

Significant Go functions

go_id	go_name	go_diffge ne_count	go_gene _count	enrichment	pvalue	FDR	-lg(P)
GO:0006810	transport	88	1712	4.891756365	7.48292E-34	1.25114E-30	33.12592893
GO:0008150	biological process	220	10237	2.045200473	7.08169E-26	5.00379E-23	25.14986318
GO:0006355	regulation of transcription, DNA-depend	80	1852	4.110881061	8.9781E-26	5.00379E-23	25.04681573
GO:0006351	transcription, DNA-dependent	73	1756	3.956254811	1.49798E-22	6.26156E-20	21.82449376
GO:0030154	cell differentiation	34	636	5.087538495	7.79648E-14	2.60714E-11	13.10810133
GO:0007275	multicellular organismal development	40	954	3.990226271	1.05428E-12	2.93792E-10	11.97704552
GO:0006811	ion transport	29	570	4.841824561	2.1724E-11	5.18893E-09	10.66306076
GO:0008152	metabolic process	37	991	3.553153554	2.2951E-10	4.79675E-08	9.639199315
GO:0045893	positive regulation of transcription, DNA	26	523	4.731050307	4.48082E-10	8.32437E-08	9.34864214
GO:0045944	positive regulation of transcription from	31	745	3.959964823	6.24556E-10	1.04426E-07	9.204428781
GO:0015031	protein transport	26	538	4.5991437	8.21518E-10	1.24871E-07	9.085383106
GO:0016310	phosphorylation	28	684	3.895720911	6.88314E-09	9.5905E-07	8.162213612
GO:0000122	negative regulation of transcription from	25	561	4.240949044	9.4768E-09	1.21886E-06	8.023338267
GO:0006468	protein phosphorylation	26	611	4.049655172	1.18358E-08	1.41353E-06	7.926802091
GO:0055085	transmembrane transport	19	385	4.696548142	1.5922E-07	1.77477E-05	6.798003136
GO:0045892	negative regulation of transcription, DN	20	429	4.436685154	1.79042E-07	1.87099E-05	6.747045421
GO:0035556	intracellular signal transduction	15	244	5.850423968	2.53814E-07	2.49634E-05	6.59548442
GO:0021766	hippocampus development	7	37	18.004548	4.30391E-07	3.99786E-05	6.366136316
GO:0007155	cell adhesion	21	500	3.997009655	4.8007E-07	4.22462E-05	6.318695109
GO:0050808	synapse organization	6	26	21.96159151	1.01528E-06	8.48772E-05	5.993415065
GO:0008285	negative regulation of cell proliferation	16	315	4.833874111	1.26189E-06	0.00010047	5.898979032
GO:0006897	endocytosis	11	143	7.320530504	1.57687E-06	0.000119842	5.802202824
GO:0006915	apoptotic process	21	540	3.700934866	1.69046E-06	0.000122889	5.771996142
GO:0009791	post-embryonic development	9	93	9.209699666	2.60753E-06	0.000181658	5.583771446
GO:0043588	skin development	7	50	13.32336552	3.70956E-06	0.000248095	5.430677805
GO:0016192	vesicle-mediated transport	12	190	6.010540835	3.92388E-06	0.000252336	5.406284217
GO:0006470	protein dephosphorylation	10	127	7.493456421	4.28303E-06	0.000265231	5.368248555
GO:0021892	cerebral cortex GABAergic interneuron	3	3	95.16689655	4.62192E-06	0.000275994	5.335177995
GO:0006816	calcium ion transport	10	132	7.209613375	6.09827E-06	0.000351597	5.214793584
GO:0043524	negative regulation of neuron apoptotic	9	114	7.513176044	1.44527E-05	0.000805498	4.840050644
GO:0048715	negative regulation of oligodendrocyte d	4	12	31.72229885	2.23885E-05	0.001199094	4.649974787
GO:0005975	carbohydrate metabolic process	11	188	5.568275862	2.30189E-05	0.001199094	4.637914903

GO:0007399	nervous system development	14	307	4.339858475	2.36663E-05	0.001199094	4.625869242
GO:0006814	sodium ion transport	9	122	7.020508762	2.52469E-05	0.001241554	4.597791623
GO:0007283	spermatogenesis	13	274	4.51521772	3.31511E-05	0.001583675	4.479502302
GO:0051209	release of sequestered calcium ion into cytosol	5	28	16.99408867	4.06573E-05	0.001868578	4.390861569
GO:0016055	Wnt receptor signaling pathway	11	200	5.23417931	4.13501E-05	0.001868578	4.383523334
GO:0001709	cell fate determination	4	14	27.19054187	4.45229E-05	0.001959006	4.351416908
GO:0009790	embryo development	8	104	7.320530504	6.07416E-05	0.002604102	4.21651366
GO:0014065	phosphatidylinositol 3-kinase cascade	4	17	22.39221095	0.000103235	0.004260312	3.986171042
GO:0034220	ion transmembrane transport	10	182	5.22895036	0.000104547	0.004260312	3.980687067
GO:0016311	dephosphorylation	9	146	5.866452527	0.000107017	0.004260312	3.970545535
GO:0070588	calcium ion transmembrane transport	7	89	7.485036807	0.000179668	0.006986174	3.745528411
GO:0048469	cell maturation	5	38	12.52196007	0.000190392	0.007234885	3.720351936
GO:0045879	negative regulation of smoothened signaling pathway	4	20	19.03337931	0.000204956	0.007615246	3.688339794
GO:0007270	neuron-neuron synaptic transmission	3	8	35.68758621	0.000248838	0.008852295	3.604082516
GO:0030206	chondroitin sulfate biosynthetic process	3	8	35.68758621	0.000248838	0.008852295	3.604082516
GO:0090103	cochlea morphogenesis	4	22	17.3030721	0.00030432	0.010218241	3.516669908
GO:0006865	amino acid transport	5	42	11.32939245	0.000311681	0.010218241	3.506289974
GO:0035335	peptidyl-tyrosine dephosphorylation	5	42	11.32939245	0.000311681	0.010218241	3.506289974
GO:0048706	embryonic skeletal system development	5	42	11.32939245	0.000311681	0.010218241	3.506289974
GO:0006836	neurotransmitter transport	5	43	11.0659182	0.000349652	0.01124266	3.45636384
GO:0007219	Notch signaling pathway	6	69	8.275382309	0.000360454	0.011371299	3.443150334
GO:0048172	regulation of short-term neuronal synaptic transmission	3	9	31.72229885	0.000370336	0.01146669	3.431404424
GO:0008104	protein localization	6	71	8.042272948	0.000423069	0.012089309	3.373588938
GO:0009954	proximal/distal pattern formation	4	24	15.86114943	0.00043475	0.012089309	3.361759957
GO:0021882	regulation of transcription from RNA polymerase II promoter	2	2	95.16689655	0.000441057	0.012089309	3.355504968
GO:0021893	cerebral cortex GABAergic interneuron development	2	2	95.16689655	0.000441057	0.012089309	3.355504968
GO:0051124	synaptic growth at neuromuscular junction	2	2	95.16689655	0.000441057	0.012089309	3.355504968
GO:0060983	epicardium-derived cardiac vascular smooth muscle cell differentiation	2	2	95.16689655	0.000441057	0.012089309	3.355504968
GO:0070072	vacuolar proton-transporting V-type ATPase activity	2	2	95.16689655	0.000441057	0.012089309	3.355504968
GO:0001764	neuron migration	7	104	6.405464191	0.000483761	0.012875856	3.315369382
GO:0009058	biosynthetic process	5	46	10.34422789	0.000485155	0.012875856	3.314119598
GO:0007422	peripheral nervous system development	4	25	15.22670345	0.000513263	0.013408995	3.289660078
GO:0030178	negative regulation of Wnt receptor signaling pathway	5	48	9.913218391	0.000595653	0.015011791	3.225006906
GO:0001892	embryonic placenta development	4	26	14.64106101	0.000601549	0.015011791	3.220728955
GO:0046034	ATP metabolic process	4	26	14.64106101	0.000601549	0.015011791	3.220728955
GO:0021795	cerebral cortex cell migration	3	11	25.95460815	0.000716109	0.017352676	3.145020731
GO:0021879	forebrain neuron differentiation	3	11	25.95460815	0.000716109	0.017352676	3.145020731
GO:0090090	negative regulation of canonical Wnt receptor signaling pathway	6	79	7.227865561	0.000764929	0.01827088	3.116378757

GO:0046326	positive regulation of glucose import	4	28	13.59527094	0.000810249	0.019080796	3.091381444
GO:0042475	odontogenesis of dentin-containing tooth	5	52	9.15066313	0.000873386	0.020281968	3.058793689
GO:0007411	axon guidance	7	115	5.792767616	0.000903583	0.020695771	3.044031813
GO:0010977	negative regulation of neuron projection	4	29	13.12646849	0.000932097	0.020919463	3.030539113
GO:0007010	cytoskeleton organization	6	82	6.963431455	0.000938373	0.020919463	3.027624481
GO:0046777	protein autophosphorylation	8	156	4.880353669	0.001062131	0.023366888	2.973821812
GO:0007165	signal transduction	42	2212	1.80696639	0.001094538	0.02376711	2.960769168
GO:0016567	protein ubiquitination	8	159	4.788271525	0.001207811	0.025381986	2.918001108
GO:0006888	ER to Golgi vesicle-mediated transport	4	31	12.27959956	0.001214449	0.025381986	2.915620689
GO:0007200	phospholipase C-activating G-protein co	4	31	12.27959956	0.001214449	0.025381986	2.915620689
GO:0021877	forebrain neuron fate commitment	2	3	63.4445977	0.001313928	0.026153426	2.881428392
GO:0042985	negative regulation of amyloid precursor	2	3	63.4445977	0.001313928	0.026153426	2.881428392
GO:0055005	ventricular cardiac myofibril developme	2	3	63.4445977	0.001313928	0.026153426	2.881428392
GO:2000171	negative regulation of dendrite developm	2	3	63.4445977	0.001313928	0.026153426	2.881428392
GO:0007626	locomotory behavior	6	88	6.488652038	0.001377261	0.02709153	2.860983807
GO:0034614	cellular response to reactive oxygen spec	3	14	20.3929064	0.001543045	0.029355417	2.811621268
GO:0045786	negative regulation of cell cycle	4	33	11.5353814	0.001553335	0.029355417	2.808734992
GO:0007389	pattern specification process	6	90	6.34445977	0.001554603	0.029355417	2.808380564
GO:0007049	cell cycle	16	565	2.694991761	0.001562579	0.029355417	2.806158018
GO:0045665	negative regulation of neuron differentia	5	60	7.930574713	0.001712996	0.031729409	2.76624376
GO:0007204	elevation of cytosolic calcium ion conce	7	128	5.204439655	0.001734325	0.031729409	2.760869591
GO:0030155	regulation of cell adhesion	4	34	11.19610548	0.001745877	0.031729409	2.757986462
GO:0006511	ubiquitin-dependent protein catabolic pr	7	130	5.124371353	0.001903691	0.03404041	2.720403568
GO:0045070	positive regulation of viral genome repli	3	15	19.03337931	0.001913755	0.03404041	2.718113642
GO:0031175	neuron projection development	6	94	6.074482759	0.001962483	0.034539705	2.707194038
GO:0010468	regulation of gene expression	8	173	4.400781343	0.002119358	0.036912157	2.673795615
GO:0007218	neuropeptide signaling pathway	6	96	5.947931034	0.002195361	0.037841692	2.658493994
GO:0007405	neuroblast proliferation	3	16	17.8437931	0.00233702	0.039469669	2.631337591
GO:0045746	negative regulation of Notch signaling p	3	16	17.8437931	0.00233702	0.039469669	2.631337591
GO:0023014	signal transduction by phosphorylation	4	37	10.28831314	0.002425162	0.040028503	2.615259316
GO:0006417	regulation of translation	6	98	5.826544687	0.002449151	0.040028503	2.610984453
GO:0006497	protein lipidation	2	4	47.58344828	0.002609514	0.040028503	2.583440422
GO:0010638	positive regulation of organelle organiza	2	4	47.58344828	0.002609514	0.040028503	2.583440422
GO:0038003	opioid receptor signaling pathway	2	4	47.58344828	0.002609514	0.040028503	2.583440422
GO:0042255	ribosome assembly	2	4	47.58344828	0.002609514	0.040028503	2.583440422
GO:0048671	negative regulation of collateral sproutin	2	4	47.58344828	0.002609514	0.040028503	2.583440422
GO:0060078	regulation of postsynaptic membrane po	2	4	47.58344828	0.002609514	0.040028503	2.583440422
GO:0060214	endocardium formation	2	4	47.58344828	0.002609514	0.040028503	2.583440422

GO:1901660	calcium ion export	2	4	47.58344828	0.002609514	0.040028503	2.583440422
GO:0001570	vasculogenesis	5	66	7.209613375	0.002661958	0.040461765	2.574798761
GO:0007030	Golgi organization	4	39	9.760707339	0.002970541	0.044745443	2.527164486
GO:0001666	response to hypoxia	6	102	5.598052738	0.003024533	0.045151952	2.519341718
GO:0009887	organ morphogenesis	6	103	5.543702712	0.003183455	0.046711504	2.497101282
GO:0006397	mRNA processing	10	278	3.42326966	0.003232086	0.046711504	2.490517144
GO:0003333	amino acid transmembrane transport	4	40	9.516689655	0.003273345	0.046711504	2.485008215
GO:0007611	learning or memory	4	40	9.516689655	0.003273345	0.046711504	2.485008215
GO:0006911	phagocytosis, engulfment	3	18	15.86114943	0.0033525	0.046711504	2.47463118
GO:0034394	protein localization to cell surface	3	18	15.86114943	0.0033525	0.046711504	2.47463118
GO:0042326	negative regulation of phosphorylation	3	18	15.86114943	0.0033525	0.046711504	2.47463118
GO:1901215	negative regulation of neuron death	3	18	15.86114943	0.0033525	0.046711504	2.47463118
GO:0001525	angiogenesis	8	189	4.028228425	0.003771428	0.052114275	2.423494202
GO:0043113	receptor clustering	3	19	15.02635209	0.003950093	0.053096553	2.403392697
GO:0045880	positive regulation of smoothened signal	3	19	15.02635209	0.003950093	0.053096553	2.403392697
GO:0007608	sensory perception of smell	2	1141	0.16681314	0.004113739	0.053096553	2.385763309
GO:0001514	selenocysteine incorporation	2	5	38.06675862	0.004318858	0.053096553	2.364631039
GO:0022405	hair cycle process	2	5	38.06675862	0.004318858	0.053096553	2.364631039
GO:0030240	skeletal muscle thin filament assembly	2	5	38.06675862	0.004318858	0.053096553	2.364631039
GO:0045162	clustering of voltage-gated sodium chan	2	5	38.06675862	0.004318858	0.053096553	2.364631039
GO:0045743	positive regulation of fibroblast growth	2	5	38.06675862	0.004318858	0.053096553	2.364631039
GO:0046321	positive regulation of fatty acid oxidatio	2	5	38.06675862	0.004318858	0.053096553	2.364631039
GO:0060029	convergent extension involved in organo	2	5	38.06675862	0.004318858	0.053096553	2.364631039
GO:0060836	lymphatic endothelial cell differentiation	2	5	38.06675862	0.004318858	0.053096553	2.364631039
GO:0071313	cellular response to caffeine	2	5	38.06675862	0.004318858	0.053096553	2.364631039
GO:0071786	endoplasmic reticulum tubular network	2	5	38.06675862	0.004318858	0.053096553	2.364631039
GO:0072091	regulation of stem cell proliferation	2	5	38.06675862	0.004318858	0.053096553	2.364631039
GO:2000272	negative regulation of receptor activity	2	5	38.06675862	0.004318858	0.053096553	2.364631039
GO:0007214	gamma-aminobutyric acid signaling path	3	20	14.27503448	0.004610999	0.055866601	2.336204936
GO:0035050	embryonic heart tube development	3	20	14.27503448	0.004610999	0.055866601	2.336204936
GO:0001942	hair follicle development	4	44	8.65153605	0.004703754	0.056580403	2.327555435
GO:0007605	sensory perception of sound	6	112	5.098226601	0.004921051	0.058771409	2.307942133
GO:0006914	autophagy	5	76	6.260980036	0.005049998	0.059046133	2.296708775
GO:0030336	negative regulation of cell migration	5	76	6.260980036	0.005049998	0.059046133	2.296708775
GO:0051216	cartilage development	5	76	6.260980036	0.005049998	0.059046133	2.296708775
GO:0007338	single fertilization	3	21	13.59527094	0.005337653	0.061976086	2.272649636
GO:0007268	synaptic transmission	6	114	5.008784029	0.00539015	0.062154003	2.268399165
GO:0016568	chromatin modification	9	251	3.412358841	0.005936104	0.067201123	2.226498499

GO:0006629	lipid metabolic process	12	409	2.792182784	0.005966149	0.067201123	2.224305912
GO:0043410	positive regulation of MAPK cascade	5	79	6.023221301	0.006004073	0.067201123	2.221554063
GO:0009968	negative regulation of signal transduction	4	47	8.099310345	0.006028809	0.067201123	2.219768486
GO:0034613	cellular protein localization	4	47	8.099310345	0.006028809	0.067201123	2.219768486
GO:0036342	post-anal tail morphogenesis	3	22	12.97730408	0.00613239	0.067456292	2.212370217
GO:0051898	negative regulation of protein kinase B signaling	3	22	12.97730408	0.00613239	0.067456292	2.212370217
GO:0006508	proteolysis	15	585	2.440176835	0.00627371	0.0676492	2.202475567
GO:0051291	protein heterooligomerization	5	80	5.947931034	0.0063497	0.0676492	2.197246804
GO:0006342	chromatin silencing	2	6	31.72229885	0.006433148	0.0676492	2.191576486
GO:0030388	fructose 1,6-bisphosphate metabolic process	2	6	31.72229885	0.006433148	0.0676492	2.191576486
GO:0051893	regulation of focal adhesion assembly	2	6	31.72229885	0.006433148	0.0676492	2.191576486
GO:0060976	coronary vasculature development	2	6	31.72229885	0.006433148	0.0676492	2.191576486
GO:0097178	ruffle assembly	2	6	31.72229885	0.006433148	0.0676492	2.191576486
GO:0007420	brain development	6	119	4.798330919	0.006712209	0.070142589	2.173134498
GO:0035235	ionotropic glutamate receptor signaling	3	23	12.41307346	0.00699745	0.072220593	2.155060208
GO:0042177	negative regulation of protein catabolic process	3	23	12.41307346	0.00699745	0.072220593	2.155060208
GO:0007498	mesoderm development	3	24	11.89586207	0.007934978	0.081394379	2.100454257
GO:0030334	regulation of cell migration	4	51	7.464070318	0.008172108	0.082471477	2.087665898
GO:0043401	steroid hormone mediated signaling pathway	4	51	7.464070318	0.008172108	0.082471477	2.087665898
GO:0007507	heart development	7	167	3.989031592	0.008187958	0.082471477	2.086824413
GO:0008219	cell death	4	52	7.320530504	0.008780335	0.083572261	2.056488919
GO:0042060	wound healing	4	52	7.320530504	0.008780335	0.083572261	2.056488919
GO:0007016	cytoskeletal anchoring at plasma membrane	2	7	27.19054187	0.008943706	0.083572261	2.048482491
GO:0015816	glycine transport	2	7	27.19054187	0.008943706	0.083572261	2.048482491
GO:0015824	proline transport	2	7	27.19054187	0.008943706	0.083572261	2.048482491
GO:0019441	tryptophan catabolic process to kynurenine	2	7	27.19054187	0.008943706	0.083572261	2.048482491
GO:0030856	regulation of epithelial cell differentiation	2	7	27.19054187	0.008943706	0.083572261	2.048482491
GO:0032962	positive regulation of inositol trisphosphate release	2	7	27.19054187	0.008943706	0.083572261	2.048482491
GO:0034389	lipid particle organization	2	7	27.19054187	0.008943706	0.083572261	2.048482491
GO:0048739	cardiac muscle fiber development	2	7	27.19054187	0.008943706	0.083572261	2.048482491
GO:0060485	mesenchyme development	2	7	27.19054187	0.008943706	0.083572261	2.048482491
GO:0007616	long-term memory	3	25	11.42002759	0.00894703	0.083572261	2.048321088
GO:0048813	dendrite morphogenesis	3	25	11.42002759	0.00894703	0.083572261	2.048321088
GO:0001701	in utero embryonic development	9	270	3.172229885	0.009721851	0.090305191	2.012251052
GO:0001702	gastrulation with mouth forming second stage	3	26	10.98079576	0.010035571	0.092704284	1.998457894
GO:0006886	intracellular protein transport	7	174	3.82855331	0.010307439	0.094692517	1.986849226
GO:0001822	kidney development	5	90	5.287049808	0.010656464	0.097363978	1.972386874
GO:0007417	central nervous system development	4	55	6.92122884	0.010790956	0.097526909	1.966940086

GO:0045454	cell redox homeostasis	4	55	6.92122884	0.010790956	0.097526909	1.966940086
GO:0030168	platelet activation	3	27	10.57409962	0.011202479	0.100701858	1.950685845
GO:0007613	memory	4	56	6.797635468	0.011525636	0.102060906	1.938335085
GO:0000578	embryonic axis specification	2	8	23.79172414	0.011841995	0.102060906	1.926575125
GO:0006390	transcription from mitochondrial promoter	2	8	23.79172414	0.011841995	0.102060906	1.926575125
GO:0010656	negative regulation of muscle cell apoptosis	2	8	23.79172414	0.011841995	0.102060906	1.926575125
GO:0016322	neuron remodeling	2	8	23.79172414	0.011841995	0.102060906	1.926575125
GO:0030431	sleep	2	8	23.79172414	0.011841995	0.102060906	1.926575125
GO:0034101	erythrocyte homeostasis	2	8	23.79172414	0.011841995	0.102060906	1.926575125
GO:0055013	cardiac muscle cell development	2	8	23.79172414	0.011841995	0.102060906	1.926575125
GO:0045669	positive regulation of osteoblast differentiation	4	57	6.678378705	0.012293784	0.105129509	1.910314413
GO:0034504	protein localization to nucleus	3	28	10.1964532	0.012449547	0.105129509	1.904846448
GO:0048663	neuron fate commitment	3	28	10.1964532	0.012449547	0.105129509	1.904846448
GO:0051930	regulation of sensory perception of pain	3	28	10.1964532	0.012449547	0.105129509	1.904846448
GO:0007018	microtubule-based movement	4	58	6.563234245	0.013096127	0.109483621	1.882857125
GO:0030326	embryonic limb morphogenesis	4	58	6.563234245	0.013096127	0.109483621	1.882857125
GO:0030501	positive regulation of bone mineralization	3	29	9.844851367	0.013778484	0.114615048	1.860798574
GO:0006983	ER overload response	2	9	21.14819923	0.015119612	0.119807611	1.820459354
GO:0010388	cullin deneddylation	2	9	21.14819923	0.015119612	0.119807611	1.820459354
GO:0016043	cellular component organization	2	9	21.14819923	0.015119612	0.119807611	1.820459354
GO:0016051	carbohydrate biosynthetic process	2	9	21.14819923	0.015119612	0.119807611	1.820459354
GO:0031529	ruffle organization	2	9	21.14819923	0.015119612	0.119807611	1.820459354
GO:0043666	regulation of phosphoprotein phosphatase activity	2	9	21.14819923	0.015119612	0.119807611	1.820459354
GO:0060124	positive regulation of growth hormone secretion	2	9	21.14819923	0.015119612	0.119807611	1.820459354
GO:0060487	lung epithelial cell differentiation	2	9	21.14819923	0.015119612	0.119807611	1.820459354
GO:1900006	positive regulation of dendrite development	2	9	21.14819923	0.015119612	0.119807611	1.820459354
GO:0007528	neuromuscular junction development	3	30	9.516689655	0.015190917	0.119807611	1.818416005
GO:0032956	regulation of actin cytoskeleton organization	3	30	9.516689655	0.015190917	0.119807611	1.818416005
GO:0019233	sensory perception of pain	4	62	6.139799778	0.016661729	0.130790661	1.778279934
GO:0008360	regulation of cell shape	5	101	4.711232503	0.017485768	0.136617778	1.757315283
GO:0051028	mRNA transport	4	63	6.042342638	0.017645686	0.137225986	1.753361453
GO:0000186	activation of MAPKK activity	3	32	8.921896552	0.018272391	0.139469227	1.73820463
GO:0009888	tissue development	3	32	8.921896552	0.018272391	0.139469227	1.73820463
GO:0035725	sodium ion transmembrane transport	4	64	5.947931034	0.018668035	0.139469227	1.728901402
GO:0015672	monovalent inorganic cation transport	2	10	19.03337931	0.018768287	0.139469227	1.726575362
GO:0016239	positive regulation of macroautophagy	2	10	19.03337931	0.018768287	0.139469227	1.726575362
GO:0016265	death	2	10	19.03337931	0.018768287	0.139469227	1.726575362
GO:0021680	cerebellar Purkinje cell layer development	2	10	19.03337931	0.018768287	0.139469227	1.726575362

GO:0021799	cerebral cortex radially oriented cell mig	2	10	19.03337931	0.018768287	0.139469227	1.726575362
GO:0033327	Leydig cell differentiation	2	10	19.03337931	0.018768287	0.139469227	1.726575362
GO:0060484	lung-associated mesenchyme developme	2	10	19.03337931	0.018768287	0.139469227	1.726575362
GO:0000165	MAPK cascade	4	65	5.856424403	0.019729443	0.14561949	1.704885165
GO:0001944	vasculature development	3	33	8.65153605	0.019944296	0.14561949	1.700181285
GO:0030217	T cell differentiation	3	33	8.65153605	0.019944296	0.14561949	1.700181285
GO:0051865	protein autoubiquitination	3	33	8.65153605	0.019944296	0.14561949	1.700181285
GO:0034765	regulation of ion transmembrane transpo	6	149	3.832224022	0.020421278	0.148453812	1.689917084
GO:0015992	proton transport	4	66	5.7676907	0.020830572	0.150773661	1.681298813
GO:0007169	transmembrane receptor protein tyrosine	4	67	5.681605764	0.021972068	0.157388277	1.658129062
GO:0001945	lymph vessel development	2	11	17.3030721	0.022779882	0.157388277	1.642448526
GO:0008347	glial cell migration	2	11	17.3030721	0.022779882	0.157388277	1.642448526
GO:0010719	negative regulation of epithelial to mese	2	11	17.3030721	0.022779882	0.157388277	1.642448526
GO:0015813	L-glutamate transport	2	11	17.3030721	0.022779882	0.157388277	1.642448526
GO:0030238	male sex determination	2	11	17.3030721	0.022779882	0.157388277	1.642448526
GO:0048339	paraxial mesoderm development	2	11	17.3030721	0.022779882	0.157388277	1.642448526
GO:0050709	negative regulation of protein secretion	2	11	17.3030721	0.022779882	0.157388277	1.642448526
GO:0051894	positive regulation of focal adhesion ass	2	11	17.3030721	0.022779882	0.157388277	1.642448526
GO:0060317	cardiac epithelial to mesenchymal transi	2	11	17.3030721	0.022779882	0.157388277	1.642448526
GO:0060402	calcium ion transport into cytosol	2	11	17.3030721	0.022779882	0.157388277	1.642448526
GO:0042472	inner ear morphogenesis	4	69	5.516921539	0.024378714	0.167741605	1.612989205
GO:0010976	positive regulation of neuron projection	4	70	5.438108374	0.025645111	0.175732075	1.590995409
GO:0051260	protein homooligomerization	6	158	3.61393278	0.027003907	0.177299851	1.568573396
GO:0001946	lymphangiogenesis	2	12	15.86114943	0.027146389	0.177299851	1.566287936
GO:0010469	regulation of receptor activity	2	12	15.86114943	0.027146389	0.177299851	1.566287936
GO:0015671	oxygen transport	2	12	15.86114943	0.027146389	0.177299851	1.566287936
GO:0016578	histone deubiquitination	2	12	15.86114943	0.027146389	0.177299851	1.566287936
GO:0021895	cerebral cortex neuron differentiation	2	12	15.86114943	0.027146389	0.177299851	1.566287936
GO:0043039	tRNA aminoacylation	2	12	15.86114943	0.027146389	0.177299851	1.566287936
GO:0045670	regulation of osteoclast differentiation	2	12	15.86114943	0.027146389	0.177299851	1.566287936
GO:0046907	intracellular transport	2	12	15.86114943	0.027146389	0.177299851	1.566287936
GO:0048856	anatomical structure development	2	12	15.86114943	0.027146389	0.177299851	1.566287936
GO:0090102	cochlea development	2	12	15.86114943	0.027146389	0.177299851	1.566287936
GO:0090307	spindle assembly involved in mitosis	2	12	15.86114943	0.027146389	0.177299851	1.566287936
GO:0070936	protein K48-linked ubiquitination	3	37	7.716234856	0.027536372	0.179147134	1.560093285
GO:0007266	Rho protein signal transduction	3	38	7.513176044	0.029666226	0.186107674	1.527737705
GO:0001503	ossification	4	74	5.14415657	0.031145262	0.186107674	1.506608011
GO:0008284	positive regulation of cell proliferation	10	382	2.491280014	0.031157825	0.186107674	1.506432861

GO:0015986	ATP synthesis coupled proton transport	2	13	14.64106101	0.031859926	0.186107674	1.496755237
GO:0019369	arachidonic acid metabolic process	2	13	14.64106101	0.031859926	0.186107674	1.496755237
GO:0042417	dopamine metabolic process	2	13	14.64106101	0.031859926	0.186107674	1.496755237
GO:0042692	muscle cell differentiation	2	13	14.64106101	0.031859926	0.186107674	1.496755237
GO:0043984	histone H4-K16 acetylation	2	13	14.64106101	0.031859926	0.186107674	1.496755237
GO:0048260	positive regulation of receptor-mediated	2	13	14.64106101	0.031859926	0.186107674	1.496755237
GO:0048488	synaptic vesicle endocytosis	2	13	14.64106101	0.031859926	0.186107674	1.496755237
GO:0050673	epithelial cell proliferation	2	13	14.64106101	0.031859926	0.186107674	1.496755237
GO:0060071	Wnt receptor signaling pathway, planar	2	13	14.64106101	0.031859926	0.186107674	1.496755237
GO:0060384	innervation	2	13	14.64106101	0.031859926	0.186107674	1.496755237
GO:0001932	regulation of protein phosphorylation	3	39	7.320530504	0.031890866	0.186107674	1.496333687
GO:0007628	adult walking behavior	3	39	7.320530504	0.031890866	0.186107674	1.496333687
GO:0030097	hemopoiesis	4	75	5.075567816	0.032631845	0.186107674	1.486358365
GO:0043086	negative regulation of catalytic activity	4	75	5.075567816	0.032631845	0.186107674	1.486358365
GO:0006874	cellular calcium ion homeostasis	4	76	5.008784029	0.03416417	0.186107674	1.466429122
GO:0021987	cerebral cortex development	3	40	7.137517241	0.034211206	0.186107674	1.465831621
GO:0030512	negative regulation of transforming growth factor	3	41	6.963431455	0.036628095	0.186107674	1.436185673
GO:0045740	positive regulation of DNA replication	3	41	6.963431455	0.036628095	0.186107674	1.436185673
GO:0051056	regulation of small GTPase mediated signaling	3	41	6.963431455	0.036628095	0.186107674	1.436185673
GO:0000132	establishment of mitotic spindle orientation	2	14	13.59527094	0.036912739	0.186107674	1.432823723
GO:0006825	copper ion transport	2	14	13.59527094	0.036912739	0.186107674	1.432823723
GO:0009314	response to radiation	2	14	13.59527094	0.036912739	0.186107674	1.432823723
GO:0015693	magnesium ion transport	2	14	13.59527094	0.036912739	0.186107674	1.432823723
GO:0021954	central nervous system neuron development	2	14	13.59527094	0.036912739	0.186107674	1.432823723
GO:0032781	positive regulation of ATPase activity	2	14	13.59527094	0.036912739	0.186107674	1.432823723
GO:0043267	negative regulation of potassium ion transport	2	14	13.59527094	0.036912739	0.186107674	1.432823723
GO:0046328	regulation of JNK cascade	2	14	13.59527094	0.036912739	0.186107674	1.432823723
GO:0050773	regulation of dendrite development	2	14	13.59527094	0.036912739	0.186107674	1.432823723
GO:0060979	vasculogenesis involved in coronary vasculature	2	14	13.59527094	0.036912739	0.186107674	1.432823723
GO:0071320	cellular response to cAMP	2	14	13.59527094	0.036912739	0.186107674	1.432823723
GO:0001658	branching involved in ureteric bud morphogenesis	3	42	6.797635468	0.039142323	0.186107674	1.407353408
GO:0003151	outflow tract morphogenesis	3	42	6.797635468	0.039142323	0.186107674	1.407353408
GO:0010466	negative regulation of peptidase activity	5	123	3.868573031	0.03957356	0.186107674	1.402594882
GO:0008203	cholesterol metabolic process	4	80	4.758344828	0.040761546	0.186107674	1.389749358
GO:0007015	actin filament organization	3	43	6.639550922	0.04175462	0.186107674	1.379295466
GO:0000338	protein deneddylation	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0001840	neural plate development	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0002030	inhibitory G-protein coupled receptor pathway	1	1	95.16689655	0.042031422	0.186107674	1.376425916

GO:0002194	hepatocyte cell migration	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0002878	negative regulation of acute inflammatory response	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0006521	regulation of cellular amino acid metabolism	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0006624	vacuolar protein processing	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0010171	body morphogenesis	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0010625	positive regulation of Schwann cell proliferation	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0010721	negative regulation of cell development	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0014739	positive regulation of muscle hyperplasia	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0015742	alpha-ketoglutarate transport	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0015781	pyrimidine nucleotide-sugar transport	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0015811	L-cystine transport	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0015812	gamma-aminobutyric acid transport	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0015964	diadenosine triphosphate catabolic process	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0017126	nucleogenesis	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0030705	cytoskeleton-dependent intracellular transport	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0030817	regulation of cAMP biosynthetic process	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0031128	developmental induction	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0032222	regulation of synaptic transmission, cholinergic	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0032460	negative regulation of protein oligomerization	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0033037	polysaccharide localization	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0035112	genitalia morphogenesis	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0038027	apolipoprotein A-I-mediated signaling pathway	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0038161	prolactin signaling pathway	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0042268	regulation of cytolysis	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0042696	menarche	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0042851	L-alanine metabolic process	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0043461	proton-transporting ATP synthase complex	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0044557	relaxation of smooth muscle	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0045226	extracellular polysaccharide biosynthesis	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0045922	negative regulation of fatty acid metabolism	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0048058	compound eye corneal lens development	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0048205	COPII coating of Golgi vesicle	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0048532	anatomical structure arrangement	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0048668	collateral sprouting	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0051389	inactivation of MAPKK activity	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0051580	regulation of neurotransmitter uptake	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0051589	negative regulation of neurotransmitter transport	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0051598	meiotic recombination checkpoint	1	1	95.16689655	0.042031422	0.186107674	1.376425916

GO:0051960	regulation of nervous system developme	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0052565	response to defense-related host nitric ox	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0052746	inositol phosphorylation	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0060004	reflex	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0060262	negative regulation of N-terminal protei	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0060479	lung cell differentiation	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0060629	regulation of homologous chromosome s	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0060816	random inactivation of X chromosome	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0060872	semicircular canal development	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0060912	cardiac cell fate specification	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0070345	negative regulation of fat cell proliferati	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0070367	negative regulation of hepatocyte differe	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0070445	regulation of oligodendrocyte progenitor	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0070571	negative regulation of neuron projection	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0070899	mitochondrial tRNA wobble uridine mo	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0071436	sodium ion export	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0071926	endocannabinoid signaling pathway	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0071929	alpha-tubulin acetylation	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0072040	negative regulation of mesenchymal cell	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0072132	mesenchyme morphogenesis	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0072363	regulation of glycolysis by positive regu	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0072366	regulation of cellular ketone metabolic p	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0072574	hepatocyte proliferation	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0080144	amino acid homeostasis	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0090075	relaxation of muscle	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0097056	selenocysteinyl-tRNA(Sec) biosynthetic	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0097254	renal tubular secretion	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0097369	sodium ion import	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:1900235	negative regulation of Kit signaling path	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:1901860	positive regulation of mitochondrial DN	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:1901863	positive regulation of muscle tissue deve	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:1901978	positive regulation of cell cycle checkpo	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:2000570	positive regulation of T-helper 2 cell act	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:2000979	positive regulation of forebrain neuron d	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:2001023	regulation of response to drug	1	1	95.16689655	0.042031422	0.186107674	1.376425916
GO:0001967	suckling behavior	2	15	12.68891954	0.042297199	0.186107674	1.373688395
GO:0007625	grooming behavior	2	15	12.68891954	0.042297199	0.186107674	1.373688395
GO:0016044	cellular membrane organization	2	15	12.68891954	0.042297199	0.186107674	1.373688395

GO:0019226	transmission of nerve impulse	2	15	12.68891954	0.042297199	0.186107674	1.373688395
GO:0043981	histone H4-K5 acetylation	2	15	12.68891954	0.042297199	0.186107674	1.373688395
GO:0043982	histone H4-K8 acetylation	2	15	12.68891954	0.042297199	0.186107674	1.373688395
GO:0045109	intermediate filament organization	2	15	12.68891954	0.042297199	0.186107674	1.373688395
GO:0046887	positive regulation of hormone secretion	2	15	12.68891954	0.042297199	0.186107674	1.373688395
GO:0060441	epithelial tube branching involved in lung morphogenesis	2	15	12.68891954	0.042297199	0.186107674	1.373688395
GO:0060070	canonical Wnt receptor signaling pathway	4	81	4.69959983	0.042530472	0.18664291	1.371299801
GO:0008542	visual learning	3	44	6.488652038	0.044465659	0.194624559	1.351975269
GO:0001933	negative regulation of protein phosphorylation	3	45	6.34445977	0.047276056	0.204759414	1.325358764
GO:0006813	potassium ion transport	5	129	3.688639401	0.04791651	0.204759414	1.319514823
GO:0006402	mRNA catabolic process	2	16	11.89586207	0.048005796	0.204759414	1.318706329
GO:0046856	phosphatidylinositol dephosphorylation	2	16	11.89586207	0.048005796	0.204759414	1.318706329
GO:0048513	organ development	2	16	11.89586207	0.048005796	0.204759414	1.318706329
GO:0048709	oligodendrocyte differentiation	2	16	11.89586207	0.048005796	0.204759414	1.318706329
GO:0048741	skeletal muscle fiber development	2	16	11.89586207	0.048005796	0.204759414	1.318706329
GO:0050768	negative regulation of neurogenesis	2	16	11.89586207	0.048005796	0.204759414	1.318706329
GO:0050877	neurological system process	2	16	11.89586207	0.048005796	0.204759414	1.318706329
GO:0060038	cardiac muscle cell proliferation	2	16	11.89586207	0.048005796	0.204759414	1.318706329
GO:0051092	positive regulation of NF-kappaB transcription	4	84	4.531756979	0.048132025	0.204775435	1.317565865
GO:0010629	negative regulation of gene expression	5	130	3.660265252	0.04941418	0.209696725	1.306148403
GO:0050896	response to stimulus	4	1142	0.333334139	0.049805724	0.210823216	1.302720743
GO:0007519	skeletal muscle tissue development	3	46	6.206536732	0.050186372	0.211364266	
GO:0048705	skeletal system morphogenesis	3	46	6.206536732	0.050186372	0.211364266	
GO:0009953	dorsal/ventral pattern formation	3	47	6.074482759	0.053197115	0.218212733	
GO:0030819	positive regulation of cAMP biosynthesis	3	47	6.074482759	0.053197115	0.218212733	
GO:0034097	response to cytokine stimulus	3	47	6.074482759	0.053197115	0.218212733	
GO:0060271	cilium morphogenesis	3	47	6.074482759	0.053197115	0.218212733	
GO:0055114	oxidation-reduction process	15	706	2.021959558	0.053712595	0.218212733	
GO:0001975	response to amphetamine	2	17	11.19610548	0.054031143	0.218212733	
GO:0002089	lens morphogenesis in camera-type eye	2	17	11.19610548	0.054031143	0.218212733	
GO:0007190	activation of adenylate cyclase activity	2	17	11.19610548	0.054031143	0.218212733	
GO:0007194	negative regulation of adenylate cyclase activity	2	17	11.19610548	0.054031143	0.218212733	
GO:0009948	anterior/posterior axis specification	2	17	11.19610548	0.054031143	0.218212733	
GO:0016925	protein sumoylation	2	17	11.19610548	0.054031143	0.218212733	
GO:0019933	cAMP-mediated signaling	2	17	11.19610548	0.054031143	0.218212733	
GO:0022604	regulation of cell morphogenesis	2	17	11.19610548	0.054031143	0.218212733	
GO:0030866	cortical actin cytoskeleton organization	2	17	11.19610548	0.054031143	0.218212733	
GO:0043001	Golgi to plasma membrane protein transport	2	17	11.19610548	0.054031143	0.218212733	

GO:0043393	regulation of protein binding	2	17	11.19610548	0.054031143	0.218212733	
GO:0045648	positive regulation of erythrocyte differ	2	17	11.19610548	0.054031143	0.218212733	
GO:0048812	neuron projection morphogenesis	3	48	5.947931034	0.05630874	0.226863165	
GO:0006357	regulation of transcription from RNA po	7	241	2.764183717	0.057633928	0.231088554	
GO:0007067	mitosis	7	241	2.764183717	0.057633928	0.231088554	
GO:0050790	regulation of catalytic activity	4	89	4.27716389	0.058477355	0.233909418	
GO:0042127	regulation of cell proliferation	5	136	3.498782961	0.059069035	0.234725367	
GO:0006396	RNA processing	3	49	5.826544687	0.059521653	0.234725367	
GO:0042552	myelination	3	49	5.826544687	0.059521653	0.234725367	
GO:0006509	membrane protein ectodomain proteolys	2	18	10.57409962	0.060365974	0.234725367	
GO:0032007	negative regulation of TOR signaling ca	2	18	10.57409962	0.060365974	0.234725367	
GO:0042157	lipoprotein metabolic process	2	18	10.57409962	0.060365974	0.234725367	
GO:0042325	regulation of phosphorylation	2	18	10.57409962	0.060365974	0.234725367	
GO:0046847	filopodium assembly	2	18	10.57409962	0.060365974	0.234725367	
GO:0048484	enteric nervous system development	2	18	10.57409962	0.060365974	0.234725367	
GO:0051480	cytosolic calcium ion homeostasis	2	18	10.57409962	0.060365974	0.234725367	
GO:0055074	calcium ion homeostasis	2	18	10.57409962	0.060365974	0.234725367	
GO:0072661	protein targeting to plasma membrane	2	18	10.57409962	0.060365974	0.234725367	
GO:0010923	negative regulation of phosphatase activ	3	50	5.710013793	0.062836209	0.24263774	
GO:0050885	neuromuscular process controlling balan	3	50	5.710013793	0.062836209	0.24263774	
GO:0090263	positive regulation of canonical Wnt rec	3	50	5.710013793	0.062836209	0.24263774	
GO:0042733	embryonic digit morphogenesis	3	51	5.598052738	0.066252715	0.254611917	
GO:0007026	negative regulation of microtubule depo	2	19	10.01756806	0.067003136	0.254611917	
GO:0008089	anterograde axon cargo transport	2	19	10.01756806	0.067003136	0.254611917	
GO:0009190	cyclic nucleotide biosynthetic process	2	19	10.01756806	0.067003136	0.254611917	
GO:0045930	negative regulation of mitotic cell cycle	2	19	10.01756806	0.067003136	0.254611917	
GO:0048821	erythrocyte development	2	19	10.01756806	0.067003136	0.254611917	
GO:0051968	positive regulation of synaptic transmiss	2	19	10.01756806	0.067003136	0.254611917	
GO:0051726	regulation of cell cycle	4	94	4.049655172	0.070128265	0.254673275	
GO:0007160	cell-matrix adhesion	3	53	5.386805465	0.073392576	0.254673275	
GO:0008344	adult locomotory behavior	3	53	5.386805465	0.073392576	0.254673275	
GO:0002052	positive regulation of neuroblast prolifer	2	20	9.516689655	0.073935596	0.254673275	
GO:0007269	neurotransmitter secretion	2	20	9.516689655	0.073935596	0.254673275	
GO:0048593	camera-type eye morphogenesis	2	20	9.516689655	0.073935596	0.254673275	
GO:0006457	protein folding	4	97	3.924408105	0.077763983	0.254673275	
GO:0016042	lipid catabolic process	4	97	3.924408105	0.077763983	0.254673275	
GO:0030030	cell projection organization	4	97	3.924408105	0.077763983	0.254673275	
GO:0043066	negative regulation of apoptotic process	11	480	2.180908046	0.079463712	0.254673275	

GO:0006513	protein monoubiquitination	2	21	9.063513957	0.081156432	0.254673275	
GO:0006885	regulation of pH	2	21	9.063513957	0.081156432	0.254673275	
GO:0034605	cellular response to heat	2	21	9.063513957	0.081156432	0.254673275	
GO:0045453	bone resorption	2	21	9.063513957	0.081156432	0.254673275	
GO:0048646	anatomical structure formation involved	2	21	9.063513957	0.081156432	0.254673275	
GO:0055007	cardiac muscle cell differentiation	2	21	9.063513957	0.081156432	0.254673275	
GO:0070059	intrinsic apoptotic signaling pathway in	2	21	9.063513957	0.081156432	0.254673275	
GO:0001504	neurotransmitter uptake	1	2	47.58344828	0.083621787	0.254673275	
GO:0001834	trophectodermal cell proliferation	1	2	47.58344828	0.083621787	0.254673275	
GO:0001869	negative regulation of complement activ	1	2	47.58344828	0.083621787	0.254673275	
GO:0002790	peptide secretion	1	2	47.58344828	0.083621787	0.254673275	
GO:0003349	epicardium-derived cardiac endothelial c	1	2	47.58344828	0.083621787	0.254673275	
GO:0005997	xylulose metabolic process	1	2	47.58344828	0.083621787	0.254673275	
GO:0006048	UDP-N-acetylglucosamine biosynthetic	1	2	47.58344828	0.083621787	0.254673275	
GO:0006438	valyl-tRNA aminoacylation	1	2	47.58344828	0.083621787	0.254673275	
GO:0006597	spermine biosynthetic process	1	2	47.58344828	0.083621787	0.254673275	
GO:0006677	glycosylceramide metabolic process	1	2	47.58344828	0.083621787	0.254673275	
GO:0006782	protoporphyrinogen IX biosynthetic pro	1	2	47.58344828	0.083621787	0.254673275	
GO:0006837	serotonin transport	1	2	47.58344828	0.083621787	0.254673275	
GO:0007109	cytokinesis, completion of separation	1	2	47.58344828	0.083621787	0.254673275	
GO:0007320	insemination	1	2	47.58344828	0.083621787	0.254673275	
GO:0009181	purine ribonucleoside diphosphate catab	1	2	47.58344828	0.083621787	0.254673275	
GO:0010045	response to nickel cation	1	2	47.58344828	0.083621787	0.254673275	
GO:0010822	positive regulation of mitochondrion org	1	2	47.58344828	0.083621787	0.254673275	
GO:0010909	positive regulation of heparan sulfate pr	1	2	47.58344828	0.083621787	0.254673275	
GO:0014010	Schwann cell proliferation	1	2	47.58344828	0.083621787	0.254673275	
GO:0014048	regulation of glutamate secretion	1	2	47.58344828	0.083621787	0.254673275	
GO:0014053	negative regulation of gamma-aminobuty	1	2	47.58344828	0.083621787	0.254673275	
GO:0019255	glucose 1-phosphate metabolic process	1	2	47.58344828	0.083621787	0.254673275	
GO:0019442	tryptophan catabolic process to acetyl-C	1	2	47.58344828	0.083621787	0.254673275	
GO:0021514	ventral spinal cord interneuron different	1	2	47.58344828	0.083621787	0.254673275	
GO:0021633	optic nerve structural organization	1	2	47.58344828	0.083621787	0.254673275	
GO:0021759	globus pallidus development	1	2	47.58344828	0.083621787	0.254673275	
GO:0021801	cerebral cortex radial glia guided migrat	1	2	47.58344828	0.083621787	0.254673275	
GO:0021831	embryonic olfactory bulb interneuron pr	1	2	47.58344828	0.083621787	0.254673275	
GO:0022898	regulation of transmembrane transporter	1	2	47.58344828	0.083621787	0.254673275	
GO:0030997	regulation of centriole-centriole cohesio	1	2	47.58344828	0.083621787	0.254673275	
GO:0031325	positive regulation of cellular metabolic	1	2	47.58344828	0.083621787	0.254673275	

GO:0032707	negative regulation of interleukin-23 pro	1	2	47.58344828	0.083621787	0.254673275	
GO:0033058	directional locomotion	1	2	47.58344828	0.083621787	0.254673275	
GO:0033126	positive regulation of GTP catabolic pro	1	2	47.58344828	0.083621787	0.254673275	
GO:0033861	negative regulation of NAD(P)H oxidase	1	2	47.58344828	0.083621787	0.254673275	
GO:0035854	eosinophil fate commitment	1	2	47.58344828	0.083621787	0.254673275	
GO:0035995	detection of muscle stretch	1	2	47.58344828	0.083621787	0.254673275	
GO:0042732	D-xylose metabolic process	1	2	47.58344828	0.083621787	0.254673275	
GO:0043252	sodium-independent organic anion trans	1	2	47.58344828	0.083621787	0.254673275	
GO:0043652	engulfment of apoptotic cell	1	2	47.58344828	0.083621787	0.254673275	
GO:0044334	canonical Wnt receptor signaling pathwa	1	2	47.58344828	0.083621787	0.254673275	
GO:0044336	canonical Wnt receptor signaling pathwa	1	2	47.58344828	0.083621787	0.254673275	
GO:0045818	negative regulation of glycogen cataboli	1	2	47.58344828	0.083621787	0.254673275	
GO:0046631	alpha-beta T cell activation	1	2	47.58344828	0.083621787	0.254673275	
GO:0046881	positive regulation of follicle-stimulating	1	2	47.58344828	0.083621787	0.254673275	
GO:0048669	collateral sprouting in absence of injury	1	2	47.58344828	0.083621787	0.254673275	
GO:0048679	regulation of axon regeneration	1	2	47.58344828	0.083621787	0.254673275	
GO:0048866	stem cell fate specification	1	2	47.58344828	0.083621787	0.254673275	
GO:0050999	regulation of nitric-oxide synthase activi	1	2	47.58344828	0.083621787	0.254673275	
GO:0051048	negative regulation of secretion	1	2	47.58344828	0.083621787	0.254673275	
GO:0051100	negative regulation of binding	1	2	47.58344828	0.083621787	0.254673275	
GO:0051177	meiotic sister chromatid cohesion	1	2	47.58344828	0.083621787	0.254673275	
GO:0051563	smooth endoplasmic reticulum calcium i	1	2	47.58344828	0.083621787	0.254673275	
GO:0051661	maintenance of centrosome location	1	2	47.58344828	0.083621787	0.254673275	
GO:0051684	maintenance of Golgi location	1	2	47.58344828	0.083621787	0.254673275	
GO:0060049	regulation of protein glycosylation	1	2	47.58344828	0.083621787	0.254673275	
GO:0060152	microtubule-based peroxisome localizati	1	2	47.58344828	0.083621787	0.254673275	
GO:0060421	positive regulation of heart growth	1	2	47.58344828	0.083621787	0.254673275	
GO:0060466	activation of meiosis involved in egg act	1	2	47.58344828	0.083621787	0.254673275	
GO:0060769	positive regulation of epithelial cell prol	1	2	47.58344828	0.083621787	0.254673275	
GO:0060849	regulation of transcription involved in ly	1	2	47.58344828	0.083621787	0.254673275	
GO:0061047	positive regulation of branching involve	1	2	47.58344828	0.083621787	0.254673275	
GO:0061324	canonical Wnt receptor signaling pathwa	1	2	47.58344828	0.083621787	0.254673275	
GO:0070602	regulation of centromeric sister chromati	1	2	47.58344828	0.083621787	0.254673275	
GO:0070682	proteasome regulatory particle assembly	1	2	47.58344828	0.083621787	0.254673275	
GO:0070858	negative regulation of bile acid biosynth	1	2	47.58344828	0.083621787	0.254673275	
GO:0071233	cellular response to leucine	1	2	47.58344828	0.083621787	0.254673275	
GO:0071492	cellular response to UV-A	1	2	47.58344828	0.083621787	0.254673275	
GO:0071600	otic vesicle morphogenesis	1	2	47.58344828	0.083621787	0.254673275	

GO:0071603	endothelial cell-cell adhesion	1	2	47.58344828	0.083621787	0.254673275	
GO:0071672	negative regulation of smooth muscle ce	1	2	47.58344828	0.083621787	0.254673275	
GO:0071673	positive regulation of smooth muscle ce	1	2	47.58344828	0.083621787	0.254673275	
GO:0072033	renal vesicle formation	1	2	47.58344828	0.083621787	0.254673275	
GO:0072054	renal outer medulla development	1	2	47.58344828	0.083621787	0.254673275	
GO:0072079	nephron tubule formation	1	2	47.58344828	0.083621787	0.254673275	
GO:0072111	cell proliferation involved in kidney dev	1	2	47.58344828	0.083621787	0.254673275	
GO:0072125	negative regulation of glomerular mesan	1	2	47.58344828	0.083621787	0.254673275	
GO:0072134	nephrogenic mesenchyme morphogenesis	1	2	47.58344828	0.083621787	0.254673275	
GO:0072136	metanephric mesenchymal cell prolifera	1	2	47.58344828	0.083621787	0.254673275	
GO:0072138	mesenchymal cell proliferation involved	1	2	47.58344828	0.083621787	0.254673275	
GO:0072180	mesonephric duct morphogenesis	1	2	47.58344828	0.083621787	0.254673275	
GO:0072182	regulation of nephron tubule epithelial c	1	2	47.58344828	0.083621787	0.254673275	
GO:0072203	cell proliferation involved in metanephro	1	2	47.58344828	0.083621787	0.254673275	
GO:0072368	regulation of lipid transport by negative	1	2	47.58344828	0.083621787	0.254673275	
GO:0072369	regulation of lipid transport by positive	1	2	47.58344828	0.083621787	0.254673275	
GO:0072383	plus-end-directed vesicle transport along	1	2	47.58344828	0.083621787	0.254673275	
GO:0085029	extracellular matrix assembly	1	2	47.58344828	0.083621787	0.254673275	
GO:0086064	cell communication by electrical couplin	1	2	47.58344828	0.083621787	0.254673275	
GO:1901857	positive regulation of cellular respiration	1	2	47.58344828	0.083621787	0.254673275	
GO:2000172	regulation of branching morphogenesis c	1	2	47.58344828	0.083621787	0.254673275	
GO:2000507	positive regulation of energy homeostas	1	2	47.58344828	0.083621787	0.254673275	
GO:2000824	negative regulation of androgen receptor	1	2	47.58344828	0.083621787	0.254673275	
GO:0006284	base-excision repair	2	22	8.65153605	0.088658836	0.264709953	
GO:0006820	anion transport	2	22	8.65153605	0.088658836	0.264709953	
GO:0007193	adenylate cyclase-inhibiting G-protein c	2	22	8.65153605	0.088658836	0.264709953	
GO:0008406	gonad development	2	22	8.65153605	0.088658836	0.264709953	
GO:0021983	pituitary gland development	2	22	8.65153605	0.088658836	0.264709953	
GO:0043552	positive regulation of phosphatidylinosit	2	22	8.65153605	0.088658836	0.264709953	
GO:0045739	positive regulation of DNA repair	2	22	8.65153605	0.088658836	0.264709953	
GO:0046580	negative regulation of Ras protein signal	2	22	8.65153605	0.088658836	0.264709953	
GO:0050714	positive regulation of protein secretion	2	22	8.65153605	0.088658836	0.264709953	
GO:0050804	regulation of synaptic transmission	2	22	8.65153605	0.088658836	0.264709953	
GO:0060291	long-term synaptic potentiation	2	22	8.65153605	0.088658836	0.264709953	
GO:0048661	positive regulation of smooth muscle ce	3	57	5.008784029	0.088904176	0.264969308	
GO:0043433	negative regulation of sequence-specific	3	58	4.922425684	0.09303916	0.27679978	
GO:0032259	methylation	5	154	3.089834304	0.095367284	0.2832222	
GO:0030316	osteoclast differentiation	2	23	8.275382309	0.096436111	0.285888612	

GO:0006006	glucose metabolic process	3	59	4.83899474	0.09727697	0.287870962	
GO:0008380	RNA splicing	6	212	2.693402733	0.101297293	0.299238646	
GO:0006486	protein glycosylation	3	60	4.758344828	0.101617533	0.299655229	
GO:0051301	cell division	8	333	2.286291809	0.102702862	0.30148121	
GO:0019048	virus-host interaction	2	24	7.930574713	0.104481668	0.30148121	
GO:0035690	cellular response to drug	2	24	7.930574713	0.104481668	0.30148121	
GO:0001568	blood vessel development	3	61	4.680339175	0.106060742	0.30148121	
GO:0007264	small GTPase mediated signal transduct	6	215	2.655820369	0.107516541	0.30148121	
GO:0030324	lung development	4	108	3.524699872	0.110039255	0.30148121	
GO:0035023	regulation of Rho protein signal transduc	3	62	4.604849833	0.110606455	0.30148121	
GO:0045664	regulation of neuron differentiation	2	25	7.613351724	0.112789028	0.30148121	
GO:0048477	oogenesis	2	25	7.613351724	0.112789028	0.30148121	
GO:0051496	positive regulation of stress fiber assembl	2	25	7.613351724	0.112789028	0.30148121	
GO:0007179	transforming growth factor beta receptor	3	63	4.531756979	0.115254493	0.30148121	
GO:0051897	positive regulation of protein kinase B si	3	63	4.531756979	0.115254493	0.30148121	
GO:0000902	cell morphogenesis	3	64	4.460948276	0.120004647	0.30148121	
GO:0042391	regulation of membrane potential	3	64	4.460948276	0.120004647	0.30148121	
GO:0006200	ATP catabolic process	4	111	3.429437714	0.120034003	0.30148121	
GO:0006812	cation transport	4	111	3.429437714	0.120034003	0.30148121	
GO:0010862	positive regulation of pathway-restricted	2	26	7.320530504	0.121351816	0.30148121	
GO:0030032	lamellipodium assembly	2	26	7.320530504	0.121351816	0.30148121	
GO:0030968	endoplasmic reticulum unfolded protein	2	26	7.320530504	0.121351816	0.30148121	
GO:0071277	cellular response to calcium ion	2	26	7.320530504	0.121351816	0.30148121	
GO:0001560	regulation of cell growth by extracellular	1	3	31.72229885	0.124775716	0.30148121	
GO:0001831	trophectodermal cellular morphogenesis	1	3	31.72229885	0.124775716	0.30148121	
GO:0001915	negative regulation of T cell mediated cy	1	3	31.72229885	0.124775716	0.30148121	
GO:0001959	regulation of cytokine-mediated signalin	1	3	31.72229885	0.124775716	0.30148121	
GO:0002016	regulation of blood volume by renin-ang	1	3	31.72229885	0.124775716	0.30148121	
GO:0002090	regulation of receptor internalization	1	3	31.72229885	0.124775716	0.30148121	
GO:0002093	auditory receptor cell morphogenesis	1	3	31.72229885	0.124775716	0.30148121	
GO:0002098	tRNA wobble uridine modification	1	3	31.72229885	0.124775716	0.30148121	
GO:0002865	negative regulation of acute inflammator	1	3	31.72229885	0.124775716	0.30148121	
GO:0003051	angiotensin-mediated drinking behavior	1	3	31.72229885	0.124775716	0.30148121	
GO:0003081	regulation of systemic arterial blood pre	1	3	31.72229885	0.124775716	0.30148121	
GO:0003136	negative regulation of heart induction by	1	3	31.72229885	0.124775716	0.30148121	
GO:0003223	ventricular compact myocardium morph	1	3	31.72229885	0.124775716	0.30148121	
GO:0003338	metanephros morphogenesis	1	3	31.72229885	0.124775716	0.30148121	
GO:0006177	GMP biosynthetic process	1	3	31.72229885	0.124775716	0.30148121	

GO:0006382	adenosine to inosine editing	1	3	31.72229885	0.124775716	0.30148121	
GO:0006419	alanyl-tRNA aminoacylation	1	3	31.72229885	0.124775716	0.30148121	
GO:0006435	threonyl-tRNA aminoacylation	1	3	31.72229885	0.124775716	0.30148121	
GO:0006533	aspartate catabolic process	1	3	31.72229885	0.124775716	0.30148121	
GO:0006556	S-adenosylmethionine biosynthetic process	1	3	31.72229885	0.124775716	0.30148121	
GO:0006568	tryptophan metabolic process	1	3	31.72229885	0.124775716	0.30148121	
GO:0006684	sphingomyelin metabolic process	1	3	31.72229885	0.124775716	0.30148121	
GO:0006741	NADP biosynthetic process	1	3	31.72229885	0.124775716	0.30148121	
GO:0006987	activation of signaling protein activity in response to stimulus	1	3	31.72229885	0.124775716	0.30148121	
GO:0007208	phospholipase C-activating serotonin receptor signaling pathway	1	3	31.72229885	0.124775716	0.30148121	
GO:0007403	glial cell fate determination	1	3	31.72229885	0.124775716	0.30148121	
GO:0010040	response to iron(II) ion	1	3	31.72229885	0.124775716	0.30148121	
GO:0010288	response to lead ion	1	3	31.72229885	0.124775716	0.30148121	
GO:0010871	negative regulation of receptor biosynthesis	1	3	31.72229885	0.124775716	0.30148121	
GO:0010960	magnesium ion homeostasis	1	3	31.72229885	0.124775716	0.30148121	
GO:0010999	regulation of eIF2 alpha phosphorylation	1	3	31.72229885	0.124775716	0.30148121	
GO:0014015	positive regulation of gliogenesis	1	3	31.72229885	0.124775716	0.30148121	
GO:0014706	striated muscle tissue development	1	3	31.72229885	0.124775716	0.30148121	
GO:0014829	vascular smooth muscle contraction	1	3	31.72229885	0.124775716	0.30148121	
GO:0015684	ferrous iron transport	1	3	31.72229885	0.124775716	0.30148121	
GO:0015819	lysine transport	1	3	31.72229885	0.124775716	0.30148121	
GO:0015842	synaptic vesicle amine transport	1	3	31.72229885	0.124775716	0.30148121	
GO:0016052	carbohydrate catabolic process	1	3	31.72229885	0.124775716	0.30148121	
GO:0016081	synaptic vesicle docking involved in exocytosis	1	3	31.72229885	0.124775716	0.30148121	
GO:0016560	protein import into peroxisome matrix, cytosolic to matrix	1	3	31.72229885	0.124775716	0.30148121	
GO:0018125	peptidyl-cysteine methylation	1	3	31.72229885	0.124775716	0.30148121	
GO:0019478	D-amino acid catabolic process	1	3	31.72229885	0.124775716	0.30148121	
GO:0021800	cerebral cortex tangential migration	1	3	31.72229885	0.124775716	0.30148121	
GO:0021885	forebrain cell migration	1	3	31.72229885	0.124775716	0.30148121	
GO:0030201	heparan sulfate proteoglycan metabolic process	1	3	31.72229885	0.124775716	0.30148121	
GO:0030204	chondroitin sulfate metabolic process	1	3	31.72229885	0.124775716	0.30148121	
GO:0030208	dermatan sulfate biosynthetic process	1	3	31.72229885	0.124775716	0.30148121	
GO:0030241	skeletal muscle myosin thick filament assembly	1	3	31.72229885	0.124775716	0.30148121	
GO:0031401	positive regulation of protein modification	1	3	31.72229885	0.124775716	0.30148121	
GO:0031989	bombesin receptor signaling pathway	1	3	31.72229885	0.124775716	0.30148121	
GO:0032446	protein modification by small protein complex	1	3	31.72229885	0.124775716	0.30148121	
GO:0032800	receptor biosynthetic process	1	3	31.72229885	0.124775716	0.30148121	
GO:0033234	negative regulation of protein sumoylation	1	3	31.72229885	0.124775716	0.30148121	

GO:0034620	cellular response to unfolded protein	1	3	31.72229885	0.124775716	0.30148121	
GO:0036023	embryonic skeletal limb joint morphogenesis	1	3	31.72229885	0.124775716	0.30148121	
GO:0036265	RNA (guanine-N7)-methylation	1	3	31.72229885	0.124775716	0.30148121	
GO:0038108	negative regulation of appetite by leptin	1	3	31.72229885	0.124775716	0.30148121	
GO:0042138	meiotic DNA double-strand break formation	1	3	31.72229885	0.124775716	0.30148121	
GO:0043490	malate-aspartate shuttle	1	3	31.72229885	0.124775716	0.30148121	
GO:0044321	response to leptin stimulus	1	3	31.72229885	0.124775716	0.30148121	
GO:0045103	intermediate filament-based process	1	3	31.72229885	0.124775716	0.30148121	
GO:0045200	establishment of neuroblast polarity	1	3	31.72229885	0.124775716	0.30148121	
GO:0045218	zonula adherens maintenance	1	3	31.72229885	0.124775716	0.30148121	
GO:0045919	positive regulation of cytolysis	1	3	31.72229885	0.124775716	0.30148121	
GO:0046813	virion attachment, binding of host cell surface	1	3	31.72229885	0.124775716	0.30148121	
GO:0046929	negative regulation of neurotransmitter secretion	1	3	31.72229885	0.124775716	0.30148121	
GO:0048208	COPII vesicle coating	1	3	31.72229885	0.124775716	0.30148121	
GO:0048672	positive regulation of collateral sprouting	1	3	31.72229885	0.124775716	0.30148121	
GO:0048769	sarcomerogenesis	1	3	31.72229885	0.124775716	0.30148121	
GO:0050882	voluntary musculoskeletal movement	1	3	31.72229885	0.124775716	0.30148121	
GO:0051224	negative regulation of protein transport	1	3	31.72229885	0.124775716	0.30148121	
GO:0051250	negative regulation of lymphocyte activation	1	3	31.72229885	0.124775716	0.30148121	
GO:0051533	positive regulation of NFAT protein import	1	3	31.72229885	0.124775716	0.30148121	
GO:0051964	negative regulation of synapse assembly	1	3	31.72229885	0.124775716	0.30148121	
GO:0055099	response to high density lipoprotein particle	1	3	31.72229885	0.124775716	0.30148121	
GO:0060020	Bergmann glial cell differentiation	1	3	31.72229885	0.124775716	0.30148121	
GO:0060066	oviduct development	1	3	31.72229885	0.124775716	0.30148121	
GO:0060263	regulation of respiratory burst	1	3	31.72229885	0.124775716	0.30148121	
GO:0060266	negative regulation of respiratory burst initiation	1	3	31.72229885	0.124775716	0.30148121	
GO:0060267	positive regulation of respiratory burst initiation	1	3	31.72229885	0.124775716	0.30148121	
GO:0060368	regulation of Fc receptor mediated stimulation	1	3	31.72229885	0.124775716	0.30148121	
GO:0060440	trachea formation	1	3	31.72229885	0.124775716	0.30148121	
GO:0060486	Clara cell differentiation	1	3	31.72229885	0.124775716	0.30148121	
GO:0060492	lung induction	1	3	31.72229885	0.124775716	0.30148121	
GO:0060916	mesenchymal cell proliferation involved in morphogenesis	1	3	31.72229885	0.124775716	0.30148121	
GO:0061028	establishment of endothelial barrier	1	3	31.72229885	0.124775716	0.30148121	
GO:0070375	ERK5 cascade	1	3	31.72229885	0.124775716	0.30148121	
GO:0070487	monocyte aggregation	1	3	31.72229885	0.124775716	0.30148121	
GO:0071294	cellular response to zinc ion	1	3	31.72229885	0.124775716	0.30148121	
GO:0071499	cellular response to laminar fluid shear stress	1	3	31.72229885	0.124775716	0.30148121	
GO:0072053	renal inner medulla development	1	3	31.72229885	0.124775716	0.30148121	

GO:0072133	metanephric mesenchyme morphogenesis	1	3	31.72229885	0.124775716	0.30148121	
GO:0072513	positive regulation of secondary heart field morphogenesis	1	3	31.72229885	0.124775716	0.30148121	
GO:0080009	mRNA methylation	1	3	31.72229885	0.124775716	0.30148121	
GO:0090274	positive regulation of somatostatin secretion	1	3	31.72229885	0.124775716	0.30148121	
GO:0090292	nuclear matrix anchoring at nuclear membrane	1	3	31.72229885	0.124775716	0.30148121	
GO:1900106	positive regulation of hyaluronan cable assembly	1	3	31.72229885	0.124775716	0.30148121	
GO:1900482	positive regulation of diacylglycerol biosynthetic process	1	3	31.72229885	0.124775716	0.30148121	
GO:2000008	regulation of protein localization to cell periphery	1	3	31.72229885	0.124775716	0.30148121	
GO:2000017	positive regulation of determination of developmental fate	1	3	31.72229885	0.124775716	0.30148121	
GO:2000188	regulation of cholesterol homeostasis	1	3	31.72229885	0.124775716	0.30148121	
GO:2000286	receptor internalization involved in cancer	1	3	31.72229885	0.124775716	0.30148121	
GO:2000318	positive regulation of T-helper 17 type 1 immune response	1	3	31.72229885	0.124775716	0.30148121	
GO:2000370	positive regulation of clathrin-mediated transport	1	3	31.72229885	0.124775716	0.30148121	
GO:2001171	positive regulation of ATP biosynthetic process	1	3	31.72229885	0.124775716	0.30148121	
GO:0009117	nucleotide metabolic process	2	27	7.049399745	0.130163763	0.312692258	
GO:0032091	negative regulation of protein binding	2	27	7.049399745	0.130163763	0.312692258	
GO:0034446	substrate adhesion-dependent cell spreading	2	27	7.049399745	0.130163763	0.312692258	
GO:0035176	social behavior	2	27	7.049399745	0.130163763	0.312692258	
GO:0071230	cellular response to amino acid stimulus	4	116	3.281617122	0.137846819	0.330674149	
GO:0001656	metanephros development	2	28	6.797635468	0.139218703	0.331586426	
GO:0006665	sphingolipid metabolic process	2	28	6.797635468	0.139218703	0.331586426	
GO:0016197	endosomal transport	2	28	6.797635468	0.139218703	0.331586426	
GO:0045600	positive regulation of fat cell differentiation	2	28	6.797635468	0.139218703	0.331586426	
GO:0048169	regulation of long-term neuronal synaptic transmission	2	28	6.797635468	0.139218703	0.331586426	
GO:0030308	negative regulation of cell growth	4	117	3.253569113	0.141583477	0.33673908	
GO:0008333	endosome to lysosome transport	2	29	6.563234245	0.148510571	0.345458545	
GO:0043523	regulation of neuron apoptotic process	2	29	6.563234245	0.148510571	0.345458545	
GO:0045787	positive regulation of cell cycle	2	29	6.563234245	0.148510571	0.345458545	
GO:0046676	negative regulation of insulin secretion	2	29	6.563234245	0.148510571	0.345458545	
GO:0048008	platelet-derived growth factor receptor signaling pathway	2	29	6.563234245	0.148510571	0.345458545	
GO:0048013	ephrin receptor signaling pathway	2	29	6.563234245	0.148510571	0.345458545	
GO:0030036	actin cytoskeleton organization	4	119	3.198887279	0.149231407	0.345458545	
GO:0042384	cilium assembly	3	70	4.078581281	0.150634238	0.345458545	
GO:0001657	ureteric bud development	2	30	6.34445977	0.158033403	0.345458545	
GO:0006506	GPI anchor biosynthetic process	2	30	6.34445977	0.158033403	0.345458545	
GO:0006913	nucleocytoplasmic transport	2	30	6.34445977	0.158033403	0.345458545	
GO:0030901	midbrain development	2	30	6.34445977	0.158033403	0.345458545	
GO:0032355	response to estradiol stimulus	2	30	6.34445977	0.158033403	0.345458545	

GO:0043491	protein kinase B signaling cascade	2	30	6.34445977	0.158033403	0.345458545	
GO:0051402	neuron apoptotic process	2	30	6.34445977	0.158033403	0.345458545	
GO:0060079	regulation of excitatory postsynaptic me	2	30	6.34445977	0.158033403	0.345458545	
GO:0060412	ventricular septum morphogenesis	2	30	6.34445977	0.158033403	0.345458545	
GO:0002175	protein localization to paranode region o	1	4	23.79172414	0.165497784	0.345458545	
GO:0002551	mast cell chemotaxis	1	4	23.79172414	0.165497784	0.345458545	
GO:0003231	cardiac ventricle development	1	4	23.79172414	0.165497784	0.345458545	
GO:0003266	regulation of secondary heart field cardi	1	4	23.79172414	0.165497784	0.345458545	
GO:0003337	mesenchymal to epithelial transition inv	1	4	23.79172414	0.165497784	0.345458545	
GO:0006116	NADH oxidation	1	4	23.79172414	0.165497784	0.345458545	
GO:0006163	purine nucleotide metabolic process	1	4	23.79172414	0.165497784	0.345458545	
GO:0006407	rRNA export from nucleus	1	4	23.79172414	0.165497784	0.345458545	
GO:0006450	regulation of translational fidelity	1	4	23.79172414	0.165497784	0.345458545	
GO:0006531	aspartate metabolic process	1	4	23.79172414	0.165497784	0.345458545	
GO:0006569	tryptophan catabolic process	1	4	23.79172414	0.165497784	0.345458545	
GO:0006651	diacylglycerol biosynthetic process	1	4	23.79172414	0.165497784	0.345458545	
GO:0006659	phosphatidylserine biosynthetic process	1	4	23.79172414	0.165497784	0.345458545	
GO:0006929	substrate-dependent cell migration	1	4	23.79172414	0.165497784	0.345458545	
GO:0006972	hyperosmotic response	1	4	23.79172414	0.165497784	0.345458545	
GO:0007028	cytoplasm organization	1	4	23.79172414	0.165497784	0.345458545	
GO:0007176	regulation of epidermal growth factor-ac	1	4	23.79172414	0.165497784	0.345458545	
GO:0007258	JUN phosphorylation	1	4	23.79172414	0.165497784	0.345458545	
GO:0007288	sperm axoneme assembly	1	4	23.79172414	0.165497784	0.345458545	
GO:0007386	compartment pattern specification	1	4	23.79172414	0.165497784	0.345458545	
GO:0007501	mesodermal cell fate specification	1	4	23.79172414	0.165497784	0.345458545	
GO:0008295	spermidine biosynthetic process	1	4	23.79172414	0.165497784	0.345458545	
GO:0008366	axon ensheathment	1	4	23.79172414	0.165497784	0.345458545	
GO:0010579	positive regulation of adenylate cyclase	1	4	23.79172414	0.165497784	0.345458545	
GO:0010887	negative regulation of cholesterol storag	1	4	23.79172414	0.165497784	0.345458545	
GO:0015810	aspartate transport	1	4	23.79172414	0.165497784	0.345458545	
GO:0015886	heme transport	1	4	23.79172414	0.165497784	0.345458545	
GO:0016576	histone dephosphorylation	1	4	23.79172414	0.165497784	0.345458545	
GO:0021533	cell differentiation in hindbrain	1	4	23.79172414	0.165497784	0.345458545	
GO:0021545	cranial nerve development	1	4	23.79172414	0.165497784	0.345458545	
GO:0021860	pyramidal neuron development	1	4	23.79172414	0.165497784	0.345458545	
GO:0022007	convergent extension involved in neural	1	4	23.79172414	0.165497784	0.345458545	
GO:0022009	central nervous system vasculogenesis	1	4	23.79172414	0.165497784	0.345458545	
GO:0030050	vesicle transport along actin filament	1	4	23.79172414	0.165497784	0.345458545	

GO:0032289	central nervous system myelin formation	1	4	23.79172414	0.165497784	0.345458545	
GO:0032489	regulation of Cdc42 protein signal transduction	1	4	23.79172414	0.165497784	0.345458545	
GO:0033004	negative regulation of mast cell activation	1	4	23.79172414	0.165497784	0.345458545	
GO:0033158	regulation of protein import into nucleus	1	4	23.79172414	0.165497784	0.345458545	
GO:0033522	histone H2A ubiquitination	1	4	23.79172414	0.165497784	0.345458545	
GO:0033572	transferrin transport	1	4	23.79172414	0.165497784	0.345458545	
GO:0033602	negative regulation of dopamine secretion	1	4	23.79172414	0.165497784	0.345458545	
GO:0035088	establishment or maintenance of apical/basal polarity	1	4	23.79172414	0.165497784	0.345458545	
GO:0036003	positive regulation of transcription from RNA polymerase II promoter	1	4	23.79172414	0.165497784	0.345458545	
GO:0040023	establishment of nucleus localization	1	4	23.79172414	0.165497784	0.345458545	
GO:0042538	hyperosmotic salinity response	1	4	23.79172414	0.165497784	0.345458545	
GO:0043305	negative regulation of mast cell degranulation	1	4	23.79172414	0.165497784	0.345458545	
GO:0043367	CD4-positive, alpha-beta T cell differentiation	1	4	23.79172414	0.165497784	0.345458545	
GO:0043374	CD8-positive, alpha-beta T cell differentiation	1	4	23.79172414	0.165497784	0.345458545	
GO:0044387	negative regulation of protein kinase activity	1	4	23.79172414	0.165497784	0.345458545	
GO:0045332	phospholipid translocation	1	4	23.79172414	0.165497784	0.345458545	
GO:0046475	glycerophospholipid catabolic process	1	4	23.79172414	0.165497784	0.345458545	
GO:0046886	positive regulation of hormone biosynthesis	1	4	23.79172414	0.165497784	0.345458545	
GO:0048311	mitochondrion distribution	1	4	23.79172414	0.165497784	0.345458545	
GO:0048312	intracellular distribution of mitochondria	1	4	23.79172414	0.165497784	0.345458545	
GO:0048755	branching morphogenesis of a nerve	1	4	23.79172414	0.165497784	0.345458545	
GO:0048845	venous blood vessel morphogenesis	1	4	23.79172414	0.165497784	0.345458545	
GO:0050702	interleukin-1 beta secretion	1	4	23.79172414	0.165497784	0.345458545	
GO:0050803	regulation of synapse structure and activity	1	4	23.79172414	0.165497784	0.345458545	
GO:0051451	myoblast migration	1	4	23.79172414	0.165497784	0.345458545	
GO:0051492	regulation of stress fiber assembly	1	4	23.79172414	0.165497784	0.345458545	
GO:0051612	negative regulation of serotonin uptake	1	4	23.79172414	0.165497784	0.345458545	
GO:0051668	localization within membrane	1	4	23.79172414	0.165497784	0.345458545	
GO:0060155	platelet dense granule organization	1	4	23.79172414	0.165497784	0.345458545	
GO:0060296	regulation of cilium beat frequency involved in cilia	1	4	23.79172414	0.165497784	0.345458545	
GO:0060393	regulation of pathway-restricted SMAD signaling	1	4	23.79172414	0.165497784	0.345458545	
GO:0060414	aorta smooth muscle tissue morphogenesis	1	4	23.79172414	0.165497784	0.345458545	
GO:0060439	trachea morphogenesis	1	4	23.79172414	0.165497784	0.345458545	
GO:0060686	negative regulation of prostatic bud formation	1	4	23.79172414	0.165497784	0.345458545	
GO:0060956	endocardial cell differentiation	1	4	23.79172414	0.165497784	0.345458545	
GO:0061154	endothelial tube morphogenesis	1	4	23.79172414	0.165497784	0.345458545	
GO:0061198	fungiform papilla formation	1	4	23.79172414	0.165497784	0.345458545	
GO:0070050	neuron homeostasis	1	4	23.79172414	0.165497784	0.345458545	

GO:0070296	sarcoplasmic reticulum calcium ion transp	1	4	23.79172414	0.165497784	0.345458545	
GO:0070309	lens fiber cell morphogenesis	1	4	23.79172414	0.165497784	0.345458545	
GO:0070849	response to epidermal growth factor stim	1	4	23.79172414	0.165497784	0.345458545	
GO:0071205	protein localization to juxtaparanode reg	1	4	23.79172414	0.165497784	0.345458545	
GO:0071340	skeletal muscle acetylcholine-gated char	1	4	23.79172414	0.165497784	0.345458545	
GO:0071599	otic vesicle development	1	4	23.79172414	0.165497784	0.345458545	
GO:0090330	regulation of platelet aggregation	1	4	23.79172414	0.165497784	0.345458545	
GO:1900165	negative regulation of interleukin-6 secr	1	4	23.79172414	0.165497784	0.345458545	
GO:1901029	negative regulation of mitochondrial out	1	4	23.79172414	0.165497784	0.345458545	
GO:0008283	cell proliferation	5	179	2.6582932	0.165764391	0.345583618	
GO:0009611	response to wounding	2	31	6.139799778	0.167781335	0.347191079	
GO:0032868	response to insulin stimulus	2	31	6.139799778	0.167781335	0.347191079	
GO:0042327	positive regulation of phosphorylation	2	31	6.139799778	0.167781335	0.347191079	
GO:0042755	eating behavior	2	31	6.139799778	0.167781335	0.347191079	
GO:0048589	developmental growth	2	31	6.139799778	0.167781335	0.347191079	
GO:0051262	protein tetramerization	2	31	6.139799778	0.167781335	0.347191079	
GO:0030900	forebrain development	3	74	3.858117428	0.173054264	0.35765974	
GO:0016477	cell migration	4	125	3.04534069	0.173574131	0.358291293	
GO:0006936	muscle contraction	2	32	5.947931034	0.177748598	0.363497059	
GO:0007339	binding of sperm to zona pellucida	2	32	5.947931034	0.177748598	0.363497059	
GO:0010942	positive regulation of cell death	2	32	5.947931034	0.177748598	0.363497059	
GO:0035116	embryonic hindlimb morphogenesis	2	32	5.947931034	0.177748598	0.363497059	
GO:0050727	regulation of inflammatory response	2	32	5.947931034	0.177748598	0.363497059	
GO:0051924	regulation of calcium ion transport	2	32	5.947931034	0.177748598	0.363497059	
GO:0072659	protein localization to plasma membrane	2	32	5.947931034	0.177748598	0.363497059	
GO:0042493	response to drug	4	126	3.021171319	0.177835284	0.363497059	
GO:0006909	phagocytosis	2	33	5.7676907	0.18792952	0.382726137	
GO:0007017	microtubule-based process	2	33	5.7676907	0.18792952	0.382726137	
GO:0043434	response to peptide hormone stimulus	2	33	5.7676907	0.18792952	0.382726137	
GO:0006412	translation	6	247	2.311746475	0.189840445	0.383168247	
GO:0050731	positive regulation of peptidyl-tyrosine p	3	77	3.707801164	0.190898487	0.383168247	
GO:0006821	chloride transport	3	78	3.660265252	0.197039699	0.383168247	
GO:0007126	meiosis	3	78	3.660265252	0.197039699	0.383168247	
GO:0010628	positive regulation of gene expression	5	188	2.531034483	0.197140331	0.383168247	
GO:0007254	JNK cascade	2	34	5.598052738	0.198318526	0.383168247	
GO:0010212	response to ionizing radiation	2	34	5.598052738	0.198318526	0.383168247	
GO:0016358	dendrite development	2	34	5.598052738	0.198318526	0.383168247	
GO:0016579	protein deubiquitination	2	34	5.598052738	0.198318526	0.383168247	

GO:0043407	negative regulation of MAP kinase activ	2	34	5.598052738	0.198318526	0.383168247	
GO:0045596	negative regulation of cell differentiation	2	34	5.598052738	0.198318526	0.383168247	
GO:0048511	rhythmic process	2	34	5.598052738	0.198318526	0.383168247	
GO:0042593	glucose homeostasis	3	79	3.61393278	0.203276491	0.383168247	
GO:0001561	fatty acid alpha-oxidation	1	5	19.03337931	0.205792515	0.383168247	
GO:0001660	fever generation	1	5	19.03337931	0.205792515	0.383168247	
GO:0001774	microglial cell activation	1	5	19.03337931	0.205792515	0.383168247	
GO:0001821	histamine secretion	1	5	19.03337931	0.205792515	0.383168247	
GO:0001842	neural fold formation	1	5	19.03337931	0.205792515	0.383168247	
GO:0002686	negative regulation of leukocyte migrati	1	5	19.03337931	0.205792515	0.383168247	
GO:0006670	sphingosine metabolic process	1	5	19.03337931	0.205792515	0.383168247	
GO:0006685	sphingomyelin catabolic process	1	5	19.03337931	0.205792515	0.383168247	
GO:0006778	porphyrin-containing compound metabo	1	5	19.03337931	0.205792515	0.383168247	
GO:0007064	mitotic sister chromatid cohesion	1	5	19.03337931	0.205792515	0.383168247	
GO:0007171	activation of transmembrane receptor pr	1	5	19.03337931	0.205792515	0.383168247	
GO:0010572	positive regulation of platelet activation	1	5	19.03337931	0.205792515	0.383168247	
GO:0010694	positive regulation of alkaline phosphata	1	5	19.03337931	0.205792515	0.383168247	
GO:0010891	negative regulation of sequestering of tr	1	5	19.03337931	0.205792515	0.383168247	
GO:0014037	Schwann cell differentiation	1	5	19.03337931	0.205792515	0.383168247	
GO:0014808	release of sequestered calcium ion into c	1	5	19.03337931	0.205792515	0.383168247	
GO:0014850	response to muscle activity	1	5	19.03337931	0.205792515	0.383168247	
GO:0015809	arginine transport	1	5	19.03337931	0.205792515	0.383168247	
GO:0015879	carnitine transport	1	5	19.03337931	0.205792515	0.383168247	
GO:0016082	synaptic vesicle priming	1	5	19.03337931	0.205792515	0.383168247	
GO:0016199	axon midline choice point recognition	1	5	19.03337931	0.205792515	0.383168247	
GO:0018026	peptidyl-lysine monomethylation	1	5	19.03337931	0.205792515	0.383168247	
GO:0021798	forebrain dorsal/ventral pattern formati	1	5	19.03337931	0.205792515	0.383168247	
GO:0021891	olfactory bulb interneuron development	1	5	19.03337931	0.205792515	0.383168247	
GO:0030072	peptide hormone secretion	1	5	19.03337931	0.205792515	0.383168247	
GO:0031102	neuron projection regeneration	1	5	19.03337931	0.205792515	0.383168247	
GO:0031952	regulation of protein autophosphorylatio	1	5	19.03337931	0.205792515	0.383168247	
GO:0032367	intracellular cholesterol transport	1	5	19.03337931	0.205792515	0.383168247	
GO:0032410	negative regulation of transporter activit	1	5	19.03337931	0.205792515	0.383168247	
GO:0033014	tetrapyrrole biosynthetic process	1	5	19.03337931	0.205792515	0.383168247	
GO:0033603	positive regulation of dopamine secretio	1	5	19.03337931	0.205792515	0.383168247	
GO:0034116	positive regulation of heterotypic cell-ce	1	5	19.03337931	0.205792515	0.383168247	
GO:0034259	negative regulation of Rho GTPase activ	1	5	19.03337931	0.205792515	0.383168247	
GO:0034333	adherens junction assembly	1	5	19.03337931	0.205792515	0.383168247	

GO:0034380	high-density lipoprotein particle assembl	1	5	19.03337931	0.205792515	0.383168247	
GO:0035065	regulation of histone acetylation	1	5	19.03337931	0.205792515	0.383168247	
GO:0035372	protein localization to microtubule	1	5	19.03337931	0.205792515	0.383168247	
GO:0035434	copper ion transmembrane transport	1	5	19.03337931	0.205792515	0.383168247	
GO:0042759	long-chain fatty acid biosynthetic proces	1	5	19.03337931	0.205792515	0.383168247	
GO:0043084	penile erection	1	5	19.03337931	0.205792515	0.383168247	
GO:0043931	ossification involved in bone maturation	1	5	19.03337931	0.205792515	0.383168247	
GO:0044030	regulation of DNA methylation	1	5	19.03337931	0.205792515	0.383168247	
GO:0045446	endothelial cell differentiation	1	5	19.03337931	0.205792515	0.383168247	
GO:0045650	negative regulation of macrophage diffe	1	5	19.03337931	0.205792515	0.383168247	
GO:0045820	negative regulation of glycolysis	1	5	19.03337931	0.205792515	0.383168247	
GO:0045824	negative regulation of innate immune res	1	5	19.03337931	0.205792515	0.383168247	
GO:0046883	regulation of hormone secretion	1	5	19.03337931	0.205792515	0.383168247	
GO:0047497	mitochondrion transport along microtub	1	5	19.03337931	0.205792515	0.383168247	
GO:0048261	negative regulation of receptor-mediated	1	5	19.03337931	0.205792515	0.383168247	
GO:0048280	vesicle fusion with Golgi apparatus	1	5	19.03337931	0.205792515	0.383168247	
GO:0050793	regulation of developmental process	1	5	19.03337931	0.205792515	0.383168247	
GO:0051645	Golgi localization	1	5	19.03337931	0.205792515	0.383168247	
GO:0055009	atrial cardiac muscle tissue morphogene	1	5	19.03337931	0.205792515	0.383168247	
GO:0060298	positive regulation of sarcomere organiz	1	5	19.03337931	0.205792515	0.383168247	
GO:0060742	epithelial cell differentiation involved in	1	5	19.03337931	0.205792515	0.383168247	
GO:0060789	hair follicle placode formation	1	5	19.03337931	0.205792515	0.383168247	
GO:0060982	coronary artery morphogenesis	1	5	19.03337931	0.205792515	0.383168247	
GO:0061180	mammary gland epithelium developmen	1	5	19.03337931	0.205792515	0.383168247	
GO:0071681	cellular response to indole-3-methanol	1	5	19.03337931	0.205792515	0.383168247	
GO:0090286	cytoskeletal anchoring at nuclear membr	1	5	19.03337931	0.205792515	0.383168247	
GO:0090370	negative regulation of cholesterol efflux	1	5	19.03337931	0.205792515	0.383168247	
GO:2000009	negative regulation of protein localizati	1	5	19.03337931	0.205792515	0.383168247	
GO:2000096	positive regulation of Wnt receptor signa	1	5	19.03337931	0.205792515	0.383168247	
GO:2000406	positive regulation of T cell migration	1	5	19.03337931	0.205792515	0.383168247	
GO:0006418	tRNA aminoacylation for protein transla	2	35	5.438108374	0.20891013	0.387248046	
GO:0019722	calcium-mediated signaling	2	35	5.438108374	0.20891013	0.387248046	
GO:0022008	neurogenesis	2	35	5.438108374	0.20891013	0.387248046	
GO:0030522	intracellular receptor signaling pathway	2	35	5.438108374	0.20891013	0.387248046	
GO:0006887	exocytosis	3	80	3.568758621	0.209608242	0.388111829	
GO:0002053	positive regulation of mesenchymal cell	2	36	5.287049808	0.219698942	0.405001799	
GO:0006096	glycolysis	2	36	5.287049808	0.219698942	0.405001799	
GO:0045471	response to ethanol	2	36	5.287049808	0.219698942	0.405001799	

GO:0060048	cardiac muscle contraction	2	36	5.287049808	0.219698942	0.405001799	
GO:0007229	integrin-mediated signaling pathway	3	82	3.481715728	0.222554036	0.409813158	
GO:0071805	potassium ion transmembrane transport	3	83	3.439767345	0.22916674	0.421525621	
GO:0030199	collagen fibril organization	2	37	5.14415657	0.230679661	0.42384219	
GO:0006974	response to DNA damage stimulus	8	361	2.108961696	0.241398609	0.425207927	
GO:0030317	sperm motility	2	38	5.008784029	0.241847074	0.425207927	
GO:0001505	regulation of neurotransmitter levels	1	6	15.86114943	0.245664389	0.425207927	
GO:0005981	regulation of glycogen catabolic process	1	6	15.86114943	0.245664389	0.425207927	
GO:0006000	fructose metabolic process	1	6	15.86114943	0.245664389	0.425207927	
GO:0006104	succinyl-CoA metabolic process	1	6	15.86114943	0.245664389	0.425207927	
GO:0006370	7-methylguanosine mRNA capping	1	6	15.86114943	0.245664389	0.425207927	
GO:0006596	polyamine biosynthetic process	1	6	15.86114943	0.245664389	0.425207927	
GO:0006824	cobalt ion transport	1	6	15.86114943	0.245664389	0.425207927	
GO:0009437	carnitine metabolic process	1	6	15.86114943	0.245664389	0.425207927	
GO:0010839	negative regulation of keratinocyte proliferation	1	6	15.86114943	0.245664389	0.425207927	
GO:0010941	regulation of cell death	1	6	15.86114943	0.245664389	0.425207927	
GO:0010971	positive regulation of G2/M transition of cell cycle	1	6	15.86114943	0.245664389	0.425207927	
GO:0014031	mesenchymal cell development	1	6	15.86114943	0.245664389	0.425207927	
GO:0015697	quaternary ammonium group transport	1	6	15.86114943	0.245664389	0.425207927	
GO:0016556	mRNA modification	1	6	15.86114943	0.245664389	0.425207927	
GO:0018095	protein polyglutamylation	1	6	15.86114943	0.245664389	0.425207927	
GO:0019439	aromatic compound catabolic process	1	6	15.86114943	0.245664389	0.425207927	
GO:0021853	cerebral cortex GABAergic interneuron	1	6	15.86114943	0.245664389	0.425207927	
GO:0030510	regulation of BMP signaling pathway	1	6	15.86114943	0.245664389	0.425207927	
GO:0030913	paranodal junction assembly	1	6	15.86114943	0.245664389	0.425207927	
GO:0032811	negative regulation of epinephrine secretion	1	6	15.86114943	0.245664389	0.425207927	
GO:0032927	positive regulation of activin receptor signaling	1	6	15.86114943	0.245664389	0.425207927	
GO:0032964	collagen biosynthetic process	1	6	15.86114943	0.245664389	0.425207927	
GO:0033119	negative regulation of RNA splicing	1	6	15.86114943	0.245664389	0.425207927	
GO:0034067	protein localization to Golgi apparatus	1	6	15.86114943	0.245664389	0.425207927	
GO:0034720	histone H3-K4 demethylation	1	6	15.86114943	0.245664389	0.425207927	
GO:0035524	proline transmembrane transport	1	6	15.86114943	0.245664389	0.425207927	
GO:0040036	regulation of fibroblast growth factor receptor signaling	1	6	15.86114943	0.245664389	0.425207927	
GO:0042129	regulation of T cell proliferation	1	6	15.86114943	0.245664389	0.425207927	
GO:0042158	lipoprotein biosynthetic process	1	6	15.86114943	0.245664389	0.425207927	
GO:0042594	response to starvation	1	6	15.86114943	0.245664389	0.425207927	
GO:0042698	ovulation cycle	1	6	15.86114943	0.245664389	0.425207927	
GO:0042713	sperm ejaculation	1	6	15.86114943	0.245664389	0.425207927	

GO:0043270	positive regulation of ion transport	1	6	15.86114943	0.245664389	0.425207927	
GO:0043619	regulation of transcription from RNA po	1	6	15.86114943	0.245664389	0.425207927	
GO:0045654	positive regulation of megakaryocyte dif	1	6	15.86114943	0.245664389	0.425207927	
GO:0045687	positive regulation of glial cell different	1	6	15.86114943	0.245664389	0.425207927	
GO:0045722	positive regulation of gluconeogenesis	1	6	15.86114943	0.245664389	0.425207927	
GO:0046785	microtubule polymerization	1	6	15.86114943	0.245664389	0.425207927	
GO:0048505	regulation of timing of cell differentiat	1	6	15.86114943	0.245664389	0.425207927	
GO:0051013	microtubule severing	1	6	15.86114943	0.245664389	0.425207927	
GO:0051054	positive regulation of DNA metabolic pr	1	6	15.86114943	0.245664389	0.425207927	
GO:0051151	negative regulation of smooth muscle ce	1	6	15.86114943	0.245664389	0.425207927	
GO:0051247	positive regulation of protein metabolic	1	6	15.86114943	0.245664389	0.425207927	
GO:0060087	relaxation of vascular smooth muscle	1	6	15.86114943	0.245664389	0.425207927	
GO:0060253	negative regulation of glial cell prolifera	1	6	15.86114943	0.245664389	0.425207927	
GO:0060430	lung sacculle development	1	6	15.86114943	0.245664389	0.425207927	
GO:0060510	Type II pneumocyte differentiation	1	6	15.86114943	0.245664389	0.425207927	
GO:0061003	positive regulation of dendritic spine mo	1	6	15.86114943	0.245664389	0.425207927	
GO:0070206	protein trimerization	1	6	15.86114943	0.245664389	0.425207927	
GO:0070544	histone H3-K36 demethylation	1	6	15.86114943	0.245664389	0.425207927	
GO:0090031	positive regulation of steroid hormone b	1	6	15.86114943	0.245664389	0.425207927	
GO:0090279	regulation of calcium ion import	1	6	15.86114943	0.245664389	0.425207927	
GO:2000252	negative regulation of feeding behavior	1	6	15.86114943	0.245664389	0.425207927	
GO:2001241	positive regulation of extrinsic apoptotic	1	6	15.86114943	0.245664389	0.425207927	
GO:0008544	epidermis development	2	39	4.880353669	0.253196058	0.436887315	
GO:0032024	positive regulation of insulin secretion	2	39	4.880353669	0.253196058	0.436887315	
GO:0045444	fat cell differentiation	2	39	4.880353669	0.253196058	0.436887315	
GO:0001501	skeletal system development	3	88	3.244326019	0.263600085	0.453902514	
GO:0030198	extracellular matrix organization	3	88	3.244326019	0.263600085	0.453902514	
GO:0007612	learning	2	40	4.758344828	0.264721576	0.455364687	
GO:0016337	cell-cell adhesion	3	89	3.207872917	0.270755529	0.465089777	
GO:0030163	protein catabolic process	2	41	4.642287637	0.276418678	0.465089777	
GO:0030183	B cell differentiation	2	41	4.642287637	0.276418678	0.465089777	
GO:0000002	mitochondrial genome maintenance	1	7	13.59527094	0.285117836	0.465089777	
GO:0000042	protein targeting to Golgi	1	7	13.59527094	0.285117836	0.465089777	
GO:0001711	endodermal cell fate commitment	1	7	13.59527094	0.285117836	0.465089777	
GO:0002674	negative regulation of acute inflammato	1	7	13.59527094	0.285117836	0.465089777	
GO:0003184	pulmonary valve morphogenesis	1	7	13.59527094	0.285117836	0.465089777	
GO:0003208	cardiac ventricle morphogenesis	1	7	13.59527094	0.285117836	0.465089777	
GO:0003300	cardiac muscle hypertrophy	1	7	13.59527094	0.285117836	0.465089777	

GO:0006002	fructose 6-phosphate metabolic process	1	7	13.59527094	0.285117836	0.465089777	
GO:0007435	salivary gland morphogenesis	1	7	13.59527094	0.285117836	0.465089777	
GO:0010642	negative regulation of platelet-derived growth factor receptor signaling	1	7	13.59527094	0.285117836	0.465089777	
GO:0010700	negative regulation of norepinephrine secretion	1	7	13.59527094	0.285117836	0.465089777	
GO:0010738	regulation of protein kinase A signaling	1	7	13.59527094	0.285117836	0.465089777	
GO:0010881	regulation of cardiac muscle contraction	1	7	13.59527094	0.285117836	0.465089777	
GO:0010886	positive regulation of cholesterol storage	1	7	13.59527094	0.285117836	0.465089777	
GO:0014824	artery smooth muscle contraction	1	7	13.59527094	0.285117836	0.465089777	
GO:0017158	regulation of calcium ion-dependent exocytosis	1	7	13.59527094	0.285117836	0.465089777	
GO:0019227	neuronal action potential propagation	1	7	13.59527094	0.285117836	0.465089777	
GO:0019674	NAD metabolic process	1	7	13.59527094	0.285117836	0.465089777	
GO:0021707	cerebellar granule cell differentiation	1	7	13.59527094	0.285117836	0.465089777	
GO:0021884	forebrain neuron development	1	7	13.59527094	0.285117836	0.465089777	
GO:0021955	central nervous system neuron axonogenesis	1	7	13.59527094	0.285117836	0.465089777	
GO:0022029	telencephalon cell migration	1	7	13.59527094	0.285117836	0.465089777	
GO:0030858	positive regulation of epithelial cell differentiation	1	7	13.59527094	0.285117836	0.465089777	
GO:0031622	positive regulation of fever generation	1	7	13.59527094	0.285117836	0.465089777	
GO:0032099	negative regulation of appetite	1	7	13.59527094	0.285117836	0.465089777	
GO:0032469	endoplasmic reticulum calcium ion homeostasis	1	7	13.59527094	0.285117836	0.465089777	
GO:0032862	activation of Rho GTPase activity	1	7	13.59527094	0.285117836	0.465089777	
GO:0034755	iron ion transmembrane transport	1	7	13.59527094	0.285117836	0.465089777	
GO:0035278	negative regulation of translation involving protein synthesis	1	7	13.59527094	0.285117836	0.465089777	
GO:0042428	serotonin metabolic process	1	7	13.59527094	0.285117836	0.465089777	
GO:0042473	outer ear morphogenesis	1	7	13.59527094	0.285117836	0.465089777	
GO:0042633	hair cycle	1	7	13.59527094	0.285117836	0.465089777	
GO:0043200	response to amino acid stimulus	1	7	13.59527094	0.285117836	0.465089777	
GO:0045839	negative regulation of mitosis	1	7	13.59527094	0.285117836	0.465089777	
GO:0046889	positive regulation of lipid biosynthetic process	1	7	13.59527094	0.285117836	0.465089777	
GO:0048642	negative regulation of skeletal muscle tissue morphogenesis	1	7	13.59527094	0.285117836	0.465089777	
GO:0048660	regulation of smooth muscle cell proliferation	1	7	13.59527094	0.285117836	0.465089777	
GO:0050798	activated T cell proliferation	1	7	13.59527094	0.285117836	0.465089777	
GO:0051099	positive regulation of binding	1	7	13.59527094	0.285117836	0.465089777	
GO:0051168	nuclear export	1	7	13.59527094	0.285117836	0.465089777	
GO:0051292	nuclear pore complex assembly	1	7	13.59527094	0.285117836	0.465089777	
GO:0051932	synaptic transmission, GABAergic	1	7	13.59527094	0.285117836	0.465089777	
GO:0060011	Sertoli cell proliferation	1	7	13.59527094	0.285117836	0.465089777	
GO:0060056	mammary gland involution	1	7	13.59527094	0.285117836	0.465089777	
GO:0060122	inner ear receptor stereocilium organization	1	7	13.59527094	0.285117836	0.465089777	

GO:0060687	regulation of branching involved in pros	1	7	13.59527094	0.285117836	0.465089777	
GO:0061037	negative regulation of cartilage developr	1	7	13.59527094	0.285117836	0.465089777	
GO:0070166	enamel mineralization	1	7	13.59527094	0.285117836	0.465089777	
GO:2000178	negative regulation of neural precursor c	1	7	13.59527094	0.285117836	0.465089777	
GO:2000543	positive regulation of gastrulation	1	7	13.59527094	0.285117836	0.465089777	
GO:0051592	response to calcium ion	2	42	4.531756979	0.288282496	0.469793697	
GO:0051781	positive regulation of cell division	2	43	4.426367281	0.300308246	0.48891469	
GO:0007409	axonogenesis	3	94	3.037241379	0.307833577	0.500678735	
GO:0008286	insulin receptor signaling pathway	2	44	4.325768025	0.312491226	0.506160704	
GO:0001553	luteinization	1	8	11.89586207	0.324157242	0.506160704	
GO:0003016	respiratory system process	1	8	11.89586207	0.324157242	0.506160704	
GO:0003197	endocardial cushion development	1	8	11.89586207	0.324157242	0.506160704	
GO:0006032	chitin catabolic process	1	8	11.89586207	0.324157242	0.506160704	
GO:0006400	tRNA modification	1	8	11.89586207	0.324157242	0.506160704	
GO:0006687	glycosphingolipid metabolic process	1	8	11.89586207	0.324157242	0.506160704	
GO:0007341	penetration of zona pellucida	1	8	11.89586207	0.324157242	0.506160704	
GO:0007617	mating behavior	1	8	11.89586207	0.324157242	0.506160704	
GO:0010592	positive regulation of lamellipodium ass	1	8	11.89586207	0.324157242	0.506160704	
GO:0014002	astrocyte development	1	8	11.89586207	0.324157242	0.506160704	
GO:0015701	bicarbonate transport	1	8	11.89586207	0.324157242	0.506160704	
GO:0015844	monoamine transport	1	8	11.89586207	0.324157242	0.506160704	
GO:0021670	lateral ventricle development	1	8	11.89586207	0.324157242	0.506160704	
GO:0031643	positive regulation of myelination	1	8	11.89586207	0.324157242	0.506160704	
GO:0032940	secretion by cell	1	8	11.89586207	0.324157242	0.506160704	
GO:0033210	leptin-mediated signaling pathway	1	8	11.89586207	0.324157242	0.506160704	
GO:0034244	negative regulation of transcription elon	1	8	11.89586207	0.324157242	0.506160704	
GO:0035058	nonmotile primary cilium assembly	1	8	11.89586207	0.324157242	0.506160704	
GO:0035239	tube morphogenesis	1	8	11.89586207	0.324157242	0.506160704	
GO:0040011	locomotion	1	8	11.89586207	0.324157242	0.506160704	
GO:0042136	neurotransmitter biosynthetic process	1	8	11.89586207	0.324157242	0.506160704	
GO:0043117	positive regulation of vascular permeabi	1	8	11.89586207	0.324157242	0.506160704	
GO:0043569	negative regulation of insulin-like growt	1	8	11.89586207	0.324157242	0.506160704	
GO:0045056	transcytosis	1	8	11.89586207	0.324157242	0.506160704	
GO:0048026	positive regulation of mRNA splicing, v	1	8	11.89586207	0.324157242	0.506160704	
GO:0048489	synaptic vesicle transport	1	8	11.89586207	0.324157242	0.506160704	
GO:0048752	semicircular canal morphogenesis	1	8	11.89586207	0.324157242	0.506160704	
GO:0050777	negative regulation of immune response	1	8	11.89586207	0.324157242	0.506160704	
GO:0050805	negative regulation of synaptic transmiss	1	8	11.89586207	0.324157242	0.506160704	

GO:0055089	fatty acid homeostasis	1	8	11.89586207	0.324157242	0.506160704	
GO:0055091	phospholipid homeostasis	1	8	11.89586207	0.324157242	0.506160704	
GO:0060119	inner ear receptor cell development	1	8	11.89586207	0.324157242	0.506160704	
GO:0060346	bone trabecula formation	1	8	11.89586207	0.324157242	0.506160704	
GO:0060406	positive regulation of penile erection	1	8	11.89586207	0.324157242	0.506160704	
GO:0060997	dendritic spine morphogenesis	1	8	11.89586207	0.324157242	0.506160704	
GO:0061337	cardiac conduction	1	8	11.89586207	0.324157242	0.506160704	
GO:0070233	negative regulation of T cell apoptotic p	1	8	11.89586207	0.324157242	0.506160704	
GO:0090129	positive regulation of synapse maturatio	1	8	11.89586207	0.324157242	0.506160704	
GO:0090136	epithelial cell-cell adhesion	1	8	11.89586207	0.324157242	0.506160704	
GO:2000179	positive regulation of neural precursor c	1	8	11.89586207	0.324157242	0.506160704	
GO:2000273	positive regulation of receptor activity	1	8	11.89586207	0.324157242	0.506160704	
GO:0014068	positive regulation of phosphatidylinosit	2	45	4.229639847	0.324826815	0.506160704	
GO:0042102	positive regulation of T cell proliferation	2	45	4.229639847	0.324826815	0.506160704	
GO:0060548	negative regulation of cell death	2	45	4.229639847	0.324826815	0.506160704	
GO:0001541	ovarian follicle development	2	46	4.137691154	0.337310472	0.524147871	
GO:0001649	osteoblast differentiation	2	46	4.137691154	0.337310472	0.524147871	
GO:0001756	somitogenesis	2	46	4.137691154	0.337310472	0.524147871	
GO:0032880	regulation of protein localization	2	47	4.049655172	0.349937732	0.537271721	
GO:0000245	spliceosomal complex assembly	1	9	10.57409962	0.362786945	0.537271721	
GO:0001101	response to acid	1	9	10.57409962	0.362786945	0.537271721	
GO:0001952	regulation of cell-matrix adhesion	1	9	10.57409962	0.362786945	0.537271721	
GO:0001973	adenosine receptor signaling pathway	1	9	10.57409962	0.362786945	0.537271721	
GO:0003203	endocardial cushion morphogenesis	1	9	10.57409962	0.362786945	0.537271721	
GO:0003382	epithelial cell morphogenesis	1	9	10.57409962	0.362786945	0.537271721	
GO:0006105	succinate metabolic process	1	9	10.57409962	0.362786945	0.537271721	
GO:0006368	transcription elongation from RNA poly	1	9	10.57409962	0.362786945	0.537271721	
GO:0006625	protein targeting to peroxisome	1	9	10.57409962	0.362786945	0.537271721	
GO:0006796	phosphate-containing compound metabo	1	9	10.57409962	0.362786945	0.537271721	
GO:0007398	ectoderm development	1	9	10.57409962	0.362786945	0.537271721	
GO:0008088	axon cargo transport	1	9	10.57409962	0.362786945	0.537271721	
GO:0009100	glycoprotein metabolic process	1	9	10.57409962	0.362786945	0.537271721	
GO:0009435	NAD biosynthetic process	1	9	10.57409962	0.362786945	0.537271721	
GO:0010389	regulation of G2/M transition of mitotic	1	9	10.57409962	0.362786945	0.537271721	
GO:0010745	negative regulation of macrophage deriv	1	9	10.57409962	0.362786945	0.537271721	
GO:0010759	positive regulation of macrophage chem	1	9	10.57409962	0.362786945	0.537271721	
GO:0014049	positive regulation of glutamate secretio	1	9	10.57409962	0.362786945	0.537271721	
GO:0014898	cardiac muscle hypertrophy in response	1	9	10.57409962	0.362786945	0.537271721	

GO:0016574	histone ubiquitination	1	9	10.57409962	0.362786945	0.537271721	
GO:0019217	regulation of fatty acid metabolic process	1	9	10.57409962	0.362786945	0.537271721	
GO:0021510	spinal cord development	1	9	10.57409962	0.362786945	0.537271721	
GO:0021756	striatum development	1	9	10.57409962	0.362786945	0.537271721	
GO:0022011	myelination in peripheral nervous system	1	9	10.57409962	0.362786945	0.537271721	
GO:0031017	exocrine pancreas development	1	9	10.57409962	0.362786945	0.537271721	
GO:0034122	negative regulation of toll-like receptor signaling	1	9	10.57409962	0.362786945	0.537271721	
GO:0035095	behavioral response to nicotine	1	9	10.57409962	0.362786945	0.537271721	
GO:0035810	positive regulation of urine volume	1	9	10.57409962	0.362786945	0.537271721	
GO:0042059	negative regulation of epidermal growth factor receptor signaling	1	9	10.57409962	0.362786945	0.537271721	
GO:0042312	regulation of vasodilation	1	9	10.57409962	0.362786945	0.537271721	
GO:0042770	signal transduction in response to DNA damage	1	9	10.57409962	0.362786945	0.537271721	
GO:0043044	ATP-dependent chromatin remodeling	1	9	10.57409962	0.362786945	0.537271721	
GO:0043206	extracellular fibril organization	1	9	10.57409962	0.362786945	0.537271721	
GO:0045603	positive regulation of endothelial cell differentiation	1	9	10.57409962	0.362786945	0.537271721	
GO:0045926	negative regulation of growth	1	9	10.57409962	0.362786945	0.537271721	
GO:0045995	regulation of embryonic development	1	9	10.57409962	0.362786945	0.537271721	
GO:0046085	adenosine metabolic process	1	9	10.57409962	0.362786945	0.537271721	
GO:0046628	positive regulation of insulin receptor signaling	1	9	10.57409962	0.362786945	0.537271721	
GO:0048016	inositol phosphate-mediated signaling	1	9	10.57409962	0.362786945	0.537271721	
GO:0048193	Golgi vesicle transport	1	9	10.57409962	0.362786945	0.537271721	
GO:0048644	muscle organ morphogenesis	1	9	10.57409962	0.362786945	0.537271721	
GO:0048762	mesenchymal cell differentiation	1	9	10.57409962	0.362786945	0.537271721	
GO:0050708	regulation of protein secretion	1	9	10.57409962	0.362786945	0.537271721	
GO:0051967	negative regulation of synaptic transmission	1	9	10.57409962	0.362786945	0.537271721	
GO:0060252	positive regulation of glial cell proliferation	1	9	10.57409962	0.362786945	0.537271721	
GO:0060644	mammary gland epithelial cell differentiation	1	9	10.57409962	0.362786945	0.537271721	
GO:0060736	prostate gland growth	1	9	10.57409962	0.362786945	0.537271721	
GO:0060947	cardiac vascular smooth muscle cell differentiation	1	9	10.57409962	0.362786945	0.537271721	
GO:0061077	chaperone-mediated protein folding	1	9	10.57409962	0.362786945	0.537271721	
GO:0090026	positive regulation of monocyte chemotaxis	1	9	10.57409962	0.362786945	0.537271721	
GO:0097150	neuronal stem cell maintenance	1	9	10.57409962	0.362786945	0.537271721	
GO:2001235	positive regulation of apoptotic signaling	1	9	10.57409962	0.362786945	0.537271721	
GO:0001938	positive regulation of endothelial cell proliferation	2	49	3.884363125	0.375605596	0.555271933	
GO:0009636	response to toxic substance	2	49	3.884363125	0.375605596	0.555271933	
GO:0006464	cellular protein modification process	2	50	3.806675862	0.388637653	0.574030174	
GO:0000413	protein peptidyl-prolyl isomerization	1	10	9.516689655	0.401011241	0.57454224	
GO:0000904	cell morphogenesis involved in differentiation	1	10	9.516689655	0.401011241	0.57454224	

GO:0003181	atrioventricular valve morphogenesis	1	10	9.516689655	0.401011241	0.57454224	
GO:0003198	epithelial to mesenchymal transition inv	1	10	9.516689655	0.401011241	0.57454224	
GO:0005979	regulation of glycogen biosynthetic proc	1	10	9.516689655	0.401011241	0.57454224	
GO:0006325	chromatin organization	1	10	9.516689655	0.401011241	0.57454224	
GO:0006744	ubiquinone biosynthetic process	1	10	9.516689655	0.401011241	0.57454224	
GO:0006839	mitochondrial transport	1	10	9.516689655	0.401011241	0.57454224	
GO:0006996	organelle organization	1	10	9.516689655	0.401011241	0.57454224	
GO:0007191	adenylate cyclase-activating dopamine r	1	10	9.516689655	0.401011241	0.57454224	
GO:0008343	adult feeding behavior	1	10	9.516689655	0.401011241	0.57454224	
GO:0009072	aromatic amino acid family metabolic pr	1	10	9.516689655	0.401011241	0.57454224	
GO:0010763	positive regulation of fibroblast migratio	1	10	9.516689655	0.401011241	0.57454224	
GO:0014823	response to activity	1	10	9.516689655	0.401011241	0.57454224	
GO:0014902	myotube differentiation	1	10	9.516689655	0.401011241	0.57454224	
GO:0015893	drug transport	1	10	9.516689655	0.401011241	0.57454224	
GO:0022904	respiratory electron transport chain	1	10	9.516689655	0.401011241	0.57454224	
GO:0030041	actin filament polymerization	1	10	9.516689655	0.401011241	0.57454224	
GO:0030520	intracellular estrogen receptor signaling	1	10	9.516689655	0.401011241	0.57454224	
GO:0031000	response to caffeine	1	10	9.516689655	0.401011241	0.57454224	
GO:0032435	negative regulation of proteasomal ubiqu	1	10	9.516689655	0.401011241	0.57454224	
GO:0032740	positive regulation of interleukin-17 pro	1	10	9.516689655	0.401011241	0.57454224	
GO:0033235	positive regulation of protein sumoylatio	1	10	9.516689655	0.401011241	0.57454224	
GO:0045737	positive regulation of cyclin-dependent p	1	10	9.516689655	0.401011241	0.57454224	
GO:0045821	positive regulation of glycolysis	1	10	9.516689655	0.401011241	0.57454224	
GO:0048703	embryonic viscerocranium morphogenesi	1	10	9.516689655	0.401011241	0.57454224	
GO:0048853	forebrain morphogenesis	1	10	9.516689655	0.401011241	0.57454224	
GO:0050771	negative regulation of axonogenesis	1	10	9.516689655	0.401011241	0.57454224	
GO:0050892	intestinal absorption	1	10	9.516689655	0.401011241	0.57454224	
GO:0061136	regulation of proteasomal protein catabol	1	10	9.516689655	0.401011241	0.57454224	
GO:0070935	3'-UTR-mediated mRNA stabilization	1	10	9.516689655	0.401011241	0.57454224	
GO:0070997	neuron death	1	10	9.516689655	0.401011241	0.57454224	
GO:0090162	establishment of epithelial cell polarity	1	10	9.516689655	0.401011241	0.57454224	
GO:2000310	regulation of N-methyl-D-aspartate sele	1	10	9.516689655	0.401011241	0.57454224	
GO:2000678	negative regulation of transcription regu	1	10	9.516689655	0.401011241	0.57454224	
GO:0000910	cytokinesis	2	51	3.732035159	0.401796222	0.574682022	
GO:0035914	skeletal muscle cell differentiation	2	51	3.732035159	0.401796222	0.574682022	
GO:0006366	transcription from RNA polymerase II p	3	106	2.693402733	0.405148176	0.578980983	
GO:0006338	chromatin remodeling	2	52	3.660265252	0.415077214	0.590646044	
GO:0008584	male gonad development	2	52	3.660265252	0.415077214	0.590646044	

GO:0017148	negative regulation of translation	2	52	3.660265252	0.415077214	0.590646044	
GO:0048704	embryonic skeletal system morphogenesis	2	52	3.660265252	0.415077214	0.590646044	
GO:0051090	regulation of sequence-specific DNA binding	2	52	3.660265252	0.415077214	0.590646044	
GO:0033138	positive regulation of peptidyl-serine phosphorylation	2	53	3.591203643	0.428476612	0.604889594	
GO:0006878	cellular copper ion homeostasis	1	11	8.65153605	0.438834377	0.604889594	
GO:0007413	axonal fasciculation	1	11	8.65153605	0.438834377	0.604889594	
GO:0008210	estrogen metabolic process	1	11	8.65153605	0.438834377	0.604889594	
GO:0009950	dorsal/ventral axis specification	1	11	8.65153605	0.438834377	0.604889594	
GO:0010875	positive regulation of cholesterol efflux	1	11	8.65153605	0.438834377	0.604889594	
GO:0014059	regulation of dopamine secretion	1	11	8.65153605	0.438834377	0.604889594	
GO:0016226	iron-sulfur cluster assembly	1	11	8.65153605	0.438834377	0.604889594	
GO:0016486	peptide hormone processing	1	11	8.65153605	0.438834377	0.604889594	
GO:0016558	protein import into peroxisome matrix	1	11	8.65153605	0.438834377	0.604889594	
GO:0019363	pyridine nucleotide biosynthetic process	1	11	8.65153605	0.438834377	0.604889594	
GO:0030031	cell projection assembly	1	11	8.65153605	0.438834377	0.604889594	
GO:0030828	positive regulation of cGMP biosynthesis	1	11	8.65153605	0.438834377	0.604889594	
GO:0031396	regulation of protein ubiquitination	1	11	8.65153605	0.438834377	0.604889594	
GO:0031571	mitotic G1 DNA damage checkpoint	1	11	8.65153605	0.438834377	0.604889594	
GO:0033700	phospholipid efflux	1	11	8.65153605	0.438834377	0.604889594	
GO:0035774	positive regulation of insulin secretion in pancreatic islet	1	11	8.65153605	0.438834377	0.604889594	
GO:0042416	dopamine biosynthetic process	1	11	8.65153605	0.438834377	0.604889594	
GO:0042789	mRNA transcription from RNA polymerase II promoter	1	11	8.65153605	0.438834377	0.604889594	
GO:0043116	negative regulation of vascular permeability	1	11	8.65153605	0.438834377	0.604889594	
GO:0043249	erythrocyte maturation	1	11	8.65153605	0.438834377	0.604889594	
GO:0044257	cellular protein catabolic process	1	11	8.65153605	0.438834377	0.604889594	
GO:0045745	positive regulation of G-protein coupled receptor signaling pathway	1	11	8.65153605	0.438834377	0.604889594	
GO:0045792	negative regulation of cell size	1	11	8.65153605	0.438834377	0.604889594	
GO:0048599	oocyte development	1	11	8.65153605	0.438834377	0.604889594	
GO:0048617	embryonic foregut morphogenesis	1	11	8.65153605	0.438834377	0.604889594	
GO:0048771	tissue remodeling	1	11	8.65153605	0.438834377	0.604889594	
GO:0050795	regulation of behavior	1	11	8.65153605	0.438834377	0.604889594	
GO:0050860	negative regulation of T cell receptor signaling pathway	1	11	8.65153605	0.438834377	0.604889594	
GO:0050884	neuromuscular process controlling posture	1	11	8.65153605	0.438834377	0.604889594	
GO:0050966	detection of mechanical stimulus involved in sensory perception of touch	1	11	8.65153605	0.438834377	0.604889594	
GO:0051481	reduction of cytosolic calcium ion concentration	1	11	8.65153605	0.438834377	0.604889594	
GO:0055003	cardiac myofibril assembly	1	11	8.65153605	0.438834377	0.604889594	
GO:0060068	vagina development	1	11	8.65153605	0.438834377	0.604889594	
GO:0060081	membrane hyperpolarization	1	11	8.65153605	0.438834377	0.604889594	

GO:0060740	prostate gland epithelium morphogenesis	1	11	8.65153605	0.438834377	0.604889594	
GO:0070208	protein heterotrimerization	1	11	8.65153605	0.438834377	0.604889594	
GO:2001141	regulation of RNA biosynthetic process	1	11	8.65153605	0.438834377	0.604889594	
GO:0006461	protein complex assembly	2	54	3.524699872	0.441990469	0.607736895	
GO:0008654	phospholipid biosynthetic process	2	54	3.524699872	0.441990469	0.607736895	
GO:0048839	inner ear development	2	54	3.524699872	0.441990469	0.607736895	
GO:0016525	negative regulation of angiogenesis	2	55	3.46061442	0.45561491	0.625955735	
GO:0001934	positive regulation of protein phosphorylation	3	112	2.5491133	0.457842669	0.628499953	
GO:0000226	microtubule cytoskeleton organization	2	56	3.398817734	0.469346127	0.637556166	
GO:0007517	muscle organ development	2	56	3.398817734	0.469346127	0.637556166	
GO:0032088	negative regulation of NF-kappaB transcription	2	56	3.398817734	0.469346127	0.637556166	
GO:0003214	cardiac left ventricle morphogenesis	1	12	7.930574713	0.476260557	0.637556166	
GO:0009303	rRNA transcription	1	12	7.930574713	0.476260557	0.637556166	
GO:0009306	protein secretion	1	12	7.930574713	0.476260557	0.637556166	
GO:0009612	response to mechanical stimulus	1	12	7.930574713	0.476260557	0.637556166	
GO:0010975	regulation of neuron projection development	1	12	7.930574713	0.476260557	0.637556166	
GO:0014912	negative regulation of smooth muscle cell proliferation	1	12	7.930574713	0.476260557	0.637556166	
GO:0016998	cell wall macromolecule catabolic process	1	12	7.930574713	0.476260557	0.637556166	
GO:0021591	ventricular system development	1	12	7.930574713	0.476260557	0.637556166	
GO:0032270	positive regulation of cellular protein metabolism	1	12	7.930574713	0.476260557	0.637556166	
GO:0032793	positive regulation of CREB transcription	1	12	7.930574713	0.476260557	0.637556166	
GO:0032924	activin receptor signaling pathway	1	12	7.930574713	0.476260557	0.637556166	
GO:0035909	aorta morphogenesis	1	12	7.930574713	0.476260557	0.637556166	
GO:0042730	fibrinolysis	1	12	7.930574713	0.476260557	0.637556166	
GO:0043583	ear development	1	12	7.930574713	0.476260557	0.637556166	
GO:0043691	reverse cholesterol transport	1	12	7.930574713	0.476260557	0.637556166	
GO:0045019	negative regulation of nitric oxide biosynthesis	1	12	7.930574713	0.476260557	0.637556166	
GO:0045086	positive regulation of interleukin-2 biosynthesis	1	12	7.930574713	0.476260557	0.637556166	
GO:0045667	regulation of osteoblast differentiation	1	12	7.930574713	0.476260557	0.637556166	
GO:0046827	positive regulation of protein export from cell	1	12	7.930574713	0.476260557	0.637556166	
GO:0046855	inositol phosphate dephosphorylation	1	12	7.930574713	0.476260557	0.637556166	
GO:0048009	insulin-like growth factor receptor signaling	1	12	7.930574713	0.476260557	0.637556166	
GO:0048255	mRNA stabilization	1	12	7.930574713	0.476260557	0.637556166	
GO:0060216	definitive hemopoiesis	1	12	7.930574713	0.476260557	0.637556166	
GO:0060272	embryonic skeletal joint morphogenesis	1	12	7.930574713	0.476260557	0.637556166	
GO:0060732	positive regulation of inositol phosphate metabolism	1	12	7.930574713	0.476260557	0.637556166	
GO:0070498	interleukin-1-mediated signaling pathway	1	12	7.930574713	0.476260557	0.637556166	
GO:1900087	positive regulation of G1/S transition of cell cycle	1	12	7.930574713	0.476260557	0.637556166	

GO:2000463	positive regulation of excitatory postsyn	1	12	7.930574713	0.476260557	0.637556166	
GO:0006334	nucleosome assembly	2	57	3.339189353	0.48318038	0.645785448	
GO:0050728	negative regulation of inflammatory resp	2	57	3.339189353	0.48318038	0.645785448	
GO:0001889	liver development	2	58	3.281617122	0.497113995	0.663877476	
GO:0009615	response to virus	2	59	3.225996493	0.5111143364	0.667361954	
GO:0001779	natural killer cell differentiation	1	13	7.320530504	0.513293943	0.667361954	
GO:0006662	glycerol ether metabolic process	1	13	7.320530504	0.513293943	0.667361954	
GO:0006779	porphyrin-containing compound biosynt	1	13	7.320530504	0.513293943	0.667361954	
GO:0006944	cellular membrane fusion	1	13	7.320530504	0.513293943	0.667361954	
GO:0006970	response to osmotic stress	1	13	7.320530504	0.513293943	0.667361954	
GO:0007202	activation of phospholipase C activity	1	13	7.320530504	0.513293943	0.667361954	
GO:0007263	nitric oxide mediated signal transduction	1	13	7.320530504	0.513293943	0.667361954	
GO:0008209	androgen metabolic process	1	13	7.320530504	0.513293943	0.667361954	
GO:0008272	sulfate transport	1	13	7.320530504	0.513293943	0.667361954	
GO:0008589	regulation of smoothened signaling path	1	13	7.320530504	0.513293943	0.667361954	
GO:0010043	response to zinc ion	1	13	7.320530504	0.513293943	0.667361954	
GO:0016045	detection of bacterium	1	13	7.320530504	0.513293943	0.667361954	
GO:0016331	morphogenesis of embryonic epithelium	1	13	7.320530504	0.513293943	0.667361954	
GO:0016601	Rac protein signal transduction	1	13	7.320530504	0.513293943	0.667361954	
GO:0017156	calcium ion-dependent exocytosis	1	13	7.320530504	0.513293943	0.667361954	
GO:0018345	protein palmitoylation	1	13	7.320530504	0.513293943	0.667361954	
GO:0021542	dentate gyrus development	1	13	7.320530504	0.513293943	0.667361954	
GO:0030517	negative regulation of axon extension	1	13	7.320530504	0.513293943	0.667361954	
GO:0031032	actomyosin structure organization	1	13	7.320530504	0.513293943	0.667361954	
GO:0032331	negative regulation of chondrocyte diffe	1	13	7.320530504	0.513293943	0.667361954	
GO:0032753	positive regulation of interleukin-4 prod	1	13	7.320530504	0.513293943	0.667361954	
GO:0043277	apoptotic cell clearance	1	13	7.320530504	0.513293943	0.667361954	
GO:0043623	cellular protein complex assembly	1	13	7.320530504	0.513293943	0.667361954	
GO:0046686	response to cadmium ion	1	13	7.320530504	0.513293943	0.667361954	
GO:0046835	carbohydrate phosphorylation	1	13	7.320530504	0.513293943	0.667361954	
GO:0048268	clathrin coat assembly	1	13	7.320530504	0.513293943	0.667361954	
GO:0048712	negative regulation of astrocyte differen	1	13	7.320530504	0.513293943	0.667361954	
GO:0050995	negative regulation of lipid catabolic pro	1	13	7.320530504	0.513293943	0.667361954	
GO:0051298	centrosome duplication	1	13	7.320530504	0.513293943	0.667361954	
GO:0060134	prepulse inhibition	1	13	7.320530504	0.513293943	0.667361954	
GO:0060445	branching involved in salivary gland mo	1	13	7.320530504	0.513293943	0.667361954	
GO:0060766	negative regulation of androgen receptor	1	13	7.320530504	0.513293943	0.667361954	
GO:0090179	planar cell polarity pathway involved in	1	13	7.320530504	0.513293943	0.667361954	

GO:0050679	positive regulation of epithelial cell prol	2	61	3.120226116	0.539475257	0.693960321	
GO:0001655	urogenital system development	1	14	6.797635468	0.549938651	0.693960321	
GO:0002092	positive regulation of receptor internaliz	1	14	6.797635468	0.549938651	0.693960321	
GO:0006103	2-oxoglutarate metabolic process	1	14	6.797635468	0.549938651	0.693960321	
GO:0006541	glutamine metabolic process	1	14	6.797635468	0.549938651	0.693960321	
GO:0006661	phosphatidylinositol biosynthetic proces	1	14	6.797635468	0.549938651	0.693960321	
GO:0006672	ceramide metabolic process	1	14	6.797635468	0.549938651	0.693960321	
GO:0006939	smooth muscle contraction	1	14	6.797635468	0.549938651	0.693960321	
GO:0007130	synaptonemal complex assembly	1	14	6.797635468	0.549938651	0.693960321	
GO:0007210	serotonin receptor signaling pathway	1	14	6.797635468	0.549938651	0.693960321	
GO:0007271	synaptic transmission, cholinergic	1	14	6.797635468	0.549938651	0.693960321	
GO:0007512	adult heart development	1	14	6.797635468	0.549938651	0.693960321	
GO:0007548	sex differentiation	1	14	6.797635468	0.549938651	0.693960321	
GO:0009967	positive regulation of signal transduction	1	14	6.797635468	0.549938651	0.693960321	
GO:0010524	positive regulation of calcium ion transp	1	14	6.797635468	0.549938651	0.693960321	
GO:0010800	positive regulation of peptidyl-threonine	1	14	6.797635468	0.549938651	0.693960321	
GO:0016079	synaptic vesicle exocytosis	1	14	6.797635468	0.549938651	0.693960321	
GO:0017144	drug metabolic process	1	14	6.797635468	0.549938651	0.693960321	
GO:0030048	actin filament-based movement	1	14	6.797635468	0.549938651	0.693960321	
GO:0030949	positive regulation of vascular endotheli	1	14	6.797635468	0.549938651	0.693960321	
GO:0031122	cytoplasmic microtubule organization	1	14	6.797635468	0.549938651	0.693960321	
GO:0031641	regulation of myelination	1	14	6.797635468	0.549938651	0.693960321	
GO:0032008	positive regulation of TOR signaling cas	1	14	6.797635468	0.549938651	0.693960321	
GO:0040015	negative regulation of multicellular orga	1	14	6.797635468	0.549938651	0.693960321	
GO:0042176	regulation of protein catabolic process	1	14	6.797635468	0.549938651	0.693960321	
GO:0042307	positive regulation of protein import into	1	14	6.797635468	0.549938651	0.693960321	
GO:0045725	positive regulation of glycogen biosynth	1	14	6.797635468	0.549938651	0.693960321	
GO:0045780	positive regulation of bone resorption	1	14	6.797635468	0.549938651	0.693960321	
GO:0046888	negative regulation of hormone secretion	1	14	6.797635468	0.549938651	0.693960321	
GO:0048490	anterograde synaptic vesicle transport	1	14	6.797635468	0.549938651	0.693960321	
GO:0048665	neuron fate specification	1	14	6.797635468	0.549938651	0.693960321	
GO:0048675	axon extension	1	14	6.797635468	0.549938651	0.693960321	
GO:0048870	cell motility	1	14	6.797635468	0.549938651	0.693960321	
GO:0050482	arachidonic acid secretion	1	14	6.797635468	0.549938651	0.693960321	
GO:0060037	pharyngeal system development	1	14	6.797635468	0.549938651	0.693960321	
GO:0061178	regulation of insulin secretion involved	1	14	6.797635468	0.549938651	0.693960321	
GO:0070527	platelet aggregation	1	14	6.797635468	0.549938651	0.693960321	
GO:0071542	dopaminergic neuron differentiation	1	14	6.797635468	0.549938651	0.693960321	

GO:0072001	renal system development	1	14	6.797635468	0.549938651	0.693960321	
GO:0030509	BMP signaling pathway	2	62	3.069899889	0.553770883	0.698269168	
GO:0050821	protein stabilization	2	64	2.973965517	0.582604722	0.730890618	
GO:0002063	chondrocyte development	1	15	6.34445977	0.586198755	0.730890618	
GO:0006171	cAMP biosynthetic process	1	15	6.34445977	0.586198755	0.730890618	
GO:0006855	drug transmembrane transport	1	15	6.34445977	0.586198755	0.730890618	
GO:0007141	male meiosis I	1	15	6.34445977	0.586198755	0.730890618	
GO:0007520	myoblast fusion	1	15	6.34445977	0.586198755	0.730890618	
GO:0008585	female gonad development	1	15	6.34445977	0.586198755	0.730890618	
GO:0010508	positive regulation of autophagy	1	15	6.34445977	0.586198755	0.730890618	
GO:0032012	regulation of ARF protein signal transduction	1	15	6.34445977	0.586198755	0.730890618	
GO:0033365	protein localization to organelle	1	15	6.34445977	0.586198755	0.730890618	
GO:0042445	hormone metabolic process	1	15	6.34445977	0.586198755	0.730890618	
GO:0043011	myeloid dendritic cell differentiation	1	15	6.34445977	0.586198755	0.730890618	
GO:0046513	ceramide biosynthetic process	1	15	6.34445977	0.586198755	0.730890618	
GO:0048566	embryonic digestive tract development	1	15	6.34445977	0.586198755	0.730890618	
GO:0090023	positive regulation of neutrophil chemotaxis	1	15	6.34445977	0.586198755	0.730890618	
GO:0030335	positive regulation of cell migration	3	129	2.213183641	0.619600182	0.763667323	
GO:0001706	endoderm formation	1	16	5.947931034	0.622078286	0.763667323	
GO:0006182	cGMP biosynthetic process	1	16	5.947931034	0.622078286	0.763667323	
GO:0007178	transmembrane receptor protein serine/threonine kinase activity	1	16	5.947931034	0.622078286	0.763667323	
GO:0007250	activation of NF-kappaB-inducing kinase activity	1	16	5.947931034	0.622078286	0.763667323	
GO:0007274	neuromuscular synaptic transmission	1	16	5.947931034	0.622078286	0.763667323	
GO:0010575	positive regulation vascular endothelial cell growth	1	16	5.947931034	0.622078286	0.763667323	
GO:0016339	calcium-dependent cell-cell adhesion	1	16	5.947931034	0.622078286	0.763667323	
GO:0032320	positive regulation of Ras GTPase activity	1	16	5.947931034	0.622078286	0.763667323	
GO:0032467	positive regulation of cytokinesis	1	16	5.947931034	0.622078286	0.763667323	
GO:0033198	response to ATP	1	16	5.947931034	0.622078286	0.763667323	
GO:0035136	forelimb morphogenesis	1	16	5.947931034	0.622078286	0.763667323	
GO:0043409	negative regulation of MAPK cascade	1	16	5.947931034	0.622078286	0.763667323	
GO:0048714	positive regulation of oligodendrocyte differentiation	1	16	5.947931034	0.622078286	0.763667323	
GO:0048747	muscle fiber development	1	16	5.947931034	0.622078286	0.763667323	
GO:0050870	positive regulation of T cell activation	1	16	5.947931034	0.622078286	0.763667323	
GO:0055008	cardiac muscle tissue morphogenesis	1	16	5.947931034	0.622078286	0.763667323	
GO:0060707	trophoblast giant cell differentiation	1	16	5.947931034	0.622078286	0.763667323	
GO:0072332	intrinsic apoptotic signaling pathway by caspase	1	16	5.947931034	0.622078286	0.763667323	
GO:0097192	extrinsic apoptotic signaling pathway in response to	1	16	5.947931034	0.622078286	0.763667323	
GO:2000311	regulation of alpha-amino-3-hydroxy-5-methyl-4-pyridine	1	16	5.947931034	0.622078286	0.763667323	

GO:0040008	regulation of growth	2	67	2.840802882	0.626413428	0.768424983	
GO:0000187	activation of MAPK activity	2	69	2.75846077	0.65595483	0.792700663	
GO:0001508	regulation of action potential	1	17	5.598052738	0.657581232	0.792700663	
GO:0001954	positive regulation of cell-matrix adhesion	1	17	5.598052738	0.657581232	0.792700663	
GO:0001964	startle response	1	17	5.598052738	0.657581232	0.792700663	
GO:0002028	regulation of sodium ion transport	1	17	5.598052738	0.657581232	0.792700663	
GO:0006783	heme biosynthetic process	1	17	5.598052738	0.657581232	0.792700663	
GO:0030100	regulation of endocytosis	1	17	5.598052738	0.657581232	0.792700663	
GO:0030539	male genitalia development	1	17	5.598052738	0.657581232	0.792700663	
GO:0032148	activation of protein kinase B activity	1	17	5.598052738	0.657581232	0.792700663	
GO:0032314	regulation of Rac GTPase activity	1	17	5.598052738	0.657581232	0.792700663	
GO:0035137	hindlimb morphogenesis	1	17	5.598052738	0.657581232	0.792700663	
GO:0042346	positive regulation of NF-kappaB import	1	17	5.598052738	0.657581232	0.792700663	
GO:0042462	eye photoreceptor cell development	1	17	5.598052738	0.657581232	0.792700663	
GO:0045671	negative regulation of osteoclast differentiation	1	17	5.598052738	0.657581232	0.792700663	
GO:0045807	positive regulation of endocytosis	1	17	5.598052738	0.657581232	0.792700663	
GO:0045987	positive regulation of smooth muscle contraction	1	17	5.598052738	0.657581232	0.792700663	
GO:0048041	focal adhesion assembly	1	17	5.598052738	0.657581232	0.792700663	
GO:0048546	digestive tract morphogenesis	1	17	5.598052738	0.657581232	0.792700663	
GO:0048565	digestive tract development	1	17	5.598052738	0.657581232	0.792700663	
GO:0048596	embryonic camera-type eye morphogenesis	1	17	5.598052738	0.657581232	0.792700663	
GO:0048738	cardiac muscle tissue development	1	17	5.598052738	0.657581232	0.792700663	
GO:0048854	brain morphogenesis	1	17	5.598052738	0.657581232	0.792700663	
GO:0050772	positive regulation of axonogenesis	1	17	5.598052738	0.657581232	0.792700663	
GO:0071260	cellular response to mechanical stimulus	1	17	5.598052738	0.657581232	0.792700663	
GO:0042254	ribosome biogenesis	2	70	2.719054187	0.6708172	0.808073746	
GO:0007596	blood coagulation	2	71	2.680757649	0.685736809	0.825451364	
GO:0006164	purine nucleotide biosynthetic process	1	18	5.287049808	0.692711541	0.826704994	
GO:0007584	response to nutrient	1	18	5.287049808	0.692711541	0.826704994	
GO:0018149	peptide cross-linking	1	18	5.287049808	0.692711541	0.826704994	
GO:0019915	lipid storage	1	18	5.287049808	0.692711541	0.826704994	
GO:0031290	retinal ganglion cell axon guidance	1	18	5.287049808	0.692711541	0.826704994	
GO:0048814	regulation of dendrite morphogenesis	1	18	5.287049808	0.692711541	0.826704994	
GO:0050890	cognition	1	18	5.287049808	0.692711541	0.826704994	
GO:0051145	smooth muscle cell differentiation	1	18	5.287049808	0.692711541	0.826704994	
GO:0051591	response to cAMP	1	18	5.287049808	0.692711541	0.826704994	
GO:0060045	positive regulation of cardiac muscle cell proliferation	1	18	5.287049808	0.692711541	0.826704994	
GO:0061098	positive regulation of protein tyrosine kinase activity	1	18	5.287049808	0.692711541	0.826704994	

GO:2000134	negative regulation of G1/S transition of	1	18	5.287049808	0.692711541	0.826704994	
GO:0006631	fatty acid metabolic process	3	139	2.053961796	0.721919583	0.856573983	
GO:0001659	temperature homeostasis	1	19	5.008784029	0.727473119	0.856573983	
GO:0006520	cellular amino acid metabolic process	1	19	5.008784029	0.727473119	0.856573983	
GO:0007163	establishment or maintenance of cell pol	1	19	5.008784029	0.727473119	0.856573983	
GO:0007610	behavior	1	19	5.008784029	0.727473119	0.856573983	
GO:0009880	embryonic pattern specification	1	19	5.008784029	0.727473119	0.856573983	
GO:0015807	L-amino acid transport	1	19	5.008784029	0.727473119	0.856573983	
GO:0015914	phospholipid transport	1	19	5.008784029	0.727473119	0.856573983	
GO:0021537	telencephalon development	1	19	5.008784029	0.727473119	0.856573983	
GO:0021772	olfactory bulb development	1	19	5.008784029	0.727473119	0.856573983	
GO:0030279	negative regulation of ossification	1	19	5.008784029	0.727473119	0.856573983	
GO:0030301	cholesterol transport	1	19	5.008784029	0.727473119	0.856573983	
GO:0030878	thyroid gland development	1	19	5.008784029	0.727473119	0.856573983	
GO:0042098	T cell proliferation	1	19	5.008784029	0.727473119	0.856573983	
GO:0045184	establishment of protein localization	1	19	5.008784029	0.727473119	0.856573983	
GO:0060395	SMAD protein signal transduction	1	19	5.008784029	0.727473119	0.856573983	
GO:0060749	mammary gland alveolus development	1	19	5.008784029	0.727473119	0.856573983	
GO:0070555	response to interleukin-1	1	19	5.008784029	0.727473119	0.856573983	
GO:2001238	positive regulation of extrinsic apoptotic	1	19	5.008784029	0.727473119	0.856573983	
GO:0001843	neural tube closure	2	74	2.572078285	0.730810945	0.859898593	
GO:0008033	tRNA processing	2	75	2.537783908	0.745931651	0.87707294	
GO:0001708	cell fate specification	1	20	4.758344828	0.761869831	0.886462323	
GO:0002026	regulation of the force of heart contracti	1	20	4.758344828	0.761869831	0.886462323	
GO:0006626	protein targeting to mitochondrion	1	20	4.758344828	0.761869831	0.886462323	
GO:0007031	peroxisome organization	1	20	4.758344828	0.761869831	0.886462323	
GO:0007259	JAK-STAT cascade	1	20	4.758344828	0.761869831	0.886462323	
GO:0030010	establishment of cell polarity	1	20	4.758344828	0.761869831	0.886462323	
GO:0030902	hindbrain development	1	20	4.758344828	0.761869831	0.886462323	
GO:0045216	cell-cell junction organization	1	20	4.758344828	0.761869831	0.886462323	
GO:0045638	negative regulation of myeloid cell diffe	1	20	4.758344828	0.761869831	0.886462323	
GO:0045672	positive regulation of osteoclast differen	1	20	4.758344828	0.761869831	0.886462323	
GO:0045859	regulation of protein kinase activity	1	20	4.758344828	0.761869831	0.886462323	
GO:0046329	negative regulation of JNK cascade	1	20	4.758344828	0.761869831	0.886462323	
GO:0051491	positive regulation of filopodium assembl	1	20	4.758344828	0.761869831	0.886462323	
GO:0071353	cellular response to interleukin-4	1	20	4.758344828	0.761869831	0.886462323	
GO:0071902	positive regulation of protein serine/thre	1	20	4.758344828	0.761869831	0.886462323	
GO:0035264	multicellular organism growth	2	77	2.471867443	0.776301191	0.902625585	

GO:0000060	protein import into nucleus, translocation	1	21	4.531756979	0.795905501	0.918394754	
GO:0000381	regulation of alternative mRNA splicing	1	21	4.531756979	0.795905501	0.918394754	
GO:0007585	respiratory gaseous exchange	1	21	4.531756979	0.795905501	0.918394754	
GO:0032715	negative regulation of interleukin-6 production	1	21	4.531756979	0.795905501	0.918394754	
GO:0045214	sarcomere organization	1	21	4.531756979	0.795905501	0.918394754	
GO:0045747	positive regulation of Notch signaling pathway	1	21	4.531756979	0.795905501	0.918394754	
GO:0045861	negative regulation of proteolysis	1	21	4.531756979	0.795905501	0.918394754	
GO:0050880	regulation of blood vessel size	1	21	4.531756979	0.795905501	0.918394754	
GO:0050918	positive chemotaxis	1	21	4.531756979	0.795905501	0.918394754	
GO:0070301	cellular response to hydrogen peroxide	1	21	4.531756979	0.795905501	0.918394754	
GO:0070371	ERK1 and ERK2 cascade	1	21	4.531756979	0.795905501	0.918394754	
GO:0008202	steroid metabolic process	2	79	2.40928852	0.806824614	0.929711065	
GO:0045666	positive regulation of neuron differentiation	2	79	2.40928852	0.806824614	0.929711065	
GO:0043065	positive regulation of apoptotic process	5	258	1.844319701	0.810154387	0.932905052	
GO:0007346	regulation of mitotic cell cycle	1	22	4.325768025	0.829583914	0.949393774	
GO:0015711	organic anion transport	1	22	4.325768025	0.829583914	0.949393774	
GO:0023019	signal transduction involved in regulation of gene expression	1	22	4.325768025	0.829583914	0.949393774	
GO:0030534	adult behavior	1	22	4.325768025	0.829583914	0.949393774	
GO:0042221	response to chemical stimulus	1	22	4.325768025	0.829583914	0.949393774	
GO:0042311	vasodilation	1	22	4.325768025	0.829583914	0.949393774	
GO:0051965	positive regulation of synapse assembly	1	22	4.325768025	0.829583914	0.949393774	
GO:0060173	limb development	1	22	4.325768025	0.829583914	0.949393774	
GO:0070509	calcium ion import	1	22	4.325768025	0.829583914	0.949393774	
GO:0002027	regulation of heart rate	1	23	4.137691154	0.862908814	0.978821938	
GO:0006378	mRNA polyadenylation	1	23	4.137691154	0.862908814	0.978821938	
GO:0006611	protein export from nucleus	1	23	4.137691154	0.862908814	0.978821938	
GO:0030318	melanocyte differentiation	1	23	4.137691154	0.862908814	0.978821938	
GO:0033344	cholesterol efflux	1	23	4.137691154	0.862908814	0.978821938	
GO:0043029	T cell homeostasis	1	23	4.137691154	0.862908814	0.978821938	
GO:0048568	embryonic organ development	1	23	4.137691154	0.862908814	0.978821938	
GO:0048873	homeostasis of number of cells within a tissue	1	23	4.137691154	0.862908814	0.978821938	
GO:0050905	neuromuscular process	1	23	4.137691154	0.862908814	0.978821938	
GO:0051017	actin filament bundle assembly	1	23	4.137691154	0.862908814	0.978821938	
GO:0051899	membrane depolarization	1	23	4.137691154	0.862908814	0.978821938	
GO:0071300	cellular response to retinoic acid	1	23	4.137691154	0.862908814	0.978821938	
GO:0071356	cellular response to tumor necrosis factor	1	23	4.137691154	0.862908814	0.978821938	
GO:0010951	negative regulation of endopeptidase activity	2	83	2.29317823	0.868255175	0.984218747	
GO:0070374	positive regulation of ERK1 and ERK2 cascade	2	84	2.265878489	0.883679161	1	

GO:0006184	GTP catabolic process	3	155	1.841939933	0.893847792	1	
GO:0000045	autophagic vacuole assembly	1	24	3.965287356	0.895883907	1	
GO:0001662	behavioral fear response	1	24	3.965287356	0.895883907	1	
GO:0006928	cellular component movement	1	24	3.965287356	0.895883907	1	
GO:0007568	aging	1	24	3.965287356	0.895883907	1	
GO:0010718	positive regulation of epithelial to mesen	1	24	3.965287356	0.895883907	1	
GO:0030177	positive regulation of Wnt receptor signa	1	24	3.965287356	0.895883907	1	
GO:0042474	middle ear morphogenesis	1	24	3.965287356	0.895883907	1	
GO:0045071	negative regulation of viral genome repl	1	24	3.965287356	0.895883907	1	
GO:0045494	photoreceptor cell maintenance	1	24	3.965287356	0.895883907	1	
GO:0046488	phosphatidylinositol metabolic process	1	24	3.965287356	0.895883907	1	
GO:0046854	phosphatidylinositol phosphorylation	1	24	3.965287356	0.895883907	1	
GO:0048468	cell development	1	24	3.965287356	0.895883907	1	
GO:0060326	cell chemotaxis	1	24	3.965287356	0.895883907	1	
GO:0060349	bone morphogenesis	1	24	3.965287356	0.895883907	1	
GO:0007154	cell communication	2	85	2.239221095	0.899125206	1	
GO:0001824	blastocyst development	1	25	3.806675862	0.928512861	1	
GO:0006637	acyl-CoA metabolic process	1	25	3.806675862	0.928512861	1	
GO:0006644	phospholipid metabolic process	1	25	3.806675862	0.928512861	1	
GO:0009966	regulation of signal transduction	1	25	3.806675862	0.928512861	1	
GO:0015991	ATP hydrolysis coupled proton transpor	1	25	3.806675862	0.928512861	1	
GO:0016571	histone methylation	1	25	3.806675862	0.928512861	1	
GO:0031016	pancreas development	1	25	3.806675862	0.928512861	1	
GO:0045909	positive regulation of vasodilation	1	25	3.806675862	0.928512861	1	
GO:0046627	negative regulation of insulin receptor si	1	25	3.806675862	0.928512861	1	
GO:0048015	phosphatidylinositol-mediated signaling	1	25	3.806675862	0.928512861	1	
GO:0050769	positive regulation of neurogenesis	1	25	3.806675862	0.928512861	1	
GO:0032496	response to lipopolysaccharide	2	87	2.187744748	0.930074862	1	
GO:0006281	DNA repair	5	291	1.635170044	0.957095559	1	
GO:0006937	regulation of muscle contraction	1	26	3.660265252	0.960799302	1	
GO:0007631	feeding behavior	1	26	3.660265252	0.960799302	1	
GO:0031663	lipopolysaccharide-mediated signaling p	1	26	3.660265252	0.960799302	1	
GO:0034599	cellular response to oxidative stress	1	26	3.660265252	0.960799302	1	
GO:0035249	synaptic transmission, glutamatergic	1	26	3.660265252	0.960799302	1	
GO:0045595	regulation of cell differentiation	1	26	3.660265252	0.960799302	1	
GO:0045931	positive regulation of mitotic cell cycle	1	26	3.660265252	0.960799302	1	
GO:0006917	induction of apoptosis	3	162	1.762349936	0.971445197	1	
GO:0001654	eye development	1	27	3.524699872	0.992746823	1	

GO:0006099	tricarboxylic acid cycle	1	27	3.524699872	0.992746823	1	
GO:0007040	lysosome organization	1	27	3.524699872	0.992746823	1	
GO:0030282	bone mineralization	1	27	3.524699872	0.992746823	1	
GO:0050796	regulation of insulin secretion	1	27	3.524699872	0.992746823	1	
GO:0050853	B cell receptor signaling pathway	1	27	3.524699872	0.992746823	1	
GO:0051928	positive regulation of calcium ion transp	1	27	3.524699872	0.992746823	1	
GO:0006730	one-carbon metabolic process	1	28	3.398817734	1	1	
GO:0007205	protein kinase C-activating G-protein co	1	28	3.398817734	1	1	
GO:0007257	activation of JUN kinase activity	1	28	3.398817734	1	1	
GO:0007265	Ras protein signal transduction	1	28	3.398817734	1	1	
GO:0007416	synapse assembly	1	28	3.398817734	1	1	
GO:0008277	regulation of G-protein coupled receptor	1	28	3.398817734	1	1	
GO:0015758	glucose transport	1	28	3.398817734	1	1	
GO:0031623	receptor internalization	1	28	3.398817734	1	1	
GO:0048863	stem cell differentiation	1	28	3.398817734	1	1	
GO:0007162	negative regulation of cell adhesion	1	29	3.281617122	1	1	
GO:0007595	lactation	1	29	3.281617122	1	1	
GO:0009725	response to hormone stimulus	1	29	3.281617122	1	1	
GO:0010595	positive regulation of endothelial cell mi	1	29	3.281617122	1	1	
GO:0030513	positive regulation of BMP signaling pat	1	29	3.281617122	1	1	
GO:0031647	regulation of protein stability	1	29	3.281617122	1	1	
GO:0034644	cellular response to UV	1	29	3.281617122	1	1	
GO:0045599	negative regulation of fat cell differentia	1	29	3.281617122	1	1	
GO:0045840	positive regulation of mitosis	1	29	3.281617122	1	1	
GO:0048701	embryonic cranial skeleton morphogene	1	29	3.281617122	1	1	
GO:0050873	brown fat cell differentiation	1	29	3.281617122	1	1	
GO:0051384	response to glucocorticoid stimulus	1	29	3.281617122	1	1	
GO:0055010	ventricular cardiac muscle tissue morpho	1	29	3.281617122	1	1	
GO:0071310	cellular response to organic substance	1	29	3.281617122	1	1	
GO:0042981	regulation of apoptotic process	3	170	1.679415822	1	1	
GO:0006955	immune response	3	171	1.669594676	1	1	
GO:0006364	rRNA processing	2	97	1.962204053	1	1	
GO:0000079	regulation of cyclin-dependent protein se	1	30	3.172229885	1	1	
GO:0002062	chondrocyte differentiation	1	30	3.172229885	1	1	
GO:0006289	nucleotide-excision repair	1	30	3.172229885	1	1	
GO:0006953	acute-phase response	1	30	3.172229885	1	1	
GO:0007157	heterophilic cell-cell adhesion	1	30	3.172229885	1	1	
GO:0008306	associative learning	1	30	3.172229885	1	1	

GO:0030838	positive regulation of actin filament polymerization	1	30	3.172229885	1	1	
GO:0071407	cellular response to organic cyclic compound	1	30	3.172229885	1	1	
GO:0006979	response to oxidative stress	2	98	1.942181562	1	1	
GO:0006605	protein targeting	1	31	3.069899889	1	1	
GO:0006879	cellular iron ion homeostasis	1	31	3.069899889	1	1	
GO:0006958	complement activation, classical pathway	1	31	3.069899889	1	1	
GO:0030879	mammary gland development	1	31	3.069899889	1	1	
GO:0031069	hair follicle morphogenesis	1	31	3.069899889	1	1	
GO:0042110	T cell activation	1	31	3.069899889	1	1	
GO:0045776	negative regulation of blood pressure	1	31	3.069899889	1	1	
GO:0000086	G2/M transition of mitotic cell cycle	1	32	2.973965517	1	1	
GO:0001707	mesoderm formation	1	32	2.973965517	1	1	
GO:0009987	cellular process	1	32	2.973965517	1	1	
GO:0010811	positive regulation of cell-substrate adhesion	1	32	2.973965517	1	1	
GO:0021915	neural tube development	1	32	2.973965517	1	1	
GO:0031424	keratinization	1	32	2.973965517	1	1	
GO:0035115	embryonic forelimb morphogenesis	1	32	2.973965517	1	1	
GO:0045429	positive regulation of nitric oxide biosynthesis	1	32	2.973965517	1	1	
GO:0045907	positive regulation of vasoconstriction	1	32	2.973965517	1	1	
GO:0048167	regulation of synaptic plasticity	1	32	2.973965517	1	1	
GO:0050715	positive regulation of cytokine secretion	1	32	2.973965517	1	1	
GO:0001755	neural crest cell migration	1	33	2.88384535	1	1	
GO:0006641	triglyceride metabolic process	1	33	2.88384535	1	1	
GO:0007565	female pregnancy	1	33	2.88384535	1	1	
GO:0030073	insulin secretion	1	33	2.88384535	1	1	
GO:0030593	neutrophil chemotaxis	1	33	2.88384535	1	1	
GO:0048662	negative regulation of smooth muscle cell proliferation	1	33	2.88384535	1	1	
GO:0005977	glycogen metabolic process	1	34	2.799026369	1	1	
GO:0008543	fibroblast growth factor receptor signaling	1	34	2.799026369	1	1	
GO:0040014	regulation of multicellular organism growth	1	34	2.799026369	1	1	
GO:0040018	positive regulation of multicellular organism growth	1	34	2.799026369	1	1	
GO:0043627	response to estrogen stimulus	1	34	2.799026369	1	1	
GO:0060325	face morphogenesis	1	34	2.799026369	1	1	
GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB activation	2	105	1.812702791	1	1	
GO:0006749	glutathione metabolic process	1	35	2.719054187	1	1	
GO:0006898	receptor-mediated endocytosis	1	35	2.719054187	1	1	
GO:0032436	positive regulation of proteasomal ubiquitination	1	35	2.719054187	1	1	
GO:0033077	T cell differentiation in thymus	1	35	2.719054187	1	1	

GO:0045597	positive regulation of cell differentiation	1	35	2.719054187	1	1	
GO:0006606	protein import into nucleus	1	36	2.643524904	1	1	
GO:0007188	adenylate cyclase-modulating G-protein	1	36	2.643524904	1	1	
GO:0007492	endoderm development	1	36	2.643524904	1	1	
GO:0007623	circadian rhythm	1	36	2.643524904	1	1	
GO:0030855	epithelial cell differentiation	1	36	2.643524904	1	1	
GO:0031047	gene silencing by RNA	1	36	2.643524904	1	1	
GO:0032313	regulation of Rab GTPase activity	1	36	2.643524904	1	1	
GO:0045785	positive regulation of cell adhesion	1	36	2.643524904	1	1	
GO:0048666	neuron development	1	36	2.643524904	1	1	
GO:0048754	branching morphogenesis of an epithelium	1	36	2.643524904	1	1	
GO:0009952	anterior/posterior pattern specification	2	109	1.746181588	1	1	
GO:0006935	chemotaxis	2	110	1.73030721	1	1	
GO:0007601	visual perception	2	110	1.73030721	1	1	
GO:0006139	nucleobase-containing compound metabolism	1	37	2.572078285	1	1	
GO:0007566	embryo implantation	1	37	2.572078285	1	1	
GO:0040007	growth	1	37	2.572078285	1	1	
GO:0043547	positive regulation of GTPase activity	1	37	2.572078285	1	1	
GO:0048538	thymus development	1	37	2.572078285	1	1	
GO:0032092	positive regulation of protein binding	1	38	2.504392015	1	1	
GO:0050766	positive regulation of phagocytosis	1	38	2.504392015	1	1	
GO:0045727	positive regulation of translation	1	39	2.440176835	1	1	
GO:0045732	positive regulation of protein catabolic process	1	39	2.440176835	1	1	
GO:0006950	response to stress	2	116	1.640808561	1	1	
GO:0000398	mRNA splicing, via spliceosome	1	40	2.379172414	1	1	
GO:0001569	patterning of blood vessels	1	40	2.379172414	1	1	
GO:0006986	response to unfolded protein	1	41	2.321143818	1	1	
GO:0007005	mitochondrion organization	1	41	2.321143818	1	1	
GO:0032755	positive regulation of interleukin-6 production	1	41	2.321143818	1	1	
GO:0035019	somatic stem cell maintenance	1	41	2.321143818	1	1	
GO:0071363	cellular response to growth factor stimulus	1	41	2.321143818	1	1	
GO:0030218	erythrocyte differentiation	1	42	2.265878489	1	1	
GO:0051607	defense response to virus	2	121	1.573006555	1	1	
GO:0007599	hemostasis	1	43	2.213183641	1	1	
GO:0016485	protein processing	1	43	2.213183641	1	1	
GO:0043473	pigmentation	1	43	2.213183641	1	1	
GO:0006260	DNA replication	2	123	1.547429212	1	1	
GO:0031398	positive regulation of protein ubiquitination	1	44	2.162884013	1	1	

GO:0032526	response to retinoic acid	1	44	2.162884013	1	1	
GO:0043406	positive regulation of MAP kinase activi	1	44	2.162884013	1	1	
GO:0042787	protein ubiquitination involved in ubiqu	1	46	2.068845577	1	1	
GO:0045668	negative regulation of osteoblast differ	1	46	2.068845577	1	1	
GO:0006302	double-strand break repair	1	47	2.024827586	1	1	
GO:0007224	smoothened signaling pathway	1	48	1.982643678	1	1	
GO:0007368	determination of left/right symmetry	1	48	1.982643678	1	1	
GO:0045860	positive regulation of protein kinase acti	1	48	1.982643678	1	1	
GO:0042632	cholesterol homeostasis	1	49	1.942181562	1	1	
GO:0050680	negative regulation of epithelial cell pro	1	49	1.942181562	1	1	
GO:0051259	protein oligomerization	1	49	1.942181562	1	1	
GO:0007166	cell surface receptor signaling pathway	2	132	1.441922675	1	1	
GO:0000082	G1/S transition of mitotic cell cycle	1	50	1.903337931	1	1	
GO:0010033	response to organic substance	1	50	1.903337931	1	1	
GO:0019827	stem cell maintenance	1	50	1.903337931	1	1	
GO:0003007	heart morphogenesis	1	53	1.795601822	1	1	
GO:0006469	negative regulation of protein kinase act	1	54	1.762349936	1	1	
GO:0008217	regulation of blood pressure	1	54	1.762349936	1	1	
GO:0060041	retina development in camera-type eye	1	56	1.699408867	1	1	
GO:0043085	positive regulation of catalytic activity	1	57	1.669594676	1	1	
GO:0006869	lipid transport	1	59	1.612998247	1	1	
GO:0007286	spermatid development	1	59	1.612998247	1	1	
GO:0018108	peptidyl-tyrosine phosphorylation	1	59	1.612998247	1	1	
GO:0043161	proteasomal ubiquitin-dependent protein	1	59	1.612998247	1	1	
GO:0051289	protein homotetramerization	1	59	1.612998247	1	1	
GO:0045165	cell fate commitment	1	62	1.534949944	1	1	
GO:0007267	cell-cell signaling	1	63	1.51058566	1	1	
GO:0006954	inflammatory response	3	214	1.334115372	1	1	
GO:0030162	regulation of proteolysis	1	66	1.441922675	1	1	
GO:0043010	camera-type eye development	1	66	1.441922675	1	1	
GO:0006633	fatty acid biosynthetic process	1	67	1.420401441	1	1	
GO:0060021	palate development	1	68	1.399513185	1	1	
GO:0006919	activation of cysteine-type endopeptidas	1	71	1.340378825	1	1	
GO:0018105	peptidyl-serine phosphorylation	1	74	1.286039143	1	1	
GO:0051091	positive regulation of sequence-specific	1	76	1.252196007	1	1	
GO:0006310	DNA recombination	1	78	1.220088417	1	1	
GO:0007243	intracellular protein kinase cascade	1	78	1.220088417	1	1	
GO:0019221	cytokine-mediated signaling pathway	1	79	1.20464426	1	1	

GO:0022900	electron transport chain	1	91	1.045790072	1	1	
GO:0045766	positive regulation of angiogenesis	1	92	1.034422789	1	1	
GO:0045087	innate immune response	2	180	1.057409962	1	1	
GO:0007186	G-protein coupled receptor signaling pat	20	1850	1.028831314	1	1	
GO:0071222	cellular response to lipopolysaccharide	1	98	0.971090781	1	1	
GO:0030182	neuron differentiation	1	100	0.951668966	1	1	