Categ	Term	Coun	Count i	P-value	Enrichment s
GO	heart development	16	114	7.38E-05	4.7787742
GO	maternal process involved in parturition	3	3	9.99E-05	7.8486767
GO	cytoplasm	247	4355	0.000189	3.66964816
GO	actin binding	27	278	0.00025	4.04491742
GO	collagen	6	22	0.000388	5.04628974
GO	synapse assembly	7	33	0.000673	4.5264191
GO	positive regulation of Wnt receptor signaling pathway	4	10	0.000775	5.31408652
GO	thrombin receptor activity	3	5	0.00093	5.8824651
GO	negative regulation of chondrocyte differentiation	3	5	0.00093	5.8824651
GO	negative regulation of DNA recombination	3	5	0.00093	5.8824651
GO	collagen fibril organization	6	26	0.001021	4.46916161
GO	nucleoplasm	36	455	0.001347	3.35258385
GO	actomyosin structure organization	3	6	0.001797	5.27996371
GO	collagen type IV	3	6	0.001797	5.27996371
GO	negative regulation of protein import into nucleus	2	2	0.002155	6.40824895
GO	regulation of acetylcholine secretion	2	2	0.002155	6.40824895
GO	DNA replication, removal of RNA primer	2	2	0.002155	6.40824895
GO	negative regulation of mitotic recombination	2	2	0.002155	6.40824895
GO	CCR2 chemokine receptor binding	2	2	0.002155	6.40824895
GO	ectoderm and mesoderm interaction	2	2	0.002155	6.40824895
GO	regulation of smooth muscle contraction	4	13	0.002359	4.47744548
GO	DNA recombination	8	52	0.002569	3.68526535
GO	proximal/distal pattern formation	5	22	0.002906	4.03262292
GO	positive regulation of filopodium assembly	3	7	0.003036	4.80499827
GO	positive regulation of Notch signaling pathway	3	7	0.003036	4.80499827
GO	DNA replication	15	146	0.003293	3.24481458
GO	damaged DNA binding	7	44	0.00388	3.55473995
GO	cell projection	11	94	0.004175	3.2596203
GO	response to drug	20	225	0.004232	3.04347188
GO	cell junction	30	387	0.004373	2.93501822
GO	DNA repair	17	182	0.004901	3.02511904
GO	organ regeneration	6	35	0.005046	3.51681207
GO	fat cell differentiation	5	25	0.005225	3.6507357
GO	muscle contraction	11	97	0.005308	3.14167838
GO	induction of apoptosis	16	170	0.005796	2.96700936
GO	collagen type V	2	3	0.006264	5.1050277
GO	branching morphogenesis of a nerve	2	3	0.006264	5.1050277
GO	5'-flap endonuclease activity	2	3	0.006264	5.1050277
GO	positive regulation of myeloid cell differentiation	2	3	0.006264	5.1050277
GO	positive regulation of muscle cell differentiation	2	3	0.006264	5.1050277
GO	guanyl-nucleotide exchange factor complex	2	3	0.006264	5.1050277
GO	prostatic bud formation	2	3	0.006264	5.1050277
GO	very-low-density lipoprotein particle clearance	2	3	0.006264	5.1050277
GO	negative regulation of cell adhesion mediated by integrin	2	3	0.006264	5.1050277
GO	regulation of cyclin-dependent protein kinase activity	6	37	0.006682	3.34799113
GO	mitochondrial large ribosomal subunit	4	17	0.006772	3.70163201
GO	Notch binding	3	9	0.006794	4.09067424
GO	auditory receptor cell differentiation	3	9	0.006794	4.09067424

GO	female pregnancy	8	61	0.006976	3.14865318
GO	DNA-dependent ATPase activity	5	27	0.007355	3.42810461
GO	sarcomere	5	27	0.007355	3.42810461
GO	polypeptide N-acetylgalactosaminyltransferase activity	4	18	0.008391	3.54539354
GO	pituitary gland development	4	18	0.008391	3.54539354
GO	actin filament	5	28	0.008618	3.32468406
GO	CTP biosynthetic process	3	10	0.009373	3.811051
GO	embryonic digestive tract development	3	10	0.009373	3.811051
GO	negative regulation of blood coagulation	3	10	0.009373	3.811051
GO	actin cytoskeleton	13	134	0.009557	2.79160476
GO	mRNA export from nucleus	5	29	0.010023	3.22593343
GO	chromosome	13	135	0.010141	2.76225848
GO	methyltransferase activity	11	106	0.010205	2.81260799
GO	heterophilic cell-cell adhesion	4	19	0.010245	3.40026933
GO	collagen catabolic process	4	19	0.010245	3.40026933
GO	basolateral plasma membrane	11	107	0.010913	2.77811331
GO	eye morphogenesis	2	4	0.012143	4.31084526
GO	apicolateral plasma membrane	2	4	0.012143	4.31084526
GO	DNA (cytosine-5-)-methyltransferase activity	2	4	0.012143	4.31084526
GO	lipoxygenase pathway	2	4	0.012143	4.31084526
GO	DNA-directed RNA polymerase I complex	2	4	0.012143	4.31084526
GO	chylomicron remnant clearance	2	4	0.012143	4.31084526
GO	regulation of axon extension	2	4	0.012143	4.31084526
GO	saliva secretion	2	4	0.012143	4.31084526
GO	regulation of DNA recombination	2	4	0.012143	4.31084526
GO	response to methylmercury	2	4	0.012143	4.31084526
GO	guanine/thymine mispair binding	2	4	0.012143	4.31084526
GO	regulation of G2/M transition of mitotic cell cycle	2	4	0.012143	4.31084526
GO	ATP-dependent 3'-5' DNA helicase activity	2	4	0.012143	4.31084526
GO	DNA strand annealing activity	2	4	0.012143	4.31084526
GO	muscle thin filament tropomyosin	2	4	0.012143	4.31084526
GO	gamma-aminobutyric acid signaling pathway	4	20	0.012344	3.26488694
GO	tissue regeneration	4	20	0.012344	3.26488694
GO	transforming growth factor beta receptor activity	3	11	0.012448	3.56723153
GO	negative regulation of DNA binding	3	11	0.012448	3.56723153
GO	positive regulation of endothelial cell proliferation	5	31	0.01329	3.04096308
GO	protein binding	321	6249	0.013619	2.25858379
GO	cell cycle	32	458	0.014412	2.41149164
GO	protein kinase inhibitor activity	4	21	0.0147	3.13810301
GO	mitotic chromosome condensation	3	12	0.016033	3.35172733
GO	blastocyst development	3	12	0.016033	3.35172733
GO	NLS-bearing substrate import into nucleus	3	12	0.016033	3.35172733
GO	rRNA transcription	3	12	0.016033	3.35172733
GO	adrenal gland development	3	12	0.016033	3.35172733
GO	dendrite	12	128	0.016044	2.55183931
GO	isomerase activity	10	99	0.016622	2.5866513
GO	actin cytoskeleton organization	11	114	0.016966	2.54684774
GO	positive regulation of neuron differentiation	4	22	0.01732	3.0189561
GO	condensin complex	2	5	0.019618	3.75713179

GO	hemidesmosome	2	5	0.019618	3.75713179
GO	cAMP-dependent protein kinase inhibitor activity	2	5	0.019618	3.75713179
GO	negative regulation of oligodendrocyte differentiation	2	5	0.019618	3.75713179
GO	positive regulation of triglyceride biosynthetic process	2	5	0.019618	3.75713179
GO	nuclear origin of replication recognition complex	2	5	0.019618	3.75713179
GO	activated T cell proliferation	2	5	0.019618	3.75713179
GO	spinal cord association neuron differentiation	2	5	0.019618	3.75713179
GO	profilin binding	2	5	0.019618	3.75713179
GO	phosphatidylcholine-sterol O-acyltransferase activator activity	2	5	0.019618	3.75713179
GO	lysosomal transport	2	5	0.019618	3.75713179
GO	positive regulation of penile erection	2	5	0.019618	3.75713179
GO	pattern recognition receptor activity	2	5	0.019618	3.75713179
GO	regulation of cell proliferation	8	73	0.019642	2.56861124
GO	cortical actin cytoskeleton organization	3	13	0.020135	3.15909193
GO	positive regulation of smooth muscle contraction	3	13	0.020135	3.15909193
GO	negative regulation of Wnt receptor signaling pathway through beta-	3	13	0.020135	3.15909193
GO	embryonic skeletal system development	4	23	0.020215	2.90663095
GO	growth factor binding	4	23	0.020215	2.90663095
GO	structural molecule activity	16	196	0.020689	2.35315212
GO	RNA binding	37	562	0.021099	2.21766831
GO	interspecies interaction between organisms	21	280	0.021382	2.28755264
GO	postsynaptic membrane	13	149	0.021572	2.37615453
GO	transmembrane receptor protein tyrosine kinase activity	5	35	0.02182	2.71287618
GO	kidney development	7	61	0.022468	2.53927267
GO	homophilic cell adhesion	12	135	0.023387	2.35183035
GO	G-protein-coupled receptor binding	4	24	0.023389	2.80043095
GO	single-stranded RNA binding	3	14	0.024758	2.98525468
GO	response to X-ray	3	14	0.024758	2.98525468
GO	tubulin binding	3	14	0.024758	2.98525468
GO	artery morphogenesis	3	14	0.024758	2.98525468
GO	anatomical structure formation involved in morphogenesis	3	14	0.024758	2.98525468
GO	identical protein binding	24	338	0.026265	2.16516909
GO	stress fiber	4	25	0.026848	2.69975673
GO	osteoblast differentiation	4	25	0.026848	2.69975673
GO	heterotrimeric G-protein complex	4	25	0.026848	2.69975673
GO	response to DNA damage stimulus	8	78	0.028053	2.36005254
GO	intronless viral mRNA export from host nucleus	2	6	0.028528	3.33975763
GO	transcription export complex	2	6	0.028528	3.33975763
GO	behavioral response to nicotine	2	6	0.028528	3.33975763
GO	thyroid hormone generation	2	6	0.028528	3.33975763
GO	forebrain neuron differentiation	2	6	0.028528	3.33975763
GO	deoxyribonuclease activity	2	6	0.028528	3.33975763
GO	regulation of blood coagulation	2	6	0.028528	3.33975763
GO	mitochondrial intermembrane space protein transporter complex	2	6	0.028528	3.33975763
GO	protein import into mitochondrial inner membrane	2	6	0.028528	3.33975763
GO	response to dietary excess	2	6	0.028528	3.33975763
GO	cerebellar Purkinje cell differentiation	2	6	0.028528	3.33975763
GO	DNA replication origin binding	2	6	0.028528	3.33975763
GO	somatic hypermutation of immunoglobulin genes	2	6	0.028528	3.33975763

GO	response to folic acid	2	6	0.028528	3.33975763
GO	sarcoglycan complex	2	6	0.028528	3.33975763
GO	parathyroid gland development	2	6	0.028528	3.33975763
GO	heart contraction	2	6	0.028528	3.33975763
GO	cell cycle arrest	10	108	0.028605	2.28545436
GO	induction of apoptosis by intracellular signals	3	15	0.029902	2.8271025
GO	digestive tract development	3	15	0.029902	2.8271025
GO	N-acetylglucosamine metabolic process	3	15	0.029902	2.8271025
GO	forebrain development	6	51	0.030028	2.41951502
GO	nucleotide-excision repair	4	26	0.030598	2.60408925
GO	triglyceride metabolic process	4	26	0.030598	2.60408925
GO	branching involved in ureteric bud morphogenesis	4	26	0.030598	2.60408925
GO	skeletal system development	11	125	0.031093	2.21507036
GO	cytoskeleton	40	635	0.031604	2.01558132
GO	ureteric bud development	5	39	0.033285	2.42876491
GO	adherens junction	4	27	0.03464	2.51297642
GO	response to wounding	6	53	0.03544	2.31283812
GO	lateral plasma membrane	3	16	0.035563	2.68220749
GO	negative regulation of endothelial cell proliferation	3	16	0.035563	2.68220749
GO	mismatch repair	3	16	0.035563	2.68220749
GO	neuron fate commitment	3	16	0.035563	2.68220749
GO	blood vessel development	5	40	0.036639	2.36334607
GO	anti-apoptosis	14	178	0.038176	2.05154979
GO	cell division	18	246	0.038621	2.00500232
GO	aging	8	83	0.038675	2.16678206
GO	Arp2/3 protein complex	2	7	0.038725	3.00866917
GO	small nucleolar ribonucleoprotein complex	2	7	0.038725	3.00866917
GO	DNA damage response, signal transduction by p53 class mediator resu	2	7	0.038725	3.00866917
GO	regulation of transcription from RNA polymerase III promoter	2	7	0.038725	3.00866917
GO	tRNA modification	2	7	0.038725	3.00866917
GO	detection of mechanical stimulus involved in sensory perception of sc	2	7	0.038725	3.00866917
GO	suckling behavior	2	7	0.038725	3.00866917
GO	positive regulation of blood coagulation	2	7	0.038725	3.00866917
GO	protein heterotetramerization	2	7	0.038725	3.00866917
GO	branched chain family amino acid catabolic process	2	7	0.038725	3.00866917
GO	receptor clustering	2	7	0.038725	3.00866917
GO	negative regulation of fatty acid biosynthetic process	2	7	0.038725	3.00866917
GO	positive regulation of cholesterol esterification	2	7	0.038725	3.00866917
GO	response to reactive oxygen species	2	7	0.038725	3.00866917
GO	negative regulation of smooth muscle cell migration	2	7	0.038725	3.00866917
GO	G2 phase of mitotic cell cycle	2	7	0.038725	3.00866917
GO	postreplication repair	2	7	0.038725	3.00866917
GO	spinal cord development	2	7	0.038725	3.00866917
GO	sympathetic nervous system development	2	7	0.038725	3.00866917
GO	3',5'-cyclic-GMP phosphodiesterase activity	2	7	0.038725	3.00866917
GO	cAMP catabolic process	2	7	0.038725	3.00866917
GO	signal peptide processing	2	7	0.038725	3.00866917
GO	transcription	7	69	0.04058	2.1751121
GO	extracellular matrix structural constituent	7	69	0.04058	2.1751121

GO	fatty acid binding	3	17	0.041732	2.54864376
GO	cardiac muscle contraction	3	17	0.041732	2.54864376
GO	lipid binding	10	116	0.04354	2.04128043
GO	G1/S transition of mitotic cell cycle	5	42	0.043948	2.23833057
GO	chromosome segregation	5	42	0.043948	2.23833057
GO	RNA splicing	18	251	0.045495	1.91508361
GO	cell adhesion	33	522	0.045547	1.84677357
GO	regulation of myelination	1	1	0.046443	4.53119698
GO	regulation of myosin II filament assembly or disassembly	1	1	0.046443	4.53119698
GO	D5 dopamine receptor binding	1	1	0.046443	4.53119698
GO	positive regulation of locomotion	1	1	0.046443	4.53119698
GO	D-ribose catabolic process	1	1	0.046443	4.53119698
GO	ribonucleoside diphosphate catabolic process	1	1	0.046443	4.53119698
GO	meiosis I	1	1	0.046443	4.53119698
GO	stem cell development	1	1	0.046443	4.53119698
GO	integrin biosynthetic process	1	1	0.046443	4.53119698
GO	glycerate kinase activity	1	1	0.046443	4.53119698
GO	nuclear mRNA 5'-splice site recognition	1	1	0.046443	4.53119698
GO	coumarin metabolic process	1	1	0.046443	4.53119698
GO	dibenzo-p-dioxin catabolic process	1	1	0.046443	4.53119698
GO	flavonoid 3'-monooxygenase activity	1	1	0.046443	4.53119698
GO	flavonoid metabolic process	1	1	0.046443	4.53119698
GO	insecticide metabolic process	1	1	0.046443	4.53119698
GO	oxidoreductase activity, acting on diphenols and related substances a	1	1	0.046443	4.53119698
GO	response to herbicide	1	1	0.046443	4.53119698
GO	response to iron(III) ion	1	1	0.046443	4.53119698
GO	(S)-2-(5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxamido)succ	1	1	0.046443	4.53119698
GO	N6-(1,2-dicarboxyethyl)AMP AMP-lyase (fumarate-forming) activity	1	1	0.046443	4.53119698
GO	deoxyguanosine kinase activity	1	1	0.046443	4.53119698
GO	dGTP metabolic process	1	1	0.046443	4.53119698
GO	guanosine metabolic process	1	1	0.046443	4.53119698
GO	site-specific endodeoxyribonuclease activity, specific for altered base	1	1	0.046443	4.53119698
GO	euchromatin	1	1	0.046443	4.53119698
GO	dTDP biosynthetic process	1	1	0.046443	4.53119698
GO	nucleoside phosphate kinase activity	1	1	0.046443	4.53119698
GO	thymidylate kinase activity	1	1	0.046443	4.53119698
GO	alpha-1,4-N-acetylgalactosaminyltransferase activity	1	1	0.046443	4.53119698
GO	mesodermal cell fate specification	1	1	0.046443	4.53119698
GO	nucleus accumbens development	1	1	0.046443	4.53119698
GO	optic cup morphogenesis involved in camera-type eye development	1	1	0.046443	4.53119698
GO	ferredoxin-NADP+ reductase activity	1	1	0.046443	4.53119698
GO	double-stranded DNA specific exodeoxyribonuclease activity	1	1	0.046443	4.53119698
GO	regulation of calcium ion transport via store-operated calcium channe	1	1	0.046443	4.53119698
GO	ribose-5-phosphate isomerase activity	1	1	0.046443	4.53119698
GO	regulation of cell cycle arrest	1	1	0.046443	4.53119698
GO	phosphoribosylamine-glycine ligase activity	1	1	0.046443	4.53119698
GO	phosphoribosylformylglycinamidine cyclo-ligase activity	1	1	0.046443	4.53119698
GO	phosphoribosylglycinamide formyltransferase activity	1	1	0.046443	4.53119698
GO	3-hydroxyisobutyryl-CoA hydrolase activity	1	1	0.046443	4.53119698

GO	glycine amidinotransferase activity	1	1	0.046443	4.53119698
GO	glycine decarboxylation via glycine cleavage system	1	1	0.046443	4.53119698
GO	cochlea morphogenesis	1	1	0.046443	4.53119698
GO	floor plate formation	1	1	0.046443	4.53119698
GO	ventral spinal cord development	1	1	0.046443	4.53119698
GO	glucose-1,6-bisphosphate synthase activity	1	1	0.046443	4.53119698
GO	intramolecular transferase activity, phosphotransferases	1	1	0.046443	4.53119698
GO	induction of programmed cell death in response to chemical stimulus	1	1	0.046443	4.53119698
GO	chondroitin-glucuronate 5-epimerase activity	1	1	0.046443	4.53119698
GO	positive regulation of calcineurin-NFAT signaling pathway	1	1	0.046443	4.53119698
GO	regulation of cardiac muscle hypertrophy	1	1	0.046443	4.53119698
GO	3-hydroxy-2-methylbutyryl-CoA dehydrogenase activity	1	1	0.046443	4.53119698
GO	7-alpha-hydroxysteroid dehydrogenase activity	1	1	0.046443	4.53119698
GO	acetoacetyl-CoA reductase activity	1	1	0.046443	4.53119698
GO	interphase microtubule organizing center	1	1	0.046443	4.53119698
GO	spindle checkpoint	1	1	0.046443	4.53119698
GO	negative regulation of phosphatidylcholine catabolic process	1	1	0.046443	4.53119698
GO	plasma lipoprotein particle remodeling	1	1	0.046443	4.53119698
GO	regulation of lipid transport	1	1	0.046443	4.53119698
GO	maintenance of location in cell	1	1	0.046443	4.53119698
GO	metal chelating activity	1	1	0.046443	4.53119698
GO	positive regulation of low-density lipoprotein receptor catabolic proc	1	1	0.046443	4.53119698
GO	recombinase activity	1	1	0.046443	4.53119698
GO	interleukin-11 receptor binding	1	1	0.046443	4.53119698
GO	activin A complex	1	1	0.046443	4.53119698
GO	cellular potassium ion homeostasis	1	1	0.046443	4.53119698
GO	eye blink reflex	1	1	0.046443	4.53119698
GO	large conductance calcium-activated potassium channel activity	1	1	0.046443	4.53119698
GO	micturition	1	1	0.046443	4.53119698
GO	negative regulation of cell volume	1	1	0.046443	4.53119698
GO	regulation of aldosterone metabolic process	1	1	0.046443	4.53119698
GO	response to carbon monoxide	1	1	0.046443	4.53119698
GO	CD8 receptor binding	1	1	0.046443	4.53119698
GO	regulation of lymphocyte activation	1	1	0.046443	4.53119698
GO	regulation of intracellular protein transport	1	1	0.046443	4.53119698
GO	negative regulation of metabolic process	1	1	0.046443	4.53119698
GO	fibrillar collagen	1	1	0.046443	4.53119698
GO	negative regulation of natural killer cell mediated cytotoxicity	1	1	0.046443	4.53119698
GO	adrenocorticotropin receptor activity	1	1	0.046443	4.53119698
GO	male meiosis chromosome segregation	1	1	0.046443	4.53119698
GO	meiotic metaphase I plate congression	1	1	0.046443	4.53119698
GO	nuclear-transcribed mRNA poly(A) tail shortening	1	1	0.046443	4.53119698
GO	resolution of meiotic recombination intermediates	1	1	0.046443	4.53119698
GO	spindle midzone assembly involved in meiosis	1	1	0.046443	4.53119698
GO	development during symbiotic interaction	1	1	0.046443	4.53119698
GO	negative regulation of sodium ion transport	1	1	0.046443	4.53119698
GO	negative regulation of transcription from RNA polymerase II promote	1	1	0.046443	4.53119698
GO	positive regulation of nucleocytoplasmic transport	1	1	0.046443	4.53119698
GO	sodium channel inhibitor activity	1	1	0.046443	4.53119698

GO	transmission of virus	1	1	0.046443	4.53119698
GO	forebrain astrocyte development	1	1	0.046443	4.53119698
GO	negative regulation of transcription factor import into nucleus	1	1	0.046443	4.53119698
GO	regulation of glial cell differentiation	1	1	0.046443	4.53119698
GO	negative regulation of myeloid leukocyte differentiation	1	1	0.046443	4.53119698
GO	nucleoside diphosphate phosphorylation	1	1	0.046443	4.53119698
GO	oxidized purine base lesion DNA N-glycosylase activity	1	1	0.046443	4.53119698
GO	oxytocin receptor activity	1	1	0.046443	4.53119698
GO	negative regulation of vascular wound healing	1	1	0.046443	4.53119698
GO	negative regulation of wound healing	1	1	0.046443	4.53119698
GO	positive regulation of leukotriene production involved in inflammator	1	1	0.046443	4.53119698
GO	satellite cell commitment	1	1	0.046443	4.53119698
GO	cyclic-nucleotide phosphodiesterase activity	1	1	0.046443	4.53119698
GO	renin secretion into blood stream	1	1	0.046443	4.53119698
GO	negative regulation of cAMP-mediated signaling	1	1	0.046443	4.53119698
GO	phytanoyl-CoA dioxygenase activity	1	1	0.046443	4.53119698
GO	bent DNA binding	1	1	0.046443	4.53119698
GO	preribosome	1	1	0.046443	4.53119698
GO	inhibition of phospholipase C activity involved in G-protein coupled re	1	1	0.046443	4.53119698
GO	negative regulation of inositol phosphate biosynthetic process	1	1	0.046443	4.53119698
GO	positive regulation of inositol-polyphosphate 5-phosphatase activity	1	1	0.046443	4.53119698
GO	protein secretion by platelet	1	1	0.046443	4.53119698
GO	regulation of cell diameter	1	1	0.046443	4.53119698
GO	epithelial tube formation	1	1	0.046443	4.53119698
GO	positive regulation of cell-cell adhesion mediated by integrin	1	1	0.046443	4.53119698
GO	regulation of microvillus assembly	1	1	0.046443	4.53119698
GO	positive regulation of mammary gland epithelial cell proliferation	1	1	0.046443	4.53119698
GO	positive regulation of mucus secretion	1	1	0.046443	4.53119698
GO	regulation of telomerase activity	1	1	0.046443	4.53119698
GO	N-acetylglucosamine kinase activity	1	1	0.046443	4.53119698
GO	N-acetylmannosamine metabolic process	1	1	0.046443	4.53119698
GO	negative regulation of activation-induced cell death of T cells	1	1	0.046443	4.53119698
GO	regulation of cytokine secretion	1	1	0.046443	4.53119698
GO	induction of retinal programmed cell death	1	1	0.046443	4.53119698
GO	mitochondrial permeability transition pore complex	1	1	0.046443	4.53119698
GO	release of matrix enzymes from mitochondria	1	1	0.046443	4.53119698
GO	ethanolamine-phosphate cytidylyltransferase activity	1	1	0.046443	4.53119698
GO	smooth muscle contractile fiber	1	1	0.046443	4.53119698
GO	vascular smooth muscle contraction	1	1	0.046443	4.53119698
GO	cocaine metabolic process	1	1	0.046443	4.53119698
GO	deoxynucleotide transmembrane transporter activity	1	1	0.046443	4.53119698
GO	deoxynucleotide transport	1	1	0.046443	4.53119698
GO	ribulose-phosphate 3-epimerase activity	1	1	0.046443	4.53119698
GO	inductive cell-cell signaling	1	1	0.046443	4.53119698
GO	kidney epithelium development	1	1	0.046443	4.53119698
GO	olfactory bulb mitral cell layer development	1	1	0.046443	4.53119698
GO	ureteric bud invasion	1	1	0.046443	4.53119698
GO	chemokine-mediated signaling pathway	1	1	0.046443	4.53119698
GO	D-ribose metabolic process	1	1	0.046443	4.53119698

GO	ribokinase activity	1	1	0.046443	4.53119698
GO	negative regulation of cell division	1	1	0.046443	4.53119698
GO	Wnt receptor signaling pathway, planar cell polarity pathway	1	1	0.046443	4.53119698
GO	negative regulation of systemic arterial blood pressure	1	1	0.046443	4.53119698
GO	regulation of lung blood pressure	1	1	0.046443	4.53119698
GO	detection of mechanical stimulus involved in equilibrioception	1	1	0.046443	4.53119698
GO	diencephalon morphogenesis	1	1	0.046443	4.53119698
GO	glial cell fate commitment	1	1	0.046443	4.53119698
GO	pigment biosynthetic process	1	1	0.046443	4.53119698
GO	endochondral bone morphogenesis	1	1	0.046443	4.53119698
GO	epithelial cell proliferation involved in prostatic bud elongation	1	1	0.046443	4.53119698
GO	male germ-line sex determination	1	1	0.046443	4.53119698
GO	microtubule plus end	1	1	0.046443	4.53119698
GO	interferon-gamma-mediated signaling pathway	1	1	0.046443	4.53119698
GO	response to type I interferon	1	1	0.046443	4.53119698
GO	type I interferon-mediated signaling pathway	1	1	0.046443	4.53119698
GO	negative regulation of centriole replication	1	1	0.046443	4.53119698
GO	histone mRNA metabolic process	1	1	0.046443	4.53119698
GO	actomyosin, actin part	1	1	0.046443	4.53119698
GO	plasma membrane part	1	1	0.046443	4.53119698
GO	regulation of systemic arterial blood pressure by ischemic conditions	1	1	0.046443	4.53119698
GO	positive regulation of heart rate by epinephrine	1	1	0.046443	4.53119698
GO	deoxyribonucleoside monophosphate biosynthetic process	1	1	0.046443	4.53119698
GO	dTMP biosynthetic process	1	1	0.046443	4.53119698
GO	dUMP metabolic process	1	1	0.046443	4.53119698
GO	thymidylate synthase activity	1	1	0.046443	4.53119698
GO	uroporphyrinogen decarboxylase activity	1	1	0.046443	4.53119698
GO	uroporphyrinogen III metabolic process	1	1	0.046443	4.53119698
GO	cerebellar molecular layer development	1	1	0.046443	4.53119698
GO	cerebellum maturation	1	1	0.046443	4.53119698
GO	negative regulation of hormone biosynthetic process	1	1	0.046443	4.53119698
GO	rhythmic synaptic transmission	1	1	0.046443	4.53119698
GO	vestibular nucleus development	1	1	0.046443	4.53119698
GO	eosinophil chemotaxis	1	1	0.046443	4.53119698
GO	fatty acid elongation	1	1	0.046443	4.53119698
GO	agmatinase activity	1	1	0.046443	4.53119698
GO	putrescine biosynthetic process	1	1	0.046443	4.53119698
GO	N-terminal peptidyl-L-cysteine N-palmitoylation	1	1	0.046443	4.53119698
GO	nucleologenesis	1	1	0.046443	4.53119698
GO	rRNA metabolic process	1	1	0.046443	4.53119698
GO	RNA polymerase II transcription termination factor activity	1	1	0.046443	4.53119698
GO	polarized epithelial cell differentiation	1	1	0.046443	4.53119698
GO	squamous basal epithelial stem cell differentiation involved in prostat	1	1	0.046443	4.53119698
GO	1-pyrroline-5-carboxylate dehydrogenase activity	1	1	0.046443	4.53119698
GO	tRNA (uracil) methyltransferase activity	1	1	0.046443	4.53119698
GO	25-hydroxycholesterol 7alpha-hydroxylase activity	1	1	0.046443	4.53119698
GO	metabotropic glutamate receptor binding	1	1	0.046443	4.53119698
GO	heparan sulfate 2-O-sulfotransferase activity	1	1	0.046443	4.53119698
GO	heparin metabolic process	1	1	0.046443	4.53119698

GO	synaptic transmission	13	167	0.047771	1.93677038
GO	structural constituent of muscle	5	43	0.047907	2.17851621
GO	tRNA processing	6	57	0.048047	2.1133471
GO	neuron migration	6	57	0.048047	2.1133471
GO	regulation of protein localization	3	18	0.0484	2.42486084
GO	response to corticosterone stimulus	3	18	0.0484	2.42486084
GO	response to inorganic substance	3	18	0.0484	2.42486084
GO	DNA helicase activity	3	18	0.0484	2.42486084
GO	beta-amyloid binding	3	18	0.0484	2.42486084
GO	beta-tubulin binding	3	18	0.0484	2.42486084
GO	response to UV	4	30	0.048538	2.26323683
GO	response to arsenic	2	8	0.05007	2.73638556
GO	response to hyperoxia	2	8	0.05007	2.73638556
GO	nucleotide biosynthetic process	2	8	0.05007	2.73638556
GO	determination of adult lifespan	2	8	0.05007	2.73638556
GO	hemopoietic progenitor cell differentiation	2	8	0.05007	2.73638556
GO	nuclear localization sequence binding	2	8	0.05007	2.73638556
GO	mismatched DNA binding	2	8	0.05007	2.73638556
GO	proline-rich region binding	2	8	0.05007	2.73638556
GO	pharyngeal system development	2	8	0.05007	2.73638556
GO	positive regulation of MAPKKK cascade	4	31	0.05376	2.18682364
GO	heparin binding	9	105	0.055356	1.91746741
GO	DNA metabolic process	3	19	0.055554	2.30959415
GO	nucleocytoplasmic transport	3	19	0.055554	2.30959415
GO	high-density lipoprotein particle	3	19	0.055554	2.30959415
GO	very-low-density lipoprotein particle	3	19	0.055554	2.30959415
GO	response to amino acid stimulus	3	19	0.055554	2.30959415
GO	neuron projection	6	60	0.059108	1.97439234
GO	nuclear pore	6	60	0.059108	1.97439234
GO	peptidyl-prolyl cis-trans isomerase activity	4	32	0.059273	2.11339496
GO	manganese ion binding	4	32	0.059273	2.11339496
GO	sensory perception of sound	8	91	0.060719	1.88426735
GO	response to hypoxia	11	140	0.061627	1.81306925
GO	Rac GTPase activator activity	2	9	0.062435	2.50637742
GO	retinal binding	2	9	0.062435	2.50637742
GO	female gonad development	2	9	0.062435	2.50637742
GO	skeletal muscle tissue regeneration	2	9	0.062435	2.50637742
GO	spectrin	2	9	0.062435	2.50637742
GO	aldehyde dehydrogenase (NAD) activity	2	9	0.062435	2.50637742
GO	lamellipodium membrane	2	9	0.062435	2.50637742
GO	regulation of smoothened signaling pathway	2	9	0.062435	2.50637742
GO	M band	2	9	0.062435	2.50637742
GO	positive regulation of synaptic transmission	2	9	0.062435	2.50637742
GO	GTP biosynthetic process	2	9	0.062435	2.50637742
GO	nucleoside diphosphate kinase activity	2	9	0.062435	2.50637742
GO	UTP biosynthetic process	2	9	0.062435	2.50637742
GO	phospholipid efflux	2	9	0.062435	2.50637742
GO	muscle filament sliding	2	9	0.062435	2.50637742
GO	smooth muscle tissue development	2	9	0.062435	2.50637742

GO	response to growth factor stimulus	2	9	0.062435	2.50637742
GO	ruffle organization	2	9	0.062435	2.50637742
GO	DNA damage response, signal transduction by p53 class mediator resu	2	9	0.062435	2.50637742
GO	positive regulation of neuron apoptosis	3	20	0.06318	2.20180026
GO	adult walking behavior	3	20	0.06318	2.20180026
GO	response to organic cyclic substance	8	92	0.063933	1.85098428
GO	elevation of cytosolic calcium ion concentration	8	92	0.063933	1.85098428
GO	negative regulation of transcription from RNA polymerase II promote	16	227	0.064357	1.73157417
GO	phosphoinositide-mediated signaling	4	33	0.065076	2.04273238
GO	apical plasma membrane	12	159	0.067096	1.74665009
GO	negative regulation of signal transduction	5	48	0.070762	1.90273605
GO	collagen binding	4	34	0.071163	1.97463975
GO	response to retinoic acid	4	34	0.071163	1.97463975
GO	ATP binding	78	1426	0.072549	1.54029133
GO	Ras GTPase activator activity	2	10	0.075701	2.30801548
GO	substrate adhesion-dependent cell spreading	2	10	0.075701	2.30801548
GO	NAD binding	2	10	0.075701	2.30801548
GO	general transcriptional repressor activity	2	10	0.075701	2.30801548
GO	limb morphogenesis	2	10	0.075701	2.30801548
GO	receptor internalization	2	10	0.075701	2.30801548
GO	isotype switching	2	10	0.075701	2.30801548
GO	prefoldin complex	2	10	0.075701	2.30801548
GO	ribosomal large subunit biogenesis	2	10	0.075701	2.30801548
GO	vascular endothelial growth factor receptor signaling pathway	2	10	0.075701	2.30801548
GO	G2/M transition DNA damage checkpoint	2	10	0.075701	2.30801548
GO	acetylglucosaminyltransferase activity	2	10	0.075701	2.30801548
GO	caveola	5	49	0.075941	1.85170262
GO	calcium ion binding	36	605	0.076793	1.55146487
GO	circadian rhythm	4	35	0.077529	1.90894029
GO	calcium-independent cell-cell adhesion	3	22	0.079776	2.00528928
GO	eating behavior	3	22	0.079776	2.00528928
GO	protein heterodimerization activity	14	199	0.080639	1.61110896
GO	activation of caspase activity	5	50	0.081319	1.80188952
GO	anterior/posterior pattern formation	7	81	0.082043	1.71329634
GO	nervous system development	24	382	0.082978	1.5371756
GO	transporter activity	19	290	0.083466	1.55539774
GO	somitogenesis	4	36	0.08417	1.84547417
GO	DNA-directed RNA polymerase activity	4	36	0.08417	1.84547417
GO	odontogenesis of dentine-containing tooth	4	36	0.08417	1.84547417
GO	lipid transport	6	66	0.085414	1.71953594
GO	synapse	17	255	0.086481	1.54496706
GO	negative regulation of neuron apoptosis	5	51	0.086894	1.75323972
GO	ATP-dependent DNA helicase activity	3	23	0.08871	1.91521911
GO	activation of MAPKK activity	3	23	0.08871	1.91521911
GO	negative regulation of cell adhesion	3	23	0.08871	1.91521911
GO	developmental growth	3	23	0.08871	1.91521911
GO	nuclear chromosome	3	23	0.08871	1.91521911
GO	somatic stem cell maintenance	2	11	0.089757	2.13410564
GO	GTPase inhibitor activity	2	11	0.089757	2.13410564

GO	glycosaminoglycan biosynthetic process	2	11	0.089757	2.13410564
GO	mitotic metaphase plate congression	2	11	0.089757	2.13410564
GO	retinol binding	2	11	0.089757	2.13410564
GO	platelet-derived growth factor binding	2	11	0.089757	2.13410564
GO	fibroblast growth factor binding	2	11	0.089757	2.13410564
GO	chylomicron	2	11	0.089757	2.13410564
GO	negative regulation of lipid catabolic process	2	11	0.089757	2.13410564
GO	vasodilation	2	11	0.089757	2.13410564
GO	3',5'-cyclic-nucleotide phosphodiesterase activity	2	11	0.089757	2.13410564
GO	large ribosomal subunit	2	11	0.089757	2.13410564
GO	dipeptidase activity	2	11	0.089757	2.13410564
GO	phosphatidylinositol-3,4-bisphosphate binding	2	11	0.089757	2.13410564
GO	replication fork	2	11	0.089757	2.13410564
GO	ubiquitin activating enzyme activity	1	2	0.090731	3.04806739
GO	C21-steroid hormone metabolic process	1	2	0.090731	3.04806739
GO	cardiac right ventricle morphogenesis	1	2	0.090731	3.04806739
GO	pulmonary myocardium development	1	2	0.090731	3.04806739
GO	semaphorin receptor binding	1	2	0.090731	3.04806739
GO	activation of phospholipase D activity	1	2	0.090731	3.04806739
GO	tRNA (guanine-N7-)-methyltransferase activity	1	2	0.090731	3.04806739
GO	ADP-sugar diphosphatase activity	1	2	0.090731	3.04806739
GO	Rab-protein geranylgeranyltransferase complex	1	2	0.090731	3.04806739
GO	regulation of cellular component organization	1	2	0.090731	3.04806739
GO	deacetylase activity	1	2	0.090731	3.04806739
GO	collagen type XI	1	2	0.090731	3.04806739
GO	cytoplasmic transport	1	2	0.090731	3.04806739
GO	radial glia guided migration of Purkinje cell	1	2	0.090731	3.04806739
GO	regulation of synapse structural plasticity	1	2	0.090731	3.04806739
GO	CTP synthase activity	1	2	0.090731	3.04806739
GO	demethylase activity	1	2	0.090731	3.04806739
GO	developmental process	1	2	0.090731	3.04806739
GO	vitamin D 24-hydroxylase activity	1	2	0.090731	3.04806739
GO	benzodiazepine receptor binding	1	2	0.090731	3.04806739
GO	cerebral cortex GABAergic interneuron fate commitment	1	2	0.090731	3.04806739
GO	regulation of transcription from RNA polymerase II promoter involvec	1	2	0.090731	3.04806739
GO	gamma DNA polymerase complex	1	2	0.090731	3.04806739
GO	tRNA (cytosine-5-)-methyltransferase activity	1	2	0.090731	3.04806739
GO	DNA (cytosine-5-)-methyltransferase activity, acting on CpG substrate	1	2	0.090731	3.04806739
GO	DNA methylation on cytosine within a CG sequence	1	2	0.090731	3.04806739
GO	annulate lamellae	1	2	0.090731	3.04806739
GO	PH domain binding	1	2	0.090731	3.04806739
GO	glucuronyl-galactosyl-proteoglycan 4-alpha-N-acetylglucosaminyltran	1	2	0.090731	3.04806739
GO	establishment of synaptic specificity at neuromuscular junction	1	2	0.090731	3.04806739
GO	platelet dense tubular network	1	2	0.090731	3.04806739
GO	olfactory pit development	1	2	0.090731	3.04806739
GO	retinoic acid biosynthetic process	1	2	0.090731	3.04806739
GO	de novo' protein folding	1	2	0.090731	3.04806739
GO	negative regulation of protein phosphatase type 2B activity	1	2	0.090731	3.04806739
GO	regulation of cardiac muscle contraction by regulation of the release	1	2	0.090731	3.04806739

GO	release of sequestered calcium ion into cytosol by sarcoplasmic reticu	1	2	0.090731	3.04806739
GO	pentose-phosphate shunt, non-oxidative branch	1	2	0.090731	3.04806739
GO	glycerol-3-phosphate catabolic process	1	2	0.090731	3.04806739
GO	negative regulation of actin filament polymerization	1	2	0.090731	3.04806739
GO	positive regulation of plasma membrane long-chain fatty acid transpo	1	2	0.090731	3.04806739
GO	trans-hexaprenyltranstransferase activity	1	2	0.090731	3.04806739
GO	trans-octaprenyltranstransferase activity	1	2	0.090731	3.04806739
GO	detection of stimulus	1	2	0.090731	3.04806739
GO	T cell mediated cytotoxicity	1	2	0.090731	3.04806739
GO	arachidonate 5-lipoxygenase activity	1	2	0.090731	3.04806739
GO	hydroxyacylglutathione hydrolase activity	1	2	0.090731	3.04806739
GO	carbon-carbon lyase activity	1	2	0.090731	3.04806739
GO	creatine biosynthetic process	1	2	0.090731	3.04806739
GO	glycine cleavage complex	1	2	0.090731	3.04806739
GO	notochord regression	1	2	0.090731	3.04806739
GO	smoothened signaling pathway involved in spinal cord motor neuron	1	2	0.090731	3.04806739
GO	smoothened signaling pathway involved in ventral spinal cord interne	1	2	0.090731	3.04806739
GO	specification of segmental identity, maxillary segment	1	2	0.090731	3.04806739
GO	spinal cord ventral commissure morphogenesis	1	2	0.090731	3.04806739
GO	response to lipid hydroperoxide	1	2	0.090731	3.04806739
GO	kainate selective glutamate receptor complex	1	2	0.090731	3.04806739
GO	voltage-gated cation channel activity	1	2	0.090731	3.04806739
GO	cytoplasm organization	1	2	0.090731	3.04806739
GO	positive regulation of growth	1	2	0.090731	3.04806739
GO	dermatan sulfate biosynthetic process	1	2	0.090731	3.04806739
GO	hydroxymethylglutaryl-CoA synthase activity	1	2	0.090731	3.04806739
GO	positive regulation of cell development	1	2	0.090731	3.04806739
GO	15-hydroxyprostaglandin dehydrogenase (NAD+) activity	1	2	0.090731	3.04806739
GO	N-methyltransferase activity	1	2	0.090731	3.04806739
GO	establishment of chromosome localization	1	2	0.090731	3.04806739
GO	follistatin binding	1	2	0.090731	3.04806739
GO	inhibin A complex	1	2	0.090731	3.04806739
GO	negative regulation of lipoprotein metabolic process	1	2	0.090731	3.04806739
GO	neuronal cell body membrane	1	2	0.090731	3.04806739
GO	smooth muscle contraction involved in micturition	1	2	0.090731	3.04806739
GO	M phase specific microtubule process	1	2	0.090731	3.04806739
GO	CD4 receptor binding	1	2	0.090731	3.04806739
GO	leptin-mediated signaling pathway	1	2	0.090731	3.04806739
GO	cerebellar Purkinje cell-granule cell precursor cell signaling involved ir	1	2	0.090731	3.04806739
GO	ectoderm formation	1	2	0.090731	3.04806739
GO	forebrain regionalization	1	2	0.090731	3.04806739
GO	head development	1	2	0.090731	3.04806739
GO	angiotensin receptor binding	1	2	0.090731	3.04806739
GO	N-acetylgalactosamine-4-sulfatase activity	1	2	0.090731	3.04806739
GO	chiasma	1	2	0.090731	3.04806739
GO	MutLalpha complex	1	2	0.090731	3.04806739
GO	B cell mediated immunity	1	2	0.090731	3.04806739
GO	dinucleotide repeat insertion binding	1	2	0.090731	3.04806739
GO	MutSalpha complex	1	2	0.090731	3.04806739

GO	MutSbeta complex	1	2	0.090731	3.04806739
GO	single thymine insertion binding	1	2	0.090731	3.04806739
GO	beta-2 adrenergic receptor binding	1	2	0.090731	3.04806739
GO	phosphothreonine binding	1	2	0.090731	3.04806739
GO	regulation of Ras GTPase activity	1	2	0.090731	3.04806739
GO	Schwann cell development	1	2	0.090731	3.04806739
GO	hydrogen:potassium-exchanging ATPase complex	1	2	0.090731	3.04806739
GO	protein import into nucleus, docking	1	2	0.090731	3.04806739
GO	regulation of fibroblast growth factor receptor signaling pathway	1	2	0.090731	3.04806739
GO	regulation of digestive system process	1	2	0.090731	3.04806739
GO	response to anoxia	1	2	0.090731	3.04806739
GO	negative regulation of norepinephrine secretion	1	2	0.090731	3.04806739
GO	UDP-activated nucleotide receptor activity	1	2	0.090731	3.04806739
GO	chronological cell aging	1	2	0.090731	3.04806739
GO	viral assembly, maturation, egress, and release	1	2	0.090731	3.04806739
GO	cGMP-inhibited cyclic-nucleotide phosphodiesterase activity	1	2	0.090731	3.04806739
GO	regulation of morphogenesis of a branching structure	1	2	0.090731	3.04806739
GO	negative regulation of calcium-mediated signaling	1	2	0.090731	3.04806739
GO	platelet degranulation	1	2	0.090731	3.04806739
GO	positive regulation of actin filament depolymerization	1	2	0.090731	3.04806739
GO	positive regulation of integrin activation	1	2	0.090731	3.04806739
GO	thrombin receptor signaling pathway	1	2	0.090731	3.04806739
GO	calcium-dependent cell-matrix adhesion	1	2	0.090731	3.04806739
GO	telomeric RNA binding	1	2	0.090731	3.04806739
GO	drug transmembrane transport	1	2	0.090731	3.04806739
GO	oleoyl-[acyl-carrier-protein] hydrolase activity	1	2	0.090731	3.04806739
GO	dosage compensation	1	2	0.090731	3.04806739
GO	N-acylmannosamine kinase activity	1	2	0.090731	3.04806739
GO	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA,	1	2	0.090731	3.04806739
GO	preribosome, large subunit precursor	1	2	0.090731	3.04806739
GO	mRNA (2'-O-methyladenosine-N6-)-methyltransferase activity	1	2	0.090731	3.04806739
GO	interleukin-2 secretion	1	2	0.090731	3.04806739
GO	BH3 domain binding	1	2	0.090731	3.04806739
GO	establishment or maintenance of transmembrane electrochemical gra	1	2	0.090731	3.04806739
GO	mitochondrial fragmentation involved in apoptosis	1	2	0.090731	3.04806739
GO	nuclear fragmentation involved in apoptotic nuclear change	1	2	0.090731	3.04806739
GO	branched chain family amino acid biosynthetic process	1	2	0.090731	3.04806739
GO	branched-chain-amino-acid transaminase activity	1	2	0.090731	3.04806739
GO	crossover junction endodeoxyribonuclease activity	1	2	0.090731	3.04806739
GO	female meiosis sister chromatid cohesion	1	2	0.090731	3.04806739
GO	acetylcholinesterase activity	1	2	0.090731	3.04806739
GO	response to alkaloid	1	2	0.090731	3.04806739
GO	DNA strand renaturation	1	2	0.090731	3.04806739
GO	class I ribonucleotide reductase activity	1	2	0.090731	3.04806739
GO	deoxyribonucleoside diphosphate metabolic process	1	2	0.090731	3.04806739
GO	olfactory bulb interneuron differentiation	1	2	0.090731	3.04806739
GO	olfactory nerve development	1	2	0.090731	3.04806739
GO	regulation of vascular endothelial growth factor production	1	2	0.090731	3.04806739
GO	response to vitamin B3	1	2	0.090731	3.04806739

GO	alpha-beta T cell differentiation	1	2	0.090731	3.04806739
GO	four-way junction helicase activity	1	2	0.090731	3.04806739
GO	replication fork processing	1	2	0.090731	3.04806739
GO	negative regulation of axon regeneration	1	2	0.090731	3.04806739
GO	protein xylosyltransferase activity	1	2	0.090731	3.04806739
GO	fructose transmembrane transporter activity	1	2	0.090731	3.04806739
GO	fructose transport	1	2	0.090731	3.04806739
GO	cytosolic calcium ion transport	1	2	0.090731	3.04806739
GO	negative regulation of vasoconstriction	1	2	0.090731	3.04806739
GO	negative regulation of viral transcription	1	2	0.090731	3.04806739
GO	nuclear periphery	1	2	0.090731	3.04806739
GO	cytokinesis, completion of separation	1	2	0.090731	3.04806739
GO	protein hexamerization	1	2	0.090731	3.04806739
GO	2,3-bisphospho-D-glycerate 2-phosphohydrolase activity	1	2	0.090731	3.04806739
GO	bisphosphoglycerate mutase activity	1	2	0.090731	3.04806739
GO	phosphoglycerate mutase activity	1	2	0.090731	3.04806739
GO	cuticular plate	1	2	0.090731	3.04806739
GO	BRCA1-BARD1 complex	1	2	0.090731	3.04806739
GO	alcohol sulfotransferase activity	1	2	0.090731	3.04806739
GO	steroid sulfotransferase activity	1	2	0.090731	3.04806739
GO	sulfonylurea receptor activity	1	2	0.090731	3.04806739
GO	transferrin receptor activity	1	2	0.090731	3.04806739
GO	negative regulation of endothelial cell differentiation	1	2	0.090731	3.04806739
GO	ISG15 ligase activity	1	2	0.090731	3.04806739
GO	musculoskeletal movement, spinal reflex action	1	2	0.090731	3.04806739
GO	sulfur amino acid metabolic process	1	2	0.090731	3.04806739
GO	regulation of fat cell differentiation	1	2	0.090731	3.04806739
GO	labyrinthine layer morphogenesis	1	2	0.090731	3.04806739
GO	carbohydrate mediated signaling	1	2	0.090731	3.04806739
GO	beta-galactoside alpha-2,6-sialyltransferase activity	1	2	0.090731	3.04806739
GO	chromatin silencing at telomere	1	2	0.090731	3.04806739
GO	internal protein amino acid acetylation	1	2	0.090731	3.04806739
GO	cloacal septation	1	2	0.090731	3.04806739
GO	female genitalia morphogenesis	1	2	0.090731	3.04806739
GO	rough microsome	1	2	0.090731	3.04806739
GO	proline metabolic process	1	2	0.090731	3.04806739
GO	JAK pathway signal transduction adaptor activity	1	2	0.090731	3.04806739
GO	prolactin receptor binding	1	2	0.090731	3.04806739
GO	male pronucleus	1	2	0.090731	3.04806739
GO	antral ovarian follicle growth	1	2	0.090731	3.04806739
GO	response to purine	1	2	0.090731	3.04806739
GO	cell-substrate adherens junction	1	2	0.090731	3.04806739
GO	D-amino acid catabolic process	1	2	0.090731	3.04806739
GO	oxysterol 7-alpha-hydroxylase activity	1	2	0.090731	3.04806739
GO	GKAP/Homer scaffold activity	1	2	0.090731	3.04806739
GO	acylphosphatase activity	1	2	0.090731	3.04806739
GO	stereocilium bundle	1	2	0.090731	3.04806739
GO	phosphatase regulator activity	1	2	0.090731	3.04806739
GO	central nervous system development	8	100	0.093389	1.59876183

GO	protein domain specific binding	9	117	0.094419	1.57146627
GO	ubiquitin thiolesterase activity	6	68	0.095409	1.64052904
GO	calcium-dependent cell-cell adhesion	3	24	0.098042	1.8298677
GO	platelet activation	3	24	0.098042	1.8298677
GO	regulation of membrane potential	3	24	0.098042	1.8298677
GO	neuromuscular junction	3	24	0.098042	1.8298677
GO	response to progesterone stimulus	3	24	0.098042	1.8298677
GO	negative regulation of cell migration	4	38	0.09825	1.72467556
GO	spliceosomal complex	9	118	0.098254	1.54445556
GO	nucleotide binding	98	1859	0.099123	1.35323039
GO	lipid metabolic process	14	206	0.099716	1.47557397
GO	voltage-gated potassium channel complex	7	85	0.099837	1.57671243
GO	ligand-dependent nuclear receptor binding	2	12	0.104501	1.9795776
GO	tissue development	2	12	0.104501	1.9795776
GO	dendrite morphogenesis	2	12	0.104501	1.9795776
GO	release of sequestered calcium ion into cytosol	2	12	0.104501	1.9795776
GO	smooth muscle contraction	2	12	0.104501	1.9795776
GO	septin complex	2	12	0.104501	1.9795776
GO	mitochondrial inner membrane presequence translocase complex	2	12	0.104501	1.9795776
GO	regulation of muscle contraction	2	12	0.104501	1.9795776
GO	caspase inhibitor activity	2	12	0.104501	1.9795776
GO	low-density lipoprotein particle	2	12	0.104501	1.9795776
GO	response to electrical stimulus	2	12	0.104501	1.9795776
GO	alpha-tubulin binding	2	12	0.104501	1.9795776
GO	response to chemical stimulus	2	12	0.104501	1.9795776
GO	ubiquitin ligase complex	5	54	0.104773	1.61375448
GO	androgen receptor signaling pathway	4	39	0.105675	1.66709121
GO	response to antibiotic	3	25	0.10775	1.74877776
GO	nucleotide metabolic process	3	25	0.10775	1.74877776
GO	midbody	3	25	0.10775	1.74877776
GO	protein polymerization	3	25	0.10775	1.74877776
GO	nucleotidyltransferase activity	6	71	0.111514	1.52690392
GO	ubiquitin-dependent protein catabolic process	10	139	0.112911	1.4337959
GO	enzyme activator activity	4	40	0.113346	1.61123371
GO	embryonic development	6	72	0.117172	1.49024583
GO	response to nutrient	6	72	0.117172	1.49024583
GO	embryo implantation	3	26	0.117814	1.67155306
GO	cellular response to hormone stimulus	3	26	0.117814	1.67155306
GO	negative regulation of phosphorylation	2	13	0.119841	1.84073838
GO	acetylcholine receptor activity	2	13	0.119841	1.84073838
GO	protein autoubiquitination	2	13	0.119841	1.84073838
GO	oogenesis	2	13	0.119841	1.84073838
GO	embryonic cranial skeleton morphogenesis	2	13	0.119841	1.84073838
GO	synaptic transmission, glutamatergic	2	13	0.119841	1.84073838
GO	high-density lipoprotein particle remodeling	2	13	0.119841	1.84073838
GO	hormone metabolic process	2	13	0.119841	1.84073838
GO	myosin binding	2	13	0.119841	1.84073838
GO	positive regulation of stress fiber assembly	2	13	0.119841	1.84073838
GO	centrosome organization	2	13	0.119841	1.84073838

GO	coated pit	4	41	0.121254	1.55700252
GO	myosin complex	4	41	0.121254	1.55700252
GO	magnesium ion binding	11	159	0.121958	1.36822318
GO	nucleolus	39	692	0.122428	1.26262769
GO	integrin-mediated signaling pathway	5	57	0.12431	1.48301391
GO	protein complex binding	7	90	0.12479	1.41590316
GO	neuron development	3	27	0.12821	1.59784823
GO	kinase binding	3	27	0.12821	1.59784823
GO	ATP synthesis coupled proton transport	3	27	0.12821	1.59784823
GO	JAK-STAT cascade	3	27	0.12821	1.59784823
GO	vasculogenesis	4	42	0.129391	1.50430533
GO	negative regulation of cell growth	7	91	0.13013	1.38494938
GO	synaptosome	7	91	0.13013	1.38494938
GO	microtubule binding	5	58	0.131171	1.44119065
GO	cholesterol metabolic process	5	58	0.131171	1.44119065
GO	positive regulation of lamellipodium assembly	1	3	0.132965	2.3613787
GO	carbonyl reductase (NADPH) activity	1	3	0.132965	2.3613787
GO	negative regulation of stress fiber assembly	1	3	0.132965	2.3613787
GO	U4/U6 snRNP	1	3	0.132965	2.3613787
GO	limb bud formation	1	3	0.132965	2.3613787
GO	regulation of Rac GTPase activity	1	3	0.132965	2.3613787
GO	ADP-ribose diphosphatase activity	1	3	0.132965	2.3613787
GO	cohesin complex	1	3	0.132965	2.3613787
GO	interphase of mitotic cell cycle	1	3	0.132965	2.3613787
GO	synaptic transmission involved in micturition	1	3	0.132965	2.3613787
GO	nucleotide-excision repair complex	1	3	0.132965	2.3613787
GO	proteoglycan binding	1	3	0.132965	2.3613787
GO	lipase activity	1	3	0.132965	2.3613787
GO	serine hydrolase activity	1	3	0.132965	2.3613787
GO	negative regulation of nuclear mRNA splicing, via spliceosome	1	3	0.132965	2.3613787
GO	NEDD8 ligase activity	1	3	0.132965	2.3613787
GO	positive regulation of vascular permeability	1	3	0.132965	2.3613787
GO	porphyrin metabolic process	1	3	0.132965	2.3613787
GO	positive regulation of S phase of mitotic cell cycle	1	3	0.132965	2.3613787
GO	response to nematode	1	3	0.132965	2.3613787
GO	AMP biosynthetic process	1	3	0.132965	2.3613787
GO	thyroxine 5'-deiodinase activity	1	3	0.132965	2.3613787
GO	DNA methylation involved in embryonic development	1	3	0.132965	2.3613787
GO	S-adenosylmethioninamine metabolic process	1	3	0.132965	2.3613787
GO	positive regulation of translational elongation	1	3	0.132965	2.3613787
GO	positive regulation of translational termination	1	3	0.132965	2.3613787
GO	translational frameshifting	1	3	0.132965	2.3613787
GO	UDP-N-acetylgalactosamine metabolic process	1	3	0.132965	2.3613787
GO	histone dephosphorylation	1	3	0.132965	2.3613787
GO	connective tissue replacement during inflammatory response	1	3	0.132965	2.3613787
GO	regulation of interleukin-1 beta production	1	3	0.132965	2.3613787
GO	STAT protein nuclear translocation	1	3	0.132965	2.3613787
GO	tyrosine phosphorylation of STAT protein	1	3	0.132965	2.3613787
GO	thyroid hormone binding	1	3	0.132965	2.3613787

GO	substrate-bound cell migration	1	3	0.132965	2.3613787
GO	negative regulation of heart rate	1	3	0.132965	2.3613787
GO	negative regulation of stress-activated MAPK cascade	1	3	0.132965	2.3613787
GO	regulation of oxygen and reactive oxygen species metabolic process	1	3	0.132965	2.3613787
GO	nicotinamide-nucleotide adenylyltransferase activity	1	3	0.132965	2.3613787
GO	nicotinate-nucleotide adenylyltransferase activity	1	3	0.132965	2.3613787
GO	glycerol-3-phosphate dehydrogenase (NAD+) activity	1	3	0.132965	2.3613787
GO	glycerol-3-phosphate dehydrogenase complex	1	3	0.132965	2.3613787
GO	intracellular receptor mediated signaling pathway	1	3	0.132965	2.3613787
GO	susceptibility to natural killer cell mediated cytotoxicity	1	3	0.132965	2.3613787
GO	cellular response to calcium ion	1	3	0.132965	2.3613787
GO	Rap GTPase activator activity	1	3	0.132965	2.3613787
GO	de novo' IMP biosynthetic process	1	3	0.132965	2.3613787
GO	organ development	1	3	0.132965	2.3613787
GO	cerebellar cortex morphogenesis	1	3	0.132965	2.3613787
GO	epidermal cell differentiation	1	3	0.132965	2.3613787
GO	smoothened signaling pathway involved in dorsal/ventral neural tube	1	3	0.132965	2.3613787
GO	tube development	1	3	0.132965	2.3613787
GO	ventral midline development	1	3	0.132965	2.3613787
GO	response to molecule of fungal origin	1	3	0.132965	2.3613787
GO	salivary gland development	1	3	0.132965	2.3613787
GO	hyaluronan synthase activity	1	3	0.132965	2.3613787
GO	peripheral nervous system neuron development	1	3	0.132965	2.3613787
GO	spinal cord motor neuron cell fate specification	1	3	0.132965	2.3613787
GO	chromosome passenger complex	1	3	0.132965	2.3613787
GO	cobalt ion binding	1	3	0.132965	2.3613787
GO	lipase inhibitor activity	1	3	0.132965	2.3613787
GO	negative regulation of cholesterol transport	1	3	0.132965	2.3613787
GO	negative regulation of lipid metabolic process	1	3	0.132965	2.3613787
GO	negative regulation of very-low-density lipoprotein particle clearance	1	3	0.132965	2.3613787
GO	intermediate-density lipoprotein particle	1	3	0.132965	2.3613787
GO	negative regulation of cholesterol biosynthetic process	1	3	0.132965	2.3613787
GO	very-low-density lipoprotein receptor binding	1	3	0.132965	2.3613787
GO	negative regulation of smooth muscle cell apoptosis	1	3	0.132965	2.3613787
GO	positive regulation of necrotic cell death	1	3	0.132965	2.3613787
GO	negative regulation of B cell differentiation	1	3	0.132965	2.3613787
GO	negative regulation of interferon-gamma biosynthetic process	1	3	0.132965	2.3613787
GO	positive regulation of follicle-stimulating hormone secretion	1	3	0.132965	2.3613787
GO	negative regulation of low-density lipoprotein receptor biosynthetic p	1	3	0.132965	2.3613787
GO	A-type (transient outward) potassium channel activity	1	3	0.132965	2.3613787
GO	locomotor rhythm	1	3	0.132965	2.3613787
GO	relaxation of vascular smooth muscle	1	3	0.132965	2.3613787
GO	miRNA catabolic process	1	3	0.132965	2.3613787
GO	positive regulation of T cell receptor signaling pathway	1	3	0.132965	2.3613787
GO	phagocytic cup	1	3	0.132965	2.3613787
GO	T cell activation during immune response	1	3	0.132965	2.3613787
GO	regulation of gluconeogenesis	1	3	0.132965	2.3613787
GO	aryl hydrocarbon receptor binding	1	3	0.132965	2.3613787
GO	desensitization of G-protein coupled receptor protein signaling pathw	1	3	0.132965	2.3613787

GO	myeloid progenitor cell differentiation	1	3	0.132965	2.3613787
GO	dinucleotide insertion or deletion binding	1	3	0.132965	2.3613787
GO	four-way junction DNA binding	1	3	0.132965	2.3613787
GO	maintenance of DNA repeat elements	1	3	0.132965	2.3613787
GO	oxidized purine DNA binding	1	3	0.132965	2.3613787
GO	single guanine insertion binding	1	3	0.132965	2.3613787
GO	negative regulation of vascular endothelial growth factor receptor sig	1	3	0.132965	2.3613787
GO	phosphoserine binding	1	3	0.132965	2.3613787
GO	positive regulation of Ras GTPase activity	1	3	0.132965	2.3613787
GO	regulation of blood vessel endothelial cell migration	1	3	0.132965	2.3613787
GO	regulation of bone resorption	1	3	0.132965	2.3613787
GO	hydrogen:potassium-exchanging ATPase activity	1	3	0.132965	2.3613787
GO	visual behavior	1	3	0.132965	2.3613787
GO	clustering of voltage-gated sodium channels	1	3	0.132965	2.3613787
GO	nuclear pore organization	1	3	0.132965	2.3613787
GO	depurination	1	3	0.132965	2.3613787
GO	origin recognition complex	1	3	0.132965	2.3613787
GO	estrous cycle phase	1	3	0.132965	2.3613787
GO	positive regulation of norepinephrine secretion	1	3	0.132965	2.3613787
GO	negative regulation of endopeptidase activity	1	3	0.132965	2.3613787
GO	negative regulation of plasminogen activation	1	3	0.132965	2.3613787
GO	positive regulation of monocyte chemotaxis	1	3	0.132965	2.3613787
GO	cGMP catabolic process	1	3	0.132965	2.3613787
GO	protein-L-isoaspartate (D-aspartate) O-methyltransferase activity	1	3	0.132965	2.3613787
GO	respiratory tube development	1	3	0.132965	2.3613787
GO	proton-transporting two-sector ATPase complex, catalytic domain	1	3	0.132965	2.3613787
GO	positive regulation of actin filament bundle assembly	1	3	0.132965	2.3613787
GO	protein kinase C signaling cascade	1	3	0.132965	2.3613787
GO	epithelial cell proliferation involved in mammary gland duct elongatic	1	3	0.132965	2.3613787
GO	mammary gland branching involved in pregnancy	1	3	0.132965	2.3613787
GO	telomerase inhibitor activity	1	3	0.132965	2.3613787
GO	telomere formation via telomerase	1	3	0.132965	2.3613787
GO	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA,	1	3	0.132965	2.3613787
GO	PeBoW complex	1	3	0.132965	2.3613787
GO	inositol 1,3,4,5 tetrakisphosphate binding	1	3	0.132965	2.3613787
GO	RNA methylation	1	3	0.132965	2.3613787
GO	Y-form DNA binding	1	3	0.132965	2.3613787
GO	peptidyl-amino acid modification	1	3	0.132965	2.3613787
GO	cAMP metabolic process	1	3	0.132965	2.3613787
GO	fatty acid homeostasis	1	3	0.132965	2.3613787
GO	glycerophospholipid metabolic process	1	3	0.132965	2.3613787
GO	B cell apoptosis	1	3	0.132965	2.3613787
GO	cleavage of lamin	1	3	0.132965	2.3613787
GO	transformed cell apoptosis	1	3	0.132965	2.3613787
GO	choline binding	1	3	0.132965	2.3613787
GO	cholinesterase activity	1	3	0.132965	2.3613787
GO	deoxyribonucleotide biosynthetic process	1	3	0.132965	2.3613787
GO	ribonucleoside-diphosphate reductase activity	1	3	0.132965	2.3613787
GO	regulation of anti-apoptosis	1	3	0.132965	2.3613787

GO	chromocenter	1	3	0.132965	2.3613787
GO	G-quadruplex DNA binding	1	3	0.132965	2.3613787
GO	replication fork protection	1	3	0.132965	2.3613787
GO	olfactory receptor binding	1	3	0.132965	2.3613787
GO	axon extension involved in axon guidance	1	3	0.132965	2.3613787
GO	chemorepulsion involved in embryonic olfactory bulb interneuron mi	1	3	0.132965	2.3613787
GO	negative regulation of chemokine-mediated signaling pathway	1	3	0.132965	2.3613787
GO	response to cortisol stimulus	1	3	0.132965	2.3613787
GO	Roundabout signaling pathway	1	3	0.132965	2.3613787
GO	miRNA binding	1	3	0.132965	2.3613787
GO	olfactory placode formation	1	3	0.132965	2.3613787
GO	positive regulation of epithelial cell differentiation	1	3	0.132965	2.3613787
GO	BH domain binding	1	3	0.132965	2.3613787
GO	prostate gland morphogenesis	1	3	0.132965	2.3613787
GO	microtubule severing	1	3	0.132965	2.3613787
GO	common-partner SMAD protein phosphorylation	1	3	0.132965	2.3613787
GO	sulfate assimilation	1	3	0.132965	2.3613787
GO	potassium ion transmembrane transporter activity	1	3	0.132965	2.3613787
GO	positive regulation of transcription from RNA polymerase II promoter	1	3	0.132965	2.3613787
GO	transforming growth factor beta receptor activity, type I	1	3	0.132965	2.3613787
GO	transforming growth factor beta receptor complex	1	3	0.132965	2.3613787
GO	bleb	1	3	0.132965	2.3613787
GO	response to organophosphorus	1	3	0.132965	2.3613787
GO	mesenchymal to epithelial transition	1	3	0.132965	2.3613787
GO	calcium ion-dependent exocytosis of neurotransmitter	1	3	0.132965	2.3613787
GO	cellular chloride ion homeostasis	1	3	0.132965	2.3613787
GO	cerebellar Purkinje cell layer development	1	3	0.132965	2.3613787
GO	gamma-aminobutyric acid secretion	1	3	0.132965	2.3613787
GO	neurotransmitter metabolic process	1	3	0.132965	2.3613787
GO	retinal rod cell development	1	3	0.132965	2.3613787
GO	transferase activity, transferring acyl groups other than amino-acyl gr	1	3	0.132965	2.3613787
GO	maintenance of mitotic sister chromatid cohesion	1	3	0.132965	2.3613787
GO	spermidine biosynthetic process	1	3	0.132965	2.3613787
GO	phagocytosis, recognition	1	3	0.132965	2.3613787
GO	ER to Golgi transport vesicle	1	3	0.132965	2.3613787
GO	ribonucleoside binding	1	3	0.132965	2.3613787
GO	malate-aspartate shuttle	1	3	0.132965	2.3613787
GO	negative regulation of keratinocyte differentiation	1	3	0.132965	2.3613787
GO	replicative cell aging	1	3	0.132965	2.3613787
GO	response to tumor cell	1	3	0.132965	2.3613787
GO	proline catabolic process	1	3	0.132965	2.3613787
GO	growth hormone receptor signaling pathway	1	3	0.132965	2.3613787
GO	female pronucleus	1	3	0.132965	2.3613787
GO	cellular response to nutrient	1	3	0.132965	2.3613787
GO	response to vitamin E	1	3	0.132965	2.3613787
GO	regulation of dendrite development	1	3	0.132965	2.3613787
GO	Fanconi anaemia nuclear complex	1	3	0.132965	2.3613787
GO	negative regulation of estrogen receptor signaling pathway	1	3	0.132965	2.3613787
GO	sodium:bicarbonate symporter activity	1	3	0.132965	2.3613787

GO	GABA-B receptor activity	1	3	0.132965	2.3613787
GO	apoptosis	26	444	0.133937	1.22750994
GO	double-stranded DNA binding	6	75	0.134978	1.38365311
GO	regulation of axonogenesis	2	14	0.135688	1.71482394
GO	senescence	2	14	0.135688	1.71482394
GO	synaptic transmission, cholinergic	2	14	0.135688	1.71482394
GO	selenium binding	2	14	0.135688	1.71482394
GO	DNA methylation	2	14	0.135688	1.71482394
GO	regulation of sensory perception of pain	2	14	0.135688	1.71482394
GO	acyl-CoA metabolic process	2	14	0.135688	1.71482394
GO	isoprenoid biosynthetic process	2	14	0.135688	1.71482394
GO	behavioral fear response	2	14	0.135688	1.71482394
GO	regulation of action potential in neuron	2	14	0.135688	1.71482394
GO	kinesin complex	2	14	0.135688	1.71482394
GO	Wnt-protein binding	2	14	0.135688	1.71482394
GO	dystrophin-associated glycoprotein complex	2	14	0.135688	1.71482394
GO	DNA damage response, signal transduction by p53 class mediator resu	2	14	0.135688	1.71482394
GO	cell fate specification	2	14	0.135688	1.71482394
GO	ubiquitin-protein ligase activity	10	145	0.137709	1.29365694
GO	nuclear mRNA splicing, via spliceosome	4	43	0.137749	1.45305721
GO	nucleoside-triphosphatase activity	5	59	0.138199	1.40018705
GO	single fertilization	3	28	0.138918	1.52736059
GO	regulation of cell migration	3	28	0.138918	1.52736059
GO	RNA polymerase II transcription mediator activity	3	28	0.138918	1.52736059
GO	camera-type eye development	3	28	0.138918	1.52736059
GO	integrin complex	3	28	0.138918	1.52736059
GO	lactation	3	28	0.138918	1.52736059
GO	protein oligomerization	3	28	0.138918	1.52736059
GO	nucleus	234	4735	0.139538	1.12317435
GO	cellular calcium ion homeostasis	5	60	0.14539	1.35997086
GO	pattern specification process	4	44	0.146317	1.40317986
GO	ubiquitin protein ligase binding	4	44	0.146317	1.40317986
GO	scavenger receptor activity	4	44	0.146317	1.40317986
GO	protein homotetramerization	3	29	0.149916	1.45982357
GO	androgen receptor binding	3	29	0.149916	1.45982357
GO	metanephros development	3	29	0.149916	1.45982357
GO	chaperone binding	3	29	0.149916	1.45982357
GO	ruffle membrane	3	29	0.149916	1.45982357
GO	neuronal cell body	10	148	0.1511	1.22594612
GO	cellular response to extracellular stimulus	2	15	0.151963	1.59971747
GO	neural tube development	2	15	0.151963	1.59971747
GO	protein disulfide oxidoreductase activity	2	15	0.151963	1.59971747
GO	acyl-CoA binding	2	15	0.151963	1.59971747
GO	cellular component organization	2	15	0.151963	1.59971747
GO	estrogen receptor binding	2	15	0.151963	1.59971747
GO	protein amino acid methylation	2	15	0.151963	1.59971747
GO	male germ cell nucleus	2	15	0.151963	1.59971747
GO	phosphatidylinositol-4,5-bisphosphate binding	2	15	0.151963	1.59971747
GO	double-strand break repair via homologous recombination	2	15	0.151963	1.59971747

GO	actin filament-based movement	2	15	0.151963	1.59971747
GO	ATP-dependent helicase activity	5	61	0.152736	1.32051163
GO	axonogenesis	5	61	0.152736	1.32051163
GO	protein tyrosine kinase activity	6	78	0.153976	1.28177323
GO	proteinaceous extracellular matrix	14	223	0.156532	1.16613896
GO	multicellular organismal development	48	890	0.157102	1.08749484
GO	cell differentiation	27	474	0.160227	1.10206193
GO	nuclear matrix	5	62	0.160235	1.28178059
GO	extracellular matrix organization	5	62	0.160235	1.28178059
GO	response to organic nitrogen	3	30	0.16118	1.39500132
GO	cellular response to insulin stimulus	4	46	0.164045	1.30725358
GO	regulation of small GTPase mediated signal transduction	4	46	0.164045	1.30725358
GO	extracellular ligand-gated ion channel activity	4	46	0.164045	1.30725358
GO	response to calcium ion	4	46	0.164045	1.30725358
GO	organ morphogenesis	8	115	0.165995	1.18181971
GO	regulation of transcription from RNA polymerase II promoter	13	207	0.167168	1.12453635
GO	gap junction	2	16	0.168591	1.49376573
GO	regulation of the force of heart contraction	2	16	0.168591	1.49376573
GO	regulation of GTPase activity	2	16	0.168591	1.49376573
GO	nicotinic acetylcholine-activated cation-selective channel activity	2	16	0.168591	1.49376573
GO	nicotinic acetylcholine-gated receptor-channel complex	2	16	0.168591	1.49376573
GO	purine nucleotide biosynthetic process	2	16	0.168591	1.49376573
GO	mitochondrial envelope	2	16	0.168591	1.49376573
GO	neuron apoptosis	2	16	0.168591	1.49376573
GO	negative regulation of MAP kinase activity	2	16	0.168591	1.49376573
GO	carbonate dehydratase activity	2	16	0.168591	1.49376573
GO	DNA-dependent DNA replication initiation	2	16	0.168591	1.49376573
GO	cerebral cortex development	2	16	0.168591	1.49376573
GO	hair follicle morphogenesis	2	16	0.168591	1.49376573
GO	spliceosome assembly	2	16	0.168591	1.49376573
GO	stereocilium	2	16	0.168591	1.49376573
GO	cellular component movement	7	98	0.170532	1.17836476
GO	mediator complex	3	31	0.172689	1.33268421
GO	SMAD binding	3	31	0.172689	1.33268421
GO	MAPKKK cascade	3	31	0.172689	1.33268421
GO	embryonic digit morphogenesis	3	31	0.172689	1.33268421
GO	ATPase activity, coupled to transmembrane movement of substances	3	31	0.172689	1.33268421
GO	keratinization	3	31	0.172689	1.33268421
GO	chromosome, centromeric region	4	47	0.173185	1.26107566
GO	RPTP-like protein binding	1	4	0.173239	1.93471296
GO	ATP-dependent protein binding	1	4	0.173239	1.93471296
GO	phenylalanyl-tRNA aminoacylation	1	4	0.173239	1.93471296
GO	excitatory synapse	1	4	0.173239	1.93471296
GO	positive regulation of programmed cell death	1	4	0.173239	1.93471296
GO	hindbrain morphogenesis	1	4	0.173239	1.93471296
GO	positive regulation of protein amino acid dephosphorylation	1	4	0.173239	1.93471296
GO	U4/U6 x U5 tri-snRNP complex	1	4	0.173239	1.93471296
GO	box C/D snoRNP complex	1	4	0.173239	1.93471296
GO	compartment pattern formation	1	4	0.173239	1.93471296

GO	protein amino acid geranylgeranylation	1	4	0.173239	1.93471296
GO	Rab geranylgeranyltransferase activity	1	4	0.173239	1.93471296
GO	regulation of dendrite morphogenesis	1	4	0.173239	1.93471296
GO	transmembrane receptor protein tyrosine kinase signaling protein act	1	4	0.173239	1.93471296
GO	TOR signaling pathway	1	4	0.173239	1.93471296
GO	9-cis-retinoic acid biosynthetic process	1	4	0.173239	1.93471296
GO	embryonic development ending in birth or egg hatching	1	4	0.173239	1.93471296
GO	hepatocyte differentiation	1	4	0.173239	1.93471296
GO	pyrimidine dimer repair	1	4	0.173239	1.93471296
GO	inner ear receptor cell differentiation	1	4	0.173239	1.93471296
GO	methylation-dependent chromatin silencing	1	4	0.173239	1.93471296
GO	unmethylated CpG binding	1	4	0.173239	1.93471296
GO	U6 snRNA binding	1	4	0.173239	1.93471296
GO	phosphopyruvate hydratase activity	1	4	0.173239	1.93471296
GO	phosphopyruvate hydratase complex	1	4	0.173239	1.93471296
GO	regulation of microtubule polymerization or depolymerization	1	4	0.173239	1.93471296
GO	paranode region of axon	1	4	0.173239	1.93471296
GO	arachidonic acid binding	1	4	0.173239	1.93471296
GO	detection of mechanical stimulus involved in sensory perception of pa	1	4	0.173239	1.93471296
GO	fatty acid alpha-oxidation	1	4	0.173239	1.93471296
GO	hindgut morphogenesis	1	4	0.173239	1.93471296
GO	mammary gland duct morphogenesis	1	4	0.173239	1.93471296
GO	smoothened signaling pathway involved in regulation of granule cell	1	4	0.173239	1.93471296
GO	procollagen-proline 4-dioxygenase activity	1	4	0.173239	1.93471296
GO	ubiquitin conjugating enzyme binding	1	4	0.173239	1.93471296
GO	epithelial cell maturation	1	4	0.173239	1.93471296
GO	positive regulation of exit from mitosis	1	4	0.173239	1.93471296
GO	protein complex localization	1	4	0.173239	1.93471296
GO	regulation of cholesterol transport	1	4	0.173239	1.93471296
GO	axon regeneration in the peripheral nervous system	1	4	0.173239	1.93471296
GO	Cdc42 protein signal transduction	1	4	0.173239	1.93471296
GO	cGMP-mediated signaling	1	4	0.173239	1.93471296
GO	death-inducing signaling complex	1	4	0.173239	1.93471296
GO	megakaryocyte differentiation	1	4	0.173239	1.93471296
GO	hemoglobin biosynthetic process	1	4	0.173239	1.93471296
GO	negative regulation of follicle-stimulating hormone secretion	1	4	0.173239	1.93471296
GO	negative regulation of macrophage differentiation	1	4	0.173239	1.93471296
GO	apoptotic cell clearance	1	4	0.173239	1.93471296
GO	negative regulation of lipid storage	1	4	0.173239	1.93471296
GO	negative regulation of lipid transport	1	4	0.173239	1.93471296
GO	G-protein activated inward rectifier potassium channel activity	1	4	0.173239	1.93471296
GO	RNA 3'-end processing	1	4	0.173239	1.93471296
GO	negative regulation of appetite	1	4	0.173239	1.93471296
GO	regulation of intestinal cholesterol absorption	1	4	0.173239	1.93471296
GO	pachytene	1	4	0.173239	1.93471296
GO	forebrain neuron development	1	4	0.173239	1.93471296
GO	positive regulation of keratinocyte migration	1	4	0.173239	1.93471296
GO	somatic recombination of immunoglobulin gene segments	1	4	0.173239	1.93471296
GO	progesterone receptor signaling pathway	1	4	0.173239	1.93471296

GO	receptor catabolic process	1	4	0.173239	1.93471296
GO	positive regulation of adenylate cyclase activity	1	4	0.173239	1.93471296
GO	positive regulation of Rac protein signal transduction	1	4	0.173239	1.93471296
GO	ERK1 and ERK2 cascade	1	4	0.173239	1.93471296
GO	positive regulation of ion transport	1	4	0.173239	1.93471296
GO	cellular response to chemical stimulus	1	4	0.173239	1.93471296
GO	Golgi cis cisterna	1	4	0.173239	1.93471296
GO	protein repair	1	4	0.173239	1.93471296
GO	cytokine biosynthetic process	1	4	0.173239	1.93471296
GO	nerve growth factor processing	1	4	0.173239	1.93471296
GO	platelet aggregation	1	4	0.173239	1.93471296
GO	positive regulation of platelet activation	1	4	0.173239	1.93471296
GO	regulation of transcription from RNA polymerase I promoter	1	4	0.173239	1.93471296
GO	peroxisome proliferator activated receptor binding	1	4	0.173239	1.93471296
GO	retinoic acid receptor binding	1	4	0.173239	1.93471296
GO	positive regulation of telomerase activity	1	4	0.173239	1.93471296
GO	DNA primase activity	1	4	0.173239	1.93471296
GO	DNA replication, synthesis of RNA primer	1	4	0.173239	1.93471296
GO	peptide-aspartate beta-dioxygenase activity	1	4	0.173239	1.93471296
GO	glycerol-3-phosphate O-acyltransferase activity	1	4	0.173239	1.93471296
GO	mitochondrial fusion	1	4	0.173239	1.93471296
GO	regulation of protein heterodimerization activity	1	4	0.173239	1.93471296
GO	choline metabolic process	1	4	0.173239	1.93471296
GO	outer ear morphogenesis	1	4	0.173239	1.93471296
GO	ventricular septum development	1	4	0.173239	1.93471296
GO	monocyte chemotaxis	1	4	0.173239	1.93471296
GO	positive regulation of macrophage chemotaxis	1	4	0.173239	1.93471296
GO	bubble DNA binding	1	4	0.173239	1.93471296
GO	lateral element	1	4	0.173239	1.93471296
GO	calcium ion transmembrane transporter activity	1	4	0.173239	1.93471296
GO	calcium:sodium antiporter activity	1	4	0.173239	1.93471296
GO	sodium ion transmembrane transporter activity	1	4	0.173239	1.93471296
GO	Roundabout binding	1	4	0.173239	1.93471296
GO	lens induction in camera-type eye	1	4	0.173239	1.93471296
GO	Sertoli cell development	1	4	0.173239	1.93471296
GO	intermediate filament cytoskeleton organization	1	4	0.173239	1.93471296
GO	soft palate development	1	4	0.173239	1.93471296
GO	cardiac myofibril assembly	1	4	0.173239	1.93471296
GO	negative regulation of membrane protein ectodomain proteolysis	1	4	0.173239	1.93471296
GO	calcium channel inhibitor activity	1	4	0.173239	1.93471296
GO	negative regulation of ATPase activity	1	4	0.173239	1.93471296
GO	troponin C binding	1	4	0.173239	1.93471296
GO	troponin T binding	1	4	0.173239	1.93471296
GO	ISG15-protein conjugation	1	4	0.173239	1.93471296
GO	protein sumoylation	1	4	0.173239	1.93471296
GO	high voltage-gated calcium channel activity	1	4	0.173239	1.93471296
GO	pantothenate kinase activity	1	4	0.173239	1.93471296
GO	AT DNA binding	1	4	0.173239	1.93471296
GO	galactose binding	1	4	0.173239	1.93471296

GO	aspartate transport	1	4	0.173239	1.93471296
GO	L-aspartate transmembrane transporter activity	1	4	0.173239	1.93471296
GO	urinary bladder development	1	4	0.173239	1.93471296
GO	growth hormone receptor binding	1	4	0.173239	1.93471296
GO	tRNA methylation	1	4	0.173239	1.93471296
GO	cardiac cell differentiation	1	4	0.173239	1.93471296
GO	metabotropic glutamate receptor signaling pathway	1	4	0.173239	1.93471296
GO	NADP metabolic process	1	4	0.173239	1.93471296
GO	NADPH:quinone reductase activity	1	4	0.173239	1.93471296
GO	heparan sulfate proteoglycan biosynthetic process, polysaccharide ch	1	4	0.173239	1.93471296
GO	cell proliferation in forebrain	1	4	0.173239	1.93471296
GO	embryonic morphogenesis	1	4	0.173239	1.93471296
GO	chromatin	6	81	0.174077	1.18419299
GO	Ras protein signal transduction	5	64	0.175662	1.20639565
GO	kinase activity	8	117	0.177237	1.13080601
GO	nucleosome assembly	5	65	0.183581	1.16969159
GO	neural tube closure	3	32	0.184422	1.27268521
GO	peptidyl-tyrosine phosphorylation	3	32	0.184422	1.27268521
GO	regulation of G-protein coupled receptor protein signaling pathway	3	32	0.184422	1.27268521
GO	regulation of gene expression	3	32	0.184422	1.27268521
GO	positive regulation of cell differentiation	2	17	0.185506	1.39565551
GO	guanyl nucleotide binding	2	17	0.185506	1.39565551
GO	regulation of excitatory postsynaptic membrane potential	2	17	0.185506	1.39565551
GO	positive regulation of DNA repair	2	17	0.185506	1.39565551
GO	anchored to plasma membrane	2	17	0.185506	1.39565551
GO	purine ribonucleoside monophosphate biosynthetic process	2	17	0.185506	1.39565551
GO	negative regulation of osteoblast differentiation	2	17	0.185506	1.39565551
GO	regulation of long-term neuronal synaptic plasticity	2	17	0.185506	1.39565551
GO	cytoplasmic microtubule	2	17	0.185506	1.39565551
GO	DNA damage response, signal transduction resulting in induction of a	2	17	0.185506	1.39565551
GO	cAMP binding	2	17	0.185506	1.39565551
GO	positive regulation of pathway-restricted SMAD protein phosphorylat	2	17	0.185506	1.39565551
GO	male genitalia development	2	17	0.185506	1.39565551
GO	nucleobase, nucleoside, nucleotide and nucleic acid metabolic proces	5	66	0.191627	1.13361519
GO	biosynthetic process	4	49	0.191968	1.17200174
GO	PDZ domain binding	4	49	0.191968	1.17200174
GO	microtubule-based movement	6	84	0.195185	1.0905498
GO	actin filament binding	4	50	0.20159	1.12900222
GO	response to estrogen stimulus	4	50	0.20159	1.12900222
GO	response to cytokine stimulus	4	50	0.20159	1.12900222
GO	rRNA processing	6	85	0.202427	1.06015394
GO	inward rectifier potassium channel activity	2	18	0.202644	1.30432814
GO	ADP binding	2	18	0.202644	1.30432814
GO	proton-transporting ATPase activity, rotational mechanism	2	18	0.202644	1.30432814
GO	hydrolase activity, acting on ester bonds	2	18	0.202644	1.30432814
GO	response to activity	2	18	0.202644	1.30432814
GO	negative regulation of apoptosis	9	140	0.203682	1.00689751
GO	calmodulin binding	9	140	0.203682	1.00689751
GO	protein homooligomerization	5	68	0.20808	1.06325857

GO	receptor signaling protein activity	3	34	0.208472	1.15898847
GO	cytokinesis	3	34	0.208472	1.15898847
GO	perikaryon	3	34	0.208472	1.15898847
GO	PML body	3	34	0.208472	1.15898847
GO	transmembrane transport	27	492	0.210605	0.90078706
GO	plasma membrane	137	2763	0.210825	0.84862898
GO	GTPase activity	12	198	0.210994	0.95196032
GO	phenylalanine-tRNA ligase activity	1	5	0.211645	1.63179848
GO	negative regulation of Rho protein signal transduction	1	5	0.211645	1.63179848
GO	CRD-mediated mRNA stability complex	1	5	0.211645	1.63179848
GO	CRD-mediated mRNA stabilization	1	5	0.211645	1.63179848
GO	histone pre-mRNA 3'end processing complex	1	5	0.211645	1.63179848
GO	dichotomous subdivision of terminal units involved in salivary gland b	1	5	0.211645	1.63179848
GO	outflow tract morphogenesis	1	5	0.211645	1.63179848
GO	negative regulation of cardiac muscle hypertrophy	1	5	0.211645	1.63179848
GO	type 1 angiotensin receptor binding	1	5	0.211645	1.63179848
GO	negative regulation of astrocyte differentiation	1	5	0.211645	1.63179848
GO	negative regulation of Notch signaling pathway	1	5	0.211645	1.63179848
GO	epithelial cell-cell adhesion	1	5	0.211645	1.63179848
GO	positive regulation of receptor recycling	1	5	0.211645	1.63179848
GO	transcription-coupled nucleotide-excision repair	1	5	0.211645	1.63179848
GO	collagen biosynthetic process	1	5	0.211645	1.63179848
GO	positive regulation of triglyceride catabolic process	1	5	0.211645	1.63179848
GO	positive regulation of fibroblast growth factor receptor signaling path	1	5	0.211645	1.63179848
GO	vitamin D metabolic process	1	5	0.211645	1.63179848
GO	establishment or maintenance of epithelial cell apical/basal polarity	1	5	0.211645	1.63179848
GO	DNA catabolic process	1	5	0.211645	1.63179848
GO	dynactin complex	1	5	0.211645	1.63179848
GO	sulfate transmembrane transporter activity	1	5	0.211645	1.63179848
GO	peptidyl-lysine modification to hypusine	1	5	0.211645	1.63179848
GO	nucleobase, nucleoside, nucleotide kinase activity	1	5	0.211645	1.63179848
GO	chemorepellent activity	1	5	0.211645	1.63179848
GO	embryonic camera-type eye development	1	5	0.211645	1.63179848
GO	embryonic eye morphogenesis	1	5	0.211645	1.63179848
GO	face development	1	5	0.211645	1.63179848
GO	ribonuclease H activity	1	5	0.211645	1.63179848
GO	fibroblast growth factor receptor activity	1	5	0.211645	1.63179848
GO	neuronal action potential propagation	1	5	0.211645	1.63179848
GO	protein maturation by protein folding	1	5	0.211645	1.63179848
GO	protein refolding	1	5	0.211645	1.63179848
GO	ryanodine-sensitive calcium-release channel activity	1	5	0.211645	1.63179848
GO	long-chain fatty acid metabolic process	1	5	0.211645	1.63179848
GO	response to gravity	1	5	0.211645	1.63179848
GO	thiamin pyrophosphate binding	1	5	0.211645	1.63179848
GO	purine base biosynthetic process	1	5	0.211645	1.63179848
GO	phosphatidylinositol transporter activity	1	5	0.211645	1.63179848
GO	dopamine receptor binding	1	5	0.211645	1.63179848
GO	neuron remodeling	1	5	0.211645	1.63179848
GO	motile primary cilium	1	5	0.211645	1.63179848

GO	spinal cord dorsal/ventral patterning	1	5	0.211645	1.63179848
GO	regulation of short-term neuronal synaptic plasticity	1	5	0.211645	1.63179848
GO	nerve-nerve synaptic transmission	1	5	0.211645	1.63179848
GO	neuromuscular process	1	5	0.211645	1.63179848
GO	cartilage development involved in endochondral bone morphogenesi	1	5	0.211645	1.63179848
GO	prostaglandin E receptor activity	1	5	0.211645	1.63179848
GO	negative regulation of lipoprotein lipase activity	1	5	0.211645	1.63179848
GO	negative regulation of receptor-mediated endocytosis	1	5	0.211645	1.63179848
GO	high-density lipoprotein particle assembly	1	5	0.211645	1.63179848
GO	high-density lipoprotein particle clearance	1	5	0.211645	1.63179848
GO	lipoprotein biosynthetic process	1	5	0.211645	1.63179848
GO	lipoprotein catabolic process	1	5	0.211645	1.63179848
GO	positive regulation of cGMP biosynthetic process	1	5	0.211645	1.63179848
GO	tau protein binding	1	5	0.211645	1.63179848
GO	magnesium ion transport	1	5	0.211645	1.63179848
GO	regulation of activin receptor signaling pathway	1	5	0.211645	1.63179848
GO	peptide hormone receptor binding	1	5	0.211645	1.63179848
GO	endoderm formation	1	5	0.211645	1.63179848
GO	G-protein coupled receptor internalization	1	5	0.211645	1.63179848
GO	melanocortin receptor activity	1	5	0.211645	1.63179848
GO	MutSalpha complex binding	1	5	0.211645	1.63179848
GO	intra-S DNA damage checkpoint	1	5	0.211645	1.63179848
GO	positive regulation of helicase activity	1	5	0.211645	1.63179848
GO	RNA polymerase binding	1	5	0.211645	1.63179848
GO	forebrain morphogenesis	1	5	0.211645	1.63179848
GO	myelination in the peripheral nervous system	1	5	0.211645	1.63179848
GO	negative regulation of neuroblast proliferation	1	5	0.211645	1.63179848
GO	structural constituent of nuclear pore	1	5	0.211645	1.63179848
GO	eukaryotic initiation factor 4E binding	1	5	0.211645	1.63179848
GO	gastric acid secretion	1	5	0.211645	1.63179848
GO	positive regulation of uterine smooth muscle contraction	1	5	0.211645	1.63179848
GO	sperm ejaculation	1	5	0.211645	1.63179848
GO	vasopressin receptor activity	1	5	0.211645	1.63179848
GO	transepithelial chloride transport	1	5	0.211645	1.63179848
GO	regulation of receptor activity	1	5	0.211645	1.63179848
GO	protein kinase B binding	1	5	0.211645	1.63179848
GO	proton-transporting two-sector ATPase complex	1	5	0.211645	1.63179848
GO	mammary gland branching involved in thelarche	1	5	0.211645	1.63179848
GO	neurotransmitter transporter activity	1	5	0.211645	1.63179848
GO	telomerase holoenzyme complex	1	5	0.211645	1.63179848
GO	spindle midzone	1	5	0.211645	1.63179848
GO	Barr body	1	5	0.211645	1.63179848
GO	negative regulation of synaptic transmission	1	5	0.211645	1.63179848
GO	mesenchymal to epithelial transition involved in metanephros morph	1	5	0.211645	1.63179848
GO	regulation of binding	1	5	0.211645	1.63179848
GO	luteolysis	1	5	0.211645	1.63179848
GO	regulation of caspase activity	1	5	0.211645	1.63179848
GO	retina morphogenesis in camera-type eye	1	5	0.211645	1.63179848
GO	pro-B cell differentiation	1	5	0.211645	1.63179848

GO	negative regulation of cellular component movement	1	5	0.211645	1.63179848
GO	microtubule-severing ATPase activity	1	5	0.211645	1.63179848
GO	cellular response to indole-3-methanol	1	5	0.211645	1.63179848
GO	skeletal muscle thin filament assembly	1	5	0.211645	1.63179848
GO	response to cholesterol	1	5	0.211645	1.63179848
GO	response to prostaglandin E stimulus	1	5	0.211645	1.63179848
GO	oligopeptide transport	1	5	0.211645	1.63179848
GO	positive regulation of protein complex assembly	1	5	0.211645	1.63179848
GO	glomerular basement membrane development	1	5	0.211645	1.63179848
GO	glomerulus development	1	5	0.211645	1.63179848
GO	behavioral response to pain	1	5	0.211645	1.63179848
GO	protein serine/threonine phosphatase inhibitor activity	1	5	0.211645	1.63179848
GO	gamma-tubulin complex	1	5	0.211645	1.63179848
GO	mitochondrion transport along microtubule	1	5	0.211645	1.63179848
GO	transcription termination	1	5	0.211645	1.63179848
GO	THO complex part of transcription export complex	1	5	0.211645	1.63179848
GO	THO complex	1	5	0.211645	1.63179848
GO	establishment of planar polarity	1	5	0.211645	1.63179848
GO	multicellular organismal aging	1	5	0.211645	1.63179848
GO	skin morphogenesis	1	5	0.211645	1.63179848
GO	mitotic cell cycle G2/M transition DNA damage checkpoint	1	5	0.211645	1.63179848
GO	AP-type membrane coat adaptor complex	1	5	0.211645	1.63179848
GO	regulation of cytoskeleton organization	1	5	0.211645	1.63179848
GO	regulation of smooth muscle cell differentiation	1	5	0.211645	1.63179848
GO	NADPH binding	1	5	0.211645	1.63179848
GO	ligand-gated ion channel activity	1	5	0.211645	1.63179848
GO	G2/M transition of mitotic cell cycle	2	19	0.219949	1.21891896
GO	hyaluronic acid binding	2	19	0.219949	1.21891896
GO	nucleotide-excision repair, DNA damage removal	2	19	0.219949	1.21891896
GO	base-excision repair	2	19	0.219949	1.21891896
GO	GABA-A receptor activity	2	19	0.219949	1.21891896
GO	extracellular-glutamate-gated ion channel activity	2	19	0.219949	1.21891896
GO	cofactor binding	2	19	0.219949	1.21891896
GO	cholesterol efflux	2	19	0.219949	1.21891896
GO	T cell differentiation	2	19	0.219949	1.21891896
GO	hydrolase activity, acting on acid anhydrides, in phosphorus-containir	2	19	0.219949	1.21891896
GO	actin cytoskeleton reorganization	2	19	0.219949	1.21891896
GO	vesicle docking involved in exocytosis	2	19	0.219949	1.21891896
GO	chromatin organization	2	19	0.219949	1.21891896
GO	negative regulation of adenylate cyclase activity	2	19	0.219949	1.21891896
GO	extracellular matrix	3	35	0.220748	1.1050044
GO	nucleosome	4	52	0.221242	1.04584484
GO	cell-cell adhesion	5	70	0.224973	0.99516284
GO	response to ethanol	5	70	0.224973	0.99516284
GO	intracellular signaling pathway	11	182	0.22649	0.90157392
GO	serine-type endopeptidase activity	9	144	0.226633	0.91907705
GO	helicase activity	7	107	0.229277	0.93543342
GO	double-strand break repair	3	36	0.233164	1.05276179
GO	response to organic substance	3	36	0.233164	1.05276179

GO	skeletal muscle tissue development	3	36	0.233164	1.05276179
GO	lamellipodium	5	71	0.233568	0.96191615
GO	regulation of Rho protein signal transduction	5	71	0.233568	0.96191615
GO	transmembrane receptor protein tyrosine kinase signaling pathway	5	71	0.233568	0.96191615
GO	spermatogenesis	15	261	0.233664	0.85248211
GO	connexon complex	2	20	0.237367	1.13871357
GO	neural crest cell migration	2	20	0.237367	1.13871357
GO	hippocampus development	2	20	0.237367	1.13871357
GO	response to amphetamine	2	20	0.237367	1.13871357
GO	L-ascorbic acid binding	2	20	0.237367	1.13871357
GO	positive regulation of protein kinase B signaling cascade	2	20	0.237367	1.13871357
GO	protein C-terminus binding	9	146	0.238457	0.87613922
GO	proton transport	4	54	0.24137	0.96619999
GO	tight junction	5	72	0.242255	0.92918048
GO	cartilage development	3	37	0.245701	1.0021492
GO	NAD or NADH binding	3	37	0.245701	1.0021492
GO	podosome	1	6	0.248268	1.39955154
GO	pre-snoRNP complex	1	6	0.248268	1.39955154
GO	paraxial mesoderm development	1	6	0.248268	1.39955154
GO	activation of transmembrane receptor protein tyrosine kinase activity	1	6	0.248268	1.39955154
GO	maintenance of gastrointestinal epithelium	1	6	0.248268	1.39955154
GO	poly(U) RNA binding	1	6	0.248268	1.39955154
GO	assembly of spliceosomal tri-snRNP	1	6	0.248268	1.39955154
GO	RS domain binding	1	6	0.248268	1.39955154
GO	protein neddylation	1	6	0.248268	1.39955154
GO	fucose metabolic process	1	6	0.248268	1.39955154
GO	amine metabolic process	1	6	0.248268	1.39955154
GO	mitochondrial DNA replication	1	6	0.248268	1.39955154
GO	S-adenosylhomocysteine metabolic process	1	6	0.248268	1.39955154
GO	endothelial cell differentiation	1	6	0.248268	1.39955154
GO	aldehyde dehydrogenase [NAD(P)+] activity	1	6	0.248268	1.39955154
GO	retinoic acid metabolic process	1	6	0.248268	1.39955154
GO	5'-3' exonuclease activity	1	6	0.248268	1.39955154
GO	regulation of ryanodine-sensitive calcium-release channel activity	1	6	0.248268	1.39955154
GO	response to redox state	1	6	0.248268	1.39955154
GO	regulation of Ras protein signal transduction	1	6	0.248268	1.39955154
GO	juxtaparanode region of axon	1	6	0.248268	1.39955154
GO	aminomethyltransferase activity	1	6	0.248268	1.39955154
GO	lipoic acid binding	1	6	0.248268	1.39955154
GO	glutathione binding	1	6	0.248268	1.39955154
GO	negative regulation of synaptic transmission, glutamatergic	1	6	0.248268	1.39955154
GO	regulation of inhibitory postsynaptic membrane potential	1	6	0.248268	1.39955154
GO	N-methyl-D-aspartate selective glutamate receptor activity	1	6	0.248268	1.39955154
GO	startle response	1	6	0.248268	1.39955154
GO	glucocorticoid receptor binding	1	6	0.248268	1.39955154
GO	Leydig cell differentiation	1	6	0.248268	1.39955154
GO	forelimb morphogenesis	1	6	0.248268	1.39955154
GO	hindlimb morphogenesis	1	6	0.248268	1.39955154
GO	parturition	1	6	0.248268	1.39955154

GO	very-low-density lipoprotein particle assembly	1	6	0.248268	1.39955154
GO	extrinsic to external side of plasma membrane	1	6	0.248268	1.39955154
GO	negative regulation of platelet activation	1	6	0.248268	1.39955154
GO	very-low-density lipoprotein particle remodeling	1	6	0.248268	1.39955154
GO	interleukin-1 receptor antagonist activity	1	6	0.248268	1.39955154
GO	pre-microRNA processing	1	6	0.248268	1.39955154
GO	regulation of steroid biosynthetic process	1	6	0.248268	1.39955154
GO	centromeric DNA binding	1	6	0.248268	1.39955154
GO	MutLalpha complex binding	1	6	0.248268	1.39955154
GO	cellular response to UV	1	6	0.248268	1.39955154
GO	glucocorticoid receptor signaling pathway	1	6	0.248268	1.39955154
GO	regulation of synaptic transmission, GABAergic	1	6	0.248268	1.39955154
GO	striated muscle cell differentiation	1	6	0.248268	1.39955154
GO	positive regulation of synaptic transmission, GABAergic	1	6	0.248268	1.39955154
GO	positive regulation of synaptogenesis	1	6	0.248268	1.39955154
GO	DNA damage response, signal transduction by p53 class mediator	1	6	0.248268	1.39955154
GO	proton-transporting ATP synthase complex, coupling factor F(o)	1	6	0.248268	1.39955154
GO	negative regulation of G-protein coupled receptor protein signaling p	1	6	0.248268	1.39955154
GO	histone mRNA 3'-end processing	1	6	0.248268	1.39955154
GO	exocytic vesicle	1	6	0.248268	1.39955154
GO	neurexin binding	1	6	0.248268	1.39955154
GO	drug transmembrane transporter activity	1	6	0.248268	1.39955154
GO	alpha DNA polymerase:primase complex	1	6	0.248268	1.39955154
GO	phospholipid homeostasis	1	6	0.248268	1.39955154
GO	response to fructose stimulus	1	6	0.248268	1.39955154
GO	apical cortex	1	6	0.248268	1.39955154
GO	negative regulation of survival gene product expression	1	6	0.248268	1.39955154
GO	nuclear envelope lumen	1	6	0.248268	1.39955154
GO	vitamin A metabolic process	1	6	0.248268	1.39955154
GO	transition metal ion binding	1	6	0.248268	1.39955154
GO	lymphocyte chemotaxis	1	6	0.248268	1.39955154
GO	prostate epithelial cord arborization involved in prostate glandular ac	1	6	0.248268	1.39955154
GO	regulation of branching involved in prostate gland morphogenesis	1	6	0.248268	1.39955154
GO	protein insertion into membrane	1	6	0.248268	1.39955154
GO	positive regulation of BMP signaling pathway	1	6	0.248268	1.39955154
GO	tongue development	1	6	0.248268	1.39955154
GO	exocrine pancreas development	1	6	0.248268	1.39955154
GO	chromo shadow domain binding	1	6	0.248268	1.39955154
GO	erythrocyte development	1	6	0.248268	1.39955154
GO	SMAD protein nuclear translocation	1	6	0.248268	1.39955154
GO	gamma-tubulin ring complex	1	6	0.248268	1.39955154
GO	G-protein coupled photoreceptor activity	1	6	0.248268	1.39955154
GO	cardiac muscle tissue morphogenesis	1	6	0.248268	1.39955154
GO	response to manganese ion	1	6	0.248268	1.39955154
GO	cell motility	1	6	0.248268	1.39955154
GO	germ cell migration	1	6	0.248268	1.39955154
GO	store-operated calcium channel activity	1	6	0.248268	1.39955154
GO	sex determination	1	6	0.248268	1.39955154
GO	spinal cord motor neuron differentiation	1	6	0.248268	1.39955154

GO	DNA packaging	1	6	0.248268	1.39955154
GO	epithelial cell development	1	6	0.248268	1.39955154
GO	prostate gland development	1	6	0.248268	1.39955154
GO	proline biosynthetic process	1	6	0.248268	1.39955154
GO	response to glucagon stimulus	1	6	0.248268	1.39955154
GO	glycoprotein biosynthetic process	1	6	0.248268	1.39955154
GO	Notch receptor processing	1	6	0.248268	1.39955154
GO	bicarbonate transport	1	6	0.248268	1.39955154
GO	response to toxin	4	55	0.251586	0.92760081
GO	post-embryonic development	4	55	0.251586	0.92760081
GO	ossification	4	55	0.251586	0.92760081
GO	transforming growth factor beta receptor signaling pathway	4	55	0.251586	0.92760081
GO	signal transducer activity	16	285	0.252492	0.78381133
GO	calcium-dependent phospholipid binding	2	21	0.254852	1.06311557
GO	ventricular cardiac muscle tissue morphogenesis	2	21	0.254852	1.06311557
GO	Wnt receptor signaling pathway, calcium modulating pathway	2	21	0.254852	1.06311557
GO	transferase activity, transferring glycosyl groups	9	149	0.256588	0.81289118
GO	response to mechanical stimulus	3	38	0.258339	0.95306527
GO	antiporter activity	3	38	0.258339	0.95306527
GO	protein amino acid phosphorylation	26	488	0.261953	0.72693669
GO	GTP binding	19	347	0.26197	0.74255574
GO	transferase activity	57	1127	0.267896	0.67989273
GO	ion channel activity	9	151	0.268915	0.77147064
GO	potassium ion transport	9	151	0.268915	0.77147064
GO	epithelial cell differentiation	3	39	0.271061	0.90541751
GO	intracellular protein kinase cascade	6	94	0.271419	0.80299775
GO	muscle organ development	6	94	0.271419	0.80299775
GO	endonuclease activity	4	57	0.272275	0.85268072
GO	response to glucose stimulus	4	57	0.272275	0.85268072
GO	regulation of cell growth	4	57	0.272275	0.85268072
GO	liver development	4	57	0.272275	0.85268072
GO	placenta development	2	22	0.27236	0.99162246
GO	germ cell development	2	22	0.27236	0.99162246
GO	microvillus	2	22	0.27236	0.99162246
GO	purinergic nucleotide receptor activity, G-protein coupled	2	22	0.27236	0.99162246
GO	voltage-gated calcium channel complex	2	22	0.27236	0.99162246
GO	basal plasma membrane	2	22	0.27236	0.99162246
GO	cysteine-type peptidase activity	5	76	0.277783	0.80303239
GO	ribosome	10	172	0.278265	0.73223424
GO	regulation of apoptosis	7	114	0.27903	0.76130658
GO	ribonucleoprotein complex	6	95	0.279429	0.7760826
GO	regulation of cell shape	4	58	0.282727	0.81629849
GO	meiosis	4	58	0.282727	0.81629849
GO	growth cone	4	58	0.282727	0.81629849
GO	alpha-catenin binding	1	7	0.283192	1.21234006
GO	proteasome binding	1	7	0.283192	1.21234006
GO	labyrinthine layer development	1	7	0.283192	1.21234006
GO	cyclosporin A binding	1	7	0.283192	1.21234006
GO	snoRNA binding	1	7	0.283192	1.21234006

GO	DNA-directed RNA polymerase III complex	1	7	0.283192	1.21234006
GO	nucleolar ribonuclease P complex	1	7	0.283192	1.21234006
GO	regulation of Cdc42 GTPase activity	1	7	0.283192	1.21234006
GO	cyclin-dependent protein kinase regulator activity	1	7	0.283192	1.21234006
GO	fibril organization	1	7	0.283192	1.21234006
GO	wound healing, spreading of epidermal cells	1	7	0.283192	1.21234006
GO	axon regeneration	1	7	0.283192	1.21234006
GO	brain morphogenesis	1	7	0.283192	1.21234006
GO	pyrimidine nucleotide biosynthetic process	1	7	0.283192	1.21234006
GO	steroid hydroxylase activity	1	7	0.283192	1.21234006
GO	morphogenesis of an epithelial sheet	1	7	0.283192	1.21234006
GO	bile acid:sodium symporter activity	1	7	0.283192	1.21234006
GO	spectrin binding	1	7	0.283192	1.21234006
GO	death	1	7	0.283192	1.21234006
GO	mitotic anaphase	1	7	0.283192	1.21234006
GO	NAD biosynthetic process	1	7	0.283192	1.21234006
GO	Ras guanyl-nucleotide exchange factor activity	1	7	0.283192	1.21234006
GO	cellular homeostasis	1	7	0.283192	1.21234006
GO	response to mercury ion	1	7	0.283192	1.21234006
GO	BBSome	1	7	0.283192	1.21234006
GO	synaptic vesicle exocytosis	1	7	0.283192	1.21234006
GO	response to selenium ion	1	7	0.283192	1.21234006
GO	kainate selective glutamate receptor activity	1	7	0.283192	1.21234006
GO	regulation of JNK cascade	1	7	0.283192	1.21234006
GO	glutamate binding	1	7	0.283192	1.21234006
GO	neurotransmitter binding	1	7	0.283192	1.21234006
GO	3-hydroxyacyl-CoA dehydrogenase activity	1	7	0.283192	1.21234006
GO	cellular zinc ion homeostasis	1	7	0.283192	1.21234006
GO	central nervous system neuron development	1	7	0.283192	1.21234006
GO	fatty acid catabolic process	1	7	0.283192	1.21234006
GO	urogenital system development	1	7	0.283192	1.21234006
GO	cell chemotaxis	1	7	0.283192	1.21234006
GO	oxidative phosphorylation	1	7	0.283192	1.21234006
GO	unconventional myosin complex	1	7	0.283192	1.21234006
GO	protein targeting to lysosome	1	7	0.283192	1.21234006
GO	regulation of cell-matrix adhesion	1	7	0.283192	1.21234006
GO	monovalent inorganic cation transmembrane transporter activity	1	7	0.283192	1.21234006
GO	ankyrin binding	1	7	0.283192	1.21234006
GO	maternal behavior	1	7	0.283192	1.21234006
GO	positive regulation of synaptic transmission, glutamatergic	1	7	0.283192	1.21234006
GO	extracellular ATP-gated cation channel activity	1	7	0.283192	1.21234006
GO	purinergic nucleotide receptor activity	1	7	0.283192	1.21234006
GO	regulation of vasodilation	1	7	0.283192	1.21234006
GO	cellular response to lipopolysaccharide	1	7	0.283192	1.21234006
GO	peptide biosynthetic process	1	7	0.283192	1.21234006
GO	extrinsic to plasma membrane	1	7	0.283192	1.21234006
GO	negative regulation of catalytic activity	1	7	0.283192	1.21234006
GO	fructose-2,6-bisphosphate 2-phosphatase activity	1	7	0.283192	1.21234006
GO	regulation of protein homodimerization activity	1	7	0.283192	1.21234006

GO	GTP-Rho binding	1	7	0.283192	1.21234006
GO	positive regulation of alpha-beta T cell proliferation	1	7	0.283192	1.21234006
GO	pronucleus	1	7	0.283192	1.21234006
GO	organic cation transmembrane transporter activity	1	7	0.283192	1.21234006
GO	U7 snRNP	1	7	0.283192	1.21234006
GO	adenohypophysis development	1	7	0.283192	1.21234006
GO	negative regulation of bone mineralization	1	7	0.283192	1.21234006
GO	negative regulation of myoblast differentiation	1	7	0.283192	1.21234006
GO	BRCA1-A complex	1	7	0.283192	1.21234006
GO	transmembrane receptor protein serine/threonine kinase activity	1	7	0.283192	1.21234006
GO	type II transforming growth factor beta receptor binding	1	7	0.283192	1.21234006
GO	contractile fiber	1	7	0.283192	1.21234006
GO	coenzyme A biosynthetic process	1	7	0.283192	1.21234006
GO	filopodium membrane	1	7	0.283192	1.21234006
GO	semaphorin receptor activity	1	7	0.283192	1.21234006
GO	male gonad development	3	40	0.283849	0.85912135
GO	non-membrane spanning protein tyrosine kinase activity	3	40	0.283849	0.85912135
GO	dendritic spine	3	40	0.283849	0.85912135
GO	brain development	7	115	0.286356	0.73736769
GO	condensed nuclear chromosome	2	23	0.28985	0.92380727
GO	neuromuscular process controlling balance	2	23	0.28985	0.92380727
GO	positive regulation of cAMP biosynthetic process	2	23	0.28985	0.92380727
GO	chromosome, telomeric region	2	23	0.28985	0.92380727
GO	regulation of ARF GTPase activity	2	23	0.28985	0.92380727
GO	positive regulation of osteoblast differentiation	2	23	0.28985	0.92380727
GO	Wnt receptor signaling pathway through beta-catenin	2	23	0.28985	0.92380727
GO	thymus development	2	23	0.28985	0.92380727
GO	cytoplasmic mRNA processing body	2	23	0.28985	0.92380727
GO	negative regulation of protein kinase activity	3	41	0.296685	0.81409928
GO	positive regulation of transcription from RNA polymerase II promoter	16	295	0.297306	0.64111953
GO	GTPase activator activity	9	156	0.300458	0.67039701
GO	chromatin binding	9	156	0.300458	0.67039701
GO	hormone activity	5	79	0.305075	0.71305694
GO	extracellular region	85	1730	0.305439	0.55764056
GO	learning	2	24	0.307288	0.85930444
GO	visual learning	2	24	0.307288	0.85930444
GO	ARF GTPase activator activity	2	24	0.307288	0.85930444
GO	cellular iron ion homeostasis	2	24	0.307288	0.85930444
GO	lung alveolus development	2	24	0.307288	0.85930444
GO	regulation of protein metabolic process	3	42	0.309554	0.77028008
GO	cell growth	3	42	0.309554	0.77028008
GO	RNA processing	5	80	0.314263	0.68387942
GO	basement membrane	4	61	0.3144	0.71113112
GO	cytoplasmic vesicle membrane	4	61	0.3144	0.71113112
GO	cytoskeleton organization	4	61	0.3144	0.71113112
GO	response to estradiol stimulus	4	61	0.3144	0.71113112
GO	catenin complex	1	8	0.316495	1.05602928
GO	positive regulation of dendrite morphogenesis	1	8	0.316495	1.05602928
GO	response to carbohydrate stimulus	1	8	0.316495	1.05602928

GO	protein K63-linked deubiquitination	1	8	0.316495	1.05602928
GO	cyclin binding	1	8	0.316495	1.05602928
GO	cyclin-dependent protein kinase holoenzyme complex	1	8	0.316495	1.05602928
GO	poly(A) RNA binding	1	8	0.316495	1.05602928
GO	negative regulation of neurogenesis	1	8	0.316495	1.05602928
GO	prepulse inhibition	1	8	0.316495	1.05602928
GO	hydrogen peroxide biosynthetic process	1	8	0.316495	1.05602928
GO	olfactory bulb development	1	8	0.316495	1.05602928
GO	secondary active sulfate transmembrane transporter activity	1	8	0.316495	1.05602928
GO	adenylate kinase activity	1	8	0.316495	1.05602928
GO	ephrin receptor binding	1	8	0.316495	1.05602928
GO	positive regulation of JAK-STAT cascade	1	8	0.316495	1.05602928
GO	positive regulation of leukocyte chemotaxis	1	8	0.316495	1.05602928
GO	retinal metabolic process	1	8	0.316495	1.05602928
GO	calcium channel complex	1	8	0.316495	1.05602928
GO	FK506 binding	1	8	0.316495	1.05602928
GO	vascular endothelial growth factor receptor activity	1	8	0.316495	1.05602928
GO	protein homotrimerization	1	8	0.316495	1.05602928
GO	diacylglycerol binding	1	8	0.316495	1.05602928
GO	creatine metabolic process	1	8	0.316495	1.05602928
GO	glycine catabolic process	1	8	0.316495	1.05602928
GO	dopamine receptor signaling pathway	1	8	0.316495	1.05602928
GO	N-methyl-D-aspartate selective glutamate receptor complex	1	8	0.316495	1.05602928
GO	positive regulation of G-protein coupled receptor protein signaling pa	1	8	0.316495	1.05602928
GO	positive regulation of chondrocyte differentiation	1	8	0.316495	1.05602928
GO	phosphatidylcholine binding	1	8	0.316495	1.05602928
GO	phospholipase inhibitor activity	1	8	0.316495	1.05602928
GO	negative regulation of programmed cell death	1	8	0.316495	1.05602928
GO	antioxidant activity	1	8	0.316495	1.05602928
GO	positive regulation of cholesterol efflux	1	8	0.316495	1.05602928
GO	protein-DNA complex	1	8	0.316495	1.05602928
GO	ciliary rootlet	1	8	0.316495	1.05602928
GO	energy reserve metabolic process	1	8	0.316495	1.05602928
GO	response to UV-B	1	8	0.316495	1.05602928
GO	actin-dependent ATPase activity	1	8	0.316495	1.05602928
GO	phosphoinositide 3-kinase cascade	1	8	0.316495	1.05602928
GO	hydrogen-exporting ATPase activity, phosphorylative mechanism	1	8	0.316495	1.05602928
GO	proton-transporting V-type ATPase, V1 domain	1	8	0.316495	1.05602928
GO	embryonic hemopoiesis	1	8	0.316495	1.05602928
GO	positive regulation of NF-kappaB import into nucleus	1	8	0.316495	1.05602928
GO	activation of caspase activity by cytochrome c	1	8	0.316495	1.05602928
GO	retinoid binding	1	8	0.316495	1.05602928
GO	heterochromatin	1	8	0.316495	1.05602928
GO	regulation of ossification	1	8	0.316495	1.05602928
GO	regulation of sodium ion transport	1	8	0.316495	1.05602928
GO	organic cation transport	1	8	0.316495	1.05602928
GO	negative chemotaxis	1	8	0.316495	1.05602928
GO	transmembrane receptor protein serine/threonine kinase signaling pa	1	8	0.316495	1.05602928
GO	positive regulation of neuroblast proliferation	1	8	0.316495	1.05602928

GO	embryonic viscerocranium morphogenesis	1	8	0.316495	1.05602928
GO	positive regulation of SMAD protein nuclear translocation	1	8	0.316495	1.05602928
GO	troponin complex	1	8	0.316495	1.05602928
GO	sarcomere organization	1	8	0.316495	1.05602928
GO	cytosolic calcium ion homeostasis	1	8	0.316495	1.05602928
GO	histone H2B ubiquitination	1	8	0.316495	1.05602928
GO	C2H2 zinc finger domain binding	1	8	0.316495	1.05602928
GO	mesonephros development	1	8	0.316495	1.05602928
GO	regulation of calcium ion-dependent exocytosis	1	8	0.316495	1.05602928
GO	epithelial cell proliferation	1	8	0.316495	1.05602928
GO	positive regulation of fat cell differentiation	1	8	0.316495	1.05602928
GO	L-glutamate transport	1	8	0.316495	1.05602928
GO	tail morphogenesis	1	8	0.316495	1.05602928
GO	glycosphingolipid biosynthetic process	1	8	0.316495	1.05602928
GO	clathrin binding	1	8	0.316495	1.05602928
GO	HAUS complex	1	8	0.316495	1.05602928
GO	bile acid biosynthetic process	1	8	0.316495	1.05602928
GO	induction of apoptosis by oxidative stress	1	8	0.316495	1.05602928
GO	protein folding	8	139	0.318496	0.62475092
GO	ion transport	26	505	0.321611	0.54571283
GO	Notch signaling pathway	3	43	0.32244	0.72759821
GO	glucose metabolic process	3	43	0.32244	0.72759821
GO	protein polyubiquitination	2	25	0.324639	0.79779879
GO	spindle microtubule	2	25	0.324639	0.79779879
GO	glycoprotein binding	2	25	0.324639	0.79779879
GO	filopodium	2	25	0.324639	0.79779879
GO	mitochondrial intermembrane space	2	25	0.324639	0.79779879
GO	protein targeting to mitochondrion	2	25	0.324639	0.79779879
GO	thyroid hormone receptor binding	2	25	0.324639	0.79779879
GO	skeletal system morphogenesis	2	25	0.324639	0.79779879
GO	spliceosomal snRNP assembly	2	25	0.324639	0.79779879
GO	negative regulation of ubiquitin-protein ligase activity involved in mit	4	62	0.325032	0.67731844
GO	integrin binding	4	62	0.325032	0.67731844
GO	positive regulation of cell migration	4	62	0.325032	0.67731844
GO	protein complex assembly	6	101	0.328457	0.62069077
GO	cellular_component	27	528	0.330143	0.51972548
GO	ligase activity	16	303	0.334766	0.53049092
GO	protein binding, bridging	3	44	0.335327	0.68599317
GO	Rab GTPase activator activity	3	44	0.335327	0.68599317
GO	regulation of Rab GTPase activity	3	44	0.335327	0.68599317
GO	anaphase-promoting complex-dependent proteasomal ubiquitin-dep	4	63	0.335686	0.64408903
GO	voltage-gated potassium channel activity	4	63	0.335686	0.64408903
GO	metalloendopeptidase activity	6	102	0.336748	0.59574689
GO	positive regulation of transcription, DNA-dependent	7	122	0.338718	0.57572252
GO	integral to plasma membrane	48	969	0.341214	0.46957629
GO	skin development	2	26	0.341874	0.73901688
GO	terminal button	2	26	0.341874	0.73901688
GO	unfolded protein binding	6	103	0.345063	0.57105947
GO	membrane raft	6	103	0.345063	0.57105947

GO	endocytosis	6	103	0.345063	0.57105947
GO	cell death	7	123	0.346313	0.55342923
GO	motor activity	4	64	0.346354	0.61142175
GO	glucose homeostasis	3	45	0.348201	0.64540907
GO	blood vessel morphogenesis	1	9	0.348252	0.9220806
GO	fascia adherens	1	9	0.348252	0.9220806
GO	myeloid dendritic cell differentiation	1	9	0.348252	0.9220806
GO	phospholipase binding	1	9	0.348252	0.9220806
GO	vinculin binding	1	9	0.348252	0.9220806
GO	ribonuclease P activity	1	9	0.348252	0.9220806
GO	regulation of alternative nuclear mRNA splicing, via spliceosome	1	9	0.348252	0.9220806
GO	response to food	1	9	0.348252	0.9220806
GO	outer kinetochore of condensed chromosome	1	9	0.348252	0.9220806
GO	UV protection	1	9	0.348252	0.9220806
GO	ubiquinone biosynthetic process	1	9	0.348252	0.9220806
GO	associative learning	1	9	0.348252	0.9220806
GO	dendrite cytoplasm	1	9	0.348252	0.9220806
GO	holo TFIIH complex	1	9	0.348252	0.9220806
GO	prostaglandin metabolic process	1	9	0.348252	0.9220806
GO	negative regulation of blood vessel endothelial cell migration	1	9	0.348252	0.9220806
GO	positive regulation of membrane protein ectodomain proteolysis	1	9	0.348252	0.9220806
GO	positive regulation of nitric-oxide synthase activity	1	9	0.348252	0.9220806
GO	regulation of gene-specific transcription from RNA polymerase II pron	1	9	0.348252	0.9220806
GO	two-component signal transduction system (phosphorelay)	1	9	0.348252	0.9220806
GO	organelle organization	1	9	0.348252	0.9220806
GO	adult feeding behavior	1	9	0.348252	0.9220806
GO	ovulation from ovarian follicle	1	9	0.348252	0.9220806
GO	anterior/posterior axis specification	1	9	0.348252	0.9220806
GO	Hsp90 protein binding	1	9	0.348252	0.9220806
GO	regulation of protein catabolic process	1	9	0.348252	0.9220806
GO	synaptonemal complex	1	9	0.348252	0.9220806
GO	macrophage differentiation	1	9	0.348252	0.9220806
GO	axonal fasciculation	1	9	0.348252	0.9220806
GO	Nup107-160 complex	1	9	0.348252	0.9220806
GO	sleep	1	9	0.348252	0.9220806
GO	telencephalon development	1	9	0.348252	0.9220806
GO	positive regulation of receptor-mediated endocytosis	1	9	0.348252	0.9220806
GO	vacuolar proton-transporting V-type ATPase complex	1	9	0.348252	0.9220806
GO	phosphoinositide metabolic process	1	9	0.348252	0.9220806
GO	respiratory burst	1	9	0.348252	0.9220806
GO	triglyceride biosynthetic process	1	9	0.348252	0.9220806
GO	male meiosis I	1	9	0.348252	0.9220806
GO	gonad development	1	9	0.348252	0.9220806
GO	proteoglycan biosynthetic process	1	9	0.348252	0.9220806
GO	sodium:hydrogen antiporter activity	1	9	0.348252	0.9220806
GO	embryonic organ development	1	9	0.348252	0.9220806
GO	epithelial tube branching involved in lung morphogenesis	1	9	0.348252	0.9220806
GO	cellular response to reactive oxygen species	1	9	0.348252	0.9220806
GO	positive regulation of ATPase activity	1	9	0.348252	0.9220806

GO	positive regulation of release of sequestered calcium ion into cytosol	1	9	0.348252	0.9220806
GO	histone monoubiquitination	1	9	0.348252	0.9220806
GO	actin polymerization or depolymerization	1	9	0.348252	0.9220806
GO	oligosaccharide metabolic process	1	9	0.348252	0.9220806
GO	clathrin coat of trans-Golgi network vesicle	1	9	0.348252	0.9220806
GO	skeletal muscle fiber development	1	9	0.348252	0.9220806
GO	quinone binding	1	9	0.348252	0.9220806
GO	melanosome	5	84	0.351306	0.5709394
GO	positive regulation of ubiquitin-protein ligase activity involved in mito	4	65	0.357028	0.57929656
GO	positive regulation of fibroblast proliferation	2	27	0.358967	0.68272004
GO	SH2 domain binding	2	27	0.358967	0.68272004
GO	cell-cell adherens junction	2	27	0.358967	0.68272004
GO	cell aging	2	27	0.358967	0.68272004
GO	protein ubiquitination	5	85	0.360611	0.54359546
GO	cytoplasmic membrane-bounded vesicle	5	85	0.360611	0.54359546
GO	early endosome	5	85	0.360611	0.54359546
GO	peptidase inhibitor activity	5	85	0.360611	0.54359546
GO	cytosol	60	1230	0.363518	0.40279803
GO	positive regulation of transcription	8	146	0.367676	0.48136
GO	structural constituent of ribosome	8	146	0.367676	0.48136
GO	RNA polymerase II transcription factor activity	7	126	0.369202	0.487667
GO	protein heterooligomerization	3	47	0.373858	0.56710035
GO	neuron differentiation	3	47	0.373858	0.56710035
GO	voltage-gated ion channel activity	8	147	0.374769	0.46145989
GO	negative regulation of angiogenesis	2	28	0.375894	0.62869885
GO	positive regulation of DNA replication	2	28	0.375894	0.62869885
GO	memory	2	28	0.375894	0.62869885
GO	activation of phospholipase C activity by G-protein coupled receptor p	2	28	0.375894	0.62869885
GO	sensory perception of pain	2	28	0.375894	0.62869885
GO	axon	7	127	0.376855	0.46610757
GO	cardiac muscle tissue development	1	10	0.378536	0.80497995
GO	regulation of actin cytoskeleton organization	1	10	0.378536	0.80497995
GO	ribonucleoprotein binding	1	10	0.378536	0.80497995
GO	acetylcholine binding	1	10	0.378536	0.80497995
GO	oxygen transporter activity	1	10	0.378536	0.80497995
GO	oxygen transport	1	10	0.378536	0.80497995
GO	transcription elongation regulator activity	1	10	0.378536	0.80497995
GO	hormone biosynthetic process	1	10	0.378536	0.80497995
GO	cytoplasmic dynein complex	1	10	0.378536	0.80497995
GO	regulation of gene expression by genetic imprinting	1	10	0.378536	0.80497995
GO	ATP metabolic process	1	10	0.378536	0.80497995
GO	elevation of cytosolic calcium ion concentration involved in G-protein	1	10	0.378536	0.80497995
GO	positive regulation of collagen biosynthetic process	1	10	0.378536	0.80497995
GO	positive regulation of positive chemotaxis	1	10	0.378536	0.80497995
GO	NAD metabolic process	1	10	0.378536	0.80497995
GO	fatty acid transport	1	10	0.378536	0.80497995
GO	cilium membrane	1	10	0.378536	0.80497995
GO	osteoblast development	1	10	0.378536	0.80497995
GO	glutathione peroxidase activity	1	10	0.378536	0.80497995

GO	outer membrane-bounded periplasmic space	1	10	0.378536	0.80497995
GO	Ran GTPase binding	1	10	0.378536	0.80497995
GO	cholesterol catabolic process	1	10	0.378536	0.80497995
GO	lipoprotein binding	1	10	0.378536	0.80497995
GO	negative regulation of hormone secretion	1	10	0.378536	0.80497995
GO	small conjugating protein ligase activity	1	10	0.378536	0.80497995
GO	phosphoinositide 3-kinase binding	1	10	0.378536	0.80497995
GO	positive regulation of T cell activation	1	10	0.378536	0.80497995
GO	double-strand break repair via nonhomologous end joining	1	10	0.378536	0.80497995
GO	cognition	1	10	0.378536	0.80497995
GO	positive regulation of smooth muscle cell migration	1	10	0.378536	0.80497995
GO	defense response to Gram-negative bacterium	1	10	0.378536	0.80497995
GO	negative regulation of fibrinolysis	1	10	0.378536	0.80497995
GO	positive regulation of interleukin-8 production	1	10	0.378536	0.80497995
GO	Golgi lumen	1	10	0.378536	0.80497995
GO	3',5'-cyclic-AMP phosphodiesterase activity	1	10	0.378536	0.80497995
GO	XY body	1	10	0.378536	0.80497995
GO	positive regulation of activated T cell proliferation	1	10	0.378536	0.80497995
GO	defense response to fungus	1	10	0.378536	0.80497995
GO	killing of cells of another organism	1	10	0.378536	0.80497995
GO	apoptotic mitochondrial changes	1	10	0.378536	0.80497995
GO	regulation of mitochondrial membrane potential	1	10	0.378536	0.80497995
GO	limb development	1	10	0.378536	0.80497995
GO	macrophage chemotaxis	1	10	0.378536	0.80497995
GO	positive regulation of epithelial cell migration	1	10	0.378536	0.80497995
GO	microtubule plus-end binding	1	10	0.378536	0.80497995
GO	microtubule bundle formation	1	10	0.378536	0.80497995
GO	I band	1	10	0.378536	0.80497995
GO	response to iron ion	1	10	0.378536	0.80497995
GO	I-SMAD binding	1	10	0.378536	0.80497995
GO	transforming growth factor beta binding	1	10	0.378536	0.80497995
GO	metalloendopeptidase inhibitor activity	1	10	0.378536	0.80497995
GO	Wnt receptor activity	1	10	0.378536	0.80497995
GO	signalosome	1	10	0.378536	0.80497995
GO	L-glutamate transmembrane transporter activity	1	10	0.378536	0.80497995
GO	G1 phase of mitotic cell cycle	1	10	0.378536	0.80497995
GO	cytokine binding	1	10	0.378536	0.80497995
GO	prostate gland epithelium morphogenesis	1	10	0.378536	0.80497995
GO	nuclear membrane	5	87	0.379235	0.48991043
GO	visual perception	10	189	0.382424	0.42458103
GO	ATPase activity	7	128	0.384516	0.44472339
GO	serine-type peptidase activity	3	48	0.386615	0.5292831
GO	fatty acid biosynthetic process	3	48	0.386615	0.5292831
GO	cytokine-mediated signaling pathway	3	48	0.386615	0.5292831
GO	positive regulation of apoptosis	6	108	0.386838	0.45127667
GO	mRNA processing	12	231	0.3873	0.40001445
GO	electron carrier activity	8	149	0.388978	0.42207534
GO	steroid metabolic process	4	68	0.389002	0.48598811
GO	Rho guanyl-nucleotide exchange factor activity	4	68	0.389002	0.48598811

GO	protein kinase C binding	2	29	0.392633	0.57676865
GO	positive regulation of smooth muscle cell proliferation	2	29	0.392633	0.57676865
GO	growth	2	29	0.392633	0.57676865
GO	positive regulation of ERK1 and ERK2 cascade	2	29	0.392633	0.57676865
GO	soluble fraction	16	315	0.392727	0.36999101
GO	microtubule	12	233	0.398695	0.36922086
GO	phospholipid biosynthetic process	3	49	0.39931	0.49230086
GO	single-stranded DNA binding	3	49	0.39931	0.49230086
GO	mRNA transport	3	49	0.39931	0.49230086
GO	protein transporter activity	4	69	0.399619	0.45585043
GO	cell communication	5	90	0.407128	0.41176115
GO	spindle	5	90	0.407128	0.41176115
GO	gamma-catenin binding	1	11	0.407414	0.70097975
GO	positive regulation of axon extension	1	11	0.407414	0.70097975
GO	mitotic sister chromatid segregation	1	11	0.407414	0.70097975
GO	cell-cell junction assembly	1	11	0.407414	0.70097975
GO	cellular response to oxidative stress	1	11	0.407414	0.70097975
GO	cyclin-dependent protein kinase inhibitor activity	1	11	0.407414	0.70097975
GO	trophectodermal cell differentiation	1	11	0.407414	0.70097975
GO	estrogen receptor signaling pathway	1	11	0.407414	0.70097975
GO	positive regulation of neurogenesis	1	11	0.407414	0.70097975
GO	gap junction channel activity	1	11	0.407414	0.70097975
GO	response to vitamin A	1	11	0.407414	0.70097975
GO	protein tetramerization	1	11	0.407414	0.70097975
GO	DNA methylation involved in gamete generation	1	11	0.407414	0.70097975
GO	cell fate determination	1	11	0.407414	0.70097975
GO	pyridine nucleotide biosynthetic process	1	11	0.407414	0.70097975
GO	positive regulation of vascular endothelial growth factor receptor sigr	1	11	0.407414	0.70097975
GO	long-chain fatty acid-CoA ligase activity	1	11	0.407414	0.70097975
GO	positive regulation of neuron projection development	1	11	0.407414	0.70097975
GO	cell recognition	1	11	0.407414	0.70097975
GO	Ras GTPase binding	1	11	0.407414	0.70097975
GO	morphogenesis of an epithelium	1	11	0.407414	0.70097975
GO	adenylate cyclase activity	1	11	0.407414	0.70097975
GO	regulation of synaptic transmission	1	11	0.407414	0.70097975
GO	RNA polymerase II carboxy-terminal domain kinase activity	1	11	0.407414	0.70097975
GO	DNA bending activity	1	11	0.407414	0.70097975
GO	low-density lipoprotein receptor binding	1	11	0.407414	0.70097975
GO	positive regulation of erythrocyte differentiation	1	11	0.407414	0.70097975
GO	delayed rectifier potassium channel activity	1	11	0.407414	0.70097975
GO	myoblast fusion	1	11	0.407414	0.70097975
GO	motor axon guidance	1	11	0.407414	0.70097975
GO	hemidesmosome assembly	1	11	0.407414	0.70097975
GO	pericentriolar material	1	11	0.407414	0.70097975
GO	bile acid metabolic process	1	11	0.407414	0.70097975
GO	cerebellum development	1	11	0.407414	0.70097975
GO	negative regulation of protein ubiquitination	1	11	0.407414	0.70097975
GO	negative regulation of MAPKKK cascade	1	11	0.407414	0.70097975
GO	gamma-tubulin binding	1	11	0.407414	0.70097975

GO	positive regulation of DNA binding	1	11	0.407414	0.70097975
GO	positive regulation of calcium ion transport into cytosol	1	11	0.407414	0.70097975
GO	endoplasmic reticulum organization	1	11	0.407414	0.70097975
GO	peptide hormone processing	1	11	0.407414	0.70097975
GO	protein maturation by peptide bond cleavage	1	11	0.407414	0.70097975
GO	phosphatidylserine binding	1	11	0.407414	0.70097975
GO	polysaccharide binding	1	11	0.407414	0.70097975
GO	glucose transmembrane transporter activity	1	11	0.407414	0.70097975
GO	regulation of calcium ion transport	1	11	0.407414	0.70097975
GO	neural crest cell development	1	11	0.407414	0.70097975
GO	oligodendrocyte differentiation	1	11	0.407414	0.70097975
GO	non-G-protein coupled 7TM receptor activity	1	11	0.407414	0.70097975
GO	phospholipase C activity	1	11	0.407414	0.70097975
GO	peptidase activity	23	465	0.408111	0.31323672
GO	DNA-directed DNA polymerase activity	2	30	0.409166	0.52676581
GO	steroid biosynthetic process	2	30	0.409166	0.52676581
GO	adult locomotory behavior	2	30	0.409166	0.52676581
GO	dorsal/ventral pattern formation	2	30	0.409166	0.52676581
GO	one-carbon metabolic process	2	30	0.409166	0.52676581
GO	response to ionizing radiation	2	30	0.409166	0.52676581
GO	negative regulation of transcription factor activity	2	30	0.409166	0.52676581
GO	nuclear speck	6	111	0.411925	0.38214759
GO	spindle pole	3	50	0.41193	0.45611491
GO	hormone-mediated signaling pathway	3	50	0.41193	0.45611491
GO	sequence-specific DNA binding	24	487	0.411949	0.30151781
GO	induction of apoptosis by extracellular signals	5	91	0.416395	0.38631346
GO	protein complex	8	153	0.417432	0.34491071
GO	axon guidance	4	71	0.420749	0.39692838
GO	response to glucocorticoid stimulus	4	71	0.420749	0.39692838
GO	hemopoiesis	3	51	0.424466	0.42068912
GO	heart morphogenesis	2	31	0.425474	0.47854477
GO	ligand-dependent nuclear receptor transcription coactivator activity	2	31	0.425474	0.47854477
GO	exonuclease activity	2	31	0.425474	0.47854477
GO	symporter activity	6	113	0.428596	0.33712577
GO	protein homodimerization activity	18	365	0.431104	0.2632706
GO	translation	10	197	0.432772	0.28951567
GO	negative regulation of cyclin-dependent protein kinase activity	1	12	0.434951	0.60742787
GO	STAGA complex	1	12	0.434951	0.60742787
GO	iron-sulfur cluster binding	1	12	0.434951	0.60742787
GO	positive regulation of innate immune response	1	12	0.434951	0.60742787
GO	positive regulation of interferon-beta production	1	12	0.434951	0.60742787
GO	regulation of lipid metabolic process	1	12	0.434951	0.60742787
GO	drug metabolic process	1	12	0.434951	0.60742787
GO	ephrin receptor activity	1	12	0.434951	0.60742787
GO	positive regulation of calcium ion transport	1	12	0.434951	0.60742787
GO	positive regulation of caspase activity	1	12	0.434951	0.60742787
GO	glutamate signaling pathway	1	12	0.434951	0.60742787
GO	estradiol 17-beta-dehydrogenase activity	1	12	0.434951	0.60742787
GO	protein methyltransferase activity	1	12	0.434951	0.60742787

GO	cholesterol transporter activity	1	12	0.434951	0.60742787
GO	positive regulation of peptidyl-serine phosphorylation	1	12	0.434951	0.60742787
GO	negative regulation of macrophage derived foam cell differentiation	1	12	0.434951	0.60742787
GO	arylsulfatase activity	1	12	0.434951	0.60742787
GO	response to pH	1	12	0.434951	0.60742787
GO	DNA unwinding involved in replication	1	12	0.434951	0.60742787
GO	positive regulation of blood pressure	1	12	0.434951	0.60742787
GO	dorsal/ventral neural tube patterning	1	12	0.434951	0.60742787
GO	cGMP binding	1	12	0.434951	0.60742787
GO	lysosphingolipid and lysophosphatidic acid receptor activity	1	12	0.434951	0.60742787
GO	microvillus membrane	1	12	0.434951	0.60742787
GO	protein serine/threonine phosphatase complex	1	12	0.434951	0.60742787
GO	acrosome reaction	1	12	0.434951	0.60742787
GO	immunological synapse	1	12	0.434951	0.60742787
GO	voltage-gated sodium channel complex	1	12	0.434951	0.60742787
GO	viral genome replication	1	12	0.434951	0.60742787
GO	retinoic acid receptor signaling pathway	1	12	0.434951	0.60742787
GO	response to copper ion	1	12	0.434951	0.60742787
GO	positive regulation of cellular component movement	1	12	0.434951	0.60742787
GO	positive regulation of survival gene product expression	1	12	0.434951	0.60742787
GO	costamere	1	12	0.434951	0.60742787
GO	neuromuscular synaptic transmission	1	12	0.434951	0.60742787
GO	endothelial cell migration	1	12	0.434951	0.60742787
GO	induction of positive chemotaxis	1	12	0.434951	0.60742787
GO	Golgi-associated vesicle	1	12	0.434951	0.60742787
GO	regulation of phosphorylation	1	12	0.434951	0.60742787
GO	nBAF complex	1	12	0.434951	0.60742787
GO	histone acetylation	1	12	0.434951	0.60742787
GO	keratinocyte proliferation	1	12	0.434951	0.60742787
GO	anion transmembrane transporter activity	1	12	0.434951	0.60742787
GO	Rac GTPase binding	1	12	0.434951	0.60742787
GO	calcium ion transport	6	114	0.436906	0.31492129
GO	peptide binding	2	32	0.441544	0.43197545
GO	carbohydrate transport	2	32	0.441544	0.43197545
GO	mitosis	10	199	0.445344	0.25661915
GO	transcription from RNA polymerase II promoter	9	178	0.445663	0.26234618
GO	ruffle	3	53	0.449248	0.35198505
GO	angiogenesis	6	116	0.453455	0.27110501
GO	Rab GTPase binding	2	33	0.457363	0.38694124
GO	learning or memory	2	33	0.457363	0.38694124
GO	positive regulation of actin filament polymerization	1	13	0.46121	0.52238484
GO	bone mineralization	1	13	0.46121	0.52238484
GO	transcription factor TFTC complex	1	13	0.46121	0.52238484
GO	spindle organization	1	13	0.46121	0.52238484
GO	extracellular matrix binding	1	13	0.46121	0.52238484
GO	autophagic vacuole membrane	1	13	0.46121	0.52238484
GO	myoblast differentiation	1	13	0.46121	0.52238484
GO	T cell proliferation	1	13	0.46121	0.52238484
GO	induction of an organ	1	13	0.46121	0.52238484

GO	lipid homeostasis	1	13	0.46121	0.52238484
GO	two-component sensor activity	1	13	0.46121	0.52238484
GO	calcium-activated potassium channel activity	1	13	0.46121	0.52238484
GO	response to osmotic stress	1	13	0.46121	0.52238484
GO	positive regulation of phosphoinositide 3-kinase cascade	1	13	0.46121	0.52238484
GO	camera-type eye morphogenesis	1	13	0.46121	0.52238484
GO	positive regulation of hormone secretion	1	13	0.46121	0.52238484
GO	transcription from RNA polymerase III promoter	1	13	0.46121	0.52238484
GO	steroid hormone receptor signaling pathway	1	13	0.46121	0.52238484
GO	positive regulation of interleukin-2 biosynthetic process	1	13	0.46121	0.52238484
GO	histone deacetylase activity	1	13	0.46121	0.52238484
GO	response to bacterium	1	13	0.46121	0.52238484
GO	syntaxin binding	1	13	0.46121	0.52238484
GO	negative regulation of microtubule depolymerization	1	13	0.46121	0.52238484
GO	labyrinthine layer blood vessel development	1	13	0.46121	0.52238484
GO	low-density lipoprotein binding	1	13	0.46121	0.52238484
GO	transcription elongation factor complex	1	13	0.46121	0.52238484
GO	insulin-like growth factor receptor binding	1	13	0.46121	0.52238484
GO	muscle cell homeostasis	1	13	0.46121	0.52238484
GO	glial cell differentiation	1	13	0.46121	0.52238484
GO	inorganic anion exchanger activity	1	13	0.46121	0.52238484
GO	cellular defense response	3	54	0.461476	0.3186455
GO	microtubule organizing center	5	96	0.462281	0.26326415
GO	defense response to bacterium	4	75	0.462412	0.28410686
GO	negative regulation of cell proliferation	14	287	0.464181	0.18960168
GO	G-protein coupled receptor activity	17	352	0.469611	0.16669562
GO	lyase activity	5	97	0.47134	0.23944578
GO	extrinsic to membrane	2	34	0.472919	0.34333718
GO	presynaptic membrane	2	34	0.472919	0.34333718
GO	B cell differentiation	2	34	0.472919	0.34333718
GO	acid-amino acid ligase activity	2	34	0.472919	0.34333718
GO	positive regulation of epithelial cell proliferation	2	34	0.472919	0.34333718
GO	humoral immune response	2	34	0.472919	0.34333718
GO	cell-cell junction	3	56	0.485568	0.25385211
GO	proteasome complex	3	56	0.485568	0.25385211
GO	condensed chromosome kinetochore	3	56	0.485568	0.25385211
GO	glutamine metabolic process	1	14	0.48625	0.44439321
GO	nuclear heterochromatin	1	14	0.48625	0.44439321
GO	protein export from nucleus	1	14	0.48625	0.44439321
GO	neuroblast proliferation	1	14	0.48625	0.44439321
GO	positive regulation of natural killer cell mediated cytotoxicity	1	14	0.48625	0.44439321
GO	hindbrain development	1	14	0.48625	0.44439321
GO	tropomyosin binding	1	14	0.48625	0.44439321
GO	nitric oxide mediated signal transduction	1	14	0.48625	0.44439321
GO	regulation of neuronal synaptic plasticity	1	14	0.48625	0.44439321
GO	regulation of action potential	1	14	0.48625	0.44439321
GO	rhythmic process	1	14	0.48625	0.44439321
GO	sensory perception	1	14	0.48625	0.44439321
GO	positive regulation of protein catabolic process	1	14	0.48625	0.44439321

GO	embryonic heart tube development	1	14	0.48625	0.44439321
GO	neurotransmitter:sodium symporter activity	1	14	0.48625	0.44439321
GO	membrane protein ectodomain proteolysis	1	14	0.48625	0.44439321
GO	positive regulation of protein secretion	1	14	0.48625	0.44439321
GO	protein kinase C activity	1	14	0.48625	0.44439321
GO	regulation of vasoconstriction	1	14	0.48625	0.44439321
GO	NuRD complex	1	14	0.48625	0.44439321
GO	chromosome organization	1	14	0.48625	0.44439321
GO	response to ATP	1	14	0.48625	0.44439321
GO	solute:hydrogen antiporter activity	1	14	0.48625	0.44439321
GO	cellular response to starvation	1	14	0.48625	0.44439321
GO	eye development	1	14	0.48625	0.44439321
GO	response to interferon-gamma	1	14	0.48625	0.44439321
GO	pathway-restricted SMAD protein phosphorylation	1	14	0.48625	0.44439321
GO	calmodulin-dependent protein kinase activity	1	14	0.48625	0.44439321
GO	mitochondrion	56	1193	0.487197	0.08433329
GO	acute-phase response	2	35	0.488202	0.30106851
GO	embryonic limb morphogenesis	2	35	0.488202	0.30106851
GO	centriole	2	35	0.488202	0.30106851
GO	transcription corepressor activity	7	142	0.490903	0.16213932
GO	locomotory behavior	3	57	0.497418	0.22234753
GO	DNA binding	65	1392	0.501026	0.04647381
GO	postsynaptic density	4	79	0.502977	0.17732626
GO	protein amino acid autophosphorylation	4	79	0.502977	0.17732626
GO	Rho protein signal transduction	2	36	0.503204	0.2600494
GO	autophagy	2	36	0.503204	0.2600494
GO	microtubule basal body	2	36	0.503204	0.2600494
GO	response to oxidative stress	5	101	0.507048	0.14661024
GO	chloride channel activity	3	58	0.509128	0.19140633
GO	oxidoreductase activity, acting on single donors with incorporation of	3	58	0.509128	0.19140633
GO	cell development	1	15	0.510128	0.37233243
GO	focal adhesion assembly	1	15	0.510128	0.37233243
GO	polysome	1	15	0.510128	0.37233243
GO	female gamete generation	1	15	0.510128	0.37233243
GO	sulfate transport	1	15	0.510128	0.37233243
GO	retinal ganglion cell axon guidance	1	15	0.510128	0.37233243
GO	homeostasis of number of cells within a tissue	1	15	0.510128	0.37233243
GO	positive regulation of cytokine secretion	1	15	0.510128	0.37233243
GO	oxidoreductase activity, acting on paired donors, with incorporation c	1	15	0.510128	0.37233243
GO	reverse cholesterol transport	1	15	0.510128	0.37233243
GO	ATPase binding	1	15	0.510128	0.37233243
GO	actin filament bundle assembly	1	15	0.510128	0.37233243
GO	binding of sperm to zona pellucida	1	15	0.510128	0.37233243
GO	leukocyte migration	1	15	0.510128	0.37233243
GO	protein deubiquitination	1	15	0.510128	0.37233243
GO	voltage-gated sodium channel activity	1	15	0.510128	0.37233243
GO	cellular metabolic process	1	15	0.510128	0.37233243
GO	cellular response to heat	1	15	0.510128	0.37233243
GO	substrate-specific transmembrane transporter activity	1	15	0.510128	0.37233243

GO	hair follicle development	1	15	0.510128	0.37233243
GO	chemoattractant activity	1	15	0.510128	0.37233243
GO	chondrocyte differentiation	1	15	0.510128	0.37233243
GO	regulation of mitotic cell cycle	1	15	0.510128	0.37233243
GO	myosin filament	1	15	0.510128	0.37233243
GO	GTPase binding	1	15	0.510128	0.37233243
GO	oxygen binding	2	37	0.517919	0.2202019
GO	protein catabolic process	2	37	0.517919	0.2202019
GO	activation of adenylate cyclase activity by G-protein signaling pathwa	2	37	0.517919	0.2202019
GO	protein serine/threonine phosphatase activity	2	37	0.517919	0.2202019
GO	NADH dehydrogenase (ubiquinone) activity	2	37	0.517919	0.2202019
GO	receptor binding	10	211	0.519722	0.06596125
GO	cell migration	3	59	0.520694	0.16100667
GO	sarcolemma	3	59	0.520694	0.16100667
GO	Golgi membrane	16	343	0.529324	0.01813299
GO	histone acetyltransferase activity	2	38	0.53234	0.18145498
GO	positive regulation of gene expression	2	38	0.53234	0.18145498
GO	positive regulation of angiogenesis	2	38	0.53234	0.18145498
GO	Cajal body	2	38	0.53234	0.18145498
GO	specific transcriptional repressor activity	2	38	0.53234	0.18145498
GO	triglyceride lipase activity	1	16	0.532897	0.30532396
GO	intrinsic to endoplasmic reticulum membrane	1	16	0.532897	0.30532396
GO	positive regulation of vasoconstriction	1	16	0.532897	0.30532396
GO	smoothened signaling pathway	1	16	0.532897	0.30532396
GO	glutathione metabolic process	1	16	0.532897	0.30532396
GO	hydrogen peroxide catabolic process	1	16	0.532897	0.30532396
GO	positive regulation of mitotic cell cycle	1	16	0.532897	0.30532396
GO	response to cocaine	1	16	0.532897	0.30532396
GO	negative regulation of insulin secretion	1	16	0.532897	0.30532396
GO	mitochondrial proton-transporting ATP synthase complex	1	16	0.532897	0.30532396
GO	cAMP-dependent protein kinase regulator activity	1	16	0.532897	0.30532396
GO	vitamin D receptor binding	1	16	0.532897	0.30532396
GO	phosphatidylinositol-3,4,5-trisphosphate binding	1	16	0.532897	0.30532396
GO	response to cadmium ion	1	16	0.532897	0.30532396
GO	response to nutrient levels	1	16	0.532897	0.30532396
GO	translation regulator activity	1	16	0.532897	0.30532396
GO	ion transmembrane transporter activity	1	16	0.532897	0.30532396
GO	positive regulation of endothelial cell migration	1	16	0.532897	0.30532396
GO	cartilage condensation	1	16	0.532897	0.30532396
GO	receptor complex	1	16	0.532897	0.30532396
GO	C-C chemokine receptor activity	1	16	0.532897	0.30532396
GO	membrane depolarization	1	16	0.532897	0.30532396
GO	protein secretion	1	16	0.532897	0.30532396
GO	mannose binding	1	16	0.532897	0.30532396
GO	response to light stimulus	1	16	0.532897	0.30532396
GO	beta-catenin binding	2	39	0.546463	0.1437438
GO	G-protein signaling, coupled to cyclic nucleotide second messenger	2	39	0.546463	0.1437438
GO	transcription cofactor activity	2	39	0.546463	0.1437438
GO	microtubule cytoskeleton organization	2	39	0.546463	0.1437438

GO	response to peptide hormone stimulus	3	62	0.554472	0.07285629
GO	peroxidase activity	1	17	0.554609	0.24266726
GO	glutathione transferase activity	1	17	0.554609	0.24266726
GO	sarcoplasmic reticulum membrane	1	17	0.554609	0.24266726
GO	intracellular transport	1	17	0.554609	0.24266726
GO	embryonic pattern specification	1	17	0.554609	0.24266726
GO	rough endoplasmic reticulum	1	17	0.554609	0.24266726
GO	regulation of angiogenesis	1	17	0.554609	0.24266726
GO	midbrain development	1	17	0.554609	0.24266726
GO	social behavior	1	17	0.554609	0.24266726
GO	positive regulation of calcium-mediated signaling	1	17	0.554609	0.24266726
GO	mitochondrial small ribosomal subunit	1	17	0.554609	0.24266726
GO	2 iron, 2 sulfur cluster binding	1	17	0.554609	0.24266726
GO	histone deacetylation	1	17	0.554609	0.24266726
GO	embryonic hindlimb morphogenesis	1	17	0.554609	0.24266726
GO	mitochondrial ribosome	1	17	0.554609	0.24266726
GO	regulation of pH	1	17	0.554609	0.24266726
GO	small nuclear ribonucleoprotein complex	1	17	0.554609	0.24266726
GO	epithelial to mesenchymal transition	1	17	0.554609	0.24266726
GO	actin filament capping	1	17	0.554609	0.24266726
GO	nuclear body	1	17	0.554609	0.24266726
GO	cis-Golgi network	1	17	0.554609	0.24266726
GO	spindle assembly	1	17	0.554609	0.24266726
GO	carbohydrate biosynthetic process	1	17	0.554609	0.24266726
GO	sodium ion transport	6	129	0.55723	0.00371365
GO	receptor-mediated endocytosis	2	40	0.560285	0.10700898
GO	cell redox homeostasis	3	63	0.565411	0.04442756
GO	glycolysis	2	41	0.573803	0.07119604
GO	peroxisomal membrane	2	41	0.573803	0.07119604
GO	negative regulation of cell cycle	2	41	0.573803	0.07119604
GO	cholesterol homeostasis	2	41	0.573803	0.07119604
GO	neuron projection development	2	41	0.573803	0.07119604
GO	ER to Golgi vesicle-mediated transport	2	41	0.573803	0.07119604
GO	ribosome binding	1	18	0.575313	0.18379545
GO	lipoprotein metabolic process	1	18	0.575313	0.18379545
GO	MHC class I protein complex	1	18	0.575313	0.18379545
GO	regulation of insulin secretion	1	18	0.575313	0.18379545
GO	protein import into nucleus, translocation	1	18	0.575313	0.18379545
GO	protein ubiquitination involved in ubiquitin-dependent protein catabo	1	18	0.575313	0.18379545
GO	endocrine pancreas development	1	18	0.575313	0.18379545
GO	cellular process	1	18	0.575313	0.18379545
GO	embryonic placenta development	1	18	0.575313	0.18379545
GO	WW domain binding	1	18	0.575313	0.18379545
GO	phosphatidylinositol binding	1	18	0.575313	0.18379545
GO	transmembrane receptor protein tyrosine phosphatase activity	1	18	0.575313	0.18379545
GO	DNA fragmentation involved in apoptotic nuclear change	1	18	0.575313	0.18379545
GO	inner ear development	1	18	0.575313	0.18379545
GO	cortical cytoskeleton	1	18	0.575313	0.18379545
GO	peptidyl-threonine phosphorylation	1	18	0.575313	0.18379545

GO	heme biosynthetic process	1	18	0.575313	0.18379545
GO	negative regulation of translation	1	18	0.575313	0.18379545
GO	cornified envelope	1	18	0.575313	0.18379545
GO	establishment or maintenance of cell polarity	1	18	0.575313	0.18379545
GO	anion transport	1	18	0.575313	0.18379545
GO	transcription initiation from RNA polymerase II promoter	3	64	0.576184	0.01644786
GO	patterning of blood vessels	1	19	0.595056	0.12824378
GO	protein amino acid O-linked glycosylation	1	19	0.595056	0.12824378
GO	cadherin binding	1	19	0.595056	0.12824378
GO	negative regulation of cell differentiation	1	19	0.595056	0.12824378
GO	leukotriene biosynthetic process	1	19	0.595056	0.12824378
GO	RNA metabolic process	1	19	0.595056	0.12824378
GO	lipid transporter activity	1	19	0.595056	0.12824378
GO	phosphoprotein binding	1	19	0.595056	0.12824378
GO	regulation of neuron differentiation	1	19	0.595056	0.12824378
GO	insulin-like growth factor binding	1	19	0.595056	0.12824378
GO	neutrophil chemotaxis	1	19	0.595056	0.12824378
GO	telomere maintenance	1	19	0.595056	0.12824378
GO	T-tubule	1	19	0.595056	0.12824378
GO	chemokine receptor activity	1	19	0.595056	0.12824378
GO	regulation of signal transduction	1	19	0.595056	0.12824378
GO	inner ear morphogenesis	2	43	0.599921	0.00213921
GO	phosphotransferase activity, alcohol group as acceptor	1	20	0.613881	0.07562688
GO	desmosome	1	20	0.613881	0.07562688
GO	translation elongation factor activity	1	20	0.613881	0.07562688
GO	phosphorylation	1	20	0.613881	0.07562688
GO	response to steroid hormone stimulus	1	20	0.613881	0.07562688
GO	proteasomal ubiquitin-dependent protein catabolic process	1	20	0.613881	0.07562688
GO	ubiquitin binding	1	20	0.613881	0.07562688
GO	hydrogen ion transmembrane transporter activity	1	20	0.613881	0.07562688
GO	positive regulation of bone mineralization	1	20	0.613881	0.07562688
GO	response to radiation	1	20	0.613881	0.07562688
GO	positive regulation of cell adhesion	1	20	0.613881	0.07562688
GO	clathrin adaptor complex	1	20	0.613881	0.07562688
GO	phosphate metabolic process	1	20	0.613881	0.07562688
GO	aromatase activity	1	21	0.631833	0.02562185
GO	translation factor activity, nucleic acid binding	1	21	0.631833	0.02562185
GO	transferase activity, transferring hexosyl groups	1	21	0.631833	0.02562185
GO	branching morphogenesis of a tube	1	21	0.631833	0.02562185
GO	regulation of multicellular organism growth	1	21	0.631833	0.02562185
GO	negative regulation of caspase activity	1	21	0.631833	0.02562185
GO	gastrulation with mouth forming second	1	21	0.631833	0.02562185
GO	positive regulation of inflammatory response	1	21	0.631833	0.02562185
GO	dephosphorylation	1	21	0.631833	0.02562185
GO	negative regulation of BMP signaling pathway	1	21	0.631833	0.02562185
GO	defense response to virus	1	21	0.631833	0.02562185
GO	release of cytochrome c from mitochondria	1	21	0.631833	0.02562185
GO	p53 binding	1	21	0.631833	0.02562185
GO	negative regulation of gene-specific transcription	1	21	0.631833	0.02562185

GO	positive regulation of mesenchymal cell proliferation	1	21	0.631833	0.02562185
GO	integral to membrane	177	3857	0.989	-0.1826334
GO	protein kinase binding	3	113	0.989	-1.0079069
GO	protein phosphatase binding	1	25	0.989	-0.1531802
GO	membrane	161	3643	0.989	-0.7174065
GO	protein kinase activity	6	170	0.989	-0.6938495
GO	protein serine/threonine kinase activity	12	335	0.989	-0.9320831
GO	signal transduction	78	1796	0.989	-0.6376905
GO	regulation of transcription, DNA-dependent	32	1013	0.989	-2.3088614
GO	transcription factor activity	39	922	0.989	-0.6129369
GO	transport	21	511	0.989	-0.5822528
GO	metabolic process	20	455	0.989	-0.2551548
GO	protein modification process	6	145	0.989	-0.2908538
GO	response to protein stimulus	1	42	0.989	-0.6977704
GO	intracellular	80	1794	0.989	-0.3912703
GO	small GTPase mediated signal transduction	8	193	0.989	-0.3312456
GO	biological_process	17	547	0.989	-1.7326533
GO	RNA splicing, via transesterification reactions	1	25	0.989	-0.1531802
GO	binding	16	500	0.989	-1.5552226
GO	nuclear envelope	4	92	0.989	-0.1354557
GO	oxidation reduction	18	515	0.989	-1.2563446
GO	oxidoreductase activity	12	418	0.989	-1.7422284
GO	hydrolase activity	39	917	0.989	-0.5771692
GO	nucleic acid binding	9	254	0.989	-0.8394256
GO	metal ion binding	116	2658	0.989	-0.7399799
GO	metallopeptidase activity	2	88	0.989	-1.0596005
GO	early endosome membrane	1	37	0.989	-0.5617454
GO	endosome	6	215	0.989	-1.2988657
GO	intracellular protein transport	7	174	0.989	-0.3912382
GO	positive regulation of anti-apoptosis	1	32	0.989	-0.4087343
GO	positive regulation of B cell proliferation	1	25	0.989	-0.1531802
GO	cell proliferation	12	286	0.989	-0.3631586
GO	perinuclear region of cytoplasm	14	309	0.989	-0.0956368
GO	zinc ion binding	81	1867	0.989	-0.661192
GO	activation of phospholipase C activity	1	22	0.989	-0.0220444
GO	focal adhesion	3	86	0.989	-0.5105313
GO	Rho GTPase activator activity	1	22	0.989	-0.0220444
GO	transcriptional repressor complex	1	29	0.989	-0.3062863
GO	endoplasmic reticulum membrane	21	518	0.989	-0.6472347
GO	endoplasmic reticulum	34	880	0.989	-1.1268491
GO	histone H3 acetylation	1	24	0.989	-0.1112588
GO	transcription coactivator activity	7	192	0.989	-0.6607663
GO	microsome	10	219	0.989	-0.0552357
GO	blood vessel remodeling	1	22	0.989	-0.0220444
GO	extracellular space	26	647	0.989	-0.7695562
GO	immune response	9	303	0.989	-1.3958099
GO	receptor activity	52	1148	0.989	-0.1904959
GO	cell cortex	2	75	0.989	-0.8154394
GO	Z disc	2	46	0.989	-0.0956653

GO	protein transport	16	388	0.989	-0.4923253
GO	response to virus	3	105	0.989	-0.8726045
GO	regulation of transcription	37	956	0.989	-1.1669373
GO	SH3 domain binding	4	97	0.989	-0.2442597
GO	brush border membrane	1	26	0.989	-0.1935193
GO	G-protein coupled receptor protein signaling pathway	27	725	0.989	-1.2004466
GO	in utero embryonic development	6	136	0.989	-0.1293253
GO	molecular_function	19	577	0.989	-1.5664987
GO	response to unfolded protein	2	49	0.989	-0.1874
GO	Golgi apparatus	34	784	0.989	-0.4179384
GO	proteolysis	18	423	0.989	-0.3844594
GO	vesicle-mediated transport	3	165	0.989	-1.7325383
GO	response to stimulus	14	477	0.989	-1.7966141
GO	sugar binding	6	161	0.989	-0.5556082
GO	SH3/SH2 adaptor activity	2	50	0.989	-0.2167724
GO	neuropeptide signaling pathway	3	85	0.989	-0.4895215
GO	chemotaxis	5	117	0.989	-0.1911748
GO	cytokine activity	6	143	0.989	-0.2558159
GO	heme binding	4	110	0.989	-0.5037882
GO	anchored to membrane	2	109	0.989	-1.3977781
GO	olfactory receptor activity	7	290	0.989	-1.8188629
GO	sensory perception of smell	8	305	0.989	-1.6910755
GO	inflammatory response	8	222	0.989	-0.7411582
GO	serine-type endopeptidase inhibitor activity	2	90	0.989	-1.0944519
GO	positive regulation of NF-kappaB transcription factor activity	1	47	0.989	-0.8208503
GO	protein amino acid dephosphorylation	3	120	0.989	-1.1197177
GO	protein tyrosine phosphatase activity	2	82	0.989	-0.9509667
GO	protein tyrosine/serine/threonine phosphatase activity	1	30	0.989	-0.3414697
GO	catalytic activity	5	114	0.989	-0.131464
GO	carbohydrate metabolic process	8	198	0.989	-0.4059095
GO	external side of plasma membrane	5	121	0.989	-0.2685147
GO	phosphoprotein phosphatase activity	1	36	0.989	-0.532663
GO	structural constituent of cytoskeleton	3	73	0.989	-0.2175083
GO	enzyme binding	5	114	0.989	-0.131464
GO	response to lipopolysaccharide	3	105	0.989	-0.8726045
GO	acyltransferase activity	3	133	0.989	-1.3135973
GO	cytoplasmic vesicle	9	229	0.989	-0.5166675
GO	lysosomal membrane	2	83	0.989	-0.9695223
GO	intracellular membrane-bounded organelle	2	127	0.989	-1.6492317
GO	microtubule motor activity	3	76	0.989	-0.2892849
GO	chromatin modification	5	204	0.989	-1.4966426
GO	growth factor activity	7	152	0.989	-0.0229643
GO	keratinocyte differentiation	1	29	0.989	-0.3062863
GO	membrane fraction	15	472	0.989	-1.532941
GO	regulation of translational initiation	1	24	0.989	-0.1112588
GO	translation initiation factor activity	1	49	0.989	-0.8671009
GO	translational initiation	1	36	0.989	-0.532663
GO	positive regulation of cell proliferation	13	290	0.989	-0.1317326
GO	protein N-terminus binding	2	72	0.989	-0.7540156

GO	chloride channel complex	2	54	0.989	-0.328909
GO	activation of protein kinase C activity by G-protein coupled receptor p	1	34	0.989	-0.4723141
GO	anatomical structure morphogenesis	4	101	0.989	-0.3274703
GO	positive regulation of I-kappaB kinase/NF-kappaB cascade	2	109	0.989	-1.3977781
GO	blood coagulation	3	71	0.989	-0.1680594
GO	phosphoinositide phospholipase C activity	1	26	0.989	-0.1935193
GO	epidermis development	3	75	0.989	-0.2656663
GO	electron transport chain	2	86	0.989	-1.0240913
GO	generation of precursor metabolites and energy	1	55	0.989	-0.9973719
GO	mitochondrial matrix	5	147	0.989	-0.7188739
GO	fibroblast growth factor receptor signaling pathway	1	33	0.989	-0.4409543
GO	cell-matrix adhesion	3	68	0.989	-0.0912824
GO	insulin secretion	1	23	0.989	-0.0676046
GO	mitochondrial outer membrane	3	81	0.989	-0.4031171
GO	peroxisome	4	92	0.989	-0.1354557
GO	synaptic vesicle	2	46	0.989	-0.0956653
GO	cell surface receptor linked signaling pathway	7	161	0.989	-0.1795191
GO	feeding behavior	1	25	0.989	-0.1531802
GO	T cell receptor signaling pathway	1	22	0.989	-0.0220444
GO	chloride transport	2	50	0.989	-0.2167724
GO	nuclear-transcribed mRNA catabolic process, nonsense-mediated dec	1	28	0.989	-0.2699629
GO	guanyl-nucleotide exchange factor activity	4	120	0.989	-0.684566
GO	mitochondrial inner membrane	7	231	0.989	-1.172796
GO	microtubule cytoskeleton	2	53	0.989	-0.3016326
GO	cilium	2	90	0.989	-1.0944519
GO	actin filament organization	1	28	0.989	-0.2699629
GO	lung development	2	60	0.989	-0.4832936
GO	mammary gland development	1	25	0.989	-0.1531802
GO	promoter binding	4	101	0.989	-0.3274703
GO	transcription activator activity	9	227	0.989	-0.4894393
GO	mitochondrial membrane	2	51	0.989	-0.2455862
GO	mitochondrion organization	1	25	0.989	-0.1531802
GO	response to stress	4	112	0.989	-0.5411256
GO	inhibition of adenylate cyclase activity by G-protein signaling pathway	1	30	0.989	-0.3414697
GO	endoplasmic reticulum lumen	3	68	0.989	-0.0912824
GO	iron ion binding	1	65	0.989	-1.1918885
GO	transcription factor binding	4	170	0.989	-1.4260212
GO	general RNA polymerase II transcription factor activity	1	22	0.989	-0.0220444
GO	RNA elongation from RNA polymerase II promoter	2	47	0.989	-0.126875
GO	cell morphogenesis	1	30	0.989	-0.3414697
GO	phosphoinositide binding	1	56	0.989	-1.0179868
GO	cell-cell signaling	8	238	0.989	-0.9464447
GO	steroid binding	1	23	0.989	-0.0676046
GO	cholesterol biosynthetic process	1	25	0.989	-0.1531802
GO	transcription repressor activity	5	173	0.989	-1.101355
GO	embryonic skeletal system morphogenesis	1	36	0.989	-0.532663
GO	fatty acid metabolic process	2	75	0.989	-0.8154394
GO	cysteine-type endopeptidase inhibitor activity	1	22	0.989	-0.0220444
GO	monooxygenase activity	2	52	0.989	-0.2738654

GO	late endosome	1	43	0.989	-0.7233198
GO	negative regulation of inflammatory response	1	24	0.989	-0.1112588
GO	phospholipid binding	2	49	0.989	-0.1874
GO	negative regulation of transcription, DNA-dependent	3	91	0.989	-0.6123225
GO	antigen processing and presentation	1	28	0.989	-0.2699629
GO	activation of pro-apoptotic gene products	1	22	0.989	-0.0220444
GO	transmembrane receptor activity	5	108	0.989	-0.0072678
GO	positive regulation of peptidyl-tyrosine phosphorylation	1	42	0.989	-0.6977704
GO	defense response	2	63	0.989	-0.5552339
GO	erythrocyte differentiation	1	23	0.989	-0.0676046
GO	ovarian follicle development	1	36	0.989	-0.532663
GO	cell surface	4	214	0.989	-1.9400301
GO	potassium channel activity	1	33	0.989	-0.4409543
GO	cell maturation	1	23	0.989	-0.0676046
GO	histone deacetylase binding	1	39	0.989	-0.6179299
GO	intermediate filament	2	80	0.989	-0.9132783
GO	keratin filament	1	64	0.989	-1.1734999
GO	gene silencing by RNA	1	30	0.989	-0.3414697
GO	post-translational protein modification	1	27	0.989	-0.2324082
GO	response to insulin stimulus	2	51	0.989	-0.2455862
GO	transcription factor complex	3	140	0.989	-1.4116177
GO	negative regulation of NF-kappaB transcription factor activity	1	22	0.989	-0.0220444
GO	lysosome organization	1	22	0.989	-0.0220444
GO	lysosome	2	144	0.989	-1.8633544
GO	mitochondrial electron transport, NADH to ubiquinone	1	36	0.989	-0.532663
GO	mitochondrial respiratory chain complex I	1	39	0.989	-0.6179299
GO	respiratory chain	1	42	0.989	-0.6977704
GO	peripheral nervous system development	1	24	0.989	-0.1112588
GO	pigmentation	1	22	0.989	-0.0220444
GO	wound healing	2	49	0.989	-0.1874
GO	ATP biosynthetic process	1	53	0.989	-0.9552503
GO	hydrolase activity, acting on acid anhydrides, catalyzing transmembra	2	47	0.989	-0.126875
GO	centrosome	4	117	0.989	-0.631835
GO	response to cAMP	2	46	0.989	-0.0956653
GO	excretion	1	35	0.989	-0.5028674
GO	transport vesicle	1	39	0.989	-0.6179299
GO	kinetochore	2	49	0.989	-0.1874
GO	hydrolase activity, acting on glycosyl bonds	1	44	0.989	-0.7483802
GO	peptide hormone binding	1	22	0.989	-0.0220444
GO	protease binding	1	23	0.989	-0.0676046
GO	translational elongation	4	87	0.989	-0.0207031
GO	secretory granule	1	51	0.989	-0.9118615
GO	Wnt receptor signaling pathway	3	90	0.989	-0.5923809
GO	drug binding	1	44	0.989	-0.7483802
GO	insoluble fraction	1	39	0.989	-0.6179299
GO	aminopeptidase activity	1	28	0.989	-0.2699629
GO	cellular amino acid metabolic process	1	36	0.989	-0.532663
GO	metallocarboxypeptidase activity	1	25	0.989	-0.1531802
GO	positive regulation of cell division	1	37	0.989	-0.5617454

GO	negative regulation of transcription	6	148	0.989	-0.342548
GO	apical part of cell	1	42	0.989	-0.6977704
GO	cell projection organization	1	28	0.989	-0.2699629
GO	calcium channel activity	2	44	0.989	-0.0311935
GO	exocytosis	2	47	0.989	-0.126875
GO	amino acid transmembrane transporter activity	1	26	0.989	-0.1935193
GO	amino acid transport	1	46	0.989	-0.7971248
GO	neurotransmitter transport	1	40	0.989	-0.6451034
GO	GDP binding	1	26	0.989	-0.1935193
GO	late endosome membrane	2	51	0.989	-0.2455862
GO	acrosomal vesicle	1	33	0.989	-0.4409543
GO	phagocytosis	1	27	0.989	-0.2324082
GO	4 iron, 4 sulfur cluster binding	1	25	0.989	-0.1531802
GO	positive regulation of T cell proliferation	1	27	0.989	-0.2324082
GO	response to heat	2	47	0.989	-0.126875
GO	negative regulation of transforming growth factor beta receptor signa	1	28	0.989	-0.2699629
GO	endomembrane system	2	77	0.989	-0.8552235
GO	integral to endoplasmic reticulum membrane	2	46	0.989	-0.0956653
GO	cilium axoneme	1	26	0.989	-0.1935193
GO	positive regulation of multicellular organism growth	1	23	0.989	-0.0676046
GO	reciprocal meiotic recombination	1	22	0.989	-0.0220444
GO	regulation of blood pressure	1	49	0.989	-0.8671009
GO	activation of MAPK activity	1	53	0.989	-0.9552503
GO	rRNA binding	1	23	0.989	-0.0676046
GO	cytosolic large ribosomal subunit	1	33	0.989	-0.4409543
GO	cytosolic small ribosomal subunit	1	34	0.989	-0.4723141
GO	chemokine activity	1	42	0.989	-0.6977704
GO	response to gamma radiation	1	24	0.989	-0.1112588
GO	response to interleukin-1	1	24	0.989	-0.1112588
GO	regulation of growth	2	51	0.989	-0.2455862
GO	glucose transport	1	22	0.989	-0.0220444
GO	heat shock protein binding	1	62	0.989	-1.136068
GO	response to hydrogen peroxide	1	40	0.989	-0.6451034
GO	cation transport	1	65	0.989	-1.1918885
GO	protein localization	1	54	0.989	-0.9764635
GO	negative regulation of gene expression	1	23	0.989	-0.0676046
GO	BMP signaling pathway	1	43	0.989	-0.7233198
GO	mesoderm formation	1	22	0.989	-0.0220444
GO	negative regulation of epithelial cell proliferation	1	26	0.989	-0.1935193
GO	negative regulation of neuron differentiation	1	27	0.989	-0.2324082
GO	protein stabilization	1	31	0.989	-0.3755947
GO	protein dimerization activity	2	84	0.989	-0.9878918
GO	specific RNA polymerase II transcription factor activity	1	33	0.989	-0.4409543
GO	positive regulation of transcription factor activity	1	25	0.989	-0.1531802
GO	respiratory gaseous exchange	1	29	0.989	-0.3062863
GO	positive regulation of gene-specific transcription from RNA polymeras	2	92	0.989	-1.1286757
GO	positive regulation of protein ubiquitination	1	25	0.989	-0.1531802
GO	mRNA binding	1	41	0.989	-0.6717072
GO	tRNA binding	1	24	0.989	-0.1112588

GO	palate development	1	34	0.989	-0.4723141
GO	peptidyl-serine phosphorylation	1	26	0.989	-0.1935193
GO	positive regulation of cell growth	1	34	0.989	-0.4723141
GO	platelet alpha granule lumen	1	34	0.989	-0.4723141
GO	enzyme inhibitor activity	1	27	0.989	-0.2324082
GO	response to hormone stimulus	1	44	0.989	-0.7483802
GO	calcium-dependent protein binding	1	31	0.989	-0.3755947
GO	regulation of heart contraction	1	32	0.989	-0.4087343
GO	ubiquitin-specific protease activity	1	28	0.989	-0.2699629
GO	positive regulation of gene-specific transcription	1	39	0.989	-0.6179299
GO	transcription regulator activity	1	102	0.989	-1.76307
GO	voltage-gated calcium channel activity	1	23	0.989	-0.0676046
GO	calcium-mediated signaling	1	33	0.989	-0.4409543
GO	cilium assembly	1	24	0.989	-0.1112588
GO	spermatid development	1	32	0.989	-0.4087343
GO	regulation of cell cycle	1	42	0.989	-0.6977704
GO	innate immune response	2	109	0.989	-1.3977781
GO	Golgi cisterna membrane	1	63	0.989	-1.1548954
GO	integral to Golgi membrane	2	45	0.989	-0.0637828
GO	protein amino acid glycosylation	3	65	0.989	-0.0110985
GO	galactosyltransferase activity	1	23	0.989	-0.0676046
GO	cellular membrane organization	1	53	0.989	-0.9552503
GO	post-Golgi vesicle-mediated transport	1	37	0.989	-0.5617454
GO	microtubule associated complex	1	25	0.989	-0.1531802
GO	myelination	1	29	0.989	-0.3062863
GO	small GTPase regulator activity	1	28	0.989	-0.2699629
GO	sulfotransferase activity	1	34	0.989	-0.4723141
GO	positive regulation of JUN kinase activity	1	9	0.348252	0.9220806

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