0014	0.002975058
GO:0033032	regulation of myeloid cell apoptotic process	14	0.296617025	0.0002	0.001341684
GO:0060795	cell fate commitment involved in formation of primary germ layer	16	0.296605534	0.0001	0.000877824
GO:0010633	negative regulation of epithelial cell migration	40	0.296602317	0.0007	0.002248538
GO:0090042	tubulin deacetylation	8	0.296557272	0.0097	0.011922488

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1903671	negative regulation of sprouting angiogenesis	17	0.296555379	0.0026	0.004377754
GO:0016579	protein deubiquitination	170	0.296552351	0.0006	0.002177563
GO:0001738	morphogenesis of a polarized epithelium	81	0.296531452	0.0006	0.002177563
GO:0005996	monosaccharide metabolic process	159	0.296513764	0.0008	0.002313249
GO:0060749	mammary gland alveolus development	11	0.296501697	0.0172	0.019442284
GO:0061377	mammary gland lobule development	11	0.296501697	0.0172	0.019442284
GO:0044346	fibroblast apoptotic process	14	0.296488325	0.0021	0.003804235
GO:0030638	polyketide metabolic process	7	0.296488325	0.0085	0.010671887
GO:0030647	aminoglycoside antibiotic metabolic process	7	0.296488325	0.0085	0.010671887
GO:0044597	daunorubicin metabolic process	7	0.296488325	0.0085	0.010671887
GO:0044598	doxorubicin metabolic process	7	0.296488325	0.0085	0.010671887
GO:0046326	positive regulation of glucose import	18	0.296439296	0.0026	0.004377754
GO:1905508	protein localization to microtubule organizing center	15	0.296422136	0.0006	0.002177563
GO:0098732	macromolecule deacylation	54	0.29639163	0.0029	0.004714719
GO:0072659	protein localization to plasma membrane	133	0.296389623	0.0009	0.002399874
GO:0010894	negative regulation of steroid biosynthetic process	11	0.296384696	0.0136	0.015813319
GO:0045939	negative regulation of steroid metabolic process	11	0.296384696	0.0136	0.015813319
GO:0030865	cortical cytoskeleton organization	22	0.296372996	0.0042	0.006097175
GO:0003157	endocardium development	8	0.296364221	0.0057	0.007745437
GO:1904019	epithelial cell apoptotic process	60	0.296332046	0.0016	0.003223775
GO:0003198	epithelial to mesenchymal transition involved in endocardial cushion formation	12	0.296310596	0.0012	0.002741075
GO:2001236	regulation of extrinsic apoptotic signaling pathway	97	0.296296886	0.0039	0.005778819
GO:0034383	low-density lipoprotein particle clearance	17	0.296252555	0.005	0.006974174
GO:0006576	cellular biogenic amine metabolic process	30	0.296216216	0.0008	0.002313249
GO:0001906	cell killing	59	0.296180442	0.0068	0.008946408
GO:0098813	nuclear chromosome segregation	123	0.296098189	0.0007	0.002248538
GO:0038128	ERBB2 signaling pathway	18	0.296024596	0.0014	0.002975058
GO:0009068	aspartate family amino acid catabolic process	17	0.296010296	0.0041	0.005981983
GO:0043536	positive regulation of blood vessel endothelial cell migration	39	0.296003696	0.0009	0.002399874
GO:1901983	regulation of protein acetylation	41	0.295978906	0.0001	0.000877824
GO:0051099	positive regulation of binding	102	0.295959825	0.0012	0.002741075
GO:0090316	positive regulation of intracellular protein transport	102	0.295937114	0.0008	0.002313249
GO:0032495	response to muramyl dipeptide	9	0.295895896	0.0003	0.001720882
GO:0033002	muscle cell proliferation	105	0.295892627	0.0018	0.003459409
GO:0050673	epithelial cell proliferation	198	0.295888096	0.0006	0.002177563
GO:0032436	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	41	0.295853345	0.0013	0.002859821
GO:0006940	regulation of smooth muscle contraction	28	0.295826439	0.0002	0.001341684
GO:2000392	regulation of lamellipodium morphogenesis	8	0.295817246	0.0285	0.030556948
GO:0048771	tissue remodeling	84	0.295801924	0.0044	0.006304227
GO:0032401	establishment of melanosome localization	11	0.295776296	0.0001	0.000877824
GO:0032402	melanosome transport	11	0.295776296	0.0001	0.000877824
GO:0032000	positive regulation of fatty acid beta-oxidation	6	0.295752896	0.0002	0.001341684
GO:0002762	negative regulation of myeloid leukocyte differentiation	24	0.295731446	0.0005	0.002177563
GO:0045988	negative regulation of striated muscle contraction	5	0.295649936	0.002	0.003693422
GO:0045010	actin nucleation	17	0.295646907	0.0002	0.001341684
GO:0043112	receptor metabolic process	94	0.295632411	0.0026	0.004377754
GO:0061298	retina vasculature development in camera-type eye	12	0.295624196	0.0021	0.003804235
GO:0071375	cellular response to peptide hormone stimulus	154	0.295610824	0.0007	0.002248538
GO:0030308	negative regulation of cell growth	90	0.295566996	0.0008	0.002313249
GO:0042035	regulation of cytokine biosynthetic process	63	0.295552696	0.0012	0.002741075
GO:0031098	stress-activated protein kinase signaling cascade	142	0.295539	0.0007	0.002248538
GO:0050774	negative regulation of dendrite morphogenesis	6	0.295538396	0.0392	0.041055316
GO:0002821	positive regulation of adaptive immune response	57	0.295531622	0.0008	0.002313249
GO:0051149	positive regulation of muscle cell differentiation	43	0.295531412	0.0017	0.003334595
GO:0030307	positive regulation of cell growth	90	0.295512656	0.0007	0.002248538
GO:0002819	regulation of adaptive immune response	85	0.295495495	0.0006	0.002177563
GO:0051438	regulation of ubiquitin-protein transferase activity	27	0.295495495	0.0009	0.002399874
GO:0035791	platelet-derived growth factor receptor-beta signaling pathway	7	0.295458724	0.023	0.025116347
GO:0007163	establishment or maintenance of cell polarity	96	0.295447233	0.0025	0.004279479
GO:0035646	endosome to melanosome transport	7	0.295421953	0.018	0.020203241
GO:0043476	pigment accumulation	7	0.295421953	0.018	0.020203241
GO:0043482	cellular pigment accumulation	7	0.295421953	0.018	0.020203241
GO:0043485	endosome to pigment granule transport	7	0.295421953	0.018	0.020203241
GO:0048757	pigment granule maturation	7	0.295421953	0.018	0.020203241
GO:0007369	gastrulation	95	0.295416921	0.0006	0.002177563
GO:0006120	mitochondrial electron transport, NADH to ubiquinone	39	0.295409695	0.0124	0.014577606
GO:0098779	mitophagy in response to mitochondrial depolarization	11	0.295378495	0.0011	0.002610912
GO:1901222	regulation of NIK/NF-kappaB signaling	72	0.295366795	0.0037	0.005561344
GO:0045429	positive regulation of nitric oxide biosynthetic process	22	0.295366795	0.001	0.002498236
GO:1904407	positive regulation of nitric oxide metabolic process	22	0.295366795	0.001	0.002498236
GO:0043200	response to amino acid	62	0.295362644	0.0004	0.002007244
GO:0061387	regulation of extent of cell growth	44	0.295302445	0.0017	0.003334595
GO:0034331	cell junction maintenance	7	0.295274867	0.0189	0.021076063
GO:0042226	interleukin-6 biosynthetic process	16	0.29527027	0.004	0.005880507
GO:0036315	cellular response to sterol	13	0.295257895	0.0001	0.000877824
GO:0009648	photoperiodism	11	0.295238095	0.0009	0.002399874
GO:2001057	reactive nitrogen species metabolic process	43	0.295160277	0.0005	0.002177563
GO:0007067	mitotic nuclear division	149	0.295115441	0.0011	0.002610912
GO:0033046	negative regulation of sister chromatid segregation	23	0.295114991	< 0.001	< 0.001
GO:2000786	positive regulation of autophagosome assembly	5	0.295083655	0.0086	0.010769857
GO:2001251	negative regulation of chromosome organization	46	0.295081417	< 0.001	< 0.001
GO:0099623	regulation of cardiac muscle cell membrane repolarization	11	0.295074295	0.0004	0.002007244
GO:0010288	response to lead ion	15	0.295066495	0.0073	0.009463568

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0007009	plasma membrane organization	176	0.295058208	0.0014	0.002975058
GO:0055069	zinc ion homeostasis	8	0.295045045	0.0039	0.005778819
GO:0002708	positive regulation of lymphocyte mediated immunity	48	0.29496997	0.0009	0.002399874
GO:1901136	carbohydrate derivative catabolic process	96	0.294964607	0.0008	0.002313249
GO:0035589	G-protein coupled purinergic nucleotide receptor signaling pathway	9	0.294952095	0.0004	0.002007244
GO:0070830	bicellular tight junction assembly	33	0.294949495	0.0012	0.002741075
GO:1901070	guanosine-containing compound biosynthetic process	8	0.29494852	0.0247	0.026793719
GO:0051767	nitric-oxide synthase biosynthetic process	13	0.294941095	0.0006	0.002177563
GO:0051769	regulation of nitric-oxide synthase biosynthetic process	13	0.294941095	0.0006	0.002177563
GO:0060155	platelet dense granule organization	6	0.294937795	< 0.001	< 0.001
GO:0044236	multicellular organism metabolic process	60	0.294907765	0.0054	0.007432873
GO:0046879	hormone secretion	138	0.294876243	0.0007	0.002248538
GO:1901606	alpha-amino acid catabolic process	59	0.294867264	0.0014	0.002975058
GO:0007020	microtubule nucleation	14	0.294851995	0.0138	0.016031243
GO:2000353	positive regulation of endothelial cell apoptotic process	13	0.294802495	0.0233	0.025417819
GO:0032275	luteinizing hormone secretion	7	0.294796838	0.0274	0.029461819
GO:0071827	plasma lipoprotein particle organization	22	0.294793495	0.0002	0.001341684
GO:0098876	vesicle-mediated transport to the plasma membrane	42	0.294778452	0.0026	0.004377754
GO:0045931	positive regulation of mitotic cell cycle	83	0.2947357	0.0011	0.002610912
GO:0001736	establishment of planar polarity	71	0.294730545	0.0006	0.002177563
GO:0007164	establishment of tissue polarity	71	0.294730545	0.0006	0.002177563
GO:0070372	regulation of ERK1 and ERK2 cascade	124	0.294704612	0.0006	0.002177563
GO:0006026	aminoglycan catabolic process	31	0.294665172	0.0005	0.002177563
GO:0006027	glycosaminoglycan catabolic process	31	0.294665172	0.0005	0.002177563
GO:0002701	negative regulation of production of molecular mediator of immune response	17	0.294617306	< 0.001	< 0.001
GO:0007250	activation of NF-kappaB-inducing kinase activity	14	0.29461298	0.0136	0.015813319
GO:0014706	striated muscle tissue development	182	0.294499837	0.0025	0.004279479
GO:0006323	DNA packaging	92	0.294491075	0.0008	0.002313249
GO:0009156	ribonucleoside monophosphate biosynthetic process	56	0.294475087	0.0044	0.006304227
GO:0000280	nuclear division	197	0.294472427	0.0011	0.002610912
GO:0042773	ATP synthesis coupled electron transport	65	0.294469854	0.0116	0.013792313
GO:0042775	mitochondrial ATP synthesis coupled electron transport	65	0.294469854	0.0116	0.013792313
GO:0022904	respiratory electron transport chain	79	0.29443657	0.0093	0.011528671
GO:0034695	response to prostaglandin E	15	0.294431574	0.0001	0.000877824
GO:0043502	regulation of muscle adaptation	44	0.294430794	0.0061	0.008182551
GO:0060711	labyrinthine layer development	26	0.294386694	0.0006	0.002177563
GO:0035710	CD4-positive, alpha-beta T cell activation	50	0.294383526	0.0036	0.005475609
GO:0034629	cellular protein complex localization	9	0.294351494	0.0006	0.002177563
GO:0051055	negative regulation of lipid biosynthetic process	26	0.294307494	0.0063	0.008390784
GO:0003222	ventricular trabecula myocardium morphogenesis	14	0.294300423	0.0038	0.005666214
GO:1901653	cellular response to peptide	185	0.294268322	0.0009	0.002399874
GO:0034101	erythrocyte homeostasis	78	0.294248094	0.0006	0.002177563
GO:0036152	phosphatidylethanolamine acyl-chain remodeling	14	0.294245266	0.0045	0.006417207
GO:0051651	maintenance of location in cell	65	0.294232254	0.0015	0.003088691
GO:0001825	blastocyst formation	25	0.294229086	0.0018	0.003459409
GO:0006513	protein monoubiquitination	40	0.294221364	0.0007	0.002248538
GO:0008593	regulation of Notch signaling pathway	52	0.294218394	0.0007	0.002248538
GO:0048747	muscle fiber development	27	0.294208494	0.0084	0.010571327
GO:0009914	hormone transport	139	0.294199235	0.0008	0.002313249
GO:0007588	excretion	32	0.294192407	0.0016	0.003223775
GO:0070199	establishment of protein localization to chromosome	18	0.294179894	< 0.001	< 0.001
GO:0042180	cellular ketone metabolic process	143	0.294165294	0.0008	0.002313249
GO:0061138	morphogenesis of a branching epithelium	91	0.294154751	0.0029	0.004714719
GO:0034694	response to prostaglandin	17	0.294132788	0.0001	0.000877824
GO:0007281	germ cell development	96	0.294103925	0.0001	0.000877824
GO:0006885	regulation of pH	36	0.294086944	0.0052	0.007215241
GO:0060323	head morphogenesis	20	0.294041184	0.0075	0.00968541
GO:0035176	social behavior	17	0.294011659	0.0002	0.001341684
GO:0051703	intraspecies interaction between organisms	17	0.294011659	0.0002	0.001341684
GO:0071354	cellular response to interleukin-6	21	0.294000123	0.0002	0.001341684
GO:2000021	regulation of ion homeostasis	86	0.293984017	0.0009	0.002399874
GO:0007219	Notch signaling pathway	103	0.29396109	0.0011	0.002610912
GO:0034145	positive regulation of toll-like receptor 4 signaling pathway	5	0.293951094	0.0005	0.002177563
GO:0016445	somatic diversification of immunoglobulins	30	0.293933934	0.0001	0.000877824
GO:1903170	negative regulation of calcium ion transmembrane transport	17	0.293920812	0.0017	0.003334595
GO:0030902	hindbrain development	75	0.293906478	0.003	0.004825593
GO:0060713	labyrinthine layer morphogenesis	9	0.293893894	0.0013	0.002859821
GO:0015807	L-amino acid transport	31	0.293884668	0.0014	0.002975058
GO:0045618	positive regulation of keratinocyte differentiation	7	0.293877551	0.0072	0.009362497
GO:0090092	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	110	0.293871534	0.0019	0.003579279
GO:0061323	cell proliferation involved in heart morphogenesis	11	0.293857494	0.002	0.003693422
GO:2000136	regulation of cell proliferation involved in heart morphogenesis	11	0.293857494	0.002	0.003693422
GO:0009612	response to mechanical stimulus	114	0.293847231	0.0018	0.003459409
GO:0007585	respiratory gaseous exchange	36	0.293843844	0.0004	0.002007244
GO:0033327	Leydig cell differentiation	10	0.293822394	0.0011	0.002610912
GO:0045844	positive regulation of striated muscle tissue development	33	0.293810694	0.0067	0.008845888
GO:0048636	positive regulation of muscle organ development	33	0.293810694	0.0067	0.008845888
GO:0071318	cellular response to ATP	11	0.293810694	0.0008	0.002313249
GO:0045061	thymic T cell selection	9	0.293808094	0.0004	0.002007244
GO:0006558	L-phenylalanine metabolic process	7	0.293804008	0.0094	0.011616482
GO:0006559	L-phenylalanine catabolic process	7	0.293804008	0.0094	0.011616482
GO:1902221	erythrose 4-phosphate/phosphoenolpyruvate family amino acid metabolic process	7	0.293804008	0.0094	0.011616482
GO:1902222	erythrose 4-phosphate/phosphoenolpyruvate family amino acid catabolic process	7	0.293804008	0.0094	0.011616482

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0090049	regulation of cell migration involved in sprouting angiogenesis	25	0.293796654	0.0017	0.003334595
GO:1903828	negative regulation of cellular protein localization	79	0.293778408	0.0024	0.004156304
GO:1904738	vascular associated smooth muscle cell migration	11	0.293740494	0.0126	0.014782732
GO:1904752	regulation of vascular associated smooth muscle cell migration	11	0.293740494	0.0126	0.014782732
GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	150	0.293734878	0.0021	0.003804235
GO:0033363	secretory granule organization	21	0.293730465	0.0002	0.001341684
GO:0002714	positive regulation of B cell mediated immunity	22	0.293717094	0.0002	0.001341684
GO:0002891	positive regulation of immunoglobulin mediated immune response	22	0.293717094	0.0002	0.001341684
GO:1902751	positive regulation of cell cycle G2/M phase transition	14	0.293693694	0.0008	0.002313249
GO:0071230	cellular response to amino acid stimulus	40	0.293635779	0.0002	0.001341684
GO:0060571	morphogenesis of an epithelial fold	8	0.293597169	0.0319	0.033911376
GO:0060326	cell chemotaxis	128	0.29357907	0.0008	0.002313249
GO:0002824	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	52	0.293574894	0.0009	0.002399874
GO:0050715	positive regulation of cytokine secretion	71	0.293526927	0.0003	0.001720882
GO:0072330	monocarboxylic acid biosynthetic process	135	0.29351256	0.0013	0.002859821
GO:0014902	myotube differentiation	41	0.29351163	0.0072	0.009362497
GO:0031398	positive regulation of protein ubiquitination	68	0.293470361	0.0004	0.002007244
GO:0061180	mammary gland epithelium development	36	0.293464893	0.0002	0.001341684
GO:0002429	immune response-activating cell surface receptor signaling pathway	191	0.29344977	0.001	0.002498236
GO:0032689	negative regulation of interferon-gamma production	12	0.293436293	0.0007	0.002248538
GO:0038089	positive regulation of cell migration by vascular endothelial growth factor signaling pathway	7	0.293436293	0.0057	0.007745437
GO:0010038	response to metal ion	186	0.293429374	0.0033	0.005149584
GO:0030326	embryonic limb morphogenesis	59	0.293427568	0.0003	0.001720882
GO:0035113	embryonic appendage morphogenesis	59	0.293427568	0.0003	0.001720882
GO:0007160	cell-matrix adhesion	112	0.293397224	0.0021	0.003804235
GO:0003298	physiological muscle hypertrophy	11	0.293342693	0.0003	0.001720882
GO:0003301	physiological cardiac muscle hypertrophy	11	0.293342693	0.0003	0.001720882
GO:0061049	cell growth involved in cardiac muscle cell development	11	0.293342693	0.0003	0.001720882
GO:0031057	negative regulation of histone modification	26	0.293337293	0.0001	0.000877824
GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling	116	0.293287623	0.0024	0.004156304
GO:0042454	ribonucleoside catabolic process	12	0.293286143	0.0036	0.005475609
GO:0031498	chromatin disassembly	12	0.293243243	0.0025	0.004279479
GO:0001657	ureteric bud development	55	0.293206973	0.0003	0.001720882
GO:0072163	mesonephric epithelium development	55	0.293206973	0.0003	0.001720882
GO:0072164	mesonephric tubule development	55	0.293206973	0.0003	0.001720882
GO:0035296	regulation of tube diameter	45	0.293173173	0.0006	0.002177563
GO:0097746	regulation of blood vessel diameter	45	0.293173173	0.0006	0.002177563
GO:0031000	response to caffeine	10	0.293153153	0.0052	0.007215241
GO:0030204	chondroitin sulfate metabolic process	19	0.293124704	0.0037	0.005561344
GO:0060537	muscle tissue development	191	0.293120944	0.0022	0.003910907
GO:0090114	COPII-coated vesicle budding	49	0.293115856	0.0009	0.002399874
GO:0021692	cerebellar Purkinje cell layer morphogenesis	9	0.293064493	0.0042	0.006097175
GO:0035094	response to nicotine	22	0.292979993	0.0008	0.002313249
GO:1902033	regulation of hematopoietic stem cell proliferation	5	0.292972973	0.0021	0.003804235
GO:1904294	positive regulation of ERAD pathway	11	0.292968293	0.0059	0.007964563
GO:0045907	positive regulation of vasoconstriction	12	0.292964393	0.0004	0.002007244
GO:0032206	positive regulation of telomere maintenance	36	0.292935793	0.0001	0.000877824
GO:1902930	regulation of alcohol biosynthetic process	43	0.292897549	0.0014	0.002975058
GO:0019319	hexose biosynthetic process	50	0.292844273	0.0011	0.002610912
GO:0060325	face morphogenesis	19	0.292840209	0.0077	0.009887588
GO:0016233	telomere capping	23	0.292820771	< 0.001	< 0.001
GO:1904029	regulation of cyclin-dependent protein kinase activity	47	0.292795531	0.0014	0.002975058
GO:0030890	positive regulation of B cell proliferation	21	0.292786664	0.0001	0.000877824
GO:0042461	photoreceptor cell development	21	0.292749893	0.0002	0.001341684
GO:0009311	oligosaccharide metabolic process	30	0.292749893	0.0056	0.007655255
GO:0051560	mitochondrial calcium ion homeostasis	14	0.292737636	0.0062	0.008281828
GO:0002790	peptide secretion	111	0.292726704	0.0008	0.002313249
GO:0033210	leptin-mediated signaling pathway	7	0.292700864	0.0001	0.000877824
GO:0036149	phosphatidylinositol acyl-chain remodeling	7	0.292700864	0.0096	0.01183839
GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	131	0.292699461	0.0007	0.002248538
GO:0045742	positive regulation of epidermal growth factor receptor signaling pathway	19	0.29267764	0.0049	0.006860215
GO:0021537	telencephalon development	120	0.292666238	0.0005	0.002177563
GO:0014742	positive regulation of muscle hypertrophy	15	0.292664093	0.0086	0.010769857
GO:0006337	nucleosome disassembly	11	0.292664093	0.0018	0.003459409
GO:1902229	regulation of intrinsic apoptotic signaling pathway in response to DNA damage	27	0.292654559	0.0002	0.001341684
GO:1902743	regulation of lamellipodium organization	19	0.292650545	0.0048	0.006748379
GO:0009166	nucleotide catabolic process	34	0.29263381	0.0013	0.002859821
GO:0050710	negative regulation of cytokine secretion	31	0.292622576	0.0008	0.002313249
GO:0035743	CD4-positive, alpha-beta T cell cytokine production	6	0.292621193	0.0162	0.018465856
GO:0032465	regulation of cytokinesis	40	0.292612613	0.0016	0.003223775
GO:0044380	protein localization to cytoskeleton	24	0.292610468	0.0006	0.002177563
GO:0033003	regulation of mast cell activation	22	0.292547093	0.0013	0.002859821
GO:1903975	regulation of glial cell migration	10	0.292535393	0.0083	0.010468217
GO:1902430	negative regulation of beta-amyloid formation	8	0.292535393	0.0026	0.004377754
GO:0007254	JNK cascade	96	0.29253003	0.0007	0.002248538
GO:0046460	neutral lipid biosynthetic process	28	0.292489428	0.001	0.002498236
GO:0046463	acylglycerol biosynthetic process	28	0.292489428	0.001	0.002498236
GO:0072006	nephron development	85	0.292488455	0.0008	0.002313249
GO:0002292	T cell differentiation involved in immune response	33	0.292437892	0.0013	0.002859821
GO:1903305	regulation of regulated secretory pathway	55	0.292392652	0.0008	0.002313249
GO:0007229	integrin-mediated signaling pathway	60	0.292389532	0.0028	0.004605006

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0034656	nucleobase-containing small molecule catabolic process	10	0.292380952	0.0037	0.005561344
GO:0044406	adhesion of symbiont to host	8	0.292374517	0.0019	0.003579279
GO:1903322	positive regulation of protein modification by small protein conjugation or removal	79	0.292361077	0.0004	0.002007244
GO:0010669	epithelial structure maintenance	16	0.29235843	< 0.001	< 0.001
GO:0001822	kidney development	163	0.292343527	0.0008	0.002313249
GO:0006293	nucleotide-excision repair, preincision complex stabilization	15	0.292286572	0.0012	0.002741075
GO:0006295	nucleotide-excision repair, DNA incision, 3'-to lesion	15	0.292286572	0.0012	0.002741075
GO:0043967	histone H4 acetylation	44	0.292242892	0.0013	0.002859821
GO:0048806	genitalia development	22	0.292231192	0.0031	0.004916949
GO:0045992	negative regulation of embryonic development	14	0.292204449	0.0003	0.001720882
GO:0071285	cellular response to lithium ion	6	0.292192192	0.0054	0.007432873
GO:0051893	regulation of focal adhesion assembly	38	0.292189934	0.0034	0.005263104
GO:0090109	regulation of cell-substrate junction assembly	38	0.292189934	0.0034	0.005263104
GO:1903729	regulation of plasma membrane organization	58	0.292171482	0.0015	0.003088691
GO:0045921	positive regulation of exocytosis	37	0.292170162	0.0053	0.007330056
GO:0009581	detection of external stimulus	41	0.292161848	0.0031	0.004916949
GO:1903052	positive regulation of proteolysis involved in cellular protein catabolic process	62	0.292157595	0.0009	0.002399874
GO:0072522	purine-containing compound biosynthetic process	100	0.292110682	0.0023	0.004032435
GO:0019317	fucose catabolic process	5	0.292097812	0.0011	0.002610912
GO:0042354	L-fucose metabolic process	5	0.292097812	0.0011	0.002610912
GO:0042355	L-fucose catabolic process	5	0.292097812	0.0011	0.002610912
GO:0008090	retrograde axonal transport	11	0.292079092	0.0085	0.010671887
GO:0006900	membrane budding	80	0.29207529	0.0009	0.002399874
GO:0006778	porphyrin-containing compound metabolic process	27	0.292063492	0.0104	0.012619802
GO:0051054	positive regulation of DNA metabolic process	135	0.292050145	0.0004	0.002007244
GO:0018242	protein O-linked glycosylation via serine	7	0.292038978	< 0.001	< 0.001
GO:0048634	regulation of muscle organ development	67	0.29203788	0.0098	0.012008345
GO:0071786	endoplasmic reticulum tubular network organization	10	0.291994852	0.0311	0.033166048
GO:0090161	Golgi ribbon formation	8	0.291956242	0.0127	0.014886353
GO:0060348	bone development	98	0.291941796	0.0014	0.002975058
GO:0045926	negative regulation of growth	131	0.291933155	0.0011	0.002610912
GO:0045444	fat cell differentiation	115	0.291932181	0.0006	0.002177563
GO:0042058	regulation of epidermal growth factor receptor signaling pathway	47	0.291930228	0.0079	0.010077402
GO:0048016	inositol phosphate-mediated signaling	21	0.291916406	0.0025	0.004279479
GO:0007007	inner mitochondrial membrane organization	24	0.291891892	0.0064	0.008500875
GO:0046459	short-chain fatty acid metabolic process	10	0.291891892	0.0022	0.003910907
GO:0055002	striated muscle cell development	68	0.291884321	0.0018	0.003459409
GO:0048871	multicellular organismal homeostasis	176	0.291883117	0.0014	0.002975058
GO:0003306	Wnt signaling pathway involved in heart development	5	0.291840412	0.0026	0.004377754
GO:1901992	positive regulation of mitotic cell cycle phase transition	42	0.29181222	0.0021	0.003804235
GO:0022605	oogenesis stage	6	0.291806092	0.0017	0.003334595
GO:0007059	chromosome segregation	153	0.291790951	0.0007	0.002248538
GO:0043401	steroid hormone mediated signaling pathway	102	0.291778333	0.0018	0.003459409
GO:0043403	skeletal muscle tissue regeneration	18	0.291777492	0.0182	0.020388223
GO:0003184	pulmonary valve morphogenesis	11	0.291774892	< 0.001	< 0.001
GO:0046165	alcohol biosynthetic process	78	0.291736792	0.0026	0.004377754
GO:0019318	hexose metabolic process	144	0.291673817	0.0006	0.002177563
GO:0051354	negative regulation of oxidoreductase activity	8	0.291666667	0.0266	0.028683892
GO:0060045	positive regulation of cardiac muscle cell proliferation	17	0.291664774	0.0011	0.002610912
GO:0080111	DNA demethylation	11	0.291657892	0.0044	0.006304227
GO:0019042	viral latency	8	0.291634492	0.0009	0.002399874
GO:0072110	glomerular mesangial cell proliferation	5	0.291634492	0.0013	0.002859821
GO:0002822	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	76	0.291627718	0.0008	0.002313249
GO:2000351	regulation of endothelial cell apoptotic process	29	0.291598988	0.0063	0.008390784
GO:0051091	positive regulation of sequence-specific DNA binding transcription factor activity	135	0.291586825	0.0011	0.002610912
GO:0016137	glycoside metabolic process	13	0.291555292	0.0049	0.006860215
GO:0007256	activation of JNKK activity	5	0.291531532	0.0013	0.002859821
GO:0010968	regulation of microtubule nucleation	5	0.291531532	0.0183	0.020489441
GO:0006687	glycosphingolipid metabolic process	42	0.291493534	0.0046	0.006532041
GO:0000187	activation of MAPK activity	78	0.291456291	0.0006	0.002177563
GO:0010761	fibroblast migration	25	0.291449163	0.0029	0.004714719
GO:0016202	regulation of striated muscle tissue development	66	0.291439491	0.0094	0.011616482
GO:1902186	regulation of viral release from host cell	25	0.291438867	0.004	0.005880507
GO:0031331	positive regulation of cellular catabolic process	141	0.291430032	0.0018	0.003459409
GO:0006751	glutathione catabolic process	5	0.291377091	0.0048	0.006748379
GO:1903320	regulation of protein modification by small protein conjugation or removal	145	0.291354014	0.0008	0.002313249
GO:0042759	long-chain fatty acid biosynthetic process	14	0.29134032	0.0011	0.002610912
GO:009574	regulation of protein catabolic process at synapse, modulating synaptic transmission	5	0.291325611	0.0041	0.005981983
GO:0031396	regulation of protein ubiquitination	129	0.291299273	0.0009	0.002399874
GO:0043433	negative regulation of sequence-specific DNA binding transcription factor activity	92	0.291295954	0.0001	0.000877824
GO:0048839	inner ear development	92	0.291290359	0.0007	0.002248538
GO:0051705	multi-organism behavior	25	0.291284427	< 0.001	< 0.001
GO:0071241	cellular response to inorganic substance	106	0.291238678	0.0033	0.005149584
GO:0001763	morphogenesis of a branching structure	96	0.291229622	0.002	0.003693422
GO:0032869	cellular response to insulin stimulus	109	0.291209427	0.002	0.003693422
GO:1902992	negative regulation of amyloid precursor protein catabolic process	9	0.291205491	0.0046	0.006532041
GO:1903391	regulation of adherens junction organization	42	0.291187105	0.0031	0.004916949
GO:0060572	morphogenesis of an epithelial bud	5	0.291171171	0.0192	0.021362011
GO:0006525	arginine metabolic process	6	0.291162591	< 0.001	< 0.001
GO:0061098	positive regulation of protein tyrosine kinase activity	21	0.291144205	0.0005	0.002177563
GO:0001890	placenta development	75	0.291136851	0.001	0.002498236
GO:0047496	vesicle transport along microtubule	19	0.291106144	0.0051	0.007095023

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0006470	protein dephosphorylation	164	0.291097718	0.001	0.002498236
GO:0010829	negative regulation of glucose transport	11	0.291096291	0.0002	0.001341684
GO:0060391	positive regulation of SMAD protein import into nucleus	9	0.291091091	0.0072	0.009362497
GO:1904814	regulation of protein localization to chromosome, telomeric region	13	0.291080091	0.0001	0.000877824
GO:1903556	negative regulation of tumor necrosis factor superfamily cytokine production	30	0.291068211	0.0065	0.008621124
GO:1990778	protein localization to cell periphery	148	0.29105708	0.001	0.002498236
GO:1903429	regulation of cell maturation	9	0.291033891	0.0033	0.005149584
GO:0031290	retinal ganglion cell axon guidance	8	0.291023166	< 0.001	< 0.001
GO:0051961	negative regulation of nervous system development	148	0.291017079	0.0007	0.002248538
GO:0009952	anterior/posterior pattern specification	74	0.291008383	0.0007	0.002248538
GO:0030072	peptide hormone secretion	107	0.291001816	0.001	0.002498236
GO:2000352	negative regulation of endothelial cell apoptotic process	15	0.290999571	0.001	0.002498236
GO:0030033	microvillus assembly	8	0.290990991	0.0072	0.009362497
GO:0032411	positive regulation of transporter activity	45	0.290976691	0.0034	0.005263104
GO:0032958	inositol phosphate biosynthetic process	12	0.290969541	0.0006	0.002177563
GO:0001823	mesonephros development	56	0.290949623	0.0002	0.001341684
GO:0002526	acute inflammatory response	75	0.290937795	0.0029	0.004714719
GO:0051983	regulation of chromosome segregation	53	0.290930283	0.0003	0.001720882
GO:0060562	epithelial tube morphogenesis	170	0.29092437	0.0006	0.002177563
GO:0000491	small nucleolar ribonucleoprotein complex assembly	5	0.290913771	0.0066	0.008731949
GO:0032462	regulation of protein homooligomerization	14	0.290899062	0.0031	0.004916949
GO:0007584	response to nutrient	84	0.290853098	0.0011	0.002610912
GO:0001773	myeloid dendritic cell activation	16	0.290846203	0.0012	0.002741075
GO:0071222	cellular response to lipopolysaccharide	88	0.290844741	0.0011	0.002610912
GO:0035855	megakaryocyte development	10	0.290836551	0.0201	0.022258436
GO:0042157	lipoprotein metabolic process	77	0.290815491	0.0031	0.004916949
GO:0032729	positive regulation of interferon-gamma production	32	0.29077381	0.0035	0.005358035
GO:0045665	negative regulation of neuron differentiation	98	0.290767736	0.0008	0.002313249
GO:0044262	cellular carbohydrate metabolic process	148	0.290766635	0.0006	0.002177563
GO:1903069	regulation of ER-associated ubiquitin-dependent protein catabolic process	7	0.290751976	0.0301	0.032169596
GO:0090313	regulation of protein targeting to membrane	18	0.290747891	0.0029	0.004714719
GO:0043583	ear development	105	0.290744622	0.0006	0.002177563
GO:0051403	stress-activated MAPK cascade	136	0.290739269	0.0007	0.002248538
GO:0002440	production of molecular mediator of immune response	98	0.290736217	0.0001	0.000877824
GO:0002093	auditory receptor cell morphogenesis	9	0.290719291	0.0001	0.000877824
GO:0044065	regulation of respiratory system process	7	0.290715205	0.006	0.00807902
GO:0050714	positive regulation of protein secretion	134	0.290687489	0.0002	0.001341684
GO:0090235	regulation of metaphase plate congression	5	0.290656371	0.0221	0.024229021
GO:0048048	embryonic eye morphogenesis	22	0.290604891	0.0023	0.004032435
GO:0002902	regulation of B cell apoptotic process	7	0.290604891	0.0038	0.005666214
GO:0045606	positive regulation of epidermal cell differentiation	10	0.290604891	0.001	0.002498236
GO:0045657	positive regulation of monocyte differentiation	7	0.290604891	0.0063	0.008390784
GO:0003009	skeletal muscle contraction	17	0.290574608	0.0001	0.000877824
GO:0006636	unsaturated fatty acid biosynthetic process	43	0.290568974	0.0013	0.002859821
GO:0042158	lipoprotein biosynthetic process	56	0.290545137	0.0021	0.003804235
GO:0010866	regulation of triglyceride biosynthetic process	14	0.290531348	0.0007	0.002248538
GO:0032868	response to insulin	142	0.290525133	0.0019	0.003579279
GO:0070741	response to interleukin-6	24	0.290508366	0.0002	0.001341684
GO:0002372	myeloid dendritic cell cytokine production	5	0.29045045	0.0269	0.028963288
GO:0002732	positive regulation of dendritic cell cytokine production	5	0.29045045	0.0269	0.028963288
GO:0002733	regulation of myeloid dendritic cell cytokine production	5	0.29045045	0.0269	0.028963288
GO:0002735	positive regulation of myeloid dendritic cell cytokine production	5	0.29045045	0.0269	0.028963288
GO:0019432	triglyceride biosynthetic process	26	0.29040689	0.0012	0.002741075
GO:0015893	drug transport	9	0.29040469	0.0025	0.004279479
GO:1903859	regulation of dendrite extension	5	0.29039897	0.0073	0.009463568
GO:1903861	positive regulation of dendrite extension	5	0.29039897	0.0073	0.009463568
GO:0048872	homeostasis of number of cells	147	0.290361499	0.0006	0.002177563
GO:0045927	positive regulation of growth	147	0.290352743	0.0007	0.002248538
GO:0015850	organic hydroxy compound transport	108	0.290352257	0.0002	0.001341684
GO:0051547	regulation of keratinocyte migration	7	0.29034749	0.0032	0.005044175
GO:0051549	positive regulation of keratinocyte migration	7	0.29034749	0.0032	0.005044175
GO:0046323	glucose import	33	0.29032409	0.0009	0.002399874
GO:0031348	negative regulation of defense response	102	0.290312161	0.0023	0.004032435
GO:0016574	histone ubiquitination	32	0.290267053	0.0006	0.002177563
GO:0010639	negative regulation of organelle organization	178	0.290189869	0.0008	0.002313249
GO:0046321	positive regulation of fatty acid oxidation	8	0.29015444	0.0029	0.004714719
GO:2000241	regulation of reproductive process	62	0.290061029	0.0004	0.002007244
GO:1903265	positive regulation of tumor necrosis factor-mediated signaling pathway	8	0.290057915	0.0027	0.004491543
GO:0036296	response to increased oxygen levels	16	0.290057915	0.0006	0.002177563
GO:0061053	somite development	42	0.290041061	0.0008	0.002313249
GO:1905515	non-motile cilium assembly	34	0.290037096	< 0.001	< 0.001
GO:0090308	regulation of methylation-dependent chromatin silencing	7	0.290016547	0.0042	0.006097175
GO:0046718	viral entry into host cell	74	0.290003131	0.0097	0.011922488
GO:0003272	endocardial cushion formation	15	0.28998713	0.002	0.003693422
GO:0006956	complement activation	33	0.28996529	0.0109	0.013101792
GO:0001654	eye development	185	0.289924519	0.0013	0.002859821
GO:0050855	regulation of B cell receptor signaling pathway	13	0.28989209	0.0033	0.005149584
GO:0051260	protein homooligomerization	193	0.289888704	0.0011	0.002610912
GO:1900087	positive regulation of G1/S transition of mitotic cell cycle	22	0.28984439	0.0035	0.005358035
GO:0045940	positive regulation of steroid metabolic process	15	0.28983269	0.0063	0.008390784
GO:0002062	chondrocyte differentiation	49	0.289816931	0.0008	0.002313249
GO:0034329	cell junction assembly	126	0.289814304	0.0033	0.005149584
GO:0031998	regulation of fatty acid beta-oxidation	12	0.28976834	0.0021	0.003804235

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0051567	histone H3-K9 methylation	24	0.289693265	0.002	0.003693422
GO:0043534	blood vessel endothelial cell migration	74	0.289690076	0.0013	0.002859821
GO:0031952	regulation of protein autophosphorylation	21	0.289624318	0.0023	0.004032435
GO:0050771	negative regulation of axonogenesis	18	0.28961819	0.0023	0.004032435
GO:0050810	regulation of steroid biosynthetic process	55	0.28958933	0.0051	0.007095023
GO:0006144	purine nucleobase metabolic process	10	0.28957529	0.0082	0.010366713
GO:0031333	negative regulation of protein complex assembly	68	0.289567719	0.0009	0.002399874
GO:0008645	hexose transport	56	0.289543115	0.0006	0.002177563
GO:0015749	monosaccharide transport	56	0.289543115	0.0006	0.002177563
GO:1990138	neuron projection extension	61	0.289524653	0.0006	0.002177563
GO:1903076	regulation of protein localization to plasma membrane	53	0.289512154	0.0021	0.003804235
GO:0006939	smooth muscle contraction	52	0.289491139	0.001	0.002498236
GO:0046328	regulation of JNK cascade	83	0.289476051	0.0008	0.002313249
GO:0050772	positive regulation of axonogenesis	32	0.289454633	0.0033	0.005149584
GO:0045080	positive regulation of chemokine biosynthetic process	5	0.289420849	0.024	0.026109935
GO:0051450	myoblast proliferation	8	0.289414414	0.0123	0.014492124
GO:0035107	appendage morphogenesis	70	0.289409818	0.0002	0.001341684
GO:0035108	limb morphogenesis	70	0.289409818	0.0002	0.001341684
GO:0036257	multivesicular body organization	23	0.28940742	0.0043	0.006204188
GO:0036258	multivesicular body assembly	23	0.28940742	0.0043	0.006204188
GO:0060324	face development	24	0.289403689	0.0083	0.010468217
GO:0031670	cellular response to nutrient	21	0.289391432	0.0008	0.002313249
GO:0043901	negative regulation of multi-organism process	78	0.289380589	0.0021	0.003804235
GO:0080154	regulation of fertilization	6	0.289360789	0.0008	0.002313249
GO:1901020	negative regulation of calcium ion transmembrane transporter activity	14	0.289354661	0.0023	0.004032435
GO:0030198	extracellular matrix organization	195	0.289331089	0.005	0.006974174
GO:0043062	extracellular structure organization	195	0.289331089	0.005	0.006974174
GO:0055001	muscle cell development	78	0.289324489	0.0023	0.004032435
GO:1903599	positive regulation of mitophagy	9	0.289317889	0.0076	0.009790742
GO:0032649	regulation of interferon-gamma production	43	0.289305917	0.0024	0.004156304
GO:0016042	lipid catabolic process	172	0.289280476	0.0028	0.004605006
GO:0032365	intracellular lipid transport	26	0.289228789	0.0047	0.006644432
GO:0010811	positive regulation of cell-substrate adhesion	67	0.289225686	0.0009	0.002399874
GO:0002064	epithelial cell development	113	0.289224496	0.0014	0.002975058
GO:0045063	T-helper 1 cell differentiation	13	0.289218889	0.0037	0.005561344
GO:0032846	positive regulation of homeostatic process	116	0.289218036	0.0004	0.002007244
GO:0048168	regulation of neuronal synaptic plasticity	11	0.289200889	0.0017	0.003334595
GO:0035239	tube morphogenesis	190	0.289197318	0.0011	0.002610912
GO:0051155	positive regulation of striated muscle cell differentiation	24	0.289189189	0.0225	0.024620965
GO:0022412	cellular process involved in reproduction in multicellular organism	116	0.289184751	0.0003	0.001720882
GO:0010508	positive regulation of autophagy	70	0.289156095	0.0045	0.006417207
GO:0010447	response to acidic pH	9	0.289146289	0.0015	0.003088691
GO:0031641	regulation of myelination	24	0.289135564	0.0057	0.007745437
GO:0048505	regulation of timing of cell differentiation	7	0.289134032	0.0016	0.003223775
GO:0019369	arachidonic acid metabolic process	19	0.289128226	0.0047	0.006644432
GO:1903523	negative regulation of blood circulation	19	0.289128226	0.0017	0.003334595
GO:1900103	positive regulation of endoplasmic reticulum unfolded protein response	8	0.289124839	0.0267	0.028781986
GO:0006771	riboflavin metabolic process	5	0.289111969	0.0103	0.012519912
GO:0034350	regulation of glial cell apoptotic process	5	0.289111969	0.0266	0.028683892
GO:1901863	positive regulation of muscle tissue development	34	0.289090771	0.008	0.010168329
GO:1901861	regulation of muscle tissue development	67	0.289079698	0.0104	0.012619802
GO:0097529	myeloid leukocyte migration	88	0.289063414	0.001	0.002498236
GO:0031102	neuron projection regeneration	29	0.289051613	0.0109	0.013101792
GO:0043491	protein kinase B signaling	126	0.289042103	0.0008	0.002313249
GO:0032611	interleukin-1 beta production	42	0.289042103	0.0003	0.001720882
GO:0035303	regulation of dephosphorylation	109	0.28901326	0.0005	0.002177563
GO:0006626	protein targeting to mitochondrion	63	0.288999203	0.0011	0.002610912
GO:0051957	positive regulation of amino acid transport	8	0.288996139	0.0047	0.006644432
GO:0006094	gluconeogenesis	49	0.288929162	0.0015	0.003088691
GO:0031937	positive regulation of chromatin silencing	9	0.288888889	0.0018	0.003459409
GO:0006643	membrane lipid metabolic process	127	0.288878079	0.0034	0.005263104
GO:0033004	negative regulation of mast cell activation	8	0.288803089	0.0006	0.002177563
GO:1902100	negative regulation of metaphase/anaphase transition of cell cycle	20	0.288777349	< 0.001	< 0.001
GO:0033273	response to vitamin	45	0.288705849	0.0021	0.003804235
GO:0048260	positive regulation of receptor-mediated endocytosis	29	0.288687702	0.0143	0.016557758
GO:0048207	vesicle targeting, rough ER to cis-Golgi	44	0.288680239	0.001	0.002498236
GO:0048208	COPII vesicle coating	44	0.288680239	0.001	0.002498236
GO:0033690	positive regulation of osteoblast proliferation	6	0.288674389	0.0065	0.008621124
GO:1901021	positive regulation of calcium ion transmembrane transporter activity	12	0.288652939	0.0015	0.003088691
GO:0035627	ceramide transport	10	0.288648649	0.0032	0.005044175
GO:0042451	purine nucleoside biosynthetic process	59	0.288641668	0.0036	0.005475609
GO:0046129	purine ribonucleoside biosynthetic process	59	0.288641668	0.0036	0.005475609
GO:0043367	CD4-positive, alpha-beta T cell differentiation	37	0.288636126	0.0014	0.002975058
GO:1904376	negative regulation of protein localization to cell periphery	17	0.288621395	0.0057	0.007745437
GO:0045663	positive regulation of myoblast differentiation	5	0.288597169	0.0003	0.001720882
GO:0030206	chondroitin sulfate biosynthetic process	13	0.288585289	0.0075	0.00968541
GO:0007045	cell-substrate adherens junction assembly	48	0.288551051	0.0031	0.004916949
GO:0048041	focal adhesion assembly	48	0.288551051	0.0031	0.004916949
GO:0030948	negative regulation of vascular endothelial growth factor receptor signaling pathway	7	0.288545689	0.0457	0.047395622
GO:0032604	granulocyte macrophage colony-stimulating factor production	7	0.288472146	0.0008	0.002313249
GO:0032645	regulation of granulocyte macrophage colony-stimulating factor production	7	0.288472146	0.0008	0.002313249
GO:2000144	positive regulation of DNA-templated transcription, initiation	13	0.288466488	0.002	0.003693422
GO:0043501	skeletal muscle adaptation	9	0.288459888	0.0054	0.007432873

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0098773	skin epidermis development	47	0.28844711	0.0009	0.002399874
GO:0071902	positive regulation of protein serine/threonine kinase activity	166	0.288429393	0.001	0.002498236
GO:1903046	meiotic cell cycle process	62	0.288387927	0.0014	0.002975058
GO:0099625	ventricular cardiac muscle cell membrane repolarization	12	0.288374088	0.0009	0.002399874
GO:0072202	cell differentiation involved in metanephros development	15	0.288356928	0.0005	0.002177563
GO:0090287	regulation of cellular response to growth factor stimulus	132	0.288352638	0.0032	0.005044175
GO:0010675	regulation of cellular carbohydrate metabolic process	74	0.288343942	0.0007	0.002248538
GO:0035459	cargo loading into vesicle	15	0.288322608	0.0066	0.008731949
GO:0050850	positive regulation of calcium-mediated signaling	21	0.288276031	0.0038	0.005666214
GO:0032103	positive regulation of response to external stimulus	154	0.288269903	0.0005	0.002177563
GO:0072075	metanephric mesenchyme development	7	0.288251517	0.0002	0.001341684
GO:0010952	positive regulation of peptidase activity	107	0.288244987	0.0026	0.004377754
GO:0046364	monosaccharide biosynthetic process	54	0.288240622	0.0021	0.003804235
GO:2000543	positive regulation of gastrulation	5	0.288236808	0.0006	0.002177563
GO:0002287	alpha-beta T cell activation involved in immune response	31	0.288221862	0.0013	0.002859821
GO:0002293	alpha-beta T cell differentiation involved in immune response	31	0.288221862	0.0013	0.002859821
GO:0002294	CD4-positive, alpha-beta T cell differentiation involved in immune response	31	0.288221862	0.0013	0.002859821
GO:0042093	T-helper cell differentiation	31	0.288221862	0.0013	0.002859821
GO:1902001	fatty acid transmembrane transport	11	0.288218088	0.0049	0.006860215
GO:0020027	hemoglobin metabolic process	9	0.288202488	0.0028	0.004605006
GO:0035562	negative regulation of chromatin binding	6	0.288202488	0.0083	0.010468217
GO:0031214	biomineral tissue development	70	0.288192682	0.001	0.002498236
GO:0001960	negative regulation of cytokine-mediated signaling pathway	31	0.288172043	0.0002	0.001341684
GO:0036344	platelet morphogenesis	12	0.288138138	0.0125	0.014684332
GO:0033629	negative regulation of cell adhesion mediated by integrin	5	0.288133848	0.0116	0.013792313
GO:0048333	mesodermal cell differentiation	19	0.288112172	0.0004	0.002007244
GO:1903532	positive regulation of secretion by cell	198	0.288098488	0.0004	0.002007244
GO:0072091	regulation of stem cell proliferation	38	0.288078304	0.0013	0.002859821
GO:0031958	corticosteroid receptor signaling pathway	10	0.288056628	0.0001	0.000877824
GO:0019835	cytolysis	13	0.288050688	0.0294	0.031463678
GO:0006749	glutathione metabolic process	35	0.288045597	0.0007	0.002248538
GO:0010543	regulation of platelet activation	14	0.288030888	0.0011	0.002610912
GO:0035357	peroxisome proliferator activated receptor signaling pathway	11	0.288030888	0.0003	0.001720882
GO:0009566	fertilization	63	0.288026802	0.0001	0.000877824
GO:0009583	detection of light stimulus	19	0.287963151	0.0073	0.009463568
GO:0009584	detection of visible light	16	0.287934363	0.004	0.005880507
GO:0070207	protein homotrimerization	18	0.287930788	0.0025	0.004279479
GO:0002250	adaptive immune response	198	0.287928188	0.0009	0.002399874
GO:0001556	oocyte maturation	11	0.287913888	0.0002	0.001341684
GO:0033014	tetrapyrrole biosynthetic process	23	0.287907784	0.0038	0.005666214
GO:0051017	actin filament bundle assembly	76	0.287844612	0.0007	0.002248538
GO:0045833	negative regulation of lipid metabolic process	42	0.287828645	0.0015	0.003088691
GO:0031589	cell-substrate adhesion	176	0.2878276	0.0019	0.003579279
GO:0031294	lymphocyte costimulation	27	0.287821154	0.0031	0.004916949
GO:1900181	negative regulation of protein localization to nucleus	28	0.287819452	0.0007	0.002248538
GO:0070861	regulation of protein exit from endoplasmic reticulum	15	0.287807808	0.0153	0.017559319
GO:0071550	death-inducing signaling complex assembly	8	0.287805663	0.0056	0.007655255
GO:0030010	establishment of cell polarity	67	0.287792697	0.0046	0.006532041
GO:0071499	cellular response to laminar fluid shear stress	6	0.287773488	0.0009	0.002399874
GO:0010975	regulation of neuron projection development	191	0.287731711	0.001	0.002498236
GO:0033119	negative regulation of RNA splicing	18	0.287716288	0.002	0.003693422
GO:0009582	detection of abiotic stimulus	42	0.287675431	0.0019	0.003579279
GO:0006497	protein lipidation	54	0.287673388	0.0029	0.004714719
GO:0046467	membrane lipid biosynthetic process	85	0.287670528	0.0039	0.005778819
GO:0090181	regulation of cholesterol metabolic process	42	0.287626402	0.0015	0.003088691
GO:0036498	IRE1-mediated unfolded protein response	46	0.287611214	0.0066	0.008731949
GO:0048793	pronephros development	6	0.287601888	0.0081	0.010256567
GO:0030260	entry into host cell	80	0.28759009	0.0081	0.010256567
GO:0044409	entry into host	80	0.28759009	0.0081	0.010256567
GO:0051806	entry into cell of other organism involved in symbiotic interaction	80	0.28759009	0.0081	0.010256567
GO:0051828	entry into other organism involved in symbiotic interaction	80	0.28759009	0.0081	0.010256567
GO:0032011	ARF protein signal transduction	7	0.28758963	0.0104	0.012619802
GO:0032012	regulation of ARF protein signal transduction	7	0.28758963	0.0104	0.012619802
GO:0055025	positive regulation of cardiac muscle tissue development	25	0.287516088	0.0068	0.008946408
GO:0007175	negative regulation of epidermal growth factor-activated receptor activity	9	0.287516088	0.0166	0.018864444
GO:1902230	negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage	21	0.287491573	< 0.001	< 0.001
GO:0006509	membrane protein ectodomain proteolysis	31	0.287491178	0.0084	0.010571327
GO:0072511	divalent inorganic cation transport	190	0.287471381	0.0017	0.003334595
GO:0006384	transcription initiation from RNA polymerase III promoter	5	0.287464607	0.0025	0.004279479
GO:0072503	cellular divalent inorganic cation homeostasis	173	0.287458061	0.0012	0.002741075
GO:0042698	ovulation cycle	61	0.287427474	0.0008	0.002313249
GO:0032201	telomere maintenance via semi-conservative replication	20	0.287413127	0.0046	0.006532041
GO:0007596	blood coagulation	151	0.287401877	0.001	0.002498236
GO:1903312	negative regulation of mRNA metabolic process	27	0.287392154	0.0011	0.002610912
GO:0030218	erythrocyte differentiation	71	0.2873892	0.0006	0.002177563
GO:0002260	lymphocyte homeostasis	34	0.287387387	0.0021	0.003804235
GO:0010939	regulation of necrotic cell death	17	0.287379817	0.0268	0.028880014
GO:0022406	membrane docking	95	0.2873481	0.0001	0.000877824
GO:0014002	astrocyte development	22	0.287317187	0.0108	0.013015961
GO:1901386	negative regulation of voltage-gated calcium channel activity	5	0.287310167	0.0027	0.004491543
GO:0031334	positive regulation of protein complex assembly	122	0.287277676	0.0013	0.002859821
GO:0070570	regulation of neuron projection regeneration	13	0.287258687	0.0124	0.014577606
GO:1904816	positive regulation of protein localization to chromosome, telomeric region	11	0.287235287	0.0002	0.001341684

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0016050	vesicle organization	179	0.287229927	0.0026	0.004377754
GO:0015833	peptide transport	123	0.28722939	0.0016	0.003223775
GO:0010770	positive regulation of cell morphogenesis involved in differentiation	67	0.287224111	0.0028	0.004605006
GO:1905049	negative regulation of metallopeptidase activity	5	0.287207207	0.008	0.010168329
GO:0006123	mitochondrial electron transport, cytochrome c to oxygen	13	0.287199287	0.0149	0.017165166
GO:1900024	regulation of substrate adhesion-dependent cell spreading	32	0.28717825	0.0038	0.005666214
GO:0009755	hormone-mediated signaling pathway	122	0.287155305	0.0011	0.002610912
GO:0010043	response to zinc ion	34	0.287152699	0.0049	0.006860215
GO:0006839	mitochondrial transport	158	0.287144649	0.0031	0.004916949
GO:0010876	lipid localization	192	0.287125965	0.0014	0.002975058
GO:0051494	negative regulation of cytoskeleton organization	65	0.287112167	0.0016	0.003223775
GO:0030238	male sex determination	8	0.287065637	0.0013	0.002859821
GO:0030835	negative regulation of actin filament depolymerization	17	0.287031569	0.0007	0.002248538
GO:0001101	response to acid chemical	177	0.287023101	0.0006	0.002177563
GO:1900364	negative regulation of mRNA polyadenylation	5	0.287001287	0.0017	0.003334595
GO:0006874	cellular calcium ion homeostasis	166	0.286991983	0.0011	0.002610912
GO:0001942	hair follicle development	46	0.286990096	0.0008	0.002313249
GO:0007599	hemostasis	154	0.286972873	0.0011	0.002610912
GO:0045839	negative regulation of mitotic nuclear division	28	0.286955323	0.0008	0.002313249
GO:0010613	positive regulation of cardiac muscle hypertrophy	14	0.286927744	0.0079	0.010077402
GO:0022408	negative regulation of cell-cell adhesion	81	0.28692502	0.0005	0.002177563
GO:0002237	response to molecule of bacterial origin	166	0.286923757	0.0006	0.002177563
GO:0052405	negative regulation by host of symbiont molecular function	6	0.286915487	0.0026	0.004377754
GO:0043524	negative regulation of neuron apoptotic process	68	0.286914225	0.0032	0.005044175
GO:0008211	glucocorticoid metabolic process	8	0.286872587	0.0133	0.015521132
GO:0048661	positive regulation of smooth muscle cell proliferation	50	0.286872587	0.0019	0.003579279
GO:0098915	membrane repolarization during ventricular cardiac muscle cell action potential	8	0.286840412	0.0036	0.005475609
GO:0014866	skeletal myofibril assembly	6	0.286829687	0.0214	0.023571068
GO:0035150	regulation of tube size	51	0.28682464	0.0016	0.003223775
GO:0050880	regulation of blood vessel size	51	0.28682464	0.0016	0.003223775
GO:0070509	calcium ion import	70	0.286802721	0.0008	0.002313249
GO:0001774	microglial cell activation	22	0.286802387	0.0114	0.01358747
GO:0070838	divalent metal ion transport	189	0.286790192	0.0017	0.003334595
GO:0036295	cellular response to increased oxygen levels	8	0.286776062	0.0006	0.002177563
GO:0018198	peptidyl-cysteine modification	16	0.286727799	0.003	0.004825593
GO:0051187	cofactor catabolic process	11	0.286720487	0.0008	0.002313249
GO:0009896	positive regulation of catabolic process	177	0.286695897	0.002	0.003693422
GO:1903432	regulation of TORC1 signaling	15	0.286692407	0.0008	0.002313249
GO:0061572	actin filament bundle organization	77	0.286680372	0.0008	0.002313249
GO:0050651	dermatan sulfate proteoglycan biosynthetic process	9	0.286629487	0.0233	0.025417819
GO:0050655	dermatan sulfate proteoglycan metabolic process	9	0.286629487	0.0233	0.025417819
GO:0072529	pyrimidine-containing compound catabolic process	17	0.286622757	0.0009	0.002399874
GO:0001909	leukocyte mediated cytotoxicity	40	0.286615187	0.0071	0.009268394
GO:0009074	aromatic amino acid family catabolic process	10	0.286589447	0.0035	0.005358035
GO:0017014	protein nitrosylation	5	0.286589447	0.0057	0.007745437
GO:0018119	peptidyl-cysteine S-nitrosylation	5	0.286589447	0.0057	0.007745437
GO:1905476	negative regulation of protein localization to membrane	18	0.286572287	0.0053	0.007330056
GO:0015758	glucose transport	53	0.286569049	0.0006	0.002177563
GO:0050707	regulation of cytokine secretion	102	0.286486486	0.0003	0.001720882
GO:0033700	phospholipid efflux	5	0.286486486	0.0035	0.005358035
GO:2001237	negative regulation of extrinsic apoptotic signaling pathway	59	0.286486486	0.0065	0.008621124
GO:0046330	positive regulation of JNK cascade	60	0.286473616	0.0007	0.002248538
GO:0032653	regulation of interleukin-10 production	25	0.286455598	0.004	0.005880507
GO:1903608	protein localization to cytoplasmic stress granule	7	0.286449715	0.0143	0.016557758
GO:2000178	negative regulation of neural precursor cell proliferation	14	0.286431329	0.0009	0.002399874
GO:0070527	platelet aggregation	32	0.28643018	0.0005	0.002177563
GO:0001656	metanephros development	50	0.286409266	0.0024	0.004156304
GO:0046503	glycerolipid catabolic process	27	0.286391153	0.0017	0.003334595
GO:2000643	positive regulation of early endosome to late endosome transport	8	0.286357786	0.0093	0.011528671
GO:2001056	positive regulation of cysteine-type endopeptidase activity	84	0.286354722	0.0031	0.004916949
GO:0051926	negative regulation of calcium ion transport	27	0.286343486	0.0011	0.002610912
GO:0001502	cartilage condensation	7	0.286339401	0.0038	0.005666214
GO:0098743	cell aggregation	7	0.286339401	0.0038	0.005666214
GO:0016486	peptide hormone processing	9	0.286314886	0.0004	0.002007244
GO:0032091	negative regulation of protein binding	56	0.286302629	0.0033	0.005149584
GO:0039702	viral budding via host ESCRT complex	17	0.286289651	0.0026	0.004377754
GO:0060996	dendritic spine development	31	0.286195873	0.0009	0.002399874
GO:0045123	cellular extravasation	29	0.286184707	0.002	0.003693422
GO:0070374	positive regulation of ERK1 and ERK2 cascade	85	0.286168521	0.0004	0.002007244
GO:0006903	vesicle targeting	59	0.28615492	0.0016	0.003223775
GO:0033147	negative regulation of intracellular estrogen receptor signaling pathway	9	0.286114686	0.0045	0.006417207
GO:0046386	deoxyribose phosphate catabolic process	13	0.286050886	0.0016	0.003223775
GO:1904031	positive regulation of cyclin-dependent protein kinase activity	18	0.286043186	0.0046	0.006532041
GO:0060415	muscle tissue morphogenesis	39	0.286024486	0.0015	0.003088691
GO:0048640	negative regulation of developmental growth	42	0.285983943	0.0014	0.002975058
GO:0035909	aorta morphogenesis	20	0.285971686	0.0007	0.002248538
GO:0071539	protein localization to centrosome	14	0.2859533	0.0006	0.002177563
GO:0032092	positive regulation of protein binding	53	0.285942546	0.007	0.009166016
GO:1903955	positive regulation of protein targeting to mitochondrion	23	0.285904538	0.0018	0.003459409
GO:0043393	regulation of protein binding	118	0.285877888	0.004	0.005880507
GO:0034113	heterotypic cell-cell adhesion	27	0.285866819	0.0018	0.003459409
GO:0046626	regulation of insulin receptor signaling pathway	27	0.285857286	0.0011	0.002610912
GO:0033173	calcineurin-NFAT signaling cascade	15	0.285851566	0.0017	0.003334595

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0097720	calcineurin-mediated signaling	15	0.285851566	0.0017	0.003334595
GO:0070302	regulation of stress-activated protein kinase signaling cascade	110	0.285847666	0.001	0.002498236
GO:0006909	phagocytosis	132	0.285833236	0.0022	0.003910907
GO:0046890	regulation of lipid biosynthetic process	111	0.285797767	0.0012	0.002741075
GO:0010921	regulation of phosphatase activity	92	0.285770242	0.0001	0.000877824
GO:0034382	chylomicron remnant clearance	5	0.285765766	0.0005	0.002177563
GO:0071830	triglyceride-rich lipoprotein particle clearance	5	0.285765766	0.0005	0.002177563
GO:0050817	coagulation	154	0.285737686	0.0012	0.002741075
GO:0014850	response to muscle activity	14	0.285732671	0.0242	0.02630058
GO:0016125	sterol metabolic process	91	0.285717114	0.003	0.004825593
GO:0043277	apoptotic cell clearance	23	0.285691903	0.0082	0.010366713
GO:0047484	regulation of response to osmotic stress	6	0.285628486	0.0015	0.003088691
GO:0021548	pons development	6	0.285628486	0.0421	0.043897791
GO:0051654	establishment of mitochondrion localization	11	0.285620686	0.001	0.002498236
GO:0045744	negative regulation of G-protein coupled receptor protein signaling pathway	18	0.285614186	0.0019	0.003579279
GO:0006491	N-glycan processing	6	0.285585586	0.0087	0.010877987
GO:1902932	positive regulation of alcohol biosynthetic process	13	0.285575686	0.001	0.002498236
GO:0007628	adult walking behavior	16	0.285553411	0.0109	0.013101792
GO:0030336	negative regulation of cell migration	142	0.285543894	0.001	0.002498236
GO:0042364	water-soluble vitamin biosynthetic process	6	0.285542686	0.0007	0.002248538
GO:0035269	protein O-linked mannosylation	14	0.285493657	< 0.001	< 0.001
GO:0009260	ribonucleotide biosynthetic process	94	0.285459624	0.0033	0.005149584
GO:0043921	modulation by host of viral transcription	21	0.285371085	0.0058	0.007856196
GO:0052312	modulation of transcription in other organism involved in symbiotic interaction	21	0.285371085	0.0058	0.007856196
GO:0052472	modulation by host of symbiont transcription	21	0.285371085	0.0058	0.007856196
GO:0032872	regulation of stress-activated MAPK cascade	108	0.285368702	0.0011	0.002610912
GO:0001821	histamine secretion	5	0.285353925	0.0009	0.002399874
GO:0071320	cellular response to cAMP	27	0.285352019	0.0002	0.001341684
GO:0009142	nucleoside triphosphate biosynthetic process	45	0.285250965	0.0026	0.004377754
GO:0043279	response to alkaloid	72	0.285199485	0.0004	0.002007244
GO:0008203	cholesterol metabolic process	86	0.285190506	0.0033	0.005149584
GO:0006359	regulation of transcription from RNA polymerase III promoter	16	0.285183398	0.0006	0.002177563
GO:0019471	4-hydroxyproline metabolic process	8	0.28516731	0.0007	0.002248538
GO:0006182	cGMP biosynthetic process	5	0.285148005	0.004	0.005880507
GO:0032927	positive regulation of activin receptor signaling pathway	6	0.285113685	0.0044	0.006304227
GO:0001935	endothelial cell proliferation	84	0.285073849	0.0027	0.004491543
GO:0048844	artery morphogenesis	42	0.285070785	0.0038	0.005666214
GO:1903441	protein localization to ciliary membrane	6	0.285027885	0.0018	0.003459409
GO:0003002	regionalization	136	0.285019684	< 0.001	< 0.001
GO:0032414	positive regulation of ion transmembrane transporter activity	39	0.285014685	0.0037	0.005561344
GO:0001837	epithelial to mesenchymal transition	72	0.285013585	0.0045	0.006417207
GO:0042754	negative regulation of circadian rhythm	8	0.285006435	0.003	0.004825593
GO:0006575	cellular modified amino acid metabolic process	107	0.284992603	0.0029	0.004714719
GO:0035335	peptidyl-tyrosine dephosphorylation	51	0.28496732	0.0008	0.002313249
GO:0090330	regulation of platelet aggregation	8	0.284942085	0.0051	0.007095023
GO:0051608	histamine transport	6	0.284942085	0.0011	0.002610912
GO:0090277	positive regulation of peptide hormone secretion	41	0.284923251	0.0003	0.001720882
GO:0042476	odontogenesis	57	0.284905959	0.0026	0.004377754
GO:0006048	UDP-N-acetylglucosamine biosynthetic process	7	0.284905313	0.0001	0.000877824
GO:0021694	cerebellar Purkinje cell layer formation	7	0.284905313	0.0046	0.006532041
GO:1903829	positive regulation of cellular protein localization	190	0.284901443	0.0009	0.002399874
GO:1901224	positive regulation of NIK/NF-kappaB signaling	52	0.284897535	0.0038	0.005666214
GO:0052548	regulation of endopeptidase activity	194	0.284817365	0.0012	0.002741075
GO:0014855	striated muscle cell proliferation	38	0.284806611	0.0034	0.005263104
GO:0051058	negative regulation of small GTPase mediated signal transduction	27	0.284799085	0.002	0.003693422
GO:0031468	nuclear envelope reassembly	12	0.284791935	0.0013	0.002859821
GO:0022404	molting cycle process	48	0.284786572	0.0012	0.002741075
GO:0022405	hair cycle process	48	0.284786572	0.0012	0.002741075
GO:1904377	positive regulation of protein localization to cell periphery	32	0.284773166	0.0013	0.002859821
GO:0030282	bone mineralization	53	0.284738107	0.0013	0.002859821
GO:0075522	IRES-dependent viral translational initiation	9	0.284713285	0.0008	0.002313249
GO:0072507	divalent inorganic cation homeostasis	182	0.284694585	0.0012	0.002741075
GO:2000647	negative regulation of stem cell proliferation	7	0.284647913	0.0107	0.012912536
GO:0031274	positive regulation of pseudopodium assembly	6	0.284641785	0.006	0.00807902
GO:0045132	meiotic chromosome segregation	27	0.284627485	0.0001	0.000877824
GO:0018394	peptidyl-lysine acetylation	109	0.284616202	0.0011	0.002610912
GO:0046827	positive regulation of protein export from nucleus	15	0.284616045	0.0059	0.007964563
GO:1902043	positive regulation of extrinsic apoptotic signaling pathway via death domain receptors	11	0.284614485	0.0015	0.003088691
GO:0031295	T cell costimulation	26	0.284605485	0.003	0.004825593
GO:0051896	regulation of protein kinase B signaling	111	0.284601204	0.0008	0.002313249
GO:0051592	response to calcium ion	60	0.284590305	0.0026	0.004377754
GO:1903825	organic acid transmembrane transport	45	0.284576005	0.0008	0.002313249
GO:1905039	carboxylic acid transmembrane transport	45	0.284576005	0.0008	0.002313249
GO:0042475	odontogenesis of dentin-containing tooth	36	0.284563135	0.0016	0.003223775
GO:0045165	cell fate commitment	105	0.284562113	0.0006	0.002177563
GO:0043550	regulation of lipid kinase activity	38	0.284535663	0.0009	0.002399874
GO:0044154	histone H3-K14 acetylation	5	0.284530245	< 0.001	< 0.001
GO:0019218	regulation of steroid metabolic process	72	0.284527385	0.0048	0.006748379
GO:0032098	regulation of appetite	18	0.284484484	0.0025	0.004279479
GO:0055074	calcium ion homeostasis	171	0.284467927	0.001	0.002498236
GO:0060088	auditory receptor cell stereocilium organization	7	0.284464056	0.0012	0.002741075
GO:0007033	vacuole organization	116	0.28443616	0.0032	0.005044175
GO:0035883	enteroendocrine cell differentiation	10	0.284427284	0.0007	0.002248538

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1904064	positive regulation of cation transmembrane transport	59	0.284427284	0.0036	0.005475609
GO:0032956	regulation of actin cytoskeleton organization	148	0.284420328	0.0007	0.002248538
GO:1904124	microglial cell migration	5	0.284221364	0.0154	0.017651835
GO:1904139	regulation of microglial cell migration	5	0.284221364	0.0154	0.017651835
GO:0008286	insulin receptor signaling pathway	67	0.28420446	0.0013	0.002859821
GO:0051701	interaction with host	129	0.284173875	0.0037	0.005561344
GO:0017121	phospholipid scrambling	8	0.284169884	0.0013	0.002859821
GO:1901292	nucleoside phosphate catabolic process	39	0.284090684	0.0014	0.002975058
GO:0022612	gland morphogenesis	67	0.284081523	0.0025	0.004279479
GO:0009127	purine nucleoside monophosphate biosynthetic process	46	0.284069162	0.0063	0.008390784
GO:0009168	purine ribonucleoside monophosphate biosynthetic process	46	0.284069162	0.0063	0.008390784
GO:0001936	regulation of endothelial cell proliferation	74	0.284065533	0.0027	0.004491543
GO:0032496	response to lipopolysaccharide	156	0.284052734	0.0006	0.002177563
GO:0010821	regulation of mitochondrion organization	137	0.284042123	0.0037	0.005561344
GO:0044351	macropinocytosis	8	0.284041184	0.0004	0.002007244
GO:0070167	regulation of biomineral tissue development	47	0.283994633	0.0006	0.002177563
GO:0010996	response to auditory stimulus	14	0.283986027	0.001	0.002498236
GO:0017157	regulation of exocytosis	82	0.283968986	0.0021	0.003804235
GO:0021517	ventral spinal cord development	23	0.28396844	0.0002	0.001341684
GO:0046365	monosaccharide catabolic process	35	0.283963964	0.0026	0.004377754
GO:0016525	negative regulation of angiogenesis	58	0.283961301	0.0016	0.003223775
GO:2000181	negative regulation of blood vessel morphogenesis	58	0.283961301	0.0016	0.003223775
GO:0031441	negative regulation of mRNA 3'-end processing	6	0.283912484	0.0033	0.005149584
GO:0009071	serine family amino acid catabolic process	8	0.283912484	0.0002	0.001341684
GO:0090192	regulation of glomerulus development	5	0.283912484	0.0002	0.001341684
GO:0046470	phosphatidylcholine metabolic process	51	0.283882202	0.0028	0.004605006
GO:0033522	histone H2A ubiquitination	19	0.283858294	0.0006	0.002177563
GO:0010971	positive regulation of G2/M transition of mitotic cell cycle	12	0.283826684	0.0019	0.003579279
GO:0034330	cell junction organization	153	0.28381659	0.0021	0.003804235
GO:0050687	negative regulation of defense response to virus	22	0.283807184	0.0142	0.016456919
GO:0031103	axon regeneration	25	0.283799228	0.0109	0.013101792
GO:0046825	regulation of protein export from nucleus	23	0.283733423	0.0031	0.004916949
GO:0034332	adherens junction organization	70	0.283721272	0.001	0.002498236
GO:0043280	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	77	0.283718598	0.0042	0.006097175
GO:0045076	regulation of interleukin-2 biosynthetic process	11	0.283678484	0.0117	0.013882722
GO:0001708	cell fate specification	35	0.283677147	0.0002	0.001341684
GO:0008344	adult locomotory behavior	39	0.283674884	0.0037	0.005561344
GO:0000422	mitophagy	38	0.283655084	0.006	0.00807902
GO:0061726	mitochondrion disassembly	38	0.283655084	0.006	0.00807902
GO:0008207	C21-steroid hormone metabolic process	21	0.283642826	0.0122	0.014387602
GO:0031109	microtubule polymerization or depolymerization	50	0.28363964	0.0097	0.011922488
GO:0006869	lipid transport	174	0.283624018	0.0017	0.003334595
GO:0032970	regulation of actin filament-based process	164	0.283618985	0.0012	0.002741075
GO:0006816	calcium ion transport	172	0.283610188	0.0017	0.003334595
GO:1901214	regulation of neuron death	157	0.283594422	0.0029	0.004714719
GO:0070536	protein K63-linked deubiquitination	21	0.283593798	0.0004	0.002007244
GO:0060761	negative regulation of response to cytokine stimulus	34	0.283564237	0.0002	0.001341684
GO:1904754	positive regulation of vascular associated smooth muscle cell migration	10	0.283552124	0.0126	0.014782732
GO:0045862	positive regulation of proteolysis	196	0.283542143	0.0026	0.004377754
GO:0007030	Golgi organization	59	0.283532928	0.0041	0.005981983
GO:0048525	negative regulation of viral process	61	0.283532713	0.0029	0.004714719
GO:0006901	vesicle coating	45	0.283506364	0.001	0.002498236
GO:0032835	glomerulus development	37	0.283488121	0.0017	0.003334595
GO:0046466	membrane lipid catabolic process	21	0.283458969	0.024	0.026109935
GO:2000146	negative regulation of cell motility	152	0.283443406	0.0011	0.002610912
GO:0007015	actin filament organization	174	0.283440583	0.0006	0.002177563
GO:0008643	carbohydrate transport	73	0.28343647	0.0008	0.002313249
GO:0060982	coronary artery morphogenesis	7	0.283397683	0.0457	0.047395622
GO:0030220	platelet formation	11	0.283374283	0.0112	0.013379119
GO:0034333	adherens junction assembly	52	0.283367983	0.0019	0.003579279
GO:0050953	sensory perception of light stimulus	89	0.28336587	0.0018	0.003459409
GO:1903358	regulation of Golgi organization	6	0.283354783	0.0062	0.008281828
GO:0032528	microvillus organization	12	0.283354783	0.0076	0.009790742
GO:0051271	negative regulation of cellular component movement	160	0.283344595	0.001	0.002498236
GO:0032387	negative regulation of intracellular transport	55	0.283341523	0.0017	0.003334595
GO:0051985	negative regulation of chromosome segregation	24	0.283333333	< 0.001	< 0.001
GO:0048511	rhythmic process	169	0.283327622	0.001	0.002498236
GO:0010466	negative regulation of peptidase activity	106	0.283324834	0.0005	0.002177563
GO:0072376	protein activation cascade	42	0.283262855	0.0105	0.012724187
GO:0006006	glucose metabolic process	120	0.283236808	0.001	0.002498236
GO:0031338	regulation of vesicle fusion	10	0.283217503	0.0116	0.013792313
GO:0071248	cellular response to metal ion	94	0.28314576	0.0038	0.005666214
GO:0097242	beta-amyloid clearance	16	0.283124196	0.0014	0.002975058
GO:0043090	amino acid import	10	0.283114543	0.0023	0.004032435
GO:0034349	glial cell apoptotic process	9	0.283083083	0.0412	0.043036814
GO:0055093	response to hyperoxia	11	0.283070083	0.0006	0.002177563
GO:0030859	polarized epithelial cell differentiation	11	0.283046683	0.0413	0.043134202
GO:0070262	peptidyl-serine dephosphorylation	7	0.282993197	0.0287	0.030750689
GO:0016573	histone acetylation	99	0.282947883	0.0017	0.003334595
GO:0010575	positive regulation of vascular endothelial growth factor production	14	0.28293804	0.0167	0.018954426
GO:0030225	macrophage differentiation	25	0.282934363	0.005	0.006974174
GO:2000177	regulation of neural precursor cell proliferation	46	0.282916457	0.0004	0.002007244
GO:0008277	regulation of G-protein coupled receptor protein signaling pathway	65	0.282886843	0.0005	0.002177563

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0010951	negative regulation of endopeptidase activity	100	0.282885457	0.0005	0.002177563
GO:0010950	positive regulation of endopeptidase activity	90	0.282842843	0.0034	0.005263104
GO:0007257	activation of JUN kinase activity	17	0.282822318	0.0019	0.003579279
GO:0006921	cellular component disassembly involved in execution phase of apoptosis	24	0.282775633	0.0024	0.004156304
GO:0032048	cardiolipin metabolic process	13	0.282764083	0.0011	0.002610912
GO:0061635	regulation of protein complex stability	6	0.282754183	0.003	0.004825593
GO:0086005	ventricular cardiac muscle cell action potential	14	0.282754183	0.008	0.010168329
GO:0090312	positive regulation of protein deacetylation	13	0.282704683	0.0024	0.004156304
GO:0007204	positive regulation of cytosolic calcium ion concentration	117	0.282687083	0.0006	0.002177563
GO:0032535	regulation of cellular component size	164	0.282641178	0.0007	0.002248538
GO:0043038	amino acid activation	35	0.282625483	0.0052	0.007215241
GO:0035329	hippo signaling	24	0.282582583	0.0024	0.004156304
GO:0002024	diet induced thermogenesis	6	0.282582583	0.02	0.022155397
GO:0021515	cell differentiation in spinal cord	24	0.282571858	0.0008	0.002313249
GO:0010507	negative regulation of autophagy	52	0.282521533	0.0047	0.006644432
GO:0007032	endosome organization	46	0.282519165	0.0086	0.010769857
GO:0008654	phospholipid biosynthetic process	159	0.28250083	0.0029	0.004714719
GO:0072077	renal vesicle morphogenesis	10	0.282496782	0.0077	0.009887588
GO:0072283	metanephric renal vesicle morphogenesis	10	0.282496782	0.0077	0.009887588
GO:0051208	sequestering of calcium ion	50	0.282486486	0.0007	0.002248538
GO:0010460	positive regulation of heart rate	10	0.282471042	0.0105	0.012724187
GO:0048635	negative regulation of muscle organ development	29	0.282465717	0.0134	0.015626386
GO:1904063	negative regulation of cation transmembrane transport	36	0.282446732	0.0009	0.002399874
GO:0040013	negative regulation of locomotion	171	0.282444851	0.0009	0.002399874
GO:0072089	stem cell proliferation	61	0.282439817	0.0015	0.003088691
GO:0002066	columnar/cuboidal epithelial cell development	30	0.282419562	0.0006	0.002177563
GO:0051402	neuron apoptotic process	119	0.282378898	0.0047	0.006644432
GO:0043010	camera-type eye development	162	0.282329949	0.0012	0.002741075
GO:0042311	vasodilation	15	0.282316602	0.0008	0.002313249
GO:0042755	eating behavior	18	0.282310882	0.0041	0.005981983
GO:0060977	coronary vasculature morphogenesis	13	0.282308682	0.0098	0.012008345
GO:0006086	acetyl-CoA biosynthetic process from pyruvate	10	0.282290862	0.0099	0.012121556
GO:0050954	sensory perception of mechanical stimulus	79	0.282289885	0.0011	0.002610912
GO:0018027	peptidyl-lysine dimethylation	11	0.282274482	0.0027	0.004491543
GO:0045746	negative regulation of Notch signaling pathway	20	0.282265122	0.0009	0.002399874
GO:0045017	glycerolipid biosynthetic process	152	0.282224141	0.0019	0.003579279
GO:1904707	positive regulation of vascular smooth muscle cell proliferation	21	0.282220997	0.0016	0.003223775
GO:0050912	detection of chemical stimulus involved in sensory perception of taste	12	0.282196482	0.0188	0.020971889
GO:0006270	DNA replication initiation	18	0.282167882	0.0008	0.002313249
GO:0016241	regulation of macroautophagy	108	0.282160732	0.0032	0.005044175
GO:0033013	tetrapyrrole metabolic process	38	0.282158098	0.0116	0.013792313
GO:0043584	nose development	8	0.282142857	0.0102	0.012424427
GO:0016578	histone deubiquitination	14	0.282092296	0.0001	0.000877824
GO:0007565	female pregnancy	101	0.282052066	0.0014	0.002975058
GO:0030168	platelet activation	65	0.282051282	0.0006	0.002177563
GO:2000027	regulation of organ morphogenesis	143	0.282044082	0.0017	0.003334595
GO:0043255	regulation of carbohydrate biosynthetic process	50	0.282043758	0.0005	0.002177563
GO:0002922	positive regulation of humoral immune response	9	0.282024882	0.0052	0.007215241
GO:0003333	amino acid transmembrane transport	25	0.281997426	0.0011	0.002610912
GO:1903539	protein localization to postsynaptic membrane	5	0.281956242	0.0001	0.000877824
GO:0043405	regulation of MAP kinase activity	175	0.281931237	0.0009	0.002399874
GO:0017158	regulation of calcium ion-dependent exocytosis	27	0.281920015	0.0002	0.001341684
GO:0072384	organelle transport along microtubule	39	0.281892882	0.0056	0.007655255
GO:0044706	multi-multicellular organism process	116	0.28185772	0.001	0.002498236
GO:0016572	histone phosphorylation	16	0.281853282	0.001	0.002498236
GO:0070997	neuron death	175	0.281835632	0.003	0.004825593
GO:0003015	heart process	119	0.28181651	0.001	0.002498236
GO:0043523	regulation of neuron apoptotic process	103	0.281765816	0.0053	0.007330056
GO:0048638	regulation of developmental growth	161	0.281725381	0.0017	0.003334595
GO:0042886	amide transport	141	0.281712716	0.0022	0.003910907
GO:0035672	oligopeptide transmembrane transport	5	0.281698842	0.0028	0.004605006
GO:1901617	organic hydroxy compound biosynthetic process	129	0.281691658	0.0013	0.002859821
GO:0071825	protein-lipid complex subunit organization	25	0.281616474	0.0007	0.002248538
GO:1903587	regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis	6	0.281552982	0.0064	0.008500875
GO:0030500	regulation of bone mineralization	37	0.281547184	0.0006	0.002177563
GO:1902652	secondary alcohol metabolic process	88	0.281543232	0.0035	0.005358035
GO:0007601	visual perception	86	0.281524049	0.0017	0.003334595
GO:1990845	adaptive thermogenesis	10	0.281518662	0.0185	0.020677043
GO:0007162	negative regulation of cell adhesion	133	0.281508791	0.0017	0.003334595
GO:0010906	regulation of glucose metabolic process	62	0.281454727	0.0008	0.002313249
GO:0032693	negative regulation of interleukin-10 production	9	0.281424281	0.0145	0.016764967
GO:0042059	negative regulation of epidermal growth factor receptor signaling pathway	23	0.281394438	0.0197	0.021861066
GO:0003417	growth plate cartilage development	5	0.281389961	0.0064	0.008500875
GO:0098911	regulation of ventricular cardiac muscle cell action potential	6	0.281381381	0.0281	0.030173766
GO:0097581	lamellipodium organization	42	0.281375253	0.0015	0.003088691
GO:0018393	internal peptidyl-lysine acetylation	102	0.281353623	0.0013	0.002859821
GO:0019076	viral release from host cell	29	0.281311854	0.0057	0.007745437
GO:0035890	exit from host	29	0.281311854	0.0057	0.007745437
GO:0035891	exit from host cell	29	0.281311854	0.0057	0.007745437
GO:0052126	movement in host environment	29	0.281311854	0.0057	0.007745437
GO:0052192	movement in environment of other organism involved in symbiotic interaction	29	0.281311854	0.0057	0.007745437
GO:0034698	response to gonadotropin	14	0.28130171	0.0057	0.007745437
GO:0048477	oogenesis	35	0.281287001	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0044331	cell-cell adhesion mediated by cadherin	9	0.281252681	0.0005	0.002177563
GO:0035313	wound healing, spreading of epidermal cells	6	0.281209781	0.0267	0.028781986
GO:1903901	negative regulation of viral life cycle	60	0.281175461	0.0035	0.005358035
GO:0001675	acrosome assembly	8	0.281145431	0.0166	0.018864444
GO:1901215	negative regulation of neuron death	102	0.281123981	0.0028	0.004605006
GO:0001845	phagolysosome assembly	7	0.281117853	0.0018	0.003459409
GO:0007043	cell-cell junction assembly	58	0.281112147	0.0075	0.00968541
GO:0050727	regulation of inflammatory response	174	0.281094395	0.0011	0.002610912
GO:0032409	regulation of transporter activity	94	0.281092034	0.0017	0.003334595
GO:0014020	primary neural tube formation	54	0.281066781	0.0006	0.002177563
GO:2000758	positive regulation of peptidyl-lysine acetylation	18	0.281052481	0.0017	0.003334595
GO:0046474	glycerophospholipid biosynthetic process	131	0.281028029	0.0022	0.003910907
GO:0055008	cardiac muscle tissue morphogenesis	37	0.28097673	0.0016	0.003223775
GO:1903510	mucopolysaccharide metabolic process	55	0.280973441	0.0009	0.002399874
GO:0034616	response to laminar fluid shear stress	12	0.280930931	0.0026	0.004377754
GO:0051954	positive regulation of amine transport	17	0.280899387	0.0002	0.001341684
GO:0007263	nitric oxide mediated signal transduction	12	0.280888031	0.003	0.004825593
GO:0071108	protein K48-linked deubiquitination	18	0.280866581	0.001	0.002498236
GO:0030514	negative regulation of BMP signaling pathway	18	0.280866581	0.0096	0.01183839
GO:0006681	galactosylceramide metabolic process	8	0.280855856	0.0078	0.009981807
GO:0019374	galactolipid metabolic process	8	0.280855856	0.0078	0.009981807
GO:0001756	somitogenesis	30	0.280815101	0.0037	0.005561344
GO:0048199	vesicle targeting, to, from or within Golgi	47	0.280812728	0.0009	0.002399874
GO:0030809	negative regulation of nucleotide biosynthetic process	11	0.280800281	0.0026	0.004377754
GO:1900372	negative regulation of purine nucleotide biosynthetic process	11	0.280800281	0.0026	0.004377754
GO:0006362	transcription elongation from RNA polymerase I promoter	21	0.280750138	< 0.001	< 0.001
GO:0007094	mitotic spindle assembly checkpoint	17	0.280747975	< 0.001	< 0.001
GO:0031577	spindle checkpoint	17	0.280747975	< 0.001	< 0.001
GO:0071173	spindle assembly checkpoint	17	0.280747975	< 0.001	< 0.001
GO:0071174	mitotic spindle checkpoint	17	0.280747975	< 0.001	< 0.001
GO:0030262	apoptotic nuclear changes	23	0.280745342	0.0019	0.003579279
GO:0001952	regulation of cell-matrix adhesion	65	0.280744481	0.0035	0.005358035
GO:0001947	heart looping	35	0.280735429	0.0069	0.009046225
GO:0045843	negative regulation of striated muscle tissue development	28	0.280713366	0.0128	0.014984276
GO:1901862	negative regulation of muscle tissue development	28	0.280713366	0.0128	0.014984276
GO:0046390	ribose phosphate biosynthetic process	98	0.280713366	0.0034	0.005263104
GO:0032366	intracellular sterol transport	15	0.280686401	0.0081	0.010256567
GO:0032367	intracellular cholesterol transport	15	0.280686401	0.0081	0.010256567
GO:0002903	negative regulation of B cell apoptotic process	5	0.280669241	0.0026	0.004377754
GO:0051255	spindle midzone assembly	5	0.280669241	0.0176	0.019838132
GO:0035315	hair cell differentiation	19	0.28062047	0.0001	0.000877824
GO:0042491	auditory receptor cell differentiation	19	0.28062047	0.0001	0.000877824
GO:0030201	heparan sulfate proteoglycan metabolic process	10	0.280617761	0.0099	0.012121556
GO:0045933	positive regulation of muscle contraction	26	0.280615781	0.0003	0.001720882
GO:0010769	regulation of cell morphogenesis involved in differentiation	114	0.280597891	0.0025	0.004279479
GO:0006691	leukotriene metabolic process	18	0.280594881	0.0136	0.015813319
GO:0003007	heart morphogenesis	135	0.280585347	0.0011	0.002610912
GO:0002190	cap-independent translational initiation	14	0.280547895	0.0002	0.001341684
GO:0003356	regulation of cilium beat frequency	7	0.280492738	< 0.001	< 0.001
GO:0022617	extracellular matrix disassembly	41	0.280484666	0.0162	0.018465856
GO:0007265	Ras protein signal transduction	177	0.280483389	0.0026	0.004377754
GO:0034111	negative regulation of homotypic cell-cell adhesion	6	0.28048048	0.0192	0.021362011
GO:0071372	cellular response to follicle-stimulating hormone stimulus	9	0.28048048	0.0029	0.004714719
GO:0060712	spongiotrophoblast layer development	8	0.280469755	0.0004	0.002007244
GO:0090207	regulation of triglyceride metabolic process	20	0.28046332	0.0011	0.002610912
GO:0045732	positive regulation of protein catabolic process	125	0.280453024	0.0023	0.004032435
GO:0035590	purinergic nucleotide receptor signaling pathway	13	0.28044748	0.001	0.002498236
GO:0051570	regulation of histone H3-K9 methylation	15	0.280429	0.0033	0.005149584
GO:0090100	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	51	0.280419916	0.0022	0.003910907
GO:0071371	cellular response to gonadotropin stimulus	10	0.2803861	0.002	0.003693422
GO:0051480	regulation of cytosolic calcium ion concentration	130	0.28034848	0.0011	0.002610912
GO:0046887	positive regulation of hormone secretion	60	0.2803432	0.0003	0.001720882
GO:0043406	positive regulation of MAP kinase activity	119	0.280315369	0.0009	0.002399874
GO:0051797	regulation of hair follicle development	10	0.28028314	< 0.001	< 0.001
GO:0002793	positive regulation of peptide secretion	43	0.28027895	0.0002	0.001341684
GO:0001570	vasculogenesis	53	0.280270027	0.0033	0.005149584
GO:0035635	entry of bacterium into host cell	8	0.28024453	0.0101	0.012328539
GO:0042108	positive regulation of cytokine biosynthetic process	38	0.28023437	0.0118	0.013977955
GO:0060261	positive regulation of transcription initiation from RNA polymerase II promoter	9	0.28022308	0.0095	0.011730963
GO:0048644	muscle organ morphogenesis	42	0.28022308	0.0014	0.002975058
GO:0030837	negative regulation of actin filament polymerization	22	0.28021528	0.0008	0.002313249
GO:0060426	lung vasculature development	5	0.28015444	0.0349	0.036866849
GO:0048741	skeletal muscle fiber development	11	0.28012168	0.0112	0.013379119
GO:0001937	negative regulation of endothelial cell proliferation	26	0.28012078	0.0078	0.009981807
GO:0010002	cardioblast differentiation	11	0.28007488	0.012	0.014185865
GO:0021761	limbic system development	52	0.28006633	0.0008	0.002313249
GO:0035970	peptidyl-threonine dephosphorylation	8	0.28005148	0.0181	0.020286898
GO:0072698	protein localization to microtubule cytoskeleton	23	0.280006715	0.0012	0.002741075
GO:0060670	branching involved in labyrinthine layer morphogenesis	5	0.28	0.0037	0.005561344
GO:0007389	pattern specification process	188	0.279976177	< 0.001	< 0.001
GO:0006069	ethanol oxidation	6	0.27996568	0.0026	0.004377754
GO:0001843	neural tube closure	52	0.27995743	0.0006	0.002177563
GO:0060606	tube closure	52	0.27995743	0.0006	0.002177563

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0061351	neural precursor cell proliferation	79	0.279908118	0.0006	0.002177563
GO:0006473	protein acetylation	126	0.279900308	0.0007	0.002248538
GO:0010954	positive regulation of protein processing	17	0.279884927	0.0142	0.016456919
GO:0034381	plasma lipoprotein particle clearance	26	0.27988318	0.0015	0.003088691
GO:0035360	positive regulation of peroxisome proliferator activated receptor signaling pathway	6	0.27987988	< 0.001	< 0.001
GO:1902837	amino acid import into cell	6	0.27987988	0.0014	0.002975058
GO:0045598	regulation of fat cell differentiation	65	0.27985744	0.0006	0.002177563
GO:0035278	miRNA mediated inhibition of translation	13	0.27983368	0.0007	0.002248538
GO:0040033	negative regulation of translation, ncRNA-mediated	13	0.27983368	0.0007	0.002248538
GO:0045974	regulation of translation, ncRNA-mediated	13	0.27983368	0.0007	0.002248538
GO:0010881	regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion	7	0.279830851	0.0103	0.012519912
GO:0035821	modification of morphology or physiology of other organism	88	0.27981748	0.0036	0.005475609
GO:0043650	dicarboxylic acid biosynthetic process	7	0.27979408	0.0001	0.000877824
GO:0032355	response to estradiol	74	0.279783645	0.0036	0.005475609
GO:0035338	long-chain fatty-acyl-CoA biosynthetic process	10	0.27976834	0.0136	0.015813319
GO:0032785	negative regulation of DNA-templated transcription, elongation	10	0.2797426	0.0111	0.013284563
GO:0010165	response to X-ray	18	0.27973688	0.0003	0.001720882
GO:1904375	regulation of protein localization to cell periphery	60	0.27972115	0.0023	0.004032435
GO:0019081	viral translation	13	0.27971488	0.0016	0.003223775
GO:1900076	regulation of cellular response to insulin stimulus	33	0.27967708	0.001	0.002498236
GO:0042416	dopamine biosynthetic process	7	0.279646994	0.0001	0.000877824
GO:0010463	mesenchymal cell proliferation	25	0.27963964	0.0112	0.013379119
GO:0048596	embryonic camera-type eye morphogenesis	17	0.279582103	0.0027	0.004491543
GO:0035265	organ growth	86	0.279557631	0.0005	0.002177563
GO:0018105	peptidyl-serine phosphorylation	104	0.279539155	0.0007	0.002248538
GO:0007586	digestion	59	0.279523591	0.0003	0.001720882
GO:0051817	modification of morphology or physiology of other organism involved in symbiotic interaction	72	0.279511655	0.0037	0.005561344
GO:0007422	peripheral nervous system development	40	0.279504505	0.0067	0.008845888
GO:0070542	response to fatty acid	46	0.279486319	0.0004	0.002007244
GO:0018209	peptidyl-serine modification	117	0.279486079	0.0007	0.002248538
GO:0070200	establishment of protein localization to telomere	14	0.279481522	< 0.001	< 0.001
GO:0006475	internal protein amino acid acetylation	104	0.279464904	0.0013	0.002859821
GO:0071277	cellular response to calcium ion	33	0.279450879	0.0016	0.003223775
GO:0042659	regulation of cell fate specification	6	0.279450879	< 0.001	< 0.001
GO:0010893	positive regulation of steroid biosynthetic process	11	0.279443079	0.0088	0.010992238
GO:0002223	stimulatory C-type lectin receptor signaling pathway	70	0.279411657	0.0013	0.002859821
GO:0030900	forebrain development	182	0.279395251	0.0006	0.002177563
GO:0048469	cell maturation	78	0.279381579	0.005	0.006974174
GO:0048863	stem cell differentiation	141	0.279381509	0.0007	0.002248538
GO:0032369	negative regulation of lipid transport	13	0.279358479	0.0148	0.017062301
GO:0006577	amino-acid betaine metabolic process	14	0.279297665	< 0.001	< 0.001
GO:0010755	regulation of plasminogen activation	6	0.279279279	0.0075	0.00968541
GO:0032897	negative regulation of viral transcription	15	0.279262119	0.019	0.02117646
GO:0010631	epithelial cell migration	166	0.279231211	0.0014	0.002975058
GO:0048675	axon extension	47	0.27922999	0.001	0.002498236
GO:0010226	response to lithium ion	10	0.279227799	0.0028	0.004605006
GO:0006821	chloride transport	45	0.279216359	0.0017	0.003334595
GO:0009988	cell-cell recognition	34	0.279211144	0.0032	0.005044175
GO:0032331	negative regulation of chondrocyte differentiation	7	0.279205736	0.0067	0.008845888
GO:0060541	respiratory system development	110	0.279103779	0.002	0.003693422
GO:0051261	protein depolymerization	47	0.279093075	0.0021	0.003804235
GO:1903115	regulation of actin filament-based movement	16	0.278973616	0.0166	0.018864444
GO:0007528	neuromuscular junction development	20	0.278970399	0.0039	0.005778819
GO:0018026	peptidyl-lysine monomethylation	6	0.278893179	0.0007	0.002248538
GO:0007623	circadian rhythm	97	0.278860009	0.0012	0.002741075
GO:1901216	positive regulation of neuron death	49	0.278848528	0.011	0.013192134
GO:0060416	response to growth hormone	19	0.278832216	0.0001	0.000877824
GO:0086091	regulation of heart rate by cardiac conduction	13	0.278784279	0.0146	0.016871405
GO:0060306	regulation of membrane repolarization	14	0.278782864	0.0022	0.003910907
GO:0010801	negative regulation of peptidyl-threonine phosphorylation	6	0.278764479	0.0169	0.019147324
GO:0006818	hydrogen transport	75	0.278740455	0.0042	0.006097175
GO:0015992	proton transport	75	0.278740455	0.0042	0.006097175
GO:0043304	regulation of mast cell degranulation	16	0.278716216	0.0036	0.005475609
GO:0090382	phagosome maturation	21	0.27871545	0.0059	0.007964563
GO:0042303	molting cycle	57	0.278710289	0.0017	0.003334595
GO:0042633	hair cycle	57	0.278710289	0.0017	0.003334595
GO:0090257	regulation of muscle system process	104	0.278702604	0.0021	0.003804235
GO:0071621	granulocyte chemotaxis	43	0.278674688	0.0031	0.004916949
GO:0042407	cristae formation	19	0.278642552	0.011	0.013192134
GO:0051238	sequestering of metal ion	53	0.278609067	0.0009	0.002399874
GO:0048013	ephrin receptor signaling pathway	38	0.27860191	0.0002	0.001341684
GO:0030252	growth hormone secretion	9	0.278592879	0.0054	0.007432873
GO:0060123	regulation of growth hormone secretion	9	0.278592879	0.0054	0.007432873
GO:0060047	heart contraction	115	0.278589894	0.0014	0.002975058
GO:0098656	anion transmembrane transport	99	0.278530479	0.0021	0.003804235
GO:0010927	cellular component assembly involved in morphogenesis	49	0.278528091	0.0092	0.011424708
GO:0048738	cardiac muscle tissue development	107	0.278478211	0.0018	0.003459409
GO:0060767	epithelial cell proliferation involved in prostate gland development	6	0.278464178	0.0001	0.000877824
GO:0050829	defense response to Gram-negative bacterium	28	0.278461114	0.0003	0.001720882
GO:0006936	muscle contraction	175	0.27842471	0.001	0.002498236
GO:0071295	cellular response to vitamin	14	0.278341607	0.0006	0.002177563
GO:0008637	apoptotic mitochondrial changes	72	0.278296153	0.004	0.005880507
GO:0090051	negative regulation of cell migration involved in sprouting angiogenesis	12	0.278271128	0.0041	0.005981983

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0070202	regulation of establishment of protein localization to chromosome	10	0.278223938	0.0001	0.000877824
GO:0070203	regulation of establishment of protein localization to telomere	10	0.278223938	0.0001	0.000877824
GO:0048259	regulation of receptor-mediated endocytosis	48	0.278201416	0.0091	0.011322589
GO:0006924	activation-induced cell death of T cells	5	0.278198198	0.0296	0.031661766
GO:0032717	negative regulation of interleukin-8 production	12	0.278185328	0.0008	0.002313249
GO:0010713	negative regulation of collagen metabolic process	5	0.278146718	0.0263	0.02839402
GO:0032966	negative regulation of collagen biosynthetic process	5	0.278146718	0.0263	0.02839402
GO:0044252	negative regulation of multicellular organismal metabolic process	5	0.278146718	0.0263	0.02839402
GO:0060768	regulation of epithelial cell proliferation involved in prostate gland development	5	0.278146718	0.0022	0.003910907
GO:0007494	midgut development	7	0.278139364	0.0399	0.04174043
GO:0008154	actin polymerization or depolymerization	88	0.278100503	0.0005	0.002177563
GO:0022898	regulation of transmembrane transporter activity	88	0.278100503	0.0017	0.003334595
GO:0043113	receptor clustering	20	0.278095238	0.0006	0.002177563
GO:0070535	histone H2A K63-linked ubiquitination	5	0.278095238	0.0062	0.008281828
GO:0003203	endocardial cushion morphogenesis	23	0.278093	0.0023	0.004032435
GO:0015908	fatty acid transport	47	0.278063474	0.0011	0.002610912
GO:0034109	homotypic cell-cell adhesion	42	0.278059692	0.0015	0.003088691
GO:1903147	negative regulation of mitophagy	6	0.278035178	0.0214	0.023571068
GO:0050679	positive regulation of epithelial cell proliferation	98	0.278023796	0.0013	0.002859821
GO:0045724	positive regulation of cilium assembly	16	0.277992278	0.0043	0.006204188
GO:0021543	pallium development	84	0.277927928	0.0006	0.002177563
GO:0014031	mesenchymal cell development	36	0.277913628	0.001	0.002498236
GO:0061371	determination of heart left/right asymmetry	36	0.277906478	0.0079	0.010077402
GO:1903071	positive regulation of ER-associated ubiquitin-dependent protein catabolic process	6	0.277906478	0.0335	0.03551156
GO:0030042	actin filament depolymerization	24	0.277863578	0.0004	0.002007244
GO:0006418	tRNA aminoacylation for protein translation	31	0.27784282	0.0059	0.007964563
GO:0090132	epithelium migration	167	0.277828898	0.0015	0.003088691
GO:0072595	maintenance of protein localization in organelle	23	0.277824408	0.0011	0.002610912
GO:0019932	second-messenger-mediated signaling	115	0.277779643	0.0011	0.002610912
GO:0033081	regulation of T cell differentiation in thymus	8	0.277767053	0.0017	0.003334595
GO:2000398	regulation of thymocyte aggregation	8	0.277767053	0.0017	0.003334595
GO:0070129	regulation of mitochondrial translation	18	0.277763478	0.0169	0.019147324
GO:0006959	humoral immune response	78	0.277741478	0.0127	0.014886353
GO:0042249	establishment of planar polarity of embryonic epithelium	5	0.277734878	0.0007	0.002248538
GO:0007350	blastoderm segmentation	8	0.277734878	0.0001	0.000877824
GO:0030838	positive regulation of actin filament polymerization	38	0.27772133	0.0022	0.003910907
GO:0099518	vesicle cytoskeletal trafficking	22	0.277711478	0.0041	0.005981983
GO:0032613	interleukin-10 production	27	0.277687211	0.0073	0.009463568
GO:0042634	regulation of hair cycle	15	0.277649078	0.0008	0.002313249
GO:0042533	tumor necrosis factor biosynthetic process	18	0.277649078	0.0136	0.015813319
GO:0042534	regulation of tumor necrosis factor biosynthetic process	18	0.277649078	0.0136	0.015813319
GO:0031128	developmental induction	14	0.277642949	0.0015	0.003088691
GO:0032460	negative regulation of protein oligomerization	13	0.277616078	0.0018	0.003459409
GO:0032922	circadian regulation of gene expression	34	0.277583466	0.0023	0.004032435
GO:0035513	oxidative RNA demethylation	5	0.277580438	0.0164	0.018653793
GO:0090075	relaxation of muscle	13	0.277576478	0.0004	0.002007244
GO:0015909	long-chain fatty acid transport	37	0.277567915	0.001	0.002498236
GO:0071971	extracellular exosome assembly	7	0.27755102	0.0098	0.012008345
GO:0007338	single fertilization	48	0.27752574	0.0001	0.000877824
GO:0008064	regulation of actin polymerization or depolymerization	70	0.277517926	0.001	0.002498236
GO:0030832	regulation of actin filament length	70	0.277517926	0.001	0.002498236
GO:0002183	cytoplasmic translational initiation	23	0.27749986	0.0007	0.002248538
GO:0051784	negative regulation of nuclear division	31	0.277494084	0.0013	0.002859821
GO:0045780	positive regulation of bone resorption	7	0.277477477	0.0435	0.045246532
GO:0046852	positive regulation of bone remodeling	7	0.277477477	0.0435	0.045246532
GO:0048736	appendage development	85	0.27745628	0.0005	0.002177563
GO:0060173	limb development	85	0.27745628	0.0005	0.002177563
GO:0038083	peptidyl-tyrosine autophosphorylation	10	0.277425997	0.0425	0.044271412
GO:0072655	establishment of protein localization to mitochondrion	85	0.277416913	0.0013	0.002859821
GO:0045995	regulation of embryonic development	67	0.2773968	0.0006	0.002177563
GO:0032456	endocytic recycling	28	0.277367163	0.0072	0.009362497
GO:2001235	positive regulation of apoptotic signaling pathway	114	0.277346519	0.0026	0.004377754
GO:0061156	pulmonary artery morphogenesis	5	0.277271557	0.0228	0.024919293
GO:0060395	SMAD protein signal transduction	21	0.277269106	0.0002	0.001341684
GO:0051495	positive regulation of cytoskeleton organization	103	0.277267559	0.0031	0.004916949
GO:0045216	cell-cell junction organization	133	0.277252978	0.0021	0.003804235
GO:0006164	purine nucleotide biosynthetic process	89	0.277251891	0.004	0.005880507
GO:0031065	positive regulation of histone deacetylation	11	0.277243477	0.0018	0.003459409
GO:0048592	eye morphogenesis	78	0.277203577	0.0046	0.006532041
GO:0022602	ovulation cycle process	51	0.27716456	0.0008	0.002313249
GO:1901879	regulation of protein depolymerization	35	0.277109763	0.0021	0.003804235
GO:0030032	lamellipodium assembly	32	0.277091377	0.0003	0.001720882
GO:0032874	positive regulation of stress-activated MAPK cascade	76	0.27708799	0.0012	0.002741075
GO:0010976	positive regulation of neuron projection development	114	0.277055251	0.0004	0.002007244
GO:0090200	positive regulation of release of cytochrome c from mitochondria	18	0.277048477	0.016	0.018267288
GO:0043271	negative regulation of ion transport	63	0.277023963	0.0025	0.004279479
GO:0033280	response to vitamin D	15	0.277014157	0.0007	0.002248538
GO:0006665	sphingolipid metabolic process	94	0.276987322	0.0058	0.007856196
GO:0043627	response to estrogen	38	0.276982998	0.0026	0.004377754
GO:0030323	respiratory tube development	101	0.276952483	0.0031	0.004916949
GO:0046148	pigment biosynthetic process	34	0.276909683	0.0014	0.002975058
GO:0006826	iron ion transport	31	0.276887948	0.0033	0.005149584
GO:0051591	response to cAMP	49	0.276883881	0.0002	0.001341684

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0010632	regulation of epithelial cell migration	129	0.276874882	0.0015	0.003088691
GO:0032799	low-density lipoprotein receptor particle metabolic process	10	0.276859717	0.0035	0.005358035
GO:0033006	regulation of mast cell activation involved in immune response	17	0.276826406	0.0023	0.004032435
GO:0002679	respiratory burst involved in defense response	8	0.276801802	0.0035	0.005358035
GO:0035268	protein mannosylation	15	0.276791077	< 0.001	< 0.001
GO:0032725	positive regulation of granulocyte macrophage colony-stimulating factor production	6	0.276791077	0.0026	0.004377754
GO:0034763	negative regulation of transmembrane transport	45	0.276779637	0.0012	0.002741075
GO:0032368	regulation of lipid transport	55	0.276752077	0.0008	0.002313249
GO:0071305	cellular response to vitamin D	11	0.276752077	0.0005	0.002177563
GO:0048332	mesoderm morphogenesis	36	0.276748177	0.0031	0.004916949
GO:0007274	neuromuscular synaptic transmission	5	0.276705277	0.0105	0.012724187
GO:0048562	embryonic organ morphogenesis	144	0.276689189	0.0027	0.004491543
GO:0060349	bone morphogenesis	37	0.276649623	0.0014	0.002975058
GO:0019530	taurine metabolic process	6	0.276576577	< 0.001	< 0.001
GO:0019694	alkanesulfonate metabolic process	6	0.276576577	< 0.001	< 0.001
GO:0002065	columnar/cuboidal epithelial cell differentiation	50	0.276571429	0.0006	0.002177563
GO:0070588	calcium ion transmembrane transport	108	0.27655036	0.002	0.003693422
GO:0050728	negative regulation of inflammatory response	59	0.276539493	0.0015	0.003088691
GO:0032273	positive regulation of protein polymerization	56	0.276526016	0.0031	0.004916949
GO:0060401	cytosolic calcium ion transport	65	0.276507277	0.0019	0.003579279
GO:0035845	photoreceptor cell outer segment organization	7	0.276447876	0.0029	0.004714719
GO:0097553	calcium ion transmembrane import into cytosol	51	0.276336841	0.0009	0.002399874
GO:1902656	calcium ion import into cytosol	51	0.276336841	0.0009	0.002399874
GO:0034767	positive regulation of ion transmembrane transport	65	0.276325116	0.0054	0.007432873
GO:0010771	negative regulation of cell morphogenesis involved in differentiation	31	0.276323328	0.0042	0.006097175
GO:0016197	endosomal transport	185	0.276310133	0.0058	0.007856196
GO:1903747	regulation of establishment of protein localization to mitochondrion	45	0.276293436	0.001	0.002498236
GO:1905247	positive regulation of aspartic-type peptidase activity	5	0.276241956	0.0071	0.009268394
GO:2000727	positive regulation of cardiac muscle cell differentiation	7	0.276227248	0.0431	0.044867086
GO:0033555	multicellular organismal response to stress	32	0.276190476	< 0.001	< 0.001
GO:1904683	regulation of metalloendopeptidase activity	5	0.276190476	0.0283	0.030373173
GO:0030203	glycosaminoglycan metabolic process	78	0.276173976	0.0009	0.002399874
GO:0021915	neural tube development	89	0.276167339	0.0002	0.001341684
GO:0023061	signal release	185	0.276137605	0.0008	0.002313249
GO:0048762	mesenchymal cell differentiation	104	0.276128601	0.0026	0.004377754
GO:0030834	regulation of actin filament depolymerization	22	0.276120276	0.0007	0.002248538
GO:0006482	protein demethylation	17	0.27611477	0.0128	0.014984276
GO:0008214	protein dealkylation	17	0.27611477	0.0128	0.014984276
GO:0016577	histone demethylation	17	0.27611477	0.0128	0.014984276
GO:0030212	hyaluronan metabolic process	17	0.27611477	0.0019	0.003579279
GO:0015696	ammonium transport	42	0.276098548	0.0005	0.002177563
GO:0051875	pigment granule localization	14	0.276098548	0.0008	0.002313249
GO:0003281	ventricular septum development	44	0.276079326	0.0028	0.004605006
GO:0009152	purine ribonucleotide biosynthetic process	85	0.276066318	0.0047	0.006644432
GO:0033622	integrin activation	14	0.27604339	0.0007	0.002248538
GO:0003229	ventricular cardiac muscle tissue development	35	0.276036036	0.0038	0.005666214
GO:0045623	negative regulation of T-helper cell differentiation	10	0.276036036	0.0001	0.000877824
GO:0009264	deoxyribonucleotide catabolic process	12	0.276018876	0.0013	0.002859821
GO:1903551	regulation of extracellular exosome assembly	6	0.275975976	0.0073	0.009463568
GO:0032412	regulation of ion transmembrane transporter activity	84	0.275975976	0.002	0.003693422
GO:0030497	fatty acid elongation	8	0.275965251	0.002	0.003693422
GO:0043542	endothelial cell migration	124	0.275922697	0.0015	0.003088691
GO:0001569	branching involved in blood vessel morphogenesis	13	0.275913276	0.0172	0.019442284
GO:1900424	regulation of defense response to bacterium	10	0.275907336	0.0063	0.008390784
GO:0030516	regulation of axon extension	37	0.275870465	0.0027	0.004491543
GO:0042117	monocyte activation	8	0.275868726	0.0089	0.011106266
GO:0035518	histone H2A monoubiquitination	12	0.275825826	0.0003	0.001720882
GO:0002693	positive regulation of cellular extravasation	9	0.275818676	0.002	0.003693422
GO:0016051	carbohydrate biosynthetic process	108	0.275813909	0.0017	0.003334595
GO:0090130	tissue migration	173	0.275733702	0.002	0.003693422
GO:0043543	protein acylation	149	0.275732684	0.001	0.002498236
GO:1901661	quinone metabolic process	24	0.275729301	0.0035	0.005358035
GO:0007605	sensory perception of sound	69	0.275724171	0.0006	0.002177563
GO:1900223	positive regulation of beta-amyloid clearance	6	0.275718576	0.0001	0.000877824
GO:0016048	detection of temperature stimulus	8	0.275707851	< 0.001	< 0.001
GO:1903522	regulation of blood circulation	111	0.27568727	0.001	0.002498236
GO:0060048	cardiac muscle contraction	59	0.275627686	0.0008	0.002313249
GO:0048149	behavioral response to ethanol	5	0.275624196	0.0003	0.001720882
GO:0001707	mesoderm formation	34	0.275622682	0.0044	0.006304227
GO:0042088	T-helper 1 type immune response	22	0.275570376	0.0013	0.002859821
GO:0032231	regulation of actin filament bundle assembly	51	0.275569687	0.0023	0.004032435
GO:1905207	regulation of cardiocyte differentiation	27	0.275532676	0.0098	0.012008345
GO:0002220	innate immune response activating cell surface receptor signaling pathway	71	0.275508909	0.0015	0.003088691
GO:0010171	body morphogenesis	29	0.275507034	0.011	0.013192134
GO:0045647	negative regulation of erythrocyte differentiation	7	0.275455047	0.0119	0.014078095
GO:0030324	lung development	98	0.275447167	0.003	0.004825593
GO:0071229	cellular response to acid chemical	106	0.275427989	0.0007	0.002248538
GO:0030858	positive regulation of epithelial cell differentiation	29	0.275400524	0.0003	0.001720882
GO:0061515	myeloid cell development	37	0.275383492	0.0067	0.008845888
GO:0021700	developmental maturation	119	0.275379341	0.0059	0.007964563
GO:0001841	neural tube formation	61	0.275257928	0.0002	0.001341684
GO:0070585	protein localization to mitochondrion	87	0.275217089	0.0016	0.003223775
GO:0042339	keratan sulfate metabolic process	19	0.275174423	0.0004	0.002007244

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0070198	protein localization to chromosome, telomeric region	22	0.275172575	< 0.001	< 0.001
GO:0051647	nucleus localization	15	0.275160875	0.0021	0.003804235
GO:0006650	glycerophospholipid metabolic process	185	0.275113569	0.0026	0.004377754
GO:0032720	negative regulation of tumor necrosis factor production	29	0.275098744	0.0094	0.011616482
GO:0045599	negative regulation of fat cell differentiation	22	0.275078975	0.0007	0.002248538
GO:0072348	sulfur compound transport	21	0.275062818	0.0008	0.002313249
GO:1903524	positive regulation of blood circulation	28	0.275059754	0.0018	0.003459409
GO:0050879	multicellular organismal movement	24	0.275010725	0.0003	0.001720882
GO:0050881	musculoskeletal movement	24	0.275010725	0.0003	0.001720882
GO:0070243	regulation of thymocyte apoptotic process	5	0.275006435	0.0016	0.003223775
GO:0035282	segmentation	41	0.274978812	0.001	0.002498236
GO:0035767	endothelial cell chemotaxis	17	0.27496404	0.0007	0.002248538
GO:0046476	glycosylceramide biosynthetic process	5	0.274954955	0.0134	0.015626386
GO:0070304	positive regulation of stress-activated protein kinase signaling cascade	77	0.274950275	0.001	0.002498236
GO:0030534	adult behavior	61	0.274924573	0.001	0.002498236
GO:1901838	positive regulation of transcription of nuclear large rRNA transcript from RNA polymerase I promoter	7	0.274903475	0.009	0.011215682
GO:0032377	regulation of intracellular lipid transport	7	0.274903475	0.0228	0.024919293
GO:0032380	regulation of intracellular sterol transport	7	0.274903475	0.0228	0.024919293
GO:0032383	regulation of intracellular cholesterol transport	7	0.274903475	0.0228	0.024919293
GO:2000679	positive regulation of transcription regulatory region DNA binding	13	0.274883675	0.0015	0.003088691
GO:0042482	positive regulation of odontogenesis	5	0.274851995	0.0119	0.014078095
GO:0006022	aminoglycan metabolic process	80	0.27484556	0.0015	0.003088691
GO:0003337	mesenchymal to epithelial transition involved in metanephros morphogenesis	8	0.2747426	0.0055	0.007544447
GO:0060393	regulation of pathway-restricted SMAD protein phosphorylation	27	0.274731875	0.0069	0.009046225
GO:0071695	anatomical structure maturation	25	0.274728443	0.0082	0.010366713
GO:0008202	steroid metabolic process	160	0.274650901	0.0053	0.007330056
GO:0010919	regulation of inositol phosphate biosynthetic process	7	0.274609303	0.0004	0.002007244
GO:0045217	cell-cell junction maintenance	6	0.274603175	0.0215	0.023664853
GO:1900120	regulation of receptor binding	12	0.274603175	0.0251	0.027199847
GO:0010594	regulation of endothelial cell migration	97	0.274590349	0.0018	0.003459409
GO:0045822	negative regulation of heart contraction	13	0.274547075	0.0004	0.002007244
GO:0010744	positive regulation of macrophage derived foam cell differentiation	5	0.274543115	0.0071	0.009268394
GO:0051693	actin filament capping	14	0.27453576	0.0006	0.002177563
GO:0051963	regulation of synapse assembly	36	0.274524525	< 0.001	< 0.001
GO:0090596	sensory organ morphogenesis	122	0.274521594	0.0046	0.006532041
GO:0050729	positive regulation of inflammatory response	69	0.27451924	0.0008	0.002313249
GO:0051924	regulation of calcium ion transport	97	0.274518701	0.0024	0.004156304
GO:0060485	mesenchyme development	133	0.274493183	0.0032	0.005044175
GO:0043567	regulation of insulin-like growth factor receptor signaling pathway	10	0.274491634	0.0315	0.033525301
GO:0006991	response to sterol depletion	6	0.274474474	0.0087	0.010877987
GO:0060193	positive regulation of lipase activity	36	0.274445874	0.0011	0.002610912
GO:0007041	lysosomal transport	64	0.274432915	0.0075	0.00968541
GO:0097484	dendrite extension	8	0.274420849	0.0011	0.002610912
GO:0007266	Rho protein signal transduction	89	0.274403135	0.003	0.004825593
GO:0048536	spleen development	18	0.274374374	0.0036	0.005475609
GO:0043931	ossification involved in bone maturation	7	0.274351903	0.0142	0.016456919
GO:0031110	regulation of microtubule polymerization or depolymerization	33	0.274349674	0.0096	0.01183839
GO:0048537	mucosal-associated lymphoid tissue development	5	0.274337194	0.021	0.023166522
GO:0048541	Peyer's patch development	5	0.274337194	0.021	0.023166522
GO:0038111	interleukin-7-mediated signaling pathway	11	0.274318474	0.0002	0.001341684
GO:0045947	negative regulation of translational initiation	14	0.274296746	0.0049	0.006860215
GO:0042147	retrograde transport, endosome to Golgi	47	0.274273666	0.004	0.005880507
GO:0003018	vascular process in circulatory system	65	0.274230274	0.0026	0.004377754
GO:0006285	base-excision repair, AP site formation	6	0.274217074	0.0078	0.009981807
GO:0042776	mitochondrial ATP synthesis coupled proton transport	12	0.274174174	0.0252	0.027298929
GO:1904923	regulation of mitophagy in response to mitochondrial depolarization	6	0.274174174	0.0265	0.028585731
GO:0031113	regulation of microtubule polymerization	22	0.274131274	0.011	0.013192134
GO:0043268	positive regulation of potassium ion transport	21	0.274069988	0.0177	0.019919142
GO:0042033	chemokine biosynthetic process	7	0.274057731	0.0111	0.013284563
GO:0045073	regulation of chemokine biosynthetic process	7	0.274057731	0.0111	0.013284563
GO:0050755	chemokine metabolic process	7	0.274057731	0.0111	0.013284563
GO:0050886	endocrine process	39	0.274038874	0.0027	0.004491543
GO:0006047	UDP-N-acetylglucosamine metabolic process	10	0.274028314	0.0002	0.001341684
GO:1900118	negative regulation of execution phase of apoptosis	5	0.273925354	0.0392	0.041055316
GO:0010717	regulation of epithelial to mesenchymal transition	48	0.273895324	0.0122	0.014387602
GO:0010712	regulation of collagen metabolic process	22	0.273850474	0.0048	0.006748379
GO:0044246	regulation of multicellular organismal metabolic process	22	0.273850474	0.0048	0.006748379
GO:0060840	artery development	55	0.273841114	0.0045	0.006417207
GO:2001212	regulation of vasculogenesis	11	0.273827074	0.003	0.004825593
GO:0010510	regulation of acetyl-CoA biosynthetic process from pyruvate	5	0.273822394	0.0022	0.003910907
GO:0050812	regulation of acyl-CoA biosynthetic process	5	0.273822394	0.0022	0.003910907
GO:0046488	phosphatidylinositol metabolic process	93	0.273818519	0.0028	0.004605006
GO:0006383	transcription from RNA polymerase III promoter	35	0.273778268	0.0021	0.003804235
GO:0031529	ruffle organization	28	0.273763559	0.0023	0.004032435
GO:0006308	DNA catabolic process	23	0.273750769	0.007	0.009166016
GO:0045736	negative regulation of cyclin-dependent protein serine/threonine kinase activity	14	0.273745174	0.0194	0.021561946
GO:1904030	negative regulation of cyclin-dependent protein kinase activity	14	0.273745174	0.0194	0.021561946
GO:0001778	plasma membrane repair	6	0.273702274	0.0102	0.012424427
GO:0034308	primary alcohol metabolic process	28	0.273662438	0.0022	0.003910907
GO:0035404	histone-serine phosphorylation	6	0.273659374	0.0017	0.003334595
GO:0032801	receptor catabolic process	19	0.273657116	0.0025	0.004279479
GO:0010257	NADH dehydrogenase complex assembly	48	0.273600386	0.0163	0.018559925
GO:0032981	mitochondrial respiratory chain complex I assembly	48	0.273600386	0.0163	0.018559925

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0097031	mitochondrial respiratory chain complex I biogenesis	48	0.273600386	0.0163	0.018559925
GO:0035850	epithelial cell differentiation involved in kidney development	27	0.273597407	0.0078	0.009981807
GO:0009303	rRNA transcription	22	0.273569674	0.0019	0.003579279
GO:0048701	embryonic cranial skeleton morphogenesis	25	0.273534106	0.0009	0.002399874
GO:0044090	positive regulation of vacuole organization	13	0.273517474	0.0206	0.022756769
GO:0045834	positive regulation of lipid metabolic process	86	0.273463829	0.001	0.002498236
GO:0030007	cellular potassium ion homeostasis	5	0.273462033	0.0341	0.036093556
GO:0072608	interleukin-10 secretion	6	0.273444873	0.0107	0.012912536
GO:0009994	oocyte differentiation	20	0.273436293	0.0004	0.002007244
GO:0002431	Fc receptor mediated stimulatory signaling pathway	41	0.273421854	0.0022	0.003910907
GO:0030321	transepithelial chloride transport	5	0.273410553	0.0147	0.016962357
GO:0016239	positive regulation of macroautophagy	42	0.273408102	0.0055	0.007544447
GO:0010959	regulation of metal ion transport	155	0.27340225	0.0019	0.003579279
GO:2000179	positive regulation of neural precursor cell proliferation	29	0.273350197	0.0001	0.000877824
GO:0051258	protein polymerization	116	0.273330227	0.0017	0.003334595
GO:0048639	positive regulation of developmental growth	89	0.273307015	0.0034	0.005263104
GO:0045666	positive regulation of neuron differentiation	153	0.273300191	0.0006	0.002177563
GO:0097530	granulocyte migration	52	0.273235323	0.0064	0.008500875
GO:0032102	negative regulation of response to external stimulus	154	0.273193602	0.0023	0.004032435
GO:0021602	cranial nerve morphogenesis	6	0.273187473	< 0.001	< 0.001
GO:0000423	macromitophagy	19	0.273155863	0.0068	0.008946408
GO:0055024	regulation of cardiac muscle tissue development	46	0.273107269	0.0092	0.011424708
GO:0001938	positive regulation of endothelial cell proliferation	54	0.273101673	0.0023	0.004032435
GO:1901019	regulation of calcium ion transmembrane transporter activity	28	0.273064902	0.0011	0.002610912
GO:0045806	negative regulation of endocytosis	33	0.273039273	0.0024	0.004156304
GO:0030041	actin filament polymerization	74	0.273035584	0.0005	0.002177563
GO:0046785	microtubule polymerization	35	0.273020776	0.0118	0.013977955
GO:0090481	pyrimidine nucleotide-sugar transmembrane transport	8	0.273005148	0.0068	0.008946408
GO:0006361	transcription initiation from RNA polymerase I promoter	25	0.272988417	0.0001	0.000877824
GO:0035871	protein K11-linked deubiquitination	5	0.272947233	0.0072	0.009362497
GO:0035733	hepatic stellate cell activation	6	0.272930073	0.0216	0.023746214
GO:0061383	trabecula morphogenesis	29	0.272906404	0.0035	0.005358035
GO:0007000	nucleolus organization	6	0.272887173	< 0.001	< 0.001
GO:0030833	regulation of actin filament polymerization	61	0.272861152	0.001	0.002498236
GO:0070979	protein K11-linked ubiquitination	18	0.272858573	0.0053	0.007330056
GO:0042440	pigment metabolic process	41	0.272806605	0.0044	0.006304227
GO:0090102	cochlea development	22	0.272797473	0.0002	0.001341684
GO:0009154	purine ribonucleotide catabolic process	15	0.272741313	0.0079	0.010077402
GO:0009261	ribonucleotide catabolic process	15	0.272741313	0.0079	0.010077402
GO:0071242	cellular response to ammonium ion	28	0.27270638	0.0002	0.001341684
GO:0019371	cyclooxygenase pathway	8	0.272651223	0.0025	0.004279479
GO:0007034	vacuolar transport	69	0.272612986	0.0077	0.009887588
GO:0032008	positive regulation of TOR signaling	21	0.272611387	0.0086	0.010769857
GO:0010762	regulation of fibroblast migration	19	0.272586873	0.0015	0.003088691
GO:0098789	pre-mRNA cleavage required for polyadenylation	7	0.272586873	0.0004	0.002007244
GO:0055023	positive regulation of cardiac muscle tissue growth	19	0.27254623	0.0048	0.006748379
GO:0006183	GTP biosynthetic process	6	0.272543973	0.0374	0.039305772
GO:0006228	UTP biosynthetic process	6	0.272543973	0.0374	0.039305772
GO:0006929	substrate-dependent cell migration	19	0.272519136	0.0114	0.01358747
GO:0002042	cell migration involved in sprouting angiogenesis	33	0.272485472	0.0037	0.005561344
GO:1902017	regulation of cilium assembly	34	0.272473314	0.0005	0.002177563
GO:0060350	endochondral bone morphogenesis	23	0.272452577	0.0011	0.002610912
GO:0070884	regulation of calcineurin-NFAT signaling cascade	13	0.272428472	0.0025	0.004279479
GO:0031346	positive regulation of cell projection organization	170	0.272399122	0.0012	0.002741075
GO:0033627	cell adhesion mediated by integrin	36	0.272386672	0.0007	0.002248538
GO:0051642	centrosome localization	14	0.27238463	0.0046	0.006532041
GO:0007626	locomotory behavior	100	0.272368082	0.0008	0.002313249
GO:0060526	prostate glandular acinus morphogenesis	5	0.272329472	0.0221	0.024229021
GO:0060527	prostate epithelial cord arborization involved in prostate glandular acinus morphogenesis	5	0.272329472	0.0221	0.024229021
GO:0035904	aorta development	34	0.272329472	0.0013	0.002859821
GO:0010634	positive regulation of epithelial cell migration	87	0.272323555	0.0021	0.003804235
GO:0006767	water-soluble vitamin metabolic process	52	0.272309672	0.0112	0.013379119
GO:0031954	positive regulation of protein autophosphorylation	11	0.272282672	0.0018	0.003459409
GO:0060314	regulation of ryanodine-sensitive calcium-release channel activity	8	0.272232947	0.0006	0.002177563
GO:0009084	glutamine family amino acid biosynthetic process	10	0.272226512	0.0001	0.000877824
GO:0031016	pancreas development	39	0.272124872	0.0038	0.005666214
GO:0060052	neurofilament cytoskeleton organization	6	0.272114972	0.0305	0.032586169
GO:0035066	positive regulation of histone acetylation	16	0.272104247	0.0051	0.007095023
GO:0046514	ceramide catabolic process	13	0.272091872	0.0168	0.019054351
GO:0017085	response to insecticide	7	0.272072072	0.008	0.010168329
GO:0031645	negative regulation of neurological system process	8	0.272039897	0.0065	0.008621124
GO:0051209	release of sequestered calcium ion into cytosol	48	0.272034535	0.0009	0.002399874
GO:0051282	regulation of sequestering of calcium ion	48	0.272034535	0.0009	0.002399874
GO:0051283	negative regulation of sequestering of calcium ion	48	0.272034535	0.0009	0.002399874
GO:0055017	cardiac muscle tissue growth	46	0.271999329	0.003	0.004825593
GO:0010835	regulation of protein ADP-ribosylation	7	0.271924986	0.007	0.009166016
GO:0030239	myofibril assembly	25	0.271907336	0.0025	0.004279479
GO:0032272	negative regulation of protein polymerization	28	0.271851443	0.0028	0.004605006
GO:0072531	pyrimidine-containing compound transmembrane transport	11	0.271838072	0.0164	0.018653793
GO:0070106	interleukin-27-mediated signaling pathway	7	0.271814672	0.0001	0.000877824
GO:1905048	regulation of metallopeptidase activity	9	0.271757472	0.002	0.003693422
GO:0006264	mitochondrial DNA replication	8	0.271750322	0.0118	0.013977955
GO:0090218	positive regulation of lipid kinase activity	25	0.2717426	0.0001	0.000877824

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0034764	positive regulation of transmembrane transport	71	0.271687784	0.006	0.00807902
GO:0032147	activation of protein kinase activity	158	0.27165176	0.0022	0.003910907
GO:0043966	histone H3 acetylation	43	0.271617132	0.0022	0.003910907
GO:1905477	positive regulation of protein localization to membrane	61	0.271603688	0.0008	0.002313249
GO:0046889	positive regulation of lipid biosynthetic process	44	0.271533872	0.0019	0.003579279
GO:0043547	positive regulation of GTPase activity	180	0.271425711	0.0056	0.007655255
GO:0060421	positive regulation of heart growth	21	0.271410186	0.0081	0.010256567
GO:0007171	activation of transmembrane receptor protein tyrosine kinase activity	5	0.271402831	0.0107	0.012912536
GO:0007498	mesoderm development	62	0.271366297	0.0002	0.001341684
GO:0038034	signal transduction in absence of ligand	37	0.271348569	0.0106	0.012825859
GO:0097192	extrinsic apoptotic signaling pathway in absence of ligand	37	0.271348569	0.0106	0.012825859
GO:0042742	defense response to bacterium	82	0.271331262	0.0044	0.006304227
GO:2000765	regulation of cytoplasmic translation	13	0.271319671	0.0169	0.019147324
GO:0035308	negative regulation of protein dephosphorylation	30	0.271274131	0.0001	0.000877824
GO:0090208	positive regulation of triglyceride metabolic process	14	0.2712631	0.0017	0.003334595
GO:0050891	multicellular organismal water homeostasis	21	0.271250843	0.0001	0.000877824
GO:0038033	positive regulation of endothelial cell chemotaxis by VEGF-activated vascular endothelial growth factor receptor signaling pathway	5	0.271248391	0.0062	0.008281828
GO:0007292	female gamete generation	54	0.271190238	0.0006	0.002177563
GO:0010569	regulation of double-strand break repair via homologous recombination	24	0.271181896	< 0.001	< 0.001
GO:0051546	keratinocyte migration	9	0.271128271	0.0076	0.009790742
GO:0021533	cell differentiation in hindbrain	9	0.271099671	0.0035	0.005358035
GO:0030728	ovulation	13	0.271082071	0.0101	0.012328539
GO:0042445	hormone metabolic process	89	0.271074285	0.004	0.005880507
GO:1902745	positive regulation of lamellipodium organization	12	0.271042471	0.0043	0.006204188
GO:0016358	dendrite development	85	0.271039443	0.0022	0.003910907
GO:0006474	N-terminal protein amino acid acetylation	12	0.271021021	0.0001	0.000877824
GO:0043039	tRNA aminoacylation	34	0.271004618	0.0062	0.008281828
GO:0034766	negative regulation of ion transmembrane transport	41	0.270992247	0.0014	0.002975058
GO:0071312	cellular response to alkaloid	21	0.270956671	0.0018	0.003459409
GO:2001259	positive regulation of cation channel activity	23	0.270930558	0.0024	0.004156304
GO:2000644	regulation of receptor catabolic process	7	0.270895385	0.0132	0.015415723
GO:0034390	smooth muscle cell apoptotic process	10	0.270836551	0.0069	0.009046225
GO:0034391	regulation of smooth muscle cell apoptotic process	10	0.270836551	0.0069	0.009046225
GO:0019748	secondary metabolic process	35	0.270792425	0.0006	0.002177563
GO:0006563	L-serine metabolic process	9	0.270785071	0.0055	0.007544447
GO:0021952	central nervous system projection neuron axonogenesis	7	0.270785071	0.0014	0.002975058
GO:1904427	positive regulation of calcium ion transmembrane transport	25	0.270754183	0.006	0.00807902
GO:0009304	tRNA transcription	6	0.270742171	0.0147	0.016962357
GO:0015671	oxygen transport	6	0.270742171	0.0154	0.017651835
GO:1902600	hydrogen ion transmembrane transport	63	0.270740128	0.0052	0.007215241
GO:0003416	endochondral bone growth	9	0.270727871	0.0009	0.002399874
GO:0010595	positive regulation of endothelial cell migration	63	0.270703356	0.0021	0.003804235
GO:0043984	histone H4-K16 acetylation	14	0.270693142	0.0059	0.007964563
GO:0016322	neuron remodeling	6	0.270613471	0.0122	0.014387602
GO:0042726	flavin-containing compound metabolic process	6	0.270613471	0.018	0.020203241
GO:0051281	positive regulation of release of sequestered calcium ion into cytosol	16	0.270608108	0.0029	0.004714719
GO:0070936	protein K48-linked ubiquitination	32	0.270608108	0.0068	0.008946408
GO:0006829	zinc II ion transport	9	0.270584871	0.006	0.00807902
GO:0035137	hindlimb morphogenesis	13	0.270567271	0.0001	0.000877824
GO:0014009	glial cell proliferation	28	0.270527671	0.0004	0.002007244
GO:0032271	regulation of protein polymerization	86	0.270470803	0.0028	0.004605006
GO:0098787	mRNA cleavage involved in mRNA processing	8	0.27046332	0.0001	0.000877824
GO:0051573	negative regulation of histone H3-K9 methylation	8	0.27046332	0.0009	0.002399874
GO:0014074	response to purine-containing compound	77	0.270407328	0.0002	0.001341684
GO:0060402	calcium ion transport into cytosol	61	0.270375762	0.0018	0.003459409
GO:0000045	autophagosome assembly	54	0.270365604	0.0037	0.005561344
GO:1904062	regulation of cation transmembrane transport	118	0.270348799	0.0013	0.002859821
GO:0046501	protoporphyrinogen IX metabolic process	7	0.270343813	0.0358	0.037748743
GO:1900363	regulation of mRNA polyadenylation	10	0.27032175	0.0006	0.002177563
GO:0032467	positive regulation of cytokinesis	15	0.27028743	0.0066	0.008731949
GO:0046135	pyrimidine nucleoside catabolic process	10	0.27024453	0.0148	0.017062301
GO:0034754	cellular hormone metabolic process	61	0.270240733	0.0056	0.007655255
GO:0003161	cardiac conduction system development	8	0.270238095	0.0044	0.006304227
GO:0042541	hemoglobin biosynthetic process	7	0.270233499	0.0041	0.005981983
GO:0006750	glutathione biosynthetic process	12	0.27014157	0.0164	0.018653793
GO:0071466	cellular response to xenobiotic stimulus	51	0.270088576	0.0001	0.000877824
GO:0001976	neurological system process involved in regulation of systemic arterial blood pressure	7	0.270086413	0.001	0.002498236
GO:1901381	positive regulation of potassium ion transmembrane transport	18	0.27008437	0.0237	0.025818821
GO:0022029	telencephalon cell migration	27	0.27007007	0.0007	0.002248538
GO:0045333	cellular respiration	129	0.270050782	0.0098	0.012008345
GO:0002566	somatic diversification of immune receptors via somatic mutation	6	0.27001287	0.0049	0.006860215
GO:0033235	positive regulation of protein sumoylation	6	0.27001287	0.0173	0.019544921
GO:0019320	hexose catabolic process	30	0.26993565	0.0022	0.003910907
GO:0050994	regulation of lipid catabolic process	33	0.26989587	0.0022	0.003910907
GO:0010810	regulation of cell-substrate adhesion	113	0.269889865	0.0024	0.004156304
GO:0035902	response to immobilization stress	16	0.269868082	0.0031	0.004916949
GO:1901379	regulation of potassium ion transmembrane transport	32	0.269843951	0.0103	0.012519912
GO:0017156	calcium ion regulated exocytosis	39	0.26978847	0.0007	0.002248538
GO:0048010	vascular endothelial growth factor receptor signaling pathway	54	0.269779303	0.0107	0.012912536
GO:0097164	ammonium ion metabolic process	122	0.269770239	0.0017	0.003334595
GO:0032042	mitochondrial DNA metabolic process	12	0.26971257	0.0175	0.019742875
GO:2001053	regulation of mesenchymal cell apoptotic process	5	0.26970399	0.0006	0.002177563

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:2001054	negative regulation of mesenchymal cell apoptotic process	5	0.26970399	0.0006	0.002177563
GO:0046683	response to organophosphorus	68	0.269664623	0.0005	0.002177563
GO:0017145	stem cell division	19	0.269660638	0.0024	0.004156304
GO:0003279	cardiac septum development	61	0.269599342	0.003	0.004825593
GO:0051881	regulation of mitochondrial membrane potential	46	0.269582004	0.0133	0.015521132
GO:0061162	establishment of monopolar cell polarity	9	0.26952667	0.0422	0.043980474
GO:0061339	establishment or maintenance of monopolar cell polarity	9	0.26952667	0.0422	0.043980474
GO:0002467	germinal center formation	9	0.269498069	0.0075	0.00968541
GO:0001829	trophectodermal cell differentiation	6	0.269498069	0.0003	0.001720882
GO:0031032	actomyosin structure organization	88	0.269486369	0.0014	0.002975058
GO:0061037	negative regulation of cartilage development	10	0.269446589	0.0127	0.014886353
GO:0046471	phosphatidylglycerol metabolic process	18	0.269440869	0.003	0.004825593
GO:0003197	endocardial cushion development	28	0.269433719	0.0046	0.006532041
GO:0006882	cellular zinc ion homeostasis	7	0.269424527	0.0091	0.011322589
GO:0051492	regulation of stress fiber assembly	45	0.269400829	0.0025	0.004279479
GO:0070076	histone lysine demethylation	16	0.269385457	0.0142	0.016456919
GO:0072148	epithelial cell fate commitment	8	0.269337194	0.0009	0.002399874
GO:0090670	RNA localization to Cajal body	17	0.269316375	< 0.001	< 0.001
GO:0090671	telomerase RNA localization to Cajal body	17	0.269316375	< 0.001	< 0.001
GO:0090672	telomerase RNA localization	17	0.269316375	< 0.001	< 0.001
GO:1904872	regulation of telomerase RNA localization to Cajal body	17	0.269316375	< 0.001	< 0.001
GO:0032964	collagen biosynthetic process	23	0.269296626	0.005	0.006974174
GO:0070935	3'-UTR-mediated mRNA stabilization	8	0.269272844	0.0126	0.014782732
GO:0016482	cytosolic transport	92	0.269263052	0.0085	0.010671887
GO:0060359	response to ammonium ion	60	0.269210639	0.0001	0.000877824
GO:0071542	dopaminergic neuron differentiation	12	0.269197769	0.0044	0.006304227
GO:0046339	diacylglycerol metabolic process	9	0.269097669	0.0015	0.003088691
GO:0006584	catecholamine metabolic process	27	0.269040469	0.0001	0.000877824
GO:0009712	catechol-containing compound metabolic process	27	0.269040469	0.0001	0.000877824
GO:0032370	positive regulation of lipid transport	34	0.26899084	0.0004	0.002007244
GO:0005976	polysaccharide metabolic process	56	0.268909726	0.0004	0.002007244
GO:0042752	regulation of circadian rhythm	49	0.268893967	0.0026	0.004377754
GO:1904837	beta-catenin-TCF complex assembly	20	0.268893179	0.0011	0.002610912
GO:0043276	anoikis	19	0.26887489	0.011	0.013192134
GO:0030148	sphingolipid biosynthetic process	58	0.268867883	0.0069	0.009046225
GO:0002532	production of molecular mediator involved in inflammatory response	35	0.268836183	0.0013	0.002859821
GO:0051340	regulation of ligase activity	6	0.268811669	0.038	0.03991002
GO:0001662	behavioral fear response	16	0.268806306	< 0.001	< 0.001
GO:0042596	fear response	16	0.268806306	< 0.001	< 0.001
GO:0014904	myotube cell development	12	0.268790219	0.0031	0.004916949
GO:1904796	regulation of core promoter binding	5	0.268777349	0.0011	0.002610912
GO:0060043	regulation of cardiac muscle cell proliferation	26	0.268775369	0.0103	0.012519912
GO:0030901	midbrain development	53	0.268764722	0.0046	0.006532041
GO:0044708	single-organism behavior	185	0.268753696	0.0012	0.002741075
GO:0050996	positive regulation of lipid catabolic process	13	0.268745669	0.008	0.010168329
GO:0006805	xenobiotic metabolic process	47	0.268709439	0.0001	0.000877824
GO:0007618	mating	18	0.268682969	< 0.001	< 0.001
GO:0021510	spinal cord development	54	0.268621002	0.0013	0.002859821
GO:0018345	protein palmitoylation	19	0.268590395	0.0073	0.009463568
GO:0099622	cardiac muscle cell membrane repolarization	16	0.268516731	0.0004	0.002007244
GO:0007409	axonogenesis	182	0.268508069	0.0014	0.002975058
GO:0003151	outflow tract morphogenesis	48	0.268500644	0.0075	0.00968541
GO:0098657	import into cell	38	0.26848879	0.0032	0.005044175
GO:0035588	G-protein coupled purinergic receptor signaling pathway	12	0.268468468	0.0005	0.002177563
GO:0048821	erythrocyte development	18	0.268411268	0.0041	0.005981983
GO:0007416	synapse assembly	57	0.268409763	0.0001	0.000877824
GO:0060433	bronchus development	5	0.268314028	0.0069	0.009046225
GO:0002192	IRES-dependent translational initiation	11	0.268304668	0.0002	0.001341684
GO:1905475	regulation of protein localization to membrane	92	0.268292205	0.0012	0.002741075
GO:0043244	regulation of protein complex disassembly	49	0.268279358	0.004	0.005880507
GO:0055022	negative regulation of cardiac muscle tissue growth	13	0.268211068	0.0212	0.023366932
GO:0061117	negative regulation of heart growth	13	0.268211068	0.0212	0.023366932
GO:0070242	thymocyte apoptotic process	9	0.268211068	0.0107	0.012912536
GO:0051491	positive regulation of filopodium assembly	15	0.268176748	0.0012	0.002741075
GO:0006309	apoptotic DNA fragmentation	17	0.268120221	0.0061	0.008182551
GO:0050999	regulation of nitric-oxide synthase activity	26	0.268102168	0.0031	0.004916949
GO:2000171	negative regulation of dendrite development	9	0.268096668	0.0411	0.042939393
GO:0015849	organic acid transport	138	0.268089829	0.0035	0.005358035
GO:0046942	carboxylic acid transport	138	0.268089829	0.0035	0.005358035
GO:0032515	negative regulation of phosphoprotein phosphatase activity	29	0.268033551	0.0001	0.000877824
GO:0015698	inorganic anion transport	70	0.268019857	0.0034	0.005263104
GO:0007006	mitochondrial membrane organization	76	0.267957055	0.0084	0.010571327
GO:1901880	negative regulation of protein depolymerization	27	0.267944135	0.003	0.004825593
GO:2001222	regulation of neuron migration	18	0.267882168	0.0012	0.002741075
GO:0035482	gastric motility	5	0.267850708	0.0006	0.002177563
GO:0055021	regulation of cardiac muscle tissue growth	33	0.267828868	0.0106	0.012825859
GO:0051668	localization within membrane	40	0.267824968	0.0005	0.002177563
GO:0008016	regulation of heart contraction	97	0.267802412	0.0015	0.003088691
GO:0002040	sprouting angiogenesis	60	0.267790648	0.0023	0.004032435
GO:0055010	ventricular cardiac muscle tissue morphogenesis	30	0.267790648	0.0034	0.005263104
GO:0021885	forebrain cell migration	28	0.267788196	0.0007	0.002248538
GO:0032233	positive regulation of actin filament bundle assembly	31	0.267770997	0.0071	0.009268394
GO:0033198	response to ATP	14	0.267751425	0.0007	0.002248538

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0097531	mast cell migration	6	0.267739168	0.0045	0.006417207
GO:0050995	negative regulation of lipid catabolic process	13	0.267696268	0.002	0.003693422
GO:0008306	associative learning	26	0.267636868	0.0024	0.004156304
GO:0043242	negative regulation of protein complex disassembly	28	0.267622725	0.0029	0.004714719
GO:0035148	tube formation	81	0.26757869	0.0006	0.002177563
GO:1900016	negative regulation of cytokine production involved in inflammatory response	10	0.267567568	0.0012	0.002741075
GO:0060419	heart growth	49	0.267559688	0.0033	0.005149584
GO:0018200	peptidyl-glutamic acid modification	16	0.26748713	0.0034	0.005263104
GO:0032400	melanosome localization	13	0.267419067	0.0018	0.003459409
GO:0060420	regulation of heart growth	35	0.267416805	0.0128	0.014984276
GO:0031272	regulation of pseudopodium assembly	7	0.267402096	0.0124	0.014577606
GO:0009268	response to pH	18	0.267381667	0.0022	0.003910907
GO:0003283	atrial septum development	11	0.267368667	< 0.001	< 0.001
GO:0045792	negative regulation of cell size	7	0.267365325	0.0307	0.03276689
GO:0042462	eye photoreceptor cell development	13	0.267359667	0.0062	0.008281828
GO:2000108	positive regulation of leukocyte apoptotic process	9	0.267353067	0.0044	0.006304227
GO:0019731	antibacterial humoral response	12	0.267310167	0.0052	0.007215241
GO:1904352	positive regulation of protein catabolic process in the vacuole	5	0.267284427	0.0154	0.017651835
GO:0061025	membrane fusion	78	0.267168267	0.0092	0.011424708
GO:0042220	response to cocaine	23	0.267159085	0.0002	0.001341684
GO:0046622	positive regulation of organ growth	28	0.267144696	0.0021	0.003804235
GO:0006941	striated muscle contraction	79	0.267073946	0.0011	0.002610912
GO:0051339	regulation of lyase activity	30	0.267069927	0.0061	0.008182551
GO:1990668	vesicle fusion with endoplasmic reticulum-Golgi intermediate compartment (ERGIC) membrane	5	0.267027027	0.039	0.040872718
GO:0043923	positive regulation by host of viral transcription	16	0.267004505	0.0066	0.008731949
GO:0007530	sex determination	10	0.266949807	0.0054	0.007432873
GO:0006029	proteoglycan metabolic process	41	0.266949179	0.0066	0.008731949
GO:2000251	positive regulation of actin cytoskeleton reorganization	9	0.266895467	0.0021	0.003804235
GO:0060412	ventricular septum morphogenesis	26	0.266884467	0.0007	0.002248538
GO:0098780	response to mitochondrial depolarisation	17	0.266818079	0.0072	0.009362497
GO:0006066	alcohol metabolic process	185	0.266797454	0.0053	0.007330056
GO:0048484	enteric nervous system development	8	0.266763192	0.0452	0.046915244
GO:0097006	regulation of plasma lipoprotein particle levels	43	0.266762444	0.0007	0.002248538
GO:0002686	negative regulation of leukocyte migration	21	0.266752467	0.0004	0.002007244
GO:0006103	2-oxoglutarate metabolic process	11	0.266690067	0.0035	0.005358035
GO:0070534	protein K63-linked ubiquitination	31	0.266683273	0.005	0.006974174
GO:0006040	amino sugar metabolic process	20	0.266602317	0.0004	0.002007244
GO:0006661	phosphatidylinositol biosynthetic process	69	0.266599519	0.0033	0.005149584
GO:0071287	cellular response to manganese ion	7	0.266593124	0.0436	0.045335748
GO:0051897	positive regulation of protein kinase B signaling	79	0.266500497	0.0013	0.002859821
GO:0090103	cochlea morphogenesis	10	0.266486486	0.0026	0.004377754
GO:0035973	aggrephagy	7	0.266482809	0.0041	0.005981983
GO:0015695	organic cation transport	9	0.266380666	0.0356	0.037550281
GO:0060038	cardiac muscle cell proliferation	32	0.266296654	0.0052	0.007215241
GO:0019730	antimicrobial humoral response	25	0.266285714	0.0118	0.013977955
GO:0051606	detection of stimulus	136	0.266282459	0.005	0.006974174
GO:0060525	prostate glandular acinus development	6	0.266280566	0.0085	0.010671887
GO:0032688	negative regulation of interferon-beta production	9	0.266180466	0.0011	0.002610912
GO:0048599	oocyte development	19	0.266151866	0.0003	0.001720882
GO:0043507	positive regulation of JUN kinase activity	35	0.266093032	0.0023	0.004032435
GO:0009069	serine family amino acid metabolic process	34	0.266091301	0.0014	0.002975058
GO:0009410	response to xenobiotic stimulus	55	0.266067626	0.0002	0.001341684
GO:0098751	bone cell development	17	0.266045878	0.0159	0.01817591
GO:0006895	Golgi to endosome transport	10	0.265997426	0.0133	0.015521132
GO:0009110	vitamin biosynthetic process	14	0.265986395	0.0013	0.002859821
GO:0001838	embryonic epithelial tube formation	70	0.265975363	0.0002	0.001341684
GO:0006672	ceramide metabolic process	57	0.265903497	0.0125	0.014684332
GO:0006544	glycine metabolic process	13	0.265894466	0.0109	0.013101792
GO:0002433	immune response-regulating cell surface receptor signaling pathway involved in phagocytosis	40	0.265810811	0.0027	0.004491543
GO:0038094	Fc-gamma receptor signaling pathway	40	0.265810811	0.0027	0.004491543
GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis	40	0.265810811	0.0027	0.004491543
GO:1905037	autophagosome organization	57	0.265768024	0.0043	0.006204188
GO:0015718	monocarboxylic acid transport	69	0.26575644	0.0041	0.005981983
GO:0010458	exit from mitosis	23	0.265726596	0.0077	0.009887588
GO:0051561	positive regulation of mitochondrial calcium ion concentration	7	0.265710609	0.0398	0.041649491
GO:0032354	response to follicle-stimulating hormone	11	0.265660466	0.0092	0.011424708
GO:0032881	regulation of polysaccharide metabolic process	24	0.265637066	0.0055	0.007544447
GO:0044321	response to leptin	12	0.265551266	0.0005	0.002177563
GO:0007019	microtubule depolymerization	17	0.265546218	0.0222	0.024321919
GO:0034637	cellular carbohydrate biosynthetic process	40	0.265540541	0.0007	0.002248538
GO:0090280	positive regulation of calcium ion import	25	0.265534106	0.0054	0.007432873
GO:0009064	glutamine family amino acid metabolic process	40	0.26547619	< 0.001	< 0.001
GO:0001702	gastrulation with mouth forming second	13	0.265458865	< 0.001	< 0.001
GO:0090151	establishment of protein localization to mitochondrial membrane	9	0.265408265	0.0093	0.011528671
GO:0032261	purine nucleotide salvage	5	0.265328185	0.0047	0.006644432
GO:0051781	positive regulation of cell division	45	0.265293865	0.0047	0.006644432
GO:0097009	energy homeostasis	20	0.265276705	0.0222	0.024321919
GO:0098868	bone growth	10	0.265276705	0.001	0.002498236
GO:1901985	positive regulation of protein acetylation	23	0.265234178	0.0009	0.002399874
GO:0034405	response to fluid shear stress	22	0.265215865	0.0085	0.010671887
GO:0010822	positive regulation of mitochondrion organization	88	0.26521294	0.0071	0.009268394
GO:0051928	positive regulation of calcium ion transport	47	0.265198938	0.0098	0.012008345
GO:0034982	mitochondrial protein processing	5	0.265122265	0.0068	0.008946408

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0008360	regulation of cell shape	82	0.265081458	0.0021	0.003804235
GO:0098661	inorganic anion transmembrane transport	37	0.265066611	0.0004	0.002007244
GO:0051650	establishment of vesicle localization	126	0.265020122	0.0021	0.003804235
GO:0006937	regulation of muscle contraction	67	0.264972435	0.0006	0.002177563
GO:0072175	epithelial tube formation	71	0.26497	0.0002	0.001341684
GO:0022027	interkinetic nuclear migration	5	0.264967825	0.0008	0.002313249
GO:0001541	ovarian follicle development	35	0.264938408	0.0017	0.003334595
GO:0060041	retina development in camera-type eye	71	0.264897493	0.0006	0.002177563
GO:0090279	regulation of calcium ion import	41	0.264871143	0.0008	0.002313249
GO:0048705	skeletal system morphogenesis	97	0.264819753	0.0011	0.002610912
GO:0016236	macroautophagy	192	0.264785768	0.0074	0.009581512
GO:0009415	response to water	8	0.26476834	0.0025	0.004279479
GO:0060491	regulation of cell projection assembly	85	0.264710425	0.0025	0.004279479
GO:1904888	cranial skeletal system development	33	0.264654265	0.0013	0.002859821
GO:0046697	decidualization	11	0.264654265	0.009	0.011215682
GO:0051181	cofactor transport	16	0.264623552	0.0271	0.029163847
GO:0051024	positive regulation of immunoglobulin secretion	6	0.264607465	0.0002	0.001341684
GO:0090311	regulation of protein deacetylation	21	0.26458295	0.0044	0.006304227
GO:0042471	ear morphogenesis	52	0.264557965	0.0037	0.005561344
GO:0010718	positive regulation of epithelial to mesenchymal transition	28	0.264524729	0.0129	0.015093024
GO:1903319	positive regulation of protein maturation	18	0.264507365	0.0174	0.019643968
GO:0046530	photoreceptor cell differentiation	29	0.264483202	0.0002	0.001341684
GO:0046173	polyol biosynthetic process	28	0.264414414	0.0075	0.00968541
GO:1901626	regulation of postsynaptic membrane organization	6	0.264392964	0.0096	0.01183839
GO:0031365	N-terminal protein amino acid modification	20	0.264337194	0.0015	0.003088691
GO:0033762	response to glucagon	13	0.264330264	0.0001	0.000877824
GO:0061050	regulation of cell growth involved in cardiac muscle cell development	7	0.264313293	0.0126	0.014782732
GO:2001257	regulation of cation channel activity	47	0.264300775	0.0016	0.003223775
GO:0019233	sensory perception of pain	40	0.264298584	0.0001	0.000877824
GO:0010661	positive regulation of muscle cell apoptotic process	10	0.264221364	0.0104	0.012619802
GO:0030149	sphingolipid catabolic process	18	0.264207064	0.0324	0.034402732
GO:0060065	uterus development	10	0.264169884	< 0.001	< 0.001
GO:0032768	regulation of monooxygenase activity	30	0.264161304	0.0021	0.003804235
GO:0043648	dicarboxylic acid metabolic process	60	0.264139854	0.0004	0.002007244
GO:0043247	telomere maintenance in response to DNA damage	6	0.264135564	0.011	0.013192134
GO:0002536	respiratory burst involved in inflammatory response	5	0.264041184	0.0158	0.018074565
GO:0090309	positive regulation of methylation-dependent chromatin silencing	6	0.263878164	0.0076	0.009790742
GO:0060135	maternal process involved in female pregnancy	33	0.263858664	0.0025	0.004279479
GO:0021826	substrate-independent telencephalic tangential migration	5	0.263835264	0.0057	0.007745437
GO:0021830	interneuron migration from the subpallium to the cortex	5	0.263835264	0.0057	0.007745437
GO:0021843	substrate-independent telencephalic tangential interneuron migration	5	0.263835264	0.0057	0.007745437
GO:0031639	plasminogen activation	10	0.263783784	0.0122	0.014387602
GO:1903564	regulation of protein localization to cilium	5	0.263783784	0.03	0.032068098
GO:1903034	regulation of response to wounding	83	0.263732924	0.0081	0.010256567
GO:0030199	collagen fibril organization	28	0.263715757	0.01	0.012232246
GO:0006865	amino acid transport	61	0.263649598	0.0041	0.005981983
GO:0006684	sphingomyelin metabolic process	8	0.263610039	0.0415	0.043328883
GO:0031063	regulation of histone deacetylation	15	0.263543544	0.0027	0.004491543
GO:0006122	mitochondrial electron transport, ubiquinol to cytochrome c	11	0.263531064	0.026	0.02809393
GO:0046884	follicle-stimulating hormone secretion	5	0.263526384	0.0349	0.036866849
GO:0002068	glandular epithelial cell development	11	0.263507664	0.0011	0.002610912
GO:0050690	regulation of defense response to virus by virus	15	0.263423423	0.0169	0.019147324
GO:0097094	craniofacial suture morphogenesis	7	0.263394006	0.0126	0.014782732
GO:0060191	regulation of lipase activity	47	0.263369753	0.001	0.002498236
GO:0009201	ribonucleoside triphosphate biosynthetic process	38	0.263320463	0.0086	0.010769857
GO:0051056	regulation of small GTPase mediated signal transduction	171	0.263308421	0.0027	0.004491543
GO:0035587	purinergic receptor signaling pathway	16	0.263304376	0.0018	0.003459409
GO:0072224	metanephric glomerulus development	9	0.263177463	0.0003	0.001720882
GO:0000271	polysaccharide biosynthetic process	35	0.263136606	0.0004	0.002007244
GO:0052428	modification by host of symbiont molecular function	7	0.263136606	0.0112	0.013379119
GO:0048663	neuron fate commitment	27	0.263091663	0.0044	0.006304227
GO:0035640	exploration behavior	9	0.263091663	0.0001	0.000877824
GO:0034110	regulation of homotypic cell-cell adhesion	12	0.263041613	0.0174	0.019643968
GO:0034393	positive regulation of smooth muscle cell apoptotic process	7	0.263026292	0.0081	0.010256567
GO:0086065	cell communication involved in cardiac conduction	20	0.262985843	0.0106	0.012825859
GO:0043517	positive regulation of DNA damage response, signal transduction by p53 class mediator	5	0.262960103	0.0382	0.040087041
GO:0044264	cellular polysaccharide metabolic process	52	0.262850213	0.0006	0.002177563
GO:0007411	axon guidance	90	0.262845703	0.0007	0.002248538
GO:0097485	neuron projection guidance	90	0.262845703	0.0007	0.002248538
GO:1900746	regulation of vascular endothelial growth factor signaling pathway	10	0.262779923	0.0094	0.011616482
GO:1902547	regulation of cellular response to vascular endothelial growth factor stimulus	10	0.262779923	0.0094	0.011616482
GO:0048679	regulation of axon regeneration	11	0.262758863	0.0163	0.018559925
GO:0015980	energy derivation by oxidation of organic compounds	183	0.262736741	0.0059	0.007964563
GO:0060263	regulation of respiratory burst	7	0.26273212	0.0061	0.008182551
GO:1901077	regulation of relaxation of muscle	5	0.262651223	0.0017	0.003334595
GO:0086011	membrane repolarization during action potential	13	0.262627463	0.0021	0.003804235
GO:0006782	protoporphyrinogen IX biosynthetic process	5	0.262599743	0.0344	0.036368812
GO:0048268	clathrin coat assembly	9	0.262548263	0.0169	0.019147324
GO:0021953	central nervous system neuron differentiation	73	0.262537684	0.0003	0.001720882
GO:0061450	trophoblast cell migration	7	0.262511491	0.0015	0.003088691
GO:1901163	regulation of trophoblast cell migration	7	0.262511491	0.0015	0.003088691
GO:0006919	activation of cysteine-type endopeptidase activity involved in apoptotic process	49	0.262464213	0.0121	0.014285532
GO:0048011	neurotrophin TRK receptor signaling pathway	14	0.262456334	0.0014	0.002975058

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0045600	positive regulation of fat cell differentiation	35	0.262401177	0.0014	0.002975058
GO:0003323	type B pancreatic cell development	8	0.262387387	0.0054	0.007432873
GO:0043266	regulation of potassium ion transport	40	0.262361647	0.0105	0.012724187
GO:0045684	positive regulation of epidermis development	17	0.262336286	0.0005	0.002177563
GO:0036148	phosphatidylglycerol acyl-chain remodeling	6	0.262333762	0.0109	0.013101792
GO:0086064	cell communication by electrical coupling involved in cardiac conduction	8	0.262323037	0.0388	0.040696577
GO:2001135	regulation of endocytic recycling	9	0.262319462	0.013	0.015198863
GO:0032925	regulation of activin receptor signaling pathway	10	0.262290862	0.001	0.002498236
GO:0010635	regulation of mitochondrial fusion	6	0.262162162	0.0021	0.003804235
GO:0034394	protein localization to cell surface	33	0.262142662	0.0012	0.002741075
GO:0060998	regulation of dendritic spine development	22	0.262080262	0.0014	0.002975058
GO:0036151	phosphatidylcholine acyl-chain remodeling	13	0.262033462	0.0097	0.011922488
GO:0003231	cardiac ventricle development	73	0.261959415	0.0016	0.003223775
GO:0046655	folic acid metabolic process	14	0.261941533	0.0081	0.010256567
GO:1901264	carbohydrate derivative transport	39	0.261934462	0.0172	0.019442284
GO:0090174	organelle membrane fusion	38	0.261925083	0.0206	0.022756769
GO:2000008	regulation of protein localization to cell surface	19	0.261721872	0.0041	0.005981983
GO:0032965	regulation of collagen biosynthetic process	19	0.261708325	0.0118	0.013977955
GO:0046578	regulation of Ras protein signal transduction	107	0.261694271	0.0039	0.005778819
GO:0016446	somatic hypermutation of immunoglobulin genes	5	0.261673102	0.0039	0.005778819
GO:0071475	cellular hyperosmotic salinity response	5	0.261673102	0.0061	0.008182551
GO:0008209	androgen metabolic process	18	0.261661662	0.0152	0.017453982
GO:0097011	cellular response to granulocyte macrophage colony-stimulating factor stimulus	5	0.261621622	0.0062	0.008281828
GO:0097012	response to granulocyte macrophage colony-stimulating factor	5	0.261621622	0.0062	0.008281828
GO:0070977	bone maturation	9	0.261575862	0.0077	0.009887588
GO:0051496	positive regulation of stress fiber assembly	26	0.261469161	0.0093	0.011528671
GO:0019674	NAD metabolic process	40	0.261389961	0.0017	0.003334595
GO:0035270	endocrine system development	61	0.261299238	0.0035	0.005358035
GO:0038179	neurotrophin signaling pathway	17	0.261276402	0.0012	0.002741075
GO:1901016	regulation of potassium ion transmembrane transporter activity	20	0.261274131	0.0211	0.023264758
GO:1905168	positive regulation of double-strand break repair via homologous recombination	6	0.261261261	0.0171	0.01934984
GO:0009145	purine nucleoside triphosphate biosynthetic process	37	0.261233434	0.008	0.010168329
GO:0060389	pathway-restricted SMAD protein phosphorylation	30	0.261226941	0.0068	0.008946408
GO:0046580	negative regulation of Ras protein signal transduction	23	0.261171731	0.0055	0.007544447
GO:0090559	regulation of membrane permeability	52	0.261157311	0.0128	0.014984276
GO:0040036	regulation of fibroblast growth factor receptor signaling pathway	11	0.261120861	0.0061	0.008182551
GO:0051043	regulation of membrane protein ectodomain proteolysis	15	0.261106821	0.0092	0.011424708
GO:0010862	positive regulation of pathway-restricted SMAD protein phosphorylation	19	0.261098693	0.0058	0.007856196
GO:0001893	maternal placenta development	16	0.261003861	0.0031	0.004916949
GO:0030038	contractile actin filament bundle assembly	51	0.260968532	0.0016	0.003223775
GO:0043149	stress fiber assembly	51	0.260968532	0.0016	0.003223775
GO:1905288	vascular associated smooth muscle cell apoptotic process	6	0.260918061	0.0093	0.011528671
GO:1905459	regulation of vascular associated smooth muscle cell apoptotic process	6	0.260918061	0.0093	0.011528671
GO:0086013	membrane repolarization during cardiac muscle cell action potential	12	0.260875161	0.0009	0.002399874
GO:2000343	positive regulation of chemokine (C-X-C motif) ligand 2 production	6	0.260875161	0.0004	0.002007244
GO:0050805	negative regulation of synaptic transmission	29	0.260861847	0.0032	0.005044175
GO:0030947	regulation of vascular endothelial growth factor receptor signaling pathway	18	0.260846561	0.0244	0.02650438
GO:0046784	viral mRNA export from host cell nucleus	6	0.260746461	0.0028	0.004605006
GO:1990126	retrograde transport, endosome to plasma membrane	15	0.260729301	0.0019	0.003579279
GO:0048799	animal organ maturation	10	0.260617761	0.0094	0.011616482
GO:0060732	positive regulation of inositol phosphate biosynthetic process	6	0.260617761	0.0008	0.002313249
GO:0086009	membrane repolarization	21	0.260599375	0.0038	0.005666214
GO:2000641	regulation of early endosome to late endosome transport	10	0.260540541	0.0186	0.020774238
GO:0033169	histone H3-K9 demethylation	7	0.260415518	0.026	0.02809393
GO:0010867	positive regulation of triglyceride biosynthetic process	12	0.26038181	0.0006	0.002177563
GO:0002209	behavioral defense response	17	0.260292225	< 0.001	< 0.001
GO:0035305	negative regulation of dephosphorylation	57	0.260159408	0.0003	0.001720882
GO:0098815	modulation of excitatory postsynaptic potential	7	0.260121346	0.0015	0.003088691
GO:0055026	negative regulation of cardiac muscle tissue development	20	0.26009009	0.0114	0.01358747
GO:0010764	negative regulation of fibroblast migration	6	0.26006006	0.001	0.002498236
GO:1902692	regulation of neuroblast proliferation	17	0.260049966	0.0011	0.002610912
GO:0044801	single-organism membrane fusion	59	0.25997426	0.015	0.017255415
GO:0035036	sperm-egg recognition	21	0.259949746	0.001	0.002498236
GO:0051899	membrane depolarization	33	0.25993526	0.0168	0.019054351
GO:1990253	cellular response to leucine starvation	5	0.25992278	< 0.001	< 0.001
GO:0032885	regulation of polysaccharide biosynthetic process	20	0.25990991	0.0032	0.005044175
GO:0070873	regulation of glycogen metabolic process	21	0.259900717	0.0049	0.006860215
GO:0003352	regulation of cilium movement	8	0.259749035	< 0.001	< 0.001
GO:0001573	ganglioside metabolic process	11	0.25974026	0.0026	0.004377754
GO:0007157	heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	14	0.259735245	0.0037	0.005561344
GO:2000291	regulation of myoblast proliferation	6	0.25967396	0.0381	0.040008453
GO:0051648	vesicle localization	132	0.25965251	0.0023	0.004032435
GO:0010923	negative regulation of phosphatase activity	54	0.259640593	0.0002	0.001341684
GO:0034315	regulation of Arp2/3 complex-mediated actin nucleation	6	0.25963106	0.039	0.040872718
GO:0021511	spinal cord patterning	14	0.259624931	0.0074	0.009581512
GO:0021846	cell proliferation in forebrain	14	0.259624931	0.0008	0.002313249
GO:0051447	negative regulation of meiotic cell cycle	6	0.25958816	0.0012	0.002741075
GO:0019043	establishment of viral latency	7	0.259533002	0.002	0.003693422
GO:0014733	regulation of skeletal muscle adaptation	5	0.25951094	0.0162	0.018465856
GO:0072378	blood coagulation, fibrin clot formation	12	0.259459459	0.0218	0.023945433
GO:0071804	cellular potassium ion transport	51	0.259449365	0.0123	0.014492124
GO:0071805	potassium ion transmembrane transport	51	0.259449365	0.0123	0.014492124
GO:0002832	negative regulation of response to biotic stimulus	34	0.259444318	0.0091	0.011322589

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0060986	endocrine hormone secretion	30	0.259433719	0.0017	0.003334595
GO:0006906	vesicle fusion	36	0.259416559	0.0229	0.025020007
GO:1904181	positive regulation of membrane depolarization	8	0.259395109	0.0443	0.046018566
GO:0046777	protein autophosphorylation	107	0.259372858	0.0009	0.002399874
GO:0021903	rostrocaudal neural tube patterning	5	0.259356499	0.0005	0.002177563
GO:1902476	chloride transmembrane transport	31	0.259343214	0.0023	0.004032435
GO:0060384	innervation	9	0.259316459	0.0006	0.002177563
GO:0071392	cellular response to estradiol stimulus	20	0.259279279	0.0166	0.018864444
GO:0042446	hormone biosynthetic process	35	0.259275602	0.0103	0.012519912
GO:0010544	negative regulation of platelet activation	8	0.259266409	0.0077	0.009887588
GO:2000242	negative regulation of reproductive process	24	0.259255684	0.0013	0.002859821
GO:0002691	regulation of cellular extravasation	12	0.259244959	0.0015	0.003088691
GO:0015732	prostaglandin transport	5	0.259202059	0.0109	0.013101792
GO:0032306	regulation of prostaglandin secretion	5	0.259202059	0.0109	0.013101792
GO:0032310	prostaglandin secretion	5	0.259202059	0.0109	0.013101792
GO:0038066	p38MAPK cascade	26	0.259172359	0.0177	0.019919142
GO:0033692	cellular polysaccharide biosynthetic process	32	0.259137709	0.0003	0.001720882
GO:0090269	fibroblast growth factor production	6	0.259116259	0.0323	0.034307983
GO:0090270	regulation of fibroblast growth factor production	6	0.259116259	0.0323	0.034307983
GO:0006743	ubiquinone metabolic process	12	0.259094809	0.0093	0.011528671
GO:0006744	ubiquinone biosynthetic process	12	0.259094809	0.0093	0.011528671
GO:1901663	quinone biosynthetic process	12	0.259094809	0.0093	0.011528671
GO:0030011	maintenance of cell polarity	8	0.259073359	0.0253	0.027397944
GO:0046320	regulation of fatty acid oxidation	19	0.259066585	0.0004	0.002007244
GO:1901748	leukotriene D4 metabolic process	7	0.259018202	0.0074	0.009581512
GO:1901750	leukotriene D4 biosynthetic process	7	0.259018202	0.0074	0.009581512
GO:0060997	dendritic spine morphogenesis	15	0.259013299	0.0005	0.002177563
GO:0043552	positive regulation of phosphatidylinositol 3-kinase activity	23	0.259000616	< 0.001	< 0.001
GO:0061299	retina vasculature morphogenesis in camera-type eye	6	0.258987559	0.0025	0.004279479
GO:0021702	cerebellar Purkinje cell differentiation	6	0.258987559	0.0063	0.008390784
GO:0016331	morphogenesis of embryonic epithelium	79	0.258987016	0.0005	0.002177563
GO:0010984	regulation of lipoprotein particle clearance	11	0.258944659	0.0063	0.008390784
GO:0015844	monoamine transport	33	0.258921259	< 0.001	< 0.001
GO:0021987	cerebral cortex development	56	0.25886652	0.0008	0.002313249
GO:1904037	positive regulation of epithelial cell apoptotic process	19	0.258863375	0.0219	0.024051129
GO:0035637	multicellular organismal signaling	70	0.258845376	0.0083	0.010468217
GO:1900027	regulation of ruffle assembly	14	0.258779187	0.0172	0.019442284
GO:0015985	energy coupled proton transport, down electrochemical gradient	13	0.258667459	0.0349	0.036866849
GO:0015986	ATP synthesis coupled proton transport	13	0.258667459	0.0349	0.036866849
GO:0051279	regulation of release of sequestered calcium ion into cytosol	28	0.258604523	0.0012	0.002741075
GO:0014066	regulation of phosphatidylinositol 3-kinase signaling	61	0.258590206	0.0012	0.002741075
GO:0006678	glucosylceramide metabolic process	6	0.258515659	0.0098	0.012008345
GO:0055075	potassium ion homeostasis	8	0.258462033	0.0419	0.043717862
GO:0071340	skeletal muscle acetylcholine-gated channel clustering	8	0.258429858	0.001	0.002498236
GO:1903036	positive regulation of response to wounding	33	0.258390858	0.0077	0.009887588
GO:0019226	transmission of nerve impulse	25	0.25834749	0.0117	0.013882722
GO:2000628	regulation of miRNA metabolic process	6	0.258301158	0.0158	0.018074565
GO:0043117	positive regulation of vascular permeability	6	0.258301158	0.0242	0.02630058
GO:0019400	alditol metabolic process	14	0.258227615	0.0044	0.006304227
GO:0016255	attachment of GPI anchor to protein	5	0.258223938	0.0439	0.045625359
GO:0034643	establishment of mitochondrion localization, microtubule-mediated	9	0.258201058	0.0054	0.007432873
GO:0047497	mitochondrion transport along microtubule	9	0.258201058	0.0054	0.007432873
GO:0048593	camera-type eye morphogenesis	62	0.258076971	0.0062	0.008281828
GO:0007631	feeding behavior	45	0.258063778	0.0001	0.000877824
GO:0001974	blood vessel remodeling	27	0.258058058	0.016	0.018267288
GO:0014831	gastro-intestinal system smooth muscle contraction	6	0.258000858	0.0177	0.019919142
GO:1905146	lysosomal protein catabolic process	10	0.257966538	0.041	0.042848967
GO:0043652	engulfment of apoptotic cell	5	0.257966538	0.0187	0.020874952
GO:0046902	regulation of mitochondrial membrane permeability	46	0.257965419	0.0134	0.015626386
GO:0060914	heart formation	14	0.257951829	0.0046	0.006532041
GO:0072087	renal vesicle development	11	0.257915058	0.0037	0.005561344
GO:2000316	regulation of T-helper 17 type immune response	7	0.257915058	0.0046	0.006532041
GO:0061041	regulation of wound healing	71	0.257886055	0.0097	0.011922488
GO:0009235	cobalamin metabolic process	11	0.257844858	0.0149	0.017165166
GO:0050913	sensory perception of bitter taste	15	0.257691978	0.0078	0.009981807
GO:0005977	glycogen metabolic process	44	0.257628408	0.0007	0.002248538
GO:0006073	cellular glucan metabolic process	44	0.257628408	0.0007	0.002248538
GO:0044042	glucan metabolic process	44	0.257628408	0.0007	0.002248538
GO:0050808	synapse organization	123	0.257576043	0.0005	0.002177563
GO:0008544	epidermis development	195	0.257571858	0.0034	0.005263104
GO:0048143	astrocyte activation	8	0.257561133	0.045	0.046730487
GO:0034721	histone H3-K4 demethylation, trimethyl-H3-K4-specific	5	0.257503218	0.0252	0.027298929
GO:0045989	positive regulation of striated muscle contraction	7	0.2574738	0.0061	0.008182551
GO:0002634	regulation of germinal center formation	6	0.257443157	0.0156	0.017858595
GO:0006564	L-serine biosynthetic process	7	0.257400257	0.008	0.010168329
GO:0002544	chronic inflammatory response	8	0.257368082	0.0117	0.013882722
GO:1901894	regulation of calcium-transporting ATPase activity	5	0.257297297	0.0306	0.032676575
GO:0021762	substantia nigra development	32	0.25725547	0.0046	0.006532041
GO:0014033	neural crest cell differentiation	36	0.257250107	0.0009	0.002399874
GO:0008347	glial cell migration	26	0.257241857	0.0007	0.002248538
GO:0071711	basement membrane organization	15	0.257211497	0.0138	0.016031243
GO:1904353	regulation of telomere capping	13	0.257202257	0.0011	0.002610912
GO:0048017	inositol lipid-mediated signaling	87	0.257196112	0.0011	0.002610912

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0042791	5S class rRNA transcription from RNA polymerase III type 1 promoter	5	0.257194337	0.0338	0.035793852
GO:0042797	tRNA transcription from RNA polymerase III promoter	5	0.257194337	0.0338	0.035793852
GO:0003205	cardiac chamber development	89	0.257163102	0.0012	0.002741075
GO:0060563	neuroepithelial cell differentiation	30	0.257134277	0.0001	0.000877824
GO:0010310	regulation of hydrogen peroxide metabolic process	7	0.257069314	0.0105	0.012724187
GO:0098901	regulation of cardiac muscle cell action potential	10	0.257039897	0.0216	0.023746214
GO:0006766	vitamin metabolic process	74	0.256989808	0.0123	0.014492124
GO:0035336	long-chain fatty-acyl-CoA metabolic process	12	0.256971257	0.011	0.013192134
GO:0070293	renal absorption	11	0.256955657	0.0344	0.036368812
GO:0030048	actin filament-based movement	65	0.256893377	0.0011	0.002610912
GO:0032410	negative regulation of transporter activity	30	0.256876877	0.001	0.002498236
GO:0007096	regulation of exit from mitosis	12	0.256864007	0.0191	0.021280472
GO:0031650	regulation of heat generation	8	0.256788932	0.0127	0.014886353
GO:0060124	positive regulation of growth hormone secretion	6	0.256756757	0.0035	0.005358035
GO:0035023	regulation of Rho protein signal transduction	67	0.256747152	0.0036	0.005475609
GO:0045981	positive regulation of nucleotide metabolic process	38	0.256743209	0.0084	0.010571327
GO:1900544	positive regulation of purine nucleotide metabolic process	38	0.256743209	0.0084	0.010571327
GO:0048015	phosphatidylinositol-mediated signaling	86	0.25672982	0.0009	0.002399874
GO:0097178	ruffle assembly	21	0.2567016	0.009	0.011215682
GO:0055117	regulation of cardiac muscle contraction	30	0.256679537	0.0011	0.002610912
GO:0045740	positive regulation of DNA replication	19	0.256628057	0.0072	0.009362497
GO:2001267	regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway	11	0.256581257	0.0059	0.007964563
GO:0070828	heterochromatin organization	11	0.256534457	0.0097	0.011922488
GO:0050795	regulation of behavior	31	0.256486902	0.0003	0.001720882
GO:0007613	memory	40	0.256486486	0.0022	0.003910907
GO:0090303	positive regulation of wound healing	28	0.256471778	0.0085	0.010671887
GO:0048521	negative regulation of behavior	10	0.256370656	0.0001	0.000877824
GO:0060339	negative regulation of type I interferon-mediated signaling pathway	6	0.256284856	0.0015	0.003088691
GO:0018243	protein O-linked glycosylation via threonine	5	0.256267696	0.0001	0.000877824
GO:1901889	negative regulation of cell junction assembly	16	0.256241956	0.0126	0.014782732
GO:0018095	protein polyglutamylation	9	0.256170456	0.001	0.002498236
GO:2000651	positive regulation of sodium ion transmembrane transporter activity	6	0.256156156	0.0163	0.018559925
GO:0061337	cardiac conduction	47	0.25609135	0.0094	0.011616482
GO:0034762	regulation of transmembrane transport	181	0.256077704	0.0041	0.005981983
GO:0034765	regulation of ion transmembrane transport	170	0.256058748	0.0046	0.006532041
GO:0072538	T-helper 17 type immune response	10	0.256036036	0.0159	0.01817591
GO:0051205	protein insertion into membrane	25	0.256	0.005	0.006974174
GO:0021536	diencephalon development	36	0.255998856	0.0005	0.002177563
GO:0006857	oligopeptide transport	6	0.255984556	0.0059	0.007964563
GO:0046620	regulation of organ growth	54	0.255970256	0.0043	0.006204188
GO:0045913	positive regulation of carbohydrate metabolic process	41	0.255937471	0.0016	0.003223775
GO:0009125	nucleoside monophosphate catabolic process	5	0.255907336	0.0022	0.003910907
GO:0015919	peroxisomal membrane transport	5	0.255907336	0.0079	0.010077402
GO:0045046	protein import into peroxisome membrane	5	0.255907336	0.0079	0.010077402
GO:0010714	positive regulation of collagen metabolic process	14	0.25583747	0.0081	0.010256567
GO:0032967	positive regulation of collagen biosynthetic process	14	0.25583747	0.0081	0.010256567
GO:0044253	positive regulation of multicellular organismal metabolic process	14	0.25583747	0.0081	0.010256567
GO:0031640	killing of cells of other organism	21	0.255831342	0.0237	0.025818821
GO:0044364	disruption of cells of other organism	21	0.255831342	0.0237	0.025818821
GO:0086003	cardiac muscle cell contraction	29	0.255820352	0.0059	0.007964563
GO:0035428	hexose transmembrane transport	12	0.255770056	0.0107	0.012912536
GO:1904659	glucose transmembrane transport	12	0.255770056	0.0107	0.012912536
GO:0095500	acetylcholine receptor signaling pathway	11	0.255692056	0.0216	0.023746214
GO:1903831	signal transduction involved in cellular response to ammonium ion	11	0.255692056	0.0216	0.023746214
GO:1905144	response to acetylcholine	11	0.255692056	0.0216	0.023746214
GO:1905145	cellular response to acetylcholine	11	0.255692056	0.0216	0.023746214
GO:0046434	organophosphate catabolic process	64	0.255678893	0.0083	0.010468217
GO:0046717	acid secretion	41	0.255629846	0.0041	0.005981983
GO:0046885	regulation of hormone biosynthetic process	9	0.255598456	0.0135	0.015731487
GO:1901526	positive regulation of macromitophagy	5	0.255598456	0.0199	0.022056122
GO:0042472	inner ear morphogenesis	43	0.255580497	0.0076	0.009790742
GO:0070141	response to UV-A	5	0.255392535	0.0338	0.035793852
GO:0033182	regulation of histone ubiquitination	7	0.255341055	0.0002	0.001341684
GO:0051955	regulation of amino acid transport	13	0.255321255	0.0056	0.007655255
GO:0035924	cellular response to vascular endothelial growth factor stimulus	35	0.255311638	0.0081	0.010256567
GO:0060397	JAK-STAT cascade involved in growth hormone signaling pathway	8	0.25530888	0.0003	0.001720882
GO:0005978	glycogen biosynthetic process	26	0.255281655	0.0005	0.002177563
GO:0009250	glucan biosynthetic process	26	0.255281655	0.0005	0.002177563
GO:0042535	positive regulation of tumor necrosis factor biosynthetic process	11	0.255247455	0.0265	0.028585731
GO:0021781	glial cell fate commitment	11	0.255060255	0.001	0.002498236
GO:0018210	peptidyl-threonine modification	43	0.255011822	0.0009	0.002399874
GO:1903169	regulation of calcium ion transmembrane transport	52	0.255009405	0.0026	0.004377754
GO:0010574	regulation of vascular endothelial growth factor production	17	0.25488682	0.0139	0.016141527
GO:0009414	response to water deprivation	5	0.254877735	0.0004	0.002007244
GO:0018107	peptidyl-threonine phosphorylation	38	0.254846576	0.0033	0.005149584
GO:0043270	positive regulation of ion transport	118	0.254841524	0.0049	0.006860215
GO:0046513	ceramide biosynthetic process	35	0.254833609	0.0156	0.017858595
GO:0060159	regulation of dopamine receptor signaling pathway	8	0.254826255	0.0039	0.005778819
GO:1903727	positive regulation of phospholipid metabolic process	30	0.254817675	0.0005	0.002177563
GO:0050885	neuromuscular process controlling balance	24	0.25481553	0.0013	0.002859821
GO:0030916	otic vesicle formation	5	0.254774775	0.0044	0.006304227
GO:0070988	demethylation	35	0.254752712	0.0034	0.005263104
GO:0043586	tongue development	7	0.254752712	0.0039	0.005778819

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0018958	phenol-containing compound metabolic process	46	0.254747916	< 0.001	< 0.001
GO:0010522	regulation of calcium ion transport into cytosol	38	0.254744971	0.0039	0.005778819
GO:0043525	positive regulation of neuron apoptotic process	29	0.254719744	0.0257	0.027793331
GO:0010470	regulation of gastrulation	20	0.254710425	0.0019	0.003579279
GO:0032463	negative regulation of protein homooligomerization	8	0.25453668	0.0073	0.009463568
GO:1902187	negative regulation of viral release from host cell	12	0.254525955	0.015	0.017255415
GO:0006531	aspartate metabolic process	6	0.254525955	0.0152	0.017453982
GO:0061437	renal system vasculature development	17	0.254493149	0.0008	0.002313249
GO:0061440	kidney vasculature development	17	0.254493149	0.0008	0.002313249
GO:0002088	lens development in camera-type eye	40	0.254465894	0.0007	0.002248538
GO:0044359	modulation of molecular function in other organism	8	0.254440154	0.0181	0.020286898
GO:0044362	negative regulation of molecular function in other organism	8	0.254440154	0.0181	0.020286898
GO:0052204	negative regulation of molecular function in other organism involved in symbiotic interaction	8	0.254440154	0.0181	0.020286898
GO:0052205	modulation of molecular function in other organism involved in symbiotic interaction	8	0.254440154	0.0181	0.020286898
GO:0002031	G-protein coupled receptor internalization	6	0.254440154	0.0132	0.015415723
GO:0006658	phosphatidylserine metabolic process	18	0.254397254	0.0329	0.034916187
GO:0001710	mesodermal cell fate commitment	10	0.254362934	< 0.001	< 0.001
GO:0035511	oxidative DNA demethylation	5	0.254362934	0.0167	0.018954426
GO:0015871	choline transport	5	0.254362934	0.0422	0.043980474
GO:0048167	regulation of synaptic plasticity	46	0.254333837	0.0056	0.007655255
GO:0032350	regulation of hormone metabolic process	17	0.254326596	0.0183	0.020489441
GO:0014065	phosphatidylinositol 3-kinase signaling	71	0.254282451	0.0014	0.002975058
GO:0050806	positive regulation of synaptic transmission	50	0.254259974	0.0004	0.002007244
GO:0048702	embryonic neurocranium morphogenesis	5	0.254208494	0.0079	0.010077402
GO:0060411	cardiac septum morphogenesis	43	0.254197719	0.0031	0.004916949
GO:0031649	heat generation	10	0.254182754	0.0168	0.019054351
GO:0009206	purine ribonucleoside triphosphate biosynthetic process	36	0.254168454	0.011	0.013192134
GO:0060343	trabecula formation	11	0.254077454	0.0009	0.002399874
GO:0061384	heart trabecula morphogenesis	23	0.254054054	0.0021	0.003804235
GO:0000737	DNA catabolic process, endonucleolytic	20	0.254015444	0.0092	0.011424708
GO:0007566	embryo implantation	28	0.25394374	0.0042	0.006097175
GO:0043551	regulation of phosphatidylinositol 3-kinase activity	32	0.253925354	0.0011	0.002610912
GO:0090043	regulation of tubulin deacetylation	6	0.253925354	0.0175	0.019742875
GO:0043588	skin development	177	0.253808288	0.0085	0.010671887
GO:0045109	intermediate filament organization	12	0.253796654	0.0174	0.019643968
GO:0009113	purine nucleobase biosynthetic process	5	0.253796654	0.0429	0.044680781
GO:0030540	female genitalia development	9	0.253682254	0.027	0.029066047
GO:0042391	regulation of membrane potential	137	0.253582467	0.0063	0.008390784
GO:0002826	negative regulation of T-helper 1 type immune response	5	0.253539254	0.0002	0.001341684
GO:0072132	mesenchyme morphogenesis	36	0.253503504	0.0062	0.008281828
GO:2001026	regulation of endothelial cell chemotaxis	14	0.253484096	0.0008	0.002313249
GO:0048311	mitochondrion distribution	5	0.253436293	0.0453	0.047003728
GO:0045022	early endosome to late endosome transport	27	0.253396253	0.0281	0.030173766
GO:0035999	tetrahydrofolate interconversion	7	0.253392168	0.0011	0.002610912
GO:0061001	regulation of dendritic spine morphogenesis	11	0.253352053	0.0002	0.001341684
GO:0061036	positive regulation of cartilage development	17	0.253296994	< 0.001	< 0.001
GO:0034163	regulation of toll-like receptor 9 signaling pathway	6	0.253281853	0.0019	0.003579279
GO:0098927	vesicle-mediated transport between endosomal compartments	29	0.253264102	0.0289	0.03094937
GO:0010457	centriole-centriole cohesion	6	0.253238953	0.0137	0.015920879
GO:1900745	positive regulation of p38MAPK cascade	16	0.253217503	0.0399	0.04174043
GO:0046854	phosphatidylinositol phosphorylation	13	0.253182853	0.0147	0.016962357
GO:0006898	receptor-mediated endocytosis	137	0.253176639	0.0082	0.010366713
GO:0031623	receptor internalization	48	0.253126341	0.0068	0.008946408
GO:0010573	vascular endothelial growth factor production	18	0.253067353	0.0081	0.010256567
GO:0051457	maintenance of protein location in nucleus	14	0.253061224	0.0036	0.005475609
GO:0007076	mitotic chromosome condensation	9	0.253053053	0.0075	0.00968541
GO:0046475	glycerophospholipid catabolic process	14	0.252969296	0.0131	0.015312968
GO:0070252	actin-mediated cell contraction	52	0.252955153	0.0015	0.003088691
GO:1905245	regulation of aspartic-type peptidase activity	7	0.252877367	0.0204	0.022555378
GO:0043647	inositol phosphate metabolic process	39	0.252846253	0.0052	0.007215241
GO:0010882	regulation of cardiac muscle contraction by calcium ion signaling	8	0.252767053	0.005	0.006974174
GO:0044539	long-chain fatty acid import	6	0.252767053	0.0459	0.047595298
GO:0050890	cognition	117	0.252685653	0.0024	0.004156304
GO:0050803	regulation of synapse structure or activity	61	0.25267	0.0003	0.001720882
GO:2001169	regulation of ATP biosynthetic process	11	0.252533053	0.0039	0.005778819
GO:0042219	cellular modified amino acid catabolic process	13	0.252430452	0.0082	0.010366713
GO:1903010	regulation of bone development	9	0.252395252	0.0032	0.005044175
GO:0072718	response to cisplatin	8	0.252348777	0.0241	0.026209778
GO:1901642	nucleoside transmembrane transport	6	0.252295152	0.0461	0.047779362
GO:0072216	positive regulation of metanephros development	7	0.252252252	0.0273	0.029359247
GO:0031018	endocrine pancreas development	23	0.252241061	0.0014	0.002975058
GO:0030317	flagellated sperm motility	27	0.252214119	< 0.001	< 0.001
GO:0097722	sperm motility	27	0.252214119	< 0.001	< 0.001
GO:0010107	potassium ion import	11	0.252182052	0.0364	0.038343339
GO:1903651	positive regulation of cytoplasmic transport	10	0.252149292	0.0054	0.007432873
GO:0098974	postsynaptic actin cytoskeleton organization	5	0.252149292	0.001	0.002498236
GO:0042415	norepinephrine metabolic process	7	0.252105166	0.0013	0.002859821
GO:1900046	regulation of hemostasis	40	0.252091377	0.0079	0.010077402
GO:0050807	regulation of synapse organization	60	0.251934792	0.0002	0.001341684
GO:1902307	positive regulation of sodium ion transmembrane transport	10	0.251891892	0.0067	0.008845888
GO:2000341	regulation of chemokine (C-X-C motif) ligand 2 production	8	0.251833977	0.0003	0.001720882
GO:0005979	regulation of glycogen biosynthetic process	17	0.251813158	0.0018	0.003459409
GO:0010962	regulation of glucan biosynthetic process	17	0.251813158	0.0018	0.003459409

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0030511	positive regulation of transforming growth factor beta receptor signaling pathway	16	0.251801802	0.0019	0.003579279
GO:1903846	positive regulation of cellular response to transforming growth factor beta stimulus	16	0.251801802	0.0019	0.003579279
GO:0009134	nucleoside diphosphate catabolic process	5	0.251788932	0.011	0.013192134
GO:0009913	epidermal cell differentiation	141	0.251779439	0.008	0.010168329
GO:0010715	regulation of extracellular matrix disassembly	8	0.251769627	0.023	0.025116347
GO:0030854	positive regulation of granulocyte differentiation	5	0.251737452	0.001	0.002498236
GO:0043497	regulation of protein heterodimerization activity	6	0.251694552	0.0075	0.00968541
GO:0032753	positive regulation of interleukin-4 production	12	0.251694552	0.0025	0.004279479
GO:0046322	negative regulation of fatty acid oxidation	8	0.251640927	< 0.001	< 0.001
GO:0021513	spinal cord dorsal/ventral patterning	13	0.251519652	0.0072	0.009362497
GO:0014874	response to stimulus involved in regulation of muscle adaptation	8	0.251512227	0.0435	0.045246532
GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	45	0.251462891	0.0009	0.002399874
GO:0072350	tricarboxylic acid metabolic process	26	0.251460251	0.0124	0.014577606
GO:0015780	nucleotide-sugar transport	9	0.251365651	0.0144	0.016652368
GO:0015781	pyrimidine nucleotide-sugar transport	9	0.251365651	0.0144	0.016652368
GO:0099003	vesicle-mediated transport in synapse	50	0.251330759	0.0035	0.005358035
GO:0042362	fat-soluble vitamin biosynthetic process	8	0.251319176	0.0124	0.014577606
GO:0038007	netrin-activated signaling pathway	8	0.251319176	0.0455	0.047203565
GO:0009225	nucleotide-sugar metabolic process	21	0.25127168	0.0016	0.003223775
GO:0060911	cardiac cell fate commitment	5	0.251222651	0.0207	0.022863276
GO:0070254	mucus secretion	5	0.251119691	0.0007	0.002248538
GO:0050432	catecholamine secretion	20	0.250978121	< 0.001	< 0.001
GO:1904749	regulation of protein localization to nucleolus	7	0.250965251	0.0016	0.003223775
GO:0048483	autonomic nervous system development	22	0.250941851	0.0075	0.00968541
GO:0044130	negative regulation of growth of symbiont in host	5	0.250862291	0.0285	0.030556948
GO:0044146	negative regulation of growth of symbiont involved in interaction with host	5	0.250862291	0.0285	0.030556948
GO:0052173	response to defenses of other organism involved in symbiotic interaction	6	0.250793651	0.0361	0.038033609
GO:0052200	response to host defenses	6	0.250793651	0.0361	0.038033609
GO:0075136	response to host	6	0.250793651	0.0361	0.038033609
GO:0007611	learning or memory	96	0.25079097	0.0029	0.004714719
GO:0071526	semaphorin-plexin signaling pathway	14	0.250744622	0.003	0.004825593
GO:0002580	regulation of antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	5	0.250707851	0.0367	0.038621054
GO:0072044	collecting duct development	5	0.250501931	0.0002	0.001341684
GO:0006754	ATP biosynthetic process	30	0.25049335	0.011	0.013192134
GO:0001659	temperature homeostasis	20	0.25048906	0.0062	0.008281828
GO:0051307	meiotic chromosome separation	7	0.250487222	0.003	0.004825593
GO:0014047	glutamate secretion	10	0.25045045	0.0016	0.003223775
GO:0021794	thalamus development	8	0.2503861	0.061	0.008182551
GO:2001214	positive regulation of vasculogenesis	8	0.2503861	0.0191	0.021280472
GO:0000186	activation of MAPKK activity	26	0.25035145	0.004	0.005880507
GO:0009226	nucleotide-sugar biosynthetic process	14	0.25032175	0.0004	0.002007244
GO:0000132	establishment of mitotic spindle orientation	13	0.25031185	0.0073	0.009463568
GO:0032892	positive regulation of organic acid transport	15	0.25029601	0.0186	0.020774238
GO:0016101	diterpenoid metabolic process	46	0.250271389	0.0035	0.005358035
GO:0060037	pharyngeal system development	14	0.250174664	0.0038	0.005666214
GO:0099624	atrial cardiac muscle cell membrane repolarization	6	0.25010725	0.0026	0.004377754
GO:0048873	homeostasis of number of cells within a tissue	16	0.25006435	0.0144	0.016652368
GO:1903749	positive regulation of establishment of protein localization to mitochondrion	36	0.24993565	0.0037	0.005561344
GO:0039692	single stranded viral RNA replication via double stranded DNA intermediate	7	0.24993565	0.0135	0.015731487
GO:0034260	negative regulation of GTPase activity	29	0.249891271	0.0118	0.013977955
GO:1904350	regulation of protein catabolic process in the vacuole	9	0.24973545	0.0308	0.032862615
GO:0072012	glomerulus vasculature development	16	0.249726512	0.0006	0.002177563
GO:0048864	stem cell development	35	0.249648833	0.0005	0.002177563
GO:0001754	eye photoreceptor cell differentiation	20	0.2496139	0.0057	0.007745437
GO:1901881	positive regulation of protein depolymerization	10	0.24960103	0.0008	0.002313249
GO:0048813	dendrite morphogenesis	45	0.24950093	0.0038	0.005666214
GO:1901099	negative regulation of signal transduction in absence of ligand	19	0.249488586	0.013	0.015198863
GO:2001240	negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	19	0.249488586	0.013	0.015198863
GO:0050773	regulation of dendrite development	54	0.249478049	0.0089	0.011106266
GO:0035162	embryonic hemopoiesis	12	0.249442299	0.0151	0.01736105
GO:0002067	glandular epithelial cell differentiation	19	0.249244733	0.0047	0.006644432
GO:0035372	protein localization to microtubule	8	0.249227799	0.0018	0.003459409
GO:0007212	dopamine receptor signaling pathway	21	0.249163449	0.0006	0.002177563
GO:1904355	positive regulation of telomere capping	10	0.249009009	0.0029	0.004714719
GO:0090383	phagosome acidification	12	0.248991849	0.0185	0.020677043
GO:0008333	endosome to lysosome transport	33	0.248984049	0.0098	0.012008345
GO:0090153	regulation of sphingolipid biosynthetic process	12	0.248927499	0.0177	0.019919142
GO:1905038	regulation of membrane lipid metabolic process	12	0.248927499	0.0177	0.019919142
GO:2000303	regulation of ceramide biosynthetic process	12	0.248927499	0.0177	0.019919142
GO:0043653	mitochondrial fragmentation involved in apoptotic process	7	0.248906049	0.0078	0.009981807
GO:1904874	positive regulation of telomerase RNA localization to Cajal body	14	0.248887663	< 0.001	< 0.001
GO:0006590	thyroid hormone generation	6	0.248863149	0.0092	0.011424708
GO:0042403	thyroid hormone metabolic process	6	0.248863149	0.0092	0.011424708
GO:0006942	regulation of striated muscle contraction	37	0.248850395	0.0009	0.002399874
GO:0051937	catecholamine transport	27	0.248801182	< 0.001	< 0.001
GO:0015748	organophosphate ester transport	55	0.248732889	0.0137	0.015920879
GO:1990440	positive regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress	10	0.248648649	0.0236	0.025731873
GO:0006862	nucleotide transport	15	0.248614329	0.039	0.040872718
GO:0006813	potassium ion transport	73	0.248613388	0.0124	0.014577606
GO:1901524	regulation of macromitophagy	10	0.248597169	0.0196	0.021765255
GO:0051445	regulation of meiotic cell cycle	15	0.248597169	0.0113	0.013488462
GO:2001239	regulation of extrinsic apoptotic signaling pathway in absence of ligand	27	0.248562849	0.016	0.018267288

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0048857	neural nucleus development	41	0.2485482	0.0082	0.010366713
GO:0044110	growth involved in symbiotic interaction	6	0.248519949	0.0035	0.005358035
GO:0044116	growth of symbiont involved in interaction with host	6	0.248519949	0.0035	0.005358035
GO:0044117	growth of symbiont in host	6	0.248519949	0.0035	0.005358035
GO:0044126	regulation of growth of symbiont in host	6	0.248519949	0.0035	0.005358035
GO:0044144	modulation of growth of symbiont involved in interaction with host	6	0.248519949	0.0035	0.005358035
GO:0014072	response to isoquinoline alkaloid	19	0.248404796	< 0.001	< 0.001
GO:0043278	response to morphine	19	0.248404796	< 0.001	< 0.001
GO:0008037	cell recognition	57	0.248382217	0.0034	0.005263104
GO:0034219	carbohydrate transmembrane transport	15	0.248339768	0.0096	0.01183839
GO:0001782	B cell homeostasis	20	0.248288288	0.0054	0.007432873
GO:0060021	palate development	38	0.248188038	0.0005	0.002177563
GO:0001578	microtubule bundle formation	39	0.248160248	< 0.001	< 0.001
GO:0010518	positive regulation of phospholipase activity	28	0.248115462	0.0008	0.002313249
GO:0099563	modification of synaptic structure	8	0.248069498	0.0216	0.023746214
GO:0033631	cell-cell adhesion mediated by integrin	10	0.248056628	0.0056	0.007655255
GO:0060900	embryonic camera-type eye formation	7	0.248023534	0.0117	0.013882722
GO:0048557	embryonic digestive tract morphogenesis	7	0.248023534	0.0312	0.033261559
GO:2000648	positive regulation of stem cell proliferation	22	0.247864748	0.0015	0.003088691
GO:0019751	polyol metabolic process	68	0.247796957	0.0076	0.009790742
GO:1900077	negative regulation of cellular response to insulin stimulus	17	0.247785601	0.0031	0.004916949
GO:0006646	phosphatidylethanolamine biosynthetic process	10	0.247747748	0.0019	0.003579279
GO:0050804	modulation of synaptic transmission	133	0.247733233	0.0014	0.002975058
GO:0030949	positive regulation of vascular endothelial growth factor receptor signaling pathway	8	0.247715573	0.0285	0.030556948
GO:0007339	binding of sperm to zona pellucida	17	0.247679612	0.0003	0.001720882
GO:0002090	regulation of receptor internalization	20	0.247541828	0.0067	0.008845888
GO:0007405	neuroblast proliferation	32	0.247369691	0.0015	0.003088691
GO:0060600	dichotomous subdivision of an epithelial terminal unit	5	0.247361647	0.0017	0.003334595
GO:0045773	positive regulation of axon extension	21	0.24734939	0.0244	0.02650438
GO:0050433	regulation of catecholamine secretion	18	0.247290147	< 0.001	< 0.001
GO:0006020	inositol metabolic process	7	0.247288104	0.0335	0.03551156
GO:0032633	interleukin-4 production	17	0.247225377	0.0098	0.012008345
GO:0097194	execution phase of apoptosis	43	0.247200024	0.0037	0.005561344
GO:0006720	isoprenoid metabolic process	64	0.247180663	0.0019	0.003579279
GO:0072539	T-helper 17 cell differentiation	9	0.247132847	0.0152	0.017453982
GO:0045722	positive regulation of gluconeogenesis	11	0.247127647	0.0014	0.002975058
GO:1900744	regulation of p38MAPK cascade	22	0.246998947	0.021	0.023166522
GO:0072015	glomerular visceral epithelial cell development	7	0.246993933	0.0204	0.022555378
GO:0072310	glomerular epithelial cell development	7	0.246993933	0.0204	0.022555378
GO:0050820	positive regulation of coagulation	13	0.246965647	0.0099	0.012121556
GO:0031268	pseudopodium organization	8	0.246943372	0.018	0.020203241
GO:0031269	pseudopodium assembly	8	0.246943372	0.018	0.020203241
GO:0060706	cell differentiation involved in embryonic placenta development	13	0.246926047	0.0039	0.005778819
GO:0030193	regulation of blood coagulation	39	0.246912847	0.0079	0.010077402
GO:0018065	protein-cofactor linkage	10	0.246898327	0.0003	0.001720882
GO:0045006	DNA deamination	5	0.246846847	0.0013	0.002859821
GO:0014032	neural crest cell development	32	0.246742278	0.0018	0.003459409
GO:0036158	outer dynein arm assembly	6	0.246675247	0.0015	0.003088691
GO:0046596	regulation of viral entry into host cell	23	0.246656594	0.0437	0.045424906
GO:0000098	sulfur amino acid catabolic process	9	0.246618047	0.0011	0.002610912
GO:0046621	negative regulation of organ growth	19	0.246589447	0.0141	0.016361854
GO:0006101	citrate metabolic process	24	0.246589447	0.0265	0.028585731
GO:0006112	energy reserve metabolic process	52	0.246554797	0.0007	0.002248538
GO:1902742	apoptotic process involved in development	23	0.246499916	0.0043	0.006204188
GO:0048704	embryonic skeletal system morphogenesis	41	0.246451329	0.0022	0.003910907
GO:0010517	regulation of phospholipase activity	33	0.246394446	0.0014	0.002975058
GO:0006023	aminoglycan biosynthetic process	55	0.246369486	0.0022	0.003910907
GO:0040001	establishment of mitotic spindle localization	15	0.246314886	0.0077	0.009887588
GO:0015865	purine nucleotide transport	11	0.246308646	0.0323	0.034307983
GO:0015868	purine ribonucleotide transport	11	0.246308646	0.0323	0.034307983
GO:0045823	positive regulation of heart contraction	16	0.246235521	0.0096	0.01183839
GO:1902369	negative regulation of RNA catabolic process	8	0.246235521	< 0.001	< 0.001
GO:1902373	negative regulation of mRNA catabolic process	8	0.246235521	< 0.001	< 0.001
GO:0048284	organelle fusion	82	0.246146844	0.0215	0.023664853
GO:0050818	regulation of coagulation	42	0.246111418	0.0102	0.012424427
GO:0030166	proteoglycan biosynthetic process	30	0.246048906	0.0168	0.019054351
GO:0060068	vagina development	6	0.245988846	0.0286	0.030648697
GO:0045091	regulation of single stranded viral RNA replication via double stranded DNA intermediate	6	0.245860146	0.0165	0.018764186
GO:0023058	adaptation of signaling pathway	9	0.245817246	0.024	0.026109935
GO:0072672	neutrophil extravasation	6	0.245817246	0.0218	0.023945433
GO:0038084	vascular endothelial growth factor signaling pathway	23	0.245705333	0.0117	0.013882722
GO:0030104	water homeostasis	25	0.245662806	0.001	0.002498236
GO:0006536	glutamate metabolic process	21	0.24558436	0.0002	0.001341684
GO:0048278	vesicle docking	19	0.245478561	0.0056	0.007655255
GO:0014854	response to inactivity	8	0.24546332	0.0319	0.033911376
GO:0044320	cellular response to leptin stimulus	10	0.245456885	0.0004	0.002007244
GO:0097479	synaptic vesicle localization	47	0.245335305	0.0039	0.005778819
GO:0090231	regulation of spindle checkpoint	10	0.245302445	< 0.001	< 0.001
GO:0090266	regulation of mitotic cell cycle spindle assembly checkpoint	10	0.245302445	< 0.001	< 0.001
GO:1903504	regulation of mitotic spindle checkpoint	10	0.245302445	< 0.001	< 0.001
GO:0034214	protein hexamerization	12	0.245045045	0.0101	0.012328539
GO:0015740	C4-dicarboxylate transport	9	0.245016445	0.0082	0.010366713
GO:0010644	cell communication by electrical coupling	10	0.244942085	0.0464	0.04806684

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:1904645	response to beta-amyloid	18	0.244916345	0.0311	0.033166048
GO:2000319	regulation of T-helper 17 cell differentiation	6	0.244873445	0.0022	0.003910907
GO:0042551	neuron maturation	24	0.244830545	0.0172	0.019442284
GO:0048286	lung alveolus development	22	0.244822745	0.0034	0.005263104
GO:0043011	myeloid dendritic cell differentiation	11	0.244764245	0.0034	0.005263104
GO:1902959	regulation of aspartic-type endopeptidase activity involved in amyloid precursor protein catabolic process	6	0.244744745	0.0178	0.020021073
GO:0006688	glycosphingolipid biosynthetic process	12	0.244723295	0.0119	0.014078095
GO:0030397	membrane disassembly	10	0.244684685	0.0026	0.004377754
GO:0051081	nuclear envelope disassembly	10	0.244684685	0.0026	0.004377754
GO:1903725	regulation of phospholipid metabolic process	49	0.244640559	0.0019	0.003579279
GO:0090073	positive regulation of protein homodimerization activity	10	0.244581725	0.038	0.03991002
GO:0071709	membrane assembly	16	0.24456242	0.023	0.025116347
GO:0070050	neuron cellular homeostasis	8	0.24456242	0.0055	0.007544447
GO:0048489	synaptic vesicle transport	45	0.244513085	0.0055	0.007544447
GO:0097480	establishment of synaptic vesicle localization	45	0.244513085	0.0055	0.007544447
GO:0010524	positive regulation of calcium ion transport into cytosol	23	0.244429523	0.0161	0.018371585
GO:0071398	cellular response to fatty acid	30	0.244375804	0.0004	0.002007244
GO:0032232	negative regulation of actin filament bundle assembly	13	0.244371844	0.0032	0.005044175
GO:0051497	negative regulation of stress fiber assembly	13	0.244371844	0.0032	0.005044175
GO:2000060	positive regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process	7	0.244346387	0.004	0.005880507
GO:0048103	somatic stem cell division	9	0.244330044	0.0046	0.006532041
GO:1903035	negative regulation of response to wounding	38	0.244327034	0.0149	0.017165166
GO:0045214	sarcomere organization	16	0.244288932	0.0106	0.012825859
GO:0032252	secretory granule localization	6	0.244187044	0.0175	0.019742875
GO:0007202	activation of phospholipase C activity	13	0.244134244	0.0019	0.003579279
GO:0006534	cysteine metabolic process	13	0.244035244	0.0005	0.002177563
GO:1903541	regulation of exosomal secretion	13	0.244035244	0.0162	0.018465856
GO:1903543	positive regulation of exosomal secretion	13	0.244035244	0.0162	0.018465856
GO:0002029	desensitization of G-protein coupled receptor protein signaling pathway	8	0.244015444	0.0184	0.020586938
GO:0022401	negative adaptation of signaling pathway	8	0.244015444	0.0184	0.020586938
GO:0070863	positive regulation of protein exit from endoplasmic reticulum	6	0.243972544	0.0415	0.043328883
GO:0036017	response to erythropoietin	5	0.243809524	0.0196	0.021765255
GO:0072010	glomerular epithelium development	12	0.243779494	0.0296	0.031661766
GO:0006290	pyrimidine dimer repair	7	0.243758044	0.0205	0.022658082
GO:0048645	animal organ formation	29	0.243731416	0.0186	0.020774238
GO:0006655	phosphatidylglycerol biosynthetic process	8	0.243725869	0.0074	0.009581512
GO:0006904	vesicle docking involved in exocytosis	15	0.243723724	0.0037	0.005561344
GO:0046348	amino sugar catabolic process	5	0.243603604	0.0072	0.009362497
GO:0032621	interleukin-18 production	5	0.243603604	0.0005	0.002177563
GO:0032661	regulation of interleukin-18 production	5	0.243603604	0.0005	0.002177563
GO:0009155	purine deoxyribonucleotide catabolic process	5	0.243603604	0.0007	0.002248538
GO:0009217	purine deoxyribonucleoside triphosphate catabolic process	5	0.243603604	0.0007	0.002248538
GO:0006024	glycosaminoglycan biosynthetic process	54	0.243595977	0.0022	0.003910907
GO:0007612	learning	51	0.243591491	0.0037	0.005561344
GO:0032836	glomerular basement membrane development	5	0.243552124	0.0411	0.042939393
GO:0015914	phospholipid transport	39	0.243546844	0.0066	0.008731949
GO:0043981	histone H4-K5 acetylation	13	0.243480843	0.0069	0.009046225
GO:0043982	histone H4-K8 acetylation	13	0.243480843	0.0069	0.009046225
GO:0090110	cargo loading into COPII-coated vesicle	11	0.243453843	0.011	0.013192134
GO:0050832	defense response to fungus	13	0.243401643	0.0322	0.034224583
GO:0032049	cardiolipin biosynthetic process	7	0.243316786	0.0039	0.005778819
GO:0051657	maintenance of organelle location	9	0.243300443	0.0193	0.021465777
GO:0042447	hormone catabolic process	6	0.243243243	0.0071	0.009268394
GO:0007200	phospholipase C-activating G-protein coupled receptor signaling pathway	31	0.24323494	0.0054	0.007432873
GO:0060920	cardiac pacemaker cell differentiation	5	0.243191763	0.0073	0.009463568
GO:0008053	mitochondrial fusion	17	0.243167537	0.0037	0.005561344
GO:1900274	regulation of phospholipase C activity	22	0.243161343	0.0014	0.002975058
GO:0044060	regulation of endocrine process	26	0.243055143	0.0029	0.004714719
GO:0003263	cardioblast proliferation	6	0.243028743	0.0353	0.037246175
GO:0003264	regulation of cardioblast proliferation	6	0.243028743	0.0353	0.037246175
GO:0033630	positive regulation of cell adhesion mediated by integrin	14	0.242967457	0.003	0.004825593
GO:0048169	regulation of long-term neuronal synaptic plasticity	7	0.242875529	0.005	0.006974174
GO:0003309	type B pancreatic cell differentiation	9	0.242871443	0.0024	0.004156304
GO:0050926	regulation of positive chemotaxis	11	0.242868843	0.0169	0.019147324
GO:0034122	negative regulation of toll-like receptor signaling pathway	16	0.242857143	0.0007	0.002248538
GO:0086002	cardiac muscle cell action potential involved in contraction	23	0.242851547	0.012	0.014185865
GO:0050918	positive chemotaxis	28	0.242737636	0.0105	0.012724187
GO:0040019	positive regulation of embryonic development	19	0.242660706	0.0009	0.002399874
GO:0034453	microtubule anchoring	11	0.242658243	0.0035	0.005358035
GO:0001764	neuron migration	65	0.242625483	0.0007	0.002248538
GO:0060291	long-term synaptic potentiation	26	0.242292842	0.0036	0.005475609
GO:0060442	branching involved in prostate gland morphogenesis	7	0.242029785	0.0476	0.049237916
GO:0010452	histone H3-K36 methylation	8	0.241891892	0.0199	0.022056122
GO:0001958	endochondral ossification	14	0.241827542	0.0053	0.007330056
GO:0036075	replacement ossification	14	0.241827542	0.0053	0.007330056
GO:0002043	blood vessel endothelial cell proliferation involved in sprouting angiogenesis	9	0.241784642	0.0062	0.008281828
GO:0051180	vitamin transport	16	0.241666667	0.0342	0.036175369
GO:1901525	negative regulation of macromitophagy	5	0.241595882	0.0383	0.040185364
GO:0006721	terpenoid metabolic process	52	0.241555292	0.0026	0.004377754
GO:0007205	protein kinase C-activating G-protein coupled receptor signaling pathway	9	0.241527242	0.0015	0.003088691
GO:1903649	regulation of cytoplasmic transport	13	0.241520642	0.0158	0.018074565
GO:0010799	regulation of peptidyl-threonine phosphorylation	16	0.241425354	0.0028	0.004605006
GO:0001523	retinoid metabolic process	43	0.241411511	0.0027	0.004491543

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0045730	respiratory burst	17	0.241396018	0.0039	0.005778819
GO:1902305	regulation of sodium ion transmembrane transport	26	0.241362241	0.0054	0.007432873
GO:0046929	negative regulation of neurotransmitter secretion	8	0.241344916	0.0202	0.02235752
GO:0015858	nucleoside transport	14	0.241331127	0.0336	0.03560572
GO:0033628	regulation of cell adhesion mediated by integrin	29	0.241263924	0.0019	0.003579279
GO:0070528	protein kinase C signaling	13	0.241263241	0.0036	0.005475609
GO:0002675	positive regulation of acute inflammatory response	17	0.241229465	0.003	0.004825593
GO:0048012	hepatocyte growth factor receptor signaling pathway	7	0.241220813	0.0142	0.016456919
GO:0021814	cell motility involved in cerebral cortex radial glia guided migration	5	0.241132561	0.0057	0.007745437
GO:0097576	vacuole fusion	28	0.241110498	0.0389	0.040788039
GO:0090140	regulation of mitochondrial fission	17	0.241093194	0.0375	0.039404369
GO:0045869	negative regulation of single stranded viral RNA replication via double stranded DNA intermediate	5	0.241081081	0.0163	0.018559925
GO:0051503	adenine nucleotide transport	10	0.240952381	0.0314	0.033430037
GO:0048706	embryonic skeletal system development	54	0.240898041	0.0052	0.007215241
GO:0044091	membrane biogenesis	20	0.240823681	0.0137	0.015920879
GO:0001539	cilium or flagellum-dependent cell motility	10	0.240772201	< 0.001	< 0.001
GO:0060285	cilium-dependent cell motility	10	0.240772201	< 0.001	< 0.001
GO:0060259	regulation of feeding behavior	12	0.240733591	< 0.001	< 0.001
GO:0042228	interleukin-8 biosynthetic process	7	0.240706012	0.0013	0.002859821
GO:0045414	regulation of interleukin-8 biosynthetic process	7	0.240706012	0.0013	0.002859821
GO:0070306	lens fiber cell differentiation	16	0.240540541	0.0022	0.003910907
GO:2000010	positive regulation of protein localization to cell surface	12	0.24041184	0.0019	0.003579279
GO:0015721	bile acid and bile salt transport	8	0.240379665	0.0108	0.013015961
GO:0032413	negative regulation of ion transmembrane transporter activity	27	0.240316507	0.0014	0.002975058
GO:0051293	establishment of spindle localization	20	0.24029601	0.0097	0.011922488
GO:0051014	actin filament severing	6	0.24028314	0.0098	0.012008345
GO:0043649	dicarboxylic acid catabolic process	11	0.24027144	0.0015	0.003088691
GO:0043114	regulation of vascular permeability	16	0.240267053	0.02	0.022155397
GO:0097061	dendritic spine organization	24	0.24011154	0.0033	0.005149584
GO:0009310	amine catabolic process	14	0.240080897	0.0061	0.008182551
GO:0042402	cellular biogenic amine catabolic process	14	0.240080897	0.0061	0.008182551
GO:0070365	hepatocyte differentiation	5	0.23994852	0.0039	0.005778819
GO:0051489	regulation of filopodium assembly	19	0.239734471	0.0018	0.003459409
GO:0051966	regulation of synaptic transmission, glutamatergic	14	0.239547711	0.0077	0.009887588
GO:0033625	positive regulation of integrin activation	5	0.23953668	0.0003	0.001720882
GO:0097734	extracellular exosome biogenesis	15	0.23950236	0.0223	0.024414688
GO:0002091	negative regulation of receptor internalization	5	0.239485199	0.0144	0.016652368
GO:0009060	aerobic respiration	38	0.239382239	0.0245	0.026594873
GO:0009620	response to fungus	20	0.239369369	0.0119	0.014078095
GO:0071599	otic vesicle development	8	0.239028314	0.0062	0.008281828
GO:0046439	L-cysteine metabolic process	7	0.238940982	0.002	0.003693422
GO:0055119	relaxation of cardiac muscle	10	0.238918919	0.0104	0.012619802
GO:0051645	Golgi localization	8	0.238899614	0.0258	0.02789201
GO:0071850	mitotic cell cycle arrest	12	0.238867439	0.0057	0.007745437
GO:0097352	autophagosome maturation	27	0.238791172	0.0389	0.040788039
GO:0090185	negative regulation of kidney development	6	0.238781639	0.0048	0.006748379
GO:0051589	negative regulation of neurotransmitter transport	10	0.238738739	0.0152	0.017453982
GO:0007341	penetration of zona pellucida	5	0.238712999	0.0113	0.013488462
GO:0071609	chemokine (C-C motif) ligand 5 production	5	0.238661519	0.0242	0.02630058
GO:0042118	endothelial cell activation	7	0.238610039	0.0109	0.013101792
GO:1900272	negative regulation of long-term synaptic potentiation	7	0.238610039	0.0025	0.004279479
GO:0003208	cardiac ventricle morphogenesis	45	0.238592879	0.0036	0.005475609
GO:0021795	cerebral cortex cell migration	20	0.238584299	0.0007	0.002248538
GO:0060074	synapse maturation	7	0.238536496	0.0406	0.042451813
GO:0003206	cardiac chamber morphogenesis	69	0.238483204	0.0018	0.003459409
GO:0030194	positive regulation of blood coagulation	12	0.238481338	0.0097	0.011922488
GO:1900048	positive regulation of hemostasis	12	0.238481338	0.0097	0.011922488
GO:0035272	exocrine system development	32	0.238433076	0.0104	0.012619802
GO:0034141	positive regulation of toll-like receptor 3 signaling pathway	5	0.238404118	0.016	0.018267288
GO:0072567	chemokine (C-X-C motif) ligand 2 production	10	0.238352638	0.0012	0.002741075
GO:0006953	acute-phase response	22	0.238340938	0.0023	0.004032435
GO:0030325	adrenal gland development	15	0.238266838	0.0142	0.016456919
GO:0060413	atrial septum morphogenesis	9	0.238181038	< 0.001	< 0.001
GO:0032780	negative regulation of ATPase activity	10	0.238146718	0.0025	0.004279479
GO:0031114	regulation of microtubule depolymerization	11	0.238118638	0.0401	0.041935888
GO:0010561	negative regulation of glycoprotein biosynthetic process	12	0.237945088	0.0431	0.044867086
GO:0032309	icosanoid secretion	18	0.237923638	0.0032	0.005044175
GO:0071715	icosanoid transport	18	0.237923638	0.0032	0.005044175
GO:1901571	fatty acid derivative transport	18	0.237923638	0.0032	0.005044175
GO:0021955	central nervous system neuron axonogenesis	12	0.237859288	0.0026	0.004377754
GO:0060117	auditory receptor cell development	12	0.237837838	0.0008	0.002313249
GO:0019626	short-chain fatty acid catabolic process	5	0.237683398	0.0298	0.031859654
GO:0061029	eyelid development in camera-type eye	9	0.237637638	0.0182	0.020388223
GO:0010863	positive regulation of phospholipase C activity	21	0.237617209	0.0012	0.002741075
GO:0002092	positive regulation of receptor internalization	14	0.237598823	0.0174	0.019643968
GO:0032793	positive regulation of CREB transcription factor activity	6	0.237580438	0.0112	0.013379119
GO:0097152	mesenchymal cell apoptotic process	6	0.237537538	0.007	0.009166016
GO:0051294	establishment of spindle orientation	16	0.237532175	0.0102	0.012424427
GO:0006107	oxaloacetate metabolic process	5	0.237425997	0.0048	0.006748379
GO:0086014	atrial cardiac muscle cell action potential	10	0.237323037	0.0369	0.038812296
GO:0086026	atrial cardiac muscle cell to AV node cell signaling	10	0.237323037	0.0369	0.038812296
GO:0086066	atrial cardiac muscle cell to AV node cell communication	10	0.237323037	0.0369	0.038812296
GO:0006600	creatine metabolic process	6	0.237237237	0.0333	0.035317174

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0086019	cell-cell signaling involved in cardiac conduction	12	0.237172887	0.0103	0.012519912
GO:0046337	phosphatidylethanolamine metabolic process	16	0.237162162	0.0013	0.002859821
GO:0032957	inositol trisphosphate metabolic process	7	0.23713918	0.0033	0.005149584
GO:0006449	regulation of translational termination	7	0.23713918	0.0395	0.041342339
GO:0032278	positive regulation of gonadotropin secretion	5	0.237117117	0.0473	0.048935536
GO:0034314	Arp2/3 complex-mediated actin nucleation	11	0.237112437	0.0015	0.003088691
GO:0060252	positive regulation of glial cell proliferation	9	0.236979837	0.0089	0.011106266
GO:0030216	keratinocyte differentiation	114	0.236945969	0.0162	0.018465856
GO:0030501	positive regulation of bone mineralization	19	0.236916616	0.0002	0.001341684
GO:0007016	cytoskeletal anchoring at plasma membrane	7	0.236734694	0.0295	0.031565396
GO:0006538	glutamate catabolic process	8	0.236711712	0.0045	0.006417207
GO:0001505	regulation of neurotransmitter levels	80	0.236631274	0.0006	0.002177563
GO:1901018	positive regulation of potassium ion transmembrane transporter activity	10	0.236576577	0.0395	0.041342339
GO:0032673	regulation of interleukin-4 production	16	0.236389961	0.0108	0.013015961
GO:0048009	insulin-like growth factor receptor signaling pathway	20	0.236267696	0.0078	0.009981807
GO:0050927	positive regulation of positive chemotaxis	10	0.236241956	0.0176	0.019838132
GO:0030049	muscle filament sliding	17	0.236111742	< 0.001	< 0.001
GO:0033275	actin-myosin filament sliding	17	0.236111742	< 0.001	< 0.001
GO:1990182	exosomal secretion	14	0.236109579	0.0221	0.024229021
GO:2000649	regulation of sodium ion transmembrane transporter activity	20	0.236087516	0.006	0.00807902
GO:0097035	regulation of membrane lipid distribution	25	0.236036036	0.0043	0.006204188
GO:0035860	glial cell-derived neurotrophic factor receptor signaling pathway	6	0.236036036	0.0003	0.001720882
GO:0002028	regulation of sodium ion transport	38	0.235907336	0.0062	0.008281828
GO:1903977	positive regulation of glial cell migration	6	0.235907336	0.0425	0.044271412
GO:0046579	positive regulation of Ras protein signal transduction	22	0.235860536	0.0009	0.002399874
GO:0042181	ketone biosynthetic process	25	0.235830116	0.0184	0.020586938
GO:0098900	regulation of action potential	17	0.235718071	0.006	0.00807902
GO:0010676	positive regulation of cellular carbohydrate metabolic process	31	0.23571221	0.0007	0.002248538
GO:0007512	adult heart development	10	0.235675676	0.0061	0.008182551
GO:0021984	adenohypophysis development	9	0.235607036	0.044	0.045721833
GO:2001223	negative regulation of neuron migration	7	0.235594778	0.0006	0.002177563
GO:2001028	positive regulation of endothelial cell chemotaxis	11	0.235591436	0.0002	0.001341684
GO:0055012	ventricular cardiac muscle cell differentiation	7	0.235521236	0.0306	0.032676575
GO:0055015	ventricular cardiac muscle cell development	7	0.235521236	0.0306	0.032676575
GO:0051653	spindle localization	21	0.235508978	0.0097	0.011922488
GO:0007026	negative regulation of microtubule depolymerization	10	0.235495495	0.0418	0.043620665
GO:0009190	cyclic nucleotide biosynthetic process	27	0.235321035	0.0069	0.009046225
GO:0052652	cyclic purine nucleotide metabolic process	27	0.235321035	0.0069	0.009046225
GO:0070989	oxidative demethylation	10	0.235315315	0.0013	0.002859821
GO:0048820	hair follicle maturation	7	0.235263835	0.0097	0.011922488
GO:0007431	salivary gland development	25	0.235212355	0.0114	0.01358747
GO:0015988	energy coupled proton transmembrane transport, against electrochemical gradient	11	0.235170235	0.017	0.019243517
GO:0015991	ATP hydrolysis coupled proton transport	11	0.235170235	0.017	0.019243517
GO:0090662	ATP hydrolysis coupled transmembrane transport	11	0.235170235	0.017	0.019243517
GO:1903715	regulation of aerobic respiration	6	0.235135135	0.0448	0.046530378
GO:0086001	cardiac muscle cell action potential	28	0.235043206	0.0164	0.018653793
GO:0072537	fibroblast activation	8	0.235006435	0.0202	0.02235752
GO:0050482	arachidonic acid secretion	13	0.234966835	0.0026	0.004377754
GO:1903963	arachidonate transport	13	0.234966835	0.0026	0.004377754
GO:0044070	regulation of anion transport	39	0.234953635	0.0098	0.012008345
GO:0018146	keratan sulfate biosynthetic process	14	0.234914506	0.0018	0.003459409
GO:0048854	brain morphogenesis	14	0.234877735	0.0167	0.018954426
GO:0007501	mesodermal cell fate specification	6	0.234749035	< 0.001	< 0.001
GO:0072583	clathrin-dependent endocytosis	27	0.234701368	0.0194	0.021561946
GO:0071391	cellular response to estrogen stimulus	10	0.234671815	0.0068	0.008946408
GO:2000300	regulation of synaptic vesicle exocytosis	19	0.23466775	0.009	0.011215682
GO:2000833	positive regulation of steroid hormone secretion	7	0.23463872	< 0.001	< 0.001
GO:0048814	regulation of dendrite morphogenesis	30	0.234448734	0.0117	0.013882722
GO:0006835	dicarboxylic acid transport	35	0.234366612	0.0077	0.009887588
GO:0018149	peptide cross-linking	12	0.234277134	0.0325	0.034497418
GO:0002026	regulation of the force of heart contraction	13	0.234254034	0.0014	0.002975058
GO:2000380	regulation of mesoderm development	7	0.234197463	0.0006	0.002177563
GO:0014029	neural crest formation	6	0.234191334	0.0051	0.007095023
GO:0046068	cGMP metabolic process	9	0.234177034	0.0294	0.031463678
GO:1900047	negative regulation of hemostasis	23	0.234099938	0.008	0.010168329
GO:2000848	positive regulation of corticosteroid hormone secretion	5	0.234028314	0.0046	0.006532041
GO:0007218	neuropeptide signaling pathway	31	0.23399344	< 0.001	< 0.001
GO:0042368	vitamin D biosynthetic process	6	0.233976834	0.0409	0.042751468
GO:0061318	renal filtration cell differentiation	9	0.233919634	0.0226	0.024717659
GO:0072112	glomerular visceral epithelial cell differentiation	9	0.233919634	0.0226	0.024717659
GO:0072311	glomerular epithelial cell differentiation	9	0.233919634	0.0226	0.024717659
GO:0051770	positive regulation of nitric-oxide synthase biosynthetic process	10	0.233899614	0.0007	0.002248538
GO:0030808	regulation of nucleotide biosynthetic process	35	0.233851811	0.0115	0.013693853
GO:1900371	regulation of purine nucleotide biosynthetic process	35	0.233851811	0.0115	0.013693853
GO:0042481	regulation of odontogenesis	11	0.233836434	0.0313	0.033357007
GO:0009143	nucleoside triphosphate catabolic process	10	0.233616474	0.0028	0.004605006
GO:0032695	negative regulation of interleukin-12 production	8	0.233429858	0.0054	0.007432873
GO:2001171	positive regulation of ATP biosynthetic process	8	0.233397683	0.0022	0.003910907
GO:1902108	regulation of mitochondrial membrane permeability involved in apoptotic process	37	0.233350725	0.0197	0.021861066
GO:0010737	protein kinase A signaling	17	0.233340904	0.0148	0.017062301
GO:0006007	glucose catabolic process	19	0.233285917	0.0179	0.020129998
GO:0002534	cytokine production involved in inflammatory response	22	0.233228033	0.0021	0.003804235
GO:1900015	regulation of cytokine production involved in inflammatory response	22	0.233228033	0.0021	0.003804235

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0039694	viral RNA genome replication	15	0.233170313	0.0159	0.01817591
GO:0039703	RNA replication	15	0.233170313	0.0159	0.01817591
GO:2000252	negative regulation of feeding behavior	5	0.233153153	0.0004	0.002007244
GO:0032890	regulation of organic acid transport	25	0.233153153	0.0122	0.014387602
GO:1900044	regulation of protein K63-linked ubiquitination	7	0.23313109	0.0276	0.029671862
GO:0015837	amine transport	34	0.232954804	0.0001	0.000877824
GO:0019048	modulation by virus of host morphology or physiology	25	0.232947233	0.013	0.015198863
GO:0032808	lacrimal gland development	6	0.232861433	0.0076	0.009790742
GO:0050905	neuromuscular process	46	0.232840915	0.0013	0.002859821
GO:0009065	glutamine family amino acid catabolic process	15	0.232792793	0.0041	0.005981983
GO:0034310	primary alcohol catabolic process	5	0.232689833	0.0348	0.036785603
GO:0003215	cardiac right ventricle morphogenesis	11	0.232666433	0.0001	0.000877824
GO:0060174	limb bud formation	6	0.232604033	0.0021	0.003804235
GO:0010812	negative regulation of cell-substrate adhesion	31	0.232515465	0.0244	0.02650438
GO:0042635	positive regulation of hair cycle	7	0.232432432	0.0011	0.002610912
GO:0007379	segment specification	5	0.232432432	0.0004	0.002007244
GO:1902803	regulation of synaptic vesicle transport	25	0.23241184	0.0181	0.020286898
GO:0015846	polyamine transport	6	0.232346632	0.0473	0.048935536
GO:0033632	regulation of cell-cell adhesion mediated by integrin	7	0.232285347	0.0256	0.02770399
GO:0032228	regulation of synaptic transmission, GABAergic	14	0.232101489	0.0005	0.002177563
GO:0090325	regulation of locomotion involved in locomotory behavior	5	0.231814672	0.0156	0.017858595
GO:0035249	synaptic transmission, glutamatergic	17	0.231811644	0.0034	0.005263104
GO:0010765	positive regulation of sodium ion transport	14	0.231788932	0.0076	0.009790742
GO:0071415	cellular response to purine-containing compound	7	0.231770546	0.0214	0.023571068
GO:0030575	nuclear body organization	10	0.231763192	0.0101	0.012328539
GO:0031111	negative regulation of microtubule polymerization or depolymerization	15	0.231574432	0.0433	0.045060565
GO:0051952	regulation of amine transport	31	0.231436044	0.0002	0.001341684
GO:0046847	filopodium assembly	29	0.231331824	0.0031	0.004916949
GO:1904646	cellular response to beta-amyloid	16	0.231081081	0.0361	0.038033609
GO:0034384	high-density lipoprotein particle clearance	6	0.231016731	0.0006	0.002177563
GO:0048384	retinoic acid receptor signaling pathway	18	0.231016731	0.0077	0.009887588
GO:0006071	glycerol metabolic process	12	0.230930931	0.0107	0.012912536
GO:0016339	calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules	9	0.230916631	0.0236	0.025731873
GO:0021799	cerebral cortex radially oriented cell migration	12	0.230909481	0.0045	0.006417207
GO:0006171	cAMP biosynthetic process	21	0.230839002	0.015	0.017255415
GO:0030814	regulation of cAMP metabolic process	21	0.230839002	0.015	0.017255415
GO:0030817	regulation of cAMP biosynthetic process	21	0.230839002	0.015	0.017255415
GO:0045761	regulation of adenylate cyclase activity	21	0.230839002	0.015	0.017255415
GO:0036035	osteoclast development	7	0.230630631	0.0257	0.027793331
GO:0008299	isoprenoid biosynthetic process	15	0.230630631	0.0025	0.004279479
GO:0044003	modification by symbiont of host morphology or physiology	32	0.230542149	0.0171	0.01934984
GO:0001941	postsynaptic membrane organization	15	0.230527671	0.0007	0.002248538
GO:0097345	mitochondrial outer membrane permeabilization	33	0.23034983	0.0177	0.019919142
GO:0032352	positive regulation of hormone metabolic process	9	0.23031603	0.0086	0.010769857
GO:1905331	negative regulation of morphogenesis of an epithelium	9	0.23031603	0.024	0.026109935
GO:0043252	sodium-independent organic anion transport	5	0.23016731	0.0285	0.030556948
GO:0003266	regulation of secondary heart field cardioblast proliferation	5	0.23006435	0.0366	0.038528543
GO:0021520	spinal cord motor neuron cell fate specification	5	0.22996139	0.0053	0.007330056
GO:0050892	intestinal absorption	15	0.22992707	0.004	0.005880507
GO:1900452	regulation of long term synaptic depression	5	0.22980695	0.0005	0.002177563
GO:0010907	positive regulation of glucose metabolic process	25	0.229734878	0.0009	0.002399874
GO:0048261	negative regulation of receptor-mediated endocytosis	13	0.22971983	0.0086	0.010769857
GO:0034204	lipid translocation	15	0.22966967	0.0068	0.008946408
GO:0045332	phospholipid translocation	15	0.22966967	0.0068	0.008946408
GO:0060999	positive regulation of dendritic spine development	15	0.22960103	0.0007	0.002248538
GO:0008542	visual learning	17	0.229570747	0.006	0.00807902
GO:0009187	cyclic nucleotide metabolic process	37	0.229545375	0.014	0.01625173
GO:0051798	positive regulation of hair follicle development	6	0.229386529	0.0004	0.002007244
GO:0031663	lipopolysaccharide-mediated signaling pathway	30	0.229377949	0.004	0.005880507
GO:1901317	regulation of flagellated sperm motility	6	0.229300729	0.0019	0.003579279
GO:1902337	regulation of apoptotic process involved in morphogenesis	8	0.229150579	0.0154	0.017651835
GO:1904748	regulation of apoptotic process involved in development	8	0.229150579	0.0154	0.017651835
GO:2000272	negative regulation of receptor activity	26	0.229016929	0.0011	0.002610912
GO:0006814	sodium ion transport	90	0.228986129	0.0038	0.005666214
GO:0007632	visual behavior	18	0.228971829	0.003	0.004825593
GO:0032924	activin receptor signaling pathway	16	0.228844916	0.019	0.02117646
GO:0000266	mitochondrial fission	21	0.228804315	0.0343	0.036275124
GO:1903624	regulation of DNA catabolic process	9	0.228800229	0.0178	0.020021073
GO:0070292	N-acylphosphatidylethanolamine metabolic process	5	0.228777349	0.0033	0.005149584
GO:0001672	regulation of chromatin assembly or disassembly	6	0.228743029	0.0198	0.02196821
GO:1900006	positive regulation of dendrite development	32	0.228684041	0.0038	0.005666214
GO:0061045	negative regulation of wound healing	33	0.228563629	0.015	0.017255415
GO:0050909	sensory perception of taste	21	0.228485628	0.0164	0.018653793
GO:1903392	negative regulation of adherens junction organization	14	0.228258871	0.0263	0.02839402
GO:0003230	cardiac atrium development	19	0.228232744	0.0018	0.003459409
GO:1902686	mitochondrial outer membrane permeabilization involved in programmed cell death	36	0.228178178	0.0196	0.021765255
GO:1900119	positive regulation of execution phase of apoptosis	11	0.228150228	0.0039	0.005778819
GO:0003334	keratinocyte development	6	0.228142428	0.0009	0.002399874
GO:0090030	regulation of steroid hormone biosynthetic process	5	0.228056628	0.0018	0.003459409
GO:0055081	anion homeostasis	20	0.227992278	0.0017	0.003334595
GO:0060561	apoptotic process involved in morphogenesis	20	0.227876448	0.0115	0.013693853
GO:0048665	neuron fate specification	15	0.227627628	0.0292	0.03126539
GO:0099504	synaptic vesicle cycle	45	0.227599028	0.0027	0.004491543

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0003339	regulation of mesenchymal to epithelial transition involved in metanephros morphogenesis	5	0.227593308	0.0023	0.004032435
GO:1903959	regulation of anion transmembrane transport	9	0.227398827	0.0072	0.009362497
GO:0015872	dopamine transport	16	0.227348777	0.0049	0.006860215
GO:0032303	regulation of icosanoid secretion	10	0.227232947	0.0443	0.046018566
GO:0035725	sodium ion transmembrane transport	51	0.227112827	0.004	0.005880507
GO:0048566	embryonic digestive tract development	16	0.22701094	0.0186	0.020774238
GO:1900117	regulation of execution phase of apoptosis	18	0.226969827	0.0069	0.009046225
GO:0009713	catechol-containing compound biosynthetic process	11	0.226933427	< 0.001	< 0.001
GO:0042423	catecholamine biosynthetic process	11	0.226933427	< 0.001	< 0.001
GO:0048703	embryonic viscerocranium morphogenesis	5	0.226924067	0.001	0.002498236
GO:1903793	positive regulation of anion transport	23	0.226769627	0.0108	0.013015961
GO:0009204	deoxyribonucleoside triphosphate catabolic process	7	0.226732855	0.0044	0.006304227
GO:0046519	sphingoid metabolic process	12	0.226726727	0.048	0.049619465
GO:0015810	aspartate transport	6	0.226340626	0.0245	0.026594873
GO:0009249	protein lipoylation	6	0.226211926	0.0102	0.012424427
GO:0061615	glycolytic process through fructose-6-phosphate	18	0.226197626	0.0314	0.033430037
GO:0061620	glycolytic process through glucose-6-phosphate	18	0.226197626	0.0314	0.033430037
GO:0045078	positive regulation of interferon-gamma biosynthetic process	8	0.226190476	0.0167	0.018954426
GO:0035794	positive regulation of mitochondrial membrane permeability	37	0.226185259	0.0215	0.023664853
GO:1905710	positive regulation of membrane permeability	37	0.226185259	0.0215	0.023664853
GO:1902018	negative regulation of cilium assembly	7	0.226181283	0.0213	0.023473094
GO:0010172	embryonic body morphogenesis	8	0.226093951	0.0451	0.046826703
GO:0015682	ferric iron transport	17	0.225755167	0.0314	0.033430037
GO:0033572	transferrin transport	17	0.225755167	0.0314	0.033430037
GO:0072512	trivalent inorganic cation transport	17	0.225755167	0.0314	0.033430037
GO:2000270	negative regulation of fibroblast apoptotic process	7	0.225740026	0.0242	0.02630058
GO:1902915	negative regulation of protein polyubiquitination	6	0.225740026	0.019	0.02117646
GO:1900025	negative regulation of substrate adhesion-dependent cell spreading	7	0.225666483	0.0222	0.024321919
GO:0090649	response to oxygen-glucose deprivation	5	0.225585586	0.0482	0.049810054
GO:0090650	cellular response to oxygen-glucose deprivation	5	0.225585586	0.0482	0.049810054
GO:0007435	salivary gland morphogenesis	23	0.225482625	0.0097	0.011922488
GO:0031664	regulation of lipopolysaccharide-mediated signaling pathway	12	0.225482625	0.0059	0.007964563
GO:0010692	regulation of alkaline phosphatase activity	6	0.225439725	< 0.001	< 0.001
GO:0016079	synaptic vesicle exocytosis	26	0.225373725	0.0073	0.009463568
GO:1900029	positive regulation of ruffle assembly	8	0.22532175	0.0175	0.019742875
GO:0030799	regulation of cyclic nucleotide metabolic process	24	0.225289575	0.0199	0.022056122
GO:0030802	regulation of cyclic nucleotide biosynthetic process	24	0.225289575	0.0199	0.022056122
GO:0031279	regulation of cyclase activity	24	0.225289575	0.0199	0.022056122
GO:0021954	central nervous system neuron development	30	0.225268125	0.0011	0.002610912
GO:0007156	homophilic cell adhesion via plasma membrane adhesion molecules	41	0.225206391	0.0002	0.001341684
GO:0060347	heart trabecula formation	8	0.2251287	0.0006	0.002177563
GO:0006910	phagocytosis, recognition	7	0.225078139	0.0225	0.024620965
GO:0051057	positive regulation of small GTPase mediated signal transduction	26	0.224948025	0.0007	0.002248538
GO:0045745	positive regulation of G-protein coupled receptor protein signaling pathway	16	0.224903475	0.022	0.024152627
GO:0070169	positive regulation of biomineral tissue development	23	0.224777573	0.0003	0.001720882
GO:0015867	ATP transport	8	0.224646075	0.0357	0.037649528
GO:0045945	positive regulation of transcription from RNA polymerase III promoter	5	0.224555985	0.0009	0.002399874
GO:2000826	regulation of heart morphogenesis	24	0.224517375	0.0232	0.025330409
GO:0042572	retinol metabolic process	14	0.224397867	0.0059	0.007964563
GO:0046058	cAMP metabolic process	27	0.224367224	0.0146	0.016871405
GO:0035330	regulation of hippo signaling	9	0.224195624	0.0039	0.005778819
GO:0030195	negative regulation of blood coagulation	22	0.224102024	0.009	0.011215682
GO:0043954	cellular component maintenance	26	0.224047124	0.0107	0.012912536
GO:1902110	positive regulation of mitochondrial membrane permeability involved in apoptotic process	34	0.223945795	0.0223	0.024414688
GO:0007271	synaptic transmission, cholinergic	11	0.223891424	0.0001	0.000877824
GO:1904321	response to forskolin	6	0.223809524	0.0015	0.003088691
GO:1904322	cellular response to forskolin	6	0.223809524	0.0015	0.003088691
GO:0051349	positive regulation of lyase activity	19	0.223328592	0.0182	0.020388223
GO:0035082	axoneme assembly	24	0.223198198	< 0.001	< 0.001
GO:0002052	positive regulation of neuroblast proliferation	11	0.223166023	0.0007	0.002248538
GO:0009070	serine family amino acid biosynthetic process	11	0.223025623	0.0059	0.007964563
GO:1900271	regulation of long-term synaptic potentiation	18	0.222880023	0.0044	0.006304227
GO:0003341	cilium movement	27	0.222794223	< 0.001	< 0.001
GO:0046627	negative regulation of insulin receptor signaling pathway	15	0.222668383	0.0185	0.020677043
GO:0015012	heparan sulfate proteoglycan biosynthetic process	8	0.222490347	0.0387	0.04059837
GO:0007288	sperm axoneme assembly	6	0.222350922	< 0.001	< 0.001
GO:0051000	positive regulation of nitric-oxide synthase activity	10	0.222290862	0.0101	0.012328539
GO:0042745	circadian sleep/wake cycle	13	0.222255222	0.0018	0.003459409
GO:0006775	fat-soluble vitamin metabolic process	20	0.222123552	0.0188	0.020971889
GO:0019935	cyclic-nucleotide-mediated signaling	34	0.221954728	0.0038	0.005666214
GO:0021872	forebrain generation of neurons	28	0.221924986	0.0008	0.002313249
GO:0030836	positive regulation of actin filament depolymerization	8	0.221589447	0.0006	0.002177563
GO:0099601	regulation of neurotransmitter receptor activity	11	0.221528022	0.0053	0.007330056
GO:0099643	signal release from synapse	50	0.221487773	0.0024	0.004156304
GO:0001755	neural crest cell migration	17	0.221379363	0.0109	0.013101792
GO:0051204	protein insertion into mitochondrial membrane	17	0.221303657	0.0188	0.020971889
GO:0009146	purine nucleoside triphosphate catabolic process	6	0.221278421	0.0037	0.005561344
GO:0042723	thiamine-containing compound metabolic process	5	0.221158301	0.0033	0.005149584
GO:0042474	middle ear morphogenesis	10	0.221003861	0.017	0.019243517
GO:0021521	ventral spinal cord interneuron specification	8	0.220978121	0.0288	0.030847462
GO:0060573	cell fate specification involved in pattern specification	8	0.220978121	0.0288	0.030847462
GO:0060445	branching involved in salivary gland morphogenesis	14	0.220849421	0.0395	0.041342339
GO:0021871	forebrain regionalization	9	0.220849421	< 0.001	< 0.001

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0046415	urate metabolic process	8	0.220785071	0.0087	0.010877987
GO:0018410	C-terminal protein amino acid modification	7	0.220702335	0.0002	0.001341684
GO:0071600	otic vesicle morphogenesis	6	0.220634921	0.0092	0.011424708
GO:0010265	SCF complex assembly	5	0.2203861	0.0418	0.043620665
GO:0050819	negative regulation of coagulation	24	0.22035607	0.0124	0.014577606
GO:0010092	specification of animal organ identity	6	0.22033462	0.0015	0.003088691
GO:0001973	adenosine receptor signaling pathway	5	0.22028314	0.0192	0.021362011
GO:0031987	locomotion involved in locomotory behavior	9	0.22013442	0.0014	0.002975058
GO:0006560	proline metabolic process	6	0.22012012	0.0054	0.007432873
GO:0051956	negative regulation of amino acid transport	5	0.21992278	0.0077	0.009887588
GO:0099565	chemical synaptic transmission, postsynaptic	26	0.21991882	0.0006	0.002177563
GO:0051443	positive regulation of ubiquitin-protein transferase activity	14	0.219838206	0.0052	0.007215241
GO:0051458	corticotropin secretion	5	0.21981982	0.0043	0.006204188
GO:0051459	regulation of corticotropin secretion	5	0.21981982	0.0043	0.006204188
GO:0048865	stem cell fate commitment	5	0.21966538	0.0061	0.008182551
GO:0070544	histone H3-K36 demethylation	6	0.21951952	0.0258	0.02789201
GO:0045725	positive regulation of glycogen biosynthetic process	9	0.21950522	0.0002	0.001341684
GO:0051932	synaptic transmission, GABAergic	15	0.219476619	0.0009	0.002399874
GO:0050906	detection of stimulus involved in sensory perception	70	0.219444751	0.0432	0.044963841
GO:0072109	glomerular mesangium development	9	0.219390819	0.0209	0.023072181
GO:0043243	positive regulation of protein complex disassembly	19	0.219345661	0.008	0.010168329
GO:0009395	phospholipid catabolic process	19	0.219305019	0.0408	0.042653937
GO:0010800	positive regulation of peptidyl-threonine phosphorylation	10	0.219021879	0.0006	0.002177563
GO:0048387	negative regulation of retinoic acid receptor signaling pathway	6	0.218833119	0.0176	0.019838132
GO:0075713	establishment of integrated proviral latency	6	0.218532819	0.0054	0.007432873
GO:0021884	forebrain neuron development	13	0.218473418	0.003	0.004825593
GO:0036465	synaptic vesicle recycling	14	0.218459276	0.0193	0.021465777
GO:0033127	regulation of histone phosphorylation	6	0.218404118	0.0111	0.013284563
GO:0006735	NADH regeneration	17	0.218366265	0.0351	0.037053553
GO:0061621	canonical glycolysis	17	0.218366265	0.0351	0.037053553
GO:0061718	glucose catabolic process to pyruvate	17	0.218366265	0.0351	0.037053553
GO:0007622	rhythmic behavior	21	0.217932218	0.0041	0.005981983
GO:0048512	circadian behavior	21	0.217932218	0.0041	0.005981983
GO:1904263	positive regulation of TORC1 signaling	7	0.217907704	0.0106	0.012825859
GO:0007269	neurotransmitter secretion	49	0.217870932	0.0029	0.004714719
GO:1901028	regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	27	0.217722484	0.0237	0.025818821
GO:0060192	negative regulation of lipase activity	8	0.217631918	0.0017	0.003334595
GO:0033189	response to vitamin A	6	0.217546118	0.0001	0.000877824
GO:0071071	regulation of phospholipid biosynthetic process	7	0.217172274	0.0019	0.003579279
GO:2000402	negative regulation of lymphocyte migration	7	0.216988417	0.0043	0.006204188
GO:0046834	lipid phosphorylation	18	0.216931217	0.0173	0.019544921
GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	84	0.216896488	0.0003	0.001720882
GO:0043249	erythrocyte maturation	8	0.216827542	0.0029	0.004714719
GO:0042095	interferon-gamma biosynthetic process	9	0.216731017	0.0095	0.011730963
GO:0045072	regulation of interferon-gamma biosynthetic process	9	0.216731017	0.0095	0.011730963
GO:0090045	positive regulation of deacetylase activity	5	0.216628057	0.0254	0.027496891
GO:0016114	terpenoid biosynthetic process	8	0.216441441	0.0149	0.017165166
GO:0051683	establishment of Golgi localization	5	0.216216216	0.0359	0.037847924
GO:0006734	NADH metabolic process	20	0.216126126	0.0392	0.041055316
GO:0008300	isoprenoid catabolic process	5	0.216061776	0.038	0.03991002
GO:0006836	neurotransmitter transport	72	0.216030316	0.001	0.002498236
GO:0035116	embryonic hindlimb morphogenesis	10	0.215933076	0.0078	0.009981807
GO:0007187	G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	69	0.215899129	0.0016	0.003223775
GO:0009593	detection of chemical stimulus	65	0.215832096	0.0471	0.048744446
GO:0035331	negative regulation of hippo signaling	6	0.215830116	0.0025	0.004279479
GO:0009954	proximal/distal pattern formation	9	0.215587016	0.0004	0.002007244
GO:1901616	organic hydroxy compound catabolic process	24	0.215551266	0.0273	0.029359247
GO:0060039	pericardium development	10	0.215546976	0.0261	0.028197203
GO:0001547	antral ovarian follicle growth	6	0.215529816	< 0.001	< 0.001
GO:1900017	positive regulation of cytokine production involved in inflammatory response	11	0.215514216	0.0102	0.012424427
GO:0034139	regulation of toll-like receptor 3 signaling pathway	6	0.215444015	0.0286	0.030648697
GO:1904778	positive regulation of protein localization to cell cortex	5	0.215289575	0.0316	0.033614889
GO:0071313	cellular response to caffeine	5	0.215289575	0.0461	0.047779362
GO:0060079	excitatory postsynaptic potential	25	0.215258687	0.0002	0.001341684
GO:0034114	regulation of heterotypic cell-cell adhesion	11	0.215186615	0.0064	0.008500875
GO:0032509	endosome transport via multivesicular body sorting pathway	11	0.215186615	0.0072	0.009362497
GO:0003376	sphingosine-1-phosphate signaling pathway	7	0.215113072	0.0014	0.002975058
GO:0030261	chromosome condensation	18	0.215043615	0.0074	0.009581512
GO:0099531	presynaptic process involved in chemical synaptic transmission	53	0.214511547	0.002	0.003693422
GO:1901096	regulation of autophagosome maturation	8	0.214060489	0.0437	0.045424906
GO:0021879	forebrain neuron differentiation	24	0.213610039	0.0008	0.002313249
GO:0008356	asymmetric cell division	8	0.213416988	0.0001	0.000877824
GO:0001508	action potential	47	0.212886443	0.0189	0.021076063
GO:0051895	negative regulation of focal adhesion assembly	13	0.212870013	0.0297	0.0317634
GO:0034115	negative regulation of heterotypic cell-cell adhesion	5	0.212715573	0.0097	0.011922488
GO:0070587	regulation of cell-cell adhesion involved in gastrulation	5	0.212715573	0.0097	0.011922488
GO:0031652	positive regulation of heat generation	6	0.212655513	0.015	0.017255415
GO:0046886	positive regulation of hormone biosynthetic process	6	0.212612613	0.0143	0.016557758
GO:0007188	adenylate cyclase-modulating G-protein coupled receptor signaling pathway	60	0.212522523	0.0014	0.002975058
GO:0021514	ventral spinal cord interneuron differentiation	10	0.211788932	0.0471	0.048744446
GO:0060579	ventral spinal cord interneuron fate commitment	10	0.211788932	0.0471	0.048744446
GO:0060581	cell fate commitment involved in pattern specification	10	0.211788932	0.0471	0.048744446
GO:0010896	regulation of triglyceride catabolic process	5	0.211788932	0.0048	0.006748379

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0090335	regulation of brown fat cell differentiation	9	0.211668812	0.0233	0.025417819
GO:0032332	positive regulation of chondrocyte differentiation	9	0.211554412	0.0017	0.003334595
GO:0090154	positive regulation of sphingolipid biosynthetic process	7	0.211472697	0.0156	0.017858595
GO:2000304	positive regulation of ceramide biosynthetic process	7	0.211472697	0.0156	0.017858595
GO:0048520	positive regulation of behavior	11	0.211419211	0.0004	0.002007244
GO:0046189	phenol-containing compound biosynthetic process	22	0.211395811	< 0.001	< 0.001
GO:0022615	protein to membrane docking	5	0.211274131	0.0181	0.020286898
GO:0006582	melanin metabolic process	12	0.211089661	0.0001	0.000877824
GO:0060452	positive regulation of cardiac muscle contraction	6	0.211025311	0.0255	0.027600459
GO:0060294	cilium movement involved in cell motility	7	0.210663725	< 0.001	< 0.001
GO:0001660	fever generation	5	0.210656371	0.0124	0.014577606
GO:0060042	retina morphogenesis in camera-type eye	25	0.210471042	0.0223	0.024414688
GO:0034720	histone H3-K4 demethylation	7	0.210406325	0.0205	0.022658082
GO:0070286	axonemal dynein complex assembly	13	0.21031581	0.0015	0.003088691
GO:0046487	glyoxylate metabolic process	6	0.20982411	0.0366	0.038528543
GO:0007270	neuron-neuron synaptic transmission	38	0.209821852	0.0011	0.002610912
GO:0061101	neuroendocrine cell differentiation	7	0.209707667	0.0178	0.020021073
GO:0048385	regulation of retinoic acid receptor signaling pathway	12	0.209459459	0.0114	0.01358747
GO:1900273	positive regulation of long-term synaptic potentiation	7	0.209413495	0.043	0.044777614
GO:0001844	protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	16	0.209411197	0.0282	0.030276044
GO:0046469	platelet activating factor metabolic process	6	0.209352209	0.0286	0.030648697
GO:1903792	negative regulation of anion transport	11	0.209289809	0.02	0.022155397
GO:0050873	brown fat cell differentiation	19	0.208832893	0.0113	0.013488462
GO:0032148	activation of protein kinase B activity	14	0.20865968	0.0094	0.011616482
GO:0097062	dendritic spine maintenance	9	0.208608609	0.0316	0.033614889
GO:1902510	regulation of apoptotic DNA fragmentation	8	0.208494208	0.0271	0.029163847
GO:0021801	cerebral cortex radial glia guided migration	7	0.208200037	0.0071	0.009268394
GO:0022030	telencephalon glial cell migration	7	0.208200037	0.0071	0.009268394
GO:0003209	cardiac atrium morphogenesis	17	0.208176243	0.0027	0.004491543
GO:0007193	adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway	30	0.207876448	0.0005	0.002177563
GO:0042573	retinoic acid metabolic process	10	0.207696268	0.0106	0.012825859
GO:0021854	hypothalamus development	10	0.207670528	0.0151	0.01736105
GO:0022410	circadian sleep/wake cycle process	11	0.207511408	0.0016	0.003223775
GO:0050802	circadian sleep/wake cycle, sleep	11	0.207511408	0.0016	0.003223775
GO:1901725	regulation of histone deacetylase activity	6	0.207507508	0.016	0.018267288
GO:2001269	positive regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway	6	0.207121407	0.0374	0.039305772
GO:0032770	positive regulation of monooxygenase activity	14	0.207004964	0.0067	0.008845888
GO:0098914	membrane repolarization during atrial cardiac muscle cell action potential	5	0.207001287	0.0112	0.013379119
GO:0070875	positive regulation of glycogen metabolic process	10	0.206924067	0.0009	0.002399874
GO:2000191	regulation of fatty acid transport	13	0.206692407	0.0283	0.030373173
GO:1900449	regulation of glutamate receptor signaling pathway	10	0.206280566	0.0047	0.006644432
GO:0023019	signal transduction involved in regulation of gene expression	9	0.205834406	0.0007	0.002248538
GO:0051482	positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G-protein coupled signaling pathway	9	0.205691406	0.0351	0.037053553
GO:0060078	regulation of postsynaptic membrane potential	28	0.20558007	0.0018	0.003459409
GO:0071379	cellular response to prostaglandin stimulus	11	0.205428805	0.0036	0.005475609
GO:1900045	negative regulation of protein K63-linked ubiquitination	5	0.204839125	0.0241	0.026209778
GO:0044550	secondary metabolite biosynthetic process	13	0.204831205	0.0002	0.001341684
GO:0048745	smooth muscle tissue development	11	0.204773605	0.0173	0.019544921
GO:0033561	regulation of water loss via skin	7	0.204081633	0.0147	0.016962357
GO:0090656	t-circle formation	9	0.203517804	0.005	0.006974174
GO:0098885	modification of postsynaptic actin cytoskeleton	5	0.203500644	0.0338	0.035793852
GO:0033598	mammary gland epithelial cell proliferation	13	0.203366003	0.0009	0.002399874
GO:0048021	regulation of melanin biosynthetic process	5	0.203243243	0.0035	0.005358035
GO:1900376	regulation of secondary metabolite biosynthetic process	5	0.203243243	0.0035	0.005358035
GO:0014821	phasic smooth muscle contraction	8	0.203120978	0.0324	0.034407232
GO:1903818	positive regulation of voltage-gated potassium channel activity	6	0.203003003	0.0313	0.033357007
GO:0002739	regulation of cytokine secretion involved in immune response	6	0.202831403	0.0024	0.004156304
GO:0006105	succinate metabolic process	7	0.202390145	0.0316	0.033614889
GO:0050775	positive regulation of dendrite morphogenesis	15	0.202230802	0.0206	0.022756769
GO:0061303	cornea development in camera-type eye	5	0.201956242	0.0177	0.019919142
GO:0070268	cornification	30	0.201818962	0.0453	0.047003728
GO:0046928	regulation of neurotransmitter secretion	30	0.201801802	0.0107	0.012912536
GO:1904668	positive regulation of ubiquitin protein ligase activity	7	0.20150763	0.0185	0.020677043
GO:0035025	positive regulation of Rho protein signal transduction	9	0.201258401	0.0019	0.003579279
GO:0007215	glutamate receptor signaling pathway	18	0.201201201	0.0073	0.009463568
GO:0042737	drug catabolic process	6	0.201115401	0.0001	0.000877824
GO:0007185	transmembrane receptor protein tyrosine phosphatase signaling pathway	5	0.201029601	0.0017	0.003334595
GO:0014046	dopamine secretion	10	0.200900901	0.0048	0.006748379
GO:0014059	regulation of dopamine secretion	10	0.200900901	0.0048	0.006748379
GO:0032736	positive regulation of interleukin-13 production	6	0.200429	0.002	0.003693422
GO:0032530	regulation of microvillus organization	5	0.20030888	0.0124	0.014577606
GO:0051593	response to folic acid	8	0.2002574	0.0382	0.040087041
GO:0001188	RNA polymerase I transcriptional preinitiation complex assembly	7	0.200220629	0.0048	0.006748379
GO:0021756	striatum development	10	0.2	0.0107	0.012912536
GO:0072697	protein localization to cell cortex	8	0.199517375	0.0236	0.025731873
GO:1902414	protein localization to cell junction	6	0.199356499	0.0192	0.021362011
GO:0090520	sphingolipid mediated signaling pathway	8	0.199292149	0.0087	0.010877987
GO:0034638	phosphatidylcholine catabolic process	5	0.198661519	0.018	0.020203241
GO:0090494	dopamine uptake	7	0.198124655	0.002	0.003693422
GO:0035115	embryonic forelimb morphogenesis	13	0.198039798	0.0072	0.009362497
GO:0035136	forelimb morphogenesis	13	0.198039798	0.0072	0.009362497
GO:0003148	outflow tract septum morphogenesis	14	0.198014341	0.0268	0.028880014

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0003407	neural retina development	30	0.197803518	0.0007	0.002248538
GO:0048488	synaptic vesicle endocytosis	10	0.197760618	0.0094	0.011616482
GO:0070307	lens fiber cell development	5	0.197477477	0.0285	0.030556948
GO:0030213	hyaluronan biosynthetic process	6	0.197425997	0.0278	0.029876796
GO:0015800	acidic amino acid transport	16	0.197265122	0.0084	0.010571327
GO:0008038	neuron recognition	12	0.197147147	0.0188	0.020971889
GO:0072079	nephron tubule formation	8	0.196943372	0.0022	0.003910907
GO:0010766	negative regulation of sodium ion transport	9	0.196911197	0.0064	0.008500875
GO:0033599	regulation of mammary gland epithelial cell proliferation	10	0.196833977	0.0011	0.002610912
GO:0001504	neurotransmitter uptake	17	0.196608373	0.0005	0.002177563
GO:0035376	sterol import	5	0.195881596	0.0333	0.035317174
GO:0070508	cholesterol import	5	0.195881596	0.0333	0.035317174
GO:0042438	melanin biosynthetic process	11	0.195858196	0.0001	0.000877824
GO:0032802	low-density lipoprotein particle receptor catabolic process	6	0.195624196	0.0111	0.013284563
GO:0003149	membranous septum morphogenesis	5	0.195469755	0.002	0.003693422
GO:0061436	establishment of skin barrier	6	0.194851995	0.0246	0.026698876
GO:1901978	positive regulation of cell cycle checkpoint	5	0.194285714	0.0006	0.002177563
GO:0019695	choline metabolic process	8	0.193983269	0.0269	0.028963288
GO:0030810	positive regulation of nucleotide biosynthetic process	23	0.193822394	0.0221	0.024229021
GO:1900373	positive regulation of purine nucleotide biosynthetic process	23	0.193822394	0.0221	0.024229021
GO:1904776	regulation of protein localization to cell cortex	6	0.193693694	0.047	0.048672571
GO:0051590	positive regulation of neurotransmitter transport	6	0.193350493	< 0.001	< 0.001
GO:0051588	regulation of neurotransmitter transport	36	0.193157443	0.0064	0.008500875
GO:0002374	cytokine secretion involved in immune response	8	0.193146718	0.0008	0.002313249
GO:0000212	meiotic spindle organization	8	0.192792793	0.0332	0.035228705
GO:0033623	regulation of integrin activation	8	0.192631918	0.001	0.002498236
GO:0007606	sensory perception of chemical stimulus	73	0.192059378	0.0467	0.048369755
GO:1901030	positive regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	20	0.191994852	0.0339	0.035893786
GO:0098810	neurotransmitter reuptake	12	0.191848992	0.0005	0.002177563
GO:0010985	negative regulation of lipoprotein particle clearance	5	0.191814672	0.0144	0.016652368
GO:0002138	retinoic acid biosynthetic process	6	0.191205491	0.0366	0.038528543
GO:0016102	diterpenoid biosynthetic process	6	0.191205491	0.0366	0.038528543
GO:0007189	adenylate cyclase-activating G-protein coupled receptor signaling pathway	29	0.190999867	0.0237	0.025818821
GO:0043949	regulation of cAMP-mediated signaling	15	0.190870871	0.0249	0.02700148
GO:0060215	primitive hemopoiesis	5	0.190682111	0.034	0.035993688
GO:0001964	startle response	11	0.18996139	0.0023	0.004032435
GO:0015813	L-glutamate transport	11	0.188604189	0.001	0.002498236
GO:0038042	dimeric G-protein coupled receptor signaling pathway	6	0.188459888	0.0247	0.026793719
GO:0097646	calcitonin family receptor signaling pathway	6	0.188459888	0.0247	0.026793719
GO:0071377	cellular response to glucagon stimulus	7	0.188380217	0.0021	0.003804235
GO:0009820	alkaloid metabolic process	6	0.188331188	0.0043	0.006204188
GO:0044793	negative regulation by host of viral process	5	0.188211068	0.0037	0.005561344
GO:2000738	positive regulation of stem cell differentiation	14	0.188067659	0.0068	0.008946408
GO:0070586	cell-cell adhesion involved in gastrulation	6	0.188030888	0.0139	0.016141527
GO:2000310	regulation of N-methyl-D-aspartate selective glutamate receptor activity	8	0.187548263	0.0015	0.003088691
GO:0043455	regulation of secondary metabolic process	6	0.187044187	0.0111	0.013284563
GO:0099558	maintenance of synapse structure	6	0.186958387	0.0058	0.007856196
GO:1900739	regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	13	0.186298386	0.0317	0.033710012
GO:1900740	positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	13	0.186298386	0.0317	0.033710012
GO:0036159	inner dynein arm assembly	10	0.186280566	0.0084	0.010571327
GO:0071380	cellular response to prostaglandin E stimulus	9	0.186214786	0.0062	0.008281828
GO:0042749	regulation of circadian sleep/wake cycle	10	0.185456885	0.0031	0.004916949
GO:0045187	regulation of circadian sleep/wake cycle, sleep	10	0.185456885	0.0031	0.004916949
GO:0002551	mast cell chemotaxis	5	0.185379665	0.0483	0.049905302
GO:0003357	noradrenergic neuron differentiation	6	0.185242385	0.008	0.010168329
GO:0051953	negative regulation of amine transport	11	0.185117585	0.0007	0.002248538
GO:0032891	negative regulation of organic acid transport	10	0.184581725	0.0367	0.038621054
GO:0034199	activation of protein kinase A activity	7	0.184482442	0.0036	0.005475609
GO:0043951	negative regulation of cAMP-mediated signaling	7	0.184261813	0.0071	0.009268394
GO:0061003	positive regulation of dendritic spine morphogenesis	6	0.184084084	0.0033	0.005149584
GO:0003207	cardiac chamber formation	9	0.183926784	0.0048	0.006748379
GO:0060004	reflex	10	0.183603604	0.0136	0.015813319
GO:0007616	long-term memory	13	0.183150183	0.0156	0.017858595
GO:0090493	catecholamine uptake	8	0.182046332	0.0004	0.002007244
GO:0033604	negative regulation of catecholamine secretion	7	0.181871668	0.0005	0.002177563
GO:0042753	positive regulation of circadian rhythm	7	0.181724582	0.0083	0.010468217
GO:0007028	cytoplasm organization	5	0.181621622	0.0003	0.001720882
GO:0060219	camera-type eye photoreceptor cell differentiation	7	0.180952381	0.0161	0.018371585
GO:1904396	regulation of neuromuscular junction development	6	0.180952381	0.0012	0.002741075
GO:0060438	trachea development	8	0.180662806	0.0078	0.009981807
GO:0001574	ganglioside biosynthetic process	5	0.180540541	0.0373	0.039220079
GO:0044068	modulation by symbiont of host cellular process	18	0.18012298	0.0325	0.034497418
GO:0060134	prepulse inhibition	6	0.18000858	0.0132	0.015415723
GO:0007413	axonal fasciculation	8	0.17960103	0.0029	0.004714719
GO:2000665	regulation of interleukin-13 secretion	5	0.179047619	0.0238	0.025923329
GO:0021978	telencephalon regionalization	6	0.178592879	0.0009	0.002399874
GO:0044241	lipid digestion	5	0.178120978	0.0026	0.004377754
GO:0010763	positive regulation of fibroblast migration	5	0.177863578	0.0461	0.047779362
GO:0019933	cAMP-mediated signaling	26	0.177833878	0.0245	0.026594873
GO:0060850	regulation of transcription involved in cell fate commitment	11	0.177278577	0.0264	0.028497154
GO:0061548	ganglion development	6	0.176490776	0.0002	0.001341684

GOIDlabel	GOName	size	categoryScores	pValPerm	pValPermCorr
GO:0051583	dopamine uptake involved in synaptic transmission	5	0.176061776	0.0116	0.013792313
GO:0051934	catecholamine uptake involved in synaptic transmission	5	0.176061776	0.0116	0.013792313
GO:0099054	presynapse assembly	10	0.175289575	0.0067	0.008845888
GO:1902306	negative regulation of sodium ion transmembrane transport	8	0.174967825	0.0086	0.010769857
GO:0001963	synaptic transmission, dopaminergic	9	0.172200772	0.0016	0.003223775
GO:0035926	chemokine (C-C motif) ligand 2 secretion	5	0.16993565	0.0064	0.008500875
GO:0006702	androgen biosynthetic process	6	0.169369369	0.0307	0.03276689
GO:0030816	positive regulation of cAMP metabolic process	12	0.169283569	0.0478	0.049420733
GO:0030819	positive regulation of cAMP biosynthetic process	12	0.169283569	0.0478	0.049420733
GO:0045762	positive regulation of adenylate cyclase activity	12	0.169283569	0.0478	0.049420733
GO:0021895	cerebral cortex neuron differentiation	9	0.168911769	0.0013	0.002859821
GO:0032656	regulation of interleukin-13 production	10	0.167078507	0.0308	0.032862615
GO:0072611	interleukin-13 secretion	6	0.166108966	0.0417	0.043530565
GO:0010918	positive regulation of mitochondrial membrane potential	5	0.163346203	0.0463	0.047971045
GO:0042730	fibrinolysis	10	0.163088803	0.0104	0.012619802
GO:0099560	synaptic membrane adhesion	7	0.162934363	0.0307	0.03276689
GO:0045760	positive regulation of action potential	5	0.162213642	0.012	0.014185865
GO:1905606	regulation of presynapse assembly	9	0.161189761	0.0311	0.033166048
GO:0032616	interleukin-13 production	11	0.161109161	0.0463	0.047971045
GO:0031665	negative regulation of lipopolysaccharide-mediated signaling pathway	6	0.16027456	0.0257	0.027793331
GO:0072017	distal tubule development	5	0.16015444	0.0336	0.03560572
GO:0021544	subpallium development	13	0.15974656	0.0054	0.007432873
GO:0021778	oligodendrocyte cell fate specification	5	0.158712999	0.0111	0.013284563
GO:0021779	oligodendrocyte cell fate commitment	5	0.158712999	0.0111	0.013284563
GO:0021780	glial cell fate specification	5	0.158712999	0.0111	0.013284563
GO:0042748	circadian sleep/wake cycle, non-REM sleep	5	0.157683398	0.0003	0.001720882
GO:0045188	regulation of circadian sleep/wake cycle, non-REM sleep	5	0.157683398	0.0003	0.001720882
GO:0019054	modulation by virus of host process	14	0.157676043	0.0423	0.044077485
GO:0051580	regulation of neurotransmitter uptake	7	0.155212355	0.0335	0.03551156
GO:0032754	positive regulation of interleukin-5 production	5	0.152535393	0.002	0.003693422
GO:0007190	activation of adenylate cyclase activity	9	0.149292149	0.0436	0.045335748
GO:0071875	adrenergic receptor signaling pathway	6	0.148691549	0.0055	0.007544447
GO:0042426	choline catabolic process	5	0.147490347	0.0305	0.032586169
GO:2000650	negative regulation of sodium ion transmembrane transporter activity	7	0.142820371	0.018	0.020203241
GO:0048485	sympathetic nervous system development	10	0.136988417	0.0401	0.041935888
GO:0021772	olfactory bulb development	12	0.134813385	0.0031	0.004916949
GO:0021988	olfactory lobe development	12	0.134813385	0.0031	0.004916949
GO:0032225	regulation of synaptic transmission, dopaminergic	6	0.133976834	0.0373	0.039220079
GO:0021889	olfactory bulb interneuron differentiation	5	0.116653797	0.0185	0.020677043
GO:0051967	negative regulation of synaptic transmission, glutamatergic	5	0.10028314	0.0452	0.046915244
GO:0097154	GABAergic neuron differentiation	7	0.097481155	0.0278	0.029876796
GO:0021892	cerebral cortex GABAergic interneuron differentiation	6	0.09021879	0.0293	0.031367193

Reward COR positive

GOIDlabel	GOName	GOID	size	categoryScores	pValZ	pValZCorr	pValPerm	pValPermCorr
GO:0051823	regulation of synapse structural plasticity	51823	6	0.541184041	1.55326E-09	6.88247E-06	< 0.001	< 0.001
GO:0099563	modification of synaptic structure	99563	11	0.441909442	2.65255E-07	0.000587672	< 0.001	< 0.001
GO:0098885	modification of postsynaptic actin cytoskeleton	98885	7	0.396102225	4.08628E-06	0.003668926	< 0.001	< 0.001