Supplement Table 3.
D90 to D135
Down Regulated

Class	GO ID	GO Description	Direction of c	GO Description and ID	Class	Size	Size in data	% in data	FDR.adj.pval
BIOLOGICAL PROCESS									
	GO:0030198	extracellular matrix organization	down	extracellular matrix organization (GO:0030198)	BP	140	134	0.02238806	4.44089E-16
	GO:0043062	extracellular structure organization	down	extracellular structure organization (GO:0043062)	BP	140	134	0.02238806	4.44089E-16
	GO:0030199	collagen fibril organization	down	collagen fibril organization (GO:0030199)	BP	24	23	0.086956522	5.15576E-10
	GO:0022612	gland morphogenesis	down	gland morphogenesis (GO:0022612)	BP	102	98	0.020408163	1.46103E-09
	GO:0043542	endothelial cell migration	down	endothelial cell migration (GO:0043542)	BP	112	108	0.018518519	2.72726E-09
	GO:0010631	epithelial cell migration	down	epithelial cell migration (GO:0010631)	BP	167	161	0.01242236	6.38758E-09
	GO:0034329	cell junction assembly	down	cell junction assembly (GO:0034329)	BP	117	113	0	7.28635E-09
	GO:0090132	epithelium migration	down	epithelium migration (GO:0090132)	BP	169	163	0.012269939	7.28635E-09
	GO:0048762	mesenchymal cell differentiation	down	mesenchymal cell differentiation (GO:0048762)	BP	127	126	0.007936508	7.28635E-09
	GO:0097485	neuron projection guidance	down	neuron projection guidance (GO:0097485)	BP	128	125	0	7.28635E-09
	GO:1905330	regulation of morphogenesis of an epithelium	down	regulation of morphogenesis of an epithelium (GO:1905330)	BP	82	79	0	7.28635E-09
	GO:0090130	tissue migration	down	tissue migration (GO:0090130)	BP	173	167	0.011976048	7.28635E-09
	GO:0007411	axon guidance	down	axon guidance (GO:0007411)	BP	126	123	0	9.7432E-09
	GO:0001945	lymph vessel development	down	lymph vessel development (GO:0001945)	BP	17	16	0.0625	9.7432E-09
	GO:0060485	mesenchyme development	down	mesenchyme development (GO:0060485)	BP	157	156	0.006410256	1.05852E-08
	GO:0014031	mesenchymal cell development	down	mesenchymal cell development (GO:0014031)	BP	45	44	0	1.22719E-08
	GO:0034330	cell junction organization	down	cell junction organization (GO:0034330)	BP	148	141	0	1.48117E-08
	GO:0010810	regulation of cell-substrate adhesion	down	regulation of cell-substrate adhesion (GO:0010810)	BP	124	119	0.016806723	2.53311E-08
	GO:0060219	camera-type eye photoreceptor cell differentiation	down	camera-type eye photoreceptor cell differentiation (GO:0060219)	BP	12	12	0	2.64876E-08
	GO:0007160	cell-matrix adhesion	down	cell-matrix adhesion (GO:0007160)	BP	127	126	0	2.70126E-08
	GO:0002063	chondrocyte development	down	chondrocyte development (GO:0002063)	BP	24	23	0	2.77281E-08
	GO:0035272	exocrine system development	down	exocrine system development (GO:0035272)	BP	40	40	0.025	2.77281E-08
	GO:0018212	peptidyl-tyrosine modification	down	peptidyl-tyrosine modification (GO:0018212)	BP	186	184	0	2.77281E-08
	GO:0018108	peptidyl-tyrosine phosphorylation	down	peptidyl-tyrosine phosphorylation (GO:0018108)	BP	184	182	0	3.21054E-08
	GO:0045216	cell-cell junction organization	down	cell-cell junction organization (GO:0045216)	BP	134	129	0	3.40338E-08
	GO:0045992	negative regulation of embryonic development	down	negative regulation of embryonic development (GO:0045992)	BP	21	20	0.05	3.40338E-08
	GO:0002062	chondrocyte differentiation	down	chondrocyte differentiation (GO:0002062)	BP	71	68	0	4.30505E-08
	GO:0014032	neural crest cell development	down	neural crest cell development (GO:0014032)	BP	42	41	0	4.30505E-08
	GO:0071526	semaphorin-plexin signaling pathway	down	semaphorin-plexin signaling pathway (GO:0071526)	BP	22	22	0.045454545	4.77953E-08
	GO:0036303	lymph vessel morphogenesis	down	lymph vessel morphogenesis (GO:0036303)	BP	12	12	0.083333333	5.00775E-08
	GO:0048864	stem cell development	down	stem cell development (GO:0048864)	BP	44	42	0	5.20044E-08
	GO:0060071	Wnt signaling pathway, planar cell polarity pathway	down	Wnt signaling pathway, planar cell polarity pathway (GO:0060071)	BP	29	28	0	5.26366E-08
	GO:0090090	negative regulation of canonical Wnt signaling pathway	down	negative regulation of canonical Wnt signaling pathway (GO:0090090)	BP	77	76	0	5.71598E-08
	GO:0061448	connective tissue development	down	connective tissue development (GO:0061448)	BP	158	153	0.013071895	5.9675E-08
	GO:0001763	morphogenesis of a branching structure	down	morphogenesis of a branching structure (GO:0001763)	BP	163	157	0.006369427	6.66401E-08
	GO:0051216	cartilage development	down	cartilage development (GO:0051216)	BP	126	121	0.008264463	7.59717E-08
	GO:0010811	positive regulation of cell-substrate adhesion	down	positive regulation of cell-substrate adhesion (GO:0010811)	BP	73	69	0.014492754	7.59717E-08
	GO:0097061	dendritic spine organization	down	dendritic spine organization (GO:0097061)	BP	29	28	0	8.43374E-08
	GO:0106027	neuron projection organization	down	neuron projection organization (GO:0106027)	BP	29	28	0	8.43374E-08
	GO:0090177	establishment of planar polarity involved in neural tube c	down	establishment of planar polarity involved in neural tube closure (GO:009	BP	14	13	0	9.1339E-08
	GO:0032467	positive regulation of cytokinesis	down	positive regulation of cytokinesis (GO:0032467)	BP	25	24	0.125	9.1339E-08
	GO:0001502	cartilage condensation	down	cartilage condensation (GO:0001502)	BP	16	15	0	1.01904E-07
	GO:0098743	cell aggregation	down	cell aggregation (GO:0098743)	BP	16	15	0	1.01904E-07
	GO:0061138	morphogenesis of a branching epithelium	down	morphogenesis of a branching epithelium (GO:0061138)	BP	153	147	0.006802721	1.09405E-07
	GO:0090175	regulation of establishment of planar polarity	down	regulation of establishment of planar polarity (GO:0090175)	BP	30	29	0	1.09405E-07
	GO:0007435	salivary gland morphogenesis	down	salivary gland morphogenesis (GO:0007435)	BP	31	31	0.032258065	1.31081E-07
	GO:0060445	branching involved in salivary gland morphogenesis	down	branching involved in salivary gland morphogenesis (GO:0060445)	BP	20	20	0.05	1.37657E-07
	GO:0001946	lymphangiogenesis	down	lymphangiogenesis (GO:0001946)	BP	11	11	0.090909091	1.48813E-07
	GO:0048863	stem cell differentiation	down	stem cell differentiation (GO:0048863)	BP	112	106	0	1.56942E-07
	GO:0048013	ephrin receptor signaling pathway	down	ephrin receptor signaling pathway (GO:0048013)	BP	26	26	0	1.61006E-07
	GO:0060070	canonical Wnt signaling pathway	down	canonical Wnt signaling pathway (GO:0060070)	BP	171	167	0.005988024	1.73993E-07
	GO:0014033	neural crest cell differentiation	down	neural crest cell differentiation (GO:0014033)	BP	49	48	0	1.73993E-07
	GO:0090179	planar cell polarity pathway involved in neural tube closu	down	planar cell polarity pathway involved in neural tube closure (GO:009017	BP	12	11	0	1.73993E-07
	GO:0060348	bone development	down	bone development (GO:0060348)	BP	140	132	0.007575758	2.24527E-07
	GO:0001822	kidney development	down	kidney development (GO:0001822)	BP	189	186	0	2.35735E-07
	GO:0097205	renal filtration	down	renal filtration (GO:0097205)	BP	11	11	0	2.37294E-07
	GO:0007044	cell-substrate junction assembly	down	cell-substrate junction assembly (GO:0007044)	BP	51	49	0	2.57577E-07
	GO:0010632	regulation of epithelial cell migration	down	regulation of epithelial cell migration (GO:0010632)	BP	126	123	0.008130081	2.66083E-07

GO:0032330	regulation of chondrocyte differentiation	down	regulation of chondrocyte differentiation (GO:0032330)	BP	32	30	0	2.70206E-07
GO:0090109	regulation of cell-substrate junction assembly	down	regulation of cell-substrate junction assembly (GO:0090109)	BP	35	35	0	2.89189E-07
GO:0051893	regulation of focal adhesion assembly	down	regulation of focal adhesion assembly (GO:0051893)	BP	35	35	0	2.89189E-07
GO:0042249	establishment of planar polarity of embryonic epithelium	down	establishment of planar polarity of embryonic epithelium (GO:0042249)	BP	15	14	0	3.99153E-07
GO:1903391	regulation of adherens junction organization	down	regulation of adherens junction organization (GO:1903391)	BP	36	36	0	3.99153E-07
GO:0051056	regulation of small GTPase mediated signal transduction	down	regulation of small GTPase mediated signal transduction (GO:0051056)	BP	173	166	0.012048193	3.99153E-07
GO:0008589	regulation of smoothened signaling pathway	down	regulation of smoothened signaling pathway (GO:0008589)	BP	49	48	0	5.05063E-07
GO:0030278	regulation of ossification	down	regulation of ossification (GO:0030278)	BP	136	130	0	5.40685E-07
GO:0034332	adherens junction organization	down	adherens junction organization (GO:0034332)	BP	57	55	0	5.50273E-07
GO:0021915	neural tube development	down	neural tube development (GO:0021915)	BP	132	130	0	6.48659E-07
GO:0032835	glomerulus development	down	glomerulus development (GO:0032835)	BP	40	40	0	8.75073E-07
GO:0050730	regulation of peptidyl-tyrosine phosphorylation	down	regulation of peptidyl-tyrosine phosphorylation (GO:0050730)	BP	110	109	0	8.75073E-07
GO:0031295	T cell costimulation	down	T cell costimulation (GO:0031295)	BP	21	21	0	9.09201E-07
GO:0003203	endocardial cushion morphogenesis	down	endocardial cushion morphogenesis (GO:0003203)	BP	24	24	0	9.10609E-07
GO:0003197	endocardial cushion development	down	endocardial cushion development (GO:0003197)	BP	32	32	0	9.26064E-07
GO:1901888	regulation of cell junction assembly	down	regulation of cell junction assembly (GO:1901888)	BP	54	54	0	9.665E-07
GO:0072006	nephron development	down	nephron development (GO:0072006)	BP	101	100	0	9.79308E-07
GO:0007416	synapse assembly	down	synapse assembly (GO:0007416)	BP	83	79	0.037974684	9.79308E-07
GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecu	down	cell-cell adhesion via plasma-membrane adhesion molecules (GO:009874	BP	108	94	0.010638298	1.01195E-06
GO:0061037	negative regulation of cartilage development	down	negative regulation of cartilage development (GO:0061037)	BP	20	19	0	1.01204E-06
GO:0007431	salivary gland development	down	salivary gland development (GO:0007431)	BP	33	33	0.03030303	1.01204E-06
GO:0034333	adherens junction assembly	down	adherens junction assembly (GO:0034333)	BP	49	48	0	1.01524E-06
GO:0048754	branching morphogenesis of an epithelial tube	down	branching morphogenesis of an epithelial tube (GO:0048754)	BP	122	117	0.008547009	1.11055E-06
GO:0035567	non-canonical Wnt signaling pathway	down	non-canonical Wnt signaling pathway (GO:0035567)	BP	38	35	0	1.1115E-06
GO:0035987	endodermal cell differentiation	down	endodermal cell differentiation (GO:0035987)	BP	39	38	0.026315789	1.14505E-06
GO:0042063	gliogenesis	down	gliogenesis (GO:0042063)	BP	139	135	0	1.14505E-06
GO:0016525	negative regulation of angiogenesis	down	negative regulation of angiogenesis (GO:0016525)	BP	49	48	0.020833333	1.14505E-06
GO:0032331	negative regulation of chondrocyte differentiation	down	negative regulation of chondrocyte differentiation (GO:0032331)	BP	16	15	0	1.14505E-06
GO:0002691	regulation of cellular extravasation	down	regulation of cellular extravasation (GO:0002691)	BP	13	13	0	1.14505E-06
GO:0090178	regulation of establishment of planar polarity involved in	down	regulation of establishment of planar polarity involved in neural tube clo	BP	13	12	0	1.14505E-06
GO:0030111	regulation of Wnt signaling pathway	down	regulation of Wnt signaling pathway (GO:0030111)	BP	176	172	0.005813953	1.14505E-06
GO:0007229	integrin-mediated signaling pathway	down	integrin-mediated signaling pathway (GO:0007229)	BP	66	64	0	1.1821E-06
GO:0003007	heart morphogenesis	down	heart morphogenesis (GO:0003007)	BP	169	168	0.017857143	1.29411E-06
GO:0060828	regulation of canonical Wnt signaling pathway	down	regulation of canonical Wnt signaling pathway (GO:0060828)	BP	133	129	0.007751938	1.30236E-06
GO:0001837	epithelial to mesenchymal transition	down	epithelial to mesenchymal transition (GO:0001837)	BP	80	80	0.0125	1.30331E-06
GO:2000027	regulation of organ morphogenesis	down	regulation of organ morphogenesis (GO:2000027)	BP	132	129	0	1.30331E-06
GO:0032963	collagen metabolic process	down	collagen metabolic process (GO:0032963)	BP	32	32	0.0625	1.31161E-06
GO:0060412	ventricular septum morphogenesis	down	ventricular septum morphogenesis (GO:0060412)	BP	27	27	0	1.31161E-06
GO:0061035	regulation of cartilage development	down	regulation of cartilage development (GO:0061035)	BP	47	45	0	1.39459E-06
GO:0007224	smoothened signaling pathway	down	smoothened signaling pathway (GO:0007224)	BP	95	93	0	1.40797E-06
GO:0032964	collagen biosynthetic process	down	collagen biosynthetic process (GO:0032964)	BP	14	14	0.142857143	1.46639E-06
GO:0001736	establishment of planar polarity	down	establishment of planar polarity (GO:0001736)	BP	39	36	0	1.46639E-06
GO:0007164	establishment of tissue polarity	down	establishment of tissue polarity (GO:0007164)	BP	39	36	0	1.46639E-06
GO:1901342	regulation of vasculature development	down	regulation of vasculature development (GO:1901342)	BP	152	148	0.013513514	1.46639E-06
GO:0098815	modulation of excitatory postsynaptic potential	down	modulation of excitatory postsynaptic potential (GO:0098815)	BP	16	15	0	1.49723E-06
GO:0044259	multicellular organismal macromolecule metabolic proce	down	multicellular organismal macromolecule metabolic process (GO:004425	BP	33	33	0.060606061	1.62514E-06
GO:0034508	centromere complex assembly	down	centromere complex assembly (GO:0034508)	BP	17	17	0.058823529	1.71182E-06
GO:0001738	morphogenesis of a polarized epithelium	down	morphogenesis of a polarized epithelium (GO:0001738)	BP	47	44	0	1.71391E-06
GO:0001952	regulation of cell-matrix adhesion	down	regulation of cell-matrix adhesion (GO:0001952)	BP	65	65	0	1.71561E-06
GO:0030178	negative regulation of Wnt signaling pathway	down	negative regulation of Wnt signaling pathway (GO:0030178)	BP	96	94	0	1.79159E-06
GO:0060351	cartilage development involved in endochondral bone mo	down	cartilage development involved in endochondral bone morphogenesis (G	BP	19	19	0.052631579	1.81378E-06
GO:0007043	cell-cell junction assembly	down	cell-cell junction assembly (GO:0007043)	BP	59	58	0	1.85834E-06
GO:0003279	cardiac septum development	down	cardiac septum development (GO:0003279)	BP	75	74	0.013513514	1.97186E-06
GO:0072132	mesenchyme morphogenesis	down	mesenchyme morphogenesis (GO:0072132)	BP	37	37	0	1.97841E-06
GO:0060350	endochondral bone morphogenesis	down	endochondral bone morphogenesis (GO:0060350)	BP	40	38	0.026315789	2.00127E-06
GO:0060026	convergent extension	down	convergent extension (GO:0060026)	BP	12	12	0	2.02742E-06
GO:1901343	negative regulation of vasculature development	down	negative regulation of vasculature development (GO:1901343)	BP	54	53	0.018867925	2.11013E-06
GO:0035641	locomotory exploration behavior	down	locomotory exploration behavior (GO:0035641)	BP	11	10	0	2.1166E-06
GO:0003094	glomerular filtration	down	glomerular filtration (GO:0003094)	BP	10	10	0	2.41759E-06
GO:0045995	regulation of embryonic development	down	regulation of embryonic development (GO:0045995)	BP	88	84	0.011904762	2.41759E-06
GO:0031294	lymphocyte costimulation	down	lymphocyte costimulation (GO:0031294)	BP	22	22	0	2.45816E-06
GO:0003158	endothelium development	down	endothelium development (GO:0003158)	BP	72	71	0	2.5566E-06
GO:0072073	kidney epithelium development	down	kidney epithelium development (GO:0072073)	BP	110	109	0	2.5775E-06
GO:0045765	regulation of angiogenesis	down	regulation of angiogenesis (GO:0045765)	BP	140	136	0.014705882	2.62927E-06

GO:0045123	cellular extravasation	down	cellular extravasation (GO:0045123)	BP	29	27	0	2.64577E-06
GO:0048565	digestive tract development	down	digestive tract development (GO:0048565)	BP	91	89	0	2.83466E-06
GO:0001706	endoderm formation	down	endoderm formation (GO:0001706)	BP	42	41	0.024390244	2.83466E-06
GO:0010594	regulation of endothelial cell migration	down	regulation of endothelial cell migration (GO:0010594)	BP	84	82	0.012195122	2.83466E-06
GO:0010634	positive regulation of epithelial cell migration	down	positive regulation of epithelial cell migration (GO:0010634)	BP	77	76	0	2.86234E-06
GO:0003205	cardiac chamber development	down	cardiac chamber development (GO:0003205)	BP	119	117	0.017094017	2.91179E-06
GO:0007045	cell-substrate adherens junction assembly	down	cell-substrate adherens junction assembly (GO:0007045)	BP	43	42	0	3.15417E-06
GO:0071560	cellular response to transforming growth factor beta stim	down	cellular response to transforming growth factor beta stimulus (GO:00715	BP	126	124	0	3.15417E-06
GO:0048041	focal adhesion assembly	down	focal adhesion assembly (GO:0048041)	BP	43	42	0	3.15417E-06
GO:0043534	blood vessel endothelial cell migration	down	blood vessel endothelial cell migration (GO:0043534)	BP	49	48	0.020833333	3.62631E-06
GO:0007492	endoderm development	down	endoderm development (GO:0007492)	BP	57	56	0.017857143	3.73946E-06
GO:0071559	response to transforming growth factor beta	down	response to transforming growth factor beta (GO:0071559)	BP	128	126	0	3.75683E-06
GO:0040013	negative regulation of locomotion	down	negative regulation of locomotion (GO:0040013)	BP	176	167	0.005988024	3.90145E-06
GO:0060976	coronary vasculature development	down	coronary vasculature development (GO:0060976)	BP	30	29	0.034482759	3.96271E-06
GO:0072234	metanephric nephron tubule development	down	metanephric nephron tubule development (GO:0072234)	BP	16	16	0	3.96271E-06
GO:2000181	negative regulation of blood vessel morphogenesis	down	negative regulation of blood vessel morphogenesis (GO:2000181)	BP	51	50	0.02	3.96271E-06
GO:0090287	regulation of cellular response to growth factor stimulus	down	regulation of cellular response to growth factor stimulus (GO:0090287)	BP	165	162	0	3.96271E-06
GO:0050808	synapse organization	down	synapse organization (GO:0050808)	BP	146	141	0.021276596	3.98004E-06
GO:0003151	outflow tract morphogenesis	down	outflow tract morphogenesis (GO:0003151)	BP	53	53	0.018867925	4.24802E-06
GO:0016331	morphogenesis of embryonic epithelium	down	morphogenesis of embryonic epithelium (GO:0016331)	BP	122	120	0	4.44109E-06
GO:0001841	neural tube formation	down	neural tube formation (GO:0001841)	BP	85	83	0	4.44109E-06
GO:0090068	positive regulation of cell cycle process	down	positive regulation of cell cycle process (GO:0090068)	BP	134	129	0.03875969	4.45347E-06
GO:0060349	bone morphogenesis	down	bone morphogenesis (GO:0060349)	BP	68	65	0.015384615	4.49565E-06
GO:0001838	embryonic epithelial tube formation	down	embryonic epithelial tube formation (GO:0001838)	BP	104	102	0	4.51589E-06
GO:0072176	nephric duct development	down	nephric duct development (GO:0072176)	BP	13	13	0	4.51589E-06
GO:0050807	regulation of synapse organization	down	regulation of synapse organization (GO:0050807)	BP	80	77	0.025974026	4.74514E-06
GO:0051301	cell division	down	cell division (GO:0051301)	BP	171	163	0.024539877	4.90111E-06
GO:0007156	homophilic cell adhesion via plasma membrane adhesion	down	homophilic cell adhesion via plasma membrane adhesion molecules (GO:	BP	79	66	0.015151515	4.90111E-06
GO:0046578	regulation of Ras protein signal transduction	down	regulation of Ras protein signal transduction (GO:0046578)	BP	152	145	0.013793103	4.90111E-06
GO:0010721	negative regulation of cell development	down	negative regulation of cell development (GO:0010721)	BP	165	159	0	5.08598E-06
GO:0035767	endothelial cell chemotaxis	down	endothelial cell chemotaxis (GO:0035767)	BP	19	19	0	5.43687E-06
GO:0055123	digestive system development	down	digestive system development (GO:0055123)	BP	97	95	0	5.50995E-06
GO:0051271	negative regulation of cellular component movement	down	negative regulation of cellular component movement (GO:0051271)	BP	163	154	0.006493506	5.50995E-06
GO:0048705	skeletal system morphogenesis	down	skeletal system morphogenesis (GO:0048705)	BP	176	168	0.005952381	5.66113E-06
GO:0030318	melanocyte differentiation	down	melanocyte differentiation (GO:0030318)	BP	21	21	0	5.8751E-06
GO:0007422	peripheral nervous system development	down	peripheral nervous system development (GO:0007422)	BP	37	37	0	5.8751E-06
GO:0034446	substrate adhesion-dependent cell spreading	down	substrate adhesion-dependent cell spreading (GO:0034446)	BP	64	60	0.016666667	5.8751E-06
GO:0051961	negative regulation of nervous system development	down	negative regulation of nervous system development (GO:0051961)	BP	157	153	0	6.43276E-06
GO:0045667	regulation of osteoblast differentiation	down	regulation of osteoblast differentiation (GO:0045667)	BP	82	79	0	6.43276E-06
GO:0010718	positive regulation of epithelial to mesenchymal transitio	down	positive regulation of epithelial to mesenchymal transition (GO:0010718	BP	29	29	0.034482759	6.73719E-06
GO:0050803	regulation of synapse structure or activity	down	regulation of synapse structure or activity (GO:0050803)	BP	82	79	0.025316456	7.32028E-06
GO:0072243	metanephric nephron epithelium development	down	metanephric nephron epithelium development (GO:0072243)	BP	19	19	0	7.43251E-06
GO:0045446	endothelial cell differentiation	down	endothelial cell differentiation (GO:0045446)	BP	62	61	0	8.11798E-06
GO:1903055	positive regulation of extracellular matrix organization	down	positive regulation of extracellular matrix organization (GO:1903055)	BP	11	9	0	8.11798E-06
GO:0035904	aorta development	down	aorta development (GO:0035904)	BP	41	41	0.024390244	8.17792E-06
GO:0036342	post-anal tail morphogenesis	down	post-anal tail morphogenesis (GO:0036342)	BP	16	16	0	8.20928E-06
GO:0001885	endothelial cell development	down	endothelial cell development (GO:0001885)	BP	40	39	0	8.46754E-06
GO:0001755	neural crest cell migration	down	neural crest cell migration (GO:0001755)	BP	28	28	0	8.80323E-06
GO:0001649	osteoblast differentiation	down	osteoblast differentiation (GO:0001649)	BP	151	145	0.013793103	8.80323E-06
GO:0001569	branching involved in blood vessel morphogenesis	down	branching involved in blood vessel morphogenesis (GO:0001569)	BP	24	23	0.043478261	8.86885E-06
GO:1903901	negative regulation of viral life cycle	down	negative regulation of viral life cycle (GO:1903901)	BP	42	40	0.025	8.99279E-06
GO:0072170	metanephric tubule development	down	metanephric tubule development (GO:0072170)	BP	18	18	0	9.11378E-06
GO:0010001	glial cell differentiation	down	glial cell differentiation (GO:0010001)	BP	110	108	0	9.24261E-06
GO:0060541	respiratory system development	down	respiratory system development (GO:0060541)	BP	156	151	0	9.62978E-06
GO:0035924	cellular response to vascular endothelial growth factor sti	down	cellular response to vascular endothelial growth factor stimulus (GO:003	BP	30	30	0	9.90087E-06
GO:0003188	heart valve formation	down	heart valve formation (GO:0003188)	BP	10	10	0	9.90508E-06
GO:0060411	cardiac septum morphogenesis	down	cardiac septum morphogenesis (GO:0060411)	BP	48	48	0	1.01368E-05
GO:0060606	tube closure	down	tube closure (GO:0060606)	BP	75	73	0	1.04039E-05
GO:0048525	negative regulation of viral process	down	negative regulation of viral process (GO:0048525)	BP	48	46	0.02173913	1.05492E-05
GO:0010717	regulation of epithelial to mesenchymal transition	down	regulation of epithelial to mesenchymal transition (GO:0010717)	BP	51	51	0.019607843	1.05492E-05
GO:0002040	sprouting angiogenesis	down	sprouting angiogenesis (GO:0002040)	BP	51	50	0	1.05492E-05
GO:0033627	cell adhesion mediated by integrin	down	cell adhesion mediated by integrin (GO:0033627)	BP	40	39	0	1.07323E-05
GO:0030323	respiratory tube development	down	respiratory tube development (GO:0030323)	BP	141	137	0	1.10172E-05
GO:0090103	cochlea morphogenesis	down	cochlea morphogenesis (GO:0090103)	BP	19	19	0	1.10767E-05

GO:0072175	epithelial tube formation	down	epithelial tube formation (GO:0072175)	BP	108	106	0	1.10767E-05
GO:0001843	neural tube closure	down	neural tube closure (GO:0001843)	BP	74	72	0	1.10767E-05
GO:0000910	cytokinesis	down	cytokinesis (GO:0000910)	BP	89	88	0.034090909	1.14822E-05
GO:0060840	artery development	down	artery development (GO:0060840)	BP	61	61	0.016393443	1.19406E-05
GO:0098901	regulation of cardiac muscle cell action potential	down	regulation of cardiac muscle cell action potential (GO:0098901)	BP	13	13	0	1.26391E-05
GO:0060560	developmental growth involved in morphogenesis	down	developmental growth involved in morphogenesis (GO:0060560)	BP	137	130	0	1.3073E-05
GO:0050764	regulation of phagocytosis	down	regulation of phagocytosis (GO:0050764)	BP	40	36	0.027777778	1.31885E-05
GO:0072207	metanephric epithelium development	down	metanephric epithelium development (GO:0072207)	BP	22	22	0	1.34077E-05
GO:2000146	negative regulation of cell motility	down	negative regulation of cell motility (GO:2000146)	BP	152	143	0.006993007	1.36128E-05
GO:0007266	Rho protein signal transduction	down	Rho protein signal transduction (GO:0007266)	BP	115	108	0	1.36128E-05
GO:1902105	regulation of leukocyte differentiation	down	regulation of leukocyte differentiation (GO:1902105)	BP	161	152	0	1.37835E-05
GO:0007163	establishment or maintenance of cell polarity	down	establishment or maintenance of cell polarity (GO:0007163)	BP	108	100	0	1.4177E-05
GO:0007369	gastrulation	down	gastrulation (GO:0007369)	BP	131	128	0.0078125	1.43017E-05
GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	down	positive regulation of peptidyl-tyrosine phosphorylation (GO:0050731)	BP	78	78	0	1.46979E-05
GO:0046777	protein autophosphorylation	down	protein autophosphorylation (GO:0046777)	BP	153	150	0	1.49984E-05
GO:0010543	regulation of platelet activation	down	regulation of platelet activation (GO:0010543)	BP	22	21	0	1.49984E-05
GO:0032092	positive regulation of protein binding	down	positive regulation of protein binding (GO:0032092)	BP	63	62	0.016129032	1.5443E-05
GO:0030336	negative regulation of cell migration	down	negative regulation of cell migration (GO:0030336)	BP	146	137	0.00729927	1.58155E-05
GO:0007179	transforming growth factor beta receptor signaling pathw	down	transforming growth factor beta receptor signaling pathway (GO:000717	BP	104	104	0	1.60806E-05
GO:0032332	positive regulation of chondrocyte differentiation	down	positive regulation of chondrocyte differentiation (GO:0032332)	BP	11	11	0	1.65143E-05
GO:0033273	response to vitamin	down	response to vitamin (GO:0033273)	BP	18	16	0	1.65143E-05
GO:0098911	regulation of ventricular cardiac muscle cell action poten	down	regulation of ventricular cardiac muscle cell action potential (GO:009891	BP	10	10	0	1.684E-05
GO:0060512	prostate gland morphogenesis	down	prostate gland morphogenesis (GO:0060512)	BP	24	22	0	1.69151E-05
GO:0017145	stem cell division	down	stem cell division (GO:0017145)	BP	22	20	0	1.78784E-05
GO:0048706	embryonic skeletal system development	down	embryonic skeletal system development (GO:0048706)	BP	100	96	0.010416667	1.80355E-05
GO:1903037	regulation of leukocyte cell-cell adhesion	down	regulation of leukocyte cell-cell adhesion (GO:1903037)	BP	184	177	0.005649718	1.80355E-05
GO:0022409	positive regulation of cell-cell adhesion	down	positive regulation of cell-cell adhesion (GO:0022409)	BP	138	133	0.007518797	1.84708E-05
GO:0090330	regulation of platelet aggregation	down	regulation of platelet aggregation (GO:0090330)	BP	13	13	0	1.84708E-05
GO:1903708	positive regulation of hemopoiesis	down	positive regulation of hemopoiesis (GO:1903708)	BP	117	113	0	1.90652E-05
GO:0021537	telencephalon development	down	telencephalon development (GO:0021537)	BP	153	149	0.013422819	1.90652E-05
GO:0035148	tube formation	down	tube formation (GO:0035148)	BP	120	118	0	1.90652E-05
GO:0035640	exploration behavior	down	exploration behavior (GO:0035640)	BP	22	21	0	1.92192E-05
GO:1903053	regulation of extracellular matrix organization	down	regulation of extracellular matrix organization (GO:1903053)	BP	20	18	0	1.92192E-05
GO:0072178	nephric duct morphogenesis	down	nephric duct morphogenesis (GO:0072178)	BP	10	10	0	2.03987E-05
GO:0003198	epithelial to mesenchymal transition involved in endocar	down	epithelial to mesenchymal transition involved in endocardial cushion for	BP	15	15	0	2.06571E-05
GO:0002011	morphogenesis of an epithelial sheet	down	morphogenesis of an epithelial sheet (GO:0002011)	BP	41	38	0.026315789	2.14099E-05
GO:0032465	regulation of cytokinesis	down	regulation of cytokinesis (GO:0032465)	BP	44	43	0.069767442	2.14099E-05
GO:0061326	renal tubule development	down	renal tubule development (GO:0061326)	BP	75	74	0	2.14099E-05
GO:0051099	positive regulation of binding	down	positive regulation of binding (GO:0051099)	BP	99	98	0.010204082	2.1436E-05
GO:0071300	cellular response to retinoic acid	down	cellular response to retinoic acid (GO:0071300)	BP	30	29	0	2.20701E-05
GO:0030324	lung development	down	lung development (GO:0030324)	BP	138	134	0	2.21103E-05
GO:0060688	regulation of morphogenesis of a branching structure	down	regulation of morphogenesis of a branching structure (GO:0060688)	BP	46	45	0	2.21556E-05
GO:0009953	dorsal/ventral pattern formation	down	dorsal/ventral pattern formation (GO:0009953)	BP	72	70	0	2.2311E-05
GO:0030903	notochord development	down	notochord development (GO:0030903)	BP	16	15	0	2.32744E-05
GO:0045778	positive regulation of ossification	down	positive regulation of ossification (GO:0045778)	BP	60	58	0	2.33815E-05
GO:0051963	regulation of synapse assembly	down	regulation of synapse assembly (GO:0051963)	BP	61	58	0.034482759	2.34037E-05
GO:0051145	smooth muscle cell differentiation	down	smooth muscle cell differentiation (GO:0051145)	BP	36	35	0	2.42729E-05
GO:0060993	kidney morphogenesis	down	kidney morphogenesis (GO:0060993)	BP	72	71	0	2.43572E-05
GO:0090596	sensory organ morphogenesis	down	sensory organ morphogenesis (GO:0090596)	BP	199	191	0.005235602	2.44338E-05
GO:0000281	mitotic cytokinesis	down	mitotic cytokinesis (GO:0000281)	BP	28	28	0	2.47233E-05
GO:0051965	positive regulation of synapse assembly	down	positive regulation of synapse assembly (GO:0051965)	BP	50	48	0.041666667	2.69936E-05
GO:0032956	regulation of actin cytoskeleton organization	down	regulation of actin cytoskeleton organization (GO:0032956)	BP	187	178	0	2.69936E-05
GO:0003018	vascular process in circulatory system	down	vascular process in circulatory system (GO:0003018)	BP	65	65	0	2.71265E-05
GO:0035023	regulation of Rho protein signal transduction	down	regulation of Rho protein signal transduction (GO:0035023)	BP	95	89	0	2.72417E-05
GO:0043406	positive regulation of MAP kinase activity	down	positive regulation of MAP kinase activity (GO:0043406)	BP	123	121	0	2.93217E-05
GO:0003206	cardiac chamber morphogenesis	down	cardiac chamber morphogenesis (GO:0003206)	BP	91	90	0.011111111	2.98102E-05
GO:0021904	dorsal/ventral neural tube patterning	down	dorsal/ventral neural tube patterning (GO:0021904)	BP	23	23	0	3.01568E-05
GO:1902850	microtubule cytoskeleton organization involved in mitosi	down	microtubule cytoskeleton organization involved in mitosis (GO:1902850	BP	65	63	0.015873016	3.01568E-05
GO:0051781	positive regulation of cell division	down	positive regulation of cell division (GO:0051781)	BP	33	32	0.09375	3.01568E-05
GO:0030010	establishment of cell polarity	down	establishment of cell polarity (GO:0030010)	BP	79	73	0	3.08693E-05
GO:0007162	negative regulation of cell adhesion	down	negative regulation of cell adhesion (GO:0007162)	BP	146	140	0.007142857	3.08693E-05
GO:0031290	retinal ganglion cell axon guidance	down	retinal ganglion cell axon guidance (GO:0031290)	BP	14	14	0	3.08693E-05
GO:0003401	axis elongation	down	axis elongation (GO:0003401)	BP	27	26	0	3.29768E-05
GO:0035050	embryonic heart tube development	down	embryonic heart tube development (GO:0035050)	BP	51	51	0	3.40752E-05

GO:0061572	actin filament bundle organization	down	actin filament bundle organization (GO:0061572)	BP	89	86	0	3.46832E-05
GO:0050768	negative regulation of neurogenesis	down	negative regulation of neurogenesis (GO:0050768)	BP	144	140	0	3.58695E-05
GO:0050918	positive chemotaxis	down	positive chemotaxis (GO:0050918)	BP	22	21	0	3.58695E-05
GO:0021700	developmental maturation	down	developmental maturation (GO:0021700)	BP	172	168	0.005952381	3.61401E-05
GO:0071773	cellular response to BMP stimulus	down	cellular response to BMP stimulus (GO:0071773)	BP	108	108	0	3.73589E-05
GO:0071772	response to BMP	down	response to BMP (GO:0071772)	BP	108	108	0	3.73589E-05
GO:0014020	primary neural tube formation	down	primary neural tube formation (GO:0014020)	BP	78	76	0	3.78048E-05
GO:0031532	actin cytoskeleton reorganization	down	actin cytoskeleton reorganization (GO:0031532)	BP	62	61	0	3.83627E-05
GO:0030279	negative regulation of ossification	down	negative regulation of ossification (GO:0030279)	BP	54	51	0	3.85886E-05
GO:0048592	eye morphogenesis	down	eye morphogenesis (GO:0048592)	BP	111	107	0.009345794	4.23193E-05
GO:0051017	actin filament bundle assembly	down	actin filament bundle assembly (GO:0051017)	BP	87	85	0	4.53852E-05
GO:0035588	G-protein coupled purinergic receptor signaling pathway	down	G-protein coupled purinergic receptor signaling pathway (GO:0035588)	BP	16	16	0	4.53852E-05
GO:0044236	multicellular organism metabolic process	down	multicellular organism metabolic process (GO:0044236)	BP	44	44	0.045454545	4.53852E-05
GO:0050920	regulation of chemotaxis	down	regulation of chemotaxis (GO:0050920)	BP	107	101	0	4.53852E-05
GO:0071604	transforming growth factor beta production	down	transforming growth factor beta production (GO:0071604)	BP	15	15	0	4.53852E-05
GO:0060443	mammary gland morphogenesis	down	mammary gland morphogenesis (GO:0060443)	BP	41	39	0	4.5643E-05
GO:0051882	mitochondrial depolarization	down	mitochondrial depolarization (GO:0051882)	BP	14	11	0	4.76203E-05
GO:0051900	regulation of mitochondrial depolarization	down	regulation of mitochondrial depolarization (GO:0051900)	BP	13	11	0	4.76203E-05
GO:0006909	phagocytosis	down	phagocytosis (GO:0006909)	BP	86	81	0.012345679	4.91091E-05
GO:1903039	positive regulation of leukocyte cell-cell adhesion	down	positive regulation of leukocyte cell-cell adhesion (GO:1903039)	BP	117	114	0.00877193	4.91671E-05
GO:0086004	regulation of cardiac muscle cell contraction	down	regulation of cardiac muscle cell contraction (GO:0086004)	BP	16	15	0	4.94477E-05
GO:0050863	regulation of T cell activation	down	regulation of T cell activation (GO:0050863)	BP	173	166	0.006024096	5.03442E-05
GO:0007626	locomotory behavior	down	locomotory behavior (GO:0007626)	BP	148	142	0	5.20416E-05
GO:0003272	endocardial cushion formation	down	endocardial cushion formation (GO:0003272)	BP	18	18	0	5.32578E-05
GO:1902107	positive regulation of leukocyte differentiation	down	positive regulation of leukocyte differentiation (GO:1902107)	BP	93	89	0	5.32578E-05
GO:0001958	endochondral ossification	down	endochondral ossification (GO:0001958)	BP	22	20	0.05	5.38502E-05
GO:0014910	regulation of smooth muscle cell migration	down	regulation of smooth muscle cell migration (GO:0014910)	BP	23	22	0	5.38502E-05
GO:0036075	replacement ossification	down	replacement ossification (GO:0036075)	BP	22	20	0.05	5.38502E-05
GO:0003281	ventricular septum development	down	ventricular septum development (GO:0003281)	BP	48	47	0	5.39123E-05
GO:0060009	Sertoli cell development	down	Sertoli cell development (GO:0060009)	BP	10	10	0	5.6898E-05
GO:0032845	negative regulation of homeostatic process	down	negative regulation of homeostatic process (GO:0032845)	BP	103	100	0	5.74406E-05
GO:0043588	skin development	down	skin development (GO:0043588)	BP	160	150	0.013333333	5.74406E-05
GO:0021781	glial cell fate commitment	down	glial cell fate commitment (GO:0021781)	BP	10	9	0	5.7817E-05
GO:0048532	anatomical structure arrangement	down	anatomical structure arrangement (GO:0048532)	BP	16	16	0.0625	5.93811E-05
GO:1901890	positive regulation of cell junction assembly	down	positive regulation of cell junction assembly (GO:1901890)	BP	20	20	0	6.03024E-05
GO:0045665	negative regulation of neuron differentiation	down	negative regulation of neuron differentiation (GO:0045665)	BP	115	112	0	6.13786E-05
GO:0001656	metanephros development	down	metanephros development (GO:0001656)	BP	65	63	0	6.14735E-05
GO:0010595	positive regulation of endothelial cell migration	down	positive regulation of endothelial cell migration (GO:0010595)	BP	48	47	0	6.17521E-05
GO:0030168	platelet activation	down	platelet activation (GO:0030168)	BP	67	65	0	6.49347E-05
GO:0061028	establishment of endothelial barrier	down	establishment of endothelial barrier (GO:0061028)	BP	27	26	0	7.08858E-05
GO:0000070	mitotic sister chromatid segregation	down	mitotic sister chromatid segregation (GO:0000070)	BP	90	86	0.034883721	7.08858E-05
GO:0019229	regulation of vasoconstriction	down	regulation of vasoconstriction (GO:0019229)	BP	21	21	0	7.08858E-05
GO:0048736	appendage development	down	appendage development (GO:0048736)	BP	137	132	0	7.15941E-05
GO:0060173	limb development	down	limb development (GO:0060173)	BP	137	132	0	7.15941E-05
GO:0035909	aorta morphogenesis	down	aorta morphogenesis (GO:0035909)	BP	24	24	0	7.17915E-05
GO:0002064	epithelial cell development	down	epithelial cell development (GO:0002064)	BP	152	148	0	7.18849E-05
GO:0014065	phosphatidylinositol 3-kinase signaling	down	phosphatidylinositol 3-kinase signaling (GO:0014065)	BP	75	72	0	7.35117E-05
GO:0045880	positive regulation of smoothened signaling pathway	down	positive regulation of smoothened signaling pathway (GO:0045880)	BP	21	20	0	7.45735E-05
GO:2001222	regulation of neuron migration	down	regulation of neuron migration (GO:2001222)	BP	19	19	0	7.48013E-05
GO:0010812	negative regulation of cell-substrate adhesion	down	negative regulation of cell-substrate adhesion (GO:0010812)	BP	38	37	0.027027027	7.63966E-05
GO:0060740	prostate gland epithelium morphogenesis	down	prostate gland epithelium morphogenesis (GO:0060740)	BP	23	21	0	7.63966E-05
GO:0048546	digestive tract morphogenesis	down	digestive tract morphogenesis (GO:0048546)	BP	34	34	0	7.87944E-05
GO:0050867	positive regulation of cell activation	down	positive regulation of cell activation (GO:0050867)	BP	176	172	0.005813953	7.87944E-05
GO:0050766	positive regulation of phagocytosis	down	positive regulation of phagocytosis (GO:0050766)	BP	27	26	0.038461538	7.87944E-05
GO:0090102	cochlea development	down	cochlea development (GO:0090102)	BP	32	32	0	8.15186E-05
GO:0048636	positive regulation of muscle organ development	down	positive regulation of muscle organ development (GO:0048636)	BP	41	40	0	8.19033E-05
GO:0045844	positive regulation of striated muscle tissue development	down	positive regulation of striated muscle tissue development (GO:0045844)	BP	41	40	0	8.19033E-05
GO:0046599	regulation of centriole replication	down	regulation of centriole replication (GO:0046599)	BP	12	11	0	8.19033E-05
GO:0050870	positive regulation of T cell activation	down	positive regulation of T cell activation (GO:0050870)	BP	113	110	0.009090909	8.35757E-05
GO:0048709	oligodendrocyte differentiation	down	oligodendrocyte differentiation (GO:0048709)	BP	46	45	0	8.44573E-05
GO:0021510	spinal cord development	down	spinal cord development (GO:0021510)	BP	63	62	0	8.64479E-05
GO:0034110	regulation of homotypic cell-cell adhesion	down	regulation of homotypic cell-cell adhesion (GO:0034110)	BP	17	17	0	8.66621E-05
GO:0043550	regulation of lipid kinase activity	down	regulation of lipid kinase activity (GO:0043550)	BP	34	34	0	8.74019E-05
GO:0070206	protein trimerization	down	protein trimerization (GO:0070206)	BP	22	22	0.045454545	9.20768E-05

GO:0001704	formation of primary germ layer	down	formation of primary germ layer (GO:0001704)	BP	91	90	0.011111111	9.22367E-05
GO:0072210	metanephric nephron development	down	metanephric nephron development (GO:0072210)	BP	30	29	0	9.23205E-05
GO:0098534	centriole assembly	down	centriole assembly (GO:0098534)	BP	26	24	0	9.32079E-05
GO:0048771	tissue remodeling	down	tissue remodeling (GO:0048771)	BP	98	96	0.010416667	9.48253E-05
GO:0021952	central nervous system projection neuron axonogenesis	down	central nervous system projection neuron axonogenesis (GO:0021952)	BP	21	20	0	9.67016E-05
GO:1903018	regulation of glycoprotein metabolic process	down	regulation of glycoprotein metabolic process (GO:1903018)	BP	28	27	0.037037037	9.67016E-05
GO:0038084	vascular endothelial growth factor signaling pathway	down	vascular endothelial growth factor signaling pathway (GO:0038084)	BP	20	20	0	9.71683E-05
GO:0021987	cerebral cortex development	down	cerebral cortex development (GO:0021987)	BP	71	69	0.028985507	9.78339E-05
GO:0045807	positive regulation of endocytosis	down	positive regulation of endocytosis (GO:0045807)	BP	74	73	0.01369863	9.82042E-05
GO:0035282	segmentation	down	segmentation (GO:0035282)	BP	77	75	0	9.85242E-05
GO:0072575	epithelial cell proliferation involved in liver morphogenes	down	epithelial cell proliferation involved in liver morphogenesis (GO:007257	BP	10	10	0.1	9.96055E-05
GO:0072574	hepatocyte proliferation	down	hepatocyte proliferation (GO:0072574)	BP	10	10	0.1	9.96055E-05
GO:0008217	regulation of blood pressure	down	regulation of blood pressure (GO:0008217)	BP	88	86	0	0.000102687
GO:0010002	cardioblast differentiation	down	cardioblast differentiation (GO:0010002)	BP	14	14	0	0.000103033
GO:0055025	positive regulation of cardiac muscle tissue development	down	positive regulation of cardiac muscle tissue development (GO:0055025)	BP	28	28	0	0.000105039
GO:0035107	appendage morphogenesis	down	appendage morphogenesis (GO:0035107)	BP	119	114	0	0.000106054
GO:0035108	limb morphogenesis	down	limb morphogenesis (GO:0035108)	BP	119	114	0	0.000106054
GO:0016358	dendrite development	down	dendrite development (GO:0016358)	BP	129	126	0	0.000106449
GO:0072009	nephron epithelium development	down	nephron epithelium development (GO:0072009)	BP	84	83	0	0.000106449
GO:0140014	mitotic nuclear division	down	mitotic nuclear division (GO:0140014)	BP	145	140	0.028571429	0.000106525
GO:0007219	Notch signaling pathway	down	Notch signaling pathway (GO:0007219)	BP	101	97	0	0.000106525
GO:1901863	positive regulation of muscle tissue development	down	positive regulation of muscle tissue development (GO:1901863)	BP	42	41	0	0.000106525
GO:0007204	positive regulation of cytosolic calcium ion concentratio	down	positive regulation of cytosolic calcium ion concentration (GO:0007204)	BP	110	104	0	0.00010713
GO:0009855	determination of bilateral symmetry	down	determination of bilateral symmetry (GO:0009855)	BP	81	81	0	0.000107624
GO:0071902	positive regulation of protein serine/threonine kinase acti	down	positive regulation of protein serine/threonine kinase activity (GO:00719	BP	165	163	0	0.000111767
GO:0050678	regulation of epithelial cell proliferation	down	regulation of epithelial cell proliferation (GO:0050678)	BP	197	189	0.005291005	0.000111767
GO:0060078	regulation of postsynaptic membrane potential	down	regulation of postsynaptic membrane potential (GO:0060078)	BP	54	53	0	0.000111767
GO:0070302	regulation of stress-activated protein kinase signaling casc	down	regulation of stress-activated protein kinase signaling cascade (GO:00703	BP	133	130	0.007692308	0.000111767
GO:0034109	homotypic cell-cell adhesion	down	homotypic cell-cell adhesion (GO:0034109)	BP	56	55	0	0.000112687
GO:0001764	neuron migration	down	neuron migration (GO:0001764)	BP	103	100	0	0.000112687
GO:0009799	specification of symmetry	down	specification of symmetry (GO:0009799)	BP	82	82	0	0.000112687
GO:0035051	cardiocyte differentiation	down	cardiocyte differentiation (GO:0035051)	BP	72	70	0	0.000113467
GO:0060326	cell chemotaxis	down	cell chemotaxis (GO:0060326)	BP	165	152	0	0.000113467
GO:0048708	astrocyte differentiation	down	astrocyte differentiation (GO:0048708)	BP	45	45	0	0.000114034
GO:0014909	smooth muscle cell migration	down	smooth muscle cell migration (GO:0014909)	BP	27	26	0	0.000114846
GO:0003143	embryonic heart tube morphogenesis	down	embryonic heart tube morphogenesis (GO:0003143)	BP	45	45	0	0.000116217
GO:0060601	lateral sprouting from an epithelium	down	lateral sprouting from an epithelium (GO:0060601)	BP	11	10	0	0.000116217
GO:0045662	negative regulation of myoblast differentiation	down	negative regulation of myoblast differentiation (GO:0045662)	BP	22	22	0	0.000116217
GO:0050921	positive regulation of chemotaxis	down	positive regulation of chemotaxis (GO:0050921)	BP	73	69	0	0.000116217
GO:0045661	regulation of myoblast differentiation	down	regulation of myoblast differentiation (GO:0045661)	BP	41	41	0	0.000116217
GO:0045428	regulation of nitric oxide biosynthetic process	down	regulation of nitric oxide biosynthetic process (GO:0045428)	BP	22	21	0.047619048	0.000116217
GO:0071634	regulation of transforming growth factor beta production	down	regulation of transforming growth factor beta production (GO:0071634)	BP	14	14	0	0.000116217
GO:0008038	neuron recognition	down	neuron recognition (GO:0008038)	BP	18	18	0	0.000129915
GO:0071695	anatomical structure maturation	down	anatomical structure maturation (GO:0071695)	BP	97	96	0	0.000130294
GO:0019722	calcium-mediated signaling	down	calcium-mediated signaling (GO:0019722)	BP	86	81	0	0.000130294
GO:0021511	spinal cord patterning	down	spinal cord patterning (GO:0021511)	BP	20	19	0	0.000130439
GO:0043535	regulation of blood vessel endothelial cell migration	down	regulation of blood vessel endothelial cell migration (GO:0043535)	BP	35	35	0.028571429	0.000130981
GO:0072080	nephron tubule development	down	nephron tubule development (GO:0072080)	BP	72	71	0	0.000132189
GO:1904018	positive regulation of vasculature development	down	positive regulation of vasculature development (GO:1904018)	BP	87	85	0	0.00013319
GO:0043537	negative regulation of blood vessel endothelial cell migrat	down	negative regulation of blood vessel endothelial cell migration (GO:00435	BP	18	18	0.055555556	0.000134435
GO:0045060	negative thymic T cell selection	down	negative thymic T cell selection (GO:0045060)	BP	10	9	0	0.000135182
GO:0030177	positive regulation of Wnt signaling pathway	down	positive regulation of Wnt signaling pathway (GO:0030177)	BP	79	76	0.013157895	0.000135903
GO:0048839	inner ear development	down	inner ear development (GO:0048839)	BP	134	128	0	0.000138322
GO:0045787	positive regulation of cell cycle	down	positive regulation of cell cycle (GO:0045787)	BP	194	186	0.02688172	0.000139277
GO:0048844	artery morphogenesis	down	artery morphogenesis (GO:0048844)	BP	42	42	0	0.000140628
GO:0030048	actin filament-based movement	down	actin filament-based movement (GO:0030048)	BP	53	51	0.019607843	0.000142702
GO:1903393	positive regulation of adherens junction organization	down	positive regulation of adherens junction organization (GO:1903393)	BP	15	15	0	0.000142702
GO:0051894	positive regulation of focal adhesion assembly	down	positive regulation of focal adhesion assembly (GO:0051894)	BP	15	15	0	0.000142702
GO:0051208	sequestering of calcium ion	down	sequestering of calcium ion (GO:0051208)	BP	64	61	0	0.000142702
GO:0032872	regulation of stress-activated MAPK cascade	down	regulation of stress-activated MAPK cascade (GO:0032872)	BP	132	129	0.007751938	0.000146277
GO:0031346	positive regulation of cell projection organization	down	positive regulation of cell projection organization (GO:0031346)	BP	169	163	0	0.000150016
GO:0060021	palate development	down	palate development (GO:0060021)	BP	67	64	0	0.000150658
GO:0051251	positive regulation of lymphocyte activation	down	positive regulation of lymphocyte activation (GO:0051251)	BP	152	149	0.006711409	0.000155348
GO:0006809	nitric oxide biosynthetic process	down	nitric oxide biosynthetic process (GO:0006809)	BP	29	27	0.037037037	0.000164545

GO:2000107	negative regulation of leukocyte apoptotic process	down	negative regulation of leukocyte apoptotic process (GO:2000107)	BP	32	31	0.032258065	0.00016729
GO:0048593	camera-type eye morphogenesis	down	camera-type eye morphogenesis (GO:0048593)	BP	81	77	0	0.000167415
GO:0009952	anterior/posterior pattern specification	down	anterior/posterior pattern specification (GO:0009952)	BP	162	155	0	0.000175554
GO:1904019	epithelial cell apoptotic process	down	epithelial cell apoptotic process (GO:1904019)	BP	52	52	0	0.000175953
GO:0045637	regulation of myeloid cell differentiation	down	regulation of myeloid cell differentiation (GO:0045637)	BP	124	118	0	0.000186125
GO:0007368	determination of left/right symmetry	down	determination of left/right symmetry (GO:0007368)	BP	77	77	0	0.000186355
GO:0043405	regulation of MAP kinase activity	down	regulation of MAP kinase activity (GO:0043405)	BP	176	173	0	0.000189856
GO:0045666	positive regulation of neuron differentiation	down	positive regulation of neuron differentiation (GO:0045666)	BP	164	158	0	0.000197353
GO:2000021	regulation of ion homeostasis	down	regulation of ion homeostasis (GO:2000021)	BP	108	102	0	0.000197353
GO:0021953	central nervous system neuron differentiation	down	central nervous system neuron differentiation (GO:0021953)	BP	126	122	0	0.000198654
GO:0050680	negative regulation of epithelial cell proliferation	down	negative regulation of epithelial cell proliferation (GO:0050680)	BP	88	86	0.011627907	0.000203997
GO:1902547	regulation of cellular response to vascular endothelial gro	down	regulation of cellular response to vascular endothelial growth factor stim	BP	12	12	0	0.000203997
GO:0002696	positive regulation of leukocyte activation	down	positive regulation of leukocyte activation (GO:0002696)	BP	170	166	0.006024096	0.000205169
GO:0048103	somatic stem cell division	down	somatic stem cell division (GO:0048103)	BP	16	14	0	0.000206964
GO:0031577	spindle checkpoint	down	spindle checkpoint (GO:0031577)	BP	25	23	0.086956522	0.000206964
GO:0048872	homeostasis of number of cells	down	homeostasis of number of cells (GO:0048872)	BP	183	180	0.005555556	0.000207443
GO:0051147	regulation of muscle cell differentiation	down	regulation of muscle cell differentiation (GO:0051147)	BP	105	103	0	0.000207443
GO:0014066	regulation of phosphatidylinositol 3-kinase signaling	down	regulation of phosphatidylinositol 3-kinase signaling (GO:0014066)	BP	57	54	0	0.000207443
GO:0030282	bone mineralization	down	bone mineralization (GO:0030282)	BP	74	70	0	0.000208436
GO:0021954	central nervous system neuron development	down	central nervous system neuron development (GO:0021954)	BP	54	51	0	0.000210752
GO:0043507	positive regulation of JUN kinase activity	down	positive regulation of JUN kinase activity (GO:0043507)	BP	40	40	0	0.00021654
GO:0071229	cellular response to acid chemical	down	cellular response to acid chemical (GO:0071229)	BP	97	95	0.031578947	0.000218117
GO:0030100	regulation of endocytosis	down	regulation of endocytosis (GO:0030100)	BP	123	119	0.008403361	0.000219195
GO:0050931	pigment cell differentiation	down	pigment cell differentiation (GO:0050931)	BP	28	28	0	0.00022066
GO:1905209	positive regulation of cardiocyte differentiation	down	positive regulation of cardiocyte differentiation (GO:1905209)	BP	16	16	0	0.00022066
GO:0010463	mesenchymal cell proliferation	down	mesenchymal cell proliferation (GO:0010463)	BP	33	33	0	0.000222099
GO:0051302	regulation of cell division	down	regulation of cell division (GO:0051302)	BP	66	64	0.046875	0.000222099
GO:0097756	negative regulation of blood vessel diameter	down	negative regulation of blood vessel diameter (GO:0097756)	BP	34	34	0	0.000222528
GO:0043506	regulation of JUN kinase activity	down	regulation of JUN kinase activity (GO:0043506)	BP	47	47	0	0.000222528
GO:0042310	vasoconstriction	down	vasoconstriction (GO:0042310)	BP	34	34	0	0.000222528
GO:0003231	cardiac ventricle development	down	cardiac ventricle development (GO:0003231)	BP	89	87	0.011494253	0.000222923
GO:0002283	neutrophil activation involved in immune response	down	neutrophil activation involved in immune response (GO:0002283)	BP	10	9	0	0.000223004
GO:0098773	skin epidermis development	down	skin epidermis development (GO:0098773)	BP	67	65	0	0.000225358
GO:0050804	modulation of chemical synaptic transmission	down	modulation of chemical synaptic transmission (GO:0050804)	BP	145	142	0.014084507	0.000226689
GO:0007099	centriole replication	down	centriole replication (GO:0007099)	BP	24	23	0	0.000236317
GO:0043583	ear development	down	ear development (GO:0043583)	BP	155	149	0	0.000236484
GO:0061008	hepaticobiliary system development	down	hepaticobiliary system development (GO:0061008)	BP	55	54	0.018518519	0.000236484
GO:0010769	regulation of cell morphogenesis involved in differentiatio	down	regulation of cell morphogenesis involved in differentiation (GO:001076	BP	155	146	0	0.000236484
GO:0021955	central nervous system neuron axonogenesis	down	central nervous system neuron axonogenesis (GO:0021955)	BP	25	24	0	0.000241671
GO:0060008	Sertoli cell differentiation	down	Sertoli cell differentiation (GO:0060008)	BP	13	13	0	0.000241671
GO:0001823	mesonephros development	down	mesonephros development (GO:0001823)	BP	81	80	0	0.000241886
GO:0098900	regulation of action potential	down	regulation of action potential (GO:0098900)	BP	20	20	0	0.000241909
GO:0021885	forebrain cell migration	down	forebrain cell migration (GO:0021885)	BP	49	49	0	0.000243596
GO:0001889	liver development	down	liver development (GO:0001889)	BP	53	52	0.019230769	0.000243596
GO:0072163	mesonephric epithelium development	down	mesonephric epithelium development (GO:0072163)	BP	79	78	0	0.000243596
GO:0072164	mesonephric tubule development	down	mesonephric tubule development (GO:0072164)	BP	79	78	0	0.000243596
GO:0048588	developmental cell growth	down	developmental cell growth (GO:0048588)	BP	106	103	0	0.000245006
GO:0046209	nitric oxide metabolic process	down	nitric oxide metabolic process (GO:0046209)	BP	30	28	0.035714286	0.000246122
GO:0002042	cell migration involved in sprouting angiogenesis	down	cell migration involved in sprouting angiogenesis (GO:0002042)	BP	24	24	0	0.000246921
GO:0022405	hair cycle process	down	hair cycle process (GO:0022405)	BP	65	63	0	0.000250367
GO:0001942	hair follicle development	down	hair follicle development (GO:0001942)	BP	65	63	0	0.000250367
GO:0022404	molting cycle process	down	molting cycle process (GO:0022404)	BP	65	63	0	0.000250367
GO:0051282	regulation of sequestering of calcium ion	down	regulation of sequestering of calcium ion (GO:0051282)	BP	63	60	0	0.000254739
GO:0045669	positive regulation of osteoblast differentiation	down	positive regulation of osteoblast differentiation (GO:0045669)	BP	43	41	0	0.000257736
GO:0042359	vitamin D metabolic process	down	vitamin D metabolic process (GO:0042359)	BP	14	11	0	0.000257736
GO:0072576	liver morphogenesis	down	liver morphogenesis (GO:0072576)	BP	12	12	0.083333333	0.000257743
GO:0030509	BMP signaling pathway	down	BMP signaling pathway (GO:0030509)	BP	101	101	0	0.000261556
GO:1902903	regulation of supramolecular fiber organization	down	regulation of supramolecular fiber organization (GO:1902903)	BP	179	171	0	0.000261556
GO:0021543	pallium development	down	pallium development (GO:0021543)	BP	101	98	0.020408163	0.000262652
GO:0098813	nuclear chromosome segregation	down	nuclear chromosome segregation (GO:0098813)	BP	162	152	0.019736842	0.00026551
GO:0046885	regulation of hormone biosynthetic process	down	regulation of hormone biosynthetic process (GO:0046885)	BP	12	12	0	0.000266483
GO:0097553	calcium ion transmembrane import into cytosol	down	calcium ion transmembrane import into cytosol (GO:0097553)	BP	62	59	0	0.00026667
GO:0051283	negative regulation of sequestering of calcium ion	down	negative regulation of sequestering of calcium ion (GO:0051283)	BP	62	59	0	0.00026667
GO:0051209	release of sequestered calcium ion into cytosol	down	release of sequestered calcium ion into cytosol (GO:0051209)	BP	62	59	0	0.00026667

GO:0046596	regulation of viral entry into host cell	down	regulation of viral entry into host cell (GO:0046596)	BP	16	15	0.066666667	0.000270831
GO:0010596	negative regulation of endothelial cell migration	down	negative regulation of endothelial cell migration (GO:0010596)	BP	32	31	0.032258065	0.000274245
GO:0032526	response to retinoic acid	down	response to retinoic acid (GO:0032526)	BP	50	47	0	0.000274497
GO:0044065	regulation of respiratory system process	down	regulation of respiratory system process (GO:0044065)	BP	11	11	0	0.000275033
GO:0031098	stress-activated protein kinase signaling cascade	down	stress-activated protein kinase signaling cascade (GO:0031098)	BP	150	147	0.006802721	0.000275033
GO:0014074	response to purine-containing compound	down	response to purine-containing compound (GO:0014074)	BP	48	48	0	0.000280071
GO:0051383	kinetochore organization	down	kinetochore organization (GO:0051383)	BP	11	11	0	0.000284371
GO:0007019	microtubule depolymerization	down	microtubule depolymerization (GO:0007019)	BP	20	20	0	0.000288178
GO:0003170	heart valve development	down	heart valve development (GO:0003170)	BP	28	28	0	0.000288515
GO:0048048	embryonic eye morphogenesis	down	embryonic eye morphogenesis (GO:0048048)	BP	27	27	0	0.000304339
GO:0071459	protein localization to chromosome, centromeric region	down	protein localization to chromosome, centromeric region (GO:0071459)	BP	12	11	0.090909091	0.000304339
GO:1905207	regulation of cardiocyte differentiation	down	regulation of cardiocyte differentiation (GO:1905207)	BP	20	20	0	0.000304339
GO:0002761	regulation of myeloid leukocyte differentiation	down	regulation of myeloid leukocyte differentiation (GO:0002761)	BP	70	68	0	0.000306079
GO:0071696	ectodermal placode development	down	ectodermal placode development (GO:0071696)	BP	12	11	0	0.000306485
GO:0051983	regulation of chromosome segregation	down	regulation of chromosome segregation (GO:0051983)	BP	53	51	0.019607843	0.000308541
GO:0048483	autonomic nervous system development	down	autonomic nervous system development (GO:0048483)	BP	33	32	0	0.000308552
GO:0061333	renal tubule morphogenesis	down	renal tubule morphogenesis (GO:0061333)	BP	61	60	0	0.000309702
GO:0001101	response to acid chemical	down	response to acid chemical (GO:0001101)	BP	129	125	0.024	0.000313354
GO:0034501	protein localization to kinetochore	down	protein localization to kinetochore (GO:0034501)	BP	11	10	0.1	0.000313401
GO:0050880	regulation of blood vessel size	down	regulation of blood vessel size (GO:0050880)	BP	53	53	0	0.000317457
GO:0061640	cytoskeleton-dependent cytokinesis	down	cytoskeleton-dependent cytokinesis (GO:0061640)	BP	34	34	0.029411765	0.000320284
GO:0035265	organ growth	down	organ growth (GO:0035265)	BP	94	89	0	0.000320284
GO:2001057	reactive nitrogen species metabolic process	down	reactive nitrogen species metabolic process (GO:2001057)	BP	33	29	0.034482759	0.000327831
GO:1903522	regulation of blood circulation	down	regulation of blood circulation (GO:1903522)	BP	112	109	0.009174312	0.000327831
GO:0019932	second-messenger-mediated signaling	down	second-messenger-mediated signaling (GO:0019932)	BP	150	142	0	0.00032897
GO:0030510	regulation of BMP signaling pathway	down	regulation of BMP signaling pathway (GO:0030510)	BP	65	65	0	0.000332626
GO:0032103	positive regulation of response to external stimulus	down	positive regulation of response to external stimulus (GO:0032103)	BP	150	143	0	0.00033502
GO:0035329	hippo signaling	down	hippo signaling (GO:0035329)	BP	23	23	0	0.000340538
GO:0051149	positive regulation of muscle cell differentiation	down	positive regulation of muscle cell differentiation (GO:0051149)	BP	53	52	0	0.000343172
GO:0090183	regulation of kidney development	down	regulation of kidney development (GO:0090183)	BP	36	35	0	0.000343397
GO:0045445	myoblast differentiation	down	myoblast differentiation (GO:0045445)	BP	59	59	0	0.000347481
GO:0048017	inositol lipid-mediated signaling	down	inositol lipid-mediated signaling (GO:0048017)	BP	99	96	0	0.000349475
GO:0046328	regulation of JNK cascade	down	regulation of JNK cascade (GO:0046328)	BP	107	104	0	0.000350488
GO:0097746	regulation of blood vessel diameter	down	regulation of blood vessel diameter (GO:0097746)	BP	48	48	0	0.000352727
GO:0070663	regulation of leukocyte proliferation	down	regulation of leukocyte proliferation (GO:0070663)	BP	134	130	0.007692308	0.000352727
GO:0035296	regulation of tube diameter	down	regulation of tube diameter (GO:0035296)	BP	48	48	0	0.000352727
GO:0010633	negative regulation of epithelial cell migration	down	negative regulation of epithelial cell migration (GO:0010633)	BP	43	41	0.024390244	0.000374559
GO:0001657	ureteric bud development	down	ureteric bud development (GO:0001657)	BP	78	77	0	0.000376777
GO:0051494	negative regulation of cytoskeleton organization	down	negative regulation of cytoskeleton organization (GO:0051494)	BP	78	75	0	0.000378941
GO:0051403	stress-activated MAPK cascade	down	stress-activated MAPK cascade (GO:0051403)	BP	147	144	0.006944444	0.000378941
GO:0070527	platelet aggregation	down	platelet aggregation (GO:0070527)	BP	43	42	0	0.000379267
GO:0035150	regulation of tube size	down	regulation of tube size (GO:0035150)	BP	54	54	0	0.000379267
GO:0051591	response to cAMP	down	response to cAMP (GO:0051591)	BP	27	27	0	0.000379352
GO:0070371	ERK1 and ERK2 cascade	down	ERK1 and ERK2 cascade (GO:0070371)	BP	157	151	0	0.000384078
GO:0048704	embryonic skeletal system morphogenesis	down	embryonic skeletal system morphogenesis (GO:0048704)	BP	77	73	0	0.000384456
GO:0007157	heterophilic cell-cell adhesion via plasma membrane cell a	down	heterophilic cell-cell adhesion via plasma membrane cell adhesion molec	BP	19	18	0	0.000384456
GO:0043393	regulation of protein binding	down	regulation of protein binding (GO:0043393)	BP	133	130	0.015384615	0.000384456
GO:0090092	regulation of transmembrane receptor protein serine/thr	down	regulation of transmembrane receptor protein serine/threonine kinase si	BP	141	141	0	0.000384456
GO:0046330	positive regulation of JNK cascade	down	positive regulation of JNK cascade (GO:0046330)	BP	82	81	0	0.000386325
GO:1903428	positive regulation of reactive oxygen species biosyntheti	down	positive regulation of reactive oxygen species biosynthetic process (GO:1	BP	20	18	0.055555556	0.000387504
GO:0061036	positive regulation of cartilage development	down	positive regulation of cartilage development (GO:0061036)	BP	21	21	0	0.000392238
GO:0046638	positive regulation of alpha-beta T cell differentiation	down	positive regulation of alpha-beta T cell differentiation (GO:0046638)	BP	24	23	0	0.000394066
GO:0042552	myelination	down	myelination (GO:0042552)	BP	61	61	0.016393443	0.00039455
GO:0014829	vascular smooth muscle contraction	down	vascular smooth muscle contraction (GO:0014829)	BP	13	13	0	0.000395717
GO:0007052	mitotic spindle organization	down	mitotic spindle organization (GO:0007052)	BP	51	50	0.02	0.000400924
GO:1903169	regulation of calcium ion transmembrane transport	down	regulation of calcium ion transmembrane transport (GO:1903169)	BP	60	58	0	0.000401123
GO:0050885	neuromuscular process controlling balance	down	neuromuscular process controlling balance (GO:0050885)	BP	40	40	0	0.000401848
GO:0006775	fat-soluble vitamin metabolic process	down	fat-soluble vitamin metabolic process (GO:0006775)	BP	24	18	0	0.00040397
GO:0045766	positive regulation of angiogenesis	down	positive regulation of angiogenesis (GO:0045766)	BP	79	77	0	0.00040397
GO:0048813	dendrite morphogenesis	down	dendrite morphogenesis (GO:0048813)	BP	79	77	0	0.00040566
GO:0045600	positive regulation of fat cell differentiation	down	positive regulation of fat cell differentiation (GO:0045600)	BP	41	40	0	0.00041152
GO:0010460	positive regulation of heart rate	down	positive regulation of heart rate (GO:0010460)	BP	13	13	0	0.00041152
GO:0030261	chromosome condensation	down	chromosome condensation (GO:0030261)	BP	16	14	0.071428571	0.000411825
GO:0003012	muscle system process	down	muscle system process (GO:0003012)	BP	197	188	0.005319149	0.000418702

GO:0008366	axon ensheathment	down	axon ensheathment (GO:0008366)	BP	63	63	0.015873016	0.000419537
GO:0061311	cell surface receptor signaling pathway involved in heart c	down	cell surface receptor signaling pathway involved in heart development (G	BP	15	15	0	0.000419537
GO:0007272	ensheathment of neurons	down	ensheathment of neurons (GO:0007272)	BP	63	63	0.015873016	0.000419537
GO:0007405	neuroblast proliferation	down	neuroblast proliferation (GO:0007405)	BP	42	41	0	0.000419537
GO:0000819	sister chromatid segregation	down	sister chromatid segregation (GO:0000819)	BP	110	104	0.028846154	0.000430488
GO:0051291	protein heterooligomerization	down	protein heterooligomerization (GO:0051291)	BP	32	27	0.074074074	0.000436666
GO:0070304	positive regulation of stress-activated protein kinase signa	down	positive regulation of stress-activated protein kinase signaling cascade (G	BP	97	96	0	0.000437592
GO:0032944	regulation of mononuclear cell proliferation	down	regulation of mononuclear cell proliferation (GO:0032944)	BP	130	126	0.007936508	0.000449374
GO:0050848	regulation of calcium-mediated signaling	down	regulation of calcium-mediated signaling (GO:0050848)	BP	42	38	0	0.000456809
GO:0061371	determination of heart left/right asymmetry	down	determination of heart left/right asymmetry (GO:0061371)	BP	42	42	0	0.000457329
GO:1903426	regulation of reactive oxygen species biosynthetic process	down	regulation of reactive oxygen species biosynthetic process (GO:1903426)	BP	27	25	0.04	0.000473942
GO:0030656	regulation of vitamin metabolic process	down	regulation of vitamin metabolic process (GO:0030656)	BP	11	10	0	0.000479651
GO:0003214	cardiac left ventricle morphogenesis	down	cardiac left ventricle morphogenesis (GO:0003214)	BP	11	11	0	0.000487984
GO:0061298	retina vasculature development in camera-type eye	down	retina vasculature development in camera-type eye (GO:0061298)	BP	15	14	0	0.000488301
GO:0001947	heart looping	down	heart looping (GO:0001947)	BP	40	40	0	0.000490837
GO:0044344	cellular response to fibroblast growth factor stimulus	down	cellular response to fibroblast growth factor stimulus (GO:0044344)	BP	71	68	0	0.000493725
GO:0071774	response to fibroblast growth factor	down	response to fibroblast growth factor (GO:0071774)	BP	71	68	0	0.000493725
GO:0014037	Schwann cell differentiation	down	Schwann cell differentiation (GO:0014037)	BP	19	19	0	0.000495031
GO:0021602	cranial nerve morphogenesis	down	cranial nerve morphogenesis (GO:0021602)	BP	22	22	0	0.000504259
GO:0007379	segment specification	down	segment specification (GO:0007379)	BP	12	11	0	0.000504259
GO:0097581	lamellipodium organization	down	lamellipodium organization (GO:0097581)	BP	52	49	0	0.000518869
GO:0008347	glial cell migration	down	glial cell migration (GO:0008347)	BP	27	25	0	0.000519066
GO:0031109	microtubule polymerization or depolymerization	down	microtubule polymerization or depolymerization (GO:0031109)	BP	58	55	0	0.000519066
GO:0045823	positive regulation of heart contraction	down	positive regulation of heart contraction (GO:0045823)	BP	19	19	0	0.000525462
GO:0070665	positive regulation of leukocyte proliferation	down	positive regulation of leukocyte proliferation (GO:0070665)	BP	92	89	0.011235955	0.000527998
GO:0007009	plasma membrane organization	down	plasma membrane organization (GO:0007009)	BP	59	59	0.016949153	0.000530073
GO:0034104	negative regulation of tissue remodeling	down	negative regulation of tissue remodeling (GO:0034104)	BP	11	11	0	0.00053142
GO:0060788	ectodermal placode formation	down	ectodermal placode formation (GO:0060788)	BP	11	10	0	0.000532782
GO:0071697	ectodermal placode morphogenesis	down	ectodermal placode morphogenesis (GO:0071697)	BP	11	10	0	0.000532782
GO:0071711	basement membrane organization	down	basement membrane organization (GO:0071711)	BP	13	13	0	0.000552477
GO:0050670	regulation of lymphocyte proliferation	down	regulation of lymphocyte proliferation (GO:0050670)	BP	129	125	0.008	0.000554685
GO:0050732	negative regulation of peptidyl-tyrosine phosphorylation	down	negative regulation of peptidyl-tyrosine phosphorylation (GO:0050732)	BP	23	23	0	0.000557031
GO:0030857	negative regulation of epithelial cell differentiation	down	negative regulation of epithelial cell differentiation (GO:0030857)	BP	22	22	0	0.00056179
GO:0033631	cell-cell adhesion mediated by integrin	down	cell-cell adhesion mediated by integrin (GO:0033631)	BP	11	11	0	0.000564168
GO:0010935	regulation of macrophage cytokine production	down	regulation of macrophage cytokine production (GO:0010935)	BP	10	10	0	0.000568248
GO:0061005	cell differentiation involved in kidney development	down	cell differentiation involved in kidney development (GO:0061005)	BP	39	39	0	0.000573902
GO:0003179	heart valve morphogenesis	down	heart valve morphogenesis (GO:0003179)	BP	25	25	0	0.000573902
GO:0050900	leukocyte migration	down	leukocyte migration (GO:0050900)	BP	179	166	0	0.000578485
GO:0009101	glycoprotein biosynthetic process	down	glycoprotein biosynthetic process (GO:0009101)	BP	185	178	0.005617978	0.00058186
GO:0042119	neutrophil activation	down	neutrophil activation (GO:0042119)	BP	14	13	0	0.00058186
GO:0061383	trabecula morphogenesis	down	trabecula morphogenesis (GO:0061383)	BP	36	36	0.027777778	0.000584054
GO:0045879	negative regulation of smoothened signaling pathway	down	negative regulation of smoothened signaling pathway (GO:0045879)	BP	19	19	0	0.000601088
GO:0110053	regulation of actin filament organization	down	regulation of actin filament organization (GO:0110053)	BP	144	138	0	0.000601088
GO:0045055	regulated exocytosis	down	regulated exocytosis (GO:0045055)	BP	99	96	0	0.000607992
GO:0086005	ventricular cardiac muscle cell action potential	down	ventricular cardiac muscle cell action potential (GO:0086005)	BP	18	18	0	0.000618887
GO:0032874	positive regulation of stress-activated MAPK cascade	down	positive regulation of stress-activated MAPK cascade (GO:0032874)	BP	96	95	0	0.000622065
GO:0043383	negative T cell selection	down	negative T cell selection (GO:0043383)	BP	11	10	0	0.000625702
GO:0033622	integrin activation	down	integrin activation (GO:0033622)	BP	16	16	0.0625	0.000627301
GO:0085029	extracellular matrix assembly	down	extracellular matrix assembly (GO:0085029)	BP	19	19	0	0.000647995
GO:0006939	smooth muscle contraction	down	smooth muscle contraction (GO:0006939)	BP	54	53	0	0.000647995
GO:0048010	vascular endothelial growth factor receptor signaling path	down	vascular endothelial growth factor receptor signaling pathway (GO:0048	BP	29	27	0	0.000665741
GO:0044091	membrane biogenesis	down	membrane biogenesis (GO:0044091)	BP	22	22	0	0.000666129
GO:0071364	cellular response to epidermal growth factor stimulus	down	cellular response to epidermal growth factor stimulus (GO:0071364)	BP	15	15	0	0.000675213
GO:0061162	establishment of monopolar cell polarity	down	establishment of monopolar cell polarity (GO:0061162)	BP	12	12	0	0.000678506
GO:0061339	establishment or maintenance of monopolar cell polarity	down	establishment or maintenance of monopolar cell polarity (GO:0061339)	BP	13	12	0	0.000678506
GO:0014068	positive regulation of phosphatidylinositol 3-kinase signa	down	positive regulation of phosphatidylinositol 3-kinase signaling (GO:0014	BP	46	44	0	0.000682147
GO:0008608	attachment of spindle microtubules to kinetochore	down	attachment of spindle microtubules to kinetochore (GO:0008608)	BP	17	16	0	0.000682816
GO:0048015	phosphatidylinositol-mediated signaling	down	phosphatidylinositol-mediated signaling (GO:0048015)	BP	96	93	0	0.000686044
GO:0043114	regulation of vascular permeability	down	regulation of vascular permeability (GO:0043114)	BP	14	14	0	0.000689119
GO:0010976	positive regulation of neuron projection development	down	positive regulation of neuron projection development (GO:0010976)	BP	119	115	0	0.000706719
GO:1900746	regulation of vascular endothelial growth factor signaling	down	regulation of vascular endothelial growth factor signaling pathway (GO:1	BP	11	11	0	0.000708866
GO:0072498	embryonic skeletal joint development	down	embryonic skeletal joint development (GO:0072498)	BP	10	10	0	0.000710657
GO:0060444	branching involved in mammary gland duct morphogenes	down	branching involved in mammary gland duct morphogenesis (GO:00604	BP	22	20	0	0.000714017
GO:0051875	pigment granule localization	down	pigment granule localization (GO:0051875)	BP	14	14	0	0.000719832

GO:0032232	negative regulation of actin filament bundle assembly	down	negative regulation of actin filament bundle assembly (GO:0032232)	BP	16	16	0	0.000721699
GO:0007051	spindle organization	down	spindle organization (GO:0007051)	BP	91	89	0.011235955	0.000722413
GO:0051905	establishment of pigment granule localization	down	establishment of pigment granule localization (GO:0051905)	BP	13	13	0	0.00073194
GO:0051904	pigment granule transport	down	pigment granule transport (GO:0051904)	BP	13	13	0	0.00073194
GO:0036293	response to decreased oxygen levels	down	response to decreased oxygen levels (GO:0036293)	BP	117	116	0	0.000747936
GO:0001666	response to hypoxia	down	response to hypoxia (GO:0001666)	BP	117	116	0	0.000747936
GO:0050890	cognition	down	cognition (GO:0050890)	BP	152	145	0.006896552	0.000750391
GO:0032147	activation of protein kinase activity	down	activation of protein kinase activity (GO:0032147)	BP	124	122	0.008196721	0.000753376
GO:0051480	regulation of cytosolic calcium ion concentration	down	regulation of cytosolic calcium ion concentration (GO:0051480)	BP	120	114	0	0.000755476
GO:2001236	regulation of extrinsic apoptotic signaling pathway	down	regulation of extrinsic apoptotic signaling pathway (GO:2001236)	BP	124	120	0	0.000755476
GO:0006182	cGMP biosynthetic process	down	cGMP biosynthetic process (GO:0006182)	BP	21	20	0	0.00077505
GO:0021782	glial cell development	down	glial cell development (GO:0021782)	BP	47	46	0	0.000785752
GO:0032102	negative regulation of response to external stimulus	down	negative regulation of response to external stimulus (GO:0032102)	BP	168	160	0	0.000795215
GO:0007254	JNK cascade	down	JNK cascade (GO:0007254)	BP	116	113	0	0.000801457
GO:0007613	memory	down	memory (GO:0007613)	BP	52	50	0.02	0.000801457
GO:0051924	regulation of calcium ion transport	down	regulation of calcium ion transport (GO:0051924)	BP	105	101	0	0.000809373
GO:0086065	cell communication involved in cardiac conduction	down	cell communication involved in cardiac conduction (GO:0086065)	BP	21	21	0	0.000810817
GO:0043901	negative regulation of multi-organism process	down	negative regulation of multi-organism process (GO:0043901)	BP	93	89	0.011235955	0.000810817
GO:1900025	negative regulation of substrate adhesion-dependent cell	down	negative regulation of substrate adhesion-dependent cell spreading (GO:1	BP	11	10	0	0.000818727
GO:0051057	positive regulation of small GTPase mediated signal transc	down	positive regulation of small GTPase mediated signal transduction (GO:005	BP	29	27	0	0.000818727
GO:0071320	cellular response to cAMP	down	cellular response to cAMP (GO:0071320)	BP	22	22	0	0.000820158
GO:0002573	myeloid leukocyte differentiation	down	myeloid leukocyte differentiation (GO:0002573)	BP	131	128	0	0.000820158
GO:1903115	regulation of actin filament-based movement	down	regulation of actin filament-based movement (GO:1903115)	BP	18	17	0	0.000820506
GO:2000727	positive regulation of cardiac muscle cell differentiation	down	positive regulation of cardiac muscle cell differentiation (GO:2000727)	BP	12	12	0	0.000847604
GO:0035313	wound healing, spreading of epidermal cells	down	wound healing, spreading of epidermal cells (GO:0035313)	BP	11	10	0.1	0.000852848
GO:0060041	retina development in camera-type eye	down	retina development in camera-type eye (GO:0060041)	BP	97	93	0	0.000853642
GO:0002027	regulation of heart rate	down	regulation of heart rate (GO:0002027)	BP	52	51	0	0.000860124
GO:0007596	blood coagulation	down	blood coagulation (GO:0007596)	BP	120	116	0	0.000887588
GO:0072089	stem cell proliferation	down	stem cell proliferation (GO:0072089)	BP	83	82	0	0.000903379
GO:0035089	establishment of apical/basal cell polarity	down	establishment of apical/basal cell polarity (GO:0035089)	BP	10	10	0	0.000907865
GO:0022029	telencephalon cell migration	down	telencephalon cell migration (GO:0022029)	BP	46	46	0	0.000907865
GO:0001935	endothelial cell proliferation	down	endothelial cell proliferation (GO:0001935)	BP	74	70	0.014285714	0.000928331
GO:0035024	negative regulation of Rho protein signal transduction	down	negative regulation of Rho protein signal transduction (GO:0035024)	BP	13	13	0	0.000928331
GO:0035455	response to interferon-alpha	down	response to interferon-alpha (GO:0035455)	BP	12	12	0	0.000928331
GO:0050817	coagulation	down	coagulation (GO:0050817)	BP	124	120	0	0.000933885
GO:2001240	negative regulation of extrinsic apoptotic signaling pathw	down	negative regulation of extrinsic apoptotic signaling pathway in absence o	BP	22	22	0	0.000933885
GO:1901099	negative regulation of signal transduction in absence of lig	down	negative regulation of signal transduction in absence of ligand (GO:19010	BP	22	22	0	0.000933885
GO:0007599	hemostasis	down	hemostasis (GO:0007599)	BP	122	118	0	0.000941656
GO:1903409	reactive oxygen species biosynthetic process	down	reactive oxygen species biosynthetic process (GO:1903409)	BP	41	37	0.027027027	0.000945696
GO:0110020	regulation of actomyosin structure organization	down	regulation of actomyosin structure organization (GO:0110020)	BP	57	54	0	0.000963641
GO:0030218	erythrocyte differentiation	down	erythrocyte differentiation (GO:0030218)	BP	74	73	0	0.000969184
GO:0048469	cell maturation	down	cell maturation (GO:0048469)	BP	108	105	0.00952381	0.000973785
GO:2000826	regulation of heart morphogenesis	down	regulation of heart morphogenesis (GO:2000826)	BP	24	24	0	0.000973785
GO:0097191	extrinsic apoptotic signaling pathway	down	extrinsic apoptotic signaling pathway (GO:0097191)	BP	172	166	0	0.000996412
GO:0050905	neuromuscular process	down	neuromuscular process (GO:0050905)	BP	78	77	0	0.000996412
GO:0051782	negative regulation of cell division	down	negative regulation of cell division (GO:0051782)	BP	10	9	0	0.001018886
GO:0007413	axonal fasciculation	down	axonal fasciculation (GO:0007413)	BP	14	14	0	0.001021468
GO:0000075	cell cycle checkpoint	down	cell cycle checkpoint (GO:0000075)	BP	118	113	0.017699115	0.001021468
GO:0021675	nerve development	down	nerve development (GO:0021675)	BP	54	54	0	0.001021468
GO:0106030	neuron projection fasciculation	down	neuron projection fasciculation (GO:0106030)	BP	14	14	0	0.001021468
GO:0051155	positive regulation of striated muscle cell differentiation	down	positive regulation of striated muscle cell differentiation (GO:0051155)	BP	41	40	0	0.001021468
GO:0060402	calcium ion transport into cytosol	down	calcium ion transport into cytosol (GO:0060402)	BP	70	66	0	0.001021523
GO:0032943	mononuclear cell proliferation	down	mononuclear cell proliferation (GO:0032943)	BP	167	163	0.006134969	0.001021523
GO:2001239	regulation of extrinsic apoptotic signaling pathway in abs	down	regulation of extrinsic apoptotic signaling pathway in absence of ligand (	BP	34	34	0	0.001030288
GO:0000187	activation of MAPK activity	down	activation of MAPK activity (GO:0000187)	BP	58	58	0	0.001031572
GO:0036230	granulocyte activation	down	granulocyte activation (GO:0036230)	BP	15	14	0	0.001031572
GO:0008543	fibroblast growth factor receptor signaling pathway	down	fibroblast growth factor receptor signaling pathway (GO:0008543)	BP	58	56	0	0.001032727
GO:0090288	negative regulation of cellular response to growth factor s	down	negative regulation of cellular response to growth factor stimulus (GO:00	BP	89	88	0	0.001032727
GO:0045619	regulation of lymphocyte differentiation	down	regulation of lymphocyte differentiation (GO:0045619)	BP	96	89	0	0.001032727
GO:0045649	regulation of macrophage differentiation	down	regulation of macrophage differentiation (GO:0045649)	BP	13	13	0	0.001046371
GO:0045621	positive regulation of lymphocyte differentiation	down	positive regulation of lymphocyte differentiation (GO:0045621)	BP	55	53	0	0.001055871
GO:0032946	positive regulation of mononuclear cell proliferation	down	positive regulation of mononuclear cell proliferation (GO:0032946)	BP	87	84	0.011904762	0.001055871
GO:1905276	regulation of epithelial tube formation	down	regulation of epithelial tube formation (GO:1905276)	BP	17	16	0	0.001055871
GO:0031102	neuron projection regeneration	down	neuron projection regeneration (GO:0031102)	BP	18	18	0	0.001065571

GO:0035115	embryonic forelimb morphogenesis	down	embryonic forelimb morphogenesis (GO:0035115)	BP	24	22	0	0.001093551
GO:0106056	regulation of calcineurin-mediated signaling	down	regulation of calcineurin-mediated signaling (GO:0106056)	BP	11	11	0	0.001093551
GO:0070884	regulation of calcineurin-NFAT signaling cascade	down	regulation of calcineurin-NFAT signaling cascade (GO:0070884)	BP	11	11	0	0.001093551
GO:0045071	negative regulation of viral genome replication	down	negative regulation of viral genome replication (GO:0045071)	BP	26	24	0	0.001098749
GO:0070588	calcium ion transmembrane transport	down	calcium ion transmembrane transport (GO:0070588)	BP	145	138	0.007246377	0.001101588
GO:0030038	contractile actin filament bundle assembly	down	contractile actin filament bundle assembly (GO:0030038)	BP	60	58	0	0.001114043
GO:0043149	stress fiber assembly	down	stress fiber assembly (GO:0043149)	BP	60	58	0	0.001114043
GO:0072028	nephron morphogenesis	down	nephron morphogenesis (GO:0072028)	BP	61	60	0	0.001123517
GO:1903672	positive regulation of sprouting angiogenesis	down	positive regulation of sprouting angiogenesis (GO:1903672)	BP	10	10	0	0.001140356
GO:2000106	regulation of leukocyte apoptotic process	down	regulation of leukocyte apoptotic process (GO:2000106)	BP	54	53	0.018867925	0.001148715
GO:0045580	regulation of T cell differentiation	down	regulation of T cell differentiation (GO:0045580)	BP	75	69	0	0.001155187
GO:0070168	negative regulation of biomineral tissue development	down	negative regulation of biomineral tissue development (GO:0070168)	BP	15	13	0	0.001174874
GO:0048566	embryonic digestive tract development	down	embryonic digestive tract development (GO:0048566)	BP	24	24	0	0.001175902
GO:0046651	lymphocyte proliferation	down	lymphocyte proliferation (GO:0046651)	BP	166	162	0.00617284	0.001210274
GO:0021513	spinal cord dorsal/ventral patterning	down	spinal cord dorsal/ventral patterning (GO:0021513)	BP	18	17	0	0.001214322
GO:0021545	cranial nerve development	down	cranial nerve development (GO:0021545)	BP	35	35	0	0.001227838
GO:0002335	mature B cell differentiation	down	mature B cell differentiation (GO:0002335)	BP	17	17	0	0.001227838
GO:0031214	biomineral tissue development	down	biomineral tissue development (GO:0031214)	BP	87	82	0.012195122	0.001234053
GO:0040001	establishment of mitotic spindle localization	down	establishment of mitotic spindle localization (GO:0040001)	BP	18	17	0	0.001250613
GO:0070661	leukocyte proliferation	down	leukocyte proliferation (GO:0070661)	BP	175	171	0.005847953	0.001250613
GO:1902743	regulation of lamellipodium organization	down	regulation of lamellipodium organization (GO:1902743)	BP	24	22	0	0.001252815
GO:0048846	axon extension involved in axon guidance	down	axon extension involved in axon guidance (GO:0048846)	BP	16	16	0	0.001262575
GO:1902284	neuron projection extension involved in neuron projectic	down	neuron projection extension involved in neuron projection guidance (GO	BP	16	16	0	0.001262575
GO:0001570	vasculogenesis	down	vasculogenesis (GO:0001570)	BP	48	47	0	0.001262575
GO:0042098	T cell proliferation	down	T cell proliferation (GO:0042098)	BP	117	113	0.008849558	0.001321858
GO:0071295	cellular response to vitamin	down	cellular response to vitamin (GO:0071295)	BP	10	9	0	0.001346487
GO:0070372	regulation of ERK1 and ERK2 cascade	down	regulation of ERK1 and ERK2 cascade (GO:0070372)	BP	149	143	0	0.001346487
GO:0035136	forelimb morphogenesis	down	forelimb morphogenesis (GO:0035136)	BP	31	29	0	0.001354671
GO:0030890	positive regulation of B cell proliferation	down	positive regulation of B cell proliferation (GO:0030890)	BP	28	28	0	0.001354671
GO:0051261	protein depolymerization	down	protein depolymerization (GO:0051261)	BP	56	53	0.018867925	0.001354671
GO:0002088	lens development in camera-type eye	down	lens development in camera-type eye (GO:0002088)	BP	47	43	0	0.001367352
GO:0043627	response to estrogen	down	response to estrogen (GO:0043627)	BP	28	25	0	0.001384238
GO:0050671	positive regulation of lymphocyte proliferation	down	positive regulation of lymphocyte proliferation (GO:0050671)	BP	86	83	0.012048193	0.001387429
GO:0030500	regulation of bone mineralization	down	regulation of bone mineralization (GO:0030500)	BP	53	50	0	0.001387429
GO:0030850	prostate gland development	down	prostate gland development (GO:0030850)	BP	35	33	0	0.001397374
GO:0072087	renal vesicle development	down	renal vesicle development (GO:0072087)	BP	16	15	0	0.001397374
GO:0018209	peptidyl-serine modification	down	peptidyl-serine modification (GO:0018209)	BP	161	155	0.006451613	0.001402046
GO:0007611	learning or memory	down	learning or memory (GO:0007611)	BP	131	128	0.0078125	0.001402449
GO:1901019	regulation of calcium ion transmembrane transporter act	down	regulation of calcium ion transmembrane transporter activity (GO:1901C	BP	27	26	0	0.001402449
GO:0055117	regulation of cardiac muscle contraction	down	regulation of cardiac muscle contraction (GO:0055117)	BP	33	32	0	0.001415013
GO:0072673	lamellipodium morphogenesis	down	lamellipodium morphogenesis (GO:0072673)	BP	14	14	0	0.001442899
GO:0070482	response to oxygen levels	down	response to oxygen levels (GO:0070482)	BP	123	122	0	0.001444541
GO:0030858	positive regulation of epithelial cell differentiation	down	positive regulation of epithelial cell differentiation (GO:0030858)	BP	41	38	0	0.001455684
GO:0008016	regulation of heart contraction	down	regulation of heart contraction (GO:0008016)	BP	95	93	0.010752688	0.001461007
GO:0050926	regulation of positive chemotaxis	down	regulation of positive chemotaxis (GO:0050926)	BP	12	11	0	0.001461007
GO:0035587	purinergic receptor signaling pathway	down	purinergic receptor signaling pathway (GO:0035587)	BP	22	22	0	0.001468225
GO:0055007	cardiac muscle cell differentiation	down	cardiac muscle cell differentiation (GO:0055007)	BP	58	56	0	0.001489824
GO:0007585	respiratory gaseous exchange	down	respiratory gaseous exchange (GO:0007585)	BP	38	36	0	0.001489824
GO:0021532	neural tube patterning	down	neural tube patterning (GO:0021532)	BP	34	34	0	0.00150709
GO:0051146	striated muscle cell differentiation	down	striated muscle cell differentiation (GO:0051146)	BP	154	151	0	0.001509226
GO:0035113	embryonic appendage morphogenesis	down	embryonic appendage morphogenesis (GO:0035113)	BP	102	97	0	0.001513538
GO:0030326	embryonic limb morphogenesis	down	embryonic limb morphogenesis (GO:0030326)	BP	102	97	0	0.001513538
GO:0072273	metanephric nephron morphogenesis	down	metanephric nephron morphogenesis (GO:0072273)	BP	20	19	0	0.001513538
GO:0008593	regulation of Notch signaling pathway	down	regulation of Notch signaling pathway (GO:0008593)	BP	46	42	0	0.001513538
GO:0090162	establishment of epithelial cell polarity	down	establishment of epithelial cell polarity (GO:0090162)	BP	18	17	0	0.001519608
GO:0014812	muscle cell migration	down	muscle cell migration (GO:0014812)	BP	37	36	0	0.001519608
GO:0099565	chemical synaptic transmission, postsynaptic	down	chemical synaptic transmission, postsynaptic (GO:0099565)	BP	38	37	0	0.001559846
GO:0046456	icosanoid biosynthetic process	down	icosanoid biosynthetic process (GO:0046456)	BP	23	22	0.045454545	0.001594325
GO:0031076	embryonic camera-type eye development	down	embryonic camera-type eye development (GO:0031076)	BP	30	30	0	0.001606848
GO:0030502	negative regulation of bone mineralization	down	negative regulation of bone mineralization (GO:0030502)	BP	13	11	0	0.001612246
GO:0050866	negative regulation of cell activation	down	negative regulation of cell activation (GO:0050866)	BP	103	98	0	0.001613252
GO:0046824	positive regulation of nucleocytoplasmic transport	down	positive regulation of nucleocytoplasmic transport (GO:0046824)	BP	83	82	0	0.00163643
GO:0031032	actomyosin structure organization	down	actomyosin structure organization (GO:0031032)	BP	108	105	0	0.00164046
GO:0072088	nephron epithelium morphogenesis	down	nephron epithelium morphogenesis (GO:0072088)	BP	60	59	0	0.001650244

GO:1901213	regulation of transcription from RNA polymerase II promo	down	regulation of transcription from RNA polymerase II promoter involved in	BP	10	10	0	0.001662496
GO:0050770	regulation of axonogenesis	down	regulation of axonogenesis (GO:0050770)	BP	87	83	0	0.001662749
GO:2001257	regulation of cation channel activity	down	regulation of cation channel activity (GO:2001257)	BP	59	58	0	0.001680713
GO:0035418	protein localization to synapse	down	protein localization to synapse (GO:0035418)	BP	11	11	0	0.001689489
GO:0045582	positive regulation of T cell differentiation	down	positive regulation of T cell differentiation (GO:0045582)	BP	44	42	0	0.001720762
GO:0045429	positive regulation of nitric oxide biosynthetic process	down	positive regulation of nitric oxide biosynthetic process (GO:0045429)	BP	16	15	0.066666667	0.001728962
GO:1904407	positive regulation of nitric oxide metabolic process	down	positive regulation of nitric oxide metabolic process (GO:1904407)	BP	16	15	0.066666667	0.001728962
GO:0006937	regulation of muscle contraction	down	regulation of muscle contraction (GO:0006937)	BP	73	71	0.014084507	0.001728962
GO:0090257	regulation of muscle system process	down	regulation of muscle system process (GO:0090257)	BP	96	94	0.010638298	0.001741188
GO:0072078	nephron tubule morphogenesis	down	nephron tubule morphogenesis (GO:0072078)	BP	58	57	0	0.001747169
GO:0043486	histone exchange	down	histone exchange (GO:0043486)	BP	11	11	0.090909091	0.001759048
GO:0042733	embryonic digit morphogenesis	down	embryonic digit morphogenesis (GO:0042733)	BP	51	48	0	0.001759823
GO:0090184	positive regulation of kidney development	down	positive regulation of kidney development (GO:0090184)	BP	24	23	0	0.001759823
GO:1903305	regulation of regulated secretory pathway	down	regulation of regulated secretory pathway (GO:1903305)	BP	56	54	0	0.001759823
GO:1902904	negative regulation of supramolecular fiber organization	down	negative regulation of supramolecular fiber organization (GO:1902904)	BP	69	66	0	0.001794032
GO:1903670	regulation of sprouting angiogenesis	down	regulation of sprouting angiogenesis (GO:1903670)	BP	21	21	0	0.001802039
GO:0042633	hair cycle	down	hair cycle (GO:0042633)	BP	76	72	0	0.001823062
GO:0042303	molting cycle	down	molting cycle (GO:0042303)	BP	76	72	0	0.001823062
GO:0006887	exocytosis	down	exocytosis (GO:0006887)	BP	166	160	0	0.001824551
GO:1903034	regulation of response to wounding	down	regulation of response to wounding (GO:1903034)	BP	98	97	0	0.001824551
GO:0031099	regeneration	down	regeneration (GO:0031099)	BP	43	42	0	0.001824613
GO:0042307	positive regulation of protein import into nucleus	down	positive regulation of protein import into nucleus (GO:0042307)	BP	70	69	0	0.001827681
GO:0050727	regulation of inflammatory response	down	regulation of inflammatory response (GO:0050727)	BP	165	161	0	0.001827681
GO:0046636	negative regulation of alpha-beta T cell activation	down	negative regulation of alpha-beta T cell activation (GO:0046636)	BP	11	11	0	0.001837112
GO:0140029	exocytic process	down	exocytic process (GO:0140029)	BP	34	34	0	0.001844674
GO:0002685	regulation of leukocyte migration	down	regulation of leukocyte migration (GO:0002685)	BP	95	89	0	0.001850681
GO:0035850	epithelial cell differentiation involved in kidney developm	down	epithelial cell differentiation involved in kidney development (GO:00358	BP	33	33	0	0.001881629
GO:0006936	muscle contraction	down	muscle contraction (GO:0006936)	BP	163	155	0.006451613	0.001893606
GO:1905476	negative regulation of protein localization to membrane	down	negative regulation of protein localization to membrane (GO:1905476)	BP	12	12	0	0.001893606
GO:2000050	regulation of non-canonical Wnt signaling pathway	down	regulation of non-canonical Wnt signaling pathway (GO:2000050)	BP	14	13	0	0.001901184
GO:0042471	ear morphogenesis	down	ear morphogenesis (GO:0042471)	BP	94	90	0	0.001952209
GO:0032231	regulation of actin filament bundle assembly	down	regulation of actin filament bundle assembly (GO:0032231)	BP	58	56	0	0.001952209
GO:0071158	positive regulation of cell cycle arrest	down	positive regulation of cell cycle arrest (GO:0071158)	BP	23	22	0	0.001984419
GO:0003338	metanephros morphogenesis	down	metanephros morphogenesis (GO:0003338)	BP	26	25	0	0.002008264
GO:1902692	regulation of neuroblast proliferation	down	regulation of neuroblast proliferation (GO:1902692)	BP	21	21	0	0.002008264
GO:0070849	response to epidermal growth factor	down	response to epidermal growth factor (GO:0070849)	BP	18	18	0	0.002008264
GO:0045061	thymic T cell selection	down	thymic T cell selection (GO:0045061)	BP	18	17	0	0.002008264
GO:0008544	epidermis development	down	epidermis development (GO:0008544)	BP	174	163	0	0.002029997
GO:1903900	regulation of viral life cycle	down	regulation of viral life cycle (GO:1903900)	BP	85	81	0.024691358	0.002034243
GO:0030071	regulation of mitotic metaphase/anaphase transition	down	regulation of mitotic metaphase/anaphase transition (GO:0030071)	BP	24	23	0.043478261	0.0020982
GO:0061351	neural precursor cell proliferation	down	neural precursor cell proliferation (GO:0061351)	BP	94	90	0.011111111	0.002151848
GO:0021761	limbic system development	down	limbic system development (GO:0021761)	BP	60	59	0.033898305	0.002206782
GO:0033002	muscle cell proliferation	down	muscle cell proliferation (GO:0033002)	BP	77	75	0	0.002212805
GO:1904062	regulation of cation transmembrane transport	down	regulation of cation transmembrane transport (GO:1904062)	BP	139	136	0	0.002220521
GO:0050864	regulation of B cell activation	down	regulation of B cell activation (GO:0050864)	BP	75	75	0	0.002228334
GO:0006693	prostaglandin metabolic process	down	prostaglandin metabolic process (GO:0006693)	BP	18	18	0	0.002262527
GO:0006692	prostanoid metabolic process	down	prostanoid metabolic process (GO:0006692)	BP	18	18	0	0.002262527
GO:0072503	cellular divalent inorganic cation homeostasis	down	cellular divalent inorganic cation homeostasis (GO:0072503)	BP	197	188	0.005319149	0.002288515
GO:0055023	positive regulation of cardiac muscle tissue growth	down	positive regulation of cardiac muscle tissue growth (GO:0055023)	BP	18	18	0	0.002293518
GO:0008045	motor neuron axon guidance	down	motor neuron axon guidance (GO:0008045)	BP	22	22	0	0.002317797
GO:0070374	positive regulation of ERK1 and ERK2 cascade	down	positive regulation of ERK1 and ERK2 cascade (GO:0070374)	BP	102	97	0	0.002324131
GO:0042472	inner ear morphogenesis	down	inner ear morphogenesis (GO:0042472)	BP	78	74	0	0.00233856
GO:0061515	myeloid cell development	down	myeloid cell development (GO:0061515)	BP	43	42	0	0.002414067
GO:0007584	response to nutrient	down	response to nutrient (GO:0007584)	BP	24	22	0	0.002419353
GO:0051492	regulation of stress fiber assembly	down	regulation of stress fiber assembly (GO:0051492)	BP	51	49	0	0.002437041
GO:1904591	positive regulation of protein import	down	positive regulation of protein import (GO:1904591)	BP	71	70	0	0.002445004
GO:0043567	regulation of insulin-like growth factor receptor signaling	down	regulation of insulin-like growth factor receptor signaling pathway (GO:0	BP	15	15	0	0.0024679
GO:0086001	cardiac muscle cell action potential	down	cardiac muscle cell action potential (GO:0086001)	BP	28	28	0	0.002469161
GO:0072224	metanephric glomerulus development	down	metanephric glomerulus development (GO:0072224)	BP	10	10	0	0.002496483
GO:0034113	heterotypic cell-cell adhesion	down	heterotypic cell-cell adhesion (GO:0034113)	BP	33	32	0	0.002507836
GO:1903524	positive regulation of blood circulation	down	positive regulation of blood circulation (GO:1903524)	BP	28	27	0	0.002518763
GO:0021591	ventricular system development	down	ventricular system development (GO:0021591)	BP	22	22	0	0.002536272
GO:2001237	negative regulation of extrinsic apoptotic signaling pathw	down	negative regulation of extrinsic apoptotic signaling pathway (GO:200123	BP	73	72	0	0.002573224
GO:2000810	regulation of bicellular tight junction assembly	down	regulation of bicellular tight junction assembly (GO:2000810)	BP	11	11	0	0.002594632

GO:0002244	hematopoietic progenitor cell differentiation	down	hematopoietic progenitor cell differentiation (GO:0002244)	BP	86	82	0.012195122	0.002610496
GO:0009187	cyclic nucleotide metabolic process	down	cyclic nucleotide metabolic process (GO:0009187)	BP	105	101	0	0.002633712
GO:0010771	negative regulation of cell morphogenesis involved in diff	down	negative regulation of cell morphogenesis involved in differentiation (GO	BP	50	49	0	0.002648752
GO:0021846	cell proliferation in forebrain	down	cell proliferation in forebrain (GO:0021846)	BP	21	20	0.05	0.002651085
GO:0009190	cyclic nucleotide biosynthetic process	down	cyclic nucleotide biosynthetic process (GO:0009190)	BP	81	80	0	0.002656821
GO:0031016	pancreas development	down	pancreas development (GO:0031016)	BP	47	47	0	0.002656821
GO:0051293	establishment of spindle localization	down	establishment of spindle localization (GO:0051293)	BP	23	22	0	0.00265754
GO:1900078	positive regulation of cellular response to insulin stimulu	down	positive regulation of cellular response to insulin stimulus (GO:1900078)	BP	15	15	0.066666667	0.00265754
GO:0008344	adult locomotory behavior	down	adult locomotory behavior (GO:0008344)	BP	63	61	0	0.002658095
GO:0051497	negative regulation of stress fiber assembly	down	negative regulation of stress fiber assembly (GO:0051497)	BP	14	14	0	0.002658095
GO:0018105	peptidyl-serine phosphorylation	down	peptidyl-serine phosphorylation (GO:0018105)	BP	151	145	0.006896552	0.002658095
GO:2000736	regulation of stem cell differentiation	down	regulation of stem cell differentiation (GO:2000736)	BP	25	24	0	0.002658095
GO:0042129	regulation of T cell proliferation	down	regulation of T cell proliferation (GO:0042129)	BP	97	93	0.010752688	0.002658095
GO:0045165	cell fate commitment	down	cell fate commitment (GO:0045165)	BP	149	146	0	0.002671981
GO:0072017	distal tubule development	down	distal tubule development (GO:0072017)	BP	10	10	0	0.002694441
GO:0007091	metaphase/anaphase transition of mitotic cell cycle	down	metaphase/anaphase transition of mitotic cell cycle (GO:0007091)	BP	25	24	0.041666667	0.002694441
GO:0010965	regulation of mitotic sister chromatid separation	down	regulation of mitotic sister chromatid separation (GO:0010965)	BP	25	24	0.041666667	0.002694441
GO:0020027	hemoglobin metabolic process	down	hemoglobin metabolic process (GO:0020027)	BP	13	13	0	0.002724254
GO:0021795	cerebral cortex cell migration	down	cerebral cortex cell migration (GO:0021795)	BP	35	35	0	0.002777424
GO:0070252	actin-mediated cell contraction	down	actin-mediated cell contraction (GO:0070252)	BP	41	39	0.025641026	0.002798723
GO:0032486	Rap protein signal transduction	down	Rap protein signal transduction (GO:0032486)	BP	10	9	0.111111111	0.002803522
GO:0050806	positive regulation of synaptic transmission	down	positive regulation of synaptic transmission (GO:0050806)	BP	61	58	0.017241379	0.002828445
GO:1903844	regulation of cellular response to transforming growth fac	down	regulation of cellular response to transforming growth factor beta stimul	BP	64	64	0	0.002828445
GO:0017015	regulation of transforming growth factor beta receptor si	down	regulation of transforming growth factor beta receptor signaling pathway	BP	64	64	0	0.002828445
GO:0030217	T cell differentiation	down	T cell differentiation (GO:0030217)	BP	153	147	0	0.002828445
GO:0043297	apical junction assembly	down	apical junction assembly (GO:0043297)	BP	34	33	0	0.002836692
GO:0034405	response to fluid shear stress	down	response to fluid shear stress (GO:0034405)	BP	16	16	0	0.002836692
GO:0033280	response to vitamin D	down	response to vitamin D (GO:0033280)	BP	13	11	0	0.002836692
GO:1904035	regulation of epithelial cell apoptotic process	down	regulation of epithelial cell apoptotic process (GO:1904035)	BP	37	37	0	0.002839965
GO:0042362	fat-soluble vitamin biosynthetic process	down	fat-soluble vitamin biosynthetic process (GO:0042362)	BP	11	10	0	0.002842023
GO:0071498	cellular response to fluid shear stress	down	cellular response to fluid shear stress (GO:0071498)	BP	10	10	0	0.002880758
GO:0060343	trabecula formation	down	trabecula formation (GO:0060343)	BP	18	18	0.055555556	0.002901261
GO:0008360	regulation of cell shape	down	regulation of cell shape (GO:0008360)	BP	79	71	0	0.002913784
GO:0046683	response to organophosphorus	down	response to organophosphorus (GO:0046683)	BP	47	47	0	0.002929818
GO:0017156	calcium ion regulated exocytosis	down	calcium ion regulated exocytosis (GO:0017156)	BP	51	51	0	0.002942584
GO:0090504	epiboly	down	epiboly (GO:0090504)	BP	21	19	0.052631579	0.002960504
GO:0010959	regulation of metal ion transport	down	regulation of metal ion transport (GO:0010959)	BP	172	167	0	0.002977855
GO:0030593	neutrophil chemotaxis	down	neutrophil chemotaxis (GO:0030593)	BP	42	39	0	0.00298477
GO:0001756	somitogenesis	down	somitogenesis (GO:0001756)	BP	57	55	0	0.002998019
GO:0051092	positive regulation of NF-kappaB transcription factor acti	down	positive regulation of NF-kappaB transcription factor activity (GO:00510	BP	79	79	0	0.002999629
GO:2000738	positive regulation of stem cell differentiation	down	positive regulation of stem cell differentiation (GO:2000738)	BP	12	11	0	0.002999629
GO:0009798	axis specification	down	axis specification (GO:0009798)	BP	62	59	0	0.003031959
GO:0010715	regulation of extracellular matrix disassembly	down	regulation of extracellular matrix disassembly (GO:0010715)	BP	10	8	0	0.003055189
GO:0035411	catenin import into nucleus	down	catenin import into nucleus (GO:0035411)	BP	19	19	0	0.003062975
GO:0035412	regulation of catenin import into nucleus	down	regulation of catenin import into nucleus (GO:0035412)	BP	19	19	0	0.003062975
GO:0046068	cGMP metabolic process	down	cGMP metabolic process (GO:0046068)	BP	31	30	0	0.003109876
GO:0043413	macromolecule glycosylation	down	macromolecule glycosylation (GO:0043413)	BP	141	136	0.007352941	0.003109876
GO:0045926	negative regulation of growth	down	negative regulation of growth (GO:0045926)	BP	144	141	0	0.003109876
GO:2000179	positive regulation of neural precursor cell proliferation	down	positive regulation of neural precursor cell proliferation (GO:2000179)	BP	31	29	0	0.003109876
GO:0006486	protein glycosylation	down	protein glycosylation (GO:0006486)	BP	141	136	0.007352941	0.003109876
GO:0048009	insulin-like growth factor receptor signaling pathway	down	insulin-like growth factor receptor signaling pathway (GO:0048009)	BP	22	22	0	0.003120394
GO:0010559	regulation of glycoprotein biosynthetic process	down	regulation of glycoprotein biosynthetic process (GO:0010559)	BP	25	24	0	0.003120394
GO:0002313	mature B cell differentiation involved in immune respons	down	mature B cell differentiation involved in immune response (GO:0002313)	BP	13	13	0	0.003121314
GO:0090505	epiboly involved in wound healing	down	epiboly involved in wound healing (GO:0090505)	BP	20	18	0.055555556	0.003126271
GO:0044319	wound healing, spreading of cells	down	wound healing, spreading of cells (GO:0044319)	BP	20	18	0.055555556	0.003126271
GO:0071230	cellular response to amino acid stimulus	down	cellular response to amino acid stimulus (GO:0071230)	BP	40	40	0.05	0.003130444
GO:0030856	regulation of epithelial cell differentiation	down	regulation of epithelial cell differentiation (GO:0030856)	BP	86	82	0	0.003135892
GO:0021515	cell differentiation in spinal cord	down	cell differentiation in spinal cord (GO:0021515)	BP	37	36	0	0.003145706
GO:0060079	excitatory postsynaptic potential	down	excitatory postsynaptic potential (GO:0060079)	BP	32	31	0	0.003154594
GO:0031062	positive regulation of histone methylation	down	positive regulation of histone methylation (GO:0031062)	BP	24	24	0	0.003171371
GO:0003073	regulation of systemic arterial blood pressure	down	regulation of systemic arterial blood pressure (GO:0003073)	BP	51	50	0	0.003171371
GO:0002764	immune response-regulating signaling pathway	down	immune response-regulating signaling pathway (GO:0002764)	BP	179	171	0	0.00317495
GO:0050851	antigen receptor-mediated signaling pathway	down	antigen receptor-mediated signaling pathway (GO:0050851)	BP	81	77	0	0.003177932
GO:0034101	erythrocyte homeostasis	down	erythrocyte homeostasis (GO:0034101)	BP	81	80	0.0125	0.003208822

GO:0044772	mitotic cell cycle phase transition	down	mitotic cell cycle phase transition (GO:0044772)	BP	190	183	0.016393443	0.003262201
GO:0034767	positive regulation of ion transmembrane transport	down	positive regulation of ion transmembrane transport (GO:0034767)	BP	58	56	0	0.003278325
GO:0002768	immune response-regulating cell surface receptor signalin	down	immune response-regulating cell surface receptor signaling pathway (GO:	BP	96	91	0	0.003295746
GO:0071675	regulation of mononuclear cell migration	down	regulation of mononuclear cell migration (GO:0071675)	BP	23	21	0	0.003295746
GO:0001578	microtubule bundle formation	down	microtubule bundle formation (GO:0001578)	BP	55	54	0	0.003307509
GO:0033048	negative regulation of mitotic sister chromatid segregatio	down	negative regulation of mitotic sister chromatid segregation (GO:0033048	BP	18	17	0.058823529	0.003307509
GO:0050878	regulation of body fluid levels	down	regulation of body fluid levels (GO:0050878)	BP	196	188	0	0.003330729
GO:0033138	positive regulation of peptidyl-serine phosphorylation	down	positive regulation of peptidyl-serine phosphorylation (GO:0033138)	BP	51	49	0	0.003335673
GO:0061337	cardiac conduction	down	cardiac conduction (GO:0061337)	BP	38	38	0	0.00337931
GO:1903429	regulation of cell maturation	down	regulation of cell maturation (GO:1903429)	BP	12	12	0.083333333	0.00341766
GO:0030947	regulation of vascular endothelial growth factor receptor	down	regulation of vascular endothelial growth factor receptor signaling pathw	BP	16	15	0	0.003425246
GO:0061053	somite development	down	somite development (GO:0061053)	BP	71	69	0	0.003425246
GO:0043536	positive regulation of blood vessel endothelial cell migrat	down	positive regulation of blood vessel endothelial cell migration (GO:00435	BP	16	16	0	0.003430911
GO:0051279	regulation of release of sequestered calcium ion into cyto	down	regulation of release of sequestered calcium ion into cytosol (GO:005127	BP	43	41	0	0.003447965
GO:0006275	regulation of DNA replication	down	regulation of DNA replication (GO:0006275)	BP	81	80	0	0.003455381
GO:0030879	mammary gland development	down	mammary gland development (GO:0030879)	BP	85	83	0	0.003455438
GO:0071174	mitotic spindle checkpoint	down	mitotic spindle checkpoint (GO:0071174)	BP	16	15	0.066666667	0.003455438
GO:0060415	muscle tissue morphogenesis	down	muscle tissue morphogenesis (GO:0060415)	BP	57	56	0.017857143	0.003455438
GO:0045841	negative regulation of mitotic metaphase/anaphase transi	down	negative regulation of mitotic metaphase/anaphase transition (GO:0045	BP	16	15	0.066666667	0.003455438
GO:2000816	negative regulation of mitotic sister chromatid separatio	down	negative regulation of mitotic sister chromatid separation (GO:2000816)	BP	16	15	0.066666667	0.003455438
GO:0031348	negative regulation of defense response	down	negative regulation of defense response (GO:0031348)	BP	99	93	0	0.003472613
GO:0006874	cellular calcium ion homeostasis	down	cellular calcium ion homeostasis (GO:0006874)	BP	181	173	0.005780347	0.003586919
GO:0001974	blood vessel remodeling	down	blood vessel remodeling (GO:0001974)	BP	26	25	0	0.003608357
GO:0046718	viral entry into host cell	down	viral entry into host cell (GO:0046718)	BP	31	27	0.037037037	0.003614047
GO:0045746	negative regulation of Notch signaling pathway	down	negative regulation of Notch signaling pathway (GO:0045746)	BP	21	19	0	0.003629296
GO:0032271	regulation of protein polymerization	down	regulation of protein polymerization (GO:0032271)	BP	105	99	0	0.003649352
GO:1900182	positive regulation of protein localization to nucleus	down	positive regulation of protein localization to nucleus (GO:1900182)	BP	89	88	0	0.003650041
GO:0002237	response to molecule of bacterial origin	down	response to molecule of bacterial origin (GO:0002237)	BP	151	142	0	0.003653748
GO:0001516	prostaglandin biosynthetic process	down	prostaglandin biosynthetic process (GO:0001516)	BP	13	13	0	0.003654003
GO:0046457	prostanoid biosynthetic process	down	prostanoid biosynthetic process (GO:0046457)	BP	13	13	0	0.003654003
GO:0022408	negative regulation of cell-cell adhesion	down	negative regulation of cell-cell adhesion (GO:0022408)	BP	89	85	0	0.003663976
GO:2001026	regulation of endothelial cell chemotaxis	down	regulation of endothelial cell chemotaxis (GO:2001026)	BP	13	13	0	0.003663976
GO:0043331	response to dsRNA	down	response to dsRNA (GO:0043331)	BP	51	50	0	0.003668845
GO:0052652	cyclic purine nucleotide metabolic process	down	cyclic purine nucleotide metabolic process (GO:0052652)	BP	80	79	0	0.003708016
GO:0003177	pulmonary valve development	down	pulmonary valve development (GO:0003177)	BP	11	11	0	0.003727125
GO:0003184	pulmonary valve morphogenesis	down	pulmonary valve morphogenesis (GO:0003184)	BP	11	11	0	0.003727125
GO:0002443	leukocyte mediated immunity	down	leukocyte mediated immunity (GO:0002443)	BP	163	158	0	0.003744271
GO:2001259	positive regulation of cation channel activity	down	positive regulation of cation channel activity (GO:2001259)	BP	18	18	0	0.003776942
GO:0000132	establishment of mitotic spindle orientation	down	establishment of mitotic spindle orientation (GO:0000132)	BP	15	14	0	0.003865451
GO:1905332	positive regulation of morphogenesis of an epithelium	down	positive regulation of morphogenesis of an epithelium (GO:1905332)	BP	25	24	0	0.003893345
GO:1904037	positive regulation of epithelial cell apoptotic process	down	positive regulation of epithelial cell apoptotic process (GO:1904037)	BP	11	11	0	0.003900614
GO:0031345	negative regulation of cell projection organization	down	negative regulation of cell projection organization (GO:0031345)	BP	82	81	0	0.00401635
GO:0030193	regulation of blood coagulation	down	regulation of blood coagulation (GO:0030193)	BP	59	58	0	0.004016353
GO:1900046	regulation of hemostasis	down	regulation of hemostasis (GO:1900046)	BP	59	58	0	0.004016353
GO:0002703	regulation of leukocyte mediated immunity	down	regulation of leukocyte mediated immunity (GO:0002703)	BP	103	100	0	0.004068487
GO:0021542	dentate gyrus development	down	dentate gyrus development (GO:0021542)	BP	14	14	0.071428571	0.004072134
GO:0051148	negative regulation of muscle cell differentiation	down	negative regulation of muscle cell differentiation (GO:0051148)	BP	43	43	0	0.004072134
GO:0043330	response to exogenous dsRNA	down	response to exogenous dsRNA (GO:0043330)	BP	25	24	0	0.004072134
GO:1901987	regulation of cell cycle phase transition	down	regulation of cell cycle phase transition (GO:1901987)	BP	137	129	0.015503876	0.004091339
GO:0090036	regulation of protein kinase C signaling	down	regulation of protein kinase C signaling (GO:0090036)	BP	12	12	0	0.004092808
GO:0007628	adult walking behavior	down	adult walking behavior (GO:0007628)	BP	28	27	0	0.004115467
GO:0090659	walking behavior	down	walking behavior (GO:0090659)	BP	28	27	0	0.004115467
GO:0042391	regulation of membrane potential	down	regulation of membrane potential (GO:0042391)	BP	199	191	0	0.004153167
GO:0021766	hippocampus development	down	hippocampus development (GO:0021766)	BP	45	44	0.045454545	0.004186316
GO:0007094	mitotic spindle assembly checkpoint	down	mitotic spindle assembly checkpoint (GO:0007094)	BP	15	14	0.071428571	0.004194863
GO:0006260	DNA replication	down	DNA replication (GO:0006260)	BP	170	168	0	0.00421481
GO:0090101	negative regulation of transmembrane receptor protein s	down	negative regulation of transmembrane receptor protein serine/threonine	BP	71	71	0	0.00421481
GO:0046822	regulation of nucleocytoplasmic transport	down	regulation of nucleocytoplasmic transport (GO:0046822)	BP	149	147	0	0.00421481
GO:0071312	cellular response to alkaloid	down	cellular response to alkaloid (GO:0071312)	BP	10	10	0	0.004237438
GO:0002757	immune response-activating signal transduction	down	immune response-activating signal transduction (GO:0002757)	BP	170	162	0	0.00427898
GO:0002275	myeloid cell activation involved in immune response	down	myeloid cell activation involved in immune response (GO:0002275)	BP	42	41	0	0.004294866
GO:2000177	regulation of neural precursor cell proliferation	down	regulation of neural precursor cell proliferation (GO:2000177)	BP	53	50	0	0.004294866
GO:0007018	microtubule-based movement	down	microtubule-based movement (GO:0007018)	BP	150	146	0.006849315	0.004327062
GO:0060441	epithelial tube branching involved in lung morphogenesis	down	epithelial tube branching involved in lung morphogenesis (GO:0060441)	BP	22	20	0	0.004340318

GO:0051897	positive regulation of protein kinase B signaling	down	positive regulation of protein kinase B signaling (GO:0051897)	BP	56	53	0.018867925	0.00438655
GO:0043491	protein kinase B signaling	down	protein kinase B signaling (GO:0043491)	BP	108	103	0.009708738	0.004399613
GO:0010453	regulation of cell fate commitment	down	regulation of cell fate commitment (GO:0010453)	BP	17	17	0	0.004485227
GO:0033135	regulation of peptidyl-serine phosphorylation	down	regulation of peptidyl-serine phosphorylation (GO:0033135)	BP	75	71	0	0.004488803
GO:0008154	actin polymerization or depolymerization	down	actin polymerization or depolymerization (GO:0008154)	BP	111	105	0.00952381	0.004491989
GO:0045137	development of primary sexual characteristics	down	development of primary sexual characteristics (GO:0045137)	BP	125	122	0	0.004491989
GO:0032414	positive regulation of ion transmembrane transporter act	down	positive regulation of ion transmembrane transporter activity (GO:00324	BP	31	30	0	0.004491989
GO:0003014	renal system process	down	renal system process (GO:0003014)	BP	48	46	0	0.004491989
GO:0003016	respiratory system process	down	respiratory system process (GO:0003016)	BP	21	20	0	0.004491989
GO:0050818	regulation of coagulation	down	regulation of coagulation (GO:0050818)	BP	63	62	0	0.004519099
GO:0030514	negative regulation of BMP signaling pathway	down	negative regulation of BMP signaling pathway (GO:0030514)	BP	35	35	0	0.00454469
GO:0072091	regulation of stem cell proliferation	down	regulation of stem cell proliferation (GO:0072091)	BP	47	47	0	0.004561818
GO:2000696	regulation of epithelial cell differentiation involved in kid	down	regulation of epithelial cell differentiation involved in kidney developmen	BP	15	15	0	0.00458225
GO:0048333	mesodermal cell differentiation	down	mesodermal cell differentiation (GO:0048333)	BP	20	20	0	0.004596961
GO:1900180	regulation of protein localization to nucleus	down	regulation of protein localization to nucleus (GO:1900180)	BP	154	152	0	0.004626846
GO:0007088	regulation of mitotic nuclear division	down	regulation of mitotic nuclear division (GO:0007088)	BP	80	78	0.025641026	0.004627829
GO:0051653	spindle localization	down	spindle localization (GO:0051653)	BP	28	27	0	0.004630572
GO:0007292	female gamete generation	down	female gamete generation (GO:0007292)	BP	73	73	0	0.004670031
GO:0048738	cardiac muscle tissue development	down	cardiac muscle tissue development (GO:0048738)	BP	122	119	0.008403361	0.004676161
GO:0070528	protein kinase C signaling	down	protein kinase C signaling (GO:0070528)	BP	22	22	0	0.004755016
GO:0046637	regulation of alpha-beta T cell differentiation	down	regulation of alpha-beta T cell differentiation (GO:0046637)	BP	32	31	0	0.004807592
GO:0006029	proteoglycan metabolic process	down	proteoglycan metabolic process (GO:0006029)	BP	51	50	0	0.004856318
GO:0060831	smoothened signaling pathway involved in dorsal/ventral	down	smoothened signaling pathway involved in dorsal/ventral neural tube pat	BP	13	13	0	0.004856318
GO:0032400	melanosome localization	down	melanosome localization (GO:0032400)	BP	13	13	0	0.004869322
GO:0002366	leukocyte activation involved in immune response	down	leukocyte activation involved in immune response (GO:0002366)	BP	138	136	0	0.004871471
GO:0071260	cellular response to mechanical stimulus	down	cellular response to mechanical stimulus (GO:0071260)	BP	36	36	0.027777778	0.004876818
GO:0071621	granulocyte chemotaxis	down	granulocyte chemotaxis (GO:0071621)	BP	55	51	0	0.004900033
GO:0010977	negative regulation of neuron projection development	down	negative regulation of neuron projection development (GO:0010977)	BP	67	67	0	0.004915785
GO:0021681	cerebellar granular layer development	down	cerebellar granular layer development (GO:0021681)	BP	10	9	0.222222222	0.004918084
GO:0002263	cell activation involved in immune response	down	cell activation involved in immune response (GO:0002263)	BP	140	137	0	0.005074663
GO:0030032	lamellipodium assembly	down	lamellipodium assembly (GO:0030032)	BP	40	37	0	0.005125739
GO:0055074	calcium ion homeostasis	down	calcium ion homeostasis (GO:0055074)	BP	191	182	0.005494505	0.005136281
GO:0043576	regulation of respiratory gaseous exchange	down	regulation of respiratory gaseous exchange (GO:0043576)	BP	15	15	0	0.005179752
GO:0002253	activation of immune response	down	activation of immune response (GO:0002253)	BP	189	179	0	0.005186719
GO:0061041	regulation of wound healing	down	regulation of wound healing (GO:0061041)	BP	86	85	0	0.005202914
GO:0030888	regulation of B cell proliferation	down	regulation of B cell proliferation (GO:0030888)	BP	40	40	0	0.005222929
GO:1901990	regulation of mitotic cell cycle phase transition	down	regulation of mitotic cell cycle phase transition (GO:1901990)	BP	124	119	0.016806723	0.005248142
GO:0032411	positive regulation of transporter activity	down	positive regulation of transporter activity (GO:0032411)	BP	36	35	0	0.005328008
GO:0006940	regulation of smooth muscle contraction	down	regulation of smooth muscle contraction (GO:0006940)	BP	26	26	0	0.005349999
GO:0072160	nephron tubule epithelial cell differentiation	down	nephron tubule epithelial cell differentiation (GO:0072160)	BP	12	12	0	0.005352435
GO:0042306	regulation of protein import into nucleus	down	regulation of protein import into nucleus (GO:0042306)	BP	122	121	0	0.005355357
GO:0032148	activation of protein kinase B activity	down	activation of protein kinase B activity (GO:0032148)	BP	12	12	0	0.005394821
GO:0051306	mitotic sister chromatid separation	down	mitotic sister chromatid separation (GO:0051306)	BP	27	26	0.038461538	0.005445168
GO:0002687	positive regulation of leukocyte migration	down	positive regulation of leukocyte migration (GO:0002687)	BP	60	56	0	0.005446955
GO:0045444	fat cell differentiation	down	fat cell differentiation (GO:0045444)	BP	162	160	0	0.005462952
GO:0010544	negative regulation of platelet activation	down	negative regulation of platelet activation (GO:0010544)	BP	11	10	0	0.005462952
GO:0032401	establishment of melanosome localization	down	establishment of melanosome localization (GO:0032401)	BP	12	12	0	0.005468638
GO:0032402	melanosome transport	down	melanosome transport (GO:0032402)	BP	12	12	0	0.005468638
GO:0044839	cell cycle G2/M phase transition	down	cell cycle G2/M phase transition (GO:0044839)	BP	63	59	0.033898305	0.005488351
GO:1901550	regulation of endothelial cell development	down	regulation of endothelial cell development (GO:1901550)	BP	10	10	0	0.005514929
GO:1903140	regulation of establishment of endothelial barrier	down	regulation of establishment of endothelial barrier (GO:1903140)	BP	10	10	0	0.005514929
GO:0007548	sex differentiation	down	sex differentiation (GO:0007548)	BP	157	154	0	0.005578264
GO:0010934	macrophage cytokine production	down	macrophage cytokine production (GO:0010934)	BP	12	12	0	0.005581587
GO:0002695	negative regulation of leukocyte activation	down	negative regulation of leukocyte activation (GO:0002695)	BP	92	88	0	0.005592189
GO:0048016	inositol phosphate-mediated signaling	down	inositol phosphate-mediated signaling (GO:0048016)	BP	22	22	0	0.005592444
GO:0030534	adult behavior	down	adult behavior (GO:0030534)	BP	105	102	0	0.005638227
GO:0034764	positive regulation of transmembrane transport	down	positive regulation of transmembrane transport (GO:0034764)	BP	62	59	0	0.005728004
GO:0033046	negative regulation of sister chromatid segregation	down	negative regulation of sister chromatid segregation (GO:0033046)	BP	19	18	0.055555556	0.005761871
GO:0072182	regulation of nephron tubule epithelial cell differentiation	down	regulation of nephron tubule epithelial cell differentiation (GO:0072182)	BP	11	11	0	0.005761871
GO:0019058	viral life cycle	down	viral life cycle (GO:0019058)	BP	123	115	0.017391304	0.005763999
GO:0061430	bone trabecula morphogenesis	down	bone trabecula morphogenesis (GO:0061430)	BP	11	11	0.090909091	0.005790481
GO:1902041	regulation of extrinsic apoptotic signaling pathway via de	down	regulation of extrinsic apoptotic signaling pathway via death domain rece	BP	41	38	0	0.005822926
GO:0035162	embryonic hemopoiesis	down	embryonic hemopoiesis (GO:0035162)	BP	15	15	0	0.00583485
GO:0045618	positive regulation of keratinocyte differentiation	down	positive regulation of keratinocyte differentiation (GO:0045618)	BP	10	7	0	0.00585787

GO:0048644	muscle organ morphogenesis	down	muscle organ morphogenesis (GO:0048644)	BP	62	61	0.016393443	0.005893533
GO:0035886	vascular smooth muscle cell differentiation	down	vascular smooth muscle cell differentiation (GO:0035886)	BP	13	13	0	0.005893533
GO:0001936	regulation of endothelial cell proliferation	down	regulation of endothelial cell proliferation (GO:0001936)	BP	62	59	0.016949153	0.005895386
GO:0042693	muscle cell fate commitment	down	muscle cell fate commitment (GO:0042693)	BP	10	10	0	0.005936003
GO:0021692	cerebellar Purkinje cell layer morphogenesis	down	cerebellar Purkinje cell layer morphogenesis (GO:0021692)	BP	14	12	0.083333333	0.005970458
GO:2000725	regulation of cardiac muscle cell differentiation	down	regulation of cardiac muscle cell differentiation (GO:2000725)	BP	15	15	0	0.005979991
GO:0072171	mesonephric tubule morphogenesis	down	mesonephric tubule morphogenesis (GO:0072171)	BP	53	52	0	0.006000943
GO:0070507	regulation of microtubule cytoskeleton organization	down	regulation of microtubule cytoskeleton organization (GO:0070507)	BP	93	91	0.010989011	0.006038014
GO:0045639	positive regulation of myeloid cell differentiation	down	positive regulation of myeloid cell differentiation (GO:0045639)	BP	63	61	0	0.006051788
GO:0071277	cellular response to calcium ion	down	cellular response to calcium ion (GO:0071277)	BP	28	27	0	0.006107954
GO:1902106	negative regulation of leukocyte differentiation	down	negative regulation of leukocyte differentiation (GO:1902106)	BP	49	46	0	0.006107954
GO:0007215	glutamate receptor signaling pathway	down	glutamate receptor signaling pathway (GO:0007215)	BP	38	38	0	0.00612393
GO:1904589	regulation of protein import	down	regulation of protein import (GO:1904589)	BP	123	122	0	0.006182205
GO:0097305	response to alcohol	down	response to alcohol (GO:0097305)	BP	54	54	0	0.006182325
GO:0051235	maintenance of location	down	maintenance of location (GO:0051235)	BP	183	178	0	0.006214209
GO:0070085	glycosylation	down	glycosylation (GO:0070085)	BP	149	144	0.006944444	0.006258143
GO:0060425	lung morphogenesis	down	lung morphogenesis (GO:0060425)	BP	44	42	0	0.006282488
GO:1901861	regulation of muscle tissue development	down	regulation of muscle tissue development (GO:1901861)	BP	78	75	0	0.006304735
GO:0048557	embryonic digestive tract morphogenesis	down	embryonic digestive tract morphogenesis (GO:0048557)	BP	11	11	0	0.006311865
GO:0061098	positive regulation of protein tyrosine kinase activity	down	positive regulation of protein tyrosine kinase activity (GO:0061098)	BP	20	20	0	0.006311865
GO:0051258	protein polymerization	down	protein polymerization (GO:0051258)	BP	138	129	0	0.006311865
GO:0070167	regulation of biomineral tissue development	down	regulation of biomineral tissue development (GO:0070167)	BP	59	56	0	0.006311865
GO:1902099	regulation of metaphase/anaphase transition of cell cycle	down	regulation of metaphase/anaphase transition of cell cycle (GO:1902099)	BP	25	24	0.041666667	0.006311865
GO:0008406	gonad development	down	gonad development (GO:0008406)	BP	123	120	0	0.006330362
GO:0060707	trophoblast giant cell differentiation	down	trophoblast giant cell differentiation (GO:0060707)	BP	12	12	0	0.006382588
GO:1901571	fatty acid derivative transport	down	fatty acid derivative transport (GO:1901571)	BP	19	19	0.052631579	0.006486541
GO:0071715	icosanoid transport	down	icosanoid transport (GO:0071715)	BP	19	19	0.052631579	0.006486541
GO:0051101	regulation of DNA binding	down	regulation of DNA binding (GO:0051101)	BP	64	62	0.016129032	0.006497517
GO:0050728	negative regulation of inflammatory response	down	negative regulation of inflammatory response (GO:0050728)	BP	73	71	0	0.006536692
GO:0070286	axonemal dynein complex assembly	down	axonemal dynein complex assembly (GO:0070286)	BP	17	17	0	0.006557193
GO:0002312	B cell activation involved in immune response	down	B cell activation involved in immune response (GO:0002312)	BP	53	53	0	0.006597105
GO:0002429	immune response-activating cell surface receptor signalin	down	immune response-activating cell surface receptor signaling pathway (GO:	BP	89	84	0	0.006597105
GO:0051806	entry into cell of other organism involved in symbiotic int	down	entry into cell of other organism involved in symbiotic interaction (GO:0	BP	34	30	0.033333333	0.006635917
GO:0044409	entry into host	down	entry into host (GO:0044409)	BP	34	30	0.033333333	0.006635917
GO:0030260	entry into host cell	down	entry into host cell (GO:0030260)	BP	34	30	0.033333333	0.006635917
GO:0051828	entry into other organism involved in symbiotic interacti	down	entry into other organism involved in symbiotic interaction (GO:005182	BP	34	30	0.033333333	0.006635917
GO:0042113	B cell activation	down	B cell activation (GO:0042113)	BP	145	143	0	0.006672859
GO:0010470	regulation of gastrulation	down	regulation of gastrulation (GO:0010470)	BP	23	22	0.045454545	0.006727806
GO:0060047	heart contraction	down	heart contraction (GO:0060047)	BP	112	110	0.009090909	0.006819675
GO:0006302	double-strand break repair	down	double-strand break repair (GO:0006302)	BP	127	123	0.016260163	0.006844456
GO:0090263	positive regulation of canonical Wnt signaling pathway	down	positive regulation of canonical Wnt signaling pathway (GO:0090263)	BP	55	52	0.019230769	0.006844456
GO:0001776	leukocyte homeostasis	down	leukocyte homeostasis (GO:0001776)	BP	63	63	0	0.006850937
GO:0090100	positive regulation of transmembrane receptor protein se	down	positive regulation of transmembrane receptor protein serine/threonine	BP	65	65	0	0.006868985
GO:1903707	negative regulation of hemopoiesis	down	negative regulation of hemopoiesis (GO:1903707)	BP	75	68	0	0.006891174
GO:1904064	positive regulation of cation transmembrane transport	down	positive regulation of cation transmembrane transport (GO:1904064)	BP	52	51	0	0.006933053
GO:1901652	response to peptide	down	response to peptide (GO:1901652)	BP	150	146	0.01369863	0.006961317
GO:0048066	developmental pigmentation	down	developmental pigmentation (GO:0048066)	BP	33	33	0	0.00710603
GO:0003015	heart process	down	heart process (GO:0003015)	BP	115	112	0.008928571	0.00710603
GO:0042438	melanin biosynthetic process	down	melanin biosynthetic process (GO:0042438)	BP	11	11	0	0.00710603
GO:0006582	melanin metabolic process	down	melanin metabolic process (GO:0006582)	BP	11	11	0	0.00710603
GO:0044550	secondary metabolite biosynthetic process	down	secondary metabolite biosynthetic process (GO:0044550)	BP	12	11	0	0.00710603
GO:0051783	regulation of nuclear division	down	regulation of nuclear division (GO:0051783)	BP	102	100	0.02	0.00711556
GO:0048640	negative regulation of developmental growth	down	negative regulation of developmental growth (GO:0048640)	BP	52	52	0	0.007219341
GO:0055024	regulation of cardiac muscle tissue development	down	regulation of cardiac muscle tissue development (GO:0055024)	BP	41	41	0	0.007252236
GO:1902042	negative regulation of extrinsic apoptotic signaling pathw	down	negative regulation of extrinsic apoptotic signaling pathway via death do	BP	19	19	0	0.007261043
GO:0010948	negative regulation of cell cycle process	down	negative regulation of cell cycle process (GO:0010948)	BP	106	100	0.01	0.007347374
GO:0046635	positive regulation of alpha-beta T cell activation	down	positive regulation of alpha-beta T cell activation (GO:0046635)	BP	34	33	0	0.0074129
GO:0048596	embryonic camera-type eye morphogenesis	down	embryonic camera-type eye morphogenesis (GO:0048596)	BP	20	20	0	0.007459005
GO:0030513	positive regulation of BMP signaling pathway	down	positive regulation of BMP signaling pathway (GO:0030513)	BP	28	28	0	0.00746612
GO:0008361	regulation of cell size	down	regulation of cell size (GO:0008361)	BP	92	89	0	0.00746612
GO:0055017	cardiac muscle tissue growth	down	cardiac muscle tissue growth (GO:0055017)	BP	33	31	0	0.007470268
GO:0050729	positive regulation of inflammatory response	down	positive regulation of inflammatory response (GO:0050729)	BP	53	53	0	0.007517399
GO:0060706	cell differentiation involved in embryonic placenta develo	down	cell differentiation involved in embryonic placenta development (GO:00	BP	21	21	0	0.007537911
GO:0044784	metaphase/anaphase transition of cell cycle	down	metaphase/anaphase transition of cell cycle (GO:0044784)	BP	26	25	0.04	0.007556314

GO:1905818	regulation of chromosome separation	down	regulation of chromosome separation (GO:1905818)	BP	26	25	0.04	0.007556314
GO:0043200	response to amino acid	down	response to amino acid (GO:0043200)	BP	46	46	0.043478261	0.007556314
GO:0030902	hindbrain development	down	hindbrain development (GO:0030902)	BP	89	83	0.024096386	0.00760924
GO:0021872	forebrain generation of neurons	down	forebrain generation of neurons (GO:0021872)	BP	47	45	0	0.007663904
GO:0046634	regulation of alpha-beta T cell activation	down	regulation of alpha-beta T cell activation (GO:0046634)	BP	46	45	0	0.007663904
GO:0050849	negative regulation of calcium-mediated signaling	down	negative regulation of calcium-mediated signaling (GO:0050849)	BP	10	10	0	0.007670288
GO:0050850	positive regulation of calcium-mediated signaling	down	positive regulation of calcium-mediated signaling (GO:0050850)	BP	22	19	0	0.007703647
GO:0030823	regulation of cGMP metabolic process	down	regulation of cGMP metabolic process (GO:0030823)	BP	16	16	0	0.007703647
GO:0032409	regulation of transporter activity	down	regulation of transporter activity (GO:0032409)	BP	108	105	0	0.007775655
GO:0097529	myeloid leukocyte migration	down	myeloid leukocyte migration (GO:0097529)	BP	97	89	0	0.007801728
GO:0017157	regulation of exocytosis	down	regulation of exocytosis (GO:0017157)	BP	95	92	0	0.007810087
GO:0042102	positive regulation of T cell proliferation	down	positive regulation of T cell proliferation (GO:0042102)	BP	65	62	0.016129032	0.007840745
GO:0042490	mechanoreceptor differentiation	down	mechanoreceptor differentiation (GO:0042490)	BP	55	54	0	0.007867869
GO:0050679	positive regulation of epithelial cell proliferation	down	positive regulation of epithelial cell proliferation (GO:0050679)	BP	100	94	0	0.007880315
GO:0048638	regulation of developmental growth	down	regulation of developmental growth (GO:0048638)	BP	192	188	0	0.00794636
GO:1903779	regulation of cardiac conduction	down	regulation of cardiac conduction (GO:1903779)	BP	11	11	0	0.00796014
GO:0031103	axon regeneration	down	axon regeneration (GO:0031103)	BP	16	16	0	0.007992667
GO:0045740	positive regulation of DNA replication	down	positive regulation of DNA replication (GO:0045740)	BP	36	35	0	0.008240015
GO:0040036	regulation of fibroblast growth factor receptor signaling p	down	regulation of fibroblast growth factor receptor signaling pathway (GO:00	BP	20	18	0	0.0083715
GO:0000086	G2/M transition of mitotic cell cycle	down	G2/M transition of mitotic cell cycle (GO:0000086)	BP	59	56	0.035714286	0.008409254
GO:0046849	bone remodeling	down	bone remodeling (GO:0046849)	BP	54	53	0.018867925	0.008479261
GO:0070228	regulation of lymphocyte apoptotic process	down	regulation of lymphocyte apoptotic process (GO:0070228)	BP	38	37	0.027027027	0.00859644
GO:0090231	regulation of spindle checkpoint	down	regulation of spindle checkpoint (GO:0090231)	BP	11	11	0.090909091	0.008652898
GO:1990266	neutrophil migration	down	neutrophil migration (GO:1990266)	BP	48	45	0	0.008713938
GO:0002052	positive regulation of neuroblast proliferation	down	positive regulation of neuroblast proliferation (GO:0002052)	BP	15	15	0	0.008782605
GO:0060113	inner ear receptor cell differentiation	down	inner ear receptor cell differentiation (GO:0060113)	BP	53	52	0	0.0088042
GO:0051648	vesicle localization	down	vesicle localization (GO:0051648)	BP	94	94	0	0.008831565
GO:0051054	positive regulation of DNA metabolic process	down	positive regulation of DNA metabolic process (GO:0051054)	BP	130	129	0.015503876	0.008891591
GO:0032350	regulation of hormone metabolic process	down	regulation of hormone metabolic process (GO:0032350)	BP	19	19	0	0.008899053
GO:0006903	vesicle targeting	down	vesicle targeting (GO:0006903)	BP	11	11	0	0.008966039
GO:0002690	positive regulation of leukocyte chemotaxis	down	positive regulation of leukocyte chemotaxis (GO:0002690)	BP	48	44	0	0.008972747
GO:0060419	heart growth	down	heart growth (GO:0060419)	BP	36	34	0	0.009006293
GO:0010469	regulation of receptor activity	down	regulation of receptor activity (GO:0010469)	BP	61	60	0	0.009018475
GO:0035637	multicellular organismal signaling	down	multicellular organismal signaling (GO:0035637)	BP	69	69	0	0.009020579
GO:0014912	negative regulation of smooth muscle cell migration	down	negative regulation of smooth muscle cell migration (GO:0014912)	BP	11	11	0	0.009051392
GO:0051091	positive regulation of DNA binding transcription factor ac	down	positive regulation of DNA binding transcription factor activity (GO:0051	BP	149	149	0	0.009118061
GO:0033077	T cell differentiation in thymus	down	T cell differentiation in thymus (GO:0033077)	BP	53	51	0	0.009118061
GO:1900076	regulation of cellular response to insulin stimulus	down	regulation of cellular response to insulin stimulus (GO:1900076)	BP	38	37	0.027027027	0.009144443
GO:1904385	cellular response to angiotensin	down	cellular response to angiotensin (GO:1904385)	BP	10	9	0	0.009187526
GO:1990776	response to angiotensin	down	response to angiotensin (GO:1990776)	BP	10	9	0	0.009187526
GO:0086003	cardiac muscle cell contraction	down	cardiac muscle cell contraction (GO:0086003)	BP	29	28	0	0.009273562
GO:0050871	positive regulation of B cell activation	down	positive regulation of B cell activation (GO:0050871)	BP	50	50	0	0.009355829
GO:1904031	positive regulation of cyclin-dependent protein kinase act	down	positive regulation of cyclin-dependent protein kinase activity (GO:1904	BP	16	15	0	0.009392717
GO:0045737	positive regulation of cyclin-dependent protein serine/thr	down	positive regulation of cyclin-dependent protein serine/threonine kinase a	BP	15	15	0	0.009392717
GO:0030865	cortical cytoskeleton organization	down	cortical cytoskeleton organization (GO:0030865)	BP	28	28	0	0.009416625
GO:0032412	regulation of ion transmembrane transporter activity	down	regulation of ion transmembrane transporter activity (GO:0032412)	BP	97	94	0	0.009416625
GO:0016202	regulation of striated muscle tissue development	down	regulation of striated muscle tissue development (GO:0016202)	BP	76	73	0	0.009416625
GO:0009880	embryonic pattern specification	down	embryonic pattern specification (GO:0009880)	BP	44	41	0	0.009441392
GO:2000311	regulation of AMPA receptor activity	down	regulation of AMPA receptor activity (GO:2000311)	BP	11	11	0	0.009444893
GO:0050777	negative regulation of immune response	down	negative regulation of immune response (GO:0050777)	BP	74	68	0	0.00945848
GO:0006813	potassium ion transport	down	potassium ion transport (GO:0006813)	BP	130	128	0	0.00945848
GO:0033045	regulation of sister chromatid segregation	down	regulation of sister chromatid segregation (GO:0033045)	BP	39	37	0.027027027	0.009462891
GO:0071219	cellular response to molecule of bacterial origin	down	cellular response to molecule of bacterial origin (GO:0071219)	BP	97	91	0	0.009466276
GO:0002260	lymphocyte homeostasis	down	lymphocyte homeostasis (GO:0002260)	BP	52	52	0	0.009466276
GO:0072010	glomerular epithelium development	down	glomerular epithelium development (GO:0072010)	BP	14	14	0	0.009501883
GO:0050857	positive regulation of antigen receptor-mediated signalin	down	positive regulation of antigen receptor-mediated signaling pathway (GO:	BP	13	12	0	0.009501883
GO:0003254	regulation of membrane depolarization	down	regulation of membrane depolarization (GO:0003254)	BP	27	25	0	0.009509697
GO:0006942	regulation of striated muscle contraction	down	regulation of striated muscle contraction (GO:0006942)	BP	45	43	0	0.009509697
GO:0050798	activated T cell proliferation	down	activated T cell proliferation (GO:0050798)	BP	28	27	0.037037037	0.009653715
GO:0032886	regulation of microtubule-based process	down	regulation of microtubule-based process (GO:0032886)	BP	112	110	0.009090909	0.009679244
GO:0051150	regulation of smooth muscle cell differentiation	down	regulation of smooth muscle cell differentiation (GO:0051150)	BP	13	13	0	0.009679244
GO:0038127	ERBB signaling pathway	down	ERBB signaling pathway (GO:0038127)	BP	66	66	0	0.009779385
GO:0030832	regulation of actin filament length	down	regulation of actin filament length (GO:0030832)	BP	97	92	0	0.009779385
GO:0008064	regulation of actin polymerization or depolymerization	down	regulation of actin polymerization or depolymerization (GO:0008064)	BP	97	92	0	0.009779385

	GO:0086019	cell-cell signaling involved in cardiac conduction	down	cell-cell signaling involved in cardiac conduction (GO:0086019)	BP	13	13	0	0.009866464
	GO:0051294	establishment of spindle orientation	down	establishment of spindle orientation (GO:0051294)	BP	17	16	0	0.00989559

D90 to D135

Down Regulated

Class	GO ID	GO Description	Direction of c	GO Description and ID	Class	Size	Size in data	% in data	FDR.adj.pval
CELLULAR COMPONENT									
	GO:0005604	basement membrane	down	basement membrane (GO:0005604)	CC	64	63	0.031746032	4.44089E-16
	GO:0005581	collagen trimer	down	collagen trimer (GO:0005581)	CC	41	39	0.051282051	4.44089E-16
	GO:0098644	complex of collagen trimers	down	complex of collagen trimers (GO:0098644)	CC	16	15	0.133333333	4.44089E-16
	GO:0044420	extracellular matrix component	down	extracellular matrix component (GO:0044420)	CC	81	80	0.0375	4.44089E-16
	GO:0005578	proteinaceous extracellular matrix	down	proteinaceous extracellular matrix (GO:0005578)	CC	190	187	0.026737968	4.44089E-16
	GO:0005605	basal lamina	down	basal lamina (GO:0005605)	CC	16	16	0	6.32022E-09
	GO:0005614	interstitial matrix	down	interstitial matrix (GO:0005614)	CC	11	10	0.1	7.69435E-09
	GO:0000775	chromosome, centromeric region	down	chromosome, centromeric region (GO:0000775)	CC	110	107	0.028037383	8.06503E-08
	GO:0000779	condensed chromosome, centromeric region	down	condensed chromosome, centromeric region (GO:0000779)	CC	23	22	0.090909091	7.2036E-07
	GO:0000777	condensed chromosome kinetochore	down	condensed chromosome kinetochore (GO:0000777)	CC	17	16	0.0625	7.65659E-07
	GO:0016459	myosin complex	down	myosin complex (GO:0016459)	CC	49	39	0	2.4324E-06
	GO:0000776	kinetochore	down	kinetochore (GO:0000776)	CC	80	79	0.025316456	3.11811E-06
	GO:0005901	caveola	down	caveola (GO:0005901)	CC	44	44	0	4.73535E-06
	GO:0005721	pericentric heterochromatin	down	pericentric heterochromatin (GO:0005721)	CC	16	15	0	4.73535E-06
	GO:0042641	actomyosin	down	actomyosin (GO:0042641)	CC	46	44	0	6.76078E-06
	GO:0044853	plasma membrane raft	down	plasma membrane raft (GO:0044853)	CC	49	49	0	6.76078E-06
	GO:0098857	membrane microdomain	down	membrane microdomain (GO:0098857)	CC	139	136	0	8.98598E-06
	GO:0045121	membrane raft	down	membrane raft (GO:0045121)	CC	139	136	0	8.98598E-06
	GO:0044448	cell cortex part	down	cell cortex part (GO:0044448)	CC	71	69	0	9.00647E-06
	GO:0097517	contractile actin filament bundle	down	contractile actin filament bundle (GO:0097517)	CC	39	37	0	9.89157E-06
	GO:0001725	stress fiber	down	stress fiber (GO:0001725)	CC	39	37	0	9.89157E-06
	GO:0098802	plasma membrane receptor complex	down	plasma membrane receptor complex (GO:0098802)	CC	120	117	0.008547009	1.02776E-05
	GO:0032432	actin filament bundle	down	actin filament bundle (GO:0032432)	CC	42	39	0	1.30535E-05
	GO:0030027	lamellipodium	down	lamellipodium (GO:0030027)	CC	103	101	0.00990099	1.30535E-05
	GO:0005874	microtubule	down	microtubule (GO:0005874)	CC	159	147	0.006802721	1.33758E-05
	GO:0051233	spindle midzone	down	spindle midzone (GO:0051233)	CC	19	19	0.052631579	1.45656E-05
	GO:0098794	postsynapse	down	postsynapse (GO:0098794)	CC	154	151	0.013245033	1.60124E-05
	GO:0000780	condensed nuclear chromosome, centromeric region	down	condensed nuclear chromosome, centromeric region (GO:0000780)	CC	10	10	0.1	1.83152E-05
	GO:0030863	cortical cytoskeleton	down	cortical cytoskeleton (GO:0030863)	CC	53	51	0	1.83152E-05
	GO:0000139	Golgi membrane	down	Golgi membrane (GO:0000139)	CC	148	143	0	1.83152E-05
	GO:0010369	chromocenter	down	chromocenter (GO:0010369)	CC	12	12	0.083333333	1.93497E-05
	GO:0098589	membrane region	down	membrane region (GO:0098589)	CC	171	168	0	3.31736E-05
	GO:0043296	apical junction complex	down	apical junction complex (GO:0043296)	CC	83	76	0.013157895	3.43275E-05
	GO:0005938	cell cortex	down	cell cortex (GO:0005938)	CC	123	116	0	3.68491E-05
	GO:0044304	main axon	down	main axon (GO:0044304)	CC	25	25	0	6.4826E-05
	GO:0005819	spindle	down	spindle (GO:0005819)	CC	165	160	0.00625	7.05986E-05
	GO:0000922	spindle pole	down	spindle pole (GO:0000922)	CC	73	70	0	7.62717E-05
	GO:0098797	plasma membrane protein complex	down	plasma membrane protein complex (GO:0098797)	CC	133	119	0	9.41434E-05
	GO:0032279	asymmetric synapse	down	asymmetric synapse (GO:0032279)	CC	72	69	0.014492754	0.00011682
	GO:0098984	neuron to neuron synapse	down	neuron to neuron synapse (GO:0098984)	CC	72	69	0.014492754	0.00011682
	GO:0014069	postsynaptic density	down	postsynaptic density (GO:0014069)	CC	72	69	0.014492754	0.00011682
	GO:0099572	postsynaptic specialization	down	postsynaptic specialization (GO:0099572)	CC	72	69	0.014492754	0.00011682
	GO:0005930	axoneme	down	axoneme (GO:0005930)	CC	51	50	0	0.000134365
	GO:0097014	ciliary plasm	down	ciliary plasm (GO:0097014)	CC	51	50	0	0.000134365
	GO:0005814	centriole	down	centriole (GO:0005814)	CC	70	68	0.014705882	0.000149744
	GO:0097546	ciliary base	down	ciliary base (GO:0097546)	CC	16	16	0	0.000156197
	GO:0030990	intraciliary transport particle	down	intraciliary transport particle (GO:0030990)	CC	26	26	0	0.000180696
	GO:0097060	synaptic membrane	down	synaptic membrane (GO:0097060)	CC	74	74	0.027027027	0.000217595
	GO:0072686	mitotic spindle	down	mitotic spindle (GO:0072686)	CC	41	40	0	0.000223645
	GO:0034702	ion channel complex	down	ion channel complex (GO:0034702)	CC	158	153	0.013071895	0.000233451
	GO:0099568	cytoplasmic region	down	cytoplasmic region (GO:0099568)	CC	141	134	0	0.000341492
	GO:0044450	microtubule organizing center part	down	microtubule organizing center part (GO:0044450)	CC	102	99	0.01010101	0.000411623
	GO:0001726	ruffle	down	ruffle (GO:0001726)	CC	89	86	0	0.000411623
	GO:0034703	cation channel complex	down	cation channel complex (GO:0034703)	CC	132	127	0.015748031	0.000446739
	GO:0030425	dendrite	down	dendrite (GO:0030425)	CC	145	137	0	0.000547714
	GO:0009897	external side of plasma membrane	down	external side of plasma membrane (GO:0009897)	CC	158	154	0	0.000564393
	GO:1902495	transmembrane transporter complex	down	transmembrane transporter complex (GO:1902495)	CC	176	166	0.012048193	0.000623615

GO:0008328	ionotropic glutamate receptor complex	down	ionotropic glutamate receptor complex (GO:0008328)	CC	27	26	0.038461538	0.000659943
GO:0042383	sarcolemma	down	sarcolemma (GO:0042383)	CC	54	52	0	0.000906751
GO:0016323	basolateral plasma membrane	down	basolateral plasma membrane (GO:0016323)	CC	97	95	0	0.000981177
GO:0005771	multivesicular body	down	multivesicular body (GO:0005771)	CC	13	13	0	0.000981177
GO:0000793	condensed chromosome	down	condensed chromosome (GO:0000793)	CC	101	94	0.053191489	0.001003121
GO:1990351	transporter complex	down	transporter complex (GO:1990351)	CC	179	169	0.01183432	0.001056596
GO:0030175	filopodium	down	filopodium (GO:0030175)	CC	51	49	0	0.00115886
GO:0032281	AMPA glutamate receptor complex	down	AMPA glutamate receptor complex (GO:0032281)	CC	16	15	0.066666667	0.00126953
GO:0032153	cell division site	down	cell division site (GO:0032153)	CC	23	23	0	0.001452595
GO:0032155	cell division site part	down	cell division site part (GO:0032155)	CC	23	23	0	0.001452595
GO:0019898	extrinsic component of membrane	down	extrinsic component of membrane (GO:0019898)	CC	124	114	0	0.001452595
GO:0019897	extrinsic component of plasma membrane	down	extrinsic component of plasma membrane (GO:0019897)	CC	69	59	0	0.001452595
GO:0043025	neuronal cell body	down	neuronal cell body (GO:0043025)	CC	127	118	0	0.001452595
GO:0005795	Golgi stack	down	Golgi stack (GO:0005795)	CC	38	36	0	0.001518531
GO:0045177	apical part of cell	down	apical part of cell (GO:0045177)	CC	197	188	0.005319149	0.001526696
GO:0031234	extrinsic component of cytoplasmic side of plasma memb	down	extrinsic component of cytoplasmic side of plasma membrane (GO:00312	CC	43	33	0	0.001547373
GO:0098878	neurotransmitter receptor complex	down	neurotransmitter receptor complex (GO:0098878)	CC	29	28	0.035714286	0.001547373
GO:0005802	trans-Golgi network	down	trans-Golgi network (GO:0005802)	CC	92	90	0	0.001558206
GO:0031253	cell projection membrane	down	cell projection membrane (GO:0031253)	CC	111	108	0	0.001941901
GO:0032588	trans-Golgi network membrane	down	trans-Golgi network membrane (GO:0032588)	CC	14	14	0	0.002006541
GO:0070160	occluding junction	down	occluding junction (GO:0070160)	CC	70	67	0.014925373	0.002098674
GO:0097610	cell surface furrow	down	cell surface furrow (GO:0097610)	CC	21	21	0	0.002109445
GO:0032154	cleavage furrow	down	cleavage furrow (GO:0032154)	CC	21	21	0	0.002109445
GO:0030139	endocytic vesicle	down	endocytic vesicle (GO:0030139)	CC	88	87	0	0.002109445
GO:0045211	postsynaptic membrane	down	postsynaptic membrane (GO:0045211)	CC	58	58	0.034482759	0.002109445
GO:0005876	spindle microtubule	down	spindle microtubule (GO:0005876)	CC	36	33	0	0.002109445
GO:0005891	voltage-gated calcium channel complex	down	voltage-gated calcium channel complex (GO:0005891)	CC	26	24	0	0.002887399
GO:0046658	anchored component of plasma membrane	down	anchored component of plasma membrane (GO:0046658)	CC	19	18	0	0.002923963
GO:0032580	Golgi cisterna membrane	down	Golgi cisterna membrane (GO:0032580)	CC	13	12	0	0.002923963
GO:0001741	XY body	down	XY body (GO:0001741)	CC	10	9	0	0.003029106
GO:0030424	axon	down	axon (GO:0030424)	CC	159	154	0	0.003178076
GO:0098643	banded collagen fibril	down	banded collagen fibril (GO:0098643)	CC	10	10	0.2	0.003609602
GO:0005583	fibrillar collagen trimer	down	fibrillar collagen trimer (GO:0005583)	CC	10	10	0.2	0.003609602
GO:0005942	phosphatidylinositol 3-kinase complex	down	phosphatidylinositol 3-kinase complex (GO:0005942)	CC	11	11	0	0.004012652
GO:0030992	intraciliary transport particle B	down	intraciliary transport particle B (GO:0030992)	CC	15	15	0	0.004136055
GO:0005881	cytoplasmic microtubule	down	cytoplasmic microtubule (GO:0005881)	CC	33	26	0	0.004708984
GO:0031594	neuromuscular junction	down	neuromuscular junction (GO:0031594)	CC	31	31	0	0.004708984
GO:0000790	nuclear chromatin	down	nuclear chromatin (GO:0000790)	CC	196	184	0	0.0050022
GO:0016460	myosin II complex	down	myosin II complex (GO:0016460)	CC	10	7	0	0.006756254
GO:0042470	melanosome	down	melanosome (GO:0042470)	CC	23	23	0	0.007535598
GO:0048770	pigment granule	down	pigment granule (GO:0048770)	CC	23	23	0	0.007535598
GO:0031256	leading edge membrane	down	leading edge membrane (GO:0031256)	CC	56	56	0	0.007713204
GO:0035098	ESC/E(Z) complex	down	ESC/E(Z) complex (GO:0035098)	CC	14	12	0	0.008763152
GO:0005903	brush border	down	brush border (GO:0005903)	CC	59	54	0	0.009192835
GO:0033267	axon part	down	axon part (GO:0033267)	CC	61	60	0	0.009697077
GO:0001518	voltage-gated sodium channel complex	down	voltage-gated sodium channel complex (GO:0001518)	CC	14	14	0	0.009977261

D90 to D135

Down Regulated

Clas	**GO ID**	**GO Description**	**Direction of c**	**GO Description and ID**	**Class**	**Size**	**Size in data**	**% in data**	**FDR.adj.pval**
MOLECULAR FUNCTION									
	GO:0048407	platelet-derived growth factor binding	down	platelet-derived growth factor binding (GO:0048407)	MF	11	10	0.2	4.44089E-16
	GO:0005201	extracellular matrix structural constituent	down	extracellular matrix structural constituent (GO:0005201)	MF	31	30	0.1	3.75922E-13
	GO:0017154	semaphorin receptor activity	down	semaphorin receptor activity (GO:0017154)	MF	11	11	0.090909091	3.75922E-13
	GO:0046875	ephrin receptor binding	down	ephrin receptor binding (GO:0046875)	MF	19	19	0	6.31305E-09
	GO:0051015	actin filament binding	down	actin filament binding (GO:0051015)	MF	80	77	0	2.6618E-07
	GO:0003774	motor activity	down	motor activity (GO:0003774)	MF	98	88	0.011363636	2.6618E-07
	GO:0017048	Rho GTPase binding	down	Rho GTPase binding (GO:0017048)	MF	115	110	0.009090909	9.0431E-07
	GO:0017147	Wnt-protein binding	down	Wnt-protein binding (GO:0017147)	MF	21	21	0	9.0431E-07
	GO:0001968	fibronectin binding	down	fibronectin binding (GO:0001968)	MF	14	13	0.076923077	1.93596E-06
	GO:0005178	integrin binding	down	integrin binding (GO:0005178)	MF	62	61	0	1.98699E-06
	GO:0017124	SH3 domain binding	down	SH3 domain binding (GO:0017124)	MF	40	38	0.052631579	2.00854E-06
	GO:0008017	microtubule binding	down	microtubule binding (GO:0008017)	MF	150	146	0.006849315	2.45431E-06
	GO:0004713	protein tyrosine kinase activity	down	protein tyrosine kinase activity (GO:0004713)	MF	95	94	0	2.66472E-06

GO:0019838	growth factor binding	down	growth factor binding (GO:0019838)	MF	89	85	0.023529412	4.2825E-06
GO:0030695	GTPase regulator activity	down	GTPase regulator activity (GO:0030695)	MF	143	142	0	8.32728E-06
GO:0004714	transmembrane receptor protein tyrosine kinase activity	down	transmembrane receptor protein tyrosine kinase activity (GO:0004714)	MF	44	44	0	8.36565E-06
GO:0005516	calmodulin binding	down	calmodulin binding (GO:0005516)	MF	56	53	0.018867925	9.80445E-06
GO:0015631	tubulin binding	down	tubulin binding (GO:0015631)	MF	198	193	0.005181347	1.03705E-05
GO:0005096	GTPase activator activity	down	GTPase activator activity (GO:0005096)	MF	122	121	0	1.0462E-05
GO:0019199	transmembrane receptor protein kinase activity	down	transmembrane receptor protein kinase activity (GO:0019199)	MF	59	58	0	1.0462E-05
GO:0005085	guanyl-nucleotide exchange factor activity	down	guanyl-nucleotide exchange factor activity (GO:0005085)	MF	158	152	0	1.69265E-05
GO:0005539	glycosaminoglycan binding	down	glycosaminoglycan binding (GO:0005539)	MF	108	106	0.028301887	1.69765E-05
GO:0003777	microtubule motor activity	down	microtubule motor activity (GO:0003777)	MF	58	56	0.017857143	2.50642E-05
GO:0005088	Ras guanyl-nucleotide exchange factor activity	down	Ras guanyl-nucleotide exchange factor activity (GO:0005088)	MF	108	102	0	2.50642E-05
GO:0005089	Rho guanyl-nucleotide exchange factor activity	down	Rho guanyl-nucleotide exchange factor activity (GO:0005089)	MF	69	64	0	2.50642E-05
GO:0050840	extracellular matrix binding	down	extracellular matrix binding (GO:0050840)	MF	31	30	0	3.75497E-05
GO:0008201	heparin binding	down	heparin binding (GO:0008201)	MF	73	72	0.041666667	3.916E-05
GO:1901681	sulfur compound binding	down	sulfur compound binding (GO:1901681)	MF	109	108	0.027777778	3.916E-05
GO:0045125	bioactive lipid receptor activity	down	bioactive lipid receptor activity (GO:0045125)	MF	12	12	0	4.49948E-05
GO:0008373	sialyltransferase activity	down	sialyltransferase activity (GO:0008373)	MF	18	18	0.055555556	6.46909E-05
GO:0003950	NAD+ ADP-ribosyltransferase activity	down	NAD+ ADP-ribosyltransferase activity (GO:0003950)	MF	16	15	0	9.06563E-05
GO:0005518	collagen binding	down	collagen binding (GO:0005518)	MF	44	42	0	0.000124156
GO:0060589	nucleoside-triphosphatase regulator activity	down	nucleoside-triphosphatase regulator activity (GO:0060589)	MF	158	155	0	0.000128044
GO:0005217	intracellular ligand-gated ion channel activity	down	intracellular ligand-gated ion channel activity (GO:0005217)	MF	20	18	0	0.000146901
GO:0008013	beta-catenin binding	down	beta-catenin binding (GO:0008013)	MF	58	58	0	0.000222558
GO:0097110	scaffold protein binding	down	scaffold protein binding (GO:0097110)	MF	29	28	0.035714286	0.000222558
GO:0043394	proteoglycan binding	down	proteoglycan binding (GO:0043394)	MF	22	22	0.045454545	0.000309978
GO:0043236	laminin binding	down	laminin binding (GO:0043236)	MF	16	15	0	0.000382412
GO:0004222	metalloendopeptidase activity	down	metalloendopeptidase activity (GO:0004222)	MF	94	88	0.011363636	0.000420461
GO:0016757	transferase activity, transferring glycosyl groups	down	transferase activity, transferring glycosyl groups (GO:0016757)	MF	188	181	0.005524862	0.000573495
GO:0008237	metallopeptidase activity	down	metallopeptidase activity (GO:0008237)	MF	149	138	0.007246377	0.000632093
GO:0005262	calcium channel activity	down	calcium channel activity (GO:0005262)	MF	66	63	0	0.000699932
GO:0008146	sulfotransferase activity	down	sulfotransferase activity (GO:0008146)	MF	36	32	0	0.000742863
GO:0048365	Rac GTPase binding	down	Rac GTPase binding (GO:0048365)	MF	34	34	0	0.001050268
GO:0072509	divalent inorganic cation transmembrane transporter act	down	divalent inorganic cation transmembrane transporter activity (GO:00725	MF	107	104	0	0.001289757
GO:0022832	voltage-gated channel activity	down	voltage-gated channel activity (GO:0022832)	MF	127	125	0	0.001414254
GO:0005244	voltage-gated ion channel activity	down	voltage-gated ion channel activity (GO:0005244)	MF	127	125	0	0.001414254
GO:0015085	calcium ion transmembrane transporter activity	down	calcium ion transmembrane transporter activity (GO:0015085)	MF	81	78	0	0.002595637
GO:0099094	ligand-gated cation channel activity	down	ligand-gated cation channel activity (GO:0099094)	MF	40	39	0.025641026	0.002595637
GO:0030971	receptor tyrosine kinase binding	down	receptor tyrosine kinase binding (GO:0030971)	MF	32	31	0	0.002595637
GO:0000149	SNARE binding	down	SNARE binding (GO:0000149)	MF	48	48	0	0.002595637
GO:0004970	ionotropic glutamate receptor activity	down	ionotropic glutamate receptor activity (GO:0004970)	MF	15	15	0.066666667	0.002960222
GO:0017022	myosin binding	down	myosin binding (GO:0017022)	MF	39	37	0	0.00310994
GO:0042169	SH2 domain binding	down	SH2 domain binding (GO:0042169)	MF	26	25	0	0.00310994
GO:1905030	voltage-gated ion channel activity involved in regulation	down	voltage-gated ion channel activity involved in regulation of postsynaptic	MF	18	18	0	0.00310994
GO:0005248	voltage-gated sodium channel activity	down	voltage-gated sodium channel activity (GO:0005248)	MF	18	18	0	0.00310994
GO:0008375	acetylglucosaminyltransferase activity	down	acetylglucosaminyltransferase activity (GO:0008375)	MF	36	36	0	0.00328881
GO:0016849	phosphorus-oxygen lyase activity	down	phosphorus-oxygen lyase activity (GO:0016849)	MF	19	19	0	0.003592632
GO:0036002	pre-mRNA binding	down	pre-mRNA binding (GO:0036002)	MF	11	11	0	0.003620555
GO:0008194	UDP-glycosyltransferase activity	down	UDP-glycosyltransferase activity (GO:0008194)	MF	81	78	0	0.003649739
GO:0051018	protein kinase A binding	down	protein kinase A binding (GO:0051018)	MF	30	26	0	0.003652792
GO:0019905	syntaxin binding	down	syntaxin binding (GO:0019905)	MF	34	34	0	0.003897705
GO:0004867	serine-type endopeptidase inhibitor activity	down	serine-type endopeptidase inhibitor activity (GO:0004867)	MF	43	38	0.026315789	0.003929931
GO:0016709	oxidoreductase activity, acting on paired donors, with in	down	oxidoreductase activity, acting on paired donors, with incorporation or	MF	17	12	0.083333333	0.004370311
GO:0035091	phosphatidylinositol binding	down	phosphatidylinositol binding (GO:0035091)	MF	147	144	0	0.004370311
GO:0022843	voltage-gated cation channel activity	down	voltage-gated cation channel activity (GO:0022843)	MF	89	88	0	0.00577183
GO:0008376	acetylgalactosaminyltransferase activity	down	acetylgalactosaminyltransferase activity (GO:0008376)	MF	21	20	0	0.006228943
GO:0042056	chemoattractant activity	down	chemoattractant activity (GO:0042056)	MF	15	14	0	0.006228943
GO:0008083	growth factor activity	down	growth factor activity (GO:0008083)	MF	86	84	0.023809524	0.006228943
GO:1990782	protein tyrosine kinase binding	down	protein tyrosine kinase binding (GO:1990782)	MF	34	33	0	0.006228943
GO:0017137	Rab GTPase binding	down	Rab GTPase binding (GO:0017137)	MF	79	74	0.013513514	0.006228943
GO:0005234	extracellularly glutamate-gated ion channel activity	down	extracellularly glutamate-gated ion channel activity (GO:0005234)	MF	16	16	0.0625	0.006448259
GO:0009975	cyclase activity	down	cyclase activity (GO:0009975)	MF	20	20	0	0.00759944
GO:0042805	actinin binding	down	actinin binding (GO:0042805)	MF	19	19	0.052631579	0.008286321
GO:0008022	protein C-terminus binding	down	protein C-terminus binding (GO:0008022)	MF	103	103	0.019417476	0.008357879
GO:0051393	alpha-actinin binding	down	alpha-actinin binding (GO:0051393)	MF	14	14	0.071428571	0.008675262
GO:0000217	DNA secondary structure binding	down	DNA secondary structure binding (GO:0000217)	MF	12	12	0	0.009226672

	GO:0022834	ligand-gated channel activity	down	ligand-gated channel activity (GO:0022834)	MF	105	100	0.01	0.009302162
	GO:0015276	ligand-gated ion channel activity	down	ligand-gated ion channel activity (GO:0015276)	MF	105	100	0.01	0.009302162
	GO:0005057	signal transducer activity, downstream of receptor	down	signal transducer activity, downstream of receptor (GO:0005057)	MF	67	67	0	0.009613034
	GO:0035064	methylated histone binding	down	methylated histone binding (GO:0035064)	MF	43	41	0	0.009692369
	GO:0140034	methylation-dependent protein binding	down	methylation-dependent protein binding (GO:0140034)	MF	43	41	0	0.009692369
	GO:0016758	transferase activity, transferring hexosyl groups	down	transferase activity, transferring hexosyl groups (GO:0016758)	MF	123	120	0	0.009692369
	GO:0005164	tumor necrosis factor receptor binding	down	tumor necrosis factor receptor binding (GO:0005164)	MF	23	23	0	0.009876734

D90 to D135

Up Regulated

Clas	GO ID	GO Description	Direction of c	GO Description and ID	Class	Size	Size in data	% in data	FDR.adj.pval
BIOLOGICAL PROCESS									
	GO:0000460	maturation of 5.8S rRNA	up	maturation of 5.8S rRNA (GO:0000460)	BP	10	10	0.1	1.14921E-06
	GO:0042273	ribosomal large subunit biogenesis	up	ribosomal large subunit biogenesis (GO:0042273)	BP	13	13	0.076923077	0.002274827
	GO:0006364	rRNA processing	up	rRNA processing (GO:0006364)	BP	54	50	0.02	0.004072134

D90 to D135

Up Regulated

Clas	GO ID	GO Description	Direction of c	GO Description and ID	Class	Size	Size in data	% in data	FDR.adj.pval
CELLULAR PROCESS									
	GO:0005838	proteasome regulatory particle	up	proteasome regulatory particle (GO:0005838)	CC	12	12	0	0.000180696
	GO:0022624	proteasome accessory complex	up	proteasome accessory complex (GO:0022624)	CC	18	18	0	0.000636237
	GO:0030684	preribosome	up	preribosome (GO:0030684)	CC	13	12	0.083333333	0.001005175
	GO:1905369	endopeptidase complex	up	endopeptidase complex (GO:1905369)	CC	44	43	0.023255814	0.002109445
	GO:0000502	proteasome complex	up	proteasome complex (GO:0000502)	CC	44	43	0.023255814	0.002109445
	GO:0044452	nucleolar part	up	nucleolar part (GO:0044452)	CC	30	29	0.034482759	0.009111643

D135 to Birth

Down Regulated

Clas	GO ID	GO Description	Direction of c	GO Description and ID	Class	Size	Size in data	% in data	FDR.adj.pval
BIOLOGICAL PROCESS									
	GO:0034508	centromere complex assembly	down	centromere complex assembly (GO:0034508)	BP	17	17	0	4.30576E-09
	GO:0007098	centrosome cycle	down	centrosome cycle (GO:0007098)	BP	60	58	0	7.34643E-06
	GO:1904666	regulation of ubiquitin protein ligase activity	down	regulation of ubiquitin protein ligase activity (GO:1904666)	BP	12	12	0	5.15011E-05
	GO:0031023	microtubule organizing center organization	down	microtubule organizing center organization (GO:0031023)	BP	69	65	0	7.29933E-05
	GO:0044782	cilium organization	down	cilium organization (GO:0044782)	BP	118	115	0	7.29933E-05
	GO:0051298	centrosome duplication	down	centrosome duplication (GO:0051298)	BP	47	45	0	0.000119224
	GO:0001502	cartilage condensation	down	cartilage condensation (GO:0001502)	BP	16	15	0	0.000161422
	GO:0098743	cell aggregation	down	cell aggregation (GO:0098743)	BP	16	15	0	0.000161422
	GO:0002063	chondrocyte development	down	chondrocyte development (GO:0002063)	BP	24	23	0	0.000242585
	GO:0060271	cilium assembly	down	cilium assembly (GO:0060271)	BP	104	102	0	0.000246141
	GO:0071539	protein localization to centrosome	down	protein localization to centrosome (GO:0071539)	BP	13	13	0	0.000246141
	GO:1905508	protein localization to microtubule organizing center	down	protein localization to microtubule organizing center (GO:1905508)	BP	13	13	0	0.000246141
	GO:0006336	DNA replication-independent nucleosome assembly	down	DNA replication-independent nucleosome assembly (GO:0006336)	BP	17	12	0	0.00025009
	GO:0034724	DNA replication-independent nucleosome organization	down	DNA replication-independent nucleosome organization (GO:0034724)	BP	17	12	0	0.00025009
	GO:0060707	trophoblast giant cell differentiation	down	trophoblast giant cell differentiation (GO:0060707)	BP	12	12	0	0.00025009
	GO:0043486	histone exchange	down	histone exchange (GO:0043486)	BP	11	11	0	0.000290816
	GO:0060219	camera-type eye photoreceptor cell differentiation	down	camera-type eye photoreceptor cell differentiation (GO:0060219)	BP	12	12	0	0.000329989
	GO:0042573	retinoic acid metabolic process	down	retinoic acid metabolic process (GO:0042573)	BP	11	8	0	0.00039237
	GO:0060831	smoothened signaling pathway involved in dorsal/ventral	down	smoothened signaling pathway involved in dorsal/ventral neural tube pat	BP	13	13	0	0.00039237
	GO:0098815	modulation of excitatory postsynaptic potential	down	modulation of excitatory postsynaptic potential (GO:0098815)	BP	16	15	0.066666667	0.00039237
	GO:0065004	protein-DNA complex assembly	down	protein-DNA complex assembly (GO:0065004)	BP	73	57	0	0.000491255
	GO:0046605	regulation of centrosome cycle	down	regulation of centrosome cycle (GO:0046605)	BP	35	34	0	0.000607172
	GO:0007018	microtubule-based movement	down	microtubule-based movement (GO:0007018)	BP	150	146	0	0.000646502
	GO:0007099	centriole replication	down	centriole replication (GO:0007099)	BP	24	23	0	0.000646502
	GO:0051383	kinetochore organization	down	kinetochore organization (GO:0051383)	BP	11	11	0	0.000646502
	GO:0072698	protein localization to microtubule cytoskeleton	down	protein localization to microtubule cytoskeleton (GO:0072698)	BP	22	22	0	0.000646502
	GO:0095500	acetylcholine receptor signaling pathway	down	acetylcholine receptor signaling pathway (GO:0095500)	BP	11	11	0.090909091	0.000646502
	GO:1903831	signal transduction involved in cellular response to ammo	down	signal transduction involved in cellular response to ammonium ion (GO:1	BP	11	11	0.090909091	0.000646502
	GO:1905144	response to acetylcholine	down	response to acetylcholine (GO:1905144)	BP	11	11	0.090909091	0.000646502
	GO:1905145	cellular response to acetylcholine	down	cellular response to acetylcholine (GO:1905145)	BP	11	11	0.090909091	0.000646502
	GO:0007224	smoothened signaling pathway	down	smoothened signaling pathway (GO:0007224)	BP	95	93	0	0.000670871
	GO:2000463	positive regulation of excitatory postsynaptic potential	down	positive regulation of excitatory postsynaptic potential (GO:2000463)	BP	12	11	0.090909091	0.000836586
	GO:0071824	protein-DNA complex subunit organization	down	protein-DNA complex subunit organization (GO:0071824)	BP	95	78	0	0.000958164
	GO:0045132	meiotic chromosome segregation	down	meiotic chromosome segregation (GO:0045132)	BP	54	51	0	0.001001623
	GO:0008589	regulation of smoothened signaling pathway	down	regulation of smoothened signaling pathway (GO:0008589)	BP	49	48	0	0.001022159

GO:0031345	negative regulation of cell projection organization	down	negative regulation of cell projection organization (GO:0031345)	BP	82	81	0.024691358	0.001401825
GO:0098534	centriole assembly	down	centriole assembly (GO:0098534)	BP	26	24	0	0.001401825
GO:0006323	DNA packaging	down	DNA packaging (GO:0006323)	BP	81	63	0	0.001426724
GO:0070507	regulation of microtubule cytoskeleton organization	down	regulation of microtubule cytoskeleton organization (GO:0070507)	BP	93	91	0	0.001600622
GO:0031572	G2 DNA damage checkpoint	down	G2 DNA damage checkpoint (GO:0031572)	BP	26	25	0	0.001687826
GO:0060997	dendritic spine morphogenesis	down	dendritic spine morphogenesis (GO:0060997)	BP	25	24	0.041666667	0.001687826
GO:0030199	collagen fibril organization	down	collagen fibril organization (GO:0030199)	BP	24	23	0	0.001717937
GO:0090190	positive regulation of branching involved in ureteric bud	down	positive regulation of branching involved in ureteric bud morphogenesis	BP	15	15	0.066666667	0.001717937
GO:0051965	positive regulation of synapse assembly	down	positive regulation of synapse assembly (GO:0051965)	BP	50	48	0.020833333	0.001768777
GO:0010824	regulation of centrosome duplication	down	regulation of centrosome duplication (GO:0010824)	BP	29	28	0	0.001883238
GO:0140013	meiotic nuclear division	down	meiotic nuclear division (GO:0140013)	BP	98	91	0	0.002033358
GO:0021513	spinal cord dorsal/ventral patterning	down	spinal cord dorsal/ventral patterning (GO:0021513)	BP	18	17	0	0.002099607
GO:0021915	neural tube development	down	neural tube development (GO:0021915)	BP	132	130	0	0.002099607
GO:0051961	negative regulation of nervous system development	down	negative regulation of nervous system development (GO:0051961)	BP	157	153	0.013071895	0.002099607
GO:0071103	DNA conformation change	down	DNA conformation change (GO:0071103)	BP	108	87	0	0.002099607
GO:0007076	mitotic chromosome condensation	down	mitotic chromosome condensation (GO:0007076)	BP	12	10	0	0.002407787
GO:0044380	protein localization to cytoskeleton	down	protein localization to cytoskeleton (GO:0044380)	BP	25	25	0	0.002507406
GO:0035107	appendage morphogenesis	down	appendage morphogenesis (GO:0035107)	BP	119	114	0	0.002580898
GO:0035108	limb morphogenesis	down	limb morphogenesis (GO:0035108)	BP	119	114	0	0.002580898
GO:2000779	regulation of double-strand break repair	down	regulation of double-strand break repair (GO:2000779)	BP	31	31	0	0.002814876
GO:0007127	meiosis I	down	meiosis I (GO:0007127)	BP	59	55	0	0.002918988
GO:0060996	dendritic spine development	down	dendritic spine development (GO:0060996)	BP	45	44	0.022727273	0.002949428
GO:0060026	convergent extension	down	convergent extension (GO:0060026)	BP	12	12	0.083333333	0.003358172
GO:0060078	regulation of postsynaptic membrane potential	down	regulation of postsynaptic membrane potential (GO:0060078)	BP	54	53	0.037735849	0.003454904
GO:0032886	regulation of microtubule-based process	down	regulation of microtubule-based process (GO:0032886)	BP	112	110	0	0.003469766
GO:0097061	dendritic spine organization	down	dendritic spine organization (GO:0097061)	BP	29	28	0.035714286	0.003469766
GO:0106027	neuron projection organization	down	neuron projection organization (GO:0106027)	BP	29	28	0.035714286	0.003469766
GO:0006260	DNA replication	down	DNA replication (GO:0006260)	BP	170	168	0	0.003486894
GO:0007143	female meiotic nuclear division	down	female meiotic nuclear division (GO:0007143)	BP	21	21	0	0.003486894
GO:0048736	appendage development	down	appendage development (GO:0048736)	BP	137	132	0	0.003486894
GO:0060173	limb development	down	limb development (GO:0060173)	BP	137	132	0	0.003486894
GO:0030177	positive regulation of Wnt signaling pathway	down	positive regulation of Wnt signaling pathway (GO:0030177)	BP	79	76	0.013157895	0.003649918
GO:0006334	nucleosome assembly	down	nucleosome assembly (GO:0006334)	BP	49	33	0	0.003952445
GO:0010977	negative regulation of neuron projection development	down	negative regulation of neuron projection development (GO:0010977)	BP	67	67	0.029850746	0.004199662
GO:0021904	dorsal/ventral neural tube patterning	down	dorsal/ventral neural tube patterning (GO:0021904)	BP	23	23	0	0.004800665
GO:0006302	double-strand break repair	down	double-strand break repair (GO:0006302)	BP	127	123	0	0.005784063
GO:0060071	Wnt signaling pathway, planar cell polarity pathway	down	Wnt signaling pathway, planar cell polarity pathway (GO:0060071)	BP	29	28	0.035714286	0.005784063
GO:0050770	regulation of axonogenesis	down	regulation of axonogenesis (GO:0050770)	BP	87	83	0.012048193	0.005891776
GO:0098693	regulation of synaptic vesicle cycle	down	regulation of synaptic vesicle cycle (GO:0098693)	BP	21	21	0.047619048	0.006256195
GO:1904037	positive regulation of epithelial cell apoptotic process	down	positive regulation of epithelial cell apoptotic process (GO:1904037)	BP	11	11	0.090909091	0.006321397
GO:1903046	meiotic cell cycle process	down	meiotic cell cycle process (GO:1903046)	BP	105	97	0	0.006471597
GO:0021511	spinal cord patterning	down	spinal cord patterning (GO:0021511)	BP	20	19	0	0.006554741
GO:0007416	synapse assembly	down	synapse assembly (GO:0007416)	BP	83	79	0.025316456	0.006695163
GO:0000075	cell cycle checkpoint	down	cell cycle checkpoint (GO:0000075)	BP	118	113	0	0.006854024
GO:0045879	negative regulation of smoothened signaling pathway	down	negative regulation of smoothened signaling pathway (GO:0045879)	BP	19	19	0	0.007042878
GO:0090175	regulation of establishment of planar polarity	down	regulation of establishment of planar polarity (GO:0090175)	BP	30	29	0.034482759	0.007414909
GO:0010721	negative regulation of cell development	down	negative regulation of cell development (GO:0010721)	BP	165	159	0.012578616	0.007543216
GO:0050771	negative regulation of axonogenesis	down	negative regulation of axonogenesis (GO:0050771)	BP	30	30	0.033333333	0.007543216
GO:0061448	connective tissue development	down	connective tissue development (GO:0061448)	BP	158	153	0	0.007665382
GO:0031497	chromatin assembly	down	chromatin assembly (GO:0031497)	BP	60	44	0	0.007670061
GO:0001841	neural tube formation	down	neural tube formation (GO:0001841)	BP	85	83	0	0.007986526
GO:0007411	axon guidance	down	axon guidance (GO:0007411)	BP	126	123	0.016260163	0.008014455
GO:0030111	regulation of Wnt signaling pathway	down	regulation of Wnt signaling pathway (GO:0030111)	BP	176	172	0.023255814	0.008103597
GO:0051216	cartilage development	down	cartilage development (GO:0051216)	BP	126	121	0	0.008103597
GO:0010769	regulation of cell morphogenesis involved in differentiati	down	regulation of cell morphogenesis involved in differentiation (GO:001076	BP	155	146	0.006849315	0.008155511
GO:0006282	regulation of DNA repair	down	regulation of DNA repair (GO:0006282)	BP	55	55	0	0.008261078
GO:0021987	cerebral cortex development	down	cerebral cortex development (GO:0021987)	BP	71	69	0.014492754	0.008381922
GO:0001736	establishment of planar polarity	down	establishment of planar polarity (GO:0001736)	BP	39	36	0.027777778	0.008406151
GO:0007164	establishment of tissue polarity	down	establishment of tissue polarity (GO:0007164)	BP	39	36	0.027777778	0.008406151
GO:0050768	negative regulation of neurogenesis	down	negative regulation of neurogenesis (GO:0050768)	BP	144	140	0.014285714	0.008406151
GO:0030326	embryonic limb morphogenesis	down	embryonic limb morphogenesis (GO:0030326)	BP	102	97	0	0.008941237
GO:0034728	nucleosome organization	down	nucleosome organization (GO:0034728)	BP	71	54	0	0.008941237
GO:0035082	axoneme assembly	down	axoneme assembly (GO:0035082)	BP	35	34	0	0.008941237
GO:0035113	embryonic appendage morphogenesis	down	embryonic appendage morphogenesis (GO:0035113)	BP	102	97	0	0.008941237

	GO:1902850	microtubule cytoskeleton organization involved in mitosi	down	microtubule cytoskeleton organization involved in mitosis (GO:1902850	BP	65	63	0	0.008941237
	GO:0030261	chromosome condensation	down	chromosome condensation (GO:0030261)	BP	16	14	0	0.009898105
	GO:0070192	chromosome organization involved in meiotic cell cycle	down	chromosome organization involved in meiotic cell cycle (GO:0070192)	BP	44	41	0	0.009898105
	GO:0071478	cellular response to radiation	down	cellular response to radiation (GO:0071478)	BP	90	88	0	0.009898105
	GO:0071479	cellular response to ionizing radiation	down	cellular response to ionizing radiation (GO:0071479)	BP	42	42	0	0.009898105
	GO:0090189	regulation of branching involved in ureteric bud morphog	down	regulation of branching involved in ureteric bud morphogenesis (GO:009	BP	19	19	0.052631579	0.009898105
	GO:2000050	regulation of non-canonical Wnt signaling pathway	down	regulation of non-canonical Wnt signaling pathway (GO:2000050)	BP	14	13	0.076923077	0.009898105

D135 to Birth

Down Regulated

Clas	GO ID	GO Description	Direction of c	GO Description and ID	Class	Size	Size in data	% in data	FDR.adj.pval
CELLULAR COMPONENT									
	GO:0000775	chromosome, centromeric region	down	chromosome, centromeric region (GO:0000775)	CC	110	107	0	6.25492E-06
	GO:0000776	kinetochore	down	kinetochore (GO:0000776)	CC	80	79	0	3.98054E-05
	GO:0001518	voltage-gated sodium channel complex	down	voltage-gated sodium channel complex (GO:0001518)	CC	14	14	0.071428571	0.000106969
	GO:0072686	mitotic spindle	down	mitotic spindle (GO:0072686)	CC	41	40	0	0.000106969
	GO:0097546	ciliary base	down	ciliary base (GO:0097546)	CC	16	16	0	0.000106969
	GO:0005819	spindle	down	spindle (GO:0005819)	CC	165	160	0	0.000310873
	GO:0000793	condensed chromosome	down	condensed chromosome (GO:0000793)	CC	101	94	0	0.000478263
	GO:0030990	intraciliary transport particle	down	intraciliary transport particle (GO:0030990)	CC	26	26	0	0.000478263
	GO:0000800	lateral element	down	lateral element (GO:0000800)	CC	11	11	0	0.000780234
	GO:0036064	ciliary basal body	down	ciliary basal body (GO:0036064)	CC	69	65	0	0.001148414
	GO:0010369	chromocenter	down	chromocenter (GO:0010369)	CC	12	12	0	0.001230126
	GO:0000777	condensed chromosome kinetochore	down	condensed chromosome kinetochore (GO:0000777)	CC	17	16	0	0.001720822
	GO:0042555	MCM complex	down	MCM complex (GO:0042555)	CC	10	10	0	0.001720822
	GO:0034706	sodium channel complex	down	sodium channel complex (GO:0034706)	CC	19	19	0.052631579	0.002037384
	GO:0044450	microtubule organizing center part	down	microtubule organizing center part (GO:0044450)	CC	102	99	0	0.002544848
	GO:0043073	germ cell nucleus	down	germ cell nucleus (GO:0043073)	CC	13	12	0	0.003221835
	GO:0033267	axon part	down	axon part (GO:0033267)	CC	61	60	0.033333333	0.003506621
	GO:0005581	collagen trimer	down	collagen trimer (GO:0005581)	CC	41	39	0.025641026	0.004516006
	GO:0000922	spindle pole	down	spindle pole (GO:0000922)	CC	73	70	0	0.005471356
	GO:0044420	extracellular matrix component	down	extracellular matrix component (GO:0044420)	CC	81	80	0.05	0.005659687
	GO:0051233	spindle midzone	down	spindle midzone (GO:0051233)	CC	19	19	0	0.005659687
	GO:0030424	axon	down	axon (GO:0030424)	CC	159	154	0.019480519	0.006385264
	GO:0005814	centriole	down	centriole (GO:0005814)	CC	70	68	0	0.007191872
	GO:0005721	pericentric heterochromatin	down	pericentric heterochromatin (GO:0005721)	CC	16	15	0	0.007407124
	GO:0001673	male germ cell nucleus	down	male germ cell nucleus (GO:0001673)	CC	11	10	0	0.008236207
	GO:0005876	spindle microtubule	down	spindle microtubule (GO:0005876)	CC	36	33	0	0.008968033
	GO:0008278	cohesin complex	down	cohesin complex (GO:0008278)	CC	11	10	0	0.008968033
	GO:0005578	proteinaceous extracellular matrix	down	proteinaceous extracellular matrix (GO:0005578)	CC	190	187	0.026737968	0.009403491

D135 to Birth

Down Regulated

Clas	GO ID	GO Description	Direction of c	GO Description and ID	Class	Size	Size in data	% in data	FDR.adj.pval
MOLECULAR FUNCTION									
	GO:0008017	microtubule binding	down	microtubule binding (GO:0008017)	MF	150	146	0	0.001023623
	GO:0005248	voltage-gated sodium channel activity	down	voltage-gated sodium channel activity (GO:0005248)	MF	18	18	0.055555556	0.001426747
	GO:0015631	tubulin binding	down	tubulin binding (GO:0015631)	MF	198	193	0	0.001426747
	GO:0043142	single-stranded DNA-dependent ATPase activity	down	single-stranded DNA-dependent ATPase activity (GO:0043142)	MF	11	11	0	0.001426747
	GO:1905030	voltage-gated ion channel activity involved in regulation	down	voltage-gated ion channel activity involved in regulation of postsynaptic	MF	18	18	0.055555556	0.001426747

D135 to Birth

Up Regulated

Clas	GO ID	GO Description	Direction of c	GO Description and ID	Class	Size	Size in data	% in data	FDR.adj.pval
BIOLOGICAL PROCESS									
	GO:0003009	skeletal muscle contraction	up	skeletal muscle contraction (GO:0003009)	BP	23	20	0.1	1.54632E-06
	GO:0006099	tricarboxylic acid cycle	up	tricarboxylic acid cycle (GO:0006099)	BP	15	15	0.066666667	0.000992187
	GO:0009060	aerobic respiration	up	aerobic respiration (GO:0009060)	BP	29	25	0.08	0.001426724
	GO:0050879	multicellular organismal movement	up	multicellular organismal movement (GO:0050879)	BP	33	29	0.068965517	0.001717937
	GO:0050881	musculoskeletal movement	up	musculoskeletal movement (GO:0050881)	BP	33	29	0.068965517	0.001717937
	GO:0043501	skeletal muscle adaptation	up	skeletal muscle adaptation (GO:0043501)	BP	12	12	0.166666667	0.00367991
	GO:0006101	citrate metabolic process	up	citrate metabolic process (GO:0006101)	BP	18	18	0.055555556	0.006421263
	GO:0072350	tricarboxylic acid metabolic process	up	tricarboxylic acid metabolic process (GO:0072350)	BP	22	22	0.045454545	0.009052534

D135 to Birth

Up Regulated

Clas	GO ID	GO Description	Direction of c	GO Description and ID	Class	Size	Size in data	% in data	FDR.adj.pval

CELLULAR COMPONENT									
	GO:0005865	striated muscle thin filament	up	striated muscle thin filament (GO:0005865)	CC	11	11	0.090909091	0.000780234
	GO:0036379	myofilament	up	myofilament (GO:0036379)	CC	13	13	0.076923077	0.005090088

D135 to Birth

Up Regulated

Class	GO ID	GO Description	Direction of c	GO Description and ID	Class	Size	Size in data	% in data	FDR.adj.pval
MOLECULAR FUNCTION									
	GO:0008137	NADH dehydrogenase (ubiquinone) activity	up	NADH dehydrogenase (ubiquinone) activity (GO:0008137)	MF	18	11	0.090909091	0.001426747
	GO:0050136	NADH dehydrogenase (quinone) activity	up	NADH dehydrogenase (quinone) activity (GO:0050136)	MF	18	11	0.090909091	0.001426747

D90 to Birth

Down Regulated

Class	GO ID	GO Description	Direction of c	GO Description and ID	Class	Size	Size in data	% in data	FDR.adj.pval
BIOLOGICAL PROCESS									
	GO.ID	GO.Description	direction	GO	class	GO.size	GO.size.in.data	pct.in.data.DE	FDR.adj.pval
	GO:0000070	mitotic sister chromatid segregation	down	mitotic sister chromatid segregation (GO:0000070)	BP	90	86	0.255813953	4.44089E-16
	GO:0000075	cell cycle checkpoint	down	cell cycle checkpoint (GO:0000075)	BP	118	113	0.168141593	4.44089E-16
	GO:0000281	mitotic cytokinesis	down	mitotic cytokinesis (GO:0000281)	BP	28	28	0.392857143	4.44089E-16
	GO:0000819	sister chromatid segregation	down	sister chromatid segregation (GO:0000819)	BP	110	104	0.221153846	4.44089E-16
	GO:0000910	cytokinesis	down	cytokinesis (GO:0000910)	BP	89	88	0.227272727	4.44089E-16
	GO:0001502	cartilage condensation	down	cartilage condensation (GO:0001502)	BP	16	15	0.533333333	4.44089E-16
	GO:0001649	osteoblast differentiation	down	osteoblast differentiation (GO:0001649)	BP	151	145	0.220689655	4.44089E-16
	GO:0001657	ureteric bud development	down	ureteric bud development (GO:0001657)	BP	78	77	0.233766234	4.44089E-16
	GO:0001704	formation of primary germ layer	down	formation of primary germ layer (GO:0001704)	BP	91	90	0.2	4.44089E-16
	GO:0001706	endoderm formation	down	endoderm formation (GO:0001706)	BP	42	41	0.268292683	4.44089E-16
	GO:0001736	establishment of planar polarity	down	establishment of planar polarity (GO:0001736)	BP	39	36	0.277777778	4.44089E-16
	GO:0001738	morphogenesis of a polarized epithelium	down	morphogenesis of a polarized epithelium (GO:0001738)	BP	47	44	0.272727273	4.44089E-16
	GO:0001763	morphogenesis of a branching structure	down	morphogenesis of a branching structure (GO:0001763)	BP	163	157	0.21656051	4.44089E-16
	GO:0001822	kidney development	down	kidney development (GO:0001822)	BP	189	186	0.215053763	4.44089E-16
	GO:0001823	mesonephros development	down	mesonephros development (GO:0001823)	BP	81	80	0.225	4.44089E-16
	GO:0001837	epithelial to mesenchymal transition	down	epithelial to mesenchymal transition (GO:0001837)	BP	80	80	0.175	4.44089E-16
	GO:0001838	embryonic epithelial tube formation	down	embryonic epithelial tube formation (GO:0001838)	BP	104	102	0.18627451	4.44089E-16
	GO:0001841	neural tube formation	down	neural tube formation (GO:0001841)	BP	85	83	0.168674699	4.44089E-16
	GO:0001843	neural tube closure	down	neural tube closure (GO:0001843)	BP	74	72	0.180555556	4.44089E-16
	GO:0001945	lymph vessel development	down	lymph vessel development (GO:0001945)	BP	17	16	0.125	4.44089E-16
	GO:0001946	lymphangiogenesis	down	lymphangiogenesis (GO:0001946)	BP	11	11	0.181818182	4.44089E-16
	GO:0001952	regulation of cell-matrix adhesion	down	regulation of cell-matrix adhesion (GO:0001952)	BP	65	65	0.107692308	4.44089E-16
	GO:0001954	positive regulation of cell-matrix adhesion	down	positive regulation of cell-matrix adhesion (GO:0001954)	BP	28	28	0.071428571	4.44089E-16
	GO:0002062	chondrocyte differentiation	down	chondrocyte differentiation (GO:0002062)	BP	71	68	0.279411765	4.44089E-16
	GO:0002063	chondrocyte development	down	chondrocyte development (GO:0002063)	BP	24	23	0.391304348	4.44089E-16
	GO:0003007	heart morphogenesis	down	heart morphogenesis (GO:0003007)	BP	169	168	0.18452381	4.44089E-16
	GO:0003188	heart valve formation	down	heart valve formation (GO:0003188)	BP	10	10	0.2	4.44089E-16
	GO:0003401	axis elongation	down	axis elongation (GO:0003401)	BP	27	26	0.230769231	4.44089E-16
	GO:0006260	DNA replication	down	DNA replication (GO:0006260)	BP	170	168	0.125	4.44089E-16
	GO:0007018	microtubule-based movement	down	microtubule-based movement (GO:0007018)	BP	150	146	0.171232877	4.44089E-16
	GO:0007019	microtubule depolymerization	down	microtubule depolymerization (GO:0007019)	BP	20	20	0.4	4.44089E-16
	GO:0007044	cell-substrate junction assembly	down	cell-substrate junction assembly (GO:0007044)	BP	51	49	0.163265306	4.44089E-16
	GO:0007051	spindle organization	down	spindle organization (GO:0007051)	BP	91	89	0.168539326	4.44089E-16
	GO:0007052	mitotic spindle organization	down	mitotic spindle organization (GO:0007052)	BP	51	50	0.2	4.44089E-16
	GO:0007076	mitotic chromosome condensation	down	mitotic chromosome condensation (GO:0007076)	BP	12	10	0.4	4.44089E-16
	GO:0007098	centrosome cycle	down	centrosome cycle (GO:0007098)	BP	60	58	0.25862069	4.44089E-16
	GO:0007099	centriole replication	down	centriole replication (GO:0007099)	BP	24	23	0.304347826	4.44089E-16
	GO:0007156	homophilic cell adhesion via plasma membrane adhesion	down	homophilic cell adhesion via plasma membrane adhesion molecules (GO:	BP	79	66	0.227272727	4.44089E-16
	GO:0007160	cell-matrix adhesion	down	cell-matrix adhesion (GO:0007160)	BP	127	126	0.150793651	4.44089E-16
	GO:0007163	establishment or maintenance of cell polarity	down	establishment or maintenance of cell polarity (GO:0007163)	BP	108	100	0.17	4.44089E-16
	GO:0007164	establishment of tissue polarity	down	establishment of tissue polarity (GO:0007164)	BP	39	36	0.277777778	4.44089E-16
	GO:0007179	transforming growth factor beta receptor signaling pathw	down	transforming growth factor beta receptor signaling pathway (GO:000717	BP	104	104	0.173076923	4.44089E-16
	GO:0007224	smoothened signaling pathway	down	smoothened signaling pathway (GO:0007224)	BP	95	93	0.247311828	4.44089E-16
	GO:0007369	gastrulation	down	gastrulation (GO:0007369)	BP	131	128	0.171875	4.44089E-16
	GO:0007405	neuroblast proliferation	down	neuroblast proliferation (GO:0007405)	BP	42	41	0.268292683	4.44089E-16
	GO:0007411	axon guidance	down	axon guidance (GO:0007411)	BP	126	123	0.276422764	4.44089E-16
	GO:0007416	synapse assembly	down	synapse assembly (GO:0007416)	BP	83	79	0.341772152	4.44089E-16
	GO:0007435	salivary gland morphogenesis	down	salivary gland morphogenesis (GO:0007435)	BP	31	31	0.322580645	4.44089E-16
	GO:0007492	endoderm development	down	endoderm development (GO:0007492)	BP	57	56	0.196428571	4.44089E-16

GO:0008045	motor neuron axon guidance	down	motor neuron axon guidance (GO:0008045)	BP	22	22	0.272727273	4.44089E-16
GO:0008347	glial cell migration	down	glial cell migration (GO:0008347)	BP	27	25	0.24	4.44089E-16
GO:0008589	regulation of smoothened signaling pathway	down	regulation of smoothened signaling pathway (GO:0008589)	BP	49	48	0.333333333	4.44089E-16
GO:0009952	anterior/posterior pattern specification	down	anterior/posterior pattern specification (GO:0009952)	BP	162	155	0.161290323	4.44089E-16
GO:0009953	dorsal/ventral pattern formation	down	dorsal/ventral pattern formation (GO:0009953)	BP	72	70	0.242857143	4.44089E-16
GO:0010001	glial cell differentiation	down	glial cell differentiation (GO:0010001)	BP	110	108	0.157407407	4.44089E-16
GO:0010631	epithelial cell migration	down	epithelial cell migration (GO:0010631)	BP	167	161	0.173913043	4.44089E-16
GO:0010632	regulation of epithelial cell migration	down	regulation of epithelial cell migration (GO:0010632)	BP	126	123	0.138211382	4.44089E-16
GO:0010715	regulation of extracellular matrix disassembly	down	regulation of extracellular matrix disassembly (GO:0010715)	BP	10	8	0.5	4.44089E-16
GO:0010717	regulation of epithelial to mesenchymal transition	down	regulation of epithelial to mesenchymal transition (GO:0010717)	BP	51	51	0.176470588	4.44089E-16
GO:0010718	positive regulation of epithelial to mesenchymal transitio	down	positive regulation of epithelial to mesenchymal transition (GO:0010718	BP	29	29	0.206896552	4.44089E-16
GO:0010721	negative regulation of cell development	down	negative regulation of cell development (GO:0010721)	BP	165	159	0.20754717	4.44089E-16
GO:0010769	regulation of cell morphogenesis involved in differentiati	down	regulation of cell morphogenesis involved in differentiation (GO:001076	BP	155	146	0.178082192	4.44089E-16
GO:0010810	regulation of cell-substrate adhesion	down	regulation of cell-substrate adhesion (GO:0010810)	BP	124	119	0.134453782	4.44089E-16
GO:0010811	positive regulation of cell-substrate adhesion	down	positive regulation of cell-substrate adhesion (GO:0010811)	BP	73	69	0.115942029	4.44089E-16
GO:0010977	negative regulation of neuron projection development	down	negative regulation of neuron projection development (GO:0010977)	BP	67	67	0.194029851	4.44089E-16
GO:0014020	primary neural tube formation	down	primary neural tube formation (GO:0014020)	BP	78	76	0.171052632	4.44089E-16
GO:0014031	mesenchymal cell development	down	mesenchymal cell development (GO:0014031)	BP	45	44	0.340909091	4.44089E-16
GO:0014032	neural crest cell development	down	neural crest cell development (GO:0014032)	BP	42	41	0.365853659	4.44089E-16
GO:0014033	neural crest cell differentiation	down	neural crest cell differentiation (GO:0014033)	BP	49	48	0.333333333	4.44089E-16
GO:0016331	morphogenesis of embryonic epithelium	down	morphogenesis of embryonic epithelium (GO:0016331)	BP	122	120	0.191666667	4.44089E-16
GO:0016358	dendrite development	down	dendrite development (GO:0016358)	BP	129	126	0.182539683	4.44089E-16
GO:0017145	stem cell division	down	stem cell division (GO:0017145)	BP	22	20	0.35	4.44089E-16
GO:0018108	peptidyl-tyrosine phosphorylation	down	peptidyl-tyrosine phosphorylation (GO:0018108)	BP	184	182	0.192307692	4.44089E-16
GO:0018212	peptidyl-tyrosine modification	down	peptidyl-tyrosine modification (GO:0018212)	BP	186	184	0.190217391	4.44089E-16
GO:0021510	spinal cord development	down	spinal cord development (GO:0021510)	BP	63	62	0.258064516	4.44089E-16
GO:0021511	spinal cord patterning	down	spinal cord patterning (GO:0021511)	BP	20	19	0.473684211	4.44089E-16
GO:0021513	spinal cord dorsal/ventral patterning	down	spinal cord dorsal/ventral patterning (GO:0021513)	BP	18	17	0.529411765	4.44089E-16
GO:0021537	telencephalon development	down	telencephalon development (GO:0021537)	BP	153	149	0.174496644	4.44089E-16
GO:0021543	pallium development	down	pallium development (GO:0021543)	BP	101	98	0.163265306	4.44089E-16
GO:0021904	dorsal/ventral neural tube patterning	down	dorsal/ventral neural tube patterning (GO:0021904)	BP	23	23	0.347826087	4.44089E-16
GO:0021915	neural tube development	down	neural tube development (GO:0021915)	BP	132	130	0.184615385	4.44089E-16
GO:0021952	central nervous system projection neuron axonogenesis	down	central nervous system projection neuron axonogenesis (GO:0021952)	BP	21	20	0.5	4.44089E-16
GO:0021955	central nervous system neuron axonogenesis	down	central nervous system neuron axonogenesis (GO:0021955)	BP	25	24	0.416666667	4.44089E-16
GO:0021987	cerebral cortex development	down	cerebral cortex development (GO:0021987)	BP	71	69	0.202898551	4.44089E-16
GO:0022612	gland morphogenesis	down	gland morphogenesis (GO:0022612)	BP	102	98	0.234693878	4.44089E-16
GO:0030111	regulation of Wnt signaling pathway	down	regulation of Wnt signaling pathway (GO:0030111)	BP	176	172	0.209302326	4.44089E-16
GO:0030177	positive regulation of Wnt signaling pathway	down	positive regulation of Wnt signaling pathway (GO:0030177)	BP	79	76	0.25	4.44089E-16
GO:0030178	negative regulation of Wnt signaling pathway	down	negative regulation of Wnt signaling pathway (GO:0030178)	BP	96	94	0.212765957	4.44089E-16
GO:0030198	extracellular matrix organization	down	extracellular matrix organization (GO:0030198)	BP	140	134	0.291044776	4.44089E-16
GO:0030199	collagen fibril organization	down	collagen fibril organization (GO:0030199)	BP	24	23	0.52173913	4.44089E-16
GO:0030261	chromosome condensation	down	chromosome condensation (GO:0030261)	BP	16	14	0.357142857	4.44089E-16
GO:0030278	regulation of ossification	down	regulation of ossification (GO:0030278)	BP	136	130	0.192307692	4.44089E-16
GO:0030323	respiratory tube development	down	respiratory tube development (GO:0030323)	BP	141	137	0.175182482	4.44089E-16
GO:0030324	lung development	down	lung development (GO:0030324)	BP	138	134	0.164179104	4.44089E-16
GO:0030326	embryonic limb morphogenesis	down	embryonic limb morphogenesis (GO:0030326)	BP	102	97	0.195876289	4.44089E-16
GO:0030509	BMP signaling pathway	down	BMP signaling pathway (GO:0030509)	BP	101	101	0.148514851	4.44089E-16
GO:0030510	regulation of BMP signaling pathway	down	regulation of BMP signaling pathway (GO:0030510)	BP	65	65	0.2	4.44089E-16
GO:0030903	notochord development	down	notochord development (GO:0030903)	BP	16	15	0.266666667	4.44089E-16
GO:0031023	microtubule organizing center organization	down	microtubule organizing center organization (GO:0031023)	BP	69	65	0.230769231	4.44089E-16
GO:0031290	retinal ganglion cell axon guidance	down	retinal ganglion cell axon guidance (GO:0031290)	BP	14	14	0.428571429	4.44089E-16
GO:0031294	lymphocyte costimulation	down	lymphocyte costimulation (GO:0031294)	BP	22	22	0.272727273	4.44089E-16
GO:0031295	T cell costimulation	down	T cell costimulation (GO:0031295)	BP	21	21	0.285714286	4.44089E-16
GO:0031345	negative regulation of cell projection organization	down	negative regulation of cell projection organization (GO:0031345)	BP	82	81	0.172839506	4.44089E-16
GO:0031577	spindle checkpoint	down	spindle checkpoint (GO:0031577)	BP	25	23	0.304347826	4.44089E-16
GO:0032330	regulation of chondrocyte differentiation	down	regulation of chondrocyte differentiation (GO:0032330)	BP	32	30	0.366666667	4.44089E-16
GO:0032331	negative regulation of chondrocyte differentiation	down	negative regulation of chondrocyte differentiation (GO:0032331)	BP	16	15	0.4	4.44089E-16
GO:0032332	positive regulation of chondrocyte differentiation	down	positive regulation of chondrocyte differentiation (GO:0032332)	BP	11	11	0.363636364	4.44089E-16
GO:0032465	regulation of cytokinesis	down	regulation of cytokinesis (GO:0032465)	BP	44	43	0.209302326	4.44089E-16
GO:0032467	positive regulation of cytokinesis	down	positive regulation of cytokinesis (GO:0032467)	BP	25	24	0.333333333	4.44089E-16
GO:0032835	glomerulus development	down	glomerulus development (GO:0032835)	BP	40	40	0.25	4.44089E-16
GO:0032886	regulation of microtubule-based process	down	regulation of microtubule-based process (GO:0032886)	BP	112	110	0.181818182	4.44089E-16
GO:0032963	collagen metabolic process	down	collagen metabolic process (GO:0032963)	BP	32	32	0.1875	4.44089E-16
GO:0034329	cell junction assembly	down	cell junction assembly (GO:0034329)	BP	117	113	0.14159292	4.44089E-16

GO:0034330	cell junction organization	down	cell junction organization (GO:0034330)	BP	148	141	0.14893617	4.44089E-16
GO:0034332	adherens junction organization	down	adherens junction organization (GO:0034332)	BP	57	55	0.163636364	4.44089E-16
GO:0034333	adherens junction assembly	down	adherens junction assembly (GO:0034333)	BP	49	48	0.145833333	4.44089E-16
GO:0034446	substrate adhesion-dependent cell spreading	down	substrate adhesion-dependent cell spreading (GO:0034446)	BP	64	60	0.133333333	4.44089E-16
GO:0034501	protein localization to kinetochore	down	protein localization to kinetochore (GO:0034501)	BP	11	10	0.3	4.44089E-16
GO:0034508	centromere complex assembly	down	centromere complex assembly (GO:0034508)	BP	17	17	0.411764706	4.44089E-16
GO:0035107	appendage morphogenesis	down	appendage morphogenesis (GO:0035107)	BP	119	114	0.219298246	4.44089E-16
GO:0035108	limb morphogenesis	down	limb morphogenesis (GO:0035108)	BP	119	114	0.219298246	4.44089E-16
GO:0035113	embryonic appendage morphogenesis	down	embryonic appendage morphogenesis (GO:0035113)	BP	102	97	0.195876289	4.44089E-16
GO:0035148	tube formation	down	tube formation (GO:0035148)	BP	120	118	0.186440678	4.44089E-16
GO:0035272	exocrine system development	down	exocrine system development (GO:0035272)	BP	40	40	0.3	4.44089E-16
GO:0035282	segmentation	down	segmentation (GO:0035282)	BP	77	75	0.213333333	4.44089E-16
GO:0035567	non-canonical Wnt signaling pathway	down	non-canonical Wnt signaling pathway (GO:0035567)	BP	38	35	0.314285714	4.44089E-16
GO:0035641	locomotory exploration behavior	down	locomotory exploration behavior (GO:0035641)	BP	11	10	0.4	4.44089E-16
GO:0035987	endodermal cell differentiation	down	endodermal cell differentiation (GO:0035987)	BP	39	38	0.289473684	4.44089E-16
GO:0036303	lymph vessel morphogenesis	down	lymph vessel morphogenesis (GO:0036303)	BP	12	12	0.166666667	4.44089E-16
GO:0036342	post-anal tail morphogenesis	down	post-anal tail morphogenesis (GO:0036342)	BP	16	16	0.25	4.44089E-16
GO:0042063	gliogenesis	down	gliogenesis (GO:0042063)	BP	139	135	0.162962963	4.44089E-16
GO:0042249	establishment of planar polarity of embryonic epithelium	down	establishment of planar polarity of embryonic epithelium (GO:0042249)	BP	15	14	0.428571429	4.44089E-16
GO:0042733	embryonic digit morphogenesis	down	embryonic digit morphogenesis (GO:0042733)	BP	51	48	0.1875	4.44089E-16
GO:0043062	extracellular structure organization	down	extracellular structure organization (GO:0043062)	BP	140	134	0.291044776	4.44089E-16
GO:0043486	histone exchange	down	histone exchange (GO:0043486)	BP	11	11	0.272727273	4.44089E-16
GO:0043542	endothelial cell migration	down	endothelial cell migration (GO:0043542)	BP	112	108	0.157407407	4.44089E-16
GO:0043583	ear development	down	ear development (GO:0043583)	BP	155	149	0.181208054	4.44089E-16
GO:0044259	multicellular organismal macromolecule metabolic proce	down	multicellular organismal macromolecule metabolic process (GO:004425	BP	33	33	0.181818182	4.44089E-16
GO:0044782	cilium organization	down	cilium organization (GO:0044782)	BP	118	115	0.104347826	4.44089E-16
GO:0045216	cell-cell junction organization	down	cell-cell junction organization (GO:0045216)	BP	134	129	0.147286822	4.44089E-16
GO:0045665	negative regulation of neuron differentiation	down	negative regulation of neuron differentiation (GO:0045665)	BP	115	112	0.214285714	4.44089E-16
GO:0045667	regulation of osteoblast differentiation	down	regulation of osteoblast differentiation (GO:0045667)	BP	82	79	0.227848101	4.44089E-16
GO:0045669	positive regulation of osteoblast differentiation	down	positive regulation of osteoblast differentiation (GO:0045669)	BP	43	41	0.268292683	4.44089E-16
GO:0045765	regulation of angiogenesis	down	regulation of angiogenesis (GO:0045765)	BP	140	136	0.139705882	4.44089E-16
GO:0045787	positive regulation of cell cycle	down	positive regulation of cell cycle (GO:0045787)	BP	194	186	0.155913978	4.44089E-16
GO:0045879	negative regulation of smoothened signaling pathway	down	negative regulation of smoothened signaling pathway (GO:0045879)	BP	19	19	0.368421053	4.44089E-16
GO:0045880	positive regulation of smoothened signaling pathway	down	positive regulation of smoothened signaling pathway (GO:0045880)	BP	21	20	0.45	4.44089E-16
GO:0045992	negative regulation of embryonic development	down	negative regulation of embryonic development (GO:0045992)	BP	21	20	0.4	4.44089E-16
GO:0045995	regulation of embryonic development	down	regulation of embryonic development (GO:0045995)	BP	88	84	0.214285714	4.44089E-16
GO:0046599	regulation of centriole replication	down	regulation of centriole replication (GO:0046599)	BP	12	11	0.363636364	4.44089E-16
GO:0048013	ephrin receptor signaling pathway	down	ephrin receptor signaling pathway (GO:0048013)	BP	26	26	0.384615385	4.44089E-16
GO:0048103	somatic stem cell division	down	somatic stem cell division (GO:0048103)	BP	16	14	0.428571429	4.44089E-16
GO:0048532	anatomical structure arrangement	down	anatomical structure arrangement (GO:0048532)	BP	16	16	0.25	4.44089E-16
GO:0048546	digestive tract morphogenesis	down	digestive tract morphogenesis (GO:0048546)	BP	34	34	0.235294118	4.44089E-16
GO:0048565	digestive tract development	down	digestive tract development (GO:0048565)	BP	91	89	0.191011236	4.44089E-16
GO:0048588	developmental cell growth	down	developmental cell growth (GO:0048588)	BP	106	103	0.174757282	4.44089E-16
GO:0048592	eye morphogenesis	down	eye morphogenesis (GO:0048592)	BP	111	107	0.242990654	4.44089E-16
GO:0048593	camera-type eye morphogenesis	down	camera-type eye morphogenesis (GO:0048593)	BP	81	77	0.25974026	4.44089E-16
GO:0048704	embryonic skeletal system morphogenesis	down	embryonic skeletal system morphogenesis (GO:0048704)	BP	77	73	0.150684932	4.44089E-16
GO:0048705	skeletal system morphogenesis	down	skeletal system morphogenesis (GO:0048705)	BP	176	168	0.19047619	4.44089E-16
GO:0048706	embryonic skeletal system development	down	embryonic skeletal system development (GO:0048706)	BP	100	96	0.15625	4.44089E-16
GO:0048736	appendage development	down	appendage development (GO:0048736)	BP	137	132	0.204545455	4.44089E-16
GO:0048754	branching morphogenesis of an epithelial tube	down	branching morphogenesis of an epithelial tube (GO:0048754)	BP	122	117	0.196581197	4.44089E-16
GO:0048762	mesenchymal cell differentiation	down	mesenchymal cell differentiation (GO:0048762)	BP	127	126	0.214285714	4.44089E-16
GO:0048813	dendrite morphogenesis	down	dendrite morphogenesis (GO:0048813)	BP	79	77	0.220779221	4.44089E-16
GO:0048839	inner ear development	down	inner ear development (GO:0048839)	BP	134	128	0.2109375	4.44089E-16
GO:0048863	stem cell differentiation	down	stem cell differentiation (GO:0048863)	BP	112	106	0.20754717	4.44089E-16
GO:0048864	stem cell development	down	stem cell development (GO:0048864)	BP	44	42	0.357142857	4.44089E-16
GO:0050730	regulation of peptidyl-tyrosine phosphorylation	down	regulation of peptidyl-tyrosine phosphorylation (GO:0050730)	BP	110	109	0.183486239	4.44089E-16
GO:0050768	negative regulation of neurogenesis	down	negative regulation of neurogenesis (GO:0050768)	BP	144	140	0.207142857	4.44089E-16
GO:0050770	regulation of axonogenesis	down	regulation of axonogenesis (GO:0050770)	BP	87	83	0.228915663	4.44089E-16
GO:0050803	regulation of synapse structure or activity	down	regulation of synapse structure or activity (GO:0050803)	BP	82	79	0.291139241	4.44089E-16
GO:0050807	regulation of synapse organization	down	regulation of synapse organization (GO:0050807)	BP	80	77	0.285714286	4.44089E-16
GO:0050808	synapse organization	down	synapse organization (GO:0050808)	BP	146	141	0.24822695	4.44089E-16
GO:0051056	regulation of small GTPase mediated signal transduction	down	regulation of small GTPase mediated signal transduction (GO:0051056)	BP	173	166	0.138554217	4.44089E-16
GO:0051216	cartilage development	down	cartilage development (GO:0051216)	BP	126	121	0.272727273	4.44089E-16
GO:0051298	centrosome duplication	down	centrosome duplication (GO:0051298)	BP	47	45	0.222222222	4.44089E-16

GO:0051301	cell division	down	cell division (GO:0051301)	BP	171	163	0.208588957	4.44089E-16
GO:0051302	regulation of cell division	down	regulation of cell division (GO:0051302)	BP	66	64	0.1875	4.44089E-16
GO:0051383	kinetochore organization	down	kinetochore organization (GO:0051383)	BP	11	11	0.454545455	4.44089E-16
GO:0051781	positive regulation of cell division	down	positive regulation of cell division (GO:0051781)	BP	33	32	0.25	4.44089E-16
GO:0051782	negative regulation of cell division	down	negative regulation of cell division (GO:0051782)	BP	10	9	0.222222222	4.44089E-16
GO:0051882	mitochondrial depolarization	down	mitochondrial depolarization (GO:0051882)	BP	14	11	0.272727273	4.44089E-16
GO:0051893	regulation of focal adhesion assembly	down	regulation of focal adhesion assembly (GO:0051893)	BP	35	35	0.171428571	4.44089E-16
GO:0051894	positive regulation of focal adhesion assembly	down	positive regulation of focal adhesion assembly (GO:0051894)	BP	15	15	0.133333333	4.44089E-16
GO:0051900	regulation of mitochondrial depolarization	down	regulation of mitochondrial depolarization (GO:0051900)	BP	13	11	0.272727273	4.44089E-16
GO:0051961	negative regulation of nervous system development	down	negative regulation of nervous system development (GO:0051961)	BP	157	153	0.215686275	4.44089E-16
GO:0051963	regulation of synapse assembly	down	regulation of synapse assembly (GO:0051963)	BP	61	58	0.344827586	4.44089E-16
GO:0051965	positive regulation of synapse assembly	down	positive regulation of synapse assembly (GO:0051965)	BP	50	48	0.375	4.44089E-16
GO:0051983	regulation of chromosome segregation	down	regulation of chromosome segregation (GO:0051983)	BP	53	51	0.274509804	4.44089E-16
GO:0055123	digestive system development	down	digestive system development (GO:0055123)	BP	97	95	0.189473684	4.44089E-16
GO:0060009	Sertoli cell development	down	Sertoli cell development (GO:0060009)	BP	10	10	0.2	4.44089E-16
GO:0060026	convergent extension	down	convergent extension (GO:0060026)	BP	12	12	0.416666667	4.44089E-16
GO:0060070	canonical Wnt signaling pathway	down	canonical Wnt signaling pathway (GO:0060070)	BP	171	167	0.19760479	4.44089E-16
GO:0060071	Wnt signaling pathway, planar cell polarity pathway	down	Wnt signaling pathway, planar cell polarity pathway (GO:0060071)	BP	29	28	0.357142857	4.44089E-16
GO:0060078	regulation of postsynaptic membrane potential	down	regulation of postsynaptic membrane potential (GO:0060078)	BP	54	53	0.339622642	4.44089E-16
GO:0060173	limb development	down	limb development (GO:0060173)	BP	137	132	0.204545455	4.44089E-16
GO:0060219	camera-type eye photoreceptor cell differentiation	down	camera-type eye photoreceptor cell differentiation (GO:0060219)	BP	12	12	0.5	4.44089E-16
GO:0060271	cilium assembly	down	cilium assembly (GO:0060271)	BP	104	102	0.088235294	4.44089E-16
GO:0060348	bone development	down	bone development (GO:0060348)	BP	140	132	0.21969697	4.44089E-16
GO:0060349	bone morphogenesis	down	bone morphogenesis (GO:0060349)	BP	68	65	0.246153846	4.44089E-16
GO:0060350	endochondral bone morphogenesis	down	endochondral bone morphogenesis (GO:0060350)	BP	40	38	0.263157895	4.44089E-16
GO:0060351	cartilage development involved in endochondral bone m	down	cartilage development involved in endochondral bone morphogenesis (G	BP	19	19	0.473684211	4.44089E-16
GO:0060412	ventricular septum morphogenesis	down	ventricular septum morphogenesis (GO:0060412)	BP	27	27	0.222222222	4.44089E-16
GO:0060485	mesenchyme development	down	mesenchyme development (GO:0060485)	BP	157	156	0.205128205	4.44089E-16
GO:0060541	respiratory system development	down	respiratory system development (GO:0060541)	BP	156	151	0.178807947	4.44089E-16
GO:0060560	developmental growth involved in morphogenesis	down	developmental growth involved in morphogenesis (GO:0060560)	BP	137	130	0.176923077	4.44089E-16
GO:0060606	tube closure	down	tube closure (GO:0060606)	BP	75	73	0.178082192	4.44089E-16
GO:0060688	regulation of morphogenesis of a branching structure	down	regulation of morphogenesis of a branching structure (GO:0060688)	BP	46	45	0.311111111	4.44089E-16
GO:0060707	trophoblast giant cell differentiation	down	trophoblast giant cell differentiation (GO:0060707)	BP	12	12	0.333333333	4.44089E-16
GO:0060828	regulation of canonical Wnt signaling pathway	down	regulation of canonical Wnt signaling pathway (GO:0060828)	BP	133	129	0.224806202	4.44089E-16
GO:0060831	smoothened signaling pathway involved in dorsal/ventral	down	smoothened signaling pathway involved in dorsal/ventral neural tube pat	BP	13	13	0.461538462	4.44089E-16
GO:0060976	coronary vasculature development	down	coronary vasculature development (GO:0060976)	BP	30	29	0.275862069	4.44089E-16
GO:0060993	kidney morphogenesis	down	kidney morphogenesis (GO:0060993)	BP	72	71	0.267605634	4.44089E-16
GO:0060996	dendritic spine development	down	dendritic spine development (GO:0060996)	BP	45	44	0.295454545	4.44089E-16
GO:0060997	dendritic spine morphogenesis	down	dendritic spine morphogenesis (GO:0060997)	BP	25	24	0.5	4.44089E-16
GO:0061001	regulation of dendritic spine morphogenesis	down	regulation of dendritic spine morphogenesis (GO:0061001)	BP	17	17	0.352941176	4.44089E-16
GO:0061035	regulation of cartilage development	down	regulation of cartilage development (GO:0061035)	BP	47	45	0.266666667	4.44089E-16
GO:0061037	negative regulation of cartilage development	down	negative regulation of cartilage development (GO:0061037)	BP	20	19	0.368421053	4.44089E-16
GO:0061138	morphogenesis of a branching epithelium	down	morphogenesis of a branching epithelium (GO:0061138)	BP	153	147	0.210884354	4.44089E-16
GO:0061326	renal tubule development	down	renal tubule development (GO:0061326)	BP	75	74	0.27027027	4.44089E-16
GO:0061333	renal tubule morphogenesis	down	renal tubule morphogenesis (GO:0061333)	BP	61	60	0.283333333	4.44089E-16
GO:0061448	connective tissue development	down	connective tissue development (GO:0061448)	BP	158	153	0.254901961	4.44089E-16
GO:0061640	cytoskeleton-dependent cytokinesis	down	cytoskeleton-dependent cytokinesis (GO:0061640)	BP	34	34	0.352941176	4.44089E-16
GO:0065004	protein-DNA complex assembly	down	protein-DNA complex assembly (GO:0065004)	BP	73	57	0.175438596	4.44089E-16
GO:0070507	regulation of microtubule cytoskeleton organization	down	regulation of microtubule cytoskeleton organization (GO:0070507)	BP	93	91	0.197802198	4.44089E-16
GO:0071459	protein localization to chromosome, centromeric region	down	protein localization to chromosome, centromeric region (GO:0071459)	BP	12	11	0.272727273	4.44089E-16
GO:0071526	semaphorin-plexin signaling pathway	down	semaphorin-plexin signaling pathway (GO:0071526)	BP	22	22	0.181818182	4.44089E-16
GO:0071559	response to transforming growth factor beta	down	response to transforming growth factor beta (GO:0071559)	BP	128	126	0.158730159	4.44089E-16
GO:0071560	cellular response to transforming growth factor beta stim	down	cellular response to transforming growth factor beta stimulus (GO:00715	BP	126	124	0.161290323	4.44089E-16
GO:0071772	response to BMP	down	response to BMP (GO:0071772)	BP	108	108	0.166666667	4.44089E-16
GO:0071773	cellular response to BMP stimulus	down	cellular response to BMP stimulus (GO:0071773)	BP	108	108	0.166666667	4.44089E-16
GO:0072006	nephron development	down	nephron development (GO:0072006)	BP	101	100	0.27	4.44089E-16
GO:0072009	nephron epithelium development	down	nephron epithelium development (GO:0072009)	BP	84	83	0.253012048	4.44089E-16
GO:0072073	kidney epithelium development	down	kidney epithelium development (GO:0072073)	BP	110	109	0.247706422	4.44089E-16
GO:0072080	nephron tubule development	down	nephron tubule development (GO:0072080)	BP	72	71	0.267605634	4.44089E-16
GO:0072089	stem cell proliferation	down	stem cell proliferation (GO:0072089)	BP	83	82	0.207317073	4.44089E-16
GO:0072163	mesonephric epithelium development	down	mesonephric epithelium development (GO:0072163)	BP	79	78	0.230769231	4.44089E-16
GO:0072164	mesonephric tubule development	down	mesonephric tubule development (GO:0072164)	BP	79	78	0.230769231	4.44089E-16
GO:0072175	epithelial tube formation	down	epithelial tube formation (GO:0072175)	BP	108	106	0.188679245	4.44089E-16
GO:0090068	positive regulation of cell cycle process	down	positive regulation of cell cycle process (GO:0090068)	BP	134	129	0.186046512	4.44089E-16

GO:0090090	negative regulation of canonical Wnt signaling pathway	down	negative regulation of canonical Wnt signaling pathway (GO:0090090)	BP	77	76	0.25	4.44089E-16
GO:0090092	regulation of transmembrane receptor protein serine/thr	down	regulation of transmembrane receptor protein serine/threonine kinase si	BP	141	141	0.156028369	4.44089E-16
GO:0090102	cochlea development	down	cochlea development (GO:0090102)	BP	32	32	0.25	4.44089E-16
GO:0090109	regulation of cell-substrate junction assembly	down	regulation of cell-substrate junction assembly (GO:0090109)	BP	35	35	0.171428571	4.44089E-16
GO:0090130	tissue migration	down	tissue migration (GO:0090130)	BP	173	167	0.167664671	4.44089E-16
GO:0090132	epithelium migration	down	epithelium migration (GO:0090132)	BP	169	163	0.171779141	4.44089E-16
GO:0090175	regulation of establishment of planar polarity	down	regulation of establishment of planar polarity (GO:0090175)	BP	30	29	0.344827586	4.44089E-16
GO:0090177	establishment of planar polarity involved in neural tube c	down	establishment of planar polarity involved in neural tube closure (GO:009	BP	14	13	0.461538462	4.44089E-16
GO:0090178	regulation of establishment of planar polarity involved in	down	regulation of establishment of planar polarity involved in neural tube clo	BP	13	12	0.416666667	4.44089E-16
GO:0090179	planar cell polarity pathway involved in neural tube closu	down	planar cell polarity pathway involved in neural tube closure (GO:009017	BP	12	11	0.454545455	4.44089E-16
GO:0090287	regulation of cellular response to growth factor stimulus	down	regulation of cellular response to growth factor stimulus (GO:0090287)	BP	165	162	0.179012346	4.44089E-16
GO:0090596	sensory organ morphogenesis	down	sensory organ morphogenesis (GO:0090596)	BP	199	191	0.214659686	4.44089E-16
GO:0095500	acetylcholine receptor signaling pathway	down	acetylcholine receptor signaling pathway (GO:0095500)	BP	11	11	0.363636364	4.44089E-16
GO:0097061	dendritic spine organization	down	dendritic spine organization (GO:0097061)	BP	29	28	0.5	4.44089E-16
GO:0097485	neuron projection guidance	down	neuron projection guidance (GO:0097485)	BP	128	125	0.272	4.44089E-16
GO:0098534	centriole assembly	down	centriole assembly (GO:0098534)	BP	26	24	0.291666667	4.44089E-16
GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecu	down	cell-cell adhesion via plasma-membrane adhesion molecules (GO:009874	BP	108	94	0.234042553	4.44089E-16
GO:0098743	cell aggregation	down	cell aggregation (GO:0098743)	BP	16	15	0.533333333	4.44089E-16
GO:0098813	nuclear chromosome segregation	down	nuclear chromosome segregation (GO:0098813)	BP	162	152	0.203947368	4.44089E-16
GO:0098815	modulation of excitatory postsynaptic potential	down	modulation of excitatory postsynaptic potential (GO:0098815)	BP	16	15	0.6	4.44089E-16
GO:0106027	neuron projection organization	down	neuron projection organization (GO:0106027)	BP	29	28	0.5	4.44089E-16
GO:0140013	meiotic nuclear division	down	meiotic nuclear division (GO:0140013)	BP	98	91	0.142857143	4.44089E-16
GO:0140014	mitotic nuclear division	down	mitotic nuclear division (GO:0140014)	BP	145	140	0.207142857	4.44089E-16
GO:1901342	regulation of vasculature development	down	regulation of vasculature development (GO:1901342)	BP	152	148	0.141891892	4.44089E-16
GO:1902850	microtubule cytoskeleton organization involved in mitosi	down	microtubule cytoskeleton organization involved in mitosis (GO:1902850	BP	65	63	0.19047619	4.44089E-16
GO:1903053	regulation of extracellular matrix organization	down	regulation of extracellular matrix organization (GO:1903053)	BP	20	18	0.277777778	4.44089E-16
GO:1903055	positive regulation of extracellular matrix organization	down	positive regulation of extracellular matrix organization (GO:1903055)	BP	11	9	0.333333333	4.44089E-16
GO:1903391	regulation of adherens junction organization	down	regulation of adherens junction organization (GO:1903391)	BP	36	36	0.166666667	4.44089E-16
GO:1903393	positive regulation of adherens junction organization	down	positive regulation of adherens junction organization (GO:1903393)	BP	15	15	0.133333333	4.44089E-16
GO:1903831	signal transduction involved in cellular response to ammo	down	signal transduction involved in cellular response to ammonium ion (GO:1	BP	11	11	0.363636364	4.44089E-16
GO:1904666	regulation of ubiquitin protein ligase activity	down	regulation of ubiquitin protein ligase activity (GO:1904666)	BP	12	12	0.333333333	4.44089E-16
GO:1905144	response to acetylcholine	down	response to acetylcholine (GO:1905144)	BP	11	11	0.363636364	4.44089E-16
GO:1905145	cellular response to acetylcholine	down	cellular response to acetylcholine (GO:1905145)	BP	11	11	0.363636364	4.44089E-16
GO:1905330	regulation of morphogenesis of an epithelium	down	regulation of morphogenesis of an epithelium (GO:1905330)	BP	82	79	0.291139241	4.44089E-16
GO:2000027	regulation of organ morphogenesis	down	regulation of organ morphogenesis (GO:2000027)	BP	132	129	0.217054264	4.44089E-16
GO:2000050	regulation of non-canonical Wnt signaling pathway	down	regulation of non-canonical Wnt signaling pathway (GO:2000050)	BP	14	13	0.461538462	4.44089E-16
GO:2000463	positive regulation of excitatory postsynaptic potential	down	positive regulation of excitatory postsynaptic potential (GO:2000463)	BP	12	11	0.636363636	4.44089E-16
GO:0001886	endothelial cell morphogenesis	down	endothelial cell morphogenesis (GO:0001886)	BP	10	10	0.2	2.79776E-14
GO:0003203	endocardial cushion morphogenesis	down	endocardial cushion morphogenesis (GO:0003203)	BP	24	24	0.25	2.79776E-14
GO:0003279	cardiac septum development	down	cardiac septum development (GO:0003279)	BP	75	74	0.189189189	2.79776E-14
GO:0006323	DNA packaging	down	DNA packaging (GO:0006323)	BP	81	63	0.19047619	2.79776E-14
GO:0007045	cell-substrate adherens junction assembly	down	cell-substrate adherens junction assembly (GO:0007045)	BP	43	42	0.142857143	2.79776E-14
GO:0007143	female meiotic nuclear division	down	female meiotic nuclear division (GO:0007143)	BP	21	21	0.238095238	2.79776E-14
GO:0008608	attachment of spindle microtubules to kinetochore	down	attachment of spindle microtubules to kinetochore (GO:0008608)	BP	17	16	0.3125	2.79776E-14
GO:0014013	regulation of gliogenesis	down	regulation of gliogenesis (GO:0014013)	BP	44	42	0.19047619	2.79776E-14
GO:0016525	negative regulation of angiogenesis	down	negative regulation of angiogenesis (GO:0016525)	BP	49	48	0.1875	2.79776E-14
GO:0030010	establishment of cell polarity	down	establishment of cell polarity (GO:0030010)	BP	79	73	0.150684932	2.79776E-14
GO:0032964	collagen biosynthetic process	down	collagen biosynthetic process (GO:0032964)	BP	14	14	0.285714286	2.79776E-14
GO:0033045	regulation of sister chromatid segregation	down	regulation of sister chromatid segregation (GO:0033045)	BP	39	37	0.243243243	2.79776E-14
GO:0035136	forelimb morphogenesis	down	forelimb morphogenesis (GO:0035136)	BP	31	29	0.24137931	2.79776E-14
GO:0042573	retinoic acid metabolic process	down	retinoic acid metabolic process (GO:0042573)	BP	11	8	0.625	2.79776E-14
GO:0048041	focal adhesion assembly	down	focal adhesion assembly (GO:0048041)	BP	43	42	0.142857143	2.79776E-14
GO:0060021	palate development	down	palate development (GO:0060021)	BP	67	64	0.1875	2.79776E-14
GO:0071103	DNA conformation change	down	DNA conformation change (GO:0071103)	BP	108	87	0.16091954	2.79776E-14
GO:0071539	protein localization to centrosome	down	protein localization to centrosome (GO:0071539)	BP	13	13	0.307692308	2.79776E-14
GO:0072028	nephron morphogenesis	down	nephron morphogenesis (GO:0072028)	BP	61	60	0.266666667	2.79776E-14
GO:0090103	cochlea morphogenesis	down	cochlea morphogenesis (GO:0090103)	BP	19	19	0.263157895	2.79776E-14
GO:0090190	positive regulation of branching involved in ureteric bud	down	positive regulation of branching involved in ureteric bud morphogenesis	BP	15	15	0.333333333	2.79776E-14
GO:0090288	negative regulation of cellular response to growth factor s	down	negative regulation of cellular response to growth factor stimulus (GO:00	BP	89	88	0.181818182	2.79776E-14
GO:0098773	skin epidermis development	down	skin epidermis development (GO:0098773)	BP	67	65	0.184615385	2.79776E-14
GO:1901888	regulation of cell junction assembly	down	regulation of cell junction assembly (GO:1901888)	BP	54	54	0.166666667	2.79776E-14
GO:1905508	protein localization to microtubule organizing center	down	protein localization to microtubule organizing center (GO:1905508)	BP	13	13	0.307692308	2.79776E-14
GO:0001755	neural crest cell migration	down	neural crest cell migration (GO:0001755)	BP	28	28	0.321428571	5.19584E-14
GO:0001756	somitogenesis	down	somitogenesis (GO:0001756)	BP	57	55	0.218181818	5.19584E-14

GO:0003197	endocardial cushion development	down	endocardial cushion development (GO:0003197)	BP	32	32	0.25	5.19584E-14
GO:0006302	double-strand break repair	down	double-strand break repair (GO:0006302)	BP	127	123	0.12195122	5.19584E-14
GO:0007088	regulation of mitotic nuclear division	down	regulation of mitotic nuclear division (GO:0007088)	BP	80	78	0.205128205	5.19584E-14
GO:0007431	salivary gland development	down	salivary gland development (GO:0007431)	BP	33	33	0.303030303	5.19584E-14
GO:0008038	neuron recognition	down	neuron recognition (GO:0008038)	BP	18	18	0.333333333	5.19584E-14
GO:0009101	glycoprotein biosynthetic process	down	glycoprotein biosynthetic process (GO:0009101)	BP	185	178	0.129213483	5.19584E-14
GO:0010463	mesenchymal cell proliferation	down	mesenchymal cell proliferation (GO:0010463)	BP	33	33	0.303030303	5.19584E-14
GO:0010771	negative regulation of cell morphogenesis involved in diff	down	negative regulation of cell morphogenesis involved in differentiation (GO	BP	50	49	0.204081633	5.19584E-14
GO:0010948	negative regulation of cell cycle process	down	negative regulation of cell cycle process (GO:0010948)	BP	106	100	0.16	5.19584E-14
GO:0035050	embryonic heart tube development	down	embryonic heart tube development (GO:0035050)	BP	51	51	0.117647059	5.19584E-14
GO:0040013	negative regulation of locomotion	down	negative regulation of locomotion (GO:0040013)	BP	176	167	0.119760479	5.19584E-14
GO:0045666	positive regulation of neuron differentiation	down	positive regulation of neuron differentiation (GO:0045666)	BP	164	158	0.158227848	5.19584E-14
GO:0060445	branching involved in salivary gland morphogenesis	down	branching involved in salivary gland morphogenesis (GO:0060445)	BP	20	20	0.3	5.19584E-14
GO:0061351	neural precursor cell proliferation	down	neural precursor cell proliferation (GO:0061351)	BP	94	90	0.211111111	5.19584E-14
GO:0071300	cellular response to retinoic acid	down	cellular response to retinoic acid (GO:0071300)	BP	30	29	0.206896552	5.19584E-14
GO:0072171	mesonephric tubule morphogenesis	down	mesonephric tubule morphogenesis (GO:0072171)	BP	53	52	0.269230769	5.19584E-14
GO:0090183	regulation of kidney development	down	regulation of kidney development (GO:0090183)	BP	36	35	0.228571429	5.19584E-14
GO:0021761	limbic system development	down	limbic system development (GO:0021761)	BP	60	59	0.169491525	7.79377E-14
GO:0090184	positive regulation of kidney development	down	positive regulation of kidney development (GO:0090184)	BP	24	23	0.304347826	7.79377E-14
GO:0001578	microtubule bundle formation	down	microtubule bundle formation (GO:0001578)	BP	55	54	0.166666667	9.99201E-14
GO:0001942	hair follicle development	down	hair follicle development (GO:0001942)	BP	65	63	0.174603175	9.99201E-14
GO:0021532	neural tube patterning	down	neural tube patterning (GO:0021532)	BP	34	34	0.235294118	9.99201E-14
GO:0022404	molting cycle process	down	molting cycle process (GO:0022404)	BP	65	63	0.174603175	9.99201E-14
GO:0022405	hair cycle process	down	hair cycle process (GO:0022405)	BP	65	63	0.174603175	9.99201E-14
GO:0035115	embryonic forelimb morphogenesis	down	embryonic forelimb morphogenesis (GO:0035115)	BP	24	22	0.227272727	9.99201E-14
GO:0060740	prostate gland epithelium morphogenesis	down	prostate gland epithelium morphogenesis (GO:0060740)	BP	23	21	0.285714286	9.99201E-14
GO:0072088	nephron epithelium morphogenesis	down	nephron epithelium morphogenesis (GO:0072088)	BP	60	59	0.271186441	9.99201E-14
GO:0035640	exploration behavior	down	exploration behavior (GO:0035640)	BP	22	21	0.285714286	1.23901E-13
GO:0044772	mitotic cell cycle phase transition	down	mitotic cell cycle phase transition (GO:0044772)	BP	190	183	0.142076503	1.23901E-13
GO:0060512	prostate gland morphogenesis	down	prostate gland morphogenesis (GO:0060512)	BP	24	22	0.272727273	1.23901E-13
GO:0060998	regulation of dendritic spine development	down	regulation of dendritic spine development (GO:0060998)	BP	29	29	0.206896552	1.23901E-13
GO:0006029	proteoglycan metabolic process	down	proteoglycan metabolic process (GO:0006029)	BP	51	50	0.22	1.48104E-13
GO:0072078	nephron tubule morphogenesis	down	nephron tubule morphogenesis (GO:0072078)	BP	58	57	0.280701754	1.48104E-13
GO:0090263	positive regulation of canonical Wnt signaling pathway	down	positive regulation of canonical Wnt signaling pathway (GO:0090263)	BP	55	52	0.230769231	1.48104E-13
GO:0010634	positive regulation of epithelial cell migration	down	positive regulation of epithelial cell migration (GO:0010634)	BP	77	76	0.171052632	1.72085E-13
GO:0051783	regulation of nuclear division	down	regulation of nuclear division (GO:0051783)	BP	102	100	0.17	1.72085E-13
GO:1904037	positive regulation of epithelial cell apoptotic process	down	positive regulation of epithelial cell apoptotic process (GO:1904037)	BP	11	11	0.181818182	1.72085E-13
GO:0009855	determination of bilateral symmetry	down	determination of bilateral symmetry (GO:0009855)	BP	81	81	0.12345679	1.94067E-13
GO:0021953	central nervous system neuron differentiation	down	central nervous system neuron differentiation (GO:0021953)	BP	126	122	0.196721311	1.94067E-13
GO:0071824	protein-DNA complex subunit organization	down	protein-DNA complex subunit organization (GO:0071824)	BP	95	78	0.128205128	1.94067E-13
GO:0002040	sprouting angiogenesis	down	sprouting angiogenesis (GO:0002040)	BP	51	50	0.16	2.18048E-13
GO:0060840	artery development	down	artery development (GO:0060840)	BP	61	61	0.180327869	2.4003E-13
GO:0090101	negative regulation of transmembrane receptor protein se	down	negative regulation of transmembrane receptor protein serine/threonine	BP	71	71	0.183098592	2.4003E-13
GO:0003205	cardiac chamber development	down	cardiac chamber development (GO:0003205)	BP	119	117	0.188034188	2.85993E-13
GO:0030100	regulation of endocytosis	down	regulation of endocytosis (GO:0030100)	BP	123	119	0.12605042	2.85993E-13
GO:0060675	ureteric bud morphogenesis	down	ureteric bud morphogenesis (GO:0060675)	BP	52	51	0.274509804	2.85993E-13
GO:0001764	neuron migration	down	neuron migration (GO:0001764)	BP	103	100	0.17	3.05977E-13
GO:0033273	response to vitamin	down	response to vitamin (GO:0033273)	BP	18	16	0.375	3.05977E-13
GO:0061162	establishment of monopolar cell polarity	down	establishment of monopolar cell polarity (GO:0061162)	BP	12	12	0.25	3.05977E-13
GO:0061339	establishment or maintenance of monopolar cell polarity	down	establishment or maintenance of monopolar cell polarity (GO:0061339)	BP	13	12	0.25	3.05977E-13
GO:1903046	meiotic cell cycle process	down	meiotic cell cycle process (GO:1903046)	BP	105	97	0.134020619	3.05977E-13
GO:0009799	specification of symmetry	down	specification of symmetry (GO:0009799)	BP	82	82	0.12195122	3.51941E-13
GO:0007422	peripheral nervous system development	down	peripheral nervous system development (GO:0007422)	BP	37	37	0.108108108	3.71925E-13
GO:0048566	embryonic digestive tract development	down	embryonic digestive tract development (GO:0048566)	BP	24	24	0.25	3.71925E-13
GO:0061036	positive regulation of cartilage development	down	positive regulation of cartilage development (GO:0061036)	BP	21	21	0.19047619	3.93907E-13
GO:1901343	negative regulation of vasculature development	down	negative regulation of vasculature development (GO:1901343)	BP	54	53	0.188679245	3.93907E-13
GO:0051271	negative regulation of cellular component movement	down	negative regulation of cellular component movement (GO:0051271)	BP	163	154	0.12987013	4.11893E-13
GO:0061053	somite development	down	somite development (GO:0061053)	BP	71	69	0.202898551	4.11893E-13
GO:0099565	chemical synaptic transmission, postsynaptic	down	chemical synaptic transmission, postsynaptic (GO:0099565)	BP	38	37	0.27027027	4.11893E-13
GO:2001222	regulation of neuron migration	down	regulation of neuron migration (GO:2001222)	BP	19	19	0.315789474	4.11893E-13
GO:0007157	heterophilic cell-cell adhesion via plasma membrane cell	down	heterophilic cell-cell adhesion via plasma membrane cell adhesion molec	BP	19	18	0.388888889	4.5608E-13
GO:0030318	melanocyte differentiation	down	melanocyte differentiation (GO:0030318)	BP	21	21	0.285714286	4.78062E-13
GO:0035767	endothelial cell chemotaxis	down	endothelial cell chemotaxis (GO:0035767)	BP	19	19	0.263157895	4.98046E-13
GO:0042471	ear morphogenesis	down	ear morphogenesis (GO:0042471)	BP	94	90	0.2	4.98046E-13

GO:0043393	regulation of protein binding	down	regulation of protein binding (GO:0043393)	BP	133	130	0.161538462	4.98046E-13
GO:0001569	branching involved in blood vessel morphogenesis	down	branching involved in blood vessel morphogenesis (GO:0001569)	BP	24	23	0.217391304	5.16032E-13
GO:0072132	mesenchyme morphogenesis	down	mesenchyme morphogenesis (GO:0072132)	BP	37	37	0.189189189	5.16032E-13
GO:0031346	positive regulation of cell projection organization	down	positive regulation of cell projection organization (GO:0031346)	BP	169	163	0.147239264	5.38014E-13
GO:2000181	negative regulation of blood vessel morphogenesis	down	negative regulation of blood vessel morphogenesis (GO:2000181)	BP	51	50	0.2	6.93889E-13
GO:0030071	regulation of mitotic metaphase/anaphase transition	down	regulation of mitotic metaphase/anaphase transition (GO:0030071)	BP	24	23	0.304347826	7.5806E-13
GO:2001236	regulation of extrinsic apoptotic signaling pathway	down	regulation of extrinsic apoptotic signaling pathway (GO:2001236)	BP	124	120	0.191666667	7.78044E-13
GO:0021766	hippocampus development	down	hippocampus development (GO:0021766)	BP	45	44	0.136363636	8.39995E-13
GO:0051225	spindle assembly	down	spindle assembly (GO:0051225)	BP	57	56	0.160714286	8.39995E-13
GO:0003151	outflow tract morphogenesis	down	outflow tract morphogenesis (GO:0003151)	BP	53	53	0.113207547	8.59979E-13
GO:0007091	metaphase/anaphase transition of mitotic cell cycle	down	metaphase/anaphase transition of mitotic cell cycle (GO:0007091)	BP	25	24	0.291666667	1.03206E-12
GO:0010965	regulation of mitotic sister chromatid separation	down	regulation of mitotic sister chromatid separation (GO:0010965)	BP	25	24	0.291666667	1.03206E-12
GO:0007127	meiosis I	down	meiosis I (GO:0007127)	BP	59	55	0.145454545	1.13798E-12
GO:0051099	positive regulation of binding	down	positive regulation of binding (GO:0051099)	BP	99	98	0.153061224	1.15796E-12
GO:0031109	microtubule polymerization or depolymerization	down	microtubule polymerization or depolymerization (GO:0031109)	BP	58	55	0.236363636	1.19793E-12
GO:0007229	integrin-mediated signaling pathway	down	integrin-mediated signaling pathway (GO:0007229)	BP	66	64	0.125	1.21592E-12
GO:0044839	cell cycle G2/M phase transition	down	cell cycle G2/M phase transition (GO:0044839)	BP	63	59	0.152542373	1.2339E-12
GO:0007413	axonal fasciculation	down	axonal fasciculation (GO:0007413)	BP	14	14	0.285714286	1.27209E-12
GO:0106030	neuron projection fasciculation	down	neuron projection fasciculation (GO:0106030)	BP	14	14	0.285714286	1.27209E-12
GO:0050919	negative chemotaxis	down	negative chemotaxis (GO:0050919)	BP	15	13	0.153846154	1.33205E-12
GO:0000086	G2/M transition of mitotic cell cycle	down	G2/M transition of mitotic cell cycle (GO:0000086)	BP	59	56	0.160714286	1.394E-12
GO:0003281	ventricular septum development	down	ventricular septum development (GO:0003281)	BP	48	47	0.191489362	1.45395E-12
GO:0007292	female gamete generation	down	female gamete generation (GO:0007292)	BP	73	73	0.178082192	1.47193E-12
GO:0042472	inner ear morphogenesis	down	inner ear morphogenesis (GO:0042472)	BP	78	74	0.243243243	1.48992E-12
GO:0046578	regulation of Ras protein signal transduction	down	regulation of Ras protein signal transduction (GO:0046578)	BP	152	145	0.137931034	1.52811E-12
GO:0060079	excitatory postsynaptic potential	down	excitatory postsynaptic potential (GO:0060079)	BP	32	31	0.322580645	1.58806E-12
GO:2000146	negative regulation of cell motility	down	negative regulation of cell motility (GO:2000146)	BP	152	143	0.13986014	1.73195E-12
GO:0046777	protein autophosphorylation	down	protein autophosphorylation (GO:0046777)	BP	153	150	0.133333333	1.81211E-12
GO:0032956	regulation of actin cytoskeleton organization	down	regulation of actin cytoskeleton organization (GO:0032956)	BP	187	178	0.129213483	1.84408E-12
GO:0045926	negative regulation of growth	down	negative regulation of growth (GO:0045926)	BP	144	141	0.141843972	1.86007E-12
GO:0008543	fibroblast growth factor receptor signaling pathway	down	fibroblast growth factor receptor signaling pathway (GO:0008543)	BP	58	56	0.25	1.97997E-12
GO:1902099	regulation of metaphase/anaphase transition of cell cycle	down	regulation of metaphase/anaphase transition of cell cycle (GO:1902099)	BP	25	24	0.291666667	2.03793E-12
GO:0060113	inner ear receptor cell differentiation	down	inner ear receptor cell differentiation (GO:0060113)	BP	53	52	0.211538462	2.0739E-12
GO:0045778	positive regulation of ossification	down	positive regulation of ossification (GO:0045778)	BP	60	58	0.275862069	2.17204E-12
GO:0032092	positive regulation of protein binding	down	positive regulation of protein binding (GO:0032092)	BP	63	62	0.161290323	2.24398E-12
GO:0051304	chromosome separation	down	chromosome separation (GO:0051304)	BP	37	36	0.222222222	2.24398E-12
GO:0072234	metanephric nephron tubule development	down	metanephric nephron tubule development (GO:0072234)	BP	16	16	0.1875	2.36211E-12
GO:0040001	establishment of mitotic spindle localization	down	establishment of mitotic spindle localization (GO:0040001)	BP	18	17	0.176470588	2.41807E-12
GO:0030308	negative regulation of cell growth	down	negative regulation of cell growth (GO:0030308)	BP	96	94	0.159574468	2.51399E-12
GO:0033048	negative regulation of mitotic sister chromatid segregatio	down	negative regulation of mitotic sister chromatid segregation (GO:0033048	BP	18	17	0.294117647	2.52798E-12
GO:0044784	metaphase/anaphase transition of cell cycle	down	metaphase/anaphase transition of cell cycle (GO:0044784)	BP	26	25	0.28	2.53597E-12
GO:1905818	regulation of chromosome separation	down	regulation of chromosome separation (GO:1905818)	BP	26	25	0.28	2.53597E-12
GO:0002011	morphogenesis of an epithelial sheet	down	morphogenesis of an epithelial sheet (GO:0002011)	BP	41	38	0.184210526	2.57194E-12
GO:0048640	negative regulation of developmental growth	down	negative regulation of developmental growth (GO:0048640)	BP	52	52	0.192307692	2.6259E-12
GO:0060008	Sertoli cell differentiation	down	Sertoli cell differentiation (GO:0060008)	BP	13	13	0.153846154	2.66009E-12
GO:0021885	forebrain cell migration	down	forebrain cell migration (GO:0021885)	BP	49	49	0.142857143	2.68607E-12
GO:0072698	protein localization to microtubule cytoskeleton	down	protein localization to microtubule cytoskeleton (GO:0072698)	BP	22	22	0.272727273	2.68607E-12
GO:0042490	mechanoreceptor differentiation	down	mechanoreceptor differentiation (GO:0042490)	BP	55	54	0.203703704	2.76001E-12
GO:0045132	meiotic chromosome segregation	down	meiotic chromosome segregation (GO:0045132)	BP	54	51	0.156862745	2.85394E-12
GO:0007368	determination of left/right symmetry	down	determination of left/right symmetry (GO:0007368)	BP	77	77	0.103896104	3.2041E-12
GO:0003158	endothelium development	down	endothelium development (GO:0003158)	BP	72	71	0.126760563	3.27605E-12
GO:0060601	lateral sprouting from an epithelium	down	lateral sprouting from an epithelium (GO:0060601)	BP	11	10	0.3	3.34799E-12
GO:0043588	skin development	down	skin development (GO:0043588)	BP	160	150	0.146666667	3.4599E-12
GO:0035089	establishment of apical/basal cell polarity	down	establishment of apical/basal cell polarity (GO:0035089)	BP	10	10	0.2	3.51008E-12
GO:1905276	regulation of epithelial tube formation	down	regulation of epithelial tube formation (GO:1905276)	BP	17	16	0.3125	3.69793E-12
GO:0030279	negative regulation of ossification	down	negative regulation of ossification (GO:0030279)	BP	54	51	0.117647059	3.74789E-12
GO:0060411	cardiac septum morphogenesis	down	cardiac septum morphogenesis (GO:0060411)	BP	48	48	0.166666667	3.79807E-12
GO:0051321	meiotic cell cycle	down	meiotic cell cycle (GO:0051321)	BP	110	102	0.12745098	3.82805E-12
GO:0072210	metanephric nephron development	down	metanephric nephron development (GO:0072210)	BP	30	29	0.206896552	3.85803E-12
GO:1901890	positive regulation of cell junction assembly	down	positive regulation of cell junction assembly (GO:1901890)	BP	20	20	0.15	4.14202E-12
GO:0021542	dentate gyrus development	down	dentate gyrus development (GO:0021542)	BP	14	14	0.142857143	4.15201E-12
GO:0044344	cellular response to fibroblast growth factor stimulus	down	cellular response to fibroblast growth factor stimulus (GO:0044344)	BP	71	68	0.235294118	4.36406E-12
GO:0071774	response to fibroblast growth factor	down	response to fibroblast growth factor (GO:0071774)	BP	71	68	0.235294118	4.36406E-12
GO:0001658	branching involved in ureteric bud morphogenesis	down	branching involved in ureteric bud morphogenesis (GO:0001658)	BP	46	46	0.260869565	4.46998E-12

GO:0071158	positive regulation of cell cycle arrest	down	positive regulation of cell cycle arrest (GO:0071158)	BP	23	22	0.090909091	4.49796E-12
GO:0003214	cardiac left ventricle morphogenesis	down	cardiac left ventricle morphogenesis (GO:0003214)	BP	11	11	0.181818182	4.62208E-12
GO:0030336	negative regulation of cell migration	down	negative regulation of cell migration (GO:0030336)	BP	146	137	0.131386861	4.63007E-12
GO:0007043	cell-cell junction assembly	down	cell-cell junction assembly (GO:0007043)	BP	59	58	0.137931034	4.67604E-12
GO:0030514	negative regulation of BMP signaling pathway	down	negative regulation of BMP signaling pathway (GO:0030514)	BP	35	35	0.2	4.70401E-12
GO:0003198	epithelial to mesenchymal transition involved in endocar	down	epithelial to mesenchymal transition involved in endocardial cushion for	BP	15	15	0.266666667	4.78795E-12
GO:0051306	mitotic sister chromatid separation	down	mitotic sister chromatid separation (GO:0051306)	BP	27	26	0.269230769	5.006E-12
GO:0045662	negative regulation of myoblast differentiation	down	negative regulation of myoblast differentiation (GO:0045662)	BP	22	22	0.454545455	5.14411E-12
GO:0072087	renal vesicle development	down	renal vesicle development (GO:0072087)	BP	16	15	0.266666667	5.4361E-12
GO:0051784	negative regulation of nuclear division	down	negative regulation of nuclear division (GO:0051784)	BP	32	31	0.193548387	5.59197E-12
GO:0090307	mitotic spindle assembly	down	mitotic spindle assembly (GO:0090307)	BP	30	29	0.206896552	5.93792E-12
GO:0055025	positive regulation of cardiac muscle tissue development	down	positive regulation of cardiac muscle tissue development (GO:0055025)	BP	28	28	0.178571429	6.112E-12
GO:0033047	regulation of mitotic sister chromatid segregation	down	regulation of mitotic sister chromatid segregation (GO:0033047)	BP	32	30	0.233333333	6.24789E-12
GO:0035088	establishment or maintenance of apical/basal cell polarit	down	establishment or maintenance of apical/basal cell polarity (GO:0035088)	BP	24	22	0.181818182	7.1021E-12
GO:0045841	negative regulation of mitotic metaphase/anaphase transi	down	negative regulation of mitotic metaphase/anaphase transition (GO:0045	BP	16	15	0.333333333	7.1021E-12
GO:0061245	establishment or maintenance of bipolar cell polarity	down	establishment or maintenance of bipolar cell polarity (GO:0061245)	BP	24	22	0.181818182	7.1021E-12
GO:0071174	mitotic spindle checkpoint	down	mitotic spindle checkpoint (GO:0071174)	BP	16	15	0.333333333	7.1021E-12
GO:2000816	negative regulation of mitotic sister chromatid separatio	down	negative regulation of mitotic sister chromatid separation (GO:2000816)	BP	16	15	0.333333333	7.1021E-12
GO:0031099	regeneration	down	regeneration (GO:0031099)	BP	43	42	0.19047619	7.10609E-12
GO:0010453	regulation of cell fate commitment	down	regulation of cell fate commitment (GO:0010453)	BP	17	17	0.294117647	7.84595E-12
GO:0060041	retina development in camera-type eye	down	retina development in camera-type eye (GO:0060041)	BP	97	93	0.182795699	8.2141E-12
GO:0033627	cell adhesion mediated by integrin	down	cell adhesion mediated by integrin (GO:0033627)	BP	40	39	0.153846154	8.32401E-12
GO:0036445	neuronal stem cell division	down	neuronal stem cell division (GO:0036445)	BP	10	10	0.4	8.41593E-12
GO:0055057	neuroblast division	down	neuroblast division (GO:0055057)	BP	10	10	0.4	8.41593E-12
GO:0042073	intraciliary transport	down	intraciliary transport (GO:0042073)	BP	20	20	0.15	8.54206E-12
GO:0098840	protein transport along microtubule	down	protein transport along microtubule (GO:0098840)	BP	20	20	0.15	8.54206E-12
GO:0099118	microtubule-based protein transport	down	microtubule-based protein transport (GO:0099118)	BP	20	20	0.15	8.54206E-12
GO:0010976	positive regulation of neuron projection development	down	positive regulation of neuron projection development (GO:0010976)	BP	119	115	0.165217391	9.5921E-12
GO:0071242	cellular response to ammonium ion	down	cellular response to ammonium ion (GO:0071242)	BP	17	17	0.294117647	9.80593E-12
GO:0010594	regulation of endothelial cell migration	down	regulation of endothelial cell migration (GO:0010594)	BP	84	82	0.12195122	1.04059E-11
GO:0050000	chromosome localization	down	chromosome localization (GO:0050000)	BP	49	46	0.260869565	1.04059E-11
GO:0051303	establishment of chromosome localization	down	establishment of chromosome localization (GO:0051303)	BP	49	46	0.260869565	1.04059E-11
GO:0031572	G2 DNA damage checkpoint	down	G2 DNA damage checkpoint (GO:0031572)	BP	26	25	0.24	1.10101E-11
GO:0003272	endocardial cushion formation	down	endocardial cushion formation (GO:0003272)	BP	18	18	0.277777778	1.1076E-11
GO:0007080	mitotic metaphase plate congression	down	mitotic metaphase plate congression (GO:0007080)	BP	30	30	0.333333333	1.1658E-11
GO:0033046	negative regulation of sister chromatid segregation	down	negative regulation of sister chromatid segregation (GO:0033046)	BP	19	18	0.277777778	1.167E-11
GO:0045839	negative regulation of mitotic nuclear division	down	negative regulation of mitotic nuclear division (GO:0045839)	BP	23	22	0.227272727	1.29581E-11
GO:0051648	vesicle localization	down	vesicle localization (GO:0051648)	BP	94	94	0.159574468	1.3054E-11
GO:0002691	regulation of cellular extravasation	down	regulation of cellular extravasation (GO:0002691)	BP	13	13	0.153846154	1.32561E-11
GO:1901987	regulation of cell cycle phase transition	down	regulation of cell cycle phase transition (GO:1901987)	BP	137	129	0.131782946	1.39699E-11
GO:0035904	aorta development	down	aorta development (GO:0035904)	BP	41	41	0.195121951	1.42739E-11
GO:0046885	regulation of hormone biosynthetic process	down	regulation of hormone biosynthetic process (GO:0046885)	BP	12	12	0.25	1.5036E-11
GO:0051310	metaphase plate congression	down	metaphase plate congression (GO:0051310)	BP	36	35	0.314285714	1.581E-11
GO:0021795	cerebral cortex cell migration	down	cerebral cortex cell migration (GO:0021795)	BP	35	35	0.171428571	1.8592E-11
GO:0017015	regulation of transforming growth factor beta receptor si	down	regulation of transforming growth factor beta receptor signaling pathway	BP	64	64	0.140625	1.8846E-11
GO:1903844	regulation of cellular response to transforming growth fac	down	regulation of cellular response to transforming growth factor beta stimul	BP	64	64	0.140625	1.8846E-11
GO:0014829	vascular smooth muscle contraction	down	vascular smooth muscle contraction (GO:0014829)	BP	13	13	0.230769231	2.0024E-11
GO:0072498	embryonic skeletal joint development	down	embryonic skeletal joint development (GO:0072498)	BP	10	10	0.2	2.01741E-11
GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	down	positive regulation of peptidyl-tyrosine phosphorylation (GO:0050731)	BP	78	78	0.153846154	2.079E-11
GO:0031062	positive regulation of histone methylation	down	positive regulation of histone methylation (GO:0031062)	BP	24	24	0.125	2.161E-11
GO:0006275	regulation of DNA replication	down	regulation of DNA replication (GO:0006275)	BP	81	80	0.125	2.1634E-11
GO:1903429	regulation of cell maturation	down	regulation of cell maturation (GO:1903429)	BP	12	12	0.166666667	2.22959E-11
GO:0035411	catenin import into nucleus	down	catenin import into nucleus (GO:0035411)	BP	19	19	0.263157895	2.23059E-11
GO:0035412	regulation of catenin import into nucleus	down	regulation of catenin import into nucleus (GO:0035412)	BP	19	19	0.263157895	2.23059E-11
GO:0031570	DNA integrity checkpoint	down	DNA integrity checkpoint (GO:0031570)	BP	75	72	0.111111111	2.2996E-11
GO:0046605	regulation of centrosome cycle	down	regulation of centrosome cycle (GO:0046605)	BP	35	34	0.235294118	2.3652E-11
GO:0071479	cellular response to ionizing radiation	down	cellular response to ionizing radiation (GO:0071479)	BP	42	42	0.214285714	2.3652E-11
GO:0051494	negative regulation of cytoskeleton organization	down	negative regulation of cytoskeleton organization (GO:0051494)	BP	78	75	0.2	2.40621E-11
GO:0021846	cell proliferation in forebrain	down	cell proliferation in forebrain (GO:0021846)	BP	21	20	0.35	2.74221E-11
GO:1902100	negative regulation of metaphase/anaphase transition of	down	negative regulation of metaphase/anaphase transition of cell cycle (GO:1	BP	17	16	0.3125	2.8038E-11
GO:1905819	negative regulation of chromosome separation	down	negative regulation of chromosome separation (GO:1905819)	BP	17	16	0.3125	2.8038E-11
GO:0001656	metanephros development	down	metanephros development (GO:0001656)	BP	65	63	0.19047619	2.8362E-11
GO:0021954	central nervous system neuron development	down	central nervous system neuron development (GO:0021954)	BP	54	51	0.215686275	2.8362E-11
GO:0050804	modulation of chemical synaptic transmission	down	modulation of chemical synaptic transmission (GO:0050804)	BP	145	142	0.147887324	2.975E-11

GO:0007093	mitotic cell cycle checkpoint	down	mitotic cell cycle checkpoint (GO:0007093)	BP	65	63	0.158730159	2.9774E-11
GO:0045807	positive regulation of endocytosis	down	positive regulation of endocytosis (GO:0045807)	BP	74	73	0.109589041	3.1636E-11
GO:0090100	positive regulation of transmembrane receptor protein se	down	positive regulation of transmembrane receptor protein serine/threonine	BP	65	65	0.138461538	3.40259E-11
GO:0051985	negative regulation of chromosome segregation	down	negative regulation of chromosome segregation (GO:0051985)	BP	20	19	0.263157895	3.45259E-11
GO:0021681	cerebellar granular layer development	down	cerebellar granular layer development (GO:0021681)	BP	10	9	0.222222222	3.45559E-11
GO:0021700	developmental maturation	down	developmental maturation (GO:0021700)	BP	172	168	0.125	3.5516E-11
GO:0021801	cerebral cortex radial glia guided migration	down	cerebral cortex radial glia guided migration (GO:0021801)	BP	16	16	0.1875	3.611E-11
GO:0022030	telencephalon glial cell migration	down	telencephalon glial cell migration (GO:0022030)	BP	16	16	0.1875	3.611E-11
GO:0050764	regulation of phagocytosis	down	regulation of phagocytosis (GO:0050764)	BP	40	36	0.138888889	3.611E-11
GO:0097205	renal filtration	down	renal filtration (GO:0097205)	BP	11	11	0.363636364	3.611E-11
GO:0048557	embryonic digestive tract morphogenesis	down	embryonic digestive tract morphogenesis (GO:0048557)	BP	11	11	0.272727273	3.635E-11
GO:0006336	DNA replication-independent nucleosome assembly	down	DNA replication-independent nucleosome assembly (GO:0006336)	BP	17	12	0.25	3.64859E-11
GO:0034724	DNA replication-independent nucleosome organization	down	DNA replication-independent nucleosome organization (GO:0034724)	BP	17	12	0.25	3.64859E-11
GO:0050931	pigment cell differentiation	down	pigment cell differentiation (GO:0050931)	BP	28	28	0.214285714	3.87981E-11
GO:0045930	negative regulation of mitotic cell cycle	down	negative regulation of mitotic cell cycle (GO:0045930)	BP	114	111	0.117117117	3.9424E-11
GO:0045844	positive regulation of striated muscle tissue development	down	positive regulation of striated muscle tissue development (GO:0045844)	BP	41	40	0.2	3.971E-11
GO:0048636	positive regulation of muscle organ development	down	positive regulation of muscle organ development (GO:0048636)	BP	41	40	0.2	3.971E-11
GO:0006775	fat-soluble vitamin metabolic process	down	fat-soluble vitamin metabolic process (GO:0006775)	BP	24	18	0.277777778	4.06699E-11
GO:0061008	hepaticobiliary system development	down	hepaticobiliary system development (GO:0061008)	BP	55	54	0.092592593	4.13021E-11
GO:0003170	heart valve development	down	heart valve development (GO:0003170)	BP	28	28	0.214285714	4.1722E-11
GO:0050771	negative regulation of axonogenesis	down	negative regulation of axonogenesis (GO:0050771)	BP	30	30	0.2	4.29481E-11
GO:0061213	positive regulation of mesonephros development	down	positive regulation of mesonephros development (GO:0061213)	BP	16	16	0.3125	4.70119E-11
GO:0060317	cardiac epithelial to mesenchymal transition	down	cardiac epithelial to mesenchymal transition (GO:0060317)	BP	25	25	0.2	4.8624E-11
GO:0050678	regulation of epithelial cell proliferation	down	regulation of epithelial cell proliferation (GO:0050678)	BP	197	189	0.153439153	4.89799E-11
GO:0048709	oligodendrocyte differentiation	down	oligodendrocyte differentiation (GO:0048709)	BP	46	45	0.111111111	5.0308E-11
GO:0042391	regulation of membrane potential	down	regulation of membrane potential (GO:0042391)	BP	199	191	0.19895288	5.251E-11
GO:0006310	DNA recombination	down	DNA recombination (GO:0006310)	BP	145	141	0.113475177	5.40179E-11
GO:2001239	regulation of extrinsic apoptotic signaling pathway in abs	down	regulation of extrinsic apoptotic signaling pathway in absence of ligand (	BP	34	34	0.323529412	5.45199E-11
GO:0060972	left/right pattern formation	down	left/right pattern formation (GO:0060972)	BP	19	19	0.210526316	5.48439E-11
GO:0007219	Notch signaling pathway	down	Notch signaling pathway (GO:0007219)	BP	101	97	0.144329897	6.18661E-11
GO:0001889	liver development	down	liver development (GO:0001889)	BP	53	52	0.096153846	6.2286E-11
GO:0030850	prostate gland development	down	prostate gland development (GO:0030850)	BP	35	33	0.242424242	6.26581E-11
GO:1901988	negative regulation of cell cycle phase transition	down	negative regulation of cell cycle phase transition (GO:1901988)	BP	64	59	0.152542373	6.3122E-11
GO:0014065	phosphatidylinositol 3-kinase signaling	down	phosphatidylinositol 3-kinase signaling (GO:0014065)	BP	75	72	0.138888889	6.478E-11
GO:0006334	nucleosome assembly	down	nucleosome assembly (GO:0006334)	BP	49	33	0.181818182	6.5898E-11
GO:0045446	endothelial cell differentiation	down	endothelial cell differentiation (GO:0045446)	BP	62	61	0.114754098	6.6134E-11
GO:0022029	telencephalon cell migration	down	telencephalon cell migration (GO:0022029)	BP	46	46	0.152173913	6.9776E-11
GO:0030513	positive regulation of BMP signaling pathway	down	positive regulation of BMP signaling pathway (GO:0030513)	BP	28	28	0.178571429	7.10341E-11
GO:0045600	positive regulation of fat cell differentiation	down	positive regulation of fat cell differentiation (GO:0045600)	BP	41	40	0.225	7.39699E-11
GO:0007626	locomotory behavior	down	locomotory behavior (GO:0007626)	BP	148	142	0.147887324	7.4982E-11
GO:0061387	regulation of extent of cell growth	down	regulation of extent of cell growth (GO:0061387)	BP	52	50	0.18	7.8844E-11
GO:0048708	astrocyte differentiation	down	astrocyte differentiation (GO:0048708)	BP	45	45	0.177777778	7.90941E-11
GO:0060384	innervation	down	innervation (GO:0060384)	BP	21	21	0.333333333	7.90941E-11
GO:0014014	negative regulation of gliogenesis	down	negative regulation of gliogenesis (GO:0014014)	BP	15	15	0.133333333	8.0552E-11
GO:0003143	embryonic heart tube morphogenesis	down	embryonic heart tube morphogenesis (GO:0003143)	BP	45	45	0.111111111	8.24061E-11
GO:0043506	regulation of JUN kinase activity	down	regulation of JUN kinase activity (GO:0043506)	BP	47	47	0.14893617	8.59119E-11
GO:0008361	regulation of cell size	down	regulation of cell size (GO:0008361)	BP	92	89	0.157303371	8.8362E-11
GO:1901990	regulation of mitotic cell cycle phase transition	down	regulation of mitotic cell cycle phase transition (GO:1901990)	BP	124	119	0.134453782	9.04059E-11
GO:0003338	metanephros morphogenesis	down	metanephros morphogenesis (GO:0003338)	BP	26	25	0.2	9.724E-11
GO:0006261	DNA-dependent DNA replication	down	DNA-dependent DNA replication (GO:0006261)	BP	81	80	0.1	1.02586E-10
GO:1901863	positive regulation of muscle tissue development	down	positive regulation of muscle tissue development (GO:1901863)	BP	42	41	0.195121951	1.0671E-10
GO:0045637	regulation of myeloid cell differentiation	down	regulation of myeloid cell differentiation (GO:0045637)	BP	124	118	0.101694915	1.15044E-10
GO:0002064	epithelial cell development	down	epithelial cell development (GO:0002064)	BP	152	148	0.121621622	1.21958E-10
GO:0022409	positive regulation of cell-cell adhesion	down	positive regulation of cell-cell adhesion (GO:0022409)	BP	138	133	0.112781955	1.21958E-10
GO:0007266	Rho protein signal transduction	down	Rho protein signal transduction (GO:0007266)	BP	115	108	0.148148148	1.23974E-10
GO:0072091	regulation of stem cell proliferation	down	regulation of stem cell proliferation (GO:0072091)	BP	47	47	0.191489362	1.24022E-10
GO:2001020	regulation of response to DNA damage stimulus	down	regulation of response to DNA damage stimulus (GO:2001020)	BP	110	110	0.145454545	1.2898E-10
GO:1902692	regulation of neuroblast proliferation	down	regulation of neuroblast proliferation (GO:1902692)	BP	21	21	0.238095238	1.30554E-10
GO:0042098	T cell proliferation	down	T cell proliferation (GO:0042098)	BP	117	113	0.088495575	1.3074E-10
GO:0007094	mitotic spindle assembly checkpoint	down	mitotic spindle assembly checkpoint (GO:0007094)	BP	15	14	0.285714286	1.32048E-10
GO:0030574	collagen catabolic process	down	collagen catabolic process (GO:0030574)	BP	12	12	0.083333333	1.3437E-10
GO:0010770	positive regulation of cell morphogenesis involved in diffe	down	positive regulation of cell morphogenesis involved in differentiation (GO:	BP	73	69	0.144927536	1.3492E-10
GO:0072170	metanephric tubule development	down	metanephric tubule development (GO:0072170)	BP	18	18	0.166666667	1.3553E-10
GO:0042303	molting cycle	down	molting cycle (GO:0042303)	BP	76	72	0.166666667	1.37714E-10

GO:0042633	hair cycle	down	hair cycle (GO:0042633)	BP	76	72	0.166666667	1.37714E-10
GO:0048483	autonomic nervous system development	down	autonomic nervous system development (GO:0048483)	BP	33	32	0.15625	1.37714E-10
GO:0072077	renal vesicle morphogenesis	down	renal vesicle morphogenesis (GO:0072077)	BP	15	14	0.285714286	1.4222E-10
GO:0009311	oligosaccharide metabolic process	down	oligosaccharide metabolic process (GO:0009311)	BP	21	21	0.142857143	1.49932E-10
GO:0072273	metanephric nephron morphogenesis	down	metanephric nephron morphogenesis (GO:0072273)	BP	20	19	0.210526316	1.562E-10
GO:0071229	cellular response to acid chemical	down	cellular response to acid chemical (GO:0071229)	BP	97	95	0.210526316	1.56234E-10
GO:0007162	negative regulation of cell adhesion	down	negative regulation of cell adhesion (GO:0007162)	BP	146	140	0.085714286	1.58794E-10
GO:0003351	epithelial cilium movement	down	epithelial cilium movement (GO:0003351)	BP	13	13	0.230769231	1.60246E-10
GO:0019233	sensory perception of pain	down	sensory perception of pain (GO:0019233)	BP	42	42	0.166666667	1.61094E-10
GO:0006582	melanin metabolic process	down	melanin metabolic process (GO:0006582)	BP	11	11	0.272727273	1.67534E-10
GO:0042438	melanin biosynthetic process	down	melanin biosynthetic process (GO:0042438)	BP	11	11	0.272727273	1.67534E-10
GO:0044550	secondary metabolite biosynthetic process	down	secondary metabolite biosynthetic process (GO:0044550)	BP	12	11	0.272727273	1.67534E-10
GO:2001237	negative regulation of extrinsic apoptotic signaling pathw	down	negative regulation of extrinsic apoptotic signaling pathway (GO:200123	BP	73	72	0.194444444	1.7175E-10
GO:0048017	inositol lipid-mediated signaling	down	inositol lipid-mediated signaling (GO:0048017)	BP	99	96	0.114583333	1.7913E-10
GO:0035418	protein localization to synapse	down	protein localization to synapse (GO:0035418)	BP	11	11	0.363636364	1.9063E-10
GO:0070302	regulation of stress-activated protein kinase signaling casc	down	regulation of stress-activated protein kinase signaling cascade (GO:00703	BP	133	130	0.161538462	1.91384E-10
GO:0061572	actin filament bundle organization	down	actin filament bundle organization (GO:0061572)	BP	89	86	0.127906977	1.9153E-10
GO:0050680	negative regulation of epithelial cell proliferation	down	negative regulation of epithelial cell proliferation (GO:0050680)	BP	88	86	0.197674419	1.94142E-10
GO:0010165	response to X-ray	down	response to X-ray (GO:0010165)	BP	18	18	0.111111111	2.00154E-10
GO:0048846	axon extension involved in axon guidance	down	axon extension involved in axon guidance (GO:0048846)	BP	16	16	0.125	2.0539E-10
GO:1902284	neuron projection extension involved in neuron projectic	down	neuron projection extension involved in neuron projection guidance (GO	BP	16	16	0.125	2.0539E-10
GO:0006909	phagocytosis	down	phagocytosis (GO:0006909)	BP	86	81	0.12345679	2.2541E-10
GO:0032872	regulation of stress-activated MAPK cascade	down	regulation of stress-activated MAPK cascade (GO:0032872)	BP	132	129	0.162790698	2.31098E-10
GO:0045123	cellular extravasation	down	cellular extravasation (GO:0045123)	BP	29	27	0.111111111	2.32672E-10
GO:0003206	cardiac chamber morphogenesis	down	cardiac chamber morphogenesis (GO:0003206)	BP	91	90	0.177777778	2.44326E-10
GO:1904018	positive regulation of vasculature development	down	positive regulation of vasculature development (GO:1904018)	BP	87	85	0.117647059	2.44878E-10
GO:0097191	extrinsic apoptotic signaling pathway	down	extrinsic apoptotic signaling pathway (GO:0097191)	BP	172	166	0.156626506	2.46932E-10
GO:1900025	negative regulation of substrate adhesion-dependent cell	down	negative regulation of substrate adhesion-dependent cell spreading (GO:1	BP	11	10	0.2	2.4769E-10
GO:0021781	glial cell fate commitment	down	glial cell fate commitment (GO:0021781)	BP	10	9	0.222222222	2.48914E-10
GO:0035329	hippo signaling	down	hippo signaling (GO:0035329)	BP	23	23	0.130434783	2.48914E-10
GO:0003177	pulmonary valve development	down	pulmonary valve development (GO:0003177)	BP	11	11	0.181818182	2.60518E-10
GO:0003184	pulmonary valve morphogenesis	down	pulmonary valve morphogenesis (GO:0003184)	BP	11	11	0.181818182	2.60518E-10
GO:0043406	positive regulation of MAP kinase activity	down	positive regulation of MAP kinase activity (GO:0043406)	BP	123	121	0.165289256	2.63482E-10
GO:0051017	actin filament bundle assembly	down	actin filament bundle assembly (GO:0051017)	BP	87	85	0.129411765	2.64232E-10
GO:0044065	regulation of respiratory system process	down	regulation of respiratory system process (GO:0044065)	BP	11	11	0.363636364	2.64952E-10
GO:1905332	positive regulation of morphogenesis of an epithelium	down	positive regulation of morphogenesis of an epithelium (GO:1905332)	BP	25	24	0.25	2.69038E-10
GO:0060359	response to ammonium ion	down	response to ammonium ion (GO:0060359)	BP	32	32	0.21875	2.71632E-10
GO:0060706	cell differentiation involved in embryonic placenta develc	down	cell differentiation involved in embryonic placenta development (GO:006	BP	21	21	0.238095238	2.7646E-10
GO:0044342	type B pancreatic cell proliferation	down	type B pancreatic cell proliferation (GO:0044342)	BP	11	11	0.181818182	2.78532E-10
GO:0061098	positive regulation of protein tyrosine kinase activity	down	positive regulation of protein tyrosine kinase activity (GO:0061098)	BP	20	20	0.15	2.8293E-10
GO:0071695	anatomical structure maturation	down	anatomical structure maturation (GO:0071695)	BP	97	96	0.15625	2.9049E-10
GO:0032943	mononuclear cell proliferation	down	mononuclear cell proliferation (GO:0032943)	BP	167	163	0.085889571	2.97968E-10
GO:1903037	regulation of leukocyte cell-cell adhesion	down	regulation of leukocyte cell-cell adhesion (GO:1903037)	BP	184	177	0.107344633	3.0071E-10
GO:0031102	neuron projection regeneration	down	neuron projection regeneration (GO:0031102)	BP	18	18	0.222222222	3.03786E-10
GO:0030166	proteoglycan biosynthetic process	down	proteoglycan biosynthetic process (GO:0030166)	BP	31	30	0.166666667	3.12858E-10
GO:0061548	ganglion development	down	ganglion development (GO:0061548)	BP	10	9	0.222222222	3.65684E-10
GO:0071902	positive regulation of protein serine/threonine kinase acti	down	positive regulation of protein serine/threonine kinase activity (GO:00719	BP	165	163	0.159509202	3.82836E-10
GO:1902105	regulation of leukocyte differentiation	down	regulation of leukocyte differentiation (GO:1902105)	BP	161	152	0.105263158	3.92624E-10
GO:0014066	regulation of phosphatidylinositol 3-kinase signaling	down	regulation of phosphatidylinositol 3-kinase signaling (GO:0014066)	BP	57	54	0.148148148	3.9599E-10
GO:0050863	regulation of T cell activation	down	regulation of T cell activation (GO:0050863)	BP	173	166	0.108433735	4.13418E-10
GO:0050773	regulation of dendrite development	down	regulation of dendrite development (GO:0050773)	BP	68	66	0.121212121	4.20286E-10
GO:0061311	cell surface receptor signaling pathway involved in heart c	down	cell surface receptor signaling pathway involved in heart development (G	BP	15	15	0.266666667	4.26288E-10
GO:0010824	regulation of centrosome duplication	down	regulation of centrosome duplication (GO:0010824)	BP	29	28	0.214285714	4.33818E-10
GO:0007131	reciprocal meiotic recombination	down	reciprocal meiotic recombination (GO:0007131)	BP	16	16	0.125	4.43252E-10
GO:0035825	homologous recombination	down	homologous recombination (GO:0035825)	BP	16	16	0.125	4.43252E-10
GO:1903018	regulation of glycoprotein metabolic process	down	regulation of glycoprotein metabolic process (GO:1903018)	BP	28	27	0.148148148	4.49516E-10
GO:0010470	regulation of gastrulation	down	regulation of gastrulation (GO:0010470)	BP	23	22	0.181818182	4.58394E-10
GO:0045165	cell fate commitment	down	cell fate commitment (GO:0045165)	BP	149	146	0.157534247	4.68496E-10
GO:0046651	lymphocyte proliferation	down	lymphocyte proliferation (GO:0046651)	BP	166	162	0.086419753	4.71026E-10
GO:0060042	retina morphogenesis in camera-type eye	down	retina morphogenesis in camera-type eye (GO:0060042)	BP	37	35	0.228571429	4.82582E-10
GO:0000132	establishment of mitotic spindle orientation	down	establishment of mitotic spindle orientation (GO:0000132)	BP	15	14	0.142857143	4.90236E-10
GO:0030033	microvillus assembly	down	microvillus assembly (GO:0030033)	BP	12	11	0.363636364	5.0238E-10
GO:1902041	regulation of extrinsic apoptotic signaling pathway via de	down	regulation of extrinsic apoptotic signaling pathway via death domain rece	BP	41	38	0.157894737	5.03756E-10
GO:1902115	regulation of organelle assembly	down	regulation of organelle assembly (GO:1902115)	BP	105	103	0.106796117	5.08948E-10

GO:0045740	positive regulation of DNA replication	down	positive regulation of DNA replication (GO:0045740)	BP	36	35	0.228571429	5.27138E-10
GO:0048872	homeostasis of number of cells	down	homeostasis of number of cells (GO:0048872)	BP	183	180	0.083333333	5.2795E-10
GO:0006493	protein O-linked glycosylation	down	protein O-linked glycosylation (GO:0006493)	BP	34	32	0.09375	5.39152E-10
GO:0021549	cerebellum development	down	cerebellum development (GO:0021549)	BP	58	53	0.169811321	5.54156E-10
GO:0035265	organ growth	down	organ growth (GO:0035265)	BP	94	89	0.157303371	5.6776E-10
GO:0072243	metanephric nephron epithelium development	down	metanephric nephron epithelium development (GO:0072243)	BP	19	19	0.157894737	5.6776E-10
GO:0003382	epithelial cell morphogenesis	down	epithelial cell morphogenesis (GO:0003382)	BP	28	27	0.111111111	5.85592E-10
GO:0048332	mesoderm morphogenesis	down	mesoderm morphogenesis (GO:0048332)	BP	52	52	0.153846154	5.97948E-10
GO:0021591	ventricular system development	down	ventricular system development (GO:0021591)	BP	22	22	0.272727273	6.05368E-10
GO:0043405	regulation of MAP kinase activity	down	regulation of MAP kinase activity (GO:0043405)	BP	176	173	0.132947977	6.14958E-10
GO:0045766	positive regulation of angiogenesis	down	positive regulation of angiogenesis (GO:0045766)	BP	79	77	0.116883117	6.27262E-10
GO:0045197	establishment or maintenance of epithelial cell apical/bas	down	establishment or maintenance of epithelial cell apical/basal polarity (GO:	BP	17	15	0.2	6.34312E-10
GO:0051653	spindle localization	down	spindle localization (GO:0051653)	BP	28	27	0.148148148	6.4083E-10
GO:2000779	regulation of double-strand break repair	down	regulation of double-strand break repair (GO:2000779)	BP	31	31	0.161290323	6.42116E-10
GO:0031497	chromatin assembly	down	chromatin assembly (GO:0031497)	BP	60	44	0.159090909	6.50452E-10
GO:0003231	cardiac ventricle development	down	cardiac ventricle development (GO:0003231)	BP	89	87	0.183908046	6.57644E-10
GO:0006486	protein glycosylation	down	protein glycosylation (GO:0006486)	BP	141	136	0.125	6.60884E-10
GO:0043413	macromolecule glycosylation	down	macromolecule glycosylation (GO:0043413)	BP	141	136	0.125	6.60884E-10
GO:1904589	regulation of protein import	down	regulation of protein import (GO:1904589)	BP	123	122	0.114754098	6.69064E-10
GO:1990138	neuron projection extension	down	neuron projection extension (GO:1990138)	BP	84	82	0.12195122	6.79612E-10
GO:0044380	protein localization to cytoskeleton	down	protein localization to cytoskeleton (GO:0044380)	BP	25	25	0.24	6.86958E-10
GO:0070286	axonemal dynein complex assembly	down	axonemal dynein complex assembly (GO:0070286)	BP	17	17	0.117647059	6.86958E-10
GO:2000177	regulation of neural precursor cell proliferation	down	regulation of neural precursor cell proliferation (GO:2000177)	BP	53	50	0.18	6.88334E-10
GO:1903039	positive regulation of leukocyte cell-cell adhesion	down	positive regulation of leukocyte cell-cell adhesion (GO:1903039)	BP	117	114	0.131578947	6.92434E-10
GO:0031532	actin cytoskeleton reorganization	down	actin cytoskeleton reorganization (GO:0031532)	BP	62	61	0.081967213	7.11688E-10
GO:0071897	DNA biosynthetic process	down	DNA biosynthetic process (GO:0071897)	BP	88	87	0.126436782	7.32728E-10
GO:0008593	regulation of Notch signaling pathway	down	regulation of Notch signaling pathway (GO:0008593)	BP	46	42	0.142857143	7.48034E-10
GO:0048771	tissue remodeling	down	tissue remodeling (GO:0048771)	BP	98	96	0.166666667	7.48034E-10
GO:0060712	spongiotrophoblast layer development	down	spongiotrophoblast layer development (GO:0060712)	BP	12	12	0.166666667	7.48034E-10
GO:0032147	activation of protein kinase activity	down	activation of protein kinase activity (GO:0032147)	BP	124	122	0.163934426	7.6424E-10
GO:0061430	bone trabecula morphogenesis	down	bone trabecula morphogenesis (GO:0061430)	BP	11	11	0.363636364	7.85792E-10
GO:0060563	neuroepithelial cell differentiation	down	neuroepithelial cell differentiation (GO:0060563)	BP	41	39	0.205128205	8.03556E-10
GO:0001754	eye photoreceptor cell differentiation	down	eye photoreceptor cell differentiation (GO:0001754)	BP	34	34	0.235294118	8.17598E-10
GO:0051145	smooth muscle cell differentiation	down	smooth muscle cell differentiation (GO:0051145)	BP	36	35	0.171428571	8.23378E-10
GO:0048670	regulation of collateral sprouting	down	regulation of collateral sprouting (GO:0048670)	BP	14	14	0.285714286	8.45228E-10
GO:0000077	DNA damage checkpoint	down	DNA damage checkpoint (GO:0000077)	BP	70	67	0.104477612	8.78152E-10
GO:0050870	positive regulation of T cell activation	down	positive regulation of T cell activation (GO:0050870)	BP	113	110	0.127272727	8.80926E-10
GO:0007272	ensheathment of neurons	down	ensheathment of neurons (GO:0007272)	BP	63	63	0.079365079	9.05634E-10
GO:0008366	axon ensheathment	down	axon ensheathment (GO:0008366)	BP	63	63	0.079365079	9.05634E-10
GO:0070986	left/right axis specification	down	left/right axis specification (GO:0070986)	BP	10	10	0.2	9.3655E-10
GO:0042552	myelination	down	myelination (GO:0042552)	BP	61	61	0.081967213	9.40296E-10
GO:0003179	heart valve morphogenesis	down	heart valve morphogenesis (GO:0003179)	BP	25	25	0.2	9.74886E-10
GO:0007063	regulation of sister chromatid cohesion	down	regulation of sister chromatid cohesion (GO:0007063)	BP	15	14	0.214285714	9.76316E-10
GO:0051054	positive regulation of DNA metabolic process	down	positive regulation of DNA metabolic process (GO:0051054)	BP	130	129	0.162790698	9.83194E-10
GO:0010595	positive regulation of endothelial cell migration	down	positive regulation of endothelial cell migration (GO:0010595)	BP	48	47	0.170212766	1.00499E-09
GO:0071173	spindle assembly checkpoint	down	spindle assembly checkpoint (GO:0071173)	BP	18	16	0.25	1.01926E-09
GO:2000052	positive regulation of non-canonical Wnt signaling pathw	down	positive regulation of non-canonical Wnt signaling pathway (GO:200005	BP	11	10	0.5	1.01926E-09
GO:0044236	multicellular organism metabolic process	down	multicellular organism metabolic process (GO:0044236)	BP	44	44	0.159090909	1.02014E-09
GO:0007379	segment specification	down	segment specification (GO:0007379)	BP	12	11	0.363636364	1.03186E-09
GO:0043473	pigmentation	down	pigmentation (GO:0043473)	BP	63	62	0.161290323	1.05167E-09
GO:0070192	chromosome organization involved in meiotic cell cycle	down	chromosome organization involved in meiotic cell cycle (GO:0070192)	BP	44	41	0.146341463	1.05512E-09
GO:0048015	phosphatidylinositol-mediated signaling	down	phosphatidylinositol-mediated signaling (GO:0048015)	BP	96	93	0.107526882	1.066E-09
GO:1902043	positive regulation of extrinsic apoptotic signaling pathw	down	positive regulation of extrinsic apoptotic signaling pathway via death dor	BP	17	15	0.066666667	1.07426E-09
GO:2001238	positive regulation of extrinsic apoptotic signaling pathw	down	positive regulation of extrinsic apoptotic signaling pathway (GO:200123	BP	47	45	0.2	1.08906E-09
GO:0021799	cerebral cortex radially oriented cell migration	down	cerebral cortex radially oriented cell migration (GO:0021799)	BP	23	23	0.130434783	1.09906E-09
GO:0021675	nerve development	down	nerve development (GO:0021675)	BP	54	54	0.203703704	1.20691E-09
GO:0043576	regulation of respiratory gaseous exchange	down	regulation of respiratory gaseous exchange (GO:0043576)	BP	15	15	0.266666667	1.22697E-09
GO:1900182	positive regulation of protein localization to nucleus	down	positive regulation of protein localization to nucleus (GO:1900182)	BP	89	88	0.136363636	1.22697E-09
GO:0097581	lamellipodium organization	down	lamellipodium organization (GO:0097581)	BP	52	49	0.142857143	1.22835E-09
GO:0001573	ganglioside metabolic process	down	ganglioside metabolic process (GO:0001573)	BP	11	11	0.181818182	1.234E-09
GO:1900180	regulation of protein localization to nucleus	down	regulation of protein localization to nucleus (GO:1900180)	BP	154	152	0.111842105	1.2514E-09
GO:0030902	hindbrain development	down	hindbrain development (GO:0030902)	BP	89	83	0.144578313	1.26781E-09
GO:2000738	positive regulation of stem cell differentiation	down	positive regulation of stem cell differentiation (GO:2000738)	BP	12	11	0.272727273	1.27174E-09
GO:0032526	response to retinoic acid	down	response to retinoic acid (GO:0032526)	BP	50	47	0.170212766	1.27832E-09

GO:0042306	regulation of protein import into nucleus	down	regulation of protein import into nucleus (GO:0042306)	BP	122	121	0.115702479	1.30324E-09
GO:0071295	cellular response to vitamin	down	cellular response to vitamin (GO:0071295)	BP	10	9	0.333333333	1.38307E-09
GO:1901991	negative regulation of mitotic cell cycle phase transition	down	negative regulation of mitotic cell cycle phase transition (GO:1901991)	BP	58	55	0.145454545	1.38307E-09
GO:0061512	protein localization to cilium	down	protein localization to cilium (GO:0061512)	BP	21	19	0.157894737	1.39213E-09
GO:0048668	collateral sprouting	down	collateral sprouting (GO:0048668)	BP	20	19	0.315789474	1.45705E-09
GO:0048477	oogenesis	down	oogenesis (GO:0048477)	BP	48	48	0.145833333	1.45933E-09
GO:0051101	regulation of DNA binding	down	regulation of DNA binding (GO:0051101)	BP	64	62	0.129032258	1.45933E-09
GO:0051293	establishment of spindle localization	down	establishment of spindle localization (GO:0051293)	BP	23	22	0.136363636	1.49659E-09
GO:0021692	cerebellar Purkinje cell layer morphogenesis	down	cerebellar Purkinje cell layer morphogenesis (GO:0021692)	BP	14	12	0.25	1.50733E-09
GO:0022037	metencephalon development	down	metencephalon development (GO:0022037)	BP	65	59	0.152542373	1.53246E-09
GO:0050766	positive regulation of phagocytosis	down	positive regulation of phagocytosis (GO:0050766)	BP	27	26	0.115384615	1.55398E-09
GO:0048675	axon extension	down	axon extension (GO:0048675)	BP	59	57	0.140350877	1.58253E-09
GO:0022412	cellular process involved in reproduction in multicellular	down	cellular process involved in reproduction in multicellular organism (GO:	BP	199	188	0.127659574	1.61987E-09
GO:0008544	epidermis development	down	epidermis development (GO:0008544)	BP	174	163	0.141104294	1.70993E-09
GO:1902903	regulation of supramolecular fiber organization	down	regulation of supramolecular fiber organization (GO:1902903)	BP	179	171	0.122807018	1.70993E-09
GO:0045005	DNA-dependent DNA replication maintenance of fidelity	down	DNA-dependent DNA replication maintenance of fidelity (GO:0045005)	BP	21	21	0.047619048	1.77103E-09
GO:0043297	apical junction assembly	down	apical junction assembly (GO:0043297)	BP	34	33	0.181818182	1.85461E-09
GO:0032944	regulation of mononuclear cell proliferation	down	regulation of mononuclear cell proliferation (GO:0032944)	BP	130	126	0.071428571	1.93074E-09
GO:0001707	mesoderm formation	down	mesoderm formation (GO:0001707)	BP	50	50	0.16	2.08026E-09
GO:0061371	determination of heart left/right asymmetry	down	determination of heart left/right asymmetry (GO:0061371)	BP	42	42	0.095238095	2.09965E-09
GO:0046822	regulation of nucleocytoplasmic transport	down	regulation of nucleocytoplasmic transport (GO:0046822)	BP	149	147	0.102040816	2.10247E-09
GO:0060491	regulation of cell projection assembly	down	regulation of cell projection assembly (GO:0060491)	BP	88	85	0.094117647	2.18524E-09
GO:0055012	ventricular cardiac muscle cell differentiation	down	ventricular cardiac muscle cell differentiation (GO:0055012)	BP	15	14	0.142857143	2.19447E-09
GO:0050890	cognition	down	cognition (GO:0050890)	BP	152	145	0.131034483	2.21112E-09
GO:0098693	regulation of synaptic vesicle cycle	down	regulation of synaptic vesicle cycle (GO:0098693)	BP	21	21	0.380952381	2.26189E-09
GO:0045577	regulation of B cell differentiation	down	regulation of B cell differentiation (GO:0045577)	BP	16	16	0.1875	2.27692E-09
GO:0001947	heart looping	down	heart looping (GO:0001947)	BP	40	40	0.1	2.29097E-09
GO:0051294	establishment of spindle orientation	down	establishment of spindle orientation (GO:0051294)	BP	17	16	0.125	2.29891E-09
GO:0051567	histone H3-K9 methylation	down	histone H3-K9 methylation (GO:0051567)	BP	24	24	0.083333333	2.31531E-09
GO:0090189	regulation of branching involved in ureteric bud morpho	down	regulation of branching involved in ureteric bud morphogenesis (GO:009	BP	19	19	0.263157895	2.34964E-09
GO:0061383	trabecula morphogenesis	down	trabecula morphogenesis (GO:0061383)	BP	36	36	0.166666667	2.39351E-09
GO:0070085	glycosylation	down	glycosylation (GO:0070085)	BP	149	144	0.118055556	2.52801E-09
GO:0060425	lung morphogenesis	down	lung morphogenesis (GO:0060425)	BP	44	42	0.166666667	2.60042E-09
GO:0010464	regulation of mesenchymal cell proliferation	down	regulation of mesenchymal cell proliferation (GO:0010464)	BP	23	23	0.260869565	2.61881E-09
GO:0033622	integrin activation	down	integrin activation (GO:0033622)	BP	16	16	0.1875	2.65309E-09
GO:1904591	positive regulation of protein import	down	positive regulation of protein import (GO:1904591)	BP	71	70	0.128571429	2.65309E-09
GO:0035082	axoneme assembly	down	axoneme assembly (GO:0035082)	BP	35	34	0.088235294	2.76031E-09
GO:0001892	embryonic placenta development	down	embryonic placenta development (GO:0001892)	BP	70	70	0.128571429	2.819E-09
GO:0003230	cardiac atrium development	down	cardiac atrium development (GO:0003230)	BP	26	26	0.192307692	2.88166E-09
GO:0070661	leukocyte proliferation	down	leukocyte proliferation (GO:0070661)	BP	175	171	0.081871345	2.945E-09
GO:0048048	embryonic eye morphogenesis	down	embryonic eye morphogenesis (GO:0048048)	BP	27	27	0.185185185	3.06142E-09
GO:0072176	nephric duct development	down	nephric duct development (GO:0072176)	BP	13	13	0.230769231	3.08505E-09
GO:0048814	regulation of dendrite morphogenesis	down	regulation of dendrite morphogenesis (GO:0048814)	BP	45	44	0.159090909	3.16579E-09
GO:0050670	regulation of lymphocyte proliferation	down	regulation of lymphocyte proliferation (GO:0050670)	BP	129	125	0.072	3.2811E-09
GO:1904019	epithelial cell apoptotic process	down	epithelial cell apoptotic process (GO:1904019)	BP	52	52	0.076923077	3.30489E-09
GO:0071230	cellular response to amino acid stimulus	down	cellular response to amino acid stimulus (GO:0071230)	BP	40	40	0.275	3.32459E-09
GO:0072583	clathrin-dependent endocytosis	down	clathrin-dependent endocytosis (GO:0072583)	BP	27	27	0.148148148	3.3925E-09
GO:0014068	positive regulation of phosphatidylinositol 3-kinase signa	down	positive regulation of phosphatidylinositol 3-kinase signaling (GO:00140	BP	46	44	0.181818182	3.47871E-09
GO:1904948	midbrain dopaminergic neuron differentiation	down	midbrain dopaminergic neuron differentiation (GO:1904948)	BP	10	10	0.2	3.54248E-09
GO:2000179	positive regulation of neural precursor cell proliferation	down	positive regulation of neural precursor cell proliferation (GO:2000179)	BP	31	29	0.172413793	3.54248E-09
GO:0007611	learning or memory	down	learning or memory (GO:0007611)	BP	131	128	0.1484375	3.55674E-09
GO:0050732	negative regulation of peptidyl-tyrosine phosphorylation	down	negative regulation of peptidyl-tyrosine phosphorylation (GO:0050732)	BP	23	23	0.217391304	3.56285E-09
GO:0010171	body morphogenesis	down	body morphogenesis (GO:0010171)	BP	38	37	0.189189189	3.60006E-09
GO:0007009	plasma membrane organization	down	plasma membrane organization (GO:0007009)	BP	59	59	0.186440678	3.74451E-09
GO:0003094	glomerular filtration	down	glomerular filtration (GO:0003094)	BP	10	10	0.3	3.84536E-09
GO:0050920	regulation of chemotaxis	down	regulation of chemotaxis (GO:0050920)	BP	107	101	0.138613861	3.85097E-09
GO:0046596	regulation of viral entry into host cell	down	regulation of viral entry into host cell (GO:0046596)	BP	16	15	0.2	3.89032E-09
GO:0051571	positive regulation of histone H3-K4 methylation	down	positive regulation of histone H3-K4 methylation (GO:0051571)	BP	11	11	0.090909091	4.09173E-09
GO:0044786	cell cycle DNA replication	down	cell cycle DNA replication (GO:0044786)	BP	23	23	0.130434783	4.11262E-09
GO:0050806	positive regulation of synaptic transmission	down	positive regulation of synaptic transmission (GO:0050806)	BP	61	58	0.172413793	4.35392E-09
GO:2000369	regulation of clathrin-dependent endocytosis	down	regulation of clathrin-dependent endocytosis (GO:2000369)	BP	10	10	0.3	4.42416E-09
GO:0035023	regulation of Rho protein signal transduction	down	regulation of Rho protein signal transduction (GO:0035023)	BP	95	89	0.146067416	4.46655E-09
GO:0060119	inner ear receptor cell development	down	inner ear receptor cell development (GO:0060119)	BP	40	39	0.205128205	4.48459E-09
GO:0061005	cell differentiation involved in kidney development	down	cell differentiation involved in kidney development (GO:0061005)	BP	39	39	0.179487179	4.59905E-09

GO:0043044	ATP-dependent chromatin remodeling	down	ATP-dependent chromatin remodeling (GO:0043044)	BP	32	32	0.125	4.66315E-09
GO:0001941	postsynaptic membrane organization	down	postsynaptic membrane organization (GO:0001941)	BP	18	18	0.277777778	4.8637E-09
GO:0060326	cell chemotaxis	down	cell chemotaxis (GO:0060326)	BP	165	152	0.125	4.8637E-09
GO:0031103	axon regeneration	down	axon regeneration (GO:0031103)	BP	16	16	0.1875	4.90993E-09
GO:0045668	negative regulation of osteoblast differentiation	down	negative regulation of osteoblast differentiation (GO:0045668)	BP	32	31	0.129032258	4.90993E-09
GO:0030858	positive regulation of epithelial cell differentiation	down	positive regulation of epithelial cell differentiation (GO:0030858)	BP	41	38	0.157894737	4.99815E-09
GO:0070663	regulation of leukocyte proliferation	down	regulation of leukocyte proliferation (GO:0070663)	BP	134	130	0.069230769	5.52722E-09
GO:0016601	Rac protein signal transduction	down	Rac protein signal transduction (GO:0016601)	BP	22	22	0.090909091	5.75875E-09
GO:0021696	cerebellar cortex morphogenesis	down	cerebellar cortex morphogenesis (GO:0021696)	BP	27	24	0.25	5.78437E-09
GO:0030705	cytoskeleton-dependent intracellular transport	down	cytoskeleton-dependent intracellular transport (GO:0030705)	BP	68	67	0.104477612	5.88095E-09
GO:1903672	positive regulation of sprouting angiogenesis	down	positive regulation of sprouting angiogenesis (GO:1903672)	BP	10	10	0.3	6.1501E-09
GO:0009798	axis specification	down	axis specification (GO:0009798)	BP	62	59	0.118644068	6.48623E-09
GO:0021587	cerebellum morphogenesis	down	cerebellum morphogenesis (GO:0021587)	BP	32	29	0.24137931	6.68297E-09
GO:0010812	negative regulation of cell-substrate adhesion	down	negative regulation of cell-substrate adhesion (GO:0010812)	BP	38	37	0.108108108	6.68727E-09
GO:0032232	negative regulation of actin filament bundle assembly	down	negative regulation of actin filament bundle assembly (GO:0032232)	BP	16	16	0.1875	6.8563E-09
GO:0043507	positive regulation of JUN kinase activity	down	positive regulation of JUN kinase activity (GO:0043507)	BP	40	40	0.125	6.90263E-09
GO:1903708	positive regulation of hemopoiesis	down	positive regulation of hemopoiesis (GO:1903708)	BP	117	113	0.079646018	6.91956E-09
GO:0048485	sympathetic nervous system development	down	sympathetic nervous system development (GO:0048485)	BP	17	16	0.125	6.92445E-09
GO:0006887	exocytosis	down	exocytosis (GO:0006887)	BP	166	160	0.09375	6.94279E-09
GO:0048638	regulation of developmental growth	down	regulation of developmental growth (GO:0048638)	BP	192	188	0.143617021	6.9493E-09
GO:0042307	positive regulation of protein import into nucleus	down	positive regulation of protein import into nucleus (GO:0042307)	BP	70	69	0.130434783	7.01997E-09
GO:0085029	extracellular matrix assembly	down	extracellular matrix assembly (GO:0085029)	BP	19	19	0.105263158	7.01997E-09
GO:0031076	embryonic camera-type eye development	down	embryonic camera-type eye development (GO:0031076)	BP	30	30	0.166666667	7.06601E-09
GO:0006333	chromatin assembly or disassembly	down	chromatin assembly or disassembly (GO:0006333)	BP	80	63	0.142857143	7.36591E-09
GO:0007498	mesoderm development	down	mesoderm development (GO:0007498)	BP	77	77	0.142857143	7.72387E-09
GO:0051904	pigment granule transport	down	pigment granule transport (GO:0051904)	BP	13	13	0.153846154	7.72387E-09
GO:0051905	establishment of pigment granule localization	down	establishment of pigment granule localization (GO:0051905)	BP	13	13	0.153846154	7.72387E-09
GO:0046824	positive regulation of nucleocytoplasmic transport	down	positive regulation of nucleocytoplasmic transport (GO:0046824)	BP	83	82	0.109756098	7.84039E-09
GO:0033044	regulation of chromosome organization	down	regulation of chromosome organization (GO:0033044)	BP	192	189	0.100529101	7.87424E-09
GO:0098901	regulation of cardiac muscle cell action potential	down	regulation of cardiac muscle cell action potential (GO:0098901)	BP	13	13	0.076923077	7.94675E-09
GO:0051251	positive regulation of lymphocyte activation	down	positive regulation of lymphocyte activation (GO:0051251)	BP	152	149	0.100671141	8.1178E-09
GO:0072207	metanephric epithelium development	down	metanephric epithelium development (GO:0072207)	BP	22	22	0.136363636	8.24735E-09
GO:0003209	cardiac atrium morphogenesis	down	cardiac atrium morphogenesis (GO:0003209)	BP	25	25	0.2	8.32059E-09
GO:0051403	stress-activated MAPK cascade	down	stress-activated MAPK cascade (GO:0051403)	BP	147	144	0.152777778	8.47169E-09
GO:2001026	regulation of endothelial cell chemotaxis	down	regulation of endothelial cell chemotaxis (GO:2001026)	BP	13	13	0.230769231	9.01866E-09
GO:0071214	cellular response to abiotic stimulus	down	cellular response to abiotic stimulus (GO:0071214)	BP	155	152	0.118421053	9.09724E-09
GO:0104004	cellular response to environmental stimulus	down	cellular response to environmental stimulus (GO:0104004)	BP	155	152	0.118421053	9.09724E-09
GO:0031297	replication fork processing	down	replication fork processing (GO:0031297)	BP	18	18	0.055555556	9.22898E-09
GO:0000187	activation of MAPK activity	down	activation of MAPK activity (GO:0000187)	BP	58	58	0.172413793	9.86796E-09
GO:0043534	blood vessel endothelial cell migration	down	blood vessel endothelial cell migration (GO:0043534)	BP	49	48	0.104166667	9.90093E-09
GO:0050772	positive regulation of axonogenesis	down	positive regulation of axonogenesis (GO:0050772)	BP	38	37	0.189189189	1.00998E-08
GO:0060343	trabecula formation	down	trabecula formation (GO:0060343)	BP	18	18	0.277777778	1.02523E-08
GO:0051125	regulation of actin nucleation	down	regulation of actin nucleation (GO:0051125)	BP	16	16	0.25	1.02928E-08
GO:2000241	regulation of reproductive process	down	regulation of reproductive process (GO:2000241)	BP	86	84	0.142857143	1.02928E-08
GO:0055024	regulation of cardiac muscle tissue development	down	regulation of cardiac muscle tissue development (GO:0055024)	BP	41	41	0.12195122	1.06688E-08
GO:0001885	endothelial cell development	down	endothelial cell development (GO:0001885)	BP	40	39	0.102564103	1.07632E-08
GO:0097306	cellular response to alcohol	down	cellular response to alcohol (GO:0097306)	BP	30	30	0.2	1.07933E-08
GO:1902042	negative regulation of extrinsic apoptotic signaling pathw	down	negative regulation of extrinsic apoptotic signaling pathway via death do	BP	19	19	0.263157895	1.07933E-08
GO:0001101	response to acid chemical	down	response to acid chemical (GO:0001101)	BP	129	125	0.176	1.08757E-08
GO:0031098	stress-activated protein kinase signaling cascade	down	stress-activated protein kinase signaling cascade (GO:0031098)	BP	150	147	0.149659864	1.09688E-08
GO:0099504	synaptic vesicle cycle	down	synaptic vesicle cycle (GO:0099504)	BP	46	46	0.239130435	1.09932E-08
GO:0033628	regulation of cell adhesion mediated by integrin	down	regulation of cell adhesion mediated by integrin (GO:0033628)	BP	29	28	0.107142857	1.16918E-08
GO:0050866	negative regulation of cell activation	down	negative regulation of cell activation (GO:0050866)	BP	103	98	0.091836735	1.20323E-08
GO:0048333	mesodermal cell differentiation	down	mesodermal cell differentiation (GO:0048333)	BP	20	20	0.25	1.20777E-08
GO:0097479	synaptic vesicle localization	down	synaptic vesicle localization (GO:0097479)	BP	56	56	0.196428571	1.21555E-08
GO:0001890	placenta development	down	placenta development (GO:0001890)	BP	108	106	0.141509434	1.24394E-08
GO:0006929	substrate-dependent cell migration	down	substrate-dependent cell migration (GO:0006929)	BP	18	18	0.277777778	1.25156E-08
GO:0014037	Schwann cell differentiation	down	Schwann cell differentiation (GO:0014037)	BP	19	19	0.052631579	1.28713E-08
GO:0010633	negative regulation of epithelial cell migration	down	negative regulation of epithelial cell migration (GO:0010633)	BP	43	41	0.097560976	1.29781E-08
GO:1901099	negative regulation of signal transduction in absence of li	down	negative regulation of signal transduction in absence of ligand (GO:19010	BP	22	22	0.272727273	1.30909E-08
GO:2001240	negative regulation of extrinsic apoptotic signaling pathw	down	negative regulation of extrinsic apoptotic signaling pathway in absence o	BP	22	22	0.272727273	1.30909E-08
GO:0090136	epithelial cell-cell adhesion	down	epithelial cell-cell adhesion (GO:0090136)	BP	12	11	0.181818182	1.30968E-08
GO:0021695	cerebellar cortex development	down	cerebellar cortex development (GO:0021695)	BP	41	37	0.216216216	1.41681E-08
GO:0051650	establishment of vesicle localization	down	establishment of vesicle localization (GO:0051650)	BP	83	83	0.13253012	1.43888E-08

GO:0072673	lamellipodium morphogenesis	down	lamellipodium morphogenesis (GO:0072673)	BP	14	14	0.285714286	1.45009E-08
GO:0030038	contractile actin filament bundle assembly	down	contractile actin filament bundle assembly (GO:0030038)	BP	60	58	0.068965517	1.47311E-08
GO:0043149	stress fiber assembly	down	stress fiber assembly (GO:0043149)	BP	60	58	0.068965517	1.47311E-08
GO:0055015	ventricular cardiac muscle cell development	down	ventricular cardiac muscle cell development (GO:0055015)	BP	10	10	0.2	1.48496E-08
GO:0048844	artery morphogenesis	down	artery morphogenesis (GO:0048844)	BP	42	42	0.119047619	1.52805E-08
GO:0061097	regulation of protein tyrosine kinase activity	down	regulation of protein tyrosine kinase activity (GO:0061097)	BP	34	34	0.147058824	1.53862E-08
GO:0046530	photoreceptor cell differentiation	down	photoreceptor cell differentiation (GO:0046530)	BP	42	40	0.2	1.55665E-08
GO:0018210	peptidyl-threonine modification	down	peptidyl-threonine modification (GO:0018210)	BP	63	59	0.13559322	1.63763E-08
GO:0034104	negative regulation of tissue remodeling	down	negative regulation of tissue remodeling (GO:0034104)	BP	11	11	0.272727273	1.63763E-08
GO:0048010	vascular endothelial growth factor receptor signaling pat	down	vascular endothelial growth factor receptor signaling pathway (GO:0048	BP	29	27	0.148148148	1.65382E-08
GO:0120032	regulation of plasma membrane bounded cell projection	down	regulation of plasma membrane bounded cell projection assembly (GO:0	BP	87	84	0.083333333	1.68162E-08
GO:0042129	regulation of T cell proliferation	down	regulation of T cell proliferation (GO:0042129)	BP	97	93	0.086021505	1.73229E-08
GO:0071604	transforming growth factor beta production	down	transforming growth factor beta production (GO:0071604)	BP	15	15	0.2	1.73759E-08
GO:0051875	pigment granule localization	down	pigment granule localization (GO:0051875)	BP	14	14	0.142857143	1.76922E-08
GO:0045840	positive regulation of mitotic nuclear division	down	positive regulation of mitotic nuclear division (GO:0045840)	BP	28	27	0.222222222	1.82877E-08
GO:0035051	cardiocyte differentiation	down	cardiocyte differentiation (GO:0035051)	BP	72	70	0.114285714	1.85138E-08
GO:0034728	nucleosome organization	down	nucleosome organization (GO:0034728)	BP	71	54	0.111111111	1.89336E-08
GO:0021575	hindbrain morphogenesis	down	hindbrain morphogenesis (GO:0021575)	BP	34	31	0.225806452	1.93834E-08
GO:0007584	response to nutrient	down	response to nutrient (GO:0007584)	BP	24	22	0.272727273	1.97925E-08
GO:0030865	cortical cytoskeleton organization	down	cortical cytoskeleton organization (GO:0030865)	BP	28	28	0.107142857	2.03389E-08
GO:0045060	negative thymic T cell selection	down	negative thymic T cell selection (GO:0045060)	BP	10	9	0.111111111	2.05396E-08
GO:0048730	epidermis morphogenesis	down	epidermis morphogenesis (GO:0048730)	BP	23	22	0.227272727	2.09214E-08
GO:0034315	regulation of Arp2/3 complex-mediated actin nucleation	down	regulation of Arp2/3 complex-mediated actin nucleation (GO:0034315)	BP	10	10	0.3	2.13377E-08
GO:0007548	sex differentiation	down	sex differentiation (GO:0007548)	BP	157	154	0.116883117	2.16737E-08
GO:0031069	hair follicle morphogenesis	down	hair follicle morphogenesis (GO:0031069)	BP	20	20	0.25	2.24798E-08
GO:0030866	cortical actin cytoskeleton organization	down	cortical actin cytoskeleton organization (GO:0030866)	BP	25	25	0.08	2.32271E-08
GO:0031954	positive regulation of protein autophosphorylation	down	positive regulation of protein autophosphorylation (GO:0031954)	BP	12	10	0.1	2.3356E-08
GO:0048384	retinoic acid receptor signaling pathway	down	retinoic acid receptor signaling pathway (GO:0048384)	BP	20	17	0.176470588	2.36107E-08
GO:0043518	negative regulation of DNA damage response, signal trans	down	negative regulation of DNA damage response, signal transduction by p53	BP	11	11	0.272727273	2.38092E-08
GO:0030282	bone mineralization	down	bone mineralization (GO:0030282)	BP	74	70	0.2	2.46819E-08
GO:0097094	craniofacial suture morphogenesis	down	craniofacial suture morphogenesis (GO:0097094)	BP	11	11	0.181818182	2.50929E-08
GO:0050864	regulation of B cell activation	down	regulation of B cell activation (GO:0050864)	BP	75	75	0.053333333	2.62202E-08
GO:0045137	development of primary sexual characteristics	down	development of primary sexual characteristics (GO:0045137)	BP	125	122	0.131147541	2.63448E-08
GO:1902547	regulation of cellular response to vascular endothelial gro	down	regulation of cellular response to vascular endothelial growth factor stim	BP	12	12	0.333333333	2.6995E-08
GO:1902904	negative regulation of supramolecular fiber organization	down	negative regulation of supramolecular fiber organization (GO:1902904)	BP	69	66	0.166666667	2.70624E-08
GO:0021872	forebrain generation of neurons	down	forebrain generation of neurons (GO:0021872)	BP	47	45	0.2	2.71257E-08
GO:0045143	homologous chromosome segregation	down	homologous chromosome segregation (GO:0045143)	BP	39	37	0.135135135	2.71257E-08
GO:1902116	negative regulation of organelle assembly	down	negative regulation of organelle assembly (GO:1902116)	BP	24	24	0.166666667	2.71257E-08
GO:0034349	glial cell apoptotic process	down	glial cell apoptotic process (GO:0034349)	BP	10	9	0.222222222	2.83412E-08
GO:0021819	layer formation in cerebral cortex	down	layer formation in cerebral cortex (GO:0021819)	BP	13	13	0.153846154	2.86105E-08
GO:0033630	positive regulation of cell adhesion mediated by integrin	down	positive regulation of cell adhesion mediated by integrin (GO:0033630)	BP	13	13	0.153846154	2.87245E-08
GO:0050885	neuromuscular process controlling balance	down	neuromuscular process controlling balance (GO:0050885)	BP	40	40	0.25	2.87516E-08
GO:2001241	positive regulation of extrinsic apoptotic signaling pathw	down	positive regulation of extrinsic apoptotic signaling pathway in absence of	BP	12	12	0.416666667	2.90614E-08
GO:0002313	mature B cell differentiation involved in immune respons	down	mature B cell differentiation involved in immune response (GO:0002313)	BP	13	13	0.230769231	2.91592E-08
GO:0007585	respiratory gaseous exchange	down	respiratory gaseous exchange (GO:0007585)	BP	38	36	0.194444444	2.91907E-08
GO:0010894	negative regulation of steroid biosynthetic process	down	negative regulation of steroid biosynthetic process (GO:0010894)	BP	19	18	0.222222222	2.95375E-08
GO:0045939	negative regulation of steroid metabolic process	down	negative regulation of steroid metabolic process (GO:0045939)	BP	19	18	0.222222222	2.95375E-08
GO:0001958	endochondral ossification	down	endochondral ossification (GO:0001958)	BP	22	20	0.15	2.96406E-08
GO:0036075	replacement ossification	down	replacement ossification (GO:0036075)	BP	22	20	0.15	2.96406E-08
GO:0110053	regulation of actin filament organization	down	regulation of actin filament organization (GO:0110053)	BP	144	138	0.123188406	3.06468E-08
GO:0071364	cellular response to epidermal growth factor stimulus	down	cellular response to epidermal growth factor stimulus (GO:0071364)	BP	15	15	0.133333333	3.09009E-08
GO:0046328	regulation of JNK cascade	down	regulation of JNK cascade (GO:0046328)	BP	107	104	0.144230769	3.10853E-08
GO:0043535	regulation of blood vessel endothelial cell migration	down	regulation of blood vessel endothelial cell migration (GO:0043535)	BP	35	35	0.114285714	3.16202E-08
GO:0072178	nephric duct morphogenesis	down	nephric duct morphogenesis (GO:0072178)	BP	10	10	0.3	3.23136E-08
GO:0006284	base-excision repair	down	base-excision repair (GO:0006284)	BP	29	29	0.137931034	3.26607E-08
GO:0032288	myelin assembly	down	myelin assembly (GO:0032288)	BP	10	10	0.1	3.28152E-08
GO:0050867	positive regulation of cell activation	down	positive regulation of cell activation (GO:0050867)	BP	176	172	0.093023256	3.28152E-08
GO:0090335	regulation of brown fat cell differentiation	down	regulation of brown fat cell differentiation (GO:0090335)	BP	10	10	0.2	3.28152E-08
GO:0050918	positive chemotaxis	down	positive chemotaxis (GO:0050918)	BP	22	21	0.047619048	3.29111E-08
GO:0048710	regulation of astrocyte differentiation	down	regulation of astrocyte differentiation (GO:0048710)	BP	16	16	0.125	3.45866E-08
GO:2000826	regulation of heart morphogenesis	down	regulation of heart morphogenesis (GO:2000826)	BP	24	24	0.166666667	3.45866E-08
GO:0035924	cellular response to vascular endothelial growth factor sti	down	cellular response to vascular endothelial growth factor stimulus (GO:003	BP	30	30	0.166666667	3.4702E-08
GO:0007613	memory	down	memory (GO:0007613)	BP	52	50	0.22	3.47138E-08
GO:0036159	inner dynein arm assembly	down	inner dynein arm assembly (GO:0036159)	BP	10	10	0.1	3.52585E-08

GO:0097150	neuronal stem cell population maintenance	down	neuronal stem cell population maintenance (GO:0097150)	BP	17	17	0.294117647	3.52837E-08
GO:0038034	signal transduction in absence of ligand	down	signal transduction in absence of ligand (GO:0038034)	BP	51	51	0.235294118	3.57406E-08
GO:0097192	extrinsic apoptotic signaling pathway in absence of ligand	down	extrinsic apoptotic signaling pathway in absence of ligand (GO:0097192)	BP	51	51	0.235294118	3.57406E-08
GO:0042113	B cell activation	down	B cell activation (GO:0042113)	BP	145	143	0.076923077	3.64452E-08
GO:0002573	myeloid leukocyte differentiation	down	myeloid leukocyte differentiation (GO:0002573)	BP	131	128	0.109375	3.64906E-08
GO:0017156	calcium ion regulated exocytosis	down	calcium ion regulated exocytosis (GO:0017156)	BP	51	51	0.176470588	3.67143E-08
GO:0007215	glutamate receptor signaling pathway	down	glutamate receptor signaling pathway (GO:0007215)	BP	38	38	0.157894737	3.81206E-08
GO:0002695	negative regulation of leukocyte activation	down	negative regulation of leukocyte activation (GO:0002695)	BP	92	88	0.079545455	3.87848E-08
GO:0007628	adult walking behavior	down	adult walking behavior (GO:0007628)	BP	28	27	0.148148148	3.8941E-08
GO:0090659	walking behavior	down	walking behavior (GO:0090659)	BP	28	27	0.148148148	3.8941E-08
GO:0000725	recombinational repair	down	recombinational repair (GO:0000725)	BP	64	63	0.142857143	3.98057E-08
GO:0051497	negative regulation of stress fiber assembly	down	negative regulation of stress fiber assembly (GO:0051497)	BP	14	14	0.142857143	4.03914E-08
GO:0007141	male meiosis I	down	male meiosis I (GO:0007141)	BP	12	12	0.166666667	4.05678E-08
GO:0110020	regulation of actomyosin structure organization	down	regulation of actomyosin structure organization (GO:0110020)	BP	57	54	0.055555556	4.07946E-08
GO:0030857	negative regulation of epithelial cell differentiation	down	negative regulation of epithelial cell differentiation (GO:0030857)	BP	22	22	0.227272727	4.15123E-08
GO:0009994	oocyte differentiation	down	oocyte differentiation (GO:0009994)	BP	31	31	0.129032258	4.18537E-08
GO:0045661	regulation of myoblast differentiation	down	regulation of myoblast differentiation (GO:0045661)	BP	41	41	0.268292683	4.24074E-08
GO:0014015	positive regulation of gliogenesis	down	positive regulation of gliogenesis (GO:0014015)	BP	21	20	0.15	4.25173E-08
GO:0140029	exocytic process	down	exocytic process (GO:0140029)	BP	34	34	0.088235294	4.29566E-08
GO:0002696	positive regulation of leukocyte activation	down	positive regulation of leukocyte activation (GO:0002696)	BP	170	166	0.090361446	4.78426E-08
GO:0042491	auditory receptor cell differentiation	down	auditory receptor cell differentiation (GO:0042491)	BP	28	28	0.214285714	4.80394E-08
GO:0090231	regulation of spindle checkpoint	down	regulation of spindle checkpoint (GO:0090231)	BP	11	11	0.181818182	4.95706E-08
GO:1902117	positive regulation of organelle assembly	down	positive regulation of organelle assembly (GO:1902117)	BP	49	49	0.102040816	5.15968E-08
GO:2001257	regulation of cation channel activity	down	regulation of cation channel activity (GO:2001257)	BP	59	58	0.120689655	5.21277E-08
GO:0002761	regulation of myeloid leukocyte differentiation	down	regulation of myeloid leukocyte differentiation (GO:0002761)	BP	70	68	0.102941176	5.25448E-08
GO:0009880	embryonic pattern specification	down	embryonic pattern specification (GO:0009880)	BP	44	41	0.170731707	5.42832E-08
GO:0072224	metanephric glomerulus development	down	metanephric glomerulus development (GO:0072224)	BP	10	10	0.2	5.68803E-08
GO:2001234	negative regulation of apoptotic signaling pathway	down	negative regulation of apoptotic signaling pathway (GO:2001234)	BP	150	148	0.168918919	5.68803E-08
GO:0006882	cellular zinc ion homeostasis	down	cellular zinc ion homeostasis (GO:0006882)	BP	16	15	0.066666667	5.86825E-08
GO:0010970	transport along microtubule	down	transport along microtubule (GO:0010970)	BP	63	62	0.096774194	6.00861E-08
GO:0099111	microtubule-based transport	down	microtubule-based transport (GO:0099111)	BP	63	62	0.096774194	6.00861E-08
GO:0072160	nephron tubule epithelial cell differentiation	down	nephron tubule epithelial cell differentiation (GO:0072160)	BP	12	12	0.166666667	6.01895E-08
GO:0030201	heparan sulfate proteoglycan metabolic process	down	heparan sulfate proteoglycan metabolic process (GO:0030201)	BP	19	19	0.210526316	6.13106E-08
GO:0033059	cellular pigmentation	down	cellular pigmentation (GO:0033059)	BP	28	28	0.107142857	6.14079E-08
GO:0060441	epithelial tube branching involved in lung morphogenesis	down	epithelial tube branching involved in lung morphogenesis (GO:0060441)	BP	22	20	0.2	6.23886E-08
GO:0070371	ERK1 and ERK2 cascade	down	ERK1 and ERK2 cascade (GO:0070371)	BP	157	151	0.112582781	6.30102E-08
GO:0045639	positive regulation of myeloid cell differentiation	down	positive regulation of myeloid cell differentiation (GO:0045639)	BP	63	61	0.081967213	6.3784E-08
GO:0046638	positive regulation of alpha-beta T cell differentiation	down	positive regulation of alpha-beta T cell differentiation (GO:0046638)	BP	24	23	0.086956522	6.424E-08
GO:0090329	regulation of DNA-dependent DNA replication	down	regulation of DNA-dependent DNA replication (GO:0090329)	BP	35	35	0.085714286	6.44028E-08
GO:0032946	positive regulation of mononuclear cell proliferation	down	positive regulation of mononuclear cell proliferation (GO:0032946)	BP	87	84	0.083333333	6.56003E-08
GO:0021988	olfactory lobe development	down	olfactory lobe development (GO:0021988)	BP	26	26	0.153846154	6.60419E-08
GO:0031016	pancreas development	down	pancreas development (GO:0031016)	BP	47	47	0.085106383	6.76619E-08
GO:0045737	positive regulation of cyclin-dependent protein serine/thr	down	positive regulation of cyclin-dependent protein serine/threonine kinase a	BP	15	15	0.133333333	6.77484E-08
GO:1904031	positive regulation of cyclin-dependent protein kinase act	down	positive regulation of cyclin-dependent protein kinase activity (GO:1904	BP	16	15	0.133333333	6.77484E-08
GO:0051170	nuclear import	down	nuclear import (GO:0051170)	BP	176	174	0.103448276	6.80451E-08
GO:0045685	regulation of glial cell differentiation	down	regulation of glial cell differentiation (GO:0045685)	BP	26	26	0.115384615	6.92958E-08
GO:0034502	protein localization to chromosome	down	protein localization to chromosome (GO:0034502)	BP	49	46	0.195652174	6.93763E-08
GO:2001251	negative regulation of chromosome organization	down	negative regulation of chromosome organization (GO:2001251)	BP	70	68	0.117647059	7.08245E-08
GO:0032873	negative regulation of stress-activated MAPK cascade	down	negative regulation of stress-activated MAPK cascade (GO:0032873)	BP	25	24	0.208333333	7.22984E-08
GO:0070303	negative regulation of stress-activated protein kinase sign	down	negative regulation of stress-activated protein kinase signaling cascade (G	BP	25	24	0.208333333	7.22984E-08
GO:0018209	peptidyl-serine modification	down	peptidyl-serine modification (GO:0018209)	BP	161	155	0.109677419	7.38359E-08
GO:0030534	adult behavior	down	adult behavior (GO:0030534)	BP	105	102	0.12745098	7.40488E-08
GO:2000311	regulation of AMPA receptor activity	down	regulation of AMPA receptor activity (GO:2000311)	BP	11	11	0.272727273	7.56142E-08
GO:0003407	neural retina development	down	neural retina development (GO:0003407)	BP	36	35	0.257142857	7.62256E-08
GO:0042359	vitamin D metabolic process	down	vitamin D metabolic process (GO:0042359)	BP	14	11	0.272727273	7.62256E-08
GO:0048678	response to axon injury	down	response to axon injury (GO:0048678)	BP	20	20	0.3	7.80232E-08
GO:0006606	protein import into nucleus	down	protein import into nucleus (GO:0006606)	BP	175	173	0.104046243	7.80558E-08
GO:0021772	olfactory bulb development	down	olfactory bulb development (GO:0021772)	BP	25	25	0.16	8.14313E-08
GO:0048525	negative regulation of viral process	down	negative regulation of viral process (GO:0048525)	BP	48	46	0.086956522	8.20279E-08
GO:0060443	mammary gland morphogenesis	down	mammary gland morphogenesis (GO:0060443)	BP	41	39	0.128205128	8.20279E-08
GO:0021782	glial cell development	down	glial cell development (GO:0021782)	BP	47	46	0.108695652	8.25053E-08
GO:0050921	positive regulation of chemotaxis	down	positive regulation of chemotaxis (GO:0050921)	BP	73	69	0.144927536	8.25053E-08
GO:0008406	gonad development	down	gonad development (GO:0008406)	BP	123	120	0.125	8.42629E-08
GO:0051147	regulation of muscle cell differentiation	down	regulation of muscle cell differentiation (GO:0051147)	BP	105	103	0.184466019	8.52731E-08

GO:0010656	negative regulation of muscle cell apoptotic process	down	negative regulation of muscle cell apoptotic process (GO:0010656)	BP	13	13	0.153846154	8.52767E-08
GO:0048841	regulation of axon extension involved in axon guidance	down	regulation of axon extension involved in axon guidance (GO:0048841)	BP	12	12	0.083333333	8.54597E-08
GO:0070830	bicellular tight junction assembly	down	bicellular tight junction assembly (GO:0070830)	BP	26	25	0.16	8.6114E-08
GO:0045055	regulated exocytosis	down	regulated exocytosis (GO:0045055)	BP	99	96	0.104166667	8.70051E-08
GO:0034109	homotypic cell-cell adhesion	down	homotypic cell-cell adhesion (GO:0034109)	BP	56	55	0.127272727	9.23095E-08
GO:0043200	response to amino acid	down	response to amino acid (GO:0043200)	BP	46	46	0.239130435	9.31433E-08
GO:0035909	aorta morphogenesis	down	aorta morphogenesis (GO:0035909)	BP	24	24	0.125	9.41464E-08
GO:0032148	activation of protein kinase B activity	down	activation of protein kinase B activity (GO:0032148)	BP	12	12	0.25	9.51928E-08
GO:0035850	epithelial cell differentiation involved in kidney developm	down	epithelial cell differentiation involved in kidney development (GO:00358	BP	33	33	0.181818182	9.60975E-08
GO:0045931	positive regulation of mitotic cell cycle	down	positive regulation of mitotic cell cycle (GO:0045931)	BP	85	82	0.146341463	1.0205E-07
GO:1903670	regulation of sprouting angiogenesis	down	regulation of sprouting angiogenesis (GO:1903670)	BP	21	21	0.142857143	1.03778E-07
GO:0000731	DNA synthesis involved in DNA repair	down	DNA synthesis involved in DNA repair (GO:0000731)	BP	18	17	0.176470588	1.05143E-07
GO:0071675	regulation of mononuclear cell migration	down	regulation of mononuclear cell migration (GO:0071675)	BP	23	21	0.095238095	1.06169E-07
GO:0015012	heparan sulfate proteoglycan biosynthetic process	down	heparan sulfate proteoglycan biosynthetic process (GO:0015012)	BP	14	14	0.214285714	1.07868E-07
GO:0071478	cellular response to radiation	down	cellular response to radiation (GO:0071478)	BP	90	88	0.170454545	1.07868E-07
GO:0048469	cell maturation	down	cell maturation (GO:0048469)	BP	108	105	0.104761905	1.09398E-07
GO:0048599	oocyte development	down	oocyte development (GO:0048599)	BP	29	29	0.137931034	1.09437E-07
GO:0043523	regulation of neuron apoptotic process	down	regulation of neuron apoptotic process (GO:0043523)	BP	107	104	0.134615385	1.10877E-07
GO:0120033	negative regulation of plasma membrane bounded cell pr	down	negative regulation of plasma membrane bounded cell projection assem	BP	16	16	0.0625	1.11638E-07
GO:0001708	cell fate specification	down	cell fate specification (GO:0001708)	BP	54	53	0.169811321	1.15785E-07
GO:0051492	regulation of stress fiber assembly	down	regulation of stress fiber assembly (GO:0051492)	BP	51	49	0.06122449	1.17635E-07
GO:0003171	atrioventricular valve development	down	atrioventricular valve development (GO:0003171)	BP	17	17	0.176470588	1.18539E-07
GO:0016197	endosomal transport	down	endosomal transport (GO:0016197)	BP	144	144	0.0625	1.18539E-07
GO:0006282	regulation of DNA repair	down	regulation of DNA repair (GO:0006282)	BP	55	55	0.163636364	1.20046E-07
GO:0032663	regulation of interleukin-2 production	down	regulation of interleukin-2 production (GO:0032663)	BP	38	35	0.057142857	1.22596E-07
GO:0060572	morphogenesis of an epithelial bud	down	morphogenesis of an epithelial bud (GO:0060572)	BP	14	14	0.214285714	1.23157E-07
GO:0051100	negative regulation of binding	down	negative regulation of binding (GO:0051100)	BP	94	88	0.147727273	1.23425E-07
GO:0021602	cranial nerve morphogenesis	down	cranial nerve morphogenesis (GO:0021602)	BP	22	22	0.181818182	1.24051E-07
GO:0061437	renal system vasculature development	down	renal system vasculature development (GO:0061437)	BP	14	14	0.071428571	1.24051E-07
GO:0061440	kidney vasculature development	down	kidney vasculature development (GO:0061440)	BP	14	14	0.071428571	1.24051E-07
GO:0033631	cell-cell adhesion mediated by integrin	down	cell-cell adhesion mediated by integrin (GO:0033631)	BP	11	11	0.272727273	1.24365E-07
GO:0007062	sister chromatid cohesion	down	sister chromatid cohesion (GO:0007062)	BP	41	38	0.105263158	1.24618E-07
GO:0000768	syncytium formation by plasma membrane fusion	down	syncytium formation by plasma membrane fusion (GO:0000768)	BP	38	38	0.131578947	1.25198E-07
GO:0006949	syncytium formation	down	syncytium formation (GO:0006949)	BP	39	39	0.128205128	1.25198E-07
GO:0050671	positive regulation of lymphocyte proliferation	down	positive regulation of lymphocyte proliferation (GO:0050671)	BP	86	83	0.084337349	1.25645E-07
GO:0007281	germ cell development	down	germ cell development (GO:0007281)	BP	148	141	0.113475177	1.26304E-07
GO:0071800	podosome assembly	down	podosome assembly (GO:0071800)	BP	13	13	0.230769231	1.27487E-07
GO:0006829	zinc II ion transport	down	zinc II ion transport (GO:0006829)	BP	13	13	0.153846154	1.27834E-07
GO:2000380	regulation of mesoderm development	down	regulation of mesoderm development (GO:2000380)	BP	10	10	0.3	1.28725E-07
GO:0051261	protein depolymerization	down	protein depolymerization (GO:0051261)	BP	56	53	0.226415094	1.28767E-07
GO:1902749	regulation of cell cycle G2/M phase transition	down	regulation of cell cycle G2/M phase transition (GO:1902749)	BP	41	38	0.105263158	1.36026E-07
GO:0072182	regulation of nephron tubule epithelial cell differentiatio	down	regulation of nephron tubule epithelial cell differentiation (GO:0072182	BP	11	11	0.181818182	1.39503E-07
GO:0014002	astrocyte development	down	astrocyte development (GO:0014002)	BP	17	17	0.235294118	1.40647E-07
GO:1905207	regulation of cardiocyte differentiation	down	regulation of cardiocyte differentiation (GO:1905207)	BP	20	20	0.15	1.42201E-07
GO:0051250	negative regulation of lymphocyte activation	down	negative regulation of lymphocyte activation (GO:0051250)	BP	81	77	0.077922078	1.43272E-07
GO:0002244	hematopoietic progenitor cell differentiation	down	hematopoietic progenitor cell differentiation (GO:0002244)	BP	86	82	0.109756098	1.46174E-07
GO:0008360	regulation of cell shape	down	regulation of cell shape (GO:0008360)	BP	79	71	0.098591549	1.48237E-07
GO:0048066	developmental pigmentation	down	developmental pigmentation (GO:0048066)	BP	33	33	0.212121212	1.51606E-07
GO:0086005	ventricular cardiac muscle cell action potential	down	ventricular cardiac muscle cell action potential (GO:0086005)	BP	18	18	0.166666667	1.57624E-07
GO:0030512	negative regulation of transforming growth factor beta re	down	negative regulation of transforming growth factor beta receptor signaling	BP	39	39	0.128205128	1.59105E-07
GO:1903845	negative regulation of cellular response to transforming g	down	negative regulation of cellular response to transforming growth factor be	BP	39	39	0.128205128	1.59105E-07
GO:0043524	negative regulation of neuron apoptotic process	down	negative regulation of neuron apoptotic process (GO:0043524)	BP	87	85	0.129411765	1.65479E-07
GO:2000648	positive regulation of stem cell proliferation	down	positive regulation of stem cell proliferation (GO:2000648)	BP	28	28	0.178571429	1.67466E-07
GO:0086065	cell communication involved in cardiac conduction	down	cell communication involved in cardiac conduction (GO:0086065)	BP	21	21	0.19047619	1.67898E-07
GO:0006335	DNA replication-dependent nucleosome assembly	down	DNA replication-dependent nucleosome assembly (GO:0006335)	BP	12	7	0.285714286	1.68861E-07
GO:0034723	DNA replication-dependent nucleosome organization	down	DNA replication-dependent nucleosome organization (GO:0034723)	BP	12	7	0.285714286	1.68861E-07
GO:2000736	regulation of stem cell differentiation	down	regulation of stem cell differentiation (GO:2000736)	BP	25	24	0.208333333	1.71592E-07
GO:0045652	regulation of megakaryocyte differentiation	down	regulation of megakaryocyte differentiation (GO:0045652)	BP	12	8	0.125	1.73275E-07
GO:0032845	negative regulation of homeostatic process	down	negative regulation of homeostatic process (GO:0032845)	BP	103	100	0.08	1.7549E-07
GO:0044728	DNA methylation or demethylation	down	DNA methylation or demethylation (GO:0044728)	BP	46	45	0.066666667	1.78167E-07
GO:0070849	response to epidermal growth factor	down	response to epidermal growth factor (GO:0070849)	BP	18	18	0.111111111	1.7847E-07
GO:0002053	positive regulation of mesenchymal cell proliferation	down	positive regulation of mesenchymal cell proliferation (GO:0002053)	BP	17	17	0.294117647	1.78927E-07
GO:0070665	positive regulation of leukocyte proliferation	down	positive regulation of leukocyte proliferation (GO:0070665)	BP	92	89	0.078651685	1.90566E-07
GO:2000696	regulation of epithelial cell differentiation involved in kid	down	regulation of epithelial cell differentiation involved in kidney developme	BP	15	15	0.133333333	1.95658E-07

GO:0010596	negative regulation of endothelial cell migration	down	negative regulation of endothelial cell migration (GO:0010596)	BP	32	31	0.064516129	1.97607E-07
GO:1901861	regulation of muscle tissue development	down	regulation of muscle tissue development (GO:1901861)	BP	78	75	0.146666667	1.97668E-07
GO:0002052	positive regulation of neuroblast proliferation	down	positive regulation of neuroblast proliferation (GO:0002052)	BP	15	15	0.2	2.00415E-07
GO:0031058	positive regulation of histone modification	down	positive regulation of histone modification (GO:0031058)	BP	57	56	0.107142857	2.02001E-07
GO:0060285	cilium-dependent cell motility	down	cilium-dependent cell motility (GO:0060285)	BP	10	10	0.1	2.07646E-07
GO:0021604	cranial nerve structural organization	down	cranial nerve structural organization (GO:0021604)	BP	10	10	0.1	2.08737E-07
GO:0048645	animal organ formation	down	animal organ formation (GO:0048645)	BP	44	44	0.136363636	2.08755E-07
GO:0007254	JNK cascade	down	JNK cascade (GO:0007254)	BP	116	113	0.14159292	2.09351E-07
GO:0010212	response to ionizing radiation	down	response to ionizing radiation (GO:0010212)	BP	86	84	0.130952381	2.18977E-07
GO:0009954	proximal/distal pattern formation	down	proximal/distal pattern formation (GO:0009954)	BP	25	24	0.291666667	2.22731E-07
GO:0002042	cell migration involved in sprouting angiogenesis	down	cell migration involved in sprouting angiogenesis (GO:0002042)	BP	24	24	0.083333333	2.36381E-07
GO:0048286	lung alveolus development	down	lung alveolus development (GO:0048286)	BP	31	31	0.064516129	2.36751E-07
GO:1900024	regulation of substrate adhesion-dependent cell spreadin	down	regulation of substrate adhesion-dependent cell spreading (GO:1900024)	BP	34	30	0.066666667	2.3763E-07
GO:1902743	regulation of lamellipodium organization	down	regulation of lamellipodium organization (GO:1902743)	BP	24	22	0.136363636	2.38274E-07
GO:0051258	protein polymerization	down	protein polymerization (GO:0051258)	BP	138	129	0.124031008	2.42139E-07
GO:0001974	blood vessel remodeling	down	blood vessel remodeling (GO:0001974)	BP	26	25	0.24	2.53164E-07
GO:0002088	lens development in camera-type eye	down	lens development in camera-type eye (GO:0002088)	BP	47	43	0.186046512	2.60903E-07
GO:0061217	regulation of mesonephros development	down	regulation of mesonephros development (GO:0061217)	BP	20	20	0.25	2.62626E-07
GO:1905269	positive regulation of chromatin organization	down	positive regulation of chromatin organization (GO:1905269)	BP	64	63	0.095238095	2.66185E-07
GO:0055023	positive regulation of cardiac muscle tissue growth	down	positive regulation of cardiac muscle tissue growth (GO:0055023)	BP	18	18	0.166666667	2.66899E-07
GO:0042310	vasoconstriction	down	vasoconstriction (GO:0042310)	BP	34	34	0.117647059	2.68711E-07
GO:0097756	negative regulation of blood vessel diameter	down	negative regulation of blood vessel diameter (GO:0097756)	BP	34	34	0.117647059	2.68711E-07
GO:0001666	response to hypoxia	down	response to hypoxia (GO:0001666)	BP	117	116	0.129310345	2.6948E-07
GO:0036293	response to decreased oxygen levels	down	response to decreased oxygen levels (GO:0036293)	BP	117	116	0.129310345	2.6948E-07
GO:0090330	regulation of platelet aggregation	down	regulation of platelet aggregation (GO:0090330)	BP	13	13	0.153846154	2.70946E-07
GO:0002283	neutrophil activation involved in immune response	down	neutrophil activation involved in immune response (GO:0002283)	BP	10	9	0.111111111	2.81417E-07
GO:1903523	negative regulation of blood circulation	down	negative regulation of blood circulation (GO:1903523)	BP	19	17	0.235294118	2.84497E-07
GO:0016202	regulation of striated muscle tissue development	down	regulation of striated muscle tissue development (GO:0016202)	BP	76	73	0.150684932	2.86307E-07
GO:0034405	response to fluid shear stress	down	response to fluid shear stress (GO:0034405)	BP	16	16	0.1875	2.86307E-07
GO:0090504	epiboly	down	epiboly (GO:0090504)	BP	21	19	0.157894737	2.88155E-07
GO:0050905	neuromuscular process	down	neuromuscular process (GO:0050905)	BP	78	77	0.155844156	2.92192E-07
GO:0048634	regulation of muscle organ development	down	regulation of muscle organ development (GO:0048634)	BP	77	74	0.148648649	2.9456E-07
GO:0045444	fat cell differentiation	down	fat cell differentiation (GO:0045444)	BP	162	160	0.13125	2.95213E-07
GO:0060603	mammary gland duct morphogenesis	down	mammary gland duct morphogenesis (GO:0060603)	BP	29	27	0.111111111	2.95621E-07
GO:0042147	retrograde transport, endosome to Golgi	down	retrograde transport, endosome to Golgi (GO:0042147)	BP	45	45	0.088888889	2.95759E-07
GO:0008217	regulation of blood pressure	down	regulation of blood pressure (GO:0008217)	BP	88	86	0.174418605	3.05533E-07
GO:0044319	wound healing, spreading of cells	down	wound healing, spreading of cells (GO:0044319)	BP	20	18	0.166666667	3.06548E-07
GO:0090505	epiboly involved in wound healing	down	epiboly involved in wound healing (GO:0090505)	BP	20	18	0.166666667	3.06548E-07
GO:0017158	regulation of calcium ion-dependent exocytosis	down	regulation of calcium ion-dependent exocytosis (GO:0017158)	BP	30	30	0.2	3.17426E-07
GO:0006305	DNA alkylation	down	DNA alkylation (GO:0006305)	BP	35	34	0.088235294	3.19547E-07
GO:0006306	DNA methylation	down	DNA methylation (GO:0006306)	BP	35	34	0.088235294	3.19547E-07
GO:0018105	peptidyl-serine phosphorylation	down	peptidyl-serine phosphorylation (GO:0018105)	BP	151	145	0.110344828	3.21033E-07
GO:0048265	response to pain	down	response to pain (GO:0048265)	BP	19	19	0.210526316	3.24482E-07
GO:0035315	hair cell differentiation	down	hair cell differentiation (GO:0035315)	BP	32	32	0.1875	3.29167E-07
GO:0098911	regulation of ventricular cardiac muscle cell action poten	down	regulation of ventricular cardiac muscle cell action potential (GO:009891	BP	10	10	0.1	3.30507E-07
GO:0042102	positive regulation of T cell proliferation	down	positive regulation of T cell proliferation (GO:0042102)	BP	65	62	0.112903226	3.35304E-07
GO:0030856	regulation of epithelial cell differentiation	down	regulation of epithelial cell differentiation (GO:0030856)	BP	86	82	0.158536585	3.36673E-07
GO:0051402	neuron apoptotic process	down	neuron apoptotic process (GO:0051402)	BP	127	124	0.120967742	3.4007E-07
GO:0070527	platelet aggregation	down	platelet aggregation (GO:0070527)	BP	43	42	0.119047619	3.4007E-07
GO:0072574	hepatocyte proliferation	down	hepatocyte proliferation (GO:0072574)	BP	10	10	0.2	3.4007E-07
GO:0072575	epithelial cell proliferation involved in liver morphogenes	down	epithelial cell proliferation involved in liver morphogenesis (GO:007257	BP	10	10	0.2	3.4007E-07
GO:0044243	multicellular organismal catabolic process	down	multicellular organismal catabolic process (GO:0044243)	BP	15	15	0.066666667	3.42094E-07
GO:0045649	regulation of macrophage differentiation	down	regulation of macrophage differentiation (GO:0045649)	BP	13	13	0	3.44969E-07
GO:0018107	peptidyl-threonine phosphorylation	down	peptidyl-threonine phosphorylation (GO:0018107)	BP	59	55	0.145454545	3.50766E-07
GO:0021545	cranial nerve development	down	cranial nerve development (GO:0021545)	BP	35	35	0.171428571	3.57124E-07
GO:0086004	regulation of cardiac muscle cell contraction	down	regulation of cardiac muscle cell contraction (GO:0086004)	BP	16	15	0.066666667	3.59616E-07
GO:0061515	myeloid cell development	down	myeloid cell development (GO:0061515)	BP	43	42	0.071428571	3.6245E-07
GO:0072012	glomerulus vasculature development	down	glomerulus vasculature development (GO:0072012)	BP	12	12	0.083333333	3.64574E-07
GO:1900449	regulation of glutamate receptor signaling pathway	down	regulation of glutamate receptor signaling pathway (GO:1900449)	BP	18	18	0.222222222	3.64574E-07
GO:1905476	negative regulation of protein localization to membrane	down	negative regulation of protein localization to membrane (GO:1905476)	BP	12	12	0.166666667	3.67206E-07
GO:0044774	mitotic DNA integrity checkpoint	down	mitotic DNA integrity checkpoint (GO:0044774)	BP	31	30	0.066666667	3.6764E-07
GO:0010559	regulation of glycoprotein biosynthetic process	down	regulation of glycoprotein biosynthetic process (GO:0010559)	BP	25	24	0.125	3.71547E-07
GO:0060122	inner ear receptor stereocilium organization	down	inner ear receptor stereocilium organization (GO:0060122)	BP	26	25	0.16	3.71547E-07
GO:0071711	basement membrane organization	down	basement membrane organization (GO:0071711)	BP	13	13	0.076923077	3.79768E-07

GO:0034968	histone lysine methylation	down	histone lysine methylation (GO:0034968)	BP	72	68	0.073529412	3.92081E-07
GO:0045861	negative regulation of proteolysis	down	negative regulation of proteolysis (GO:0045861)	BP	169	160	0.175	3.95586E-07
GO:0033260	nuclear DNA replication	down	nuclear DNA replication (GO:0033260)	BP	14	14	0.142857143	3.99468E-07
GO:0035313	wound healing, spreading of epidermal cells	down	wound healing, spreading of epidermal cells (GO:0035313)	BP	11	10	0.2	4.03565E-07
GO:0003283	atrial septum development	down	atrial septum development (GO:0003283)	BP	14	14	0.285714286	4.1233E-07
GO:0051785	positive regulation of nuclear division	down	positive regulation of nuclear division (GO:0051785)	BP	37	36	0.166666667	4.15609E-07
GO:0016045	detection of bacterium	down	detection of bacterium (GO:0016045)	BP	11	10	0.2	4.16613E-07
GO:0098543	detection of other organism	down	detection of other organism (GO:0098543)	BP	11	10	0.2	4.16613E-07
GO:0043383	negative T cell selection	down	negative T cell selection (GO:0043383)	BP	11	10	0.1	4.19615E-07
GO:0001556	oocyte maturation	down	oocyte maturation (GO:0001556)	BP	17	17	0.176470588	4.23751E-07
GO:0006338	chromatin remodeling	down	chromatin remodeling (GO:0006338)	BP	80	79	0.126582278	4.40717E-07
GO:0072215	regulation of metanephros development	down	regulation of metanephros development (GO:0072215)	BP	16	15	0.2	4.57998E-07
GO:0042770	signal transduction in response to DNA damage	down	signal transduction in response to DNA damage (GO:0042770)	BP	60	57	0.105263158	4.58017E-07
GO:0045598	regulation of fat cell differentiation	down	regulation of fat cell differentiation (GO:0045598)	BP	83	82	0.12195122	4.58017E-07
GO:0001935	endothelial cell proliferation	down	endothelial cell proliferation (GO:0001935)	BP	74	70	0.128571429	4.67982E-07
GO:1903901	negative regulation of viral life cycle	down	negative regulation of viral life cycle (GO:1903901)	BP	42	40	0.075	4.72321E-07
GO:0070997	neuron death	down	neuron death (GO:0070997)	BP	160	156	0.121794872	4.74998E-07
GO:0086019	cell-cell signaling involved in cardiac conduction	down	cell-cell signaling involved in cardiac conduction (GO:0086019)	BP	13	13	0.230769231	4.77535E-07
GO:0019229	regulation of vasoconstriction	down	regulation of vasoconstriction (GO:0019229)	BP	21	21	0.142857143	4.85958E-07
GO:0030330	DNA damage response, signal transduction by p53 class m	down	DNA damage response, signal transduction by p53 class mediator (GO:003	BP	47	44	0.113636364	4.87679E-07
GO:0030032	lamellipodium assembly	down	lamellipodium assembly (GO:0030032)	BP	40	37	0.081081081	4.89334E-07
GO:0051291	protein heterooligomerization	down	protein heterooligomerization (GO:0051291)	BP	32	27	0.296296296	4.93953E-07
GO:0016572	histone phosphorylation	down	histone phosphorylation (GO:0016572)	BP	24	22	0.136363636	5.00193E-07
GO:0071156	regulation of cell cycle arrest	down	regulation of cell cycle arrest (GO:0071156)	BP	34	32	0.15625	5.13236E-07
GO:0072576	liver morphogenesis	down	liver morphogenesis (GO:0072576)	BP	12	12	0.166666667	5.2046E-07
GO:0090316	positive regulation of intracellular protein transport	down	positive regulation of intracellular protein transport (GO:0090316)	BP	178	173	0.080924855	5.2046E-07
GO:0006903	vesicle targeting	down	vesicle targeting (GO:0006903)	BP	11	11	0.272727273	5.21908E-07
GO:0033555	multicellular organismal response to stress	down	multicellular organismal response to stress (GO:0033555)	BP	49	48	0.166666667	5.26705E-07
GO:0008211	glucocorticoid metabolic process	down	glucocorticoid metabolic process (GO:0008211)	BP	12	11	0.181818182	5.27331E-07
GO:0000082	G1/S transition of mitotic cell cycle	down	G1/S transition of mitotic cell cycle (GO:0000082)	BP	91	89	0.101123596	5.37418E-07
GO:0003181	atrioventricular valve morphogenesis	down	atrioventricular valve morphogenesis (GO:0003181)	BP	14	14	0.214285714	5.42825E-07
GO:0071801	regulation of podosome assembly	down	regulation of podosome assembly (GO:0071801)	BP	10	10	0.2	5.70945E-07
GO:0010951	negative regulation of endopeptidase activity	down	negative regulation of endopeptidase activity (GO:0010951)	BP	104	98	0.214285714	5.77898E-07
GO:0071498	cellular response to fluid shear stress	down	cellular response to fluid shear stress (GO:0071498)	BP	10	10	0.2	5.81419E-07
GO:0000724	double-strand break repair via homologous recombinatio	down	double-strand break repair via homologous recombination (GO:0000724	BP	63	62	0.129032258	5.96194E-07
GO:0036035	osteoclast development	down	osteoclast development (GO:0036035)	BP	11	11	0.181818182	6.00936E-07
GO:0045445	myoblast differentiation	down	myoblast differentiation (GO:0045445)	BP	59	59	0.271186441	6.01311E-07
GO:2001021	negative regulation of response to DNA damage stimulus	down	negative regulation of response to DNA damage stimulus (GO:2001021)	BP	37	37	0.162162162	6.05061E-07
GO:0010466	negative regulation of peptidase activity	down	negative regulation of peptidase activity (GO:0010466)	BP	115	108	0.222222222	6.09895E-07
GO:0042551	neuron maturation	down	neuron maturation (GO:0042551)	BP	29	29	0.137931034	6.13169E-07
GO:0071709	membrane assembly	down	membrane assembly (GO:0071709)	BP	20	20	0.3	6.15087E-07
GO:0032486	Rap protein signal transduction	down	Rap protein signal transduction (GO:0032486)	BP	10	9	0.111111111	6.15919E-07
GO:0016571	histone methylation	down	histone methylation (GO:0016571)	BP	95	91	0.076923077	6.18294E-07
GO:0031214	biomineral tissue development	down	biomineral tissue development (GO:0031214)	BP	87	82	0.182926829	6.32543E-07
GO:1901214	regulation of neuron death	down	regulation of neuron death (GO:1901214)	BP	137	133	0.127819549	6.34793E-07
GO:2001252	positive regulation of chromosome organization	down	positive regulation of chromosome organization (GO:2001252)	BP	109	107	0.074766355	6.3691E-07
GO:0051057	positive regulation of small GTPase mediated signal transc	down	positive regulation of small GTPase mediated signal transduction (GO:005	BP	29	27	0.111111111	6.59062E-07
GO:0051055	negative regulation of lipid biosynthetic process	down	negative regulation of lipid biosynthetic process (GO:0051055)	BP	35	33	0.212121212	6.64798E-07
GO:1902107	positive regulation of leukocyte differentiation	down	positive regulation of leukocyte differentiation (GO:1902107)	BP	93	89	0.06741573	6.69855E-07
GO:0044091	membrane biogenesis	down	membrane biogenesis (GO:0044091)	BP	22	22	0.272727273	7.02185E-07
GO:0008584	male gonad development	down	male gonad development (GO:0008584)	BP	78	76	0.144736842	7.02372E-07
GO:0046546	development of primary male sexual characteristics	down	development of primary male sexual characteristics (GO:0046546)	BP	78	76	0.144736842	7.02372E-07
GO:0045746	negative regulation of Notch signaling pathway	down	negative regulation of Notch signaling pathway (GO:0045746)	BP	21	19	0.157894737	7.16303E-07
GO:0010560	positive regulation of glycoprotein biosynthetic process	down	positive regulation of glycoprotein biosynthetic process (GO:0010560)	BP	11	11	0.090909091	7.18782E-07
GO:0030517	negative regulation of axon extension	down	negative regulation of axon extension (GO:0030517)	BP	18	18	0.166666667	7.65674E-07
GO:0002260	lymphocyte homeostasis	down	lymphocyte homeostasis (GO:0002260)	BP	52	52	0.076923077	7.87145E-07
GO:0032743	positive regulation of interleukin-2 production	down	positive regulation of interleukin-2 production (GO:0032743)	BP	25	23	0.086956522	7.87629E-07
GO:0045185	maintenance of protein location	down	maintenance of protein location (GO:0045185)	BP	59	58	0.120689655	8.07704E-07
GO:0042119	neutrophil activation	down	neutrophil activation (GO:0042119)	BP	14	13	0.153846154	8.08533E-07
GO:0071674	mononuclear cell migration	down	mononuclear cell migration (GO:0071674)	BP	32	29	0.068965517	8.10798E-07
GO:0070482	response to oxygen levels	down	response to oxygen levels (GO:0070482)	BP	123	122	0.12295082	8.17343E-07
GO:0046883	regulation of hormone secretion	down	regulation of hormone secretion (GO:0046883)	BP	123	120	0.116666667	8.29337E-07
GO:1901985	positive regulation of protein acetylation	down	positive regulation of protein acetylation (GO:1901985)	BP	21	20	0.2	8.54248E-07
GO:2000021	regulation of ion homeostasis	down	regulation of ion homeostasis (GO:2000021)	BP	108	102	0.117647059	8.56734E-07

GO:0099601	regulation of neurotransmitter receptor activity	down	regulation of neurotransmitter receptor activity (GO:0099601)	BP	19	19	0.210526316	8.63822E-07
GO:0010762	regulation of fibroblast migration	down	regulation of fibroblast migration (GO:0010762)	BP	20	19	0.105263158	8.66265E-07
GO:0035336	long-chain fatty-acyl-CoA metabolic process	down	long-chain fatty-acyl-CoA metabolic process (GO:0035336)	BP	11	11	0.181818182	8.76884E-07
GO:2000278	regulation of DNA biosynthetic process	down	regulation of DNA biosynthetic process (GO:2000278)	BP	55	55	0.109090909	8.88636E-07
GO:0060389	pathway-restricted SMAD protein phosphorylation	down	pathway-restricted SMAD protein phosphorylation (GO:0060389)	BP	39	39	0.076923077	8.92869E-07
GO:0033280	response to vitamin D	down	response to vitamin D (GO:0033280)	BP	13	11	0.272727273	9.08711E-07
GO:0003222	ventricular trabecula myocardium morphogenesis	down	ventricular trabecula myocardium morphogenesis (GO:0003222)	BP	15	15	0.066666667	9.14895E-07
GO:1904888	cranial skeletal system development	down	cranial skeletal system development (GO:1904888)	BP	49	48	0.104166667	9.14895E-07
GO:0060571	morphogenesis of an epithelial fold	down	morphogenesis of an epithelial fold (GO:0060571)	BP	20	20	0.15	9.16392E-07
GO:0045686	negative regulation of glial cell differentiation	down	negative regulation of glial cell differentiation (GO:0045686)	BP	12	12	0.083333333	9.23134E-07
GO:1904062	regulation of cation transmembrane transport	down	regulation of cation transmembrane transport (GO:1904062)	BP	139	136	0.132352941	9.40799E-07
GO:0006301	postreplication repair	down	postreplication repair (GO:0006301)	BP	15	14	0.142857143	9.48854E-07
GO:0055017	cardiac muscle tissue growth	down	cardiac muscle tissue growth (GO:0055017)	BP	33	31	0.129032258	9.4956E-07
GO:0060438	trachea development	down	trachea development (GO:0060438)	BP	14	14	0.142857143	1.00961E-06
GO:0035337	fatty-acyl-CoA metabolic process	down	fatty-acyl-CoA metabolic process (GO:0035337)	BP	12	12	0.166666667	1.00964E-06
GO:0030168	platelet activation	down	platelet activation (GO:0030168)	BP	67	65	0.107692308	1.02291E-06
GO:2000105	positive regulation of DNA-dependent DNA replication	down	positive regulation of DNA-dependent DNA replication (GO:2000105)	BP	12	12	0.166666667	1.02851E-06
GO:1905209	positive regulation of cardiocyte differentiation	down	positive regulation of cardiocyte differentiation (GO:1905209)	BP	16	16	0.125	1.03541E-06
GO:0032506	cytokinetic process	down	cytokinetic process (GO:0032506)	BP	12	12	0.333333333	1.04212E-06
GO:0021515	cell differentiation in spinal cord	down	cell differentiation in spinal cord (GO:0021515)	BP	37	36	0.222222222	1.09422E-06
GO:0044843	cell cycle G1/S phase transition	down	cell cycle G1/S phase transition (GO:0044843)	BP	97	93	0.096774194	1.10688E-06
GO:0030516	regulation of axon extension	down	regulation of axon extension (GO:0030516)	BP	41	39	0.128205128	1.11211E-06
GO:0071634	regulation of transforming growth factor beta production	down	regulation of transforming growth factor beta production (GO:0071634)	BP	14	14	0.142857143	1.12589E-06
GO:0051127	positive regulation of actin nucleation	down	positive regulation of actin nucleation (GO:0051127)	BP	10	10	0.2	1.12657E-06
GO:0043627	response to estrogen	down	response to estrogen (GO:0043627)	BP	28	25	0.16	1.12707E-06
GO:0032271	regulation of protein polymerization	down	regulation of protein polymerization (GO:0032271)	BP	105	99	0.121212121	1.1301E-06
GO:0034113	heterotypic cell-cell adhesion	down	heterotypic cell-cell adhesion (GO:0034113)	BP	33	32	0.125	1.13697E-06
GO:0036230	granulocyte activation	down	granulocyte activation (GO:0036230)	BP	15	14	0.142857143	1.13746E-06
GO:0002065	columnar/cuboidal epithelial cell differentiation	down	columnar/cuboidal epithelial cell differentiation (GO:0002065)	BP	83	80	0.125	1.15165E-06
GO:0045619	regulation of lymphocyte differentiation	down	regulation of lymphocyte differentiation (GO:0045619)	BP	96	89	0.112359551	1.16584E-06
GO:0003341	cilium movement	down	cilium movement (GO:0003341)	BP	33	32	0.15625	1.16982E-06
GO:0007193	adenylate cyclase-inhibiting G-protein coupled receptor s	down	adenylate cyclase-inhibiting G-protein coupled receptor signaling pathwa	BP	31	31	0.225806452	1.17616E-06
GO:0030218	erythrocyte differentiation	down	erythrocyte differentiation (GO:0030218)	BP	74	73	0.068493151	1.18012E-06
GO:0055007	cardiac muscle cell differentiation	down	cardiac muscle cell differentiation (GO:0055007)	BP	58	56	0.089285714	1.20737E-06
GO:0018022	peptidyl-lysine methylation	down	peptidyl-lysine methylation (GO:0018022)	BP	79	73	0.082191781	1.21574E-06
GO:0002455	humoral immune response mediated by circulating immu	down	humoral immune response mediated by circulating immunoglobulin (GO	BP	10	10	0.2	1.22948E-06
GO:0032231	regulation of actin filament bundle assembly	down	regulation of actin filament bundle assembly (GO:0032231)	BP	58	56	0.089285714	1.23822E-06
GO:0043537	negative regulation of blood vessel endothelial cell migrat	down	negative regulation of blood vessel endothelial cell migration (GO:00435	BP	18	18	0.111111111	1.24215E-06
GO:0034767	positive regulation of ion transmembrane transport	down	positive regulation of ion transmembrane transport (GO:0034767)	BP	58	56	0.125	1.25513E-06
GO:0008344	adult locomotory behavior	down	adult locomotory behavior (GO:0008344)	BP	63	61	0.131147541	1.26198E-06
GO:1900746	regulation of vascular endothelial growth factor signaling	down	regulation of vascular endothelial growth factor signaling pathway (GO:1	BP	11	11	0.272727273	1.28874E-06
GO:1903522	regulation of blood circulation	down	regulation of blood circulation (GO:1903522)	BP	112	109	0.201834862	1.39531E-06
GO:1904035	regulation of epithelial cell apoptotic process	down	regulation of epithelial cell apoptotic process (GO:1904035)	BP	37	37	0.054054054	1.40196E-06
GO:0051149	positive regulation of muscle cell differentiation	down	positive regulation of muscle cell differentiation (GO:0051149)	BP	53	52	0.115384615	1.41209E-06
GO:1905314	semi-lunar valve development	down	semi-lunar valve development (GO:1905314)	BP	14	14	0.142857143	1.42817E-06
GO:0007204	positive regulation of cytosolic calcium ion concentratio	down	positive regulation of cytosolic calcium ion concentration (GO:0007204)	BP	110	104	0.096153846	1.44453E-06
GO:0061647	histone H3-K9 modification	down	histone H3-K9 modification (GO:0061647)	BP	31	31	0.064516129	1.44632E-06
GO:0032401	establishment of melanosome localization	down	establishment of melanosome localization (GO:0032401)	BP	12	12	0.083333333	1.44757E-06
GO:0032402	melanosome transport	down	melanosome transport (GO:0032402)	BP	12	12	0.083333333	1.44757E-06
GO:0045732	positive regulation of protein catabolic process	down	positive regulation of protein catabolic process (GO:0045732)	BP	110	105	0.133333333	1.48901E-06
GO:0098868	bone growth	down	bone growth (GO:0098868)	BP	19	18	0.166666667	1.51041E-06
GO:0061298	retina vasculature development in camera-type eye	down	retina vasculature development in camera-type eye (GO:0061298)	BP	15	14	0.071428571	1.55071E-06
GO:1901522	positive regulation of transcription from RNA polymerase	down	positive regulation of transcription from RNA polymerase II promoter inv	BP	19	18	0.055555556	1.57118E-06
GO:1903305	regulation of regulated secretory pathway	down	regulation of regulated secretory pathway (GO:1903305)	BP	56	54	0.12962963	1.58924E-06
GO:0098900	regulation of action potential	down	regulation of action potential (GO:0098900)	BP	20	20	0.05	1.66371E-06
GO:0032350	regulation of hormone metabolic process	down	regulation of hormone metabolic process (GO:0032350)	BP	19	19	0.157894737	1.6762E-06
GO:0032102	negative regulation of response to external stimulus	down	negative regulation of response to external stimulus (GO:0032102)	BP	168	160	0.08125	1.68632E-06
GO:0050679	positive regulation of epithelial cell proliferation	down	positive regulation of epithelial cell proliferation (GO:0050679)	BP	100	94	0.095744681	1.69811E-06
GO:0043113	receptor clustering	down	receptor clustering (GO:0043113)	BP	28	28	0.214285714	1.70807E-06
GO:0031110	regulation of microtubule polymerization or depolymeriz	down	regulation of microtubule polymerization or depolymerization (GO:0031	BP	37	36	0.166666667	1.72899E-06
GO:0007129	synapsis	down	synapsis (GO:0007129)	BP	34	32	0.09375	1.74373E-06
GO:0007350	blastoderm segmentation	down	blastoderm segmentation (GO:0007350)	BP	11	11	0.181818182	1.78054E-06
GO:0001776	leukocyte homeostasis	down	leukocyte homeostasis (GO:0001776)	BP	63	63	0.063492063	1.78201E-06
GO:0070372	regulation of ERK1 and ERK2 cascade	down	regulation of ERK1 and ERK2 cascade (GO:0070372)	BP	149	143	0.097902098	1.78963E-06

GO:0021522	spinal cord motor neuron differentiation	down	spinal cord motor neuron differentiation (GO:0021522)	BP	24	24	0.208333333	1.79731E-06
GO:0060413	atrial septum morphogenesis	down	atrial septum morphogenesis (GO:0060413)	BP	13	13	0.307692308	1.79731E-06
GO:1902667	regulation of axon guidance	down	regulation of axon guidance (GO:1902667)	BP	15	15	0.066666667	1.82137E-06
GO:2001235	positive regulation of apoptotic signaling pathway	down	positive regulation of apoptotic signaling pathway (GO:2001235)	BP	120	113	0.115044248	1.83898E-06
GO:0009948	anterior/posterior axis specification	down	anterior/posterior axis specification (GO:0009948)	BP	34	33	0.121212121	1.87402E-06
GO:0010862	positive regulation of pathway-restricted SMAD protein p	down	positive regulation of pathway-restricted SMAD protein phosphorylation	BP	25	25	0.08	1.95582E-06
GO:0071804	cellular potassium ion transport	down	cellular potassium ion transport (GO:0071804)	BP	109	108	0.138888889	2.01291E-06
GO:0071805	potassium ion transmembrane transport	down	potassium ion transmembrane transport (GO:0071805)	BP	109	108	0.138888889	2.01291E-06
GO:0038084	vascular endothelial growth factor signaling pathway	down	vascular endothelial growth factor signaling pathway (GO:0038084)	BP	20	20	0.15	2.0553E-06
GO:0030890	positive regulation of B cell proliferation	down	positive regulation of B cell proliferation (GO:0030890)	BP	28	28	0.035714286	2.08334E-06
GO:0046785	microtubule polymerization	down	microtubule polymerization (GO:0046785)	BP	34	31	0.129032258	2.10428E-06
GO:0014009	glial cell proliferation	down	glial cell proliferation (GO:0014009)	BP	11	11	0.181818182	2.11452E-06
GO:0098727	maintenance of cell number	down	maintenance of cell number (GO:0098727)	BP	101	99	0.121212121	2.18485E-06
GO:0070304	positive regulation of stress-activated protein kinase signa	down	positive regulation of stress-activated protein kinase signaling cascade (G	BP	97	96	0.135416667	2.23608E-06
GO:1903020	positive regulation of glycoprotein metabolic process	down	positive regulation of glycoprotein metabolic process (GO:1903020)	BP	13	13	0.076923077	2.23608E-06
GO:0043488	regulation of mRNA stability	down	regulation of mRNA stability (GO:0043488)	BP	38	38	0.131578947	2.25436E-06
GO:0051053	negative regulation of DNA metabolic process	down	negative regulation of DNA metabolic process (GO:0051053)	BP	80	79	0.037974684	2.27171E-06
GO:0051048	negative regulation of secretion	down	negative regulation of secretion (GO:0051048)	BP	102	101	0.069306931	2.28126E-06
GO:0071542	dopaminergic neuron differentiation	down	dopaminergic neuron differentiation (GO:0071542)	BP	21	20	0.1	2.28597E-06
GO:0010389	regulation of G2/M transition of mitotic cell cycle	down	regulation of G2/M transition of mitotic cell cycle (GO:0010389)	BP	38	36	0.111111111	2.3009E-06
GO:0032400	melanosome localization	down	melanosome localization (GO:0032400)	BP	13	13	0.076923077	2.42759E-06
GO:0048738	cardiac muscle tissue development	down	cardiac muscle tissue development (GO:0048738)	BP	122	119	0.134453782	2.50186E-06
GO:0016482	cytosolic transport	down	cytosolic transport (GO:0016482)	BP	80	80	0.075	2.56E-06
GO:0050805	negative regulation of synaptic transmission	down	negative regulation of synaptic transmission (GO:0050805)	BP	32	32	0.1875	2.64117E-06
GO:0002027	regulation of heart rate	down	regulation of heart rate (GO:0002027)	BP	52	51	0.176470588	2.67261E-06
GO:0006813	potassium ion transport	down	potassium ion transport (GO:0006813)	BP	130	128	0.1328125	2.68339E-06
GO:2001258	negative regulation of cation channel activity	down	negative regulation of cation channel activity (GO:2001258)	BP	14	14	0	2.78609E-06
GO:0030947	regulation of vascular endothelial growth factor receptor	down	regulation of vascular endothelial growth factor receptor signaling pathw	BP	16	15	0.133333333	2.79859E-06
GO:0032874	positive regulation of stress-activated MAPK cascade	down	positive regulation of stress-activated MAPK cascade (GO:0032874)	BP	96	95	0.136842105	2.82653E-06
GO:2000727	positive regulation of cardiac muscle cell differentiation	down	positive regulation of cardiac muscle cell differentiation (GO:2000727)	BP	12	12	0.083333333	2.82981E-06
GO:0045724	positive regulation of cilium assembly	down	positive regulation of cilium assembly (GO:0045724)	BP	14	14	0.071428571	2.95698E-06
GO:0090162	establishment of epithelial cell polarity	down	establishment of epithelial cell polarity (GO:0090162)	BP	18	17	0.117647059	3.04117E-06
GO:2000780	negative regulation of double-strand break repair	down	negative regulation of double-strand break repair (GO:2000780)	BP	11	11	0.090909091	3.07398E-06
GO:0046661	male sex differentiation	down	male sex differentiation (GO:0046661)	BP	95	93	0.129032258	3.08947E-06
GO:0042246	tissue regeneration	down	tissue regeneration (GO:0042246)	BP	21	20	0.15	3.1365E-06
GO:0031529	ruffle organization	down	ruffle organization (GO:0031529)	BP	33	30	0.1	3.14939E-06
GO:0030203	glycosaminoglycan metabolic process	down	glycosaminoglycan metabolic process (GO:0030203)	BP	60	58	0.103448276	3.16587E-06
GO:0016050	vesicle organization	down	vesicle organization (GO:0016050)	BP	121	119	0.075630252	3.18494E-06
GO:0016233	telomere capping	down	telomere capping (GO:0016233)	BP	23	23	0.130434783	3.19228E-06
GO:0051092	positive regulation of NF-kappaB transcription factor acti	down	positive regulation of NF-kappaB transcription factor activity (GO:00510	BP	79	79	0.113924051	3.24261E-06
GO:0000079	regulation of cyclin-dependent protein serine/threonine	down	regulation of cyclin-dependent protein serine/threonine kinase activity (	BP	44	44	0.090909091	3.3096E-06
GO:1904029	regulation of cyclin-dependent protein kinase activity	down	regulation of cyclin-dependent protein kinase activity (GO:1904029)	BP	45	44	0.090909091	3.3096E-06
GO:0051091	positive regulation of DNA binding transcription factor ac	down	positive regulation of DNA binding transcription factor activity (GO:0051	BP	149	149	0.087248322	3.32806E-06
GO:0043392	negative regulation of DNA binding	down	negative regulation of DNA binding (GO:0043392)	BP	27	25	0.12	3.35035E-06
GO:0030316	osteoclast differentiation	down	osteoclast differentiation (GO:0030316)	BP	62	60	0.166666667	3.36778E-06
GO:2000242	negative regulation of reproductive process	down	negative regulation of reproductive process (GO:2000242)	BP	39	39	0.153846154	3.42065E-06
GO:0043154	negative regulation of cysteine-type endopeptidase activit	down	negative regulation of cysteine-type endopeptidase activity involved in a	BP	45	45	0.288888889	3.42588E-06
GO:0003085	negative regulation of systemic arterial blood pressure	down	negative regulation of systemic arterial blood pressure (GO:0003085)	BP	12	12	0.416666667	3.46767E-06
GO:0051966	regulation of synaptic transmission, glutamatergic	down	regulation of synaptic transmission, glutamatergic (GO:0051966)	BP	21	21	0.142857143	3.49068E-06
GO:0007520	myoblast fusion	down	myoblast fusion (GO:0007520)	BP	28	28	0.142857143	3.54893E-06
GO:0009914	hormone transport	down	hormone transport (GO:0009914)	BP	163	160	0.10625	3.5993E-06
GO:0030048	actin filament-based movement	down	actin filament-based movement (GO:0030048)	BP	53	51	0.235294118	3.63307E-06
GO:0045683	negative regulation of epidermis development	down	negative regulation of epidermis development (GO:0045683)	BP	10	10	0.2	3.63307E-06
GO:0055069	zinc ion homeostasis	down	zinc ion homeostasis (GO:0055069)	BP	17	16	0.0625	3.68282E-06
GO:0043536	positive regulation of blood vessel endothelial cell migrat	down	positive regulation of blood vessel endothelial cell migration (GO:00435	BP	16	16	0.125	3.70195E-06
GO:0008625	extrinsic apoptotic signaling pathway via death domain r	down	extrinsic apoptotic signaling pathway via death domain receptors (GO:00	BP	60	56	0.125	3.70685E-06
GO:0050871	positive regulation of B cell activation	down	positive regulation of B cell activation (GO:0050871)	BP	50	50	0.04	3.75101E-06
GO:0032456	endocytic recycling	down	endocytic recycling (GO:0032456)	BP	25	25	0.12	3.80637E-06
GO:0045061	thymic T cell selection	down	thymic T cell selection (GO:0045061)	BP	18	17	0.117647059	3.90802E-06
GO:0043624	cellular protein complex disassembly	down	cellular protein complex disassembly (GO:0043624)	BP	68	63	0.19047619	3.93122E-06
GO:0043516	regulation of DNA damage response, signal transduction b	down	regulation of DNA damage response, signal transduction by p53 class me	BP	22	22	0.181818182	3.9613E-06
GO:0071168	protein localization to chromatin	down	protein localization to chromatin (GO:0071168)	BP	13	11	0.363636364	3.97901E-06
GO:0098751	bone cell development	down	bone cell development (GO:0098751)	BP	26	25	0.08	3.97901E-06
GO:0034764	positive regulation of transmembrane transport	down	positive regulation of transmembrane transport (GO:0034764)	BP	62	59	0.118644068	4.04767E-06

GO:0048745	smooth muscle tissue development	down	smooth muscle tissue development (GO:0048745)	BP	19	19	0.157894737	4.11154E-06
GO:0032623	interleukin-2 production	down	interleukin-2 production (GO:0032623)	BP	42	39	0.051282051	4.19527E-06
GO:0010469	regulation of receptor activity	down	regulation of receptor activity (GO:0010469)	BP	61	60	0.133333333	4.19918E-06
GO:0045494	photoreceptor cell maintenance	down	photoreceptor cell maintenance (GO:0045494)	BP	23	22	0.136363636	4.29107E-06
GO:0010569	regulation of double-strand break repair via homologous	down	regulation of double-strand break repair via homologous recombination	BP	16	16	0.1875	4.2935E-06
GO:2000573	positive regulation of DNA biosynthetic process	down	positive regulation of DNA biosynthetic process (GO:2000573)	BP	37	37	0.135135135	4.2935E-06
GO:1904064	positive regulation of cation transmembrane transport	down	positive regulation of cation transmembrane transport (GO:1904064)	BP	52	51	0.137254902	4.35686E-06
GO:2001022	positive regulation of response to DNA damage stimulus	down	positive regulation of response to DNA damage stimulus (GO:2001022)	BP	47	47	0.127659574	4.40783E-06
GO:0070555	response to interleukin-1	down	response to interleukin-1 (GO:0070555)	BP	53	52	0.153846154	4.40862E-06
GO:0006687	glycosphingolipid metabolic process	down	glycosphingolipid metabolic process (GO:0006687)	BP	20	20	0.2	4.45454E-06
GO:0007030	Golgi organization	down	Golgi organization (GO:0007030)	BP	59	58	0.103448276	4.54621E-06
GO:0033138	positive regulation of peptidyl-serine phosphorylation	down	positive regulation of peptidyl-serine phosphorylation (GO:0033138)	BP	51	49	0.102040816	4.56445E-06
GO:0097305	response to alcohol	down	response to alcohol (GO:0097305)	BP	54	54	0.12962963	4.65441E-06
GO:0000723	telomere maintenance	down	telomere maintenance (GO:0000723)	BP	68	65	0.076923077	4.91132E-06
GO:0032200	telomere organization	down	telomere organization (GO:0032200)	BP	68	65	0.076923077	4.91132E-06
GO:0051924	regulation of calcium ion transport	down	regulation of calcium ion transport (GO:0051924)	BP	105	101	0.069306931	4.9389E-06
GO:0043687	post-translational protein modification	down	post-translational protein modification (GO:0043687)	BP	11	10	0.1	5.2008E-06
GO:2000107	negative regulation of leukocyte apoptotic process	down	negative regulation of leukocyte apoptotic process (GO:2000107)	BP	32	31	0.064516129	5.29128E-06
GO:0050798	activated T cell proliferation	down	activated T cell proliferation (GO:0050798)	BP	28	27	0.148148148	5.29458E-06
GO:2000117	negative regulation of cysteine-type endopeptidase activit	down	negative regulation of cysteine-type endopeptidase activity (GO:2000117	BP	46	46	0.282608696	5.37518E-06
GO:0020027	hemoglobin metabolic process	down	hemoglobin metabolic process (GO:0020027)	BP	13	13	0.230769231	5.45788E-06
GO:0061337	cardiac conduction	down	cardiac conduction (GO:0061337)	BP	38	38	0.131578947	5.47012E-06
GO:0030219	megakaryocyte differentiation	down	megakaryocyte differentiation (GO:0030219)	BP	29	24	0.041666667	5.49205E-06
GO:0050796	regulation of insulin secretion	down	regulation of insulin secretion (GO:0050796)	BP	73	72	0.097222222	5.52524E-06
GO:0030833	regulation of actin filament polymerization	down	regulation of actin filament polymerization (GO:0030833)	BP	86	81	0.135802469	5.6194E-06
GO:0019827	stem cell population maintenance	down	stem cell population maintenance (GO:0019827)	BP	100	98	0.112244898	5.64176E-06
GO:0030497	fatty acid elongation	down	fatty acid elongation (GO:0030497)	BP	10	10	0	5.66011E-06
GO:0042761	very long-chain fatty acid biosynthetic process	down	very long-chain fatty acid biosynthetic process (GO:0042761)	BP	10	10	0	5.66011E-06
GO:0014812	muscle cell migration	down	muscle cell migration (GO:0014812)	BP	37	36	0.138888889	5.66479E-06
GO:1904357	negative regulation of telomere maintenance via telomere	down	negative regulation of telomere maintenance via telomere lengthening (G	BP	10	10	0.1	5.70051E-06
GO:0043491	protein kinase B signaling	down	protein kinase B signaling (GO:0043491)	BP	108	103	0.087378641	5.73936E-06
GO:0055117	regulation of cardiac muscle contraction	down	regulation of cardiac muscle contraction (GO:0055117)	BP	33	32	0.125	5.82295E-06
GO:1903900	regulation of viral life cycle	down	regulation of viral life cycle (GO:1903900)	BP	85	81	0.086419753	5.8299E-06
GO:0010800	positive regulation of peptidyl-threonine phosphorylatio	down	positive regulation of peptidyl-threonine phosphorylation (GO:0010800	BP	17	16	0.125	6.02409E-06
GO:0060393	regulation of pathway-restricted SMAD protein phosphor	down	regulation of pathway-restricted SMAD protein phosphorylation (GO:006	BP	35	35	0.057142857	6.05813E-06
GO:0070734	histone H3-K27 methylation	down	histone H3-K27 methylation (GO:0070734)	BP	14	11	0.181818182	6.16761E-06
GO:0010669	epithelial structure maintenance	down	epithelial structure maintenance (GO:0010669)	BP	15	15	0.133333333	6.25637E-06
GO:0051208	sequestering of calcium ion	down	sequestering of calcium ion (GO:0051208)	BP	64	61	0.098360656	6.52199E-06
GO:0035066	positive regulation of histone acetylation	down	positive regulation of histone acetylation (GO:0035066)	BP	18	18	0.222222222	6.6041E-06
GO:2000758	positive regulation of peptidyl-lysine acetylation	down	positive regulation of peptidyl-lysine acetylation (GO:2000758)	BP	18	18	0.222222222	6.6041E-06
GO:0021680	cerebellar Purkinje cell layer development	down	cerebellar Purkinje cell layer development (GO:0021680)	BP	25	22	0.181818182	6.70391E-06
GO:0050775	positive regulation of dendrite morphogenesis	down	positive regulation of dendrite morphogenesis (GO:0050775)	BP	13	13	0.230769231	6.70688E-06
GO:0008154	actin polymerization or depolymerization	down	actin polymerization or depolymerization (GO:0008154)	BP	111	105	0.133333333	6.75531E-06
GO:0046879	hormone secretion	down	hormone secretion (GO:0046879)	BP	157	154	0.103896104	7.02484E-06
GO:0090382	phagosome maturation	down	phagosome maturation (GO:0090382)	BP	12	12	0.166666667	7.05085E-06
GO:0051224	negative regulation of protein transport	down	negative regulation of protein transport (GO:0051224)	BP	137	135	0.088888889	7.05449E-06
GO:0030511	positive regulation of transforming growth factor beta rec	down	positive regulation of transforming growth factor beta receptor signaling	BP	16	16	0.125	7.29191E-06
GO:1903846	positive regulation of cellular response to transforming gr	down	positive regulation of cellular response to transforming growth factor bet	BP	16	16	0.125	7.29191E-06
GO:0010737	protein kinase A signaling	down	protein kinase A signaling (GO:0010737)	BP	14	13	0.230769231	7.29683E-06
GO:0051489	regulation of filopodium assembly	down	regulation of filopodium assembly (GO:0051489)	BP	24	23	0.130434783	7.47447E-06
GO:0032103	positive regulation of response to external stimulus	down	positive regulation of response to external stimulus (GO:0032103)	BP	150	143	0.090909091	7.54966E-06
GO:0032528	microvillus organization	down	microvillus organization (GO:0032528)	BP	18	17	0.235294118	7.64148E-06
GO:0060045	positive regulation of cardiac muscle cell proliferation	down	positive regulation of cardiac muscle cell proliferation (GO:0060045)	BP	16	16	0.125	7.6421E-06
GO:0072148	epithelial cell fate commitment	down	epithelial cell fate commitment (GO:0072148)	BP	12	12	0.166666667	7.71571E-06
GO:0048679	regulation of axon regeneration	down	regulation of axon regeneration (GO:0048679)	BP	12	12	0.166666667	7.76475E-06
GO:0070570	regulation of neuron projection regeneration	down	regulation of neuron projection regeneration (GO:0070570)	BP	12	12	0.166666667	7.76475E-06
GO:0031503	protein complex localization	down	protein complex localization (GO:0031503)	BP	66	65	0.076923077	7.8006E-06
GO:0086001	cardiac muscle cell action potential	down	cardiac muscle cell action potential (GO:0086001)	BP	28	28	0.178571429	7.81089E-06
GO:1901215	negative regulation of neuron death	down	negative regulation of neuron death (GO:1901215)	BP	102	99	0.121212121	7.81089E-06
GO:0045646	regulation of erythrocyte differentiation	down	regulation of erythrocyte differentiation (GO:0045646)	BP	27	27	0.074074074	7.84374E-06
GO:0001539	cilium or flagellum-dependent cell motility	down	cilium or flagellum-dependent cell motility (GO:0001539)	BP	11	11	0.090909091	7.87562E-06
GO:0097529	myeloid leukocyte migration	down	myeloid leukocyte migration (GO:0097529)	BP	97	89	0.078651685	8.00865E-06
GO:0051642	centrosome localization	down	centrosome localization (GO:0051642)	BP	18	18	0.222222222	8.05131E-06
GO:0061842	microtubule organizing center localization	down	microtubule organizing center localization (GO:0061842)	BP	18	18	0.222222222	8.05131E-06

GO:1904950	negative regulation of establishment of protein localizati	down	negative regulation of establishment of protein localization (GO:190495	BP	139	137	0.087591241	8.21351E-06
GO:0035637	multicellular organismal signaling	down	multicellular organismal signaling (GO:0035637)	BP	69	69	0.115942029	8.21879E-06
GO:0097152	mesenchymal cell apoptotic process	down	mesenchymal cell apoptotic process (GO:0097152)	BP	10	10	0.1	8.24783E-06
GO:1905475	regulation of protein localization to membrane	down	regulation of protein localization to membrane (GO:1905475)	BP	44	42	0.095238095	8.27323E-06
GO:0001570	vasculogenesis	down	vasculogenesis (GO:0001570)	BP	48	47	0.106382979	8.47898E-06
GO:0032228	regulation of synaptic transmission, GABAergic	down	regulation of synaptic transmission, GABAergic (GO:0032228)	BP	16	15	0.066666667	8.73479E-06
GO:0044331	cell-cell adhesion mediated by cadherin	down	cell-cell adhesion mediated by cadherin (GO:0044331)	BP	10	10	0.1	8.87288E-06
GO:1903649	regulation of cytoplasmic transport	down	regulation of cytoplasmic transport (GO:1903649)	BP	10	10	0.2	8.89985E-06
GO:0048193	Golgi vesicle transport	down	Golgi vesicle transport (GO:0048193)	BP	127	125	0.04	8.93325E-06
GO:0090049	regulation of cell migration involved in sprouting angioge	down	regulation of cell migration involved in sprouting angiogenesis (GO:0090	BP	15	15	0.066666667	8.93718E-06
GO:0061013	regulation of mRNA catabolic process	down	regulation of mRNA catabolic process (GO:0061013)	BP	53	53	0.113207547	9.02171E-06
GO:0007601	visual perception	down	visual perception (GO:0007601)	BP	94	91	0.10989011	9.16096E-06
GO:0044773	mitotic DNA damage checkpoint	down	mitotic DNA damage checkpoint (GO:0044773)	BP	28	27	0.037037037	9.39919E-06
GO:0048259	regulation of receptor-mediated endocytosis	down	regulation of receptor-mediated endocytosis (GO:0048259)	BP	47	47	0.085106383	9.64905E-06
GO:0045580	regulation of T cell differentiation	down	regulation of T cell differentiation (GO:0045580)	BP	75	69	0.115942029	9.66783E-06
GO:0014909	smooth muscle cell migration	down	smooth muscle cell migration (GO:0014909)	BP	27	26	0.115384615	1.03381E-05
GO:0021520	spinal cord motor neuron cell fate specification	down	spinal cord motor neuron cell fate specification (GO:0021520)	BP	10	10	0.3	1.05492E-05
GO:0051148	negative regulation of muscle cell differentiation	down	negative regulation of muscle cell differentiation (GO:0051148)	BP	43	43	0.279069767	1.05616E-05
GO:0050953	sensory perception of light stimulus	down	sensory perception of light stimulus (GO:0050953)	BP	99	95	0.115789474	1.07588E-05
GO:0051984	positive regulation of chromosome segregation	down	positive regulation of chromosome segregation (GO:0051984)	BP	14	13	0.153846154	1.0793E-05
GO:0048167	regulation of synaptic plasticity	down	regulation of synaptic plasticity (GO:0048167)	BP	81	80	0.1	1.07965E-05
GO:0042133	neurotransmitter metabolic process	down	neurotransmitter metabolic process (GO:0042133)	BP	12	12	0.166666667	1.09306E-05
GO:0007187	G-protein coupled receptor signaling pathway, coupled t	down	G-protein coupled receptor signaling pathway, coupled to cyclic nucleoti	BP	74	73	0.150684932	1.10064E-05
GO:0017157	regulation of exocytosis	down	regulation of exocytosis (GO:0017157)	BP	95	92	0.086956522	1.10064E-05
GO:0051146	striated muscle cell differentiation	down	striated muscle cell differentiation (GO:0051146)	BP	154	151	0.125827815	1.10919E-05
GO:0044818	mitotic G2/M transition checkpoint	down	mitotic G2/M transition checkpoint (GO:0044818)	BP	13	13	0.076923077	1.10923E-05
GO:0010002	cardioblast differentiation	down	cardioblast differentiation (GO:0010002)	BP	14	14	0.142857143	1.12726E-05
GO:0048663	neuron fate commitment	down	neuron fate commitment (GO:0048663)	BP	47	46	0.195652174	1.12989E-05
GO:0003254	regulation of membrane depolarization	down	regulation of membrane depolarization (GO:0003254)	BP	27	25	0.24	1.14787E-05
GO:0046330	positive regulation of JNK cascade	down	positive regulation of JNK cascade (GO:0046330)	BP	82	81	0.12345679	1.14879E-05
GO:0060419	heart growth	down	heart growth (GO:0060419)	BP	36	34	0.147058824	1.16827E-05
GO:1902745	positive regulation of lamellipodium organization	down	positive regulation of lamellipodium organization (GO:1902745)	BP	18	16	0.1875	1.17424E-05
GO:0034101	erythrocyte homeostasis	down	erythrocyte homeostasis (GO:0034101)	BP	81	80	0.075	1.17497E-05
GO:0034698	response to gonadotropin	down	response to gonadotropin (GO:0034698)	BP	10	10	0.1	1.19422E-05
GO:0072395	signal transduction involved in cell cycle checkpoint	down	signal transduction involved in cell cycle checkpoint (GO:0072395)	BP	12	11	0.090909091	1.19829E-05
GO:0008064	regulation of actin polymerization or depolymerization	down	regulation of actin polymerization or depolymerization (GO:0008064)	BP	97	92	0.130434783	1.20078E-05
GO:0030832	regulation of actin filament length	down	regulation of actin filament length (GO:0030832)	BP	97	92	0.130434783	1.20078E-05
GO:0060579	ventral spinal cord interneuron fate commitment	down	ventral spinal cord interneuron fate commitment (GO:0060579)	BP	12	11	0.454545455	1.21972E-05
GO:0060581	cell fate commitment involved in pattern specification	down	cell fate commitment involved in pattern specification (GO:0060581)	BP	12	11	0.454545455	1.21972E-05
GO:0010959	regulation of metal ion transport	down	regulation of metal ion transport (GO:0010959)	BP	172	167	0.095808383	1.22098E-05
GO:0051932	synaptic transmission, GABAergic	down	synaptic transmission, GABAergic (GO:0051932)	BP	19	18	0.055555556	1.22158E-05
GO:0006022	aminoglycan metabolic process	down	aminoglycan metabolic process (GO:0006022)	BP	69	66	0.090909091	1.22658E-05
GO:0043901	negative regulation of multi-organism process	down	negative regulation of multi-organism process (GO:0043901)	BP	93	89	0.06741573	1.24367E-05
GO:0030217	T cell differentiation	down	T cell differentiation (GO:0030217)	BP	153	147	0.068027211	1.25015E-05
GO:0007612	learning	down	learning (GO:0007612)	BP	85	84	0.142857143	1.25274E-05
GO:0034110	regulation of homotypic cell-cell adhesion	down	regulation of homotypic cell-cell adhesion (GO:0034110)	BP	17	17	0.117647059	1.26617E-05
GO:0002066	columnar/cuboidal epithelial cell development	down	columnar/cuboidal epithelial cell development (GO:0002066)	BP	44	44	0.159090909	1.29295E-05
GO:0035455	response to interferon-alpha	down	response to interferon-alpha (GO:0035455)	BP	12	12	0	1.29406E-05
GO:0010935	regulation of macrophage cytokine production	down	regulation of macrophage cytokine production (GO:0010935)	BP	10	10	0.2	1.32941E-05
GO:0030593	neutrophil chemotaxis	down	neutrophil chemotaxis (GO:0030593)	BP	42	39	0.076923077	1.32941E-05
GO:0021517	ventral spinal cord development	down	ventral spinal cord development (GO:0021517)	BP	35	34	0.235294118	1.36696E-05
GO:0006346	methylation-dependent chromatin silencing	down	methylation-dependent chromatin silencing (GO:0006346)	BP	10	10	0.1	1.38404E-05
GO:0014855	striated muscle cell proliferation	down	striated muscle cell proliferation (GO:0014855)	BP	35	33	0.151515152	1.38939E-05
GO:0036465	synaptic vesicle recycling	down	synaptic vesicle recycling (GO:0036465)	BP	11	11	0.181818182	1.39186E-05
GO:1903510	mucopolysaccharide metabolic process	down	mucopolysaccharide metabolic process (GO:1903510)	BP	38	37	0.108108108	1.39487E-05
GO:0032613	interleukin-10 production	down	interleukin-10 production (GO:0032613)	BP	31	30	0.133333333	1.39623E-05
GO:0003018	vascular process in circulatory system	down	vascular process in circulatory system (GO:0003018)	BP	65	65	0.123076923	1.41181E-05
GO:0060999	positive regulation of dendritic spine development	down	positive regulation of dendritic spine development (GO:0060999)	BP	14	14	0.214285714	1.41364E-05
GO:0061318	renal filtration cell differentiation	down	renal filtration cell differentiation (GO:0061318)	BP	12	12	0.333333333	1.41947E-05
GO:0072112	glomerular visceral epithelial cell differentiation	down	glomerular visceral epithelial cell differentiation (GO:0072112)	BP	12	12	0.333333333	1.41947E-05
GO:0072503	cellular divalent inorganic cation homeostasis	down	cellular divalent inorganic cation homeostasis (GO:0072503)	BP	197	188	0.111702128	1.42516E-05
GO:0003208	cardiac ventricle morphogenesis	down	cardiac ventricle morphogenesis (GO:0003208)	BP	52	51	0.176470588	1.4547E-05
GO:0048266	behavioral response to pain	down	behavioral response to pain (GO:0048266)	BP	10	10	0.3	1.47195E-05
GO:0030041	actin filament polymerization	down	actin filament polymerization (GO:0030041)	BP	93	87	0.126436782	1.53408E-05

GO:0060325	face morphogenesis	down	face morphogenesis (GO:0060325)	BP	25	25	0.2	1.54478E-05
GO:0050900	leukocyte migration	down	leukocyte migration (GO:0050900)	BP	179	166	0.078313253	1.56087E-05
GO:0032878	regulation of establishment or maintenance of cell polarit	down	regulation of establishment or maintenance of cell polarity (GO:0032878	BP	16	16	0.1875	1.57361E-05
GO:0061178	regulation of insulin secretion involved in cellular respons	down	regulation of insulin secretion involved in cellular response to glucose sti	BP	29	29	0.103448276	1.62225E-05
GO:0007528	neuromuscular junction development	down	neuromuscular junction development (GO:0007528)	BP	27	27	0.222222222	1.6251E-05
GO:0048260	positive regulation of receptor-mediated endocytosis	down	positive regulation of receptor-mediated endocytosis (GO:0048260)	BP	30	30	0.066666667	1.6251E-05
GO:1903509	liposaccharide metabolic process	down	liposaccharide metabolic process (GO:1903509)	BP	46	46	0.086956522	1.68224E-05
GO:0014911	positive regulation of smooth muscle cell migration	down	positive regulation of smooth muscle cell migration (GO:0014911)	BP	10	10	0.2	1.68603E-05
GO:0010035	response to inorganic substance	down	response to inorganic substance (GO:0010035)	BP	175	167	0.101796407	1.69595E-05
GO:1901550	regulation of endothelial cell development	down	regulation of endothelial cell development (GO:1901550)	BP	10	10	0.2	1.70465E-05
GO:1903140	regulation of establishment of endothelial barrier	down	regulation of establishment of endothelial barrier (GO:1903140)	BP	10	10	0.2	1.70465E-05
GO:0003417	growth plate cartilage development	down	growth plate cartilage development (GO:0003417)	BP	12	12	0.25	1.73299E-05
GO:0046209	nitric oxide metabolic process	down	nitric oxide metabolic process (GO:0046209)	BP	30	28	0.178571429	1.75285E-05
GO:1902230	negative regulation of intrinsic apoptotic signaling pathw	down	negative regulation of intrinsic apoptotic signaling pathway in response t	BP	18	18	0.277777778	1.7899E-05
GO:0006939	smooth muscle contraction	down	smooth muscle contraction (GO:0006939)	BP	54	53	0.132075472	1.79473E-05
GO:1905517	macrophage migration	down	macrophage migration (GO:1905517)	BP	20	18	0.166666667	1.8031E-05
GO:0046849	bone remodeling	down	bone remodeling (GO:0046849)	BP	54	53	0.188679245	1.80714E-05
GO:0070206	protein trimerization	down	protein trimerization (GO:0070206)	BP	22	22	0.318181818	1.81453E-05
GO:0031032	actomyosin structure organization	down	actomyosin structure organization (GO:0031032)	BP	108	105	0.114285714	1.81825E-05
GO:0048665	neuron fate specification	down	neuron fate specification (GO:0048665)	BP	24	23	0.217391304	1.83788E-05
GO:0038127	ERBB signaling pathway	down	ERBB signaling pathway (GO:0038127)	BP	66	66	0.106060606	1.84176E-05
GO:0032273	positive regulation of protein polymerization	down	positive regulation of protein polymerization (GO:0032273)	BP	69	63	0.142857143	1.84211E-05
GO:0051573	negative regulation of histone H3-K9 methylation	down	negative regulation of histone H3-K9 methylation (GO:0051573)	BP	10	10	0.2	1.86752E-05
GO:0006304	DNA modification	down	DNA modification (GO:0006304)	BP	51	50	0.06	1.89468E-05
GO:1990266	neutrophil migration	down	neutrophil migration (GO:1990266)	BP	48	45	0.066666667	1.89468E-05
GO:0090630	activation of GTPase activity	down	activation of GTPase activity (GO:0090630)	BP	24	24	0.083333333	1.92747E-05
GO:0045738	negative regulation of DNA repair	down	negative regulation of DNA repair (GO:0045738)	BP	12	12	0.083333333	1.93027E-05
GO:0022408	negative regulation of cell-cell adhesion	down	negative regulation of cell-cell adhesion (GO:0022408)	BP	89	85	0.070588235	1.98172E-05
GO:0014074	response to purine-containing compound	down	response to purine-containing compound (GO:0014074)	BP	48	48	0.125	2.0404E-05
GO:0051668	localization within membrane	down	localization within membrane (GO:0051668)	BP	46	46	0.173913043	2.0404E-05
GO:2001057	reactive nitrogen species metabolic process	down	reactive nitrogen species metabolic process (GO:2001057)	BP	33	29	0.172413793	2.0404E-05
GO:0071347	cellular response to interleukin-1	down	cellular response to interleukin-1 (GO:0071347)	BP	41	40	0.15	2.05116E-05
GO:2000725	regulation of cardiac muscle cell differentiation	down	regulation of cardiac muscle cell differentiation (GO:2000725)	BP	15	15	0.066666667	2.07351E-05
GO:0003073	regulation of systemic arterial blood pressure	down	regulation of systemic arterial blood pressure (GO:0003073)	BP	51	50	0.2	2.07444E-05
GO:0030073	insulin secretion	down	insulin secretion (GO:0030073)	BP	92	91	0.098901099	2.07444E-05
GO:0031952	regulation of protein autophosphorylation	down	regulation of protein autophosphorylation (GO:0031952)	BP	23	21	0.095238095	2.08095E-05
GO:0032392	DNA geometric change	down	DNA geometric change (GO:0032392)	BP	24	22	0.090909091	2.10181E-05
GO:0086091	regulation of heart rate by cardiac conduction	down	regulation of heart rate by cardiac conduction (GO:0086091)	BP	22	22	0.136363636	2.10503E-05
GO:0061384	heart trabecula morphogenesis	down	heart trabecula morphogenesis (GO:0061384)	BP	24	24	0.083333333	2.11595E-05
GO:0035249	synaptic transmission, glutamatergic	down	synaptic transmission, glutamatergic (GO:0035249)	BP	34	34	0.117647059	2.1831E-05
GO:0072657	protein localization to membrane	down	protein localization to membrane (GO:0072657)	BP	182	175	0.125714286	2.19965E-05
GO:2000106	regulation of leukocyte apoptotic process	down	regulation of leukocyte apoptotic process (GO:2000106)	BP	54	53	0.075471698	2.20986E-05
GO:0021514	ventral spinal cord interneuron differentiation	down	ventral spinal cord interneuron differentiation (GO:0021514)	BP	13	12	0.416666667	2.22881E-05
GO:0051899	membrane depolarization	down	membrane depolarization (GO:0051899)	BP	42	39	0.179487179	2.22909E-05
GO:0097530	granulocyte migration	down	granulocyte migration (GO:0097530)	BP	62	58	0.068965517	2.23291E-05
GO:0051495	positive regulation of cytoskeleton organization	down	positive regulation of cytoskeleton organization (GO:0051495)	BP	119	112	0.107142857	2.2998E-05
GO:0051282	regulation of sequestering of calcium ion	down	regulation of sequestering of calcium ion (GO:0051282)	BP	63	60	0.1	2.30081E-05
GO:1903169	regulation of calcium ion transmembrane transport	down	regulation of calcium ion transmembrane transport (GO:1903169)	BP	60	58	0.103448276	2.32795E-05
GO:0044246	regulation of multicellular organismal metabolic process	down	regulation of multicellular organismal metabolic process (GO:0044246)	BP	13	13	0.076923077	2.33264E-05
GO:0035024	negative regulation of Rho protein signal transduction	down	negative regulation of Rho protein signal transduction (GO:0035024)	BP	13	13	0.230769231	2.33724E-05
GO:0090276	regulation of peptide hormone secretion	down	regulation of peptide hormone secretion (GO:0090276)	BP	91	89	0.08988764	2.34E-05
GO:0051438	regulation of ubiquitin-protein transferase activity	down	regulation of ubiquitin-protein transferase activity (GO:0051438)	BP	27	27	0.148148148	2.3473E-05
GO:0010712	regulation of collagen metabolic process	down	regulation of collagen metabolic process (GO:0010712)	BP	12	12	0.083333333	2.49007E-05
GO:0060415	muscle tissue morphogenesis	down	muscle tissue morphogenesis (GO:0060415)	BP	57	56	0.232142857	2.4932E-05
GO:0071621	granulocyte chemotaxis	down	granulocyte chemotaxis (GO:0071621)	BP	55	51	0.078431373	2.54083E-05
GO:0006644	phospholipid metabolic process	down	phospholipid metabolic process (GO:0006644)	BP	196	191	0.047120419	2.57726E-05
GO:0060323	head morphogenesis	down	head morphogenesis (GO:0060323)	BP	28	28	0.178571429	2.57726E-05
GO:0072659	protein localization to plasma membrane	down	protein localization to plasma membrane (GO:0072659)	BP	77	74	0.108108108	2.58479E-05
GO:1903034	regulation of response to wounding	down	regulation of response to wounding (GO:1903034)	BP	98	97	0.072164948	2.58479E-05
GO:1902807	negative regulation of cell cycle G1/S phase transition	down	negative regulation of cell cycle G1/S phase transition (GO:1902807)	BP	29	27	0.111111111	2.63016E-05
GO:0003416	endochondral bone growth	down	endochondral bone growth (GO:0003416)	BP	17	16	0.1875	2.68907E-05
GO:0048255	mRNA stabilization	down	mRNA stabilization (GO:0048255)	BP	18	18	0.166666667	2.68907E-05
GO:0060004	reflex	down	reflex (GO:0060004)	BP	19	18	0.277777778	2.75615E-05
GO:0006470	protein dephosphorylation	down	protein dephosphorylation (GO:0006470)	BP	172	169	0.124260355	2.93093E-05

GO:0032091	negative regulation of protein binding	down	negative regulation of protein binding (GO:0032091)	BP	62	59	0.152542373	2.96265E-05
GO:0003016	respiratory system process	down	respiratory system process (GO:0003016)	BP	21	20	0.25	2.97701E-05
GO:0043487	regulation of RNA stability	down	regulation of RNA stability (GO:0043487)	BP	41	41	0.12195122	2.97991E-05
GO:0006809	nitric oxide biosynthetic process	down	nitric oxide biosynthetic process (GO:0006809)	BP	29	27	0.185185185	3.02303E-05
GO:0060038	cardiac muscle cell proliferation	down	cardiac muscle cell proliferation (GO:0060038)	BP	28	26	0.115384615	3.09048E-05
GO:0055021	regulation of cardiac muscle tissue growth	down	regulation of cardiac muscle tissue growth (GO:0055021)	BP	26	26	0.115384615	3.10277E-05
GO:0070168	negative regulation of biomineral tissue development	down	negative regulation of biomineral tissue development (GO:0070168)	BP	15	13	0.153846154	3.26572E-05
GO:0007040	lysosome organization	down	lysosome organization (GO:0007040)	BP	36	36	0.111111111	3.38449E-05
GO:0080171	lytic vacuole organization	down	lytic vacuole organization (GO:0080171)	BP	36	36	0.111111111	3.38449E-05
GO:0032409	regulation of transporter activity	down	regulation of transporter activity (GO:0032409)	BP	108	105	0.133333333	3.43236E-05
GO:0046847	filopodium assembly	down	filopodium assembly (GO:0046847)	BP	29	28	0.142857143	3.5081E-05
GO:1902017	regulation of cilium assembly	down	regulation of cilium assembly (GO:1902017)	BP	26	26	0.038461538	3.50868E-05
GO:0045638	negative regulation of myeloid cell differentiation	down	negative regulation of myeloid cell differentiation (GO:0045638)	BP	46	42	0.119047619	3.53921E-05
GO:0072010	glomerular epithelium development	down	glomerular epithelium development (GO:0072010)	BP	14	14	0.285714286	3.64818E-05
GO:1902905	positive regulation of supramolecular fiber organization	down	positive regulation of supramolecular fiber organization (GO:1902905)	BP	107	100	0.11	3.66143E-05
GO:2000811	negative regulation of anoikis	down	negative regulation of anoikis (GO:2000811)	BP	12	11	0.363636364	3.69515E-05
GO:0051209	release of sequestered calcium ion into cytosol	down	release of sequestered calcium ion into cytosol (GO:0051209)	BP	62	59	0.101694915	3.71427E-05
GO:0051283	negative regulation of sequestering of calcium ion	down	negative regulation of sequestering of calcium ion (GO:0051283)	BP	62	59	0.101694915	3.71427E-05
GO:0097553	calcium ion transmembrane import into cytosol	down	calcium ion transmembrane import into cytosol (GO:0097553)	BP	62	59	0.101694915	3.71427E-05
GO:0030879	mammary gland development	down	mammary gland development (GO:0030879)	BP	85	83	0.144578313	3.71483E-05
GO:0030656	regulation of vitamin metabolic process	down	regulation of vitamin metabolic process (GO:0030656)	BP	11	10	0.2	3.77869E-05
GO:0001702	gastrulation with mouth forming second	down	gastrulation with mouth forming second (GO:0001702)	BP	21	21	0.142857143	3.78743E-05
GO:2000810	regulation of bicellular tight junction assembly	down	regulation of bicellular tight junction assembly (GO:2000810)	BP	11	11	0.272727273	3.79263E-05
GO:0010038	response to metal ion	down	response to metal ion (GO:0010038)	BP	104	99	0.090909091	3.80217E-05
GO:0071260	cellular response to mechanical stimulus	down	cellular response to mechanical stimulus (GO:0071260)	BP	36	36	0.083333333	3.82029E-05
GO:0046636	negative regulation of alpha-beta T cell activation	down	negative regulation of alpha-beta T cell activation (GO:0046636)	BP	11	11	0.181818182	3.84605E-05
GO:0001936	regulation of endothelial cell proliferation	down	regulation of endothelial cell proliferation (GO:0001936)	BP	62	59	0.13559322	3.86329E-05
GO:0046006	regulation of activated T cell proliferation	down	regulation of activated T cell proliferation (GO:0046006)	BP	24	23	0.173913043	3.87083E-05
GO:0032205	negative regulation of telomere maintenance	down	negative regulation of telomere maintenance (GO:0032205)	BP	18	18	0.055555556	3.88056E-05
GO:0048596	embryonic camera-type eye morphogenesis	down	embryonic camera-type eye morphogenesis (GO:0048596)	BP	20	20	0.15	3.89326E-05
GO:0070228	regulation of lymphocyte apoptotic process	down	regulation of lymphocyte apoptotic process (GO:0070228)	BP	38	37	0.108108108	3.90077E-05
GO:1902229	regulation of intrinsic apoptotic signaling pathway in resp	down	regulation of intrinsic apoptotic signaling pathway in response to DNA da	BP	25	25	0.2	3.91448E-05
GO:0045806	negative regulation of endocytosis	down	negative regulation of endocytosis (GO:0045806)	BP	27	25	0.16	3.91905E-05
GO:0030888	regulation of B cell proliferation	down	regulation of B cell proliferation (GO:0030888)	BP	40	40	0.025	3.99879E-05
GO:0021516	dorsal spinal cord development	down	dorsal spinal cord development (GO:0021516)	BP	13	12	0.166666667	4.02634E-05
GO:0050851	antigen receptor-mediated signaling pathway	down	antigen receptor-mediated signaling pathway (GO:0050851)	BP	81	77	0.064935065	4.0572E-05
GO:0045747	positive regulation of Notch signaling pathway	down	positive regulation of Notch signaling pathway (GO:0045747)	BP	23	21	0.142857143	4.07458E-05
GO:0045823	positive regulation of heart contraction	down	positive regulation of heart contraction (GO:0045823)	BP	19	19	0.157894737	4.08714E-05
GO:0032438	melanosome organization	down	melanosome organization (GO:0032438)	BP	11	11	0.090909091	4.0885E-05
GO:0048753	pigment granule organization	down	pigment granule organization (GO:0048753)	BP	11	11	0.090909091	4.0885E-05
GO:1990778	protein localization to cell periphery	down	protein localization to cell periphery (GO:1990778)	BP	82	79	0.101265823	4.133E-05
GO:0008016	regulation of heart contraction	down	regulation of heart contraction (GO:0008016)	BP	95	93	0.215053763	4.19245E-05
GO:0031061	negative regulation of histone methylation	down	negative regulation of histone methylation (GO:0031061)	BP	17	16	0.125	4.19245E-05
GO:1903707	negative regulation of hemopoiesis	down	negative regulation of hemopoiesis (GO:1903707)	BP	75	68	0.102941176	4.21067E-05
GO:0009913	epidermal cell differentiation	down	epidermal cell differentiation (GO:0009913)	BP	108	100	0.12	4.25816E-05
GO:0046718	viral entry into host cell	down	viral entry into host cell (GO:0046718)	BP	31	27	0.111111111	4.25816E-05
GO:0090036	regulation of protein kinase C signaling	down	regulation of protein kinase C signaling (GO:0090036)	BP	12	12	0.166666667	4.31766E-05
GO:1905331	negative regulation of morphogenesis of an epithelium	down	negative regulation of morphogenesis of an epithelium (GO:1905331)	BP	13	13	0.153846154	4.35177E-05
GO:0021561	facial nerve development	down	facial nerve development (GO:0021561)	BP	10	10	0.1	4.39788E-05
GO:0021610	facial nerve morphogenesis	down	facial nerve morphogenesis (GO:0021610)	BP	10	10	0.1	4.39788E-05
GO:0040036	regulation of fibroblast growth factor receptor signaling p	down	regulation of fibroblast growth factor receptor signaling pathway (GO:00	BP	20	18	0.111111111	4.39802E-05
GO:0042104	positive regulation of activated T cell proliferation	down	positive regulation of activated T cell proliferation (GO:0042104)	BP	17	17	0.235294118	4.48645E-05
GO:0050850	positive regulation of calcium-mediated signaling	down	positive regulation of calcium-mediated signaling (GO:0050850)	BP	22	19	0.157894737	4.51669E-05
GO:1902106	negative regulation of leukocyte differentiation	down	negative regulation of leukocyte differentiation (GO:1902106)	BP	49	46	0.130434783	4.54688E-05
GO:0046683	response to organophosphorus	down	response to organophosphorus (GO:0046683)	BP	47	47	0.127659574	4.70427E-05
GO:0071901	negative regulation of protein serine/threonine kinase act	down	negative regulation of protein serine/threonine kinase activity (GO:0071	BP	80	77	0.064935065	4.70754E-05
GO:0052548	regulation of endopeptidase activity	down	regulation of endopeptidase activity (GO:0052548)	BP	186	177	0.152542373	4.72591E-05
GO:0032411	positive regulation of transporter activity	down	positive regulation of transporter activity (GO:0032411)	BP	36	35	0.114285714	4.75893E-05
GO:0061028	establishment of endothelial barrier	down	establishment of endothelial barrier (GO:0061028)	BP	27	26	0.076923077	4.78722E-05
GO:0071320	cellular response to cAMP	down	cellular response to cAMP (GO:0071320)	BP	22	22	0.136363636	4.78845E-05
GO:0007140	male meiotic nuclear division	down	male meiotic nuclear division (GO:0007140)	BP	28	26	0.115384615	4.79728E-05
GO:1903428	positive regulation of reactive oxygen species biosyntheti	down	positive regulation of reactive oxygen species biosynthetic process (GO:1	BP	20	18	0.111111111	4.79728E-05
GO:0006692	prostanoid metabolic process	down	prostanoid metabolic process (GO:0006692)	BP	18	18	0.222222222	4.85298E-05
GO:0006693	prostaglandin metabolic process	down	prostaglandin metabolic process (GO:0006693)	BP	18	18	0.222222222	4.85298E-05

GO:0030838	positive regulation of actin filament polymerization	down	positive regulation of actin filament polymerization (GO:0030838)	BP	59	54	0.148148148	4.85668E-05
GO:0031334	positive regulation of protein complex assembly	down	positive regulation of protein complex assembly (GO:0031334)	BP	125	116	0.146551724	4.8726E-05
GO:0060444	branching involved in mammary gland duct morphogene	down	branching involved in mammary gland duct morphogenesis (GO:006044	BP	22	20	0.05	4.89365E-05
GO:0070374	positive regulation of ERK1 and ERK2 cascade	down	positive regulation of ERK1 and ERK2 cascade (GO:0070374)	BP	102	97	0.082474227	4.91197E-05
GO:1902806	regulation of cell cycle G1/S phase transition	down	regulation of cell cycle G1/S phase transition (GO:1902806)	BP	59	56	0.071428571	5.0081E-05
GO:0051155	positive regulation of striated muscle cell differentiation	down	positive regulation of striated muscle cell differentiation (GO:0051155)	BP	41	40	0.075	5.01733E-05
GO:0060324	face development	down	face development (GO:0060324)	BP	42	42	0.19047619	5.03248E-05
GO:0002768	immune response-regulating cell surface receptor signalin	down	immune response-regulating cell surface receptor signaling pathway (GO:	BP	96	91	0.054945055	5.1705E-05
GO:0007286	spermatid development	down	spermatid development (GO:0007286)	BP	91	84	0.095238095	5.233E-05
GO:0001937	negative regulation of endothelial cell proliferation	down	negative regulation of endothelial cell proliferation (GO:0001937)	BP	24	23	0.217391304	5.23844E-05
GO:0050727	regulation of inflammatory response	down	regulation of inflammatory response (GO:0050727)	BP	165	161	0.080745342	5.24224E-05
GO:0002763	positive regulation of myeloid leukocyte differentiation	down	positive regulation of myeloid leukocyte differentiation (GO:0002763)	BP	38	36	0.055555556	5.26775E-05
GO:0051570	regulation of histone H3-K9 methylation	down	regulation of histone H3-K9 methylation (GO:0051570)	BP	16	16	0.125	5.29951E-05
GO:0001818	negative regulation of cytokine production	down	negative regulation of cytokine production (GO:0001818)	BP	137	131	0.076335878	5.30012E-05
GO:0048639	positive regulation of developmental growth	down	positive regulation of developmental growth (GO:0048639)	BP	106	103	0.13592233	5.31936E-05
GO:0048489	synaptic vesicle transport	down	synaptic vesicle transport (GO:0048489)	BP	50	50	0.14	5.33026E-05
GO:0097480	establishment of synaptic vesicle localization	down	establishment of synaptic vesicle localization (GO:0097480)	BP	50	50	0.14	5.33026E-05
GO:0099003	vesicle-mediated transport in synapse	down	vesicle-mediated transport in synapse (GO:0099003)	BP	50	50	0.14	5.33026E-05
GO:0019058	viral life cycle	down	viral life cycle (GO:0019058)	BP	123	115	0.069565217	5.44339E-05
GO:0060039	pericardium development	down	pericardium development (GO:0060039)	BP	15	15	0.066666667	5.45131E-05
GO:0060402	calcium ion transport into cytosol	down	calcium ion transport into cytosol (GO:0060402)	BP	70	66	0.090909091	5.48429E-05
GO:0000041	transition metal ion transport	down	transition metal ion transport (GO:0000041)	BP	39	35	0.085714286	5.5282E-05
GO:0042953	lipoprotein transport	down	lipoprotein transport (GO:0042953)	BP	10	10	0.1	5.59442E-05
GO:0044872	lipoprotein localization	down	lipoprotein localization (GO:0044872)	BP	10	10	0.1	5.59442E-05
GO:0001990	regulation of systemic arterial blood pressure by hormon	down	regulation of systemic arterial blood pressure by hormone (GO:0001990)	BP	26	25	0.16	5.65913E-05
GO:0032480	negative regulation of type I interferon production	down	negative regulation of type I interferon production (GO:0032480)	BP	10	10	0.1	5.65913E-05
GO:1902750	negative regulation of cell cycle G2/M phase transition	down	negative regulation of cell cycle G2/M phase transition (GO:1902750)	BP	18	17	0.058823529	5.74796E-05
GO:0030307	positive regulation of cell growth	down	positive regulation of cell growth (GO:0030307)	BP	85	84	0.130952381	5.7628E-05
GO:0034314	Arp2/3 complex-mediated actin nucleation	down	Arp2/3 complex-mediated actin nucleation (GO:0034314)	BP	20	20	0.2	5.87819E-05
GO:0030072	peptide hormone secretion	down	peptide hormone secretion (GO:0030072)	BP	121	119	0.092436975	5.91113E-05
GO:0007569	cell aging	down	cell aging (GO:0007569)	BP	63	62	0.080645161	5.93476E-05
GO:0050810	regulation of steroid biosynthetic process	down	regulation of steroid biosynthetic process (GO:0050810)	BP	39	37	0.135135135	5.94852E-05
GO:0033559	unsaturated fatty acid metabolic process	down	unsaturated fatty acid metabolic process (GO:0033559)	BP	35	33	0.151515152	6.04202E-05
GO:0008306	associative learning	down	associative learning (GO:0008306)	BP	51	51	0.137254902	6.14903E-05
GO:0030260	entry into host cell	down	entry into host cell (GO:0030260)	BP	34	30	0.1	6.23687E-05
GO:0044409	entry into host	down	entry into host (GO:0044409)	BP	34	30	0.1	6.23687E-05
GO:0051806	entry into cell of other organism involved in symbiotic int	down	entry into cell of other organism involved in symbiotic interaction (GO:0	BP	34	30	0.1	6.23687E-05
GO:0051828	entry into other organism involved in symbiotic interacti	down	entry into other organism involved in symbiotic interaction (GO:005182	BP	34	30	0.1	6.23687E-05
GO:0014910	regulation of smooth muscle cell migration	down	regulation of smooth muscle cell migration (GO:0014910)	BP	23	22	0.136363636	6.27654E-05
GO:0060479	lung cell differentiation	down	lung cell differentiation (GO:0060479)	BP	23	22	0.227272727	6.31802E-05
GO:0045076	regulation of interleukin-2 biosynthetic process	down	regulation of interleukin-2 biosynthetic process (GO:0045076)	BP	12	12	0.083333333	6.37691E-05
GO:0006664	glycolipid metabolic process	down	glycolipid metabolic process (GO:0006664)	BP	45	45	0.088888889	6.3841E-05
GO:0006814	sodium ion transport	down	sodium ion transport (GO:0006814)	BP	102	100	0.19	6.55389E-05
GO:0043551	regulation of phosphatidylinositol 3-kinase activity	down	regulation of phosphatidylinositol 3-kinase activity (GO:0043551)	BP	26	26	0	6.56018E-05
GO:0030502	negative regulation of bone mineralization	down	negative regulation of bone mineralization (GO:0030502)	BP	13	11	0.090909091	6.56542E-05
GO:0060421	positive regulation of heart growth	down	positive regulation of heart growth (GO:0060421)	BP	20	20	0.2	6.68967E-05
GO:0051480	regulation of cytosolic calcium ion concentration	down	regulation of cytosolic calcium ion concentration (GO:0051480)	BP	120	114	0.087719298	6.71021E-05
GO:0050792	regulation of viral process	down	regulation of viral process (GO:0050792)	BP	108	103	0.067961165	6.735E-05
GO:0007050	cell cycle arrest	down	cell cycle arrest (GO:0007050)	BP	79	75	0.106666667	6.74803E-05
GO:0033135	regulation of peptidyl-serine phosphorylation	down	regulation of peptidyl-serine phosphorylation (GO:0033135)	BP	75	71	0.126760563	6.85547E-05
GO:0048873	homeostasis of number of cells within a tissue	down	homeostasis of number of cells within a tissue (GO:0048873)	BP	28	28	0.107142857	6.9698E-05
GO:0043029	T cell homeostasis	down	T cell homeostasis (GO:0043029)	BP	32	32	0.125	7.00557E-05
GO:0000018	regulation of DNA recombination	down	regulation of DNA recombination (GO:0000018)	BP	48	48	0.083333333	7.09997E-05
GO:1901976	regulation of cell cycle checkpoint	down	regulation of cell cycle checkpoint (GO:1901976)	BP	24	24	0.083333333	7.10263E-05
GO:0032635	interleukin-6 production	down	interleukin-6 production (GO:0032635)	BP	86	84	0.05952381	7.15481E-05
GO:0006636	unsaturated fatty acid biosynthetic process	down	unsaturated fatty acid biosynthetic process (GO:0006636)	BP	24	23	0.173913043	7.19835E-05
GO:0032781	positive regulation of ATPase activity	down	positive regulation of ATPase activity (GO:0032781)	BP	17	16	0.1875	7.37011E-05
GO:0033688	regulation of osteoblast proliferation	down	regulation of osteoblast proliferation (GO:0033688)	BP	17	17	0.235294118	7.38652E-05
GO:0008037	cell recognition	down	cell recognition (GO:0008037)	BP	63	63	0.111111111	7.46582E-05
GO:0072311	glomerular epithelial cell differentiation	down	glomerular epithelial cell differentiation (GO:0072311)	BP	13	13	0.307692308	7.75081E-05
GO:0046823	negative regulation of nucleocytoplasmic transport	down	negative regulation of nucleocytoplasmic transport (GO:0046823)	BP	54	53	0.113207547	7.85114E-05
GO:1903828	negative regulation of cellular protein localization	down	negative regulation of cellular protein localization (GO:1903828)	BP	93	91	0.098901099	7.88022E-05
GO:0036294	cellular response to decreased oxygen levels	down	cellular response to decreased oxygen levels (GO:0036294)	BP	55	54	0.092592593	7.94972E-05
GO:0071456	cellular response to hypoxia	down	cellular response to hypoxia (GO:0071456)	BP	55	54	0.092592593	7.94972E-05

GO:0048644	muscle organ morphogenesis	down	muscle organ morphogenesis (GO:0048644)	BP	62	61	0.213114754	8.00495E-05
GO:0048486	parasympathetic nervous system development	down	parasympathetic nervous system development (GO:0048486)	BP	14	14	0.071428571	8.04492E-05
GO:0003156	regulation of animal organ formation	down	regulation of animal organ formation (GO:0003156)	BP	27	27	0.111111111	8.0704E-05
GO:0035235	ionotropic glutamate receptor signaling pathway	down	ionotropic glutamate receptor signaling pathway (GO:0035235)	BP	12	12	0.166666667	8.07175E-05
GO:0033690	positive regulation of osteoblast proliferation	down	positive regulation of osteoblast proliferation (GO:0033690)	BP	11	11	0.272727273	8.1189E-05
GO:0030183	B cell differentiation	down	B cell differentiation (GO:0030183)	BP	68	66	0.121212121	8.2579E-05
GO:0030852	regulation of granulocyte differentiation	down	regulation of granulocyte differentiation (GO:0030852)	BP	14	14	0.071428571	8.31286E-05
GO:0002792	negative regulation of peptide secretion	down	negative regulation of peptide secretion (GO:0002792)	BP	71	70	0.071428571	8.33896E-05
GO:0002335	mature B cell differentiation	down	mature B cell differentiation (GO:0002335)	BP	17	17	0.176470588	8.35574E-05
GO:0032897	negative regulation of viral transcription	down	negative regulation of viral transcription (GO:0032897)	BP	15	15	0.066666667	8.42701E-05
GO:0035561	regulation of chromatin binding	down	regulation of chromatin binding (GO:0035561)	BP	12	12	0.083333333	8.52658E-05
GO:0001710	mesodermal cell fate commitment	down	mesodermal cell fate commitment (GO:0001710)	BP	11	11	0.181818182	8.54888E-05
GO:0048701	embryonic cranial skeleton morphogenesis	down	embryonic cranial skeleton morphogenesis (GO:0048701)	BP	40	39	0.076923077	8.6076E-05
GO:0043403	skeletal muscle tissue regeneration	down	skeletal muscle tissue regeneration (GO:0043403)	BP	16	15	0.133333333	8.67548E-05
GO:0042308	negative regulation of protein import into nucleus	down	negative regulation of protein import into nucleus (GO:0042308)	BP	46	46	0.108695652	8.80721E-05
GO:1904590	negative regulation of protein import	down	negative regulation of protein import (GO:1904590)	BP	46	46	0.108695652	8.80721E-05
GO:0048515	spermatid differentiation	down	spermatid differentiation (GO:0048515)	BP	94	87	0.114942529	8.83159E-05
GO:0042772	DNA damage response, signal transduction resulting in tra	down	DNA damage response, signal transduction resulting in transcription (GO:	BP	13	11	0.090909091	8.84076E-05
GO:0060850	regulation of transcription involved in cell fate commitm	down	regulation of transcription involved in cell fate commitment (GO:006085	BP	10	10	0.1	8.86307E-05
GO:0032508	DNA duplex unwinding	down	DNA duplex unwinding (GO:0032508)	BP	20	18	0.111111111	9.11934E-05
GO:2000243	positive regulation of reproductive process	down	positive regulation of reproductive process (GO:2000243)	BP	33	32	0.09375	9.29521E-05
GO:0003014	renal system process	down	renal system process (GO:0003014)	BP	48	46	0.152173913	9.37036E-05
GO:2000279	negative regulation of DNA biosynthetic process	down	negative regulation of DNA biosynthetic process (GO:2000279)	BP	18	18	0.055555556	9.45091E-05
GO:0031111	negative regulation of microtubule polymerization or dep	down	negative regulation of microtubule polymerization or depolymerization (	BP	18	18	0.166666667	9.55821E-05
GO:0002262	myeloid cell homeostasis	down	myeloid cell homeostasis (GO:0002262)	BP	94	93	0.075268817	9.77985E-05
GO:0002429	immune response-activating cell surface receptor signalin	down	immune response-activating cell surface receptor signaling pathway (GO:	BP	89	84	0.05952381	9.87318E-05
GO:0006978	DNA damage response, signal transduction by p53 class m	down	DNA damage response, signal transduction by p53 class mediator resultin	BP	12	10	0.1	0.000102785
GO:0043279	response to alkaloid	down	response to alkaloid (GO:0043279)	BP	27	27	0.111111111	0.000104323
GO:0071453	cellular response to oxygen levels	down	cellular response to oxygen levels (GO:0071453)	BP	61	60	0.083333333	0.000105874
GO:0034260	negative regulation of GTPase activity	down	negative regulation of GTPase activity (GO:0034260)	BP	20	18	0.111111111	0.000106075
GO:0051447	negative regulation of meiotic cell cycle	down	negative regulation of meiotic cell cycle (GO:0051447)	BP	11	11	0.090909091	0.000107243
GO:0009595	detection of biotic stimulus	down	detection of biotic stimulus (GO:0009595)	BP	18	17	0.176470588	0.000107847
GO:0051592	response to calcium ion	down	response to calcium ion (GO:0051592)	BP	54	52	0.076923077	0.000108995
GO:0006874	cellular calcium ion homeostasis	down	cellular calcium ion homeostasis (GO:0006874)	BP	181	173	0.115606936	0.000109324
GO:1900078	positive regulation of cellular response to insulin stimulu	down	positive regulation of cellular response to insulin stimulus (GO:1900078)	BP	15	15	0.133333333	0.000109324
GO:0043267	negative regulation of potassium ion transport	down	negative regulation of potassium ion transport (GO:0043267)	BP	16	16	0.125	0.000109443
GO:0050880	regulation of blood vessel size	down	regulation of blood vessel size (GO:0050880)	BP	53	53	0.132075472	0.000109443
GO:0007605	sensory perception of sound	down	sensory perception of sound (GO:0007605)	BP	89	87	0.149425287	0.000110423
GO:0060487	lung epithelial cell differentiation	down	lung epithelial cell differentiation (GO:0060487)	BP	22	21	0.238095238	0.000111816
GO:0042220	response to cocaine	down	response to cocaine (GO:0042220)	BP	13	13	0.153846154	0.000112127
GO:0030225	macrophage differentiation	down	macrophage differentiation (GO:0030225)	BP	21	21	0.095238095	0.000112158
GO:0050954	sensory perception of mechanical stimulus	down	sensory perception of mechanical stimulus (GO:0050954)	BP	98	96	0.135416667	0.000115358
GO:0010665	regulation of cardiac muscle cell apoptotic process	down	regulation of cardiac muscle cell apoptotic process (GO:0010665)	BP	10	10	0.1	0.000116005
GO:0010543	regulation of platelet activation	down	regulation of platelet activation (GO:0010543)	BP	22	21	0.095238095	0.00011621
GO:0042698	ovulation cycle	down	ovulation cycle (GO:0042698)	BP	47	46	0.130434783	0.000116532
GO:0032490	detection of molecule of bacterial origin	down	detection of molecule of bacterial origin (GO:0032490)	BP	10	10	0.2	0.000117305
GO:0046717	acid secretion	down	acid secretion (GO:0046717)	BP	34	34	0.117647059	0.000117671
GO:0007188	adenylate cyclase-modulating G-protein coupled recepto	down	adenylate cyclase-modulating G-protein coupled receptor signaling path	BP	72	71	0.14084507	0.000117683
GO:0043954	cellular component maintenance	down	cellular component maintenance (GO:0043954)	BP	18	16	0.1875	0.000118716
GO:0070301	cellular response to hydrogen peroxide	down	cellular response to hydrogen peroxide (GO:0070301)	BP	40	38	0.184210526	0.000118716
GO:0010799	regulation of peptidyl-threonine phosphorylation	down	regulation of peptidyl-threonine phosphorylation (GO:0010799)	BP	24	22	0.136363636	0.0001191
GO:0001508	action potential	down	action potential (GO:0001508)	BP	56	56	0.125	0.000121145
GO:0008156	negative regulation of DNA replication	down	negative regulation of DNA replication (GO:0008156)	BP	27	27	0.037037037	0.000123016
GO:0000245	spliceosomal complex assembly	down	spliceosomal complex assembly (GO:0000245)	BP	23	23	0.043478261	0.000123619
GO:0048291	isotype switching to IgG isotypes	down	isotype switching to IgG isotypes (GO:0048291)	BP	10	10	0	0.000124294
GO:0050709	negative regulation of protein secretion	down	negative regulation of protein secretion (GO:0050709)	BP	68	67	0.074626866	0.000124294
GO:1905521	regulation of macrophage migration	down	regulation of macrophage migration (GO:1905521)	BP	13	13	0.153846154	0.0001252
GO:0031670	cellular response to nutrient	down	cellular response to nutrient (GO:0031670)	BP	14	13	0.230769231	0.000128182
GO:0060788	ectodermal placode formation	down	ectodermal placode formation (GO:0060788)	BP	11	10	0.2	0.000128182
GO:0071697	ectodermal placode morphogenesis	down	ectodermal placode morphogenesis (GO:0071697)	BP	11	10	0.2	0.000128182
GO:0050848	regulation of calcium-mediated signaling	down	regulation of calcium-mediated signaling (GO:0050848)	BP	42	38	0.157894737	0.000128821
GO:1903531	negative regulation of secretion by cell	down	negative regulation of secretion by cell (GO:1903531)	BP	94	93	0.064516129	0.000130644
GO:0035019	somatic stem cell population maintenance	down	somatic stem cell population maintenance (GO:0035019)	BP	32	31	0.129032258	0.000131427
GO:0035335	peptidyl-tyrosine dephosphorylation	down	peptidyl-tyrosine dephosphorylation (GO:0035335)	BP	62	61	0.163934426	0.000131427

GO:0046635	positive regulation of alpha-beta T cell activation	down	positive regulation of alpha-beta T cell activation (GO:0046635)	BP	34	33	0.060606061	0.000131427
GO:0010575	positive regulation of vascular endothelial growth factor p	down	positive regulation of vascular endothelial growth factor production (GO:	BP	21	20	0.15	0.000131783
GO:0055006	cardiac cell development	down	cardiac cell development (GO:0055006)	BP	33	33	0.151515152	0.000132155
GO:0007173	epidermal growth factor receptor signaling pathway	down	epidermal growth factor receptor signaling pathway (GO:0007173)	BP	58	58	0.103448276	0.000132222
GO:0051865	protein autoubiquitination	down	protein autoubiquitination (GO:0051865)	BP	40	40	0.125	0.00013226
GO:0001840	neural plate development	down	neural plate development (GO:0001840)	BP	11	11	0.090909091	0.000132299
GO:1903725	regulation of phospholipid metabolic process	down	regulation of phospholipid metabolic process (GO:1903725)	BP	40	38	0.052631579	0.000134248
GO:0030500	regulation of bone mineralization	down	regulation of bone mineralization (GO:0030500)	BP	53	50	0.16	0.000137342
GO:0045582	positive regulation of T cell differentiation	down	positive regulation of T cell differentiation (GO:0045582)	BP	44	42	0.095238095	0.00013872
GO:0006910	phagocytosis, recognition	down	phagocytosis, recognition (GO:0006910)	BP	10	10	0.1	0.000140202
GO:0046887	positive regulation of hormone secretion	down	positive regulation of hormone secretion (GO:0046887)	BP	56	56	0.107142857	0.000141139
GO:0022617	extracellular matrix disassembly	down	extracellular matrix disassembly (GO:0022617)	BP	23	20	0.3	0.000142481
GO:0031348	negative regulation of defense response	down	negative regulation of defense response (GO:0031348)	BP	99	93	0.064516129	0.00014291
GO:0035886	vascular smooth muscle cell differentiation	down	vascular smooth muscle cell differentiation (GO:0035886)	BP	13	13	0.076923077	0.00014291
GO:0070229	negative regulation of lymphocyte apoptotic process	down	negative regulation of lymphocyte apoptotic process (GO:0070229)	BP	22	21	0.095238095	0.000144888
GO:0045927	positive regulation of growth	down	positive regulation of growth (GO:0045927)	BP	153	150	0.12	0.000147211
GO:2000351	regulation of endothelial cell apoptotic process	down	regulation of endothelial cell apoptotic process (GO:2000351)	BP	29	29	0.034482759	0.000147327
GO:0031128	developmental induction	down	developmental induction (GO:0031128)	BP	26	26	0.153846154	0.000148321
GO:1902275	regulation of chromatin organization	down	regulation of chromatin organization (GO:1902275)	BP	108	106	0.066037736	0.000149013
GO:0046637	regulation of alpha-beta T cell differentiation	down	regulation of alpha-beta T cell differentiation (GO:0046637)	BP	32	31	0.096774194	0.00015105
GO:0043271	negative regulation of ion transport	down	negative regulation of ion transport (GO:0043271)	BP	49	49	0.102040816	0.000152259
GO:0002762	negative regulation of myeloid leukocyte differentiation	down	negative regulation of myeloid leukocyte differentiation (GO:0002762)	BP	23	23	0.130434783	0.000153131
GO:0046660	female sex differentiation	down	female sex differentiation (GO:0046660)	BP	71	70	0.1	0.000153195
GO:0060612	adipose tissue development	down	adipose tissue development (GO:0060612)	BP	23	23	0.217391304	0.000153272
GO:0071696	ectodermal placode development	down	ectodermal placode development (GO:0071696)	BP	12	11	0.181818182	0.000153668
GO:0001894	tissue homeostasis	down	tissue homeostasis (GO:0001894)	BP	139	134	0.104477612	0.000153922
GO:0021879	forebrain neuron differentiation	down	forebrain neuron differentiation (GO:0021879)	BP	38	36	0.111111111	0.000154154
GO:0040037	negative regulation of fibroblast growth factor receptor si	down	negative regulation of fibroblast growth factor receptor signaling pathwa	BP	11	10	0.1	0.000154154
GO:0048246	macrophage chemotaxis	down	macrophage chemotaxis (GO:0048246)	BP	19	17	0.117647059	0.000154239
GO:0019722	calcium-mediated signaling	down	calcium-mediated signaling (GO:0019722)	BP	86	81	0.12345679	0.000155417
GO:0031018	endocrine pancreas development	down	endocrine pancreas development (GO:0031018)	BP	29	29	0.103448276	0.000155417
GO:0050817	coagulation	down	coagulation (GO:0050817)	BP	124	120	0.091666667	0.00015586
GO:0051354	negative regulation of oxidoreductase activity	down	negative regulation of oxidoreductase activity (GO:0051354)	BP	12	9	0.222222222	0.000157358
GO:0021670	lateral ventricle development	down	lateral ventricle development (GO:0021670)	BP	10	10	0.3	0.000160483
GO:0034605	cellular response to heat	down	cellular response to heat (GO:0034605)	BP	24	22	0.045454545	0.000166442
GO:0055074	calcium ion homeostasis	down	calcium ion homeostasis (GO:0055074)	BP	191	182	0.120879121	0.000166732
GO:0032945	negative regulation of mononuclear cell proliferation	down	negative regulation of mononuclear cell proliferation (GO:0032945)	BP	38	36	0.027777778	0.000168142
GO:0050672	negative regulation of lymphocyte proliferation	down	negative regulation of lymphocyte proliferation (GO:0050672)	BP	38	36	0.027777778	0.000168142
GO:0070664	negative regulation of leukocyte proliferation	down	negative regulation of leukocyte proliferation (GO:0070664)	BP	38	36	0.027777778	0.000168142
GO:1900015	regulation of cytokine production involved in inflammato	down	regulation of cytokine production involved in inflammatory response (GO	BP	18	17	0.176470588	0.000168142
GO:0007596	blood coagulation	down	blood coagulation (GO:0007596)	BP	120	116	0.094827586	0.000168492
GO:2001259	positive regulation of cation channel activity	down	positive regulation of cation channel activity (GO:2001259)	BP	18	18	0.111111111	0.000171503
GO:0045428	regulation of nitric oxide biosynthetic process	down	regulation of nitric oxide biosynthetic process (GO:0045428)	BP	22	21	0.142857143	0.000171696
GO:0045833	negative regulation of lipid metabolic process	down	negative regulation of lipid metabolic process (GO:0045833)	BP	52	49	0.204081633	0.000174523
GO:0036158	outer dynein arm assembly	down	outer dynein arm assembly (GO:0036158)	BP	10	10	0.1	0.000174857
GO:0003159	morphogenesis of an endothelium	down	morphogenesis of an endothelium (GO:0003159)	BP	13	13	0.153846154	0.00017561
GO:0061154	endothelial tube morphogenesis	down	endothelial tube morphogenesis (GO:0061154)	BP	13	13	0.153846154	0.00017561
GO:0003323	type B pancreatic cell development	down	type B pancreatic cell development (GO:0003323)	BP	14	14	0.142857143	0.000183936
GO:0032436	positive regulation of proteasomal ubiquitin-dependent p	down	positive regulation of proteasomal ubiquitin-dependent protein cataboli	BP	37	34	0.176470588	0.000186601
GO:0032414	positive regulation of ion transmembrane transporter act	down	positive regulation of ion transmembrane transporter activity (GO:00324	BP	31	30	0.1	0.000188765
GO:0002714	positive regulation of B cell mediated immunity	down	positive regulation of B cell mediated immunity (GO:0002714)	BP	26	25	0.08	0.0001903
GO:0002891	positive regulation of immunoglobulin mediated immune	down	positive regulation of immunoglobulin mediated immune response (GO:0	BP	26	25	0.08	0.0001903
GO:0006479	protein methylation	down	protein methylation (GO:0006479)	BP	121	114	0.070175439	0.0001903
GO:0008213	protein alkylation	down	protein alkylation (GO:0008213)	BP	121	114	0.070175439	0.0001903
GO:0046189	phenol-containing compound biosynthetic process	down	phenol-containing compound biosynthetic process (GO:0046189)	BP	23	23	0.217391304	0.000193629
GO:2000136	regulation of cell proliferation involved in heart morphog	down	regulation of cell proliferation involved in heart morphogenesis (GO:200	BP	13	13	0.076923077	0.000196447
GO:0032653	regulation of interleukin-10 production	down	regulation of interleukin-10 production (GO:0032653)	BP	28	27	0.111111111	0.000197616
GO:0001881	receptor recycling	down	receptor recycling (GO:0001881)	BP	20	19	0.210526316	0.000198292
GO:0032412	regulation of ion transmembrane transporter activity	down	regulation of ion transmembrane transporter activity (GO:0032412)	BP	97	94	0.127659574	0.000199467
GO:1903038	negative regulation of leukocyte cell-cell adhesion	down	negative regulation of leukocyte cell-cell adhesion (GO:1903038)	BP	61	58	0.051724138	0.000199467
GO:0010092	specification of animal organ identity	down	specification of animal organ identity (GO:0010092)	BP	25	25	0.16	0.000200927
GO:0051220	cytoplasmic sequestering of protein	down	cytoplasmic sequestering of protein (GO:0051220)	BP	17	17	0.117647059	0.000200927
GO:0019083	viral transcription	down	viral transcription (GO:0019083)	BP	29	29	0.034482759	0.000201218
GO:0045671	negative regulation of osteoclast differentiation	down	negative regulation of osteoclast differentiation (GO:0045671)	BP	13	13	0.230769231	0.000201266

GO:2000045	regulation of G1/S transition of mitotic cell cycle	down	regulation of G1/S transition of mitotic cell cycle (GO:2000045)	BP	52	51	0.058823529	0.000208535
GO:0006672	ceramide metabolic process	down	ceramide metabolic process (GO:0006672)	BP	43	43	0.093023256	0.000209476
GO:2000269	regulation of fibroblast apoptotic process	down	regulation of fibroblast apoptotic process (GO:2000269)	BP	13	13	0.153846154	0.000210083
GO:0072577	endothelial cell apoptotic process	down	endothelial cell apoptotic process (GO:0072577)	BP	32	32	0.03125	0.000210958
GO:0070167	regulation of biomineral tissue development	down	regulation of biomineral tissue development (GO:0070167)	BP	59	56	0.160714286	0.000212303
GO:0051928	positive regulation of calcium ion transport	down	positive regulation of calcium ion transport (GO:0051928)	BP	56	54	0.074074074	0.000214423
GO:0006694	steroid biosynthetic process	down	steroid biosynthetic process (GO:0006694)	BP	71	66	0.090909091	0.00021526
GO:0007599	hemostasis	down	hemostasis (GO:0007599)	BP	122	118	0.093220339	0.00021526
GO:0040034	regulation of development, heterochronic	down	regulation of development, heterochronic (GO:0040034)	BP	12	11	0.090909091	0.000219801
GO:0048505	regulation of timing of cell differentiation	down	regulation of timing of cell differentiation (GO:0048505)	BP	12	11	0.090909091	0.000219801
GO:0090317	negative regulation of intracellular protein transport	down	negative regulation of intracellular protein transport (GO:0090317)	BP	67	66	0.106060606	0.000221067
GO:0002685	regulation of leukocyte migration	down	regulation of leukocyte migration (GO:0002685)	BP	95	89	0.123595506	0.000221754
GO:0045648	positive regulation of erythrocyte differentiation	down	positive regulation of erythrocyte differentiation (GO:0045648)	BP	18	18	0.111111111	0.000224715
GO:0035773	insulin secretion involved in cellular response to glucose s	down	insulin secretion involved in cellular response to glucose stimulus (GO:00	BP	32	32	0.125	0.000228264
GO:0033687	osteoblast proliferation	down	osteoblast proliferation (GO:0033687)	BP	19	19	0.210526316	0.000229688
GO:0002312	B cell activation involved in immune response	down	B cell activation involved in immune response (GO:0002312)	BP	53	53	0.094339623	0.000229922
GO:0009187	cyclic nucleotide metabolic process	down	cyclic nucleotide metabolic process (GO:0009187)	BP	105	101	0.079207921	0.000230558
GO:0070232	regulation of T cell apoptotic process	down	regulation of T cell apoptotic process (GO:0070232)	BP	22	21	0.095238095	0.000234813
GO:0006487	protein N-linked glycosylation	down	protein N-linked glycosylation (GO:0006487)	BP	28	27	0.037037037	0.000236708
GO:0002687	positive regulation of leukocyte migration	down	positive regulation of leukocyte migration (GO:0002687)	BP	60	56	0.142857143	0.000236959
GO:0051235	maintenance of location	down	maintenance of location (GO:0051235)	BP	183	178	0.106741573	0.000240563
GO:1904063	negative regulation of cation transmembrane transport	down	negative regulation of cation transmembrane transport (GO:1904063)	BP	28	28	0.035714286	0.000247239
GO:0071241	cellular response to inorganic substance	down	cellular response to inorganic substance (GO:0071241)	BP	67	64	0.125	0.000247406
GO:0042476	odontogenesis	down	odontogenesis (GO:0042476)	BP	75	73	0.150684932	0.00024843
GO:0021884	forebrain neuron development	down	forebrain neuron development (GO:0021884)	BP	22	21	0.095238095	0.000249635
GO:0022898	regulation of transmembrane transporter activity	down	regulation of transmembrane transporter activity (GO:0022898)	BP	99	96	0.125	0.000250329
GO:0035883	enteroendocrine cell differentiation	down	enteroendocrine cell differentiation (GO:0035883)	BP	18	18	0.111111111	0.000257876
GO:2001242	regulation of intrinsic apoptotic signaling pathway	down	regulation of intrinsic apoptotic signaling pathway (GO:2001242)	BP	107	105	0.133333333	0.000259564
GO:1902186	regulation of viral release from host cell	down	regulation of viral release from host cell (GO:1902186)	BP	27	26	0.038461538	0.000259654
GO:0032210	regulation of telomere maintenance via telomerase	down	regulation of telomere maintenance via telomerase (GO:0032210)	BP	31	31	0.096774194	0.000268218
GO:0035116	embryonic hindlimb morphogenesis	down	embryonic hindlimb morphogenesis (GO:0035116)	BP	23	21	0.095238095	0.000268218
GO:0002902	regulation of B cell apoptotic process	down	regulation of B cell apoptotic process (GO:0002902)	BP	13	13	0.153846154	0.000270207
GO:0048799	animal organ maturation	down	animal organ maturation (GO:0048799)	BP	16	15	0.466666667	0.000271973
GO:0033002	muscle cell proliferation	down	muscle cell proliferation (GO:0033002)	BP	77	75	0.093333333	0.000273043
GO:0006911	phagocytosis, engulfment	down	phagocytosis, engulfment (GO:0006911)	BP	20	19	0.052631579	0.00027584
GO:1900181	negative regulation of protein localization to nucleus	down	negative regulation of protein localization to nucleus (GO:1900181)	BP	55	55	0.090909091	0.000278389
GO:0006509	membrane protein ectodomain proteolysis	down	membrane protein ectodomain proteolysis (GO:0006509)	BP	30	30	0.066666667	0.000282904
GO:0019932	second-messenger-mediated signaling	down	second-messenger-mediated signaling (GO:0019932)	BP	150	142	0.112676056	0.000282969
GO:1900006	positive regulation of dendrite development	down	positive regulation of dendrite development (GO:1900006)	BP	29	28	0.142857143	0.000286874
GO:0051896	regulation of protein kinase B signaling	down	regulation of protein kinase B signaling (GO:0051896)	BP	87	83	0.072289157	0.000286911
GO:0051705	multi-organism behavior	down	multi-organism behavior (GO:0051705)	BP	38	37	0.162162162	0.000288107
GO:0035150	regulation of tube size	down	regulation of tube size (GO:0035150)	BP	54	54	0.12962963	0.000288246
GO:0051591	response to cAMP	down	response to cAMP (GO:0051591)	BP	27	27	0.185185185	0.000289445
GO:2001244	positive regulation of intrinsic apoptotic signaling pathwa	down	positive regulation of intrinsic apoptotic signaling pathway (GO:200124	BP	40	39	0.051282051	0.000289454
GO:0002366	leukocyte activation involved in immune response	down	leukocyte activation involved in immune response (GO:0002366)	BP	138	136	0.058823529	0.000292079
GO:0046427	positive regulation of JAK-STAT cascade	down	positive regulation of JAK-STAT cascade (GO:0046427)	BP	16	15	0.066666667	0.00029342
GO:1904894	positive regulation of STAT cascade	down	positive regulation of STAT cascade (GO:1904894)	BP	16	15	0.066666667	0.00029342
GO:0001953	negative regulation of cell-matrix adhesion	down	negative regulation of cell-matrix adhesion (GO:0001953)	BP	22	22	0	0.000297425
GO:0006278	RNA-dependent DNA biosynthetic process	down	RNA-dependent DNA biosynthetic process (GO:0006278)	BP	32	32	0.09375	0.000298241
GO:0007004	telomere maintenance via telomerase	down	telomere maintenance via telomerase (GO:0007004)	BP	32	32	0.09375	0.000298241
GO:0002263	cell activation involved in immune response	down	cell activation involved in immune response (GO:0002263)	BP	140	137	0.058394161	0.000302331
GO:0060420	regulation of heart growth	down	regulation of heart growth (GO:0060420)	BP	29	29	0.137931034	0.00030634
GO:0050868	negative regulation of T cell activation	down	negative regulation of T cell activation (GO:0050868)	BP	54	51	0.058823529	0.000306441
GO:0051496	positive regulation of stress fiber assembly	down	positive regulation of stress fiber assembly (GO:0051496)	BP	29	27	0.037037037	0.000312406
GO:0010591	regulation of lamellipodium assembly	down	regulation of lamellipodium assembly (GO:0010591)	BP	15	14	0.071428571	0.000313383
GO:0045776	negative regulation of blood pressure	down	negative regulation of blood pressure (GO:0045776)	BP	19	19	0.263157895	0.000314312
GO:0032495	response to muramyl dipeptide	down	response to muramyl dipeptide (GO:0032495)	BP	14	13	0.076923077	0.00031434
GO:0010460	positive regulation of heart rate	down	positive regulation of heart rate (GO:0010460)	BP	13	13	0.076923077	0.000314533
GO:0032675	regulation of interleukin-6 production	down	regulation of interleukin-6 production (GO:0032675)	BP	81	79	0.050632911	0.000314582
GO:0045682	regulation of epidermis development	down	regulation of epidermis development (GO:0045682)	BP	52	49	0.142857143	0.000314613
GO:0045589	regulation of regulatory T cell differentiation	down	regulation of regulatory T cell differentiation (GO:0045589)	BP	10	9	0	0.000314733
GO:0061041	regulation of wound healing	down	regulation of wound healing (GO:0061041)	BP	86	85	0.058823529	0.000314985
GO:1900076	regulation of cellular response to insulin stimulus	down	regulation of cellular response to insulin stimulus (GO:1900076)	BP	38	37	0.135135135	0.000314985
GO:0051348	negative regulation of transferase activity	down	negative regulation of transferase activity (GO:0051348)	BP	146	142	0.098591549	0.000315875

GO:0051972	regulation of telomerase activity	down	regulation of telomerase activity (GO:0051972)	BP	29	29	0.103448276	0.00031811
GO:0016573	histone acetylation	down	histone acetylation (GO:0016573)	BP	97	94	0.042553191	0.000318539
GO:1903035	negative regulation of response to wounding	down	negative regulation of response to wounding (GO:1903035)	BP	43	42	0.095238095	0.000319346
GO:0046634	regulation of alpha-beta T cell activation	down	regulation of alpha-beta T cell activation (GO:0046634)	BP	46	45	0.066666667	0.000325964
GO:0034249	negative regulation of cellular amide metabolic process	down	negative regulation of cellular amide metabolic process (GO:0034249)	BP	88	87	0.045977011	0.000330253
GO:0002275	myeloid cell activation involved in immune response	down	myeloid cell activation involved in immune response (GO:0002275)	BP	42	41	0.048780488	0.000332568
GO:0007026	negative regulation of microtubule depolymerization	down	negative regulation of microtubule depolymerization (GO:0007026)	BP	12	12	0.25	0.000337059
GO:1904375	regulation of protein localization to cell periphery	down	regulation of protein localization to cell periphery (GO:1904375)	BP	19	18	0.111111111	0.000337206
GO:0072017	distal tubule development	down	distal tubule development (GO:0072017)	BP	10	10	0.2	0.000338394
GO:0048385	regulation of retinoic acid receptor signaling pathway	down	regulation of retinoic acid receptor signaling pathway (GO:0048385)	BP	10	8	0.25	0.000342048
GO:0002764	immune response-regulating signaling pathway	down	immune response-regulating signaling pathway (GO:0002764)	BP	179	171	0.052631579	0.000343885
GO:0002253	activation of immune response	down	activation of immune response (GO:0002253)	BP	189	179	0.061452514	0.00034599
GO:0006270	DNA replication initiation	down	DNA replication initiation (GO:0006270)	BP	16	16	0.125	0.000347931
GO:2000114	regulation of establishment of cell polarity	down	regulation of establishment of cell polarity (GO:2000114)	BP	14	14	0.142857143	0.00034895
GO:0071715	icosanoid transport	down	icosanoid transport (GO:0071715)	BP	19	19	0.105263158	0.000349572
GO:1901571	fatty acid derivative transport	down	fatty acid derivative transport (GO:1901571)	BP	19	19	0.105263158	0.000349572
GO:1900026	positive regulation of substrate adhesion-dependent cell s	down	positive regulation of substrate adhesion-dependent cell spreading (GO:1	BP	23	20	0	0.000352693
GO:0007566	embryo implantation	down	embryo implantation (GO:0007566)	BP	30	27	0.074074074	0.000352982
GO:1904427	positive regulation of calcium ion transmembrane transp	down	positive regulation of calcium ion transmembrane transport (GO:190442	BP	30	30	0.133333333	0.00035457
GO:0017148	negative regulation of translation	down	negative regulation of translation (GO:0017148)	BP	81	80	0.05	0.000356481
GO:0008356	asymmetric cell division	down	asymmetric cell division (GO:0008356)	BP	11	11	0.090909091	0.000358462
GO:0035296	regulation of tube diameter	down	regulation of tube diameter (GO:0035296)	BP	48	48	0.125	0.000359752
GO:0097746	regulation of blood vessel diameter	down	regulation of blood vessel diameter (GO:0097746)	BP	48	48	0.125	0.000359752
GO:0045687	positive regulation of glial cell differentiation	down	positive regulation of glial cell differentiation (GO:0045687)	BP	12	12	0.083333333	0.000361252
GO:0002443	leukocyte mediated immunity	down	leukocyte mediated immunity (GO:0002443)	BP	163	158	0.056962025	0.000362014
GO:0006024	glycosaminoglycan biosynthetic process	down	glycosaminoglycan biosynthetic process (GO:0006024)	BP	30	29	0.103448276	0.000362014
GO:0050729	positive regulation of inflammatory response	down	positive regulation of inflammatory response (GO:0050729)	BP	53	53	0.094339623	0.000362427
GO:0018393	internal peptidyl-lysine acetylation	down	internal peptidyl-lysine acetylation (GO:0018393)	BP	100	96	0.041666667	0.000362838
GO:0019724	B cell mediated immunity	down	B cell mediated immunity (GO:0019724)	BP	60	59	0.06779661	0.000363115
GO:0032507	maintenance of protein location in cell	down	maintenance of protein location in cell (GO:0032507)	BP	38	37	0.081081081	0.000363115
GO:1901568	fatty acid derivative metabolic process	down	fatty acid derivative metabolic process (GO:1901568)	BP	53	51	0.196078431	0.000363436
GO:0097193	intrinsic apoptotic signaling pathway	down	intrinsic apoptotic signaling pathway (GO:0097193)	BP	197	191	0.115183246	0.000365211
GO:0002093	auditory receptor cell morphogenesis	down	auditory receptor cell morphogenesis (GO:0002093)	BP	13	13	0.230769231	0.000365788
GO:0046326	positive regulation of glucose import	down	positive regulation of glucose import (GO:0046326)	BP	25	25	0.16	0.000368259
GO:0030595	leukocyte chemotaxis	down	leukocyte chemotaxis (GO:0030595)	BP	115	104	0.086538462	0.000371243
GO:0015693	magnesium ion transport	down	magnesium ion transport (GO:0015693)	BP	11	11	0	0.000378492
GO:0031056	regulation of histone modification	down	regulation of histone modification (GO:0031056)	BP	92	90	0.066666667	0.000378492
GO:0045621	positive regulation of lymphocyte differentiation	down	positive regulation of lymphocyte differentiation (GO:0045621)	BP	55	53	0.075471698	0.000379727
GO:0060074	synapse maturation	down	synapse maturation (GO:0060074)	BP	15	15	0.066666667	0.000382542
GO:0098581	detection of external biotic stimulus	down	detection of external biotic stimulus (GO:0098581)	BP	16	15	0.133333333	0.000387423
GO:0030501	positive regulation of bone mineralization	down	positive regulation of bone mineralization (GO:0030501)	BP	28	28	0.25	0.000387491
GO:0060117	auditory receptor cell development	down	auditory receptor cell development (GO:0060117)	BP	17	17	0.235294118	0.000387491
GO:0046329	negative regulation of JNK cascade	down	negative regulation of JNK cascade (GO:0046329)	BP	18	17	0.176470588	0.000390035
GO:0001782	B cell homeostasis	down	B cell homeostasis (GO:0001782)	BP	23	23	0.043478261	0.000390102
GO:0034643	establishment of mitochondrion localization, microtubul	down	establishment of mitochondrion localization, microtubule-mediated (GC	BP	11	10	0.1	0.000390229
GO:0047497	mitochondrion transport along microtubule	down	mitochondrion transport along microtubule (GO:0047497)	BP	11	10	0.1	0.000390229
GO:0051654	establishment of mitochondrion localization	down	establishment of mitochondrion localization (GO:0051654)	BP	12	10	0.1	0.000390229
GO:0010922	positive regulation of phosphatase activity	down	positive regulation of phosphatase activity (GO:0010922)	BP	18	17	0.117647059	0.0003919
GO:0060043	regulation of cardiac muscle cell proliferation	down	regulation of cardiac muscle cell proliferation (GO:0060043)	BP	24	24	0.083333333	0.000393806
GO:0002703	regulation of leukocyte mediated immunity	down	regulation of leukocyte mediated immunity (GO:0002703)	BP	103	100	0.05	0.000395216
GO:0010828	positive regulation of glucose transport	down	positive regulation of glucose transport (GO:0010828)	BP	27	27	0.148148148	0.000396116
GO:0061180	mammary gland epithelium development	down	mammary gland epithelium development (GO:0061180)	BP	50	48	0.145833333	0.000398903
GO:0007568	aging	down	aging (GO:0007568)	BP	92	87	0.091954023	0.000400423
GO:0043266	regulation of potassium ion transport	down	regulation of potassium ion transport (GO:0043266)	BP	45	45	0.133333333	0.000400423
GO:0010659	cardiac muscle cell apoptotic process	down	cardiac muscle cell apoptotic process (GO:0010659)	BP	11	11	0.090909091	0.000402024
GO:0045429	positive regulation of nitric oxide biosynthetic process	down	positive regulation of nitric oxide biosynthetic process (GO:0045429)	BP	16	15	0.133333333	0.000403197
GO:1904407	positive regulation of nitric oxide metabolic process	down	positive regulation of nitric oxide metabolic process (GO:1904407)	BP	16	15	0.133333333	0.000403197
GO:0070588	calcium ion transmembrane transport	down	calcium ion transmembrane transport (GO:0070588)	BP	145	138	0.123188406	0.000404535
GO:0071277	cellular response to calcium ion	down	cellular response to calcium ion (GO:0071277)	BP	28	27	0.111111111	0.000410761
GO:0050728	negative regulation of inflammatory response	down	negative regulation of inflammatory response (GO:0050728)	BP	73	71	0.070422535	0.000419177
GO:1900027	regulation of ruffle assembly	down	regulation of ruffle assembly (GO:1900027)	BP	16	14	0.071428571	0.000425325
GO:0007269	neurotransmitter secretion	down	neurotransmitter secretion (GO:0007269)	BP	56	55	0.145454545	0.000426447
GO:0099643	signal release from synapse	down	signal release from synapse (GO:0099643)	BP	56	55	0.145454545	0.000426447
GO:0043112	receptor metabolic process	down	receptor metabolic process (GO:0043112)	BP	103	100	0.05	0.000426502

GO:0035303	regulation of dephosphorylation	down	regulation of dephosphorylation (GO:0035303)	BP	102	98	0.091836735	0.000433833
GO:0007184	SMAD protein import into nucleus	down	SMAD protein import into nucleus (GO:0007184)	BP	21	21	0.047619048	0.000434801
GO:0045987	positive regulation of smooth muscle contraction	down	positive regulation of smooth muscle contraction (GO:0045987)	BP	10	10	0.1	0.00043753
GO:0010719	negative regulation of epithelial to mesenchymal transiti	down	negative regulation of epithelial to mesenchymal transition (GO:001071	BP	17	17	0.235294118	0.000441846
GO:0007257	activation of JUN kinase activity	down	activation of JUN kinase activity (GO:0007257)	BP	15	15	0.066666667	0.000442316
GO:1904385	cellular response to angiotensin	down	cellular response to angiotensin (GO:1904385)	BP	10	9	0.222222222	0.00044504
GO:1990776	response to angiotensin	down	response to angiotensin (GO:1990776)	BP	10	9	0.222222222	0.00044504
GO:0048535	lymph node development	down	lymph node development (GO:0048535)	BP	16	16	0	0.000447674
GO:0042693	muscle cell fate commitment	down	muscle cell fate commitment (GO:0042693)	BP	10	10	0.1	0.000448826
GO:0043414	macromolecule methylation	down	macromolecule methylation (GO:0043414)	BP	176	165	0.066666667	0.000451072
GO:0046324	regulation of glucose import	down	regulation of glucose import (GO:0046324)	BP	40	39	0.102564103	0.000451674
GO:0042445	hormone metabolic process	down	hormone metabolic process (GO:0042445)	BP	96	91	0.164835165	0.000451974
GO:2000677	regulation of transcription regulatory region DNA binding	down	regulation of transcription regulatory region DNA binding (GO:2000677)	BP	26	26	0.076923077	0.000452131
GO:0035137	hindlimb morphogenesis	down	hindlimb morphogenesis (GO:0035137)	BP	30	28	0.107142857	0.000454809
GO:0050869	negative regulation of B cell activation	down	negative regulation of B cell activation (GO:0050869)	BP	21	21	0.095238095	0.000454809
GO:2000116	regulation of cysteine-type endopeptidase activity	down	regulation of cysteine-type endopeptidase activity (GO:2000116)	BP	123	120	0.158333333	0.000457858
GO:0043270	positive regulation of ion transport	down	positive regulation of ion transport (GO:0043270)	BP	114	109	0.091743119	0.000458859
GO:0008202	steroid metabolic process	down	steroid metabolic process (GO:0008202)	BP	139	128	0.0859375	0.000458942
GO:0120034	positive regulation of plasma membrane bounded cell pr	down	positive regulation of plasma membrane bounded cell projection assemb	BP	48	46	0.065217391	0.000463229
GO:0046633	alpha-beta T cell proliferation	down	alpha-beta T cell proliferation (GO:0046633)	BP	18	17	0.058823529	0.000464746
GO:1903321	negative regulation of protein modification by small prot	down	negative regulation of protein modification by small protein conjugation	BP	53	52	0.076923077	0.000464746
GO:0090344	negative regulation of cell aging	down	negative regulation of cell aging (GO:0090344)	BP	12	12	0.083333333	0.000467524
GO:0002757	immune response-activating signal transduction	down	immune response-activating signal transduction (GO:0002757)	BP	170	162	0.055555556	0.000472934
GO:0071359	cellular response to dsRNA	down	cellular response to dsRNA (GO:0071359)	BP	33	32	0.0625	0.000474532
GO:0042596	fear response	down	fear response (GO:0042596)	BP	25	24	0.166666667	0.000476998
GO:0007033	vacuole organization	down	vacuole organization (GO:0007033)	BP	90	90	0.055555556	0.000483268
GO:0010972	negative regulation of G2/M transition of mitotic cell cycl	down	negative regulation of G2/M transition of mitotic cell cycle (GO:0010972	BP	16	16	0.0625	0.000483552
GO:1903532	positive regulation of secretion by cell	down	positive regulation of secretion by cell (GO:1903532)	BP	185	178	0.073033708	0.000484231
GO:0051279	regulation of release of sequestered calcium ion into cyto	down	regulation of release of sequestered calcium ion into cytosol (GO:005127	BP	43	41	0.097560976	0.00048854
GO:0051047	positive regulation of secretion	down	positive regulation of secretion (GO:0051047)	BP	196	188	0.074468085	0.000489037
GO:0090305	nucleic acid phosphodiester bond hydrolysis	down	nucleic acid phosphodiester bond hydrolysis (GO:0090305)	BP	76	75	0.133333333	0.000492713
GO:1901617	organic hydroxy compound biosynthetic process	down	organic hydroxy compound biosynthetic process (GO:1901617)	BP	106	99	0.121212121	0.000494732
GO:0035306	positive regulation of dephosphorylation	down	positive regulation of dephosphorylation (GO:0035306)	BP	34	33	0.151515152	0.000496582
GO:0061323	cell proliferation involved in heart morphogenesis	down	cell proliferation involved in heart morphogenesis (GO:0061323)	BP	13	13	0.076923077	0.00049671
GO:0043407	negative regulation of MAP kinase activity	down	negative regulation of MAP kinase activity (GO:0043407)	BP	51	50	0.06	0.000498143
GO:0002449	lymphocyte mediated immunity	down	lymphocyte mediated immunity (GO:0002449)	BP	128	124	0.064516129	0.000499442
GO:0043489	RNA stabilization	down	RNA stabilization (GO:0043489)	BP	19	19	0.157894737	0.000499442
GO:0046620	regulation of organ growth	down	regulation of organ growth (GO:0046620)	BP	53	52	0.115384615	0.000506683
GO:2000171	negative regulation of dendrite development	down	negative regulation of dendrite development (GO:2000171)	BP	14	14	0.142857143	0.000506754
GO:1901213	regulation of transcription from RNA polymerase II prom	down	regulation of transcription from RNA polymerase II promoter involved in	BP	10	10	0.1	0.000507921
GO:0045603	positive regulation of endothelial cell differentiation	down	positive regulation of endothelial cell differentiation (GO:0045603)	BP	12	12	0.083333333	0.000514215
GO:0097178	ruffle assembly	down	ruffle assembly (GO:0097178)	BP	24	22	0.045454545	0.000518031
GO:0046916	cellular transition metal ion homeostasis	down	cellular transition metal ion homeostasis (GO:0046916)	BP	48	46	0.086956522	0.000520363
GO:1901798	positive regulation of signal transduction by p53 class me	down	positive regulation of signal transduction by p53 class mediator (GO:190	BP	12	12	0	0.000527714
GO:0016079	synaptic vesicle exocytosis	down	synaptic vesicle exocytosis (GO:0016079)	BP	32	32	0.1875	0.000529665
GO:0007214	gamma-aminobutyric acid signaling pathway	down	gamma-aminobutyric acid signaling pathway (GO:0007214)	BP	15	15	0.2	0.000530599
GO:0006892	post-Golgi vesicle-mediated transport	down	post-Golgi vesicle-mediated transport (GO:0006892)	BP	46	44	0.068181818	0.000531814
GO:0003309	type B pancreatic cell differentiation	down	type B pancreatic cell differentiation (GO:0003309)	BP	17	17	0.117647059	0.000537323
GO:0060428	lung epithelium development	down	lung epithelium development (GO:0060428)	BP	32	31	0.193548387	0.000541602
GO:1903426	regulation of reactive oxygen species biosynthetic process	down	regulation of reactive oxygen species biosynthetic process (GO:1903426)	BP	27	25	0.16	0.00054887
GO:0002237	response to molecule of bacterial origin	down	response to molecule of bacterial origin (GO:0002237)	BP	151	142	0.077464789	0.000549534
GO:0009411	response to UV	down	response to UV (GO:0009411)	BP	89	88	0.102272727	0.000549534
GO:0042474	middle ear morphogenesis	down	middle ear morphogenesis (GO:0042474)	BP	15	15	0.066666667	0.000561227
GO:0046456	icosanoid biosynthetic process	down	icosanoid biosynthetic process (GO:0046456)	BP	23	22	0.318181818	0.000567994
GO:0046782	regulation of viral transcription	down	regulation of viral transcription (GO:0046782)	BP	27	27	0.037037037	0.000569578
GO:0086002	cardiac muscle cell action potential involved in contracti	down	cardiac muscle cell action potential involved in contraction (GO:00860	BP	25	25	0.16	0.000573123
GO:0002532	production of molecular mediator involved in inflammat	down	production of molecular mediator involved in inflammatory response (G	BP	36	35	0.114285714	0.000580195
GO:0002092	positive regulation of receptor internalization	down	positive regulation of receptor internalization (GO:0002092)	BP	14	14	0.071428571	0.000580856
GO:0001662	behavioral fear response	down	behavioral fear response (GO:0001662)	BP	24	23	0.173913043	0.000591123
GO:0002209	behavioral defense response	down	behavioral defense response (GO:0002209)	BP	24	23	0.173913043	0.000591123
GO:0021783	preganglionic parasympathetic fiber development	down	preganglionic parasympathetic fiber development (GO:0021783)	BP	13	13	0.076923077	0.0005932
GO:0060291	long-term synaptic potentiation	down	long-term synaptic potentiation (GO:0060291)	BP	29	28	0.107142857	0.000604557
GO:0006898	receptor-mediated endocytosis	down	receptor-mediated endocytosis (GO:0006898)	BP	142	139	0.09352518	0.000605494
GO:0010761	fibroblast migration	down	fibroblast migration (GO:0010761)	BP	30	29	0.068965517	0.000609517

GO:0051150	regulation of smooth muscle cell differentiation	down	regulation of smooth muscle cell differentiation (GO:0051150)	BP	13	13	0.153846154	0.000616509
GO:1903311	regulation of mRNA metabolic process	down	regulation of mRNA metabolic process (GO:1903311)	BP	116	115	0.060869565	0.000619077
GO:0002068	glandular epithelial cell development	down	glandular epithelial cell development (GO:0002068)	BP	19	19	0.105263158	0.000619899
GO:0032365	intracellular lipid transport	down	intracellular lipid transport (GO:0032365)	BP	10	10	0.1	0.000622581
GO:0001505	regulation of neurotransmitter levels	down	regulation of neurotransmitter levels (GO:0001505)	BP	82	81	0.12345679	0.00062337
GO:0001523	retinoid metabolic process	down	retinoid metabolic process (GO:0001523)	BP	29	23	0.304347826	0.00062337
GO:0043543	protein acylation	down	protein acylation (GO:0043543)	BP	142	138	0.057971014	0.00062924
GO:0019076	viral release from host cell	down	viral release from host cell (GO:0019076)	BP	29	28	0.035714286	0.000634255
GO:0035890	exit from host	down	exit from host (GO:0035890)	BP	29	28	0.035714286	0.000634255
GO:0035891	exit from host cell	down	exit from host cell (GO:0035891)	BP	29	28	0.035714286	0.000634255
GO:0052126	movement in host environment	down	movement in host environment (GO:0052126)	BP	29	28	0.035714286	0.000634255
GO:0052192	movement in environment of other organism involved in	down	movement in environment of other organism involved in symbiotic inter	BP	29	28	0.035714286	0.000634255
GO:0099531	presynaptic process involved in chemical synaptic transm	down	presynaptic process involved in chemical synaptic transmission (GO:009	BP	61	60	0.133333333	0.000634255
GO:1903115	regulation of actin filament-based movement	down	regulation of actin filament-based movement (GO:1903115)	BP	18	17	0.117647059	0.00063794
GO:0034629	cellular protein complex localization	down	cellular protein complex localization (GO:0034629)	BP	12	12	0.083333333	0.000641443
GO:0071248	cellular response to metal ion	down	cellular response to metal ion (GO:0071248)	BP	60	57	0.122807018	0.000641443
GO:0003015	heart process	down	heart process (GO:0003015)	BP	115	112	0.196428571	0.000642516
GO:0042362	fat-soluble vitamin biosynthetic process	down	fat-soluble vitamin biosynthetic process (GO:0042362)	BP	11	10	0.2	0.000647111
GO:0016064	immunoglobulin mediated immune response	down	immunoglobulin mediated immune response (GO:0016064)	BP	59	58	0.068965517	0.000655558
GO:0002089	lens morphogenesis in camera-type eye	down	lens morphogenesis in camera-type eye (GO:0002089)	BP	16	13	0.153846154	0.000661219
GO:0002698	negative regulation of immune effector process	down	negative regulation of immune effector process (GO:0002698)	BP	62	56	0.089285714	0.000663165
GO:0043241	protein complex disassembly	down	protein complex disassembly (GO:0043241)	BP	90	83	0.156626506	0.000663659
GO:0070884	regulation of calcineurin-NFAT signaling cascade	down	regulation of calcineurin-NFAT signaling cascade (GO:0070884)	BP	11	11	0.363636364	0.000673203
GO:0106056	regulation of calcineurin-mediated signaling	down	regulation of calcineurin-mediated signaling (GO:0106056)	BP	11	11	0.363636364	0.000673203
GO:2000104	negative regulation of DNA-dependent DNA replication	down	negative regulation of DNA-dependent DNA replication (GO:2000104)	BP	13	13	0	0.000675171
GO:0032204	regulation of telomere maintenance	down	regulation of telomere maintenance (GO:0032204)	BP	49	49	0.06122449	0.000676932
GO:0032387	negative regulation of intracellular transport	down	negative regulation of intracellular transport (GO:0032387)	BP	86	84	0.095238095	0.000684586
GO:0048643	positive regulation of skeletal muscle tissue development	down	positive regulation of skeletal muscle tissue development (GO:0048643)	BP	13	12	0.25	0.000684586
GO:0072079	nephron tubule formation	down	nephron tubule formation (GO:0072079)	BP	16	16	0.25	0.000696793
GO:0033619	membrane protein proteolysis	down	membrane protein proteolysis (GO:0033619)	BP	38	38	0.078947368	0.000697071
GO:0002706	regulation of lymphocyte mediated immunity	down	regulation of lymphocyte mediated immunity (GO:0002706)	BP	83	80	0.05	0.000697843
GO:0006643	membrane lipid metabolic process	down	membrane lipid metabolic process (GO:0006643)	BP	93	92	0.065217391	0.00069879
GO:0071219	cellular response to molecule of bacterial origin	down	cellular response to molecule of bacterial origin (GO:0071219)	BP	97	91	0.087912088	0.00069879
GO:1903409	reactive oxygen species biosynthetic process	down	reactive oxygen species biosynthetic process (GO:1903409)	BP	41	37	0.189189189	0.00069879
GO:0031641	regulation of myelination	down	regulation of myelination (GO:0031641)	BP	17	17	0.058823529	0.000701657
GO:1901652	response to peptide	down	response to peptide (GO:1901652)	BP	150	146	0.102739726	0.000701657
GO:0006303	double-strand break repair via nonhomologous end joini	down	double-strand break repair via nonhomologous end joining (GO:000630	BP	15	15	0.066666667	0.000704964
GO:0010522	regulation of calcium ion transport into cytosol	down	regulation of calcium ion transport into cytosol (GO:0010522)	BP	50	48	0.083333333	0.000713751
GO:0032846	positive regulation of homeostatic process	down	positive regulation of homeostatic process (GO:0032846)	BP	129	128	0.0703125	0.000714226
GO:0031396	regulation of protein ubiquitination	down	regulation of protein ubiquitination (GO:0031396)	BP	130	128	0.078125	0.000715307
GO:0046622	positive regulation of organ growth	down	positive regulation of organ growth (GO:0046622)	BP	29	28	0.178571429	0.000717585
GO:0019884	antigen processing and presentation of exogenous antige	down	antigen processing and presentation of exogenous antigen (GO:0019884)	BP	10	9	0	0.000722356
GO:0000726	non-recombinational repair	down	non-recombinational repair (GO:0000726)	BP	19	19	0.052631579	0.000726007
GO:0045921	positive regulation of exocytosis	down	positive regulation of exocytosis (GO:0045921)	BP	53	50	0.04	0.00072966
GO:0016032	viral process	down	viral process (GO:0016032)	BP	162	152	0.059210526	0.000732463
GO:0006690	icosanoid metabolic process	down	icosanoid metabolic process (GO:0006690)	BP	35	33	0.242424242	0.000732591
GO:1903320	regulation of protein modification by small protein conju	down	regulation of protein modification by small protein conjugation or remo	BP	147	144	0.069444444	0.000732591
GO:0070252	actin-mediated cell contraction	down	actin-mediated cell contraction (GO:0070252)	BP	41	39	0.205128205	0.000734243
GO:0031397	negative regulation of protein ubiquitination	down	negative regulation of protein ubiquitination (GO:0031397)	BP	47	46	0.086956522	0.000736422
GO:1901380	negative regulation of potassium ion transmembrane tra	down	negative regulation of potassium ion transmembrane transport (GO:1901	BP	13	13	0.076923077	0.00073937
GO:0099024	plasma membrane invagination	down	plasma membrane invagination (GO:0099024)	BP	27	26	0.076923077	0.000744422
GO:0014044	Schwann cell development	down	Schwann cell development (GO:0014044)	BP	15	15	0	0.000744556
GO:0034754	cellular hormone metabolic process	down	cellular hormone metabolic process (GO:0034754)	BP	46	41	0.170731707	0.000763988
GO:0002467	germinal center formation	down	germinal center formation (GO:0002467)	BP	13	13	0	0.000768929
GO:0006312	mitotic recombination	down	mitotic recombination (GO:0006312)	BP	13	12	0.083333333	0.000785883
GO:0045670	regulation of osteoclast differentiation	down	regulation of osteoclast differentiation (GO:0045670)	BP	41	39	0.128205128	0.000785886
GO:0034766	negative regulation of ion transmembrane transport	down	negative regulation of ion transmembrane transport (GO:0034766)	BP	31	31	0.032258065	0.000790068
GO:0031114	regulation of microtubule depolymerization	down	regulation of microtubule depolymerization (GO:0031114)	BP	13	13	0.230769231	0.000793062
GO:0042100	B cell proliferation	down	B cell proliferation (GO:0042100)	BP	54	54	0.055555556	0.000805578
GO:0071216	cellular response to biotic stimulus	down	cellular response to biotic stimulus (GO:0071216)	BP	113	107	0.074766355	0.00081427
GO:0071887	leukocyte apoptotic process	down	leukocyte apoptotic process (GO:0071887)	BP	67	66	0.090909091	0.000814474
GO:0050654	chondroitin sulfate proteoglycan metabolic process	down	chondroitin sulfate proteoglycan metabolic process (GO:0050654)	BP	20	19	0.052631579	0.000823778
GO:0002690	positive regulation of leukocyte chemotaxis	down	positive regulation of leukocyte chemotaxis (GO:0002690)	BP	48	44	0.159090909	0.000827289
GO:0018149	peptide cross-linking	down	peptide cross-linking (GO:0018149)	BP	22	21	0.142857143	0.000827289

GO:0030224	monocyte differentiation	down	monocyte differentiation (GO:0030224)	BP	20	20	0	0.000827289
GO:0034204	lipid translocation	down	lipid translocation (GO:0034204)	BP	17	16	0.125	0.000827289
GO:0045332	phospholipid translocation	down	phospholipid translocation (GO:0045332)	BP	17	16	0.125	0.000827289
GO:1903131	mononuclear cell differentiation	down	mononuclear cell differentiation (GO:1903131)	BP	20	20	0	0.000827289
GO:0050710	negative regulation of cytokine secretion	down	negative regulation of cytokine secretion (GO:0050710)	BP	35	34	0.088235294	0.000836575
GO:0046928	regulation of neurotransmitter secretion	down	regulation of neurotransmitter secretion (GO:0046928)	BP	28	28	0.214285714	0.000840016
GO:0043281	regulation of cysteine-type endopeptidase activity involve	down	regulation of cysteine-type endopeptidase activity involved in apoptotic	BP	114	111	0.162162162	0.000844099
GO:0022602	ovulation cycle process	down	ovulation cycle process (GO:0022602)	BP	45	44	0.136363636	0.000848501
GO:0043409	negative regulation of MAPK cascade	down	negative regulation of MAPK cascade (GO:0043409)	BP	104	101	0.089108911	0.000855607
GO:1903779	regulation of cardiac conduction	down	regulation of cardiac conduction (GO:1903779)	BP	11	11	0.090909091	0.000855607
GO:0070169	positive regulation of biomineral tissue development	down	positive regulation of biomineral tissue development (GO:0070169)	BP	31	31	0.225806452	0.000860544
GO:0060216	definitive hemopoiesis	down	definitive hemopoiesis (GO:0060216)	BP	13	12	0.083333333	0.000862057
GO:0030851	granulocyte differentiation	down	granulocyte differentiation (GO:0030851)	BP	26	26	0.038461538	0.00086555
GO:0001919	regulation of receptor recycling	down	regulation of receptor recycling (GO:0001919)	BP	14	13	0.230769231	0.000866492
GO:0009065	glutamine family amino acid catabolic process	down	glutamine family amino acid catabolic process (GO:0009065)	BP	11	11	0.272727273	0.000875445
GO:0006904	vesicle docking involved in exocytosis	down	vesicle docking involved in exocytosis (GO:0006904)	BP	17	17	0.058823529	0.000883113
GO:2000134	negative regulation of G1/S transition of mitotic cell cycle	down	negative regulation of G1/S transition of mitotic cell cycle (GO:2000134)	BP	27	26	0.076923077	0.000884549
GO:0002534	cytokine production involved in inflammatory response	down	cytokine production involved in inflammatory response (GO:0002534)	BP	20	19	0.157894737	0.000885933
GO:0008299	isoprenoid biosynthetic process	down	isoprenoid biosynthetic process (GO:0008299)	BP	22	21	0.142857143	0.000887272
GO:0048145	regulation of fibroblast proliferation	down	regulation of fibroblast proliferation (GO:0048145)	BP	52	51	0.117647059	0.0009009
GO:0071496	cellular response to external stimulus	down	cellular response to external stimulus (GO:0071496)	BP	133	129	0.085271318	0.00090204
GO:0008542	visual learning	down	visual learning (GO:0008542)	BP	37	37	0.135135135	0.000902491
GO:0001895	retina homeostasis	down	retina homeostasis (GO:0001895)	BP	42	39	0.102564103	0.000910543
GO:0007200	phospholipase C-activating G-protein coupled receptor si	down	phospholipase C-activating G-protein coupled receptor signaling pathwa	BP	31	29	0.103448276	0.000913568
GO:0043388	positive regulation of DNA binding	down	positive regulation of DNA binding (GO:0043388)	BP	29	29	0.103448276	0.000916064
GO:0048169	regulation of long-term neuronal synaptic plasticity	down	regulation of long-term neuronal synaptic plasticity (GO:0048169)	BP	15	15	0.2	0.000933554
GO:0007249	I-kappaB kinase/NF-kappaB signaling	down	I-kappaB kinase/NF-kappaB signaling (GO:0007249)	BP	184	178	0.073033708	0.000943262
GO:0046834	lipid phosphorylation	down	lipid phosphorylation (GO:0046834)	BP	28	28	0.035714286	0.000944149
GO:0010934	macrophage cytokine production	down	macrophage cytokine production (GO:0010934)	BP	12	12	0.166666667	0.0009447
GO:0060047	heart contraction	down	heart contraction (GO:0060047)	BP	112	110	0.190909091	0.000945097
GO:0050878	regulation of body fluid levels	down	regulation of body fluid levels (GO:0050878)	BP	196	188	0.085106383	0.000948154
GO:0050922	negative regulation of chemotaxis	down	negative regulation of chemotaxis (GO:0050922)	BP	26	24	0.125	0.000962389
GO:0002274	myeloid leukocyte activation	down	myeloid leukocyte activation (GO:0002274)	BP	92	90	0.044444444	0.000972356
GO:0021544	subpallium development	down	subpallium development (GO:0021544)	BP	19	18	0.166666667	0.00098329
GO:0032885	regulation of polysaccharide biosynthetic process	down	regulation of polysaccharide biosynthetic process (GO:0032885)	BP	17	17	0.117647059	0.000995065
GO:0035510	DNA dealkylation	down	DNA dealkylation (GO:0035510)	BP	15	15	0	0.001003102
GO:1902373	negative regulation of mRNA catabolic process	down	negative regulation of mRNA catabolic process (GO:1902373)	BP	22	22	0.136363636	0.00100925
GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signalin	down	positive regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043123)	BP	128	123	0.097560976	0.00102652
GO:1903524	positive regulation of blood circulation	down	positive regulation of blood circulation (GO:1903524)	BP	28	27	0.111111111	0.001030303
GO:1901019	regulation of calcium ion transmembrane transporter act	down	regulation of calcium ion transmembrane transporter activity (GO:1901	BP	27	26	0.115384615	0.001034089
GO:0002067	glandular epithelial cell differentiation	down	glandular epithelial cell differentiation (GO:0002067)	BP	36	34	0.058823529	0.001037989
GO:2001243	negative regulation of intrinsic apoptotic signaling pathw	down	negative regulation of intrinsic apoptotic signaling pathway (GO:20012	BP	61	60	0.166666667	0.001042099
GO:0006023	aminoglycan biosynthetic process	down	aminoglycan biosynthetic process (GO:0006023)	BP	35	34	0.088235294	0.001043041
GO:0051341	regulation of oxidoreductase activity	down	regulation of oxidoreductase activity (GO:0051341)	BP	45	41	0.170731707	0.001045861
GO:1903076	regulation of protein localization to plasma membrane	down	regulation of protein localization to plasma membrane (GO:1903076)	BP	18	17	0.117647059	0.001045916
GO:0043331	response to dsRNA	down	response to dsRNA (GO:0043331)	BP	51	50	0.06	0.001058094
GO:0043372	positive regulation of CD4-positive, alpha-beta T cell diffe	down	positive regulation of CD4-positive, alpha-beta T cell differentiation (GO:	BP	15	15	0.066666667	0.001082372
GO:0010827	regulation of glucose transport	down	regulation of glucose transport (GO:0010827)	BP	47	46	0.086956522	0.001111026
GO:0042493	response to drug	down	response to drug (GO:0042493)	BP	101	94	0.106382979	0.001111026
GO:0043903	regulation of symbiosis, encompassing mutualism throug	down	regulation of symbiosis, encompassing mutualism through parasitism (G	BP	127	122	0.057377049	0.001114301
GO:0071322	cellular response to carbohydrate stimulus	down	cellular response to carbohydrate stimulus (GO:0071322)	BP	49	47	0.127659574	0.001120985
GO:0071480	cellular response to gamma radiation	down	cellular response to gamma radiation (GO:0071480)	BP	12	12	0	0.001122489
GO:0046323	glucose import	down	glucose import (GO:0046323)	BP	45	44	0.090909091	0.001122814
GO:0086003	cardiac muscle cell contraction	down	cardiac muscle cell contraction (GO:0086003)	BP	29	28	0.142857143	0.001126139
GO:0007632	visual behavior	down	visual behavior (GO:0007632)	BP	39	39	0.128205128	0.00114005
GO:0032309	icosanoid secretion	down	icosanoid secretion (GO:0032309)	BP	18	18	0.111111111	0.001141209
GO:0042094	interleukin-2 biosynthetic process	down	interleukin-2 biosynthetic process (GO:0042094)	BP	13	13	0.076923077	0.001150517
GO:0045620	negative regulation of lymphocyte differentiation	down	negative regulation of lymphocyte differentiation (GO:0045620)	BP	27	24	0.166666667	0.00115242
GO:0000209	protein polyubiquitination	down	protein polyubiquitination (GO:0000209)	BP	111	111	0.063063063	0.001159532
GO:0055013	cardiac muscle cell development	down	cardiac muscle cell development (GO:0055013)	BP	31	31	0.129032258	0.001159532
GO:0050777	negative regulation of immune response	down	negative regulation of immune response (GO:0050777)	BP	74	68	0.088235294	0.00116836
GO:0051568	histone H3-K4 methylation	down	histone H3-K4 methylation (GO:0051568)	BP	36	32	0.0625	0.001203292
GO:0002495	antigen processing and presentation of peptide antigen vi	down	antigen processing and presentation of peptide antigen via MHC class II (G	BP	10	6	0	0.001211412
GO:0030317	flagellated sperm motility	down	flagellated sperm motility (GO:0030317)	BP	47	43	0.093023256	0.001211642

GO:0097722	sperm motility	down	sperm motility (GO:0097722)	BP	47	43	0.093023256	0.001211642
GO:0046854	phosphatidylinositol phosphorylation	down	phosphatidylinositol phosphorylation (GO:0046854)	BP	27	27	0.037037037	0.001238266
GO:0045010	actin nucleation	down	actin nucleation (GO:0045010)	BP	30	29	0.206896552	0.001258973
GO:0001516	prostaglandin biosynthetic process	down	prostaglandin biosynthetic process (GO:0001516)	BP	13	13	0.230769231	0.001263263
GO:0046457	prostanoid biosynthetic process	down	prostanoid biosynthetic process (GO:0046457)	BP	13	13	0.230769231	0.001263263
GO:0048144	fibroblast proliferation	down	fibroblast proliferation (GO:0048144)	BP	53	52	0.115384615	0.001293865
GO:0048339	paraxial mesoderm development	down	paraxial mesoderm development (GO:0048339)	BP	14	14	0.071428571	0.00131787
GO:0097035	regulation of membrane lipid distribution	down	regulation of membrane lipid distribution (GO:0097035)	BP	26	25	0.12	0.001327093
GO:0018394	peptidyl-lysine acetylation	down	peptidyl-lysine acetylation (GO:0018394)	BP	102	98	0.051020408	0.001335355
GO:0006475	internal protein amino acid acetylation	down	internal protein amino acid acetylation (GO:0006475)	BP	103	99	0.04040404	0.00133767
GO:0045069	regulation of viral genome replication	down	regulation of viral genome replication (GO:0045069)	BP	50	48	0.083333333	0.001343744
GO:0051923	sulfation	down	sulfation (GO:0051923)	BP	10	7	0.142857143	0.001344002
GO:1901379	regulation of potassium ion transmembrane transport	down	regulation of potassium ion transmembrane transport (GO:1901379)	BP	38	38	0.131578947	0.001345957
GO:0051607	defense response to virus	down	defense response to virus (GO:0051607)	BP	170	163	0.09202454	0.001347457
GO:0009416	response to light stimulus	down	response to light stimulus (GO:0009416)	BP	173	169	0.082840237	0.001347836
GO:0031113	regulation of microtubule polymerization	down	regulation of microtubule polymerization (GO:0031113)	BP	18	17	0.058823529	0.001355361
GO:0044788	modulation by host of viral process	down	modulation by host of viral process (GO:0044788)	BP	16	15	0.066666667	0.001374961
GO:0043550	regulation of lipid kinase activity	down	regulation of lipid kinase activity (GO:0043550)	BP	34	34	0.058823529	0.001380862
GO:0006473	protein acetylation	down	protein acetylation (GO:0006473)	BP	116	112	0.053571429	0.001392195
GO:0045862	positive regulation of proteolysis	down	positive regulation of proteolysis (GO:0045862)	BP	167	161	0.105590062	0.001398496
GO:0001991	regulation of systemic arterial blood pressure by circulat	down	regulation of systemic arterial blood pressure by circulatory renin-angio	BP	11	10	0.1	0.001417927
GO:0034763	negative regulation of transmembrane transport	down	negative regulation of transmembrane transport (GO:0034763)	BP	36	36	0.083333333	0.001419483
GO:0010613	positive regulation of cardiac muscle hypertrophy	down	positive regulation of cardiac muscle hypertrophy (GO:0010613)	BP	11	11	0.090909091	0.00144654
GO:0014742	positive regulation of muscle hypertrophy	down	positive regulation of muscle hypertrophy (GO:0014742)	BP	11	11	0.090909091	0.00144654
GO:0019221	cytokine-mediated signaling pathway	down	cytokine-mediated signaling pathway (GO:0019221)	BP	170	163	0.09202454	0.001452968
GO:0071222	cellular response to lipopolysaccharide	down	cellular response to lipopolysaccharide (GO:0071222)	BP	91	85	0.082352941	0.001453243
GO:0046676	negative regulation of insulin secretion	down	negative regulation of insulin secretion (GO:0046676)	BP	16	16	0.125	0.001463077
GO:0060711	labyrinthine layer development	down	labyrinthine layer development (GO:0060711)	BP	39	39	0.076923077	0.001464765
GO:0050774	negative regulation of dendrite morphogenesis	down	negative regulation of dendrite morphogenesis (GO:0050774)	BP	10	10	0.2	0.001467014
GO:0072202	cell differentiation involved in metanephros developmen	down	cell differentiation involved in metanephros development (GO:0072202)	BP	20	20	0.1	0.001512732
GO:0071514	genetic imprinting	down	genetic imprinting (GO:0071514)	BP	16	15	0.066666667	0.001531924
GO:0010758	regulation of macrophage chemotaxis	down	regulation of macrophage chemotaxis (GO:0010758)	BP	12	12	0.083333333	0.001544987
GO:0033077	T cell differentiation in thymus	down	T cell differentiation in thymus (GO:0033077)	BP	53	51	0.058823529	0.001548552
GO:0046579	positive regulation of Ras protein signal transduction	down	positive regulation of Ras protein signal transduction (GO:0046579)	BP	24	22	0.090909091	0.001558556
GO:0032703	negative regulation of interleukin-2 production	down	negative regulation of interleukin-2 production (GO:0032703)	BP	11	10	0	0.001559211
GO:2001275	positive regulation of glucose import in response to insuli	down	positive regulation of glucose import in response to insulin stimulus (GO:	BP	10	10	0.1	0.001571719
GO:0006298	mismatch repair	down	mismatch repair (GO:0006298)	BP	18	18	0.111111111	0.001577572
GO:0032984	macromolecular complex disassembly	down	macromolecular complex disassembly (GO:0032984)	BP	110	102	0.12745098	0.001596449
GO:0006665	sphingolipid metabolic process	down	sphingolipid metabolic process (GO:0006665)	BP	66	66	0.090909091	0.001610094
GO:0010574	regulation of vascular endothelial growth factor producti	down	regulation of vascular endothelial growth factor production (GO:001057	BP	23	22	0.136363636	0.001628882
GO:1904356	regulation of telomere maintenance via telomere lengthe	down	regulation of telomere maintenance via telomere lengthening (GO:19043	BP	34	34	0.088235294	0.001630173
GO:0060538	skeletal muscle organ development	down	skeletal muscle organ development (GO:0060538)	BP	119	116	0.181034483	0.001649071
GO:0032755	positive regulation of interleukin-6 production	down	positive regulation of interleukin-6 production (GO:0032755)	BP	52	50	0.02	0.001674862
GO:0018023	peptidyl-lysine trimethylation	down	peptidyl-lysine trimethylation (GO:0018023)	BP	25	22	0.045454545	0.001689055
GO:0045822	negative regulation of heart contraction	down	negative regulation of heart contraction (GO:0045822)	BP	13	11	0.272727273	0.001703137
GO:0035725	sodium ion transmembrane transport	down	sodium ion transmembrane transport (GO:0035725)	BP	62	61	0.180327869	0.001703281
GO:0009612	response to mechanical stimulus	down	response to mechanical stimulus (GO:0009612)	BP	83	82	0.097560976	0.001722577
GO:0060841	venous blood vessel development	down	venous blood vessel development (GO:0060841)	BP	13	13	0	0.001728775
GO:0035176	social behavior	down	social behavior (GO:0035176)	BP	26	25	0.16	0.001745982
GO:0050857	positive regulation of antigen receptor-mediated signalin	down	positive regulation of antigen receptor-mediated signaling pathway (GO:	BP	13	12	0.083333333	0.001745982
GO:0051703	intraspecies interaction between organisms	down	intraspecies interaction between organisms (GO:0051703)	BP	26	25	0.16	0.001745982
GO:0034614	cellular response to reactive oxygen species	down	cellular response to reactive oxygen species (GO:0034614)	BP	67	64	0.1875	0.001746411
GO:1903205	regulation of hydrogen peroxide-induced cell death	down	regulation of hydrogen peroxide-induced cell death (GO:1903205)	BP	17	16	0.25	0.001755621
GO:0009395	phospholipid catabolic process	down	phospholipid catabolic process (GO:0009395)	BP	21	21	0.095238095	0.001765881
GO:0051651	maintenance of location in cell	down	maintenance of location in cell (GO:0051651)	BP	48	47	0.127659574	0.001765881
GO:0090278	negative regulation of peptide hormone secretion	down	negative regulation of peptide hormone secretion (GO:0090278)	BP	18	18	0.111111111	0.001783032
GO:0031060	regulation of histone methylation	down	regulation of histone methylation (GO:0031060)	BP	48	47	0.085106383	0.001786967
GO:0072331	signal transduction by p53 class mediator	down	signal transduction by p53 class mediator (GO:0072331)	BP	92	88	0.102272727	0.001791262
GO:1901880	negative regulation of protein depolymerization	down	negative regulation of protein depolymerization (GO:1901880)	BP	35	32	0.1875	0.001795665
GO:0010921	regulation of phosphatase activity	down	regulation of phosphatase activity (GO:0010921)	BP	81	77	0.077922078	0.001806631
GO:0072520	seminiferous tubule development	down	seminiferous tubule development (GO:0072520)	BP	12	11	0.090909091	0.00181709
GO:2000403	positive regulation of lymphocyte migration	down	positive regulation of lymphocyte migration (GO:2000403)	BP	14	13	0.153846154	0.00182653
GO:1901224	positive regulation of NIK/NF-kappaB signaling	down	positive regulation of NIK/NF-kappaB signaling (GO:1901224)	BP	23	23	0.043478261	0.001830724
GO:0008585	female gonad development	down	female gonad development (GO:0008585)	BP	59	58	0.120689655	0.001831205

GO:0046545	development of primary female sexual characteristics	down	development of primary female sexual characteristics (GO:0046545)	BP	60	59	0.118644068	0.001831205
GO:0045071	negative regulation of viral genome replication	down	negative regulation of viral genome replication (GO:0045071)	BP	26	24	0.083333333	0.001858234
GO:0002822	regulation of adaptive immune response based on somati	down	regulation of adaptive immune response based on somatic recombinatio	BP	85	84	0.047619048	0.001874354
GO:1903306	negative regulation of regulated secretory pathway	down	negative regulation of regulated secretory pathway (GO:1903306)	BP	11	11	0.090909091	0.001885745
GO:0006342	chromatin silencing	down	chromatin silencing (GO:0006342)	BP	26	26	0.038461538	0.001895258
GO:0007519	skeletal muscle tissue development	down	skeletal muscle tissue development (GO:0007519)	BP	116	113	0.185840708	0.001912562
GO:0010833	telomere maintenance via telomere lengthening	down	telomere maintenance via telomere lengthening (GO:0010833)	BP	36	36	0.083333333	0.001916296
GO:0032733	positive regulation of interleukin-10 production	down	positive regulation of interleukin-10 production (GO:0032733)	BP	20	20	0.1	0.001922233
GO:0002250	adaptive immune response	down	adaptive immune response (GO:0002250)	BP	153	151	0.052980132	0.001924124
GO:0080111	DNA demethylation	down	DNA demethylation (GO:0080111)	BP	13	13	0	0.001938648
GO:0071677	positive regulation of mononuclear cell migration	down	positive regulation of mononuclear cell migration (GO:0071677)	BP	13	11	0.181818182	0.001938802
GO:0097194	execution phase of apoptosis	down	execution phase of apoptosis (GO:0097194)	BP	38	38	0.105263158	0.001945153
GO:0043931	ossification involved in bone maturation	down	ossification involved in bone maturation (GO:0043931)	BP	13	12	0.416666667	0.00197554
GO:0070977	bone maturation	down	bone maturation (GO:0070977)	BP	13	12	0.416666667	0.00197554
GO:0006836	neurotransmitter transport	down	neurotransmitter transport (GO:0006836)	BP	84	82	0.134146341	0.001981728
GO:0034453	microtubule anchoring	down	microtubule anchoring (GO:0034453)	BP	17	17	0	0.002001852
GO:0044381	glucose import in response to insulin stimulus	down	glucose import in response to insulin stimulus (GO:0044381)	BP	13	12	0.083333333	0.002015437
GO:2001273	regulation of glucose import in response to insulin stimul	down	regulation of glucose import in response to insulin stimulus (GO:200127	BP	13	12	0.083333333	0.002015437
GO:0051973	positive regulation of telomerase activity	down	positive regulation of telomerase activity (GO:0051973)	BP	21	21	0.095238095	0.002017879
GO:0040029	regulation of gene expression, epigenetic	down	regulation of gene expression, epigenetic (GO:0040029)	BP	99	97	0.041237113	0.002022855
GO:0045814	negative regulation of gene expression, epigenetic	down	negative regulation of gene expression, epigenetic (GO:0045814)	BP	31	29	0.034482759	0.002026838
GO:0018958	phenol-containing compound metabolic process	down	phenol-containing compound metabolic process (GO:0018958)	BP	51	50	0.16	0.002045274
GO:0050901	leukocyte tethering or rolling	down	leukocyte tethering or rolling (GO:0050901)	BP	15	13	0.076923077	0.002079479
GO:0008277	regulation of G-protein coupled receptor protein signalin	down	regulation of G-protein coupled receptor protein signaling pathway (GO:	BP	60	57	0.105263158	0.002085919
GO:0003071	renal system process involved in regulation of systemic ar	down	renal system process involved in regulation of systemic arterial blood pre	BP	11	10	0.1	0.002099938
GO:1903317	regulation of protein maturation	down	regulation of protein maturation (GO:1903317)	BP	39	37	0.108108108	0.002101703
GO:0046631	alpha-beta T cell activation	down	alpha-beta T cell activation (GO:0046631)	BP	79	78	0.064102564	0.002131499
GO:0010544	negative regulation of platelet activation	down	negative regulation of platelet activation (GO:0010544)	BP	11	10	0.2	0.002147508
GO:0002548	monocyte chemotaxis	down	monocyte chemotaxis (GO:0002548)	BP	23	20	0.1	0.002193785
GO:0002712	regulation of B cell mediated immunity	down	regulation of B cell mediated immunity (GO:0002712)	BP	35	34	0.058823529	0.002368276
GO:0002889	regulation of immunoglobulin mediated immune respons	down	regulation of immunoglobulin mediated immune response (GO:0002889	BP	35	34	0.058823529	0.002368276
GO:0061756	leukocyte adhesion to vascular endothelial cell	down	leukocyte adhesion to vascular endothelial cell (GO:0061756)	BP	17	15	0.066666667	0.002380851
GO:0031398	positive regulation of protein ubiquitination	down	positive regulation of protein ubiquitination (GO:0031398)	BP	75	74	0.081081081	0.002403715
GO:0042991	transcription factor import into nucleus	down	transcription factor import into nucleus (GO:0042991)	BP	64	63	0.031746032	0.002422616
GO:0055083	monovalent inorganic anion homeostasis	down	monovalent inorganic anion homeostasis (GO:0055083)	BP	13	13	0.153846154	0.002423143
GO:0002460	adaptive immune response based on somatic recombinati	down	adaptive immune response based on somatic recombination of immune r	BP	136	135	0.059259259	0.002428262
GO:0071622	regulation of granulocyte chemotaxis	down	regulation of granulocyte chemotaxis (GO:0071622)	BP	25	25	0.12	0.00243543
GO:0010573	vascular endothelial growth factor production	down	vascular endothelial growth factor production (GO:0010573)	BP	25	24	0.125	0.002437377
GO:0070613	regulation of protein processing	down	regulation of protein processing (GO:0070613)	BP	38	36	0.111111111	0.002449715
GO:0003148	outflow tract septum morphogenesis	down	outflow tract septum morphogenesis (GO:0003148)	BP	16	16	0.0625	0.002484625
GO:0045830	positive regulation of isotype switching	down	positive regulation of isotype switching (GO:0045830)	BP	17	17	0.058823529	0.002494613
GO:0051353	positive regulation of oxidoreductase activity	down	positive regulation of oxidoreductase activity (GO:0051353)	BP	29	28	0.142857143	0.002511988
GO:0045066	regulatory T cell differentiation	down	regulatory T cell differentiation (GO:0045066)	BP	11	10	0	0.002535284
GO:2000249	regulation of actin cytoskeleton reorganization	down	regulation of actin cytoskeleton reorganization (GO:2000249)	BP	20	20	0.05	0.00253619
GO:0000381	regulation of alternative mRNA splicing, via spliceosome	down	regulation of alternative mRNA splicing, via spliceosome (GO:0000381)	BP	25	24	0.041666667	0.002542916
GO:0048538	thymus development	down	thymus development (GO:0048538)	BP	36	35	0.171428571	0.002557485
GO:0018126	protein hydroxylation	down	protein hydroxylation (GO:0018126)	BP	12	12	0.166666667	0.002560773
GO:0033209	tumor necrosis factor-mediated signaling pathway	down	tumor necrosis factor-mediated signaling pathway (GO:0033209)	BP	33	32	0.125	0.002561447
GO:0090311	regulation of protein deacetylation	down	regulation of protein deacetylation (GO:0090311)	BP	25	24	0	0.002561679
GO:0006721	terpenoid metabolic process	down	terpenoid metabolic process (GO:0006721)	BP	32	25	0.28	0.00256743
GO:0016101	diterpenoid metabolic process	down	diterpenoid metabolic process (GO:0016101)	BP	30	24	0.291666667	0.00256743
GO:0051897	positive regulation of protein kinase B signaling	down	positive regulation of protein kinase B signaling (GO:0051897)	BP	56	53	0.056603774	0.002574712
GO:1901021	positive regulation of calcium ion transmembrane transp	down	positive regulation of calcium ion transmembrane transporter activity (G	BP	11	11	0.181818182	0.002585206
GO:0070227	lymphocyte apoptotic process	down	lymphocyte apoptotic process (GO:0070227)	BP	49	48	0.125	0.002612976
GO:1905477	positive regulation of protein localization to membrane	down	positive regulation of protein localization to membrane (GO:1905477)	BP	28	26	0.038461538	0.002630235
GO:0060602	branch elongation of an epithelium	down	branch elongation of an epithelium (GO:0060602)	BP	17	16	0.0625	0.002642318
GO:0006891	intra-Golgi vesicle-mediated transport	down	intra-Golgi vesicle-mediated transport (GO:0006891)	BP	16	16	0	0.002654194
GO:0043242	negative regulation of protein complex disassembly	down	negative regulation of protein complex disassembly (GO:0043242)	BP	40	37	0.162162162	0.002654194
GO:0046068	cGMP metabolic process	down	cGMP metabolic process (GO:0046068)	BP	31	30	0.066666667	0.002664392
GO:0050853	B cell receptor signaling pathway	down	B cell receptor signaling pathway (GO:0050853)	BP	32	32	0.09375	0.002730088
GO:0061014	positive regulation of mRNA catabolic process	down	positive regulation of mRNA catabolic process (GO:0061014)	BP	22	22	0.045454545	0.00277169
GO:0045773	positive regulation of axon extension	down	positive regulation of axon extension (GO:0045773)	BP	19	18	0.111111111	0.002793335
GO:0019882	antigen processing and presentation	down	antigen processing and presentation (GO:0019882)	BP	49	43	0.023255814	0.002806013
GO:0022011	myelination in peripheral nervous system	down	myelination in peripheral nervous system (GO:0022011)	BP	12	12	0	0.002819513

GO:0032292	peripheral nervous system axon ensheathment	down	peripheral nervous system axon ensheathment (GO:0032292)	BP	12	12	0	0.002819513
GO:0099518	vesicle cytoskeletal trafficking	down	vesicle cytoskeletal trafficking (GO:0099518)	BP	23	23	0.043478261	0.002827722
GO:2000273	positive regulation of receptor activity	down	positive regulation of receptor activity (GO:2000273)	BP	15	15	0.133333333	0.002852468
GO:0090342	regulation of cell aging	down	regulation of cell aging (GO:0090342)	BP	22	22	0.090909091	0.002869758
GO:0016125	sterol metabolic process	down	sterol metabolic process (GO:0016125)	BP	58	54	0.092592593	0.002891901
GO:0051588	regulation of neurotransmitter transport	down	regulation of neurotransmitter transport (GO:0051588)	BP	34	34	0.176470588	0.002903271
GO:0002437	inflammatory response to antigenic stimulus	down	inflammatory response to antigenic stimulus (GO:0002437)	BP	24	24	0.041666667	0.002930076
GO:0051604	protein maturation	down	protein maturation (GO:0051604)	BP	144	140	0.092857143	0.002974995
GO:0071356	cellular response to tumor necrosis factor	down	cellular response to tumor necrosis factor (GO:0071356)	BP	75	71	0.154929577	0.003071166
GO:0043902	positive regulation of multi-organism process	down	positive regulation of multi-organism process (GO:0043902)	BP	105	99	0.070707071	0.003077762
GO:0046621	negative regulation of organ growth	down	negative regulation of organ growth (GO:0046621)	BP	14	14	0.071428571	0.003083982
GO:0016574	histone ubiquitination	down	histone ubiquitination (GO:0016574)	BP	33	33	0.060606061	0.003084398
GO:0051058	negative regulation of small GTPase mediated signal trans	down	negative regulation of small GTPase mediated signal transduction (GO:00	BP	30	29	0.137931034	0.003084398
GO:0006349	regulation of gene expression by genetic imprinting	down	regulation of gene expression by genetic imprinting (GO:0006349)	BP	12	12	0.083333333	0.003088209
GO:0072384	organelle transport along microtubule	down	organelle transport along microtubule (GO:0072384)	BP	39	38	0.052631579	0.003101542
GO:0070193	synaptonemal complex organization	down	synaptonemal complex organization (GO:0070193)	BP	20	20	0.1	0.003103425
GO:0042542	response to hydrogen peroxide	down	response to hydrogen peroxide (GO:0042542)	BP	52	50	0.14	0.003112414
GO:0016485	protein processing	down	protein processing (GO:0016485)	BP	115	112	0.098214286	0.003137223
GO:0051043	regulation of membrane protein ectodomain proteolysis	down	regulation of membrane protein ectodomain proteolysis (GO:0051043)	BP	15	15	0.133333333	0.003137223
GO:0051974	negative regulation of telomerase activity	down	negative regulation of telomerase activity (GO:0051974)	BP	10	10	0.1	0.003199209
GO:0035728	response to hepatocyte growth factor	down	response to hepatocyte growth factor (GO:0035728)	BP	13	13	0.230769231	0.003232677
GO:0035729	cellular response to hepatocyte growth factor stimulus	down	cellular response to hepatocyte growth factor stimulus (GO:0035729)	BP	13	13	0.230769231	0.003232677
GO:1903362	regulation of cellular protein catabolic process	down	regulation of cellular protein catabolic process (GO:1903362)	BP	128	122	0.098360656	0.003233284
GO:0009950	dorsal/ventral axis specification	down	dorsal/ventral axis specification (GO:0009950)	BP	12	12	0.083333333	0.003273409
GO:2000516	positive regulation of CD4-positive, alpha-beta T cell activ	down	positive regulation of CD4-positive, alpha-beta T cell activation (GO:2000	BP	16	16	0.0625	0.003305472
GO:0032924	activin receptor signaling pathway	down	activin receptor signaling pathway (GO:0032924)	BP	28	28	0.142857143	0.003314215
GO:0019079	viral genome replication	down	viral genome replication (GO:0019079)	BP	58	54	0.074074074	0.003415367
GO:0032693	negative regulation of interleukin-10 production	down	negative regulation of interleukin-10 production (GO:0032693)	BP	11	10	0.1	0.003415367
GO:0006906	vesicle fusion	down	vesicle fusion (GO:0006906)	BP	31	31	0.064516129	0.003428397
GO:0043277	apoptotic cell clearance	down	apoptotic cell clearance (GO:0043277)	BP	19	18	0.055555556	0.003441823
GO:0008630	intrinsic apoptotic signaling pathway in response to DNA	down	intrinsic apoptotic signaling pathway in response to DNA damage (GO:00	BP	74	74	0.121621622	0.003443547
GO:0040020	regulation of meiotic nuclear division	down	regulation of meiotic nuclear division (GO:0040020)	BP	23	23	0.043478261	0.003487236
GO:0009190	cyclic nucleotide biosynthetic process	down	cyclic nucleotide biosynthetic process (GO:0009190)	BP	81	80	0.0875	0.003519147
GO:0042446	hormone biosynthetic process	down	hormone biosynthetic process (GO:0042446)	BP	24	24	0.125	0.003539889
GO:0034114	regulation of heterotypic cell-cell adhesion	down	regulation of heterotypic cell-cell adhesion (GO:0034114)	BP	14	13	0.076923077	0.003550046
GO:0014902	myotube differentiation	down	myotube differentiation (GO:0014902)	BP	73	72	0.166666667	0.003575195
GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	down	regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043122)	BP	168	162	0.074074074	0.00359463
GO:0070231	T cell apoptotic process	down	T cell apoptotic process (GO:0070231)	BP	33	32	0.125	0.003613378
GO:0050886	endocrine process	down	endocrine process (GO:0050886)	BP	52	50	0.12	0.003671731
GO:0071312	cellular response to alkaloid	down	cellular response to alkaloid (GO:0071312)	BP	10	10	0.1	0.003751961
GO:0048008	platelet-derived growth factor receptor signaling pathwa	down	platelet-derived growth factor receptor signaling pathway (GO:0048008)	BP	36	35	0.085714286	0.003783214
GO:0051044	positive regulation of membrane protein ectodomain pro	down	positive regulation of membrane protein ectodomain proteolysis (GO:00	BP	11	11	0.181818182	0.003789286
GO:0051281	positive regulation of release of sequestered calcium ion i	down	positive regulation of release of sequestered calcium ion into cytosol (GO:	BP	21	21	0.095238095	0.003798966
GO:0046425	regulation of JAK-STAT cascade	down	regulation of JAK-STAT cascade (GO:0046425)	BP	30	29	0.068965517	0.003830064
GO:1904892	regulation of STAT cascade	down	regulation of STAT cascade (GO:1904892)	BP	30	29	0.068965517	0.003830064
GO:0051445	regulation of meiotic cell cycle	down	regulation of meiotic cell cycle (GO:0051445)	BP	30	30	0.066666667	0.00388055
GO:0090025	regulation of monocyte chemotaxis	down	regulation of monocyte chemotaxis (GO:0090025)	BP	14	12	0.166666667	0.00388055
GO:0042982	amyloid precursor protein metabolic process	down	amyloid precursor protein metabolic process (GO:0042982)	BP	18	18	0.111111111	0.003881213
GO:0090279	regulation of calcium ion import	down	regulation of calcium ion import (GO:0090279)	BP	17	16	0	0.003941448
GO:1902652	secondary alcohol metabolic process	down	secondary alcohol metabolic process (GO:1902652)	BP	59	54	0.092592593	0.003942033
GO:0060442	branching involved in prostate gland morphogenesis	down	branching involved in prostate gland morphogenesis (GO:0060442)	BP	10	9	0.222222222	0.003942214
GO:0042462	eye photoreceptor cell development	down	eye photoreceptor cell development (GO:0042462)	BP	26	26	0.153846154	0.003951338
GO:0046580	negative regulation of Ras protein signal transduction	down	negative regulation of Ras protein signal transduction (GO:0046580)	BP	29	28	0.142857143	0.004095819
GO:0036474	cell death in response to hydrogen peroxide	down	cell death in response to hydrogen peroxide (GO:0036474)	BP	19	18	0.222222222	0.004120302
GO:1903364	positive regulation of cellular protein catabolic process	down	positive regulation of cellular protein catabolic process (GO:1903364)	BP	67	62	0.129032258	0.00413812
GO:0032413	negative regulation of ion transmembrane transporter act	down	negative regulation of ion transmembrane transporter activity (GO:0032	BP	23	23	0	0.004167527
GO:0010829	negative regulation of glucose transport	down	negative regulation of glucose transport (GO:0010829)	BP	13	13	0	0.00417241
GO:0000271	polysaccharide biosynthetic process	down	polysaccharide biosynthetic process (GO:0000271)	BP	37	36	0.083333333	0.004182757
GO:0043496	regulation of protein homodimerization activity	down	regulation of protein homodimerization activity (GO:0043496)	BP	12	12	0.333333333	0.004184791
GO:0048641	regulation of skeletal muscle tissue development	down	regulation of skeletal muscle tissue development (GO:0048641)	BP	32	29	0.172413793	0.004197879
GO:0035304	regulation of protein dephosphorylation	down	regulation of protein dephosphorylation (GO:0035304)	BP	40	38	0.105263158	0.004207372
GO:0007259	JAK-STAT cascade	down	JAK-STAT cascade (GO:0007259)	BP	37	36	0.055555556	0.004212804
GO:0051701	interaction with host	down	interaction with host (GO:0051701)	BP	87	79	0.050632911	0.004212804
GO:0097696	STAT cascade	down	STAT cascade (GO:0097696)	BP	37	36	0.055555556	0.004212804

GO:0010662	regulation of striated muscle cell apoptotic process	down	regulation of striated muscle cell apoptotic process (GO:0010662)	BP	11	11	0.090909091	0.004276382
GO:1903322	positive regulation of protein modification by small prote	down	positive regulation of protein modification by small protein conjugation	BP	87	85	0.070588235	0.004324184
GO:0010517	regulation of phospholipase activity	down	regulation of phospholipase activity (GO:0010517)	BP	28	28	0.107142857	0.004336823
GO:0048642	negative regulation of skeletal muscle tissue development	down	negative regulation of skeletal muscle tissue development (GO:0048642)	BP	11	10	0.1	0.004349611
GO:1904353	regulation of telomere capping	down	regulation of telomere capping (GO:1904353)	BP	17	17	0.117647059	0.00437841
GO:0042990	regulation of transcription factor import into nucleus	down	regulation of transcription factor import into nucleus (GO:0042990)	BP	63	62	0.032258065	0.004382702
GO:0006720	isoprenoid metabolic process	down	isoprenoid metabolic process (GO:0006720)	BP	52	44	0.159090909	0.004470436
GO:0034644	cellular response to UV	down	cellular response to UV (GO:0034644)	BP	47	46	0.152173913	0.004497071
GO:0048278	vesicle docking	down	vesicle docking (GO:0048278)	BP	21	21	0.047619048	0.004497071
GO:0140056	organelle localization by membrane tethering	down	organelle localization by membrane tethering (GO:0140056)	BP	21	21	0.047619048	0.004497071
GO:0010324	membrane invagination	down	membrane invagination (GO:0010324)	BP	33	32	0.0625	0.004501173
GO:0001938	positive regulation of endothelial cell proliferation	down	positive regulation of endothelial cell proliferation (GO:0001938)	BP	41	39	0.051282051	0.004537178
GO:0006402	mRNA catabolic process	down	mRNA catabolic process (GO:0006402)	BP	99	98	0.071428571	0.00455515
GO:0033144	negative regulation of intracellular steroid hormone recep	down	negative regulation of intracellular steroid hormone receptor signaling pa	BP	25	23	0.086956522	0.004565103
GO:0021533	cell differentiation in hindbrain	down	cell differentiation in hindbrain (GO:0021533)	BP	16	15	0.066666667	0.004609082
GO:0048016	inositol phosphate-mediated signaling	down	inositol phosphate-mediated signaling (GO:0048016)	BP	22	22	0.227272727	0.004623531
GO:1901570	fatty acid derivative biosynthetic process	down	fatty acid derivative biosynthetic process (GO:1901570)	BP	33	32	0.21875	0.004649629
GO:0032088	negative regulation of NF-kappaB transcription factor acti	down	negative regulation of NF-kappaB transcription factor activity (GO:00320	BP	50	48	0.0625	0.004655632
GO:0043114	regulation of vascular permeability	down	regulation of vascular permeability (GO:0043114)	BP	14	14	0.071428571	0.004738542
GO:0008088	axo-dendritic transport	down	axo-dendritic transport (GO:0008088)	BP	21	20	0.05	0.004756549
GO:0071482	cellular response to light stimulus	down	cellular response to light stimulus (GO:0071482)	BP	53	51	0.137254902	0.004763127
GO:0046325	negative regulation of glucose import	down	negative regulation of glucose import (GO:0046325)	BP	10	10	0	0.004812128
GO:0050926	regulation of positive chemotaxis	down	regulation of positive chemotaxis (GO:0050926)	BP	12	11	0	0.004819893
GO:0048147	negative regulation of fibroblast proliferation	down	negative regulation of fibroblast proliferation (GO:0048147)	BP	21	21	0.095238095	0.004850982
GO:0051260	protein homooligomerization	down	protein homooligomerization (GO:0051260)	BP	168	163	0.128834356	0.004873354
GO:0072310	glomerular epithelial cell development	down	glomerular epithelial cell development (GO:0072310)	BP	10	10	0.2	0.004907195
GO:0051926	negative regulation of calcium ion transport	down	negative regulation of calcium ion transport (GO:0051926)	BP	19	19	0.052631579	0.00493542
GO:0033673	negative regulation of kinase activity	down	negative regulation of kinase activity (GO:0033673)	BP	130	126	0.087301587	0.004938167
GO:0034103	regulation of tissue remodeling	down	regulation of tissue remodeling (GO:0034103)	BP	38	38	0.157894737	0.005009163
GO:1901186	positive regulation of ERBB signaling pathway	down	positive regulation of ERBB signaling pathway (GO:1901186)	BP	14	14	0.142857143	0.005048031
GO:0035855	megakaryocyte development	down	megakaryocyte development (GO:0035855)	BP	15	14	0	0.005050736
GO:0010955	negative regulation of protein processing	down	negative regulation of protein processing (GO:0010955)	BP	15	14	0.142857143	0.005052516
GO:1903318	negative regulation of protein maturation	down	negative regulation of protein maturation (GO:1903318)	BP	15	14	0.142857143	0.005052516
GO:2000379	positive regulation of reactive oxygen species metabolic p	down	positive regulation of reactive oxygen species metabolic process (GO:200	BP	43	41	0.12195122	0.005065545
GO:1901264	carbohydrate derivative transport	down	carbohydrate derivative transport (GO:1901264)	BP	37	36	0.027777778	0.005086213
GO:0070098	chemokine-mediated signaling pathway	down	chemokine-mediated signaling pathway (GO:0070098)	BP	22	20	0.25	0.005252417
GO:0045739	positive regulation of DNA repair	down	positive regulation of DNA repair (GO:0045739)	BP	26	26	0.192307692	0.005302169
GO:0043434	response to peptide hormone	down	response to peptide hormone (GO:0043434)	BP	136	134	0.104477612	0.00535971
GO:0002824	positive regulation of adaptive immune response based o	down	positive regulation of adaptive immune response based on somatic recom	BP	56	55	0.054545455	0.005497387
GO:0043967	histone H4 acetylation	down	histone H4 acetylation (GO:0043967)	BP	47	46	0.043478261	0.005521322
GO:0001541	ovarian follicle development	down	ovarian follicle development (GO:0001541)	BP	30	29	0.137931034	0.005635037
GO:0048009	insulin-like growth factor receptor signaling pathway	down	insulin-like growth factor receptor signaling pathway (GO:0048009)	BP	22	22	0.045454545	0.005674003
GO:0050779	RNA destabilization	down	RNA destabilization (GO:0050779)	BP	11	11	0	0.005692186
GO:0007212	dopamine receptor signaling pathway	down	dopamine receptor signaling pathway (GO:0007212)	BP	19	18	0.055555556	0.005710829
GO:1901797	negative regulation of signal transduction by p53 class me	down	negative regulation of signal transduction by p53 class mediator (GO:190	BP	20	20	0.15	0.005718557
GO:0043161	proteasome-mediated ubiquitin-dependent protein catab	down	proteasome-mediated ubiquitin-dependent protein catabolic process (G	BP	172	167	0.077844311	0.005764151
GO:0043567	regulation of insulin-like growth factor receptor signaling	down	regulation of insulin-like growth factor receptor signaling pathway (GO:0	BP	15	15	0.066666667	0.005774344
GO:0071326	cellular response to monosaccharide stimulus	down	cellular response to monosaccharide stimulus (GO:0071326)	BP	45	43	0.139534884	0.005774344
GO:0071331	cellular response to hexose stimulus	down	cellular response to hexose stimulus (GO:0071331)	BP	45	43	0.139534884	0.005774344
GO:0071333	cellular response to glucose stimulus	down	cellular response to glucose stimulus (GO:0071333)	BP	45	43	0.139534884	0.005774344
GO:0042074	cell migration involved in gastrulation	down	cell migration involved in gastrulation (GO:0042074)	BP	12	12	0.083333333	0.005906626
GO:0021697	cerebellar cortex formation	down	cerebellar cortex formation (GO:0021697)	BP	20	18	0.111111111	0.005913315
GO:0050873	brown fat cell differentiation	down	brown fat cell differentiation (GO:0050873)	BP	36	36	0.25	0.00596204
GO:0005979	regulation of glycogen biosynthetic process	down	regulation of glycogen biosynthetic process (GO:0005979)	BP	13	13	0.153846154	0.00598602
GO:0010962	regulation of glucan biosynthetic process	down	regulation of glucan biosynthetic process (GO:0010962)	BP	13	13	0.153846154	0.00598602
GO:0048002	antigen processing and presentation of peptide antigen	down	antigen processing and presentation of peptide antigen (GO:0048002)	BP	23	18	0	0.00604056
GO:0000380	alternative mRNA splicing, via spliceosome	down	alternative mRNA splicing, via spliceosome (GO:0000380)	BP	35	34	0.029411765	0.006066991
GO:0010837	regulation of keratinocyte proliferation	down	regulation of keratinocyte proliferation (GO:0010837)	BP	23	23	0.173913043	0.006068086
GO:0055062	phosphate ion homeostasis	down	phosphate ion homeostasis (GO:0055062)	BP	10	10	0.1	0.006079241
GO:0072505	divalent inorganic anion homeostasis	down	divalent inorganic anion homeostasis (GO:0072505)	BP	10	10	0.1	0.006079241
GO:0072506	trivalent inorganic anion homeostasis	down	trivalent inorganic anion homeostasis (GO:0072506)	BP	10	10	0.1	0.006079241
GO:0090174	organelle membrane fusion	down	organelle membrane fusion (GO:0090174)	BP	32	32	0.0625	0.006142504
GO:0046467	membrane lipid biosynthetic process	down	membrane lipid biosynthetic process (GO:0046467)	BP	61	61	0.049180328	0.006185667
GO:0002381	immunoglobulin production involved in immunoglobuli	down	immunoglobulin production involved in immunoglobulin mediated imm	BP	38	38	0.052631579	0.006191564

GO:1901222	regulation of NIK/NF-kappaB signaling	down	regulation of NIK/NF-kappaB signaling (GO:1901222)	BP	33	33	0.060606061	0.006223907
GO:0030799	regulation of cyclic nucleotide metabolic process	down	regulation of cyclic nucleotide metabolic process (GO:0030799)	BP	72	70	0.071428571	0.006270619
GO:0031349	positive regulation of defense response	down	positive regulation of defense response (GO:0031349)	BP	177	172	0.069767442	0.006291728
GO:0060401	cytosolic calcium ion transport	down	cytosolic calcium ion transport (GO:0060401)	BP	77	73	0.109589041	0.006333726
GO:0042108	positive regulation of cytokine biosynthetic process	down	positive regulation of cytokine biosynthetic process (GO:0042108)	BP	44	44	0.068181818	0.006360053
GO:0002204	somatic recombination of immunoglobulin genes involve	down	somatic recombination of immunoglobulin genes involved in immune re	BP	35	35	0.057142857	0.006414191
GO:0002208	somatic diversification of immunoglobulins involved in ir	down	somatic diversification of immunoglobulins involved in immune respons	BP	35	35	0.057142857	0.006414191
GO:0045190	isotype switching	down	isotype switching (GO:0045190)	BP	35	35	0.057142857	0.006414191
GO:2000272	negative regulation of receptor activity	down	negative regulation of receptor activity (GO:2000272)	BP	17	17	0.058823529	0.006420849
GO:0032011	ARF protein signal transduction	down	ARF protein signal transduction (GO:0032011)	BP	15	15	0.066666667	0.006442822
GO:0032012	regulation of ARF protein signal transduction	down	regulation of ARF protein signal transduction (GO:0032012)	BP	15	15	0.066666667	0.006442822
GO:0006940	regulation of smooth muscle contraction	down	regulation of smooth muscle contraction (GO:0006940)	BP	26	26	0.153846154	0.006503786
GO:0050854	regulation of antigen receptor-mediated signaling pathwa	down	regulation of antigen receptor-mediated signaling pathway (GO:0050854	BP	31	30	0.066666667	0.006557458
GO:0035065	regulation of histone acetylation	down	regulation of histone acetylation (GO:0035065)	BP	32	32	0.125	0.006559247
GO:0035162	embryonic hemopoiesis	down	embryonic hemopoiesis (GO:0035162)	BP	15	15	0	0.006667011
GO:0006182	cGMP biosynthetic process	down	cGMP biosynthetic process (GO:0006182)	BP	21	20	0.1	0.006701744
GO:0007588	excretion	down	excretion (GO:0007588)	BP	21	21	0.142857143	0.00671761
GO:0031333	negative regulation of protein complex assembly	down	negative regulation of protein complex assembly (GO:0031333)	BP	70	66	0.106060606	0.006749174
GO:0070979	protein K11-linked ubiquitination	down	protein K11-linked ubiquitination (GO:0070979)	BP	16	16	0.125	0.006749174
GO:0035270	endocrine system development	down	endocrine system development (GO:0035270)	BP	91	89	0.112359551	0.0068322
GO:0043616	keratinocyte proliferation	down	keratinocyte proliferation (GO:0043616)	BP	31	31	0.193548387	0.0068322
GO:1901184	regulation of ERBB signaling pathway	down	regulation of ERBB signaling pathway (GO:1901184)	BP	37	37	0.108108108	0.006859447
GO:0080182	histone H3-K4 trimethylation	down	histone H3-K4 trimethylation (GO:0080182)	BP	12	10	0	0.00695969
GO:0043299	leukocyte degranulation	down	leukocyte degranulation (GO:0043299)	BP	36	35	0.028571429	0.007017942
GO:0045058	T cell selection	down	T cell selection (GO:0045058)	BP	32	31	0.096774194	0.007025195
GO:0050860	negative regulation of T cell receptor signaling pathway	down	negative regulation of T cell receptor signaling pathway (GO:0050860)	BP	10	10	0.1	0.007083518
GO:0035914	skeletal muscle cell differentiation	down	skeletal muscle cell differentiation (GO:0035914)	BP	55	53	0.226415094	0.00715368
GO:0015695	organic cation transport	down	organic cation transport (GO:0015695)	BP	16	16	0.125	0.007177876
GO:1901032	negative regulation of response to reactive oxygen species	down	negative regulation of response to reactive oxygen species (GO:1901032)	BP	14	13	0.230769231	0.007207997
GO:1903206	negative regulation of hydrogen peroxide-induced cell dea	down	negative regulation of hydrogen peroxide-induced cell death (GO:190320	BP	14	13	0.230769231	0.007207997
GO:0006469	negative regulation of protein kinase activity	down	negative regulation of protein kinase activity (GO:0006469)	BP	121	118	0.084745763	0.007350252
GO:1903312	negative regulation of mRNA metabolic process	down	negative regulation of mRNA metabolic process (GO:1903312)	BP	42	42	0.071428571	0.007363912
GO:1903533	regulation of protein targeting	down	regulation of protein targeting (GO:1903533)	BP	86	81	0.061728395	0.007390024
GO:0016925	protein sumoylation	down	protein sumoylation (GO:0016925)	BP	25	24	0	0.007439156
GO:0060218	hematopoietic stem cell differentiation	down	hematopoietic stem cell differentiation (GO:0060218)	BP	11	10	0.1	0.007503187
GO:0009166	nucleotide catabolic process	down	nucleotide catabolic process (GO:0009166)	BP	29	24	0	0.007552838
GO:0015748	organophosphate ester transport	down	organophosphate ester transport (GO:0015748)	BP	50	48	0.083333333	0.007557267
GO:0035307	positive regulation of protein dephosphorylation	down	positive regulation of protein dephosphorylation (GO:0035307)	BP	25	24	0.166666667	0.007641735
GO:0038061	NIK/NF-kappaB signaling	down	NIK/NF-kappaB signaling (GO:0038061)	BP	35	35	0.057142857	0.007649722
GO:2000377	regulation of reactive oxygen species metabolic process	down	regulation of reactive oxygen species metabolic process (GO:2000377)	BP	85	81	0.172839506	0.007695675
GO:0032606	type I interferon production	down	type I interferon production (GO:0032606)	BP	44	44	0.090909091	0.007776887
GO:0031644	regulation of neurological system process	down	regulation of neurological system process (GO:0031644)	BP	24	23	0.043478261	0.007866719
GO:0006650	glycerophospholipid metabolic process	down	glycerophospholipid metabolic process (GO:0006650)	BP	138	134	0.037313433	0.007903113
GO:0061157	mRNA destabilization	down	mRNA destabilization (GO:0061157)	BP	10	10	0	0.007963257
GO:0002821	positive regulation of adaptive immune response	down	positive regulation of adaptive immune response (GO:0002821)	BP	57	56	0.053571429	0.008025425
GO:0022406	membrane docking	down	membrane docking (GO:0022406)	BP	27	27	0.037037037	0.008027187
GO:0006401	RNA catabolic process	down	RNA catabolic process (GO:0006401)	BP	116	115	0.069565217	0.008156007
GO:1900119	positive regulation of execution phase of apoptosis	down	positive regulation of execution phase of apoptosis (GO:1900119)	BP	10	10	0.2	0.008156007
GO:0070306	lens fiber cell differentiation	down	lens fiber cell differentiation (GO:0070306)	BP	17	16	0.125	0.008174973
GO:0055010	ventricular cardiac muscle tissue morphogenesis	down	ventricular cardiac muscle tissue morphogenesis (GO:0055010)	BP	36	35	0.142857143	0.008225233
GO:0002819	regulation of adaptive immune response	down	regulation of adaptive immune response (GO:0002819)	BP	91	89	0.04494382	0.008314019
GO:0061045	negative regulation of wound healing	down	negative regulation of wound healing (GO:0061045)	BP	37	36	0.083333333	0.00831614
GO:0060142	regulation of syncytium formation by plasma membrane f	down	regulation of syncytium formation by plasma membrane fusion (GO:006C	BP	21	21	0.047619048	0.008373403
GO:0032496	response to lipopolysaccharide	down	response to lipopolysaccharide (GO:0032496)	BP	139	130	0.069230769	0.00838316
GO:0032233	positive regulation of actin filament bundle assembly	down	positive regulation of actin filament bundle assembly (GO:0032233)	BP	33	31	0.064516129	0.008409032
GO:0050852	T cell receptor signaling pathway	down	T cell receptor signaling pathway (GO:0050852)	BP	51	47	0.063829787	0.00846587
GO:0031623	receptor internalization	down	receptor internalization (GO:0031623)	BP	55	53	0.037735849	0.008490522
GO:0008654	phospholipid biosynthetic process	down	phospholipid biosynthetic process (GO:0008654)	BP	76	71	0.042253521	0.008559347
GO:1903902	positive regulation of viral life cycle	down	positive regulation of viral life cycle (GO:1903902)	BP	43	41	0.097560976	0.008657851
GO:0035588	G-protein coupled purinergic receptor signaling pathway	down	G-protein coupled purinergic receptor signaling pathway (GO:0035588)	BP	16	16	0.125	0.00867584
GO:0051023	regulation of immunoglobulin secretion	down	regulation of immunoglobulin secretion (GO:0051023)	BP	11	11	0	0.008709913
GO:0010658	striated muscle cell apoptotic process	down	striated muscle cell apoptotic process (GO:0010658)	BP	12	12	0.083333333	0.008974381
GO:0052652	cyclic purine nucleotide metabolic process	down	cyclic purine nucleotide metabolic process (GO:0052652)	BP	80	79	0.075949367	0.008974381
GO:0032868	response to insulin	down	response to insulin (GO:0032868)	BP	107	106	0.103773585	0.008993791

	GO:0034599	cellular response to oxidative stress	down	cellular response to oxidative stress (GO:0034599)	BP	125	121	0.140495868	0.008993791
	GO:0042058	regulation of epidermal growth factor receptor signaling p	down	regulation of epidermal growth factor receptor signaling pathway (GO:00	BP	34	34	0.117647059	0.009023533
	GO:0051443	positive regulation of ubiquitin-protein transferase activit	down	positive regulation of ubiquitin-protein transferase activity (GO:0051443	BP	17	17	0.117647059	0.009055674
	GO:0016458	gene silencing	down	gene silencing (GO:0016458)	BP	75	74	0.027027027	0.009169915
	GO:0032637	interleukin-8 production	down	interleukin-8 production (GO:0032637)	BP	51	51	0.058823529	0.009290139
	GO:0051895	negative regulation of focal adhesion assembly	down	negative regulation of focal adhesion assembly (GO:0051895)	BP	11	11	0	0.009340892
	GO:0005976	polysaccharide metabolic process	down	polysaccharide metabolic process (GO:0005976)	BP	58	57	0.087719298	0.00938382
	GO:0045601	regulation of endothelial cell differentiation	down	regulation of endothelial cell differentiation (GO:0045601)	BP	20	20	0.15	0.009413718
	GO:0060765	regulation of androgen receptor signaling pathway	down	regulation of androgen receptor signaling pathway (GO:0060765)	BP	19	19	0.052631579	0.009429039
	GO:0050482	arachidonic acid secretion	down	arachidonic acid secretion (GO:0050482)	BP	12	12	0.083333333	0.009431091
	GO:1903963	arachidonate transport	down	arachidonate transport (GO:1903963)	BP	12	12	0.083333333	0.009431091
	GO:1904355	positive regulation of telomere capping	down	positive regulation of telomere capping (GO:1904355)	BP	12	12	0.166666667	0.009462053
	GO:0042461	photoreceptor cell development	down	photoreceptor cell development (GO:0042461)	BP	32	30	0.133333333	0.009717896
	GO:0045070	positive regulation of viral genome replication	down	positive regulation of viral genome replication (GO:0045070)	BP	28	27	0.111111111	0.00976694
	GO:0048511	rhythmic process	down	rhythmic process (GO:0048511)	BP	144	142	0.112676056	0.00976694
	GO:0044346	fibroblast apoptotic process	down	fibroblast apoptotic process (GO:0044346)	BP	15	15	0.133333333	0.00982577
	GO:0001678	cellular glucose homeostasis	down	cellular glucose homeostasis (GO:0001678)	BP	58	56	0.107142857	0.009838374
	GO:1901136	carbohydrate derivative catabolic process	down	carbohydrate derivative catabolic process (GO:1901136)	BP	74	68	0.058823529	0.009910628
	GO:0048821	erythrocyte development	down	erythrocyte development (GO:0048821)	BP	19	19	0	0.009921851
	GO:0042267	natural killer cell mediated cytotoxicity	down	natural killer cell mediated cytotoxicity (GO:0042267)	BP	30	26	0.038461538	0.009928355
	GO:1903747	regulation of establishment of protein localization to mit	down	regulation of establishment of protein localization to mitochondrion (GC	BP	69	65	0.061538462	0.009999502

D90 to Birth

Down Regulated

Clas	**GO ID**	**GO Description**	**Direction of c**	**GO Description and ID**	**Class**	**Size**	**Size in data**	**% in data**	**FDR.adj.pval**
CELLULAR COMPONENT									
	GO:0000775	chromosome, centromeric region	down	chromosome, centromeric region (GO:0000775)	CC	110	107	0.242990654	4.44089E-16
	GO:0000776	kinetochore	down	kinetochore (GO:0000776)	CC	80	79	0.265822785	4.44089E-16
	GO:0000777	condensed chromosome kinetochore	down	condensed chromosome kinetochore (GO:0000777)	CC	17	16	0.375	4.44089E-16
	GO:0000779	condensed chromosome, centromeric region	down	condensed chromosome, centromeric region (GO:0000779)	CC	23	22	0.363636364	4.44089E-16
	GO:0000780	condensed nuclear chromosome, centromeric region	down	condensed nuclear chromosome, centromeric region (GO:0000780)	CC	10	10	0.4	4.44089E-16
	GO:0000793	condensed chromosome	down	condensed chromosome (GO:0000793)	CC	101	94	0.20212766	4.44089E-16
	GO:0000922	spindle pole	down	spindle pole (GO:0000922)	CC	73	70	0.214285714	4.44089E-16
	GO:0001518	voltage-gated sodium channel complex	down	voltage-gated sodium channel complex (GO:0001518)	CC	14	14	0.5	4.44089E-16
	GO:0005578	proteinaceous extracellular matrix	down	proteinaceous extracellular matrix (GO:0005578)	CC	190	187	0.368983957	4.44089E-16
	GO:0005581	collagen trimer	down	collagen trimer (GO:0005581)	CC	41	39	0.435897436	4.44089E-16
	GO:0005583	fibrillar collagen trimer	down	fibrillar collagen trimer (GO:0005583)	CC	10	10	1	4.44089E-16
	GO:0005604	basement membrane	down	basement membrane (GO:0005604)	CC	64	63	0.349206349	4.44089E-16
	GO:0005605	basal lamina	down	basal lamina (GO:0005605)	CC	16	16	0.375	4.44089E-16
	GO:0005614	interstitial matrix	down	interstitial matrix (GO:0005614)	CC	11	10	0.4	4.44089E-16
	GO:0005721	pericentric heterochromatin	down	pericentric heterochromatin (GO:0005721)	CC	16	15	0.133333333	4.44089E-16
	GO:0005814	centriole	down	centriole (GO:0005814)	CC	70	68	0.191176471	4.44089E-16
	GO:0005819	spindle	down	spindle (GO:0005819)	CC	165	160	0.1875	4.44089E-16
	GO:0005874	microtubule	down	microtubule (GO:0005874)	CC	159	147	0.210884354	4.44089E-16
	GO:0005930	axoneme	down	axoneme (GO:0005930)	CC	51	50	0.2	4.44089E-16
	GO:0010369	chromocenter	down	chromocenter (GO:0010369)	CC	12	12	0.25	4.44089E-16
	GO:0030496	midbody	down	midbody (GO:0030496)	CC	87	84	0.226190476	4.44089E-16
	GO:0030990	intraciliary transport particle	down	intraciliary transport particle (GO:0030990)	CC	26	26	0.115384615	4.44089E-16
	GO:0044420	extracellular matrix component	down	extracellular matrix component (GO:0044420)	CC	81	80	0.425	4.44089E-16
	GO:0044450	microtubule organizing center part	down	microtubule organizing center part (GO:0044450)	CC	102	99	0.151515152	4.44089E-16
	GO:0051233	spindle midzone	down	spindle midzone (GO:0051233)	CC	19	19	0.473684211	4.44089E-16
	GO:0072686	mitotic spindle	down	mitotic spindle (GO:0072686)	CC	41	40	0.25	4.44089E-16
	GO:0097014	ciliary plasm	down	ciliary plasm (GO:0097014)	CC	51	50	0.2	4.44089E-16
	GO:0097546	ciliary base	down	ciliary base (GO:0097546)	CC	16	16	0.25	4.44089E-16
	GO:0098643	banded collagen fibril	down	banded collagen fibril (GO:0098643)	CC	10	10	1	4.44089E-16
	GO:0098644	complex of collagen trimers	down	complex of collagen trimers (GO:0098644)	CC	16	15	0.733333333	4.44089E-16
	GO:0030424	axon	down	axon (GO:0030424)	CC	159	154	0.162337662	1.79856E-14
	GO:0036064	ciliary basal body	down	ciliary basal body (GO:0036064)	CC	69	65	0.123076923	1.79856E-14
	GO:0098794	postsynapse	down	postsynapse (GO:0098794)	CC	154	151	0.125827815	1.79856E-14
	GO:0005876	spindle microtubule	down	spindle microtubule (GO:0005876)	CC	36	33	0.272727273	3.19744E-14
	GO:0030425	dendrite	down	dendrite (GO:0030425)	CC	145	137	0.153284672	3.19744E-14
	GO:0033267	axon part	down	axon part (GO:0033267)	CC	61	60	0.133333333	3.19744E-14
	GO:0035869	ciliary transition zone	down	ciliary transition zone (GO:0035869)	CC	49	44	0.090909091	3.19744E-14
	GO:0098802	plasma membrane receptor complex	down	plasma membrane receptor complex (GO:0098802)	CC	120	117	0.145299145	5.9952E-14

GO:0000139	Golgi membrane	down	Golgi membrane (GO:0000139)	CC	148	143	0.097902098	1.7808E-13
GO:0042555	MCM complex	down	MCM complex (GO:0042555)	CC	10	10	0.3	3.63931E-13
GO:0030992	intraciliary transport particle B	down	intraciliary transport particle B (GO:0030992)	CC	15	15	0.066666667	4.84057E-13
GO:0030027	lamellipodium	down	lamellipodium (GO:0030027)	CC	103	101	0.118811881	6.29941E-13
GO:0043025	neuronal cell body	down	neuronal cell body (GO:0043025)	CC	127	118	0.13559322	6.29941E-13
GO:0030139	endocytic vesicle	down	endocytic vesicle (GO:0030139)	CC	88	87	0.114942529	1.04805E-12
GO:0044853	plasma membrane raft	down	plasma membrane raft (GO:0044853)	CC	49	49	0.224489796	1.17395E-12
GO:0034706	sodium channel complex	down	sodium channel complex (GO:0034706)	CC	19	19	0.368421053	1.61804E-12
GO:0032588	trans-Golgi network membrane	down	trans-Golgi network membrane (GO:0032588)	CC	14	14	0.071428571	2.00795E-12
GO:0014069	postsynaptic density	down	postsynaptic density (GO:0014069)	CC	72	69	0.144927536	3.07998E-12
GO:0032279	asymmetric synapse	down	asymmetric synapse (GO:0032279)	CC	72	69	0.144927536	3.07998E-12
GO:0098984	neuron to neuron synapse	down	neuron to neuron synapse (GO:0098984)	CC	72	69	0.144927536	3.07998E-12
GO:0099572	postsynaptic specialization	down	postsynaptic specialization (GO:0099572)	CC	72	69	0.144927536	3.07998E-12
GO:0031253	cell projection membrane	down	cell projection membrane (GO:0031253)	CC	111	108	0.138888889	3.36597E-12
GO:0043296	apical junction complex	down	apical junction complex (GO:0043296)	CC	83	76	0.078947368	5.23603E-12
GO:0097060	synaptic membrane	down	synaptic membrane (GO:0097060)	CC	74	74	0.162162162	7.9261E-12
GO:0045121	membrane raft	down	membrane raft (GO:0045121)	CC	139	136	0.176470588	8.79607E-12
GO:0098857	membrane microdomain	down	membrane microdomain (GO:0098857)	CC	139	136	0.176470588	8.79607E-12
GO:0099568	cytoplasmic region	down	cytoplasmic region (GO:0099568)	CC	141	134	0.097014925	8.79607E-12
GO:0005938	cell cortex	down	cell cortex (GO:0005938)	CC	123	116	0.103448276	1.2244E-11
GO:0044304	main axon	down	main axon (GO:0044304)	CC	25	25	0.2	1.25719E-11
GO:0098797	plasma membrane protein complex	down	plasma membrane protein complex (GO:0098797)	CC	133	119	0.100840336	1.68181E-11
GO:0032153	cell division site	down	cell division site (GO:0032153)	CC	23	23	0.260869565	1.8044E-11
GO:0032155	cell division site part	down	cell division site part (GO:0032155)	CC	23	23	0.260869565	1.8044E-11
GO:0005901	caveola	down	caveola (GO:0005901)	CC	44	44	0.227272727	1.8558E-11
GO:0032580	Golgi cisterna membrane	down	Golgi cisterna membrane (GO:0032580)	CC	13	12	0.166666667	2.14759E-11
GO:0032281	AMPA glutamate receptor complex	down	AMPA glutamate receptor complex (GO:0032281)	CC	16	15	0.2	2.9694E-11
GO:0098636	protein complex involved in cell adhesion	down	protein complex involved in cell adhesion (GO:0098636)	CC	31	31	0.193548387	3.34861E-11
GO:0098589	membrane region	down	membrane region (GO:0098589)	CC	171	168	0.154761905	4.87179E-11
GO:0008305	integrin complex	down	integrin complex (GO:0008305)	CC	28	28	0.214285714	5.5048E-11
GO:0035371	microtubule plus-end	down	microtubule plus-end (GO:0035371)	CC	12	12	0.333333333	5.7484E-11
GO:0034702	ion channel complex	down	ion channel complex (GO:0034702)	CC	158	153	0.176470588	6.09319E-11
GO:0001772	immunological synapse	down	immunological synapse (GO:0001772)	CC	28	26	0.076923077	1.04614E-10
GO:0034703	cation channel complex	down	cation channel complex (GO:0034703)	CC	132	127	0.181102362	1.08278E-10
GO:0005798	Golgi-associated vesicle	down	Golgi-associated vesicle (GO:0005798)	CC	55	54	0.148148148	1.0872E-10
GO:0005802	trans-Golgi network	down	trans-Golgi network (GO:0005802)	CC	92	90	0.1	1.166E-10
GO:0031256	leading edge membrane	down	leading edge membrane (GO:0031256)	CC	56	56	0.107142857	1.29428E-10
GO:0043073	germ cell nucleus	down	germ cell nucleus (GO:0043073)	CC	13	12	0.166666667	1.71518E-10
GO:0000794	condensed nuclear chromosome	down	condensed nuclear chromosome (GO:0000794)	CC	61	58	0.137931034	1.7177E-10
GO:0035861	site of double-strand break	down	site of double-strand break (GO:0035861)	CC	24	22	0.090909091	2.00354E-10
GO:0090734	site of DNA damage	down	site of DNA damage (GO:0090734)	CC	24	22	0.090909091	2.00354E-10
GO:0001741	XY body	down	XY body (GO:0001741)	CC	10	9	0.222222222	2.31472E-10
GO:0055038	recycling endosome membrane	down	recycling endosome membrane (GO:0055038)	CC	21	20	0.1	2.31856E-10
GO:0044448	cell cortex part	down	cell cortex part (GO:0044448)	CC	71	69	0.072463768	2.9094E-10
GO:0044297	cell body	down	cell body (GO:0044297)	CC	157	144	0.125	3.47114E-10
GO:0032154	cleavage furrow	down	cleavage furrow (GO:0032154)	CC	21	21	0.238095238	4.12336E-10
GO:0097610	cell surface furrow	down	cell surface furrow (GO:0097610)	CC	21	21	0.238095238	4.12336E-10
GO:1902495	transmembrane transporter complex	down	transmembrane transporter complex (GO:1902495)	CC	176	166	0.180722892	5.40484E-10
GO:0019898	extrinsic component of membrane	down	extrinsic component of membrane (GO:0019898)	CC	124	114	0.122807018	5.41124E-10
GO:0008328	ionotropic glutamate receptor complex	down	ionotropic glutamate receptor complex (GO:0008328)	CC	27	26	0.230769231	5.77186E-10
GO:0005795	Golgi stack	down	Golgi stack (GO:0005795)	CC	38	36	0.083333333	6.96474E-10
GO:0030863	cortical cytoskeleton	down	cortical cytoskeleton (GO:0030863)	CC	53	51	0.098039216	6.96632E-10
GO:0002102	podosome	down	podosome (GO:0002102)	CC	10	10	0.2	9.37446E-10
GO:1990351	transporter complex	down	transporter complex (GO:1990351)	CC	179	169	0.177514793	1.1363E-09
GO:0001726	ruffle	down	ruffle (GO:0001726)	CC	89	86	0.081395349	1.32406E-09
GO:0030864	cortical actin cytoskeleton	down	cortical actin cytoskeleton (GO:0030864)	CC	34	32	0.0625	1.43094E-09
GO:0000790	nuclear chromatin	down	nuclear chromatin (GO:0000790)	CC	196	184	0.086956522	1.62948E-09
GO:1990752	microtubule end	down	microtubule end (GO:1990752)	CC	16	16	0.3125	2.32587E-09
GO:0045177	apical part of cell	down	apical part of cell (GO:0045177)	CC	197	188	0.154255319	2.74986E-09
GO:0001673	male germ cell nucleus	down	male germ cell nucleus (GO:0001673)	CC	11	10	0.2	4.42761E-09
GO:0097731	9+0 non-motile cilium	down	9+0 non-motile cilium (GO:0097731)	CC	64	59	0.101694915	4.44536E-09
GO:0097733	photoreceptor cell cilium	down	photoreceptor cell cilium (GO:0097733)	CC	64	59	0.101694915	4.44536E-09
GO:0016328	lateral plasma membrane	down	lateral plasma membrane (GO:0016328)	CC	32	31	0.096774194	5.12557E-09
GO:0000800	lateral element	down	lateral element (GO:0000800)	CC	11	11	0.181818182	6.14819E-09

GO:0016459	myosin complex	down	myosin complex (GO:0016459)	CC	49	39	0.282051282	6.20741E-09
GO:0019897	extrinsic component of plasma membrane	down	extrinsic component of plasma membrane (GO:0019897)	CC	69	59	0.152542373	9.17113E-09
GO:0035098	ESC/E(Z) complex	down	ESC/E(Z) complex (GO:0035098)	CC	14	12	0.25	9.17113E-09
GO:0042470	melanosome	down	melanosome (GO:0042470)	CC	23	23	0.173913043	9.90237E-09
GO:0048770	pigment granule	down	pigment granule (GO:0048770)	CC	23	23	0.173913043	9.90237E-09
GO:0000792	heterochromatin	down	heterochromatin (GO:0000792)	CC	52	51	0.078431373	1.06888E-08
GO:0098793	presynapse	down	presynapse (GO:0098793)	CC	118	117	0.11965812	1.23928E-08
GO:0098878	neurotransmitter receptor complex	down	neurotransmitter receptor complex (GO:0098878)	CC	29	28	0.214285714	1.27565E-08
GO:0005720	nuclear heterochromatin	down	nuclear heterochromatin (GO:0005720)	CC	24	24	0.083333333	1.55403E-08
GO:0097730	non-motile cilium	down	non-motile cilium (GO:0097730)	CC	68	63	0.095238095	1.58914E-08
GO:0005881	cytoplasmic microtubule	down	cytoplasmic microtubule (GO:0005881)	CC	33	26	0.153846154	1.9352E-08
GO:0000803	sex chromosome	down	sex chromosome (GO:0000803)	CC	21	18	0.166666667	2.09347E-08
GO:0070160	occluding junction	down	occluding junction (GO:0070160)	CC	70	67	0.044776119	2.14676E-08
GO:0005942	phosphatidylinositol 3-kinase complex	down	phosphatidylinositol 3-kinase complex (GO:0005942)	CC	11	11	0.181818182	2.30517E-08
GO:0030175	filopodium	down	filopodium (GO:0030175)	CC	51	49	0.163265306	2.96925E-08
GO:0043197	dendritic spine	down	dendritic spine (GO:0043197)	CC	33	33	0.151515152	3.9618E-08
GO:0005923	bicellular tight junction	down	bicellular tight junction (GO:0005923)	CC	67	64	0.046875	4.54411E-08
GO:0045211	postsynaptic membrane	down	postsynaptic membrane (GO:0045211)	CC	58	58	0.137931034	4.54411E-08
GO:0044309	neuron spine	down	neuron spine (GO:0044309)	CC	37	37	0.135135135	4.60704E-08
GO:0042641	actomyosin	down	actomyosin (GO:0042641)	CC	46	44	0.227272727	7.59035E-08
GO:0042101	T cell receptor complex	down	T cell receptor complex (GO:0042101)	CC	15	13	0.153846154	7.872E-08
GO:0070382	exocytic vesicle	down	exocytic vesicle (GO:0070382)	CC	57	57	0.157894737	8.76449E-08
GO:0005637	nuclear inner membrane	down	nuclear inner membrane (GO:0005637)	CC	20	18	0.166666667	8.82222E-08
GO:0030135	coated vesicle	down	coated vesicle (GO:0030135)	CC	85	84	0.095238095	9.35255E-08
GO:0030133	transport vesicle	down	transport vesicle (GO:0030133)	CC	106	106	0.169811321	1.40444E-07
GO:0008076	voltage-gated potassium channel complex	down	voltage-gated potassium channel complex (GO:0008076)	CC	47	47	0.127659574	1.48325E-07
GO:0032587	ruffle membrane	down	ruffle membrane (GO:0032587)	CC	37	37	0.108108108	1.55157E-07
GO:0045335	phagocytic vesicle	down	phagocytic vesicle (GO:0045335)	CC	40	40	0.075	1.55157E-07
GO:0016323	basolateral plasma membrane	down	basolateral plasma membrane (GO:0016323)	CC	97	95	0.105263158	1.55397E-07
GO:0044440	endosomal part	down	endosomal part (GO:0044440)	CC	126	122	0.057377049	1.69259E-07
GO:0010008	endosome membrane	down	endosome membrane (GO:0010008)	CC	114	110	0.054545455	1.96822E-07
GO:0044306	neuron projection terminus	down	neuron projection terminus (GO:0044306)	CC	28	27	0.111111111	2.1971E-07
GO:0032391	photoreceptor connecting cilium	down	photoreceptor connecting cilium (GO:0032391)	CC	29	26	0.076923077	2.72919E-07
GO:0060170	ciliary membrane	down	ciliary membrane (GO:0060170)	CC	23	22	0.227272727	2.96362E-07
GO:0045178	basal part of cell	down	basal part of cell (GO:0045178)	CC	29	29	0.034482759	3.70903E-07
GO:0031965	nuclear membrane	down	nuclear membrane (GO:0031965)	CC	143	136	0.125	3.80882E-07
GO:0055037	recycling endosome	down	recycling endosome (GO:0055037)	CC	72	70	0.071428571	4.64073E-07
GO:0005657	replication fork	down	replication fork (GO:0005657)	CC	44	43	0.093023256	4.74798E-07
GO:0000152	nuclear ubiquitin ligase complex	down	nuclear ubiquitin ligase complex (GO:0000152)	CC	29	29	0.137931034	5.08821E-07
GO:0001725	stress fiber	down	stress fiber (GO:0001725)	CC	39	37	0.243243243	6.22142E-07
GO:0097517	contractile actin filament bundle	down	contractile actin filament bundle (GO:0097517)	CC	39	37	0.243243243	6.22142E-07
GO:0008278	cohesin complex	down	cohesin complex (GO:0008278)	CC	11	10	0.2	9.01914E-07
GO:0032432	actin filament bundle	down	actin filament bundle (GO:0032432)	CC	42	39	0.230769231	1.04948E-06
GO:0031519	PcG protein complex	down	PcG protein complex (GO:0031519)	CC	34	32	0.1875	1.09947E-06
GO:0045171	intercellular bridge	down	intercellular bridge (GO:0045171)	CC	38	37	0.135135135	1.2823E-06
GO:0008021	synaptic vesicle	down	synaptic vesicle (GO:0008021)	CC	53	53	0.150943396	1.8612E-06
GO:0000795	synaptonemal complex	down	synaptonemal complex (GO:0000795)	CC	28	28	0.107142857	1.91256E-06
GO:0099086	synaptonemal structure	down	synaptonemal structure (GO:0099086)	CC	28	28	0.107142857	1.91256E-06
GO:0005769	early endosome	down	early endosome (GO:0005769)	CC	133	133	0.090225564	2.09789E-06
GO:0034705	potassium channel complex	down	potassium channel complex (GO:0034705)	CC	51	51	0.137254902	2.09789E-06
GO:0034399	nuclear periphery	down	nuclear periphery (GO:0034399)	CC	60	58	0.103448276	2.21444E-06
GO:0031985	Golgi cisterna	down	Golgi cisterna (GO:0031985)	CC	24	22	0.136363636	2.22437E-06
GO:0098858	actin-based cell projection	down	actin-based cell projection (GO:0098858)	CC	103	100	0.12	2.61178E-06
GO:0031201	SNARE complex	down	SNARE complex (GO:0031201)	CC	19	18	0.166666667	2.6405E-06
GO:0030057	desmosome	down	desmosome (GO:0030057)	CC	16	16	0.125	3.08346E-06
GO:0043240	Fanconi anaemia nuclear complex	down	Fanconi anaemia nuclear complex (GO:0043240)	CC	12	11	0	3.42446E-06
GO:0001750	photoreceptor outer segment	down	photoreceptor outer segment (GO:0001750)	CC	43	41	0.12195122	5.36668E-06
GO:0000242	pericentriolar material	down	pericentriolar material (GO:0000242)	CC	17	15	0	5.47619E-06
GO:0000781	chromosome, telomeric region	down	chromosome, telomeric region (GO:0000781)	CC	102	89	0.04494382	6.40281E-06
GO:0016363	nuclear matrix	down	nuclear matrix (GO:0016363)	CC	47	46	0.108695652	8.35881E-06
GO:0016324	apical plasma membrane	down	apical plasma membrane (GO:0016324)	CC	140	136	0.132352941	8.62296E-06
GO:0031234	extrinsic component of cytoplasmic side of plasma memb	down	extrinsic component of cytoplasmic side of plasma membrane (GO:00312	CC	43	33	0.151515152	9.20491E-06
GO:0009897	external side of plasma membrane	down	external side of plasma membrane (GO:0009897)	CC	158	154	0.103896104	1.00338E-05
GO:0030136	clathrin-coated vesicle	down	clathrin-coated vesicle (GO:0030136)	CC	56	56	0.089285714	1.13296E-05

GO:0043198	dendritic shaft	down	dendritic shaft (GO:0043198)	CC	14	14	0.142857143	1.25299E-05
GO:0030426	growth cone	down	growth cone (GO:0030426)	CC	42	40	0.2	1.32488E-05
GO:0045111	intermediate filament cytoskeleton	down	intermediate filament cytoskeleton (GO:0045111)	CC	117	102	0.088235294	1.87212E-05
GO:0030134	COPII-coated ER to Golgi transport vesicle	down	COPII-coated ER to Golgi transport vesicle (GO:0030134)	CC	14	14	0.142857143	1.94249E-05
GO:0030427	site of polarized growth	down	site of polarized growth (GO:0030427)	CC	44	42	0.19047619	2.17261E-05
GO:0005771	multivesicular body	down	multivesicular body (GO:0005771)	CC	13	13	0.153846154	2.24888E-05
GO:0000307	cyclin-dependent protein kinase holoenzyme complex	down	cyclin-dependent protein kinase holoenzyme complex (GO:0000307)	CC	29	29	0.137931034	2.46466E-05
GO:0005875	microtubule associated complex	down	microtubule associated complex (GO:0005875)	CC	60	60	0.116666667	2.4737E-05
GO:0034451	centriolar satellite	down	centriolar satellite (GO:0034451)	CC	20	20	0.1	2.4737E-05
GO:0005921	gap junction	down	gap junction (GO:0005921)	CC	23	23	0.086956522	2.80985E-05
GO:0005882	intermediate filament	down	intermediate filament (GO:0005882)	CC	79	66	0.121212121	3.10418E-05
GO:0099503	secretory vesicle	down	secretory vesicle (GO:0099503)	CC	194	185	0.102702703	3.62542E-05
GO:0031594	neuromuscular junction	down	neuromuscular junction (GO:0031594)	CC	31	31	0.193548387	3.91352E-05
GO:0017053	transcriptional repressor complex	down	transcriptional repressor complex (GO:0017053)	CC	54	53	0.075471698	3.99846E-05
GO:0016592	mediator complex	down	mediator complex (GO:0016592)	CC	28	28	0.071428571	4.3239E-05
GO:0016605	PML body	down	PML body (GO:0016605)	CC	56	55	0.054545455	5.61667E-05
GO:0016234	inclusion body	down	inclusion body (GO:0016234)	CC	46	45	0.111111111	5.66165E-05
GO:0001891	phagocytic cup	down	phagocytic cup (GO:0001891)	CC	11	10	0.2	6.52657E-05
GO:0000784	nuclear chromosome, telomeric region	down	nuclear chromosome, telomeric region (GO:0000784)	CC	86	74	0.054054054	6.5998E-05
GO:0031527	filopodium membrane	down	filopodium membrane (GO:0031527)	CC	11	11	0.090909091	6.8832E-05
GO:0030660	Golgi-associated vesicle membrane	down	Golgi-associated vesicle membrane (GO:0030660)	CC	30	29	0.103448276	7.52209E-05
GO:0043596	nuclear replication fork	down	nuclear replication fork (GO:0043596)	CC	23	23	0.086956522	7.62165E-05
GO:0016604	nuclear body	down	nuclear body (GO:0016604)	CC	174	171	0.052631579	8.31949E-05
GO:0005788	endoplasmic reticulum lumen	down	endoplasmic reticulum lumen (GO:0005788)	CC	28	27	0	8.78525E-05
GO:0090568	nuclear transcriptional repressor complex	down	nuclear transcriptional repressor complex (GO:0090568)	CC	23	23	0.086956522	8.78525E-05
GO:0005884	actin filament	down	actin filament (GO:0005884)	CC	55	49	0.142857143	9.09058E-05
GO:0000123	histone acetyltransferase complex	down	histone acetyltransferase complex (GO:0000123)	CC	69	65	0.030769231	0.000107968
GO:0000151	ubiquitin ligase complex	down	ubiquitin ligase complex (GO:0000151)	CC	141	139	0.086330935	0.000111014
GO:0030137	COPI-coated vesicle	down	COPI-coated vesicle (GO:0030137)	CC	13	12	0.083333333	0.000112945
GO:0031514	motile cilium	down	motile cilium (GO:0031514)	CC	73	69	0.101449275	0.000113522
GO:0044815	DNA packaging complex	down	DNA packaging complex (GO:0044815)	CC	46	15	0.133333333	0.000127553
GO:0042734	presynaptic membrane	down	presynaptic membrane (GO:0042734)	CC	17	17	0.058823529	0.000146553
GO:0043679	axon terminus	down	axon terminus (GO:0043679)	CC	21	21	0.095238095	0.000156811
GO:0030286	dynein complex	down	dynein complex (GO:0030286)	CC	27	27	0.111111111	0.000158646
GO:0030140	trans-Golgi network transport vesicle	down	trans-Golgi network transport vesicle (GO:0030140)	CC	15	15	0.133333333	0.00016016
GO:0045120	pronucleus	down	pronucleus (GO:0045120)	CC	11	11	0.090909091	0.000183394
GO:0098562	cytoplasmic side of membrane	down	cytoplasmic side of membrane (GO:0098562)	CC	86	75	0.08	0.000185496
GO:0031463	Cul3-RING ubiquitin ligase complex	down	Cul3-RING ubiquitin ligase complex (GO:0031463)	CC	24	23	0.130434783	0.000194708
GO:0032993	protein-DNA complex	down	protein-DNA complex (GO:0032993)	CC	80	49	0.040816327	0.000239898
GO:0070603	SWI/SNF superfamily-type complex	down	SWI/SNF superfamily-type complex (GO:0070603)	CC	55	54	0.055555556	0.000257451
GO:1902554	serine/threonine protein kinase complex	down	serine/threonine protein kinase complex (GO:1902554)	CC	52	52	0.096153846	0.000257451
GO:0005765	lysosomal membrane	down	lysosomal membrane (GO:0005765)	CC	141	136	0.058823529	0.000260739
GO:0098852	lytic vacuole membrane	down	lytic vacuole membrane (GO:0098852)	CC	141	136	0.058823529	0.000260739
GO:1902911	protein kinase complex	down	protein kinase complex (GO:1902911)	CC	59	59	0.084745763	0.000280358
GO:0031228	intrinsic component of Golgi membrane	down	intrinsic component of Golgi membrane (GO:0031228)	CC	28	28	0.107142857	0.000294173
GO:0005770	late endosome	down	late endosome (GO:0005770)	CC	100	98	0.06122449	0.000313807
GO:0000159	protein phosphatase type 2A complex	down	protein phosphatase type 2A complex (GO:0000159)	CC	17	16	0.1875	0.000325966
GO:0043189	H4/H2A histone acetyltransferase complex	down	H4/H2A histone acetyltransferase complex (GO:0043189)	CC	16	15	0.066666667	0.000328827
GO:0031248	protein acetyltransferase complex	down	protein acetyltransferase complex (GO:0031248)	CC	76	72	0.027777778	0.000377308
GO:1902493	acetyltransferase complex	down	acetyltransferase complex (GO:1902493)	CC	76	72	0.027777778	0.000377308
GO:0016581	NuRD complex	down	NuRD complex (GO:0016581)	CC	14	14	0.142857143	0.000414256
GO:0090545	CHD-type complex	down	CHD-type complex (GO:0090545)	CC	14	14	0.142857143	0.000414256
GO:0030173	integral component of Golgi membrane	down	integral component of Golgi membrane (GO:0030173)	CC	26	26	0.115384615	0.000418174
GO:0031461	cullin-RING ubiquitin ligase complex	down	cullin-RING ubiquitin ligase complex (GO:0031461)	CC	88	86	0.093023256	0.000467794
GO:0012506	vesicle membrane	down	vesicle membrane (GO:0012506)	CC	120	119	0.075630252	0.000491471
GO:0044447	axoneme part	down	axoneme part (GO:0044447)	CC	11	11	0.181818182	0.000570499
GO:0005774	vacuolar membrane	down	vacuolar membrane (GO:0005774)	CC	155	150	0.053333333	0.000749685
GO:0031901	early endosome membrane	down	early endosome membrane (GO:0031901)	CC	25	25	0.08	0.000788626
GO:0005801	cis-Golgi network	down	cis-Golgi network (GO:0005801)	CC	27	27	0	0.000921003
GO:0000118	histone deacetylase complex	down	histone deacetylase complex (GO:0000118)	CC	38	37	0.108108108	0.00094635
GO:0009898	cytoplasmic side of plasma membrane	down	cytoplasmic side of plasma membrane (GO:0009898)	CC	75	64	0.078125	0.001013853
GO:0005793	endoplasmic reticulum-Golgi intermediate compartment	down	endoplasmic reticulum-Golgi intermediate compartment (GO:0005793)	CC	42	41	0.12195122	0.001017947
GO:0044798	nuclear transcription factor complex	down	nuclear transcription factor complex (GO:0044798)	CC	85	84	0.035714286	0.001313012
GO:0030014	CCR4-NOT complex	down	CCR4-NOT complex (GO:0030014)	CC	15	14	0.071428571	0.001375841

	GO:0005892	acetylcholine-gated channel complex	down	acetylcholine-gated channel complex (GO:0005892)	CC	11	11	0.090909091	0.001377012
	GO:1904949	ATPase complex	down	ATPase complex (GO:1904949)	CC	66	65	0.092307692	0.00150478
	GO:0061695	transferase complex, transferring phosphorus-containing	down	transferase complex, transferring phosphorus-containing groups (GO:006	CC	155	154	0.064935065	0.001509253
	GO:0035097	histone methyltransferase complex	down	histone methyltransferase complex (GO:0035097)	CC	54	51	0.078431373	0.001525445
	GO:0044437	vacuolar part	down	vacuolar part (GO:0044437)	CC	159	154	0.051948052	0.001553435
	GO:0035102	PRC1 complex	down	PRC1 complex (GO:0035102)	CC	11	11	0.090909091	0.001745881
	GO:0035145	exon-exon junction complex	down	exon-exon junction complex (GO:0035145)	CC	14	14	0	0.001935416
	GO:0005680	anaphase-promoting complex	down	anaphase-promoting complex (GO:0005680)	CC	14	14	0.071428571	0.00206707
	GO:0030894	replisome	down	replisome (GO:0030894)	CC	18	18	0.055555556	0.002095131
	GO:0030659	cytoplasmic vesicle membrane	down	cytoplasmic vesicle membrane (GO:0030659)	CC	105	104	0.086538462	0.002114091
	GO:0016235	aggresome	down	aggresome (GO:0016235)	CC	24	24	0.041666667	0.002601114
	GO:0016607	nuclear speck	down	nuclear speck (GO:0016607)	CC	70	68	0.044117647	0.002601114
	GO:0045334	clathrin-coated endocytic vesicle	down	clathrin-coated endocytic vesicle (GO:0045334)	CC	14	14	0.071428571	0.002601114
	GO:0043204	perikaryon	down	perikaryon (GO:0043204)	CC	14	13	0.153846154	0.002709107
	GO:0032838	cell projection cytoplasm	down	cell projection cytoplasm (GO:0032838)	CC	19	19	0.052631579	0.003054334
	GO:0030662	coated vesicle membrane	down	coated vesicle membrane (GO:0030662)	CC	34	33	0.060606061	0.003367587
	GO:0070461	SAGA-type complex	down	SAGA-type complex (GO:0070461)	CC	19	18	0.055555556	0.003367587
	GO:0035267	NuA4 histone acetyltransferase complex	down	NuA4 histone acetyltransferase complex (GO:0035267)	CC	15	14	0.071428571	0.004217852
	GO:0005902	microvillus	down	microvillus (GO:0005902)	CC	40	40	0.075	0.004382449
	GO:0080008	Cul4-RING E3 ubiquitin ligase complex	down	Cul4-RING E3 ubiquitin ligase complex (GO:0080008)	CC	19	19	0.052631579	0.004533922
	GO:0044291	cell-cell contact zone	down	cell-cell contact zone (GO:0044291)	CC	44	40	0.175	0.004844728
	GO:0005922	connexin complex	down	connexin complex (GO:0005922)	CC	16	16	0	0.004890002
	GO:0000109	nucleotide-excision repair complex	down	nucleotide-excision repair complex (GO:0000109)	CC	10	10	0.1	0.005657414
	GO:0097223	sperm part	down	sperm part (GO:0097223)	CC	97	89	0.06741573	0.005700219
	GO:0042405	nuclear inclusion body	down	nuclear inclusion body (GO:0042405)	CC	10	10	0.1	0.005730699
	GO:1902562	H4 histone acetyltransferase complex	down	H4 histone acetyltransferase complex (GO:1902562)	CC	31	28	0.035714286	0.006767594
	GO:1904115	axon cytoplasm	down	axon cytoplasm (GO:1904115)	CC	16	16	0	0.006935148
	GO:1902555	endoribonuclease complex	down	endoribonuclease complex (GO:1902555)	CC	13	13	0.076923077	0.007288128
	GO:1905348	endonuclease complex	down	endonuclease complex (GO:1905348)	CC	13	13	0.076923077	0.007288128
	GO:0005834	heterotrimeric G-protein complex	down	heterotrimeric G-protein complex (GO:0005834)	CC	17	9	0.111111111	0.00813902
	GO:1905360	GTPase complex	down	GTPase complex (GO:1905360)	CC	17	9	0.111111111	0.00813902
	GO:0009925	basal plasma membrane	down	basal plasma membrane (GO:0009925)	CC	18	18	0	0.008737578
	GO:0036464	cytoplasmic ribonucleoprotein granule	down	cytoplasmic ribonucleoprotein granule (GO:0036464)	CC	88	85	0.047058824	0.009923476

D90 to Birth

Down Regulated

Clas	**GO ID**	**GO Description**	**Direction of c**	**GO Description and ID**	**Class**	**Size**	**Size in data**	**% in data**	**FDR.adj.pval**
MOLECULAR FUNCTION									
	GO:0003774	motor activity	down	motor activity (GO:0003774)	MF	98	88	0.329545455	4.44089E-16
	GO:0003777	microtubule motor activity	down	microtubule motor activity (GO:0003777)	MF	58	56	0.321428571	4.44089E-16
	GO:0004713	protein tyrosine kinase activity	down	protein tyrosine kinase activity (GO:0004713)	MF	95	94	0.212765957	4.44089E-16
	GO:0004714	transmembrane receptor protein tyrosine kinase activity	down	transmembrane receptor protein tyrosine kinase activity (GO:0004714)	MF	44	44	0.318181818	4.44089E-16
	GO:0005003	ephrin receptor activity	down	ephrin receptor activity (GO:0005003)	MF	11	11	0.636363636	4.44089E-16
	GO:0005201	extracellular matrix structural constituent	down	extracellular matrix structural constituent (GO:0005201)	MF	31	30	0.466666667	4.44089E-16
	GO:0005248	voltage-gated sodium channel activity	down	voltage-gated sodium channel activity (GO:0005248)	MF	18	18	0.444444444	4.44089E-16
	GO:0008017	microtubule binding	down	microtubule binding (GO:0008017)	MF	150	146	0.239726027	4.44089E-16
	GO:0015631	tubulin binding	down	tubulin binding (GO:0015631)	MF	198	193	0.222797927	4.44089E-16
	GO:0017048	Rho GTPase binding	down	Rho GTPase binding (GO:0017048)	MF	115	110	0.154545455	4.44089E-16
	GO:0017147	Wnt-protein binding	down	Wnt-protein binding (GO:0017147)	MF	21	21	0.333333333	4.44089E-16
	GO:0017154	semaphorin receptor activity	down	semaphorin receptor activity (GO:0017154)	MF	11	11	0.181818182	4.44089E-16
	GO:0019199	transmembrane receptor protein kinase activity	down	transmembrane receptor protein kinase activity (GO:0019199)	MF	59	58	0.25862069	4.44089E-16
	GO:0019838	growth factor binding	down	growth factor binding (GO:0019838)	MF	89	85	0.247058824	4.44089E-16
	GO:0030695	GTPase regulator activity	down	GTPase regulator activity (GO:0030695)	MF	143	142	0.098591549	4.44089E-16
	GO:0043394	proteoglycan binding	down	proteoglycan binding (GO:0043394)	MF	22	22	0.318181818	4.44089E-16
	GO:0046875	ephrin receptor binding	down	ephrin receptor binding (GO:0046875)	MF	19	19	0.315789474	4.44089E-16
	GO:0048407	platelet-derived growth factor binding	down	platelet-derived growth factor binding (GO:0048407)	MF	11	10	0.7	4.44089E-16
	GO:1905030	voltage-gated ion channel activity involved in regulation c	down	voltage-gated ion channel activity involved in regulation of postsynaptic r	MF	18	18	0.444444444	4.44089E-16
	GO:0008194	UDP-glycosyltransferase activity	down	UDP-glycosyltransferase activity (GO:0008194)	MF	81	78	0.153846154	4.79616E-14
	GO:0017124	SH3 domain binding	down	SH3 domain binding (GO:0017124)	MF	40	38	0.184210526	4.79616E-14
	GO:0016757	transferase activity, transferring glycosyl groups	down	transferase activity, transferring glycosyl groups (GO:0016757)	MF	188	181	0.160220994	8.59313E-14
	GO:0043142	single-stranded DNA-dependent ATPase activity	down	single-stranded DNA-dependent ATPase activity (GO:0043142)	MF	11	11	0.181818182	8.59313E-14
	GO:0005096	GTPase activator activity	down	GTPase activator activity (GO:0005096)	MF	122	121	0.099173554	1.25899E-13
	GO:0008094	DNA-dependent ATPase activity	down	DNA-dependent ATPase activity (GO:0008094)	MF	57	55	0.090909091	1.50102E-13
	GO:0035064	methylated histone binding	down	methylated histone binding (GO:0035064)	MF	43	41	0.146341463	1.50102E-13

GO:0140034	methylation-dependent protein binding	down	methylation-dependent protein binding (GO:0140034)	MF	43	41	0.146341463	1.50102E-13
GO:0005178	integrin binding	down	integrin binding (GO:0005178)	MF	62	61	0.196721311	1.82077E-13
GO:0005516	calmodulin binding	down	calmodulin binding (GO:0005516)	MF	56	53	0.301886792	2.74003E-13
GO:0140097	catalytic activity, acting on DNA	down	catalytic activity, acting on DNA (GO:0140097)	MF	118	113	0.088495575	2.74003E-13
GO:0008146	sulfotransferase activity	down	sulfotransferase activity (GO:0008146)	MF	36	32	0.1875	4.98046E-13
GO:0005272	sodium channel activity	down	sodium channel activity (GO:0005272)	MF	32	31	0.290322581	8.71969E-13
GO:0004222	metalloendopeptidase activity	down	metalloendopeptidase activity (GO:0004222)	MF	94	88	0.215909091	8.77964E-13
GO:0005539	glycosaminoglycan binding	down	glycosaminoglycan binding (GO:0005539)	MF	108	106	0.216981132	9.4591E-13
GO:0008013	beta-catenin binding	down	beta-catenin binding (GO:0008013)	MF	58	58	0.172413793	1.15996E-12
GO:0060589	nucleoside-triphosphatase regulator activity	down	nucleoside-triphosphatase regulator activity (GO:0060589)	MF	158	155	0.096774194	1.56408E-12
GO:0050431	transforming growth factor beta binding	down	transforming growth factor beta binding (GO:0050431)	MF	12	12	0.333333333	1.69398E-12
GO:0045125	bioactive lipid receptor activity	down	bioactive lipid receptor activity (GO:0045125)	MF	12	12	0.333333333	4.90408E-12
GO:0035173	histone kinase activity	down	histone kinase activity (GO:0035173)	MF	15	14	0.142857143	8.66196E-12
GO:0008237	metallopeptidase activity	down	metallopeptidase activity (GO:0008237)	MF	149	138	0.18115942	1.2454E-11
GO:0031996	thioesterase binding	down	thioesterase binding (GO:0031996)	MF	10	10	0.2	1.51741E-11
GO:0008376	acetylgalactosaminyltransferase activity	down	acetylgalactosaminyltransferase activity (GO:0008376)	MF	21	20	0.2	1.9708E-11
GO:0051018	protein kinase A binding	down	protein kinase A binding (GO:0051018)	MF	30	26	0.192307692	2.54441E-11
GO:0016758	transferase activity, transferring hexosyl groups	down	transferase activity, transferring hexosyl groups (GO:0016758)	MF	123	120	0.116666667	3.67539E-11
GO:0048365	Rac GTPase binding	down	Rac GTPase binding (GO:0048365)	MF	34	34	0.088235294	5.997E-11
GO:0042169	SH2 domain binding	down	SH2 domain binding (GO:0042169)	MF	26	25	0.2	7.0836E-11
GO:0016894	endonuclease activity, active with either ribo- or deoxyrib	down	endonuclease activity, active with either ribo- or deoxyribonucleic acids	MF	10	10	0.2	1.07968E-10
GO:0001968	fibronectin binding	down	fibronectin binding (GO:0001968)	MF	14	13	0.153846154	1.2777E-10
GO:0008201	heparin binding	down	heparin binding (GO:0008201)	MF	73	72	0.236111111	1.60488E-10
GO:0004520	endodeoxyribonuclease activity	down	endodeoxyribonuclease activity (GO:0004520)	MF	22	21	0.142857143	1.74986E-10
GO:0005089	Rho guanyl-nucleotide exchange factor activity	down	Rho guanyl-nucleotide exchange factor activity (GO:0005089)	MF	69	64	0.140625	2.07484E-10
GO:1901681	sulfur compound binding	down	sulfur compound binding (GO:1901681)	MF	109	108	0.222222222	2.16186E-10
GO:0000217	DNA secondary structure binding	down	DNA secondary structure binding (GO:0000217)	MF	12	12	0.166666667	2.76096E-10
GO:0004715	non-membrane spanning protein tyrosine kinase activity	down	non-membrane spanning protein tyrosine kinase activity (GO:0004715)	MF	35	34	0.117647059	3.37406E-10
GO:0005085	guanyl-nucleotide exchange factor activity	down	guanyl-nucleotide exchange factor activity (GO:0005085)	MF	158	152	0.105263158	3.81856E-10
GO:0017137	Rab GTPase binding	down	Rab GTPase binding (GO:0017137)	MF	79	74	0.108108108	3.95098E-10
GO:0051015	actin filament binding	down	actin filament binding (GO:0051015)	MF	80	77	0.181818182	3.95098E-10
GO:0050840	extracellular matrix binding	down	extracellular matrix binding (GO:0050840)	MF	31	30	0.233333333	4.46362E-10
GO:0030676	Rac guanyl-nucleotide exchange factor activity	down	Rac guanyl-nucleotide exchange factor activity (GO:0030676)	MF	10	10	0.1	5.42854E-10
GO:0008083	growth factor activity	down	growth factor activity (GO:0008083)	MF	86	84	0.202380952	1.3252E-09
GO:0008022	protein C-terminus binding	down	protein C-terminus binding (GO:0008022)	MF	103	103	0.106796117	1.53056E-09
GO:0015278	calcium-release channel activity	down	calcium-release channel activity (GO:0015278)	MF	13	12	0.166666667	1.53056E-09
GO:0099604	ligand-gated calcium channel activity	down	ligand-gated calcium channel activity (GO:0099604)	MF	13	12	0.166666667	1.53056E-09
GO:0042393	histone binding	down	histone binding (GO:0042393)	MF	117	107	0.093457944	1.89469E-09
GO:0005109	frizzled binding	down	frizzled binding (GO:0005109)	MF	22	21	0.19047619	2.38137E-09
GO:0003950	NAD+ ADP-ribosyltransferase activity	down	NAD+ ADP-ribosyltransferase activity (GO:0003950)	MF	16	15	0.133333333	2.76668E-09
GO:0035091	phosphatidylinositol binding	down	phosphatidylinositol binding (GO:0035091)	MF	147	144	0.104166667	2.94479E-09
GO:0005217	intracellular ligand-gated ion channel activity	down	intracellular ligand-gated ion channel activity (GO:0005217)	MF	20	18	0.166666667	3.49007E-09
GO:0004970	ionotropic glutamate receptor activity	down	ionotropic glutamate receptor activity (GO:0004970)	MF	15	15	0.2	4.42697E-09
GO:0000149	SNARE binding	down	SNARE binding (GO:0000149)	MF	48	48	0.166666667	4.5813E-09
GO:0008375	acetylglucosaminyltransferase activity	down	acetylglucosaminyltransferase activity (GO:0008375)	MF	36	36	0.111111111	5.2585E-09
GO:0017022	myosin binding	down	myosin binding (GO:0017022)	MF	39	37	0.108108108	6.48063E-09
GO:0003678	DNA helicase activity	down	DNA helicase activity (GO:0003678)	MF	31	29	0.103448276	6.61795E-09
GO:0036002	pre-mRNA binding	down	pre-mRNA binding (GO:0036002)	MF	11	11	0.090909091	7.21769E-09
GO:0097110	scaffold protein binding	down	scaffold protein binding (GO:0097110)	MF	29	28	0.285714286	1.30484E-08
GO:0005088	Ras guanyl-nucleotide exchange factor activity	down	Ras guanyl-nucleotide exchange factor activity (GO:0005088)	MF	108	102	0.107843137	1.37898E-08
GO:0005518	collagen binding	down	collagen binding (GO:0005518)	MF	44	42	0.166666667	1.731E-08
GO:0008373	sialyltransferase activity	down	sialyltransferase activity (GO:0008373)	MF	18	18	0.222222222	2.06505E-08
GO:0008484	sulfuric ester hydrolase activity	down	sulfuric ester hydrolase activity (GO:0008484)	MF	15	13	0.230769231	2.87321E-08
GO:0030165	PDZ domain binding	down	PDZ domain binding (GO:0030165)	MF	45	43	0.186046512	3.11407E-08
GO:0004536	deoxyribonuclease activity	down	deoxyribonuclease activity (GO:0004536)	MF	32	31	0.096774194	4.01652E-08
GO:0005234	extracellularly glutamate-gated ion channel activity	down	extracellularly glutamate-gated ion channel activity (GO:0005234)	MF	16	16	0.1875	4.1737E-08
GO:0035591	signaling adaptor activity	down	signaling adaptor activity (GO:0035591)	MF	27	25	0.12	4.1737E-08
GO:0015276	ligand-gated ion channel activity	down	ligand-gated ion channel activity (GO:0015276)	MF	105	100	0.12	4.71567E-08
GO:0022834	ligand-gated channel activity	down	ligand-gated channel activity (GO:0022834)	MF	105	100	0.12	4.71567E-08
GO:0005244	voltage-gated ion channel activity	down	voltage-gated ion channel activity (GO:0005244)	MF	127	125	0.2	6.98827E-08
GO:0022832	voltage-gated channel activity	down	voltage-gated channel activity (GO:0022832)	MF	127	125	0.2	6.98827E-08
GO:0005057	signal transducer activity, downstream of receptor	down	signal transducer activity, downstream of receptor (GO:0005057)	MF	67	67	0.134328358	9.09506E-08
GO:0060090	molecular adaptor activity	down	molecular adaptor activity (GO:0060090)	MF	67	65	0.153846154	9.09506E-08
GO:0004386	helicase activity	down	helicase activity (GO:0004386)	MF	79	77	0.103896104	1.58621E-07

GO:0043236	laminin binding	down	laminin binding (GO:0043236)	MF	16	15	0.133333333	1.73476E-07
GO:0004697	protein kinase C activity	down	protein kinase C activity (GO:0004697)	MF	11	11	0.090909091	2.66467E-07
GO:0005484	SNAP receptor activity	down	SNAP receptor activity (GO:0005484)	MF	17	17	0.117647059	2.66467E-07
GO:0140030	modification-dependent protein binding	down	modification-dependent protein binding (GO:0140030)	MF	90	86	0.151162791	3.64171E-07
GO:0019104	DNA N-glycosylase activity	down	DNA N-glycosylase activity (GO:0019104)	MF	10	10	0.1	3.71507E-07
GO:0001664	G-protein coupled receptor binding	down	G-protein coupled receptor binding (GO:0001664)	MF	121	109	0.082568807	4.76083E-07
GO:0005501	retinoid binding	down	retinoid binding (GO:0005501)	MF	16	13	0.153846154	4.83541E-07
GO:0019840	isoprenoid binding	down	isoprenoid binding (GO:0019840)	MF	16	13	0.153846154	4.83541E-07
GO:0005540	hyaluronic acid binding	down	hyaluronic acid binding (GO:0005540)	MF	21	20	0.2	6.59493E-07
GO:0019905	syntaxin binding	down	syntaxin binding (GO:0019905)	MF	34	34	0.147058824	9.61843E-07
GO:0030594	neurotransmitter receptor activity	down	neurotransmitter receptor activity (GO:0030594)	MF	43	43	0.139534884	1.00649E-06
GO:0030276	clathrin binding	down	clathrin binding (GO:0030276)	MF	19	19	0.210526316	1.01544E-06
GO:0031418	L-ascorbic acid binding	down	L-ascorbic acid binding (GO:0031418)	MF	16	16	0.1875	1.1447E-06
GO:0005104	fibroblast growth factor receptor binding	down	fibroblast growth factor receptor binding (GO:0005104)	MF	24	24	0.291666667	1.18867E-06
GO:0005160	transforming growth factor beta receptor binding	down	transforming growth factor beta receptor binding (GO:0005160)	MF	16	16	0.1875	1.21803E-06
GO:0005230	extracellular ligand-gated ion channel activity	down	extracellular ligand-gated ion channel activity (GO:0005230)	MF	66	63	0.142857143	1.63307E-06
GO:0072509	divalent inorganic cation transmembrane transporter act	down	divalent inorganic cation transmembrane transporter activity (GO:00725	MF	107	104	0.105769231	1.79193E-06
GO:0030674	protein binding, bridging	down	protein binding, bridging (GO:0030674)	MF	56	56	0.142857143	1.83643E-06
GO:0022824	transmitter-gated ion channel activity	down	transmitter-gated ion channel activity (GO:0022824)	MF	26	26	0.153846154	2.84668E-06
GO:0022835	transmitter-gated channel activity	down	transmitter-gated channel activity (GO:0022835)	MF	26	26	0.153846154	2.84668E-06
GO:0004003	ATP-dependent DNA helicase activity	down	ATP-dependent DNA helicase activity (GO:0004003)	MF	22	21	0.047619048	3.14883E-06
GO:0042623	ATPase activity, coupled	down	ATPase activity, coupled (GO:0042623)	MF	190	185	0.124324324	3.47213E-06
GO:0003713	transcription coactivator activity	down	transcription coactivator activity (GO:0003713)	MF	146	143	0.055944056	3.69698E-06
GO:0005267	potassium channel activity	down	potassium channel activity (GO:0005267)	MF	86	84	0.142857143	3.69698E-06
GO:0099094	ligand-gated cation channel activity	down	ligand-gated cation channel activity (GO:0099094)	MF	40	39	0.102564103	4.32493E-06
GO:0008409	5'-3' exonuclease activity	down	5'-3' exonuclease activity (GO:0008409)	MF	10	9	0.222222222	4.86938E-06
GO:0030742	GTP-dependent protein binding	down	GTP-dependent protein binding (GO:0030742)	MF	16	15	0.066666667	4.989E-06
GO:0001158	enhancer sequence-specific DNA binding	down	enhancer sequence-specific DNA binding (GO:0001158)	MF	67	67	0.119402985	5.53166E-06
GO:0030971	receptor tyrosine kinase binding	down	receptor tyrosine kinase binding (GO:0030971)	MF	32	31	0.096774194	5.66013E-06
GO:0050699	WW domain binding	down	WW domain binding (GO:0050699)	MF	19	18	0.166666667	5.66013E-06
GO:0005520	insulin-like growth factor binding	down	insulin-like growth factor binding (GO:0005520)	MF	19	18	0.111111111	6.01926E-06
GO:0051219	phosphoprotein binding	down	phosphoprotein binding (GO:0051219)	MF	45	45	0.111111111	6.81524E-06
GO:0016782	transferase activity, transferring sulfur-containing groups	down	transferase activity, transferring sulfur-containing groups (GO:0016782)	MF	48	43	0.139534884	7.66783E-06
GO:0046332	SMAD binding	down	SMAD binding (GO:0046332)	MF	59	59	0.118644068	8.96894E-06
GO:0005262	calcium channel activity	down	calcium channel activity (GO:0005262)	MF	66	63	0.111111111	9.96901E-06
GO:0030414	peptidase inhibitor activity	down	peptidase inhibitor activity (GO:0030414)	MF	92	85	0.188235294	1.00175E-05
GO:0005249	voltage-gated potassium channel activity	down	voltage-gated potassium channel activity (GO:0005249)	MF	59	58	0.155172414	1.18249E-05
GO:0019902	phosphatase binding	down	phosphatase binding (GO:0019902)	MF	107	103	0.058252427	1.37789E-05
GO:0008026	ATP-dependent helicase activity	down	ATP-dependent helicase activity (GO:0008026)	MF	52	51	0.098039216	1.53526E-05
GO:0070035	purine NTP-dependent helicase activity	down	purine NTP-dependent helicase activity (GO:0070035)	MF	52	51	0.098039216	1.53526E-05
GO:0005231	excitatory extracellular ligand-gated ion channel activity	down	excitatory extracellular ligand-gated ion channel activity (GO:0005231)	MF	28	28	0.107142857	1.57524E-05
GO:0042056	chemoattractant activity	down	chemoattractant activity (GO:0042056)	MF	15	14	0.214285714	1.57524E-05
GO:0035326	enhancer binding	down	enhancer binding (GO:0035326)	MF	72	72	0.111111111	1.60298E-05
GO:0018024	histone-lysine N-methyltransferase activity	down	histone-lysine N-methyltransferase activity (GO:0018024)	MF	29	28	0.035714286	1.61107E-05
GO:0019003	GDP binding	down	GDP binding (GO:0019003)	MF	40	40	0.025	2.03383E-05
GO:0015079	potassium ion transmembrane transporter activity	down	potassium ion transmembrane transporter activity (GO:0015079)	MF	101	98	0.163265306	2.3804E-05
GO:0008066	glutamate receptor activity	down	glutamate receptor activity (GO:0008066)	MF	20	20	0.15	2.48361E-05
GO:0015020	glucuronosyltransferase activity	down	glucuronosyltransferase activity (GO:0015020)	MF	11	8	0.125	2.52617E-05
GO:0061134	peptidase regulator activity	down	peptidase regulator activity (GO:0061134)	MF	115	106	0.179245283	2.84904E-05
GO:0001540	amyloid-beta binding	down	amyloid-beta binding (GO:0001540)	MF	21	19	0.263157895	3.13332E-05
GO:0004725	protein tyrosine phosphatase activity	down	protein tyrosine phosphatase activity (GO:0004725)	MF	79	78	0.192307692	3.23634E-05
GO:0004012	phospholipid-translocating ATPase activity	down	phospholipid-translocating ATPase activity (GO:0004012)	MF	14	13	0.153846154	3.63491E-05
GO:0001786	phosphatidylserine binding	down	phosphatidylserine binding (GO:0001786)	MF	22	22	0.136363636	4.19856E-05
GO:0022843	voltage-gated cation channel activity	down	voltage-gated cation channel activity (GO:0022843)	MF	89	88	0.136363636	4.81109E-05
GO:1901981	phosphatidylinositol phosphate binding	down	phosphatidylinositol phosphate binding (GO:1901981)	MF	82	80	0.075	4.81109E-05
GO:0031625	ubiquitin protein ligase binding	down	ubiquitin protein ligase binding (GO:0031625)	MF	189	182	0.076923077	4.96772E-05
GO:0070851	growth factor receptor binding	down	growth factor receptor binding (GO:0070851)	MF	97	94	0.117021277	5.28359E-05
GO:0004867	serine-type endopeptidase inhibitor activity	down	serine-type endopeptidase inhibitor activity (GO:0004867)	MF	43	38	0.184210526	5.37357E-05
GO:0004857	enzyme inhibitor activity	down	enzyme inhibitor activity (GO:0004857)	MF	169	157	0.140127389	5.71264E-05
GO:0008353	RNA polymerase II carboxy-terminal domain kinase activit	down	RNA polymerase II carboxy-terminal domain kinase activity (GO:0008353	MF	14	14	0.071428571	6.79117E-05
GO:0042813	Wnt-activated receptor activity	down	Wnt-activated receptor activity (GO:0042813)	MF	10	10	0.1	7.42773E-05
GO:0005112	Notch binding	down	Notch binding (GO:0005112)	MF	14	13	0.230769231	7.74059E-05
GO:1990782	protein tyrosine kinase binding	down	protein tyrosine kinase binding (GO:1990782)	MF	34	33	0.090909091	8.19873E-05
GO:0004519	endonuclease activity	down	endonuclease activity (GO:0004519)	MF	53	52	0.096153846	8.20983E-05

GO:0004518	nuclease activity	down	nuclease activity (GO:0004518)	MF	107	106	0.075471698	8.35058E-05
GO:0004866	endopeptidase inhibitor activity	down	endopeptidase inhibitor activity (GO:0004866)	MF	85	79	0.17721519	9.03849E-05
GO:0019215	intermediate filament binding	down	intermediate filament binding (GO:0019215)	MF	10	9	0.111111111	0.000104648
GO:0015085	calcium ion transmembrane transporter activity	down	calcium ion transmembrane transporter activity (GO:0015085)	MF	81	78	0.128205128	0.000106165
GO:0030551	cyclic nucleotide binding	down	cyclic nucleotide binding (GO:0030551)	MF	22	19	0.157894737	0.000109046
GO:0043395	heparan sulfate proteoglycan binding	down	heparan sulfate proteoglycan binding (GO:0043395)	MF	10	10	0.3	0.000110398
GO:0032813	tumor necrosis factor receptor superfamily binding	down	tumor necrosis factor receptor superfamily binding (GO:0032813)	MF	33	32	0.15625	0.000121069
GO:0019903	protein phosphatase binding	down	protein phosphatase binding (GO:0019903)	MF	71	68	0.073529412	0.000122872
GO:0015081	sodium ion transmembrane transporter activity	down	sodium ion transmembrane transporter activity (GO:0015081)	MF	93	90	0.177777778	0.000123859
GO:0016849	phosphorus-oxygen lyase activity	down	phosphorus-oxygen lyase activity (GO:0016849)	MF	19	19	0.105263158	0.000128635
GO:0044389	ubiquitin-like protein ligase binding	down	ubiquitin-like protein ligase binding (GO:0044389)	MF	192	185	0.081081081	0.000138916
GO:0005126	cytokine receptor binding	down	cytokine receptor binding (GO:0005126)	MF	153	142	0.084507042	0.000155118
GO:0019209	kinase activator activity	down	kinase activator activity (GO:0019209)	MF	41	40	0.1	0.000161383
GO:0005158	insulin receptor binding	down	insulin receptor binding (GO:0005158)	MF	23	23	0.130434783	0.00017736
GO:0030507	spectrin binding	down	spectrin binding (GO:0030507)	MF	19	18	0.055555556	0.000182255
GO:0030246	carbohydrate binding	down	carbohydrate binding (GO:0030246)	MF	109	108	0.138888889	0.00021663
GO:0030552	cAMP binding	down	cAMP binding (GO:0030552)	MF	12	10	0.2	0.000221925
GO:0030295	protein kinase activator activity	down	protein kinase activator activity (GO:0030295)	MF	35	34	0.117647059	0.000223699
GO:0061135	endopeptidase regulator activity	down	endopeptidase regulator activity (GO:0061135)	MF	90	84	0.19047619	0.000239878
GO:0004712	protein serine/threonine/tyrosine kinase activity	down	protein serine/threonine/tyrosine kinase activity (GO:0004712)	MF	14	14	0.214285714	0.000247163
GO:0001047	core promoter binding	down	core promoter binding (GO:0001047)	MF	111	110	0.072727273	0.000248069
GO:0004197	cysteine-type endopeptidase activity	down	cysteine-type endopeptidase activity (GO:0004197)	MF	49	47	0.085106383	0.000252917
GO:0000980	RNA polymerase II distal enhancer sequence-specific DNA	down	RNA polymerase II distal enhancer sequence-specific DNA binding (GO:00	MF	53	53	0.075471698	0.000262384
GO:1990841	promoter-specific chromatin binding	down	promoter-specific chromatin binding (GO:1990841)	MF	11	11	0.090909091	0.000276219
GO:0009975	cyclase activity	down	cyclase activity (GO:0009975)	MF	20	20	0.1	0.000287942
GO:0043621	protein self-association	down	protein self-association (GO:0043621)	MF	29	29	0.034482759	0.000287942
GO:0004721	phosphoprotein phosphatase activity	down	phosphoprotein phosphatase activity (GO:0004721)	MF	129	128	0.140625	0.000291352
GO:0005092	GDP-dissociation inhibitor activity	down	GDP-dissociation inhibitor activity (GO:0005092)	MF	13	13	0.076923077	0.000292357
GO:0019207	kinase regulator activity	down	kinase regulator activity (GO:0019207)	MF	88	83	0.108433735	0.000302333
GO:0070411	I-SMAD binding	down	I-SMAD binding (GO:0070411)	MF	10	10	0.1	0.000320023
GO:0015095	magnesium ion transmembrane transporter activity	down	magnesium ion transmembrane transporter activity (GO:0015095)	MF	13	13	0	0.000322381
GO:0031683	G-protein beta/gamma-subunit complex binding	down	G-protein beta/gamma-subunit complex binding (GO:0031683)	MF	18	17	0.117647059	0.000325546
GO:0042277	peptide binding	down	peptide binding (GO:0042277)	MF	71	64	0.125	0.000356291
GO:0019789	SUMO transferase activity	down	SUMO transferase activity (GO:0019789)	MF	10	9	0	0.00039281
GO:0033218	amide binding	down	amide binding (GO:0033218)	MF	80	73	0.109589041	0.000395158
GO:0005164	tumor necrosis factor receptor binding	down	tumor necrosis factor receptor binding (GO:0005164)	MF	23	23	0.173913043	0.000474104
GO:0019955	cytokine binding	down	cytokine binding (GO:0019955)	MF	67	65	0.123076923	0.000481261
GO:0042800	histone methyltransferase activity (H3-K4 specific)	down	histone methyltransferase activity (H3-K4 specific) (GO:0042800)	MF	13	12	0	0.000490655
GO:0004702	signal transducer, downstream of receptor, with serine/t	down	signal transducer, downstream of receptor, with serine/threonine kinase	MF	40	40	0.1	0.00051959
GO:0031406	carboxylic acid binding	down	carboxylic acid binding (GO:0031406)	MF	104	98	0.153061224	0.000541094
GO:0043177	organic acid binding	down	organic acid binding (GO:0043177)	MF	104	98	0.153061224	0.000541094
GO:0005507	copper ion binding	down	copper ion binding (GO:0005507)	MF	34	31	0.129032258	0.000546476
GO:0031489	myosin V binding	down	myosin V binding (GO:0031489)	MF	15	14	0	0.000586967
GO:0042805	actinin binding	down	actinin binding (GO:0042805)	MF	19	19	0.105263158	0.000593887
GO:0003730	mRNA 3'-UTR binding	down	mRNA 3'-UTR binding (GO:0003730)	MF	29	28	0.178571429	0.000640486
GO:0047485	protein N-terminus binding	down	protein N-terminus binding (GO:0047485)	MF	60	58	0.017241379	0.000643763
GO:0031690	adrenergic receptor binding	down	adrenergic receptor binding (GO:0031690)	MF	10	10	0.1	0.000684534
GO:0003887	DNA-directed DNA polymerase activity	down	DNA-directed DNA polymerase activity (GO:0003887)	MF	19	19	0.052631579	0.000731377
GO:0015459	potassium channel regulator activity	down	potassium channel regulator activity (GO:0015459)	MF	17	17	0.235294118	0.000822638
GO:0001784	phosphotyrosine residue binding	down	phosphotyrosine residue binding (GO:0001784)	MF	12	12	0.083333333	0.000843261
GO:0019894	kinesin binding	down	kinesin binding (GO:0019894)	MF	24	24	0.166666667	0.000843671
GO:0072341	modified amino acid binding	down	modified amino acid binding (GO:0072341)	MF	34	34	0.088235294	0.000849964
GO:0043548	phosphatidylinositol 3-kinase binding	down	phosphatidylinositol 3-kinase binding (GO:0043548)	MF	16	16	0	0.000855353
GO:0042054	histone methyltransferase activity	down	histone methyltransferase activity (GO:0042054)	MF	39	38	0.052631579	0.000865188
GO:0003785	actin monomer binding	down	actin monomer binding (GO:0003785)	MF	16	14	0.285714286	0.000978561
GO:0003684	damaged DNA binding	down	damaged DNA binding (GO:0003684)	MF	37	36	0.111111111	0.000984118
GO:0042826	histone deacetylase binding	down	histone deacetylase binding (GO:0042826)	MF	71	71	0.070422535	0.001351603
GO:0016917	GABA receptor activity	down	GABA receptor activity (GO:0016917)	MF	21	21	0.19047619	0.001385779
GO:0030291	protein serine/threonine kinase inhibitor activity	down	protein serine/threonine kinase inhibitor activity (GO:0030291)	MF	16	14	0.142857143	0.001385779
GO:0005343	organic acid:sodium symporter activity	down	organic acid:sodium symporter activity (GO:0005343)	MF	14	14	0.142857143	0.001489574
GO:0008080	N-acetyltransferase activity	down	N-acetyltransferase activity (GO:0008080)	MF	55	51	0.019607843	0.001566648
GO:0003705	transcription factor activity, RNA polymerase II distal enh	down	transcription factor activity, RNA polymerase II distal enhancer sequence-	MF	54	54	0.148148148	0.001635507
GO:0004527	exonuclease activity	down	exonuclease activity (GO:0004527)	MF	51	50	0.06	0.001785904
GO:0017112	Rab guanyl-nucleotide exchange factor activity	down	Rab guanyl-nucleotide exchange factor activity (GO:0017112)	MF	24	23	0.043478261	0.001785904

	GO:0045309	protein phosphorylated amino acid binding	down	protein phosphorylated amino acid binding (GO:0045309)	MF	18	18	0.055555556	0.001850945
	GO:0043015	gamma-tubulin binding	down	gamma-tubulin binding (GO:0043015)	MF	17	17	0.176470588	0.001951323
	GO:0034061	DNA polymerase activity	down	DNA polymerase activity (GO:0034061)	MF	24	23	0.043478261	0.002036108
	GO:0015026	coreceptor activity	down	coreceptor activity (GO:0015026)	MF	14	14	0.071428571	0.00207537
	GO:0001077	transcriptional activator activity, RNA polymerase II core	down	transcriptional activator activity, RNA polymerase II core promoter proxi	MF	157	155	0.103225806	0.00215467
	GO:0005545	1-phosphatidylinositol binding	down	1-phosphatidylinositol binding (GO:0005545)	MF	13	13	0.153846154	0.002216065
	GO:1902936	phosphatidylinositol bisphosphate binding	down	phosphatidylinositol bisphosphate binding (GO:1902936)	MF	47	46	0.086956522	0.002246177
	GO:0016278	lysine N-methyltransferase activity	down	lysine N-methyltransferase activity (GO:0016278)	MF	38	35	0.057142857	0.002439768
	GO:0016279	protein-lysine N-methyltransferase activity	down	protein-lysine N-methyltransferase activity (GO:0016279)	MF	38	35	0.057142857	0.002439768
	GO:0005080	protein kinase C binding	down	protein kinase C binding (GO:0005080)	MF	23	22	0.045454545	0.002655455
	GO:0017134	fibroblast growth factor binding	down	fibroblast growth factor binding (GO:0017134)	MF	17	16	0.25	0.002968159
	GO:0005070	SH3/SH2 adaptor activity	down	SH3/SH2 adaptor activity (GO:0005070)	MF	14	14	0	0.003124861
	GO:0015296	anion:cation symporter activity	down	anion:cation symporter activity (GO:0015296)	MF	25	24	0.083333333	0.003124861
	GO:0015297	antiporter activity	down	antiporter activity (GO:0015297)	MF	35	34	0.088235294	0.003155569
	GO:0035497	cAMP response element binding	down	cAMP response element binding (GO:0035497)	MF	11	11	0.090909091	0.003348797
	GO:0140103	catalytic activity, acting on a glycoprotein	down	catalytic activity, acting on a glycoprotein (GO:0140103)	MF	11	11	0	0.00348986
	GO:0005548	phospholipid transporter activity	down	phospholipid transporter activity (GO:0005548)	MF	29	28	0.071428571	0.003731422
	GO:0032947	protein complex scaffold activity	down	protein complex scaffold activity (GO:0032947)	MF	38	37	0.081081081	0.003802028
	GO:0070577	lysine-acetylated histone binding	down	lysine-acetylated histone binding (GO:0070577)	MF	14	13	0.153846154	0.00407021
	GO:0140033	acetylation-dependent protein binding	down	acetylation-dependent protein binding (GO:0140033)	MF	14	13	0.153846154	0.00407021
	GO:0043014	alpha-tubulin binding	down	alpha-tubulin binding (GO:0043014)	MF	14	13	0.153846154	0.004391016
	GO:0001076	transcription factor activity, RNA polymerase II transcript	down	transcription factor activity, RNA polymerase II transcription factor bindi	MF	90	89	0.06741573	0.004496303
	GO:0043178	alcohol binding	down	alcohol binding (GO:0043178)	MF	36	33	0	0.004716798
	GO:0099516	ion antiporter activity	down	ion antiporter activity (GO:0099516)	MF	28	28	0.107142857	0.004836606
	GO:0044325	ion channel binding	down	ion channel binding (GO:0044325)	MF	61	59	0.152542373	0.005018022
	GO:0004181	metallocarboxypeptidase activity	down	metallocarboxypeptidase activity (GO:0004181)	MF	22	18	0.111111111	0.005055811
	GO:0001104	RNA polymerase II transcription cofactor activity	down	RNA polymerase II transcription cofactor activity (GO:0001104)	MF	55	54	0.037037037	0.005085481
	GO:0003823	antigen binding	down	antigen binding (GO:0003823)	MF	10	8	0.125	0.005526441
	GO:0030332	cyclin binding	down	cyclin binding (GO:0030332)	MF	17	17	0.117647059	0.005582159
	GO:0016763	transferase activity, transferring pentosyl groups	down	transferase activity, transferring pentosyl groups (GO:0016763)	MF	32	29	0.172413793	0.005648546
	GO:0016791	phosphatase activity	down	phosphatase activity (GO:0016791)	MF	191	188	0.132978723	0.00565826
	GO:0019206	nucleoside kinase activity	down	nucleoside kinase activity (GO:0019206)	MF	12	12	0.166666667	0.00565826
	GO:0048029	monosaccharide binding	down	monosaccharide binding (GO:0048029)	MF	41	41	0.12195122	0.006353555
	GO:0001653	peptide receptor activity	down	peptide receptor activity (GO:0001653)	MF	90	87	0.126436782	0.006490967
	GO:0004890	GABA-A receptor activity	down	GABA-A receptor activity (GO:0004890)	MF	18	18	0.222222222	0.006643879
	GO:0015464	acetylcholine receptor activity	down	acetylcholine receptor activity (GO:0015464)	MF	14	14	0.142857143	0.007013276
	GO:0051721	protein phosphatase 2A binding	down	protein phosphatase 2A binding (GO:0051721)	MF	13	12	0.083333333	0.007174341
	GO:0032182	ubiquitin-like protein binding	down	ubiquitin-like protein binding (GO:0032182)	MF	49	48	0.0625	0.007315725
	GO:0016410	N-acyltransferase activity	down	N-acyltransferase activity (GO:0016410)	MF	67	63	0.031746032	0.007418578
	GO:0070273	phosphatidylinositol-4-phosphate binding	down	phosphatidylinositol-4-phosphate binding (GO:0070273)	MF	15	14	0.071428571	0.007418578
	GO:0005086	ARF guanyl-nucleotide exchange factor activity	down	ARF guanyl-nucleotide exchange factor activity (GO:0005086)	MF	15	15	0.066666667	0.007522837
	GO:0000146	microfilament motor activity	down	microfilament motor activity (GO:0000146)	MF	13	11	0.454545455	0.007593301
	GO:0030506	ankyrin binding	down	ankyrin binding (GO:0030506)	MF	14	13	0.076923077	0.007617217
	GO:0016706	oxidoreductase activity, acting on paired donors, with inc	down	oxidoreductase activity, acting on paired donors, with incorporation or r	MF	36	34	0.058823529	0.008696824
	GO:0016705	oxidoreductase activity, acting on paired donors, with inc	down	oxidoreductase activity, acting on paired donors, with incorporation or r	MF	105	77	0.168831169	0.009359657
	GO:0015298	solute:cation antiporter activity	down	solute:cation antiporter activity (GO:0015298)	MF	25	25	0.12	0.009629726

D90 to Birth

Up Regulated

Clas	**GO ID**	**GO Description**	**Direction of c**	**GO Description and ID**	**Class**	**Size**	**Size in data**	**% in data**	**FDR.adj.pval**
BIOLOGICAL PROCESS									
	GO:0006099	tricarboxylic acid cycle	up	tricarboxylic acid cycle (GO:0006099)	BP	15	15	0.266666667	1.8184E-12
	GO:0006101	citrate metabolic process	up	citrate metabolic process (GO:0006101)	BP	18	18	0.222222222	1.69192E-09
	GO:0072350	tricarboxylic acid metabolic process	up	tricarboxylic acid metabolic process (GO:0072350)	BP	22	22	0.227272727	4.70122E-09
	GO:0045333	cellular respiration	up	cellular respiration (GO:0045333)	BP	74	60	0.116666667	1.22823E-08
	GO:0009060	aerobic respiration	up	aerobic respiration (GO:0009060)	BP	29	25	0.2	4.73648E-08
	GO:0002082	regulation of oxidative phosphorylation	up	regulation of oxidative phosphorylation (GO:0002082)	BP	12	10	0.4	6.00218E-08
	GO:0006119	oxidative phosphorylation	up	oxidative phosphorylation (GO:0006119)	BP	36	25	0.16	1.10393E-07
	GO:0003009	skeletal muscle contraction	up	skeletal muscle contraction (GO:0003009)	BP	23	20	0.35	1.19296E-07
	GO:0000460	maturation of 5.8S rRNA	up	maturation of 5.8S rRNA (GO:0000460)	BP	10	10	0.2	1.28338E-06
	GO:0015985	energy coupled proton transport, down electrochemical	up	energy coupled proton transport, down electrochemical gradient (GO:00	BP	13	11	0.090909091	1.29766E-06
	GO:0015986	ATP synthesis coupled proton transport	up	ATP synthesis coupled proton transport (GO:0015986)	BP	13	11	0.090909091	1.29766E-06
	GO:0022904	respiratory electron transport chain	up	respiratory electron transport chain (GO:0022904)	BP	34	24	0.041666667	2.28126E-06
	GO:0006085	acetyl-CoA biosynthetic process	up	acetyl-CoA biosynthetic process (GO:0006085)	BP	11	11	0.090909091	3.10904E-06

GO:0046034	ATP metabolic process	up	ATP metabolic process (GO:0046034)	BP	123	104	0.115384615	3.18698E-06
GO:0022900	electron transport chain	up	electron transport chain (GO:0022900)	BP	39	28	0.035714286	3.90167E-06
GO:0046320	regulation of fatty acid oxidation	up	regulation of fatty acid oxidation (GO:0046320)	BP	15	14	0.357142857	4.2935E-06
GO:1903579	negative regulation of ATP metabolic process	up	negative regulation of ATP metabolic process (GO:1903579)	BP	13	13	0.230769231	5.20371E-06
GO:0009123	nucleoside monophosphate metabolic process	up	nucleoside monophosphate metabolic process (GO:0009123)	BP	151	132	0.106060606	8.08899E-06
GO:0009126	purine nucleoside monophosphate metabolic process	up	purine nucleoside monophosphate metabolic process (GO:0009126)	BP	141	122	0.114754098	1.0793E-05
GO:0009167	purine ribonucleoside monophosphate metabolic proces	up	purine ribonucleoside monophosphate metabolic process (GO:0009167)	BP	140	121	0.107438017	2.21643E-05
GO:0009205	purine ribonucleoside triphosphate metabolic process	up	purine ribonucleoside triphosphate metabolic process (GO:0009205)	BP	136	116	0.112068966	2.45123E-05
GO:0033108	mitochondrial respiratory chain complex assembly	up	mitochondrial respiratory chain complex assembly (GO:0033108)	BP	25	20	0.15	2.99026E-05
GO:0009161	ribonucleoside monophosphate metabolic process	up	ribonucleoside monophosphate metabolic process (GO:0009161)	BP	146	127	0.102362205	3.41962E-05
GO:0006084	acetyl-CoA metabolic process	up	acetyl-CoA metabolic process (GO:0006084)	BP	18	18	0.111111111	4.133E-05
GO:0006090	pyruvate metabolic process	up	pyruvate metabolic process (GO:0006090)	BP	61	58	0.103448276	5.3505E-05
GO:0009199	ribonucleoside triphosphate metabolic process	up	ribonucleoside triphosphate metabolic process (GO:0009199)	BP	138	118	0.110169492	6.14456E-05
GO:0042773	ATP synthesis coupled electron transport	up	ATP synthesis coupled electron transport (GO:0042773)	BP	22	14	0	6.84407E-05
GO:0006414	translational elongation	up	translational elongation (GO:0006414)	BP	21	21	0.142857143	7.38652E-05
GO:0009144	purine nucleoside triphosphate metabolic process	up	purine nucleoside triphosphate metabolic process (GO:0009144)	BP	142	122	0.106557377	8.9544E-05
GO:0042775	mitochondrial ATP synthesis coupled electron transport	up	mitochondrial ATP synthesis coupled electron transport (GO:0042775)	BP	19	13	0	0.000147977
GO:0046365	monosaccharide catabolic process	up	monosaccharide catabolic process (GO:0046365)	BP	12	12	0.166666667	0.000254371
GO:0006754	ATP biosynthetic process	up	ATP biosynthetic process (GO:0006754)	BP	22	18	0.111111111	0.000313181
GO:0010257	NADH dehydrogenase complex assembly	up	NADH dehydrogenase complex assembly (GO:0010257)	BP	15	13	0.153846154	0.000389046
GO:0032981	mitochondrial respiratory chain complex I assembly	up	mitochondrial respiratory chain complex I assembly (GO:0032981)	BP	15	13	0.153846154	0.000389046
GO:0097031	mitochondrial respiratory chain complex I biogenesis	up	mitochondrial respiratory chain complex I biogenesis (GO:0097031)	BP	15	13	0.153846154	0.000389046
GO:0009127	purine nucleoside monophosphate biosynthetic process	up	purine nucleoside monophosphate biosynthetic process (GO:0009127)	BP	36	32	0.125	0.000441846
GO:0009168	purine ribonucleoside monophosphate biosynthetic proc	up	purine ribonucleoside monophosphate biosynthetic process (GO:00091	BP	36	32	0.125	0.000441846
GO:0010889	regulation of sequestering of triglyceride	up	regulation of sequestering of triglyceride (GO:0010889)	BP	11	11	0.181818182	0.00044388
GO:0051193	regulation of cofactor metabolic process	up	regulation of cofactor metabolic process (GO:0051193)	BP	26	26	0.192307692	0.000617326
GO:0051196	regulation of coenzyme metabolic process	up	regulation of coenzyme metabolic process (GO:0051196)	BP	26	26	0.192307692	0.000617326
GO:0033013	tetrapyrrole metabolic process	up	tetrapyrrole metabolic process (GO:0033013)	BP	27	24	0.208333333	0.000655477
GO:0000959	mitochondrial RNA metabolic process	up	mitochondrial RNA metabolic process (GO:0000959)	BP	21	19	0.105263158	0.000766566
GO:0009141	nucleoside triphosphate metabolic process	up	nucleoside triphosphate metabolic process (GO:0009141)	BP	154	134	0.097014925	0.000770947
GO:0019433	triglyceride catabolic process	up	triglyceride catabolic process (GO:0019433)	BP	13	12	0.166666667	0.000778847
GO:0009145	purine nucleoside triphosphate biosynthetic process	up	purine nucleoside triphosphate biosynthetic process (GO:0009145)	BP	30	25	0.08	0.00120042
GO:0042273	ribosomal large subunit biogenesis	up	ribosomal large subunit biogenesis (GO:0042273)	BP	13	13	0.153846154	0.001259199
GO:0009124	nucleoside monophosphate biosynthetic process	up	nucleoside monophosphate biosynthetic process (GO:0009124)	BP	45	41	0.097560976	0.001440113
GO:0009156	ribonucleoside monophosphate biosynthetic process	up	ribonucleoside monophosphate biosynthetic process (GO:0009156)	BP	42	38	0.105263158	0.001443029
GO:0009206	purine ribonucleoside triphosphate biosynthetic process	up	purine ribonucleoside triphosphate biosynthetic process (GO:0009206)	BP	29	24	0.083333333	0.001466984
GO:0034440	lipid oxidation	up	lipid oxidation (GO:0034440)	BP	53	51	0.098039216	0.003004319
GO:0006635	fatty acid beta-oxidation	up	fatty acid beta-oxidation (GO:0006635)	BP	36	35	0.085714286	0.00327279
GO:0019395	fatty acid oxidation	up	fatty acid oxidation (GO:0019395)	BP	51	49	0.102040816	0.003397879
GO:0090075	relaxation of muscle	up	relaxation of muscle (GO:0090075)	BP	18	17	0.176470588	0.003413745
GO:1905039	carboxylic acid transmembrane transport	up	carboxylic acid transmembrane transport (GO:1905039)	BP	27	27	0.074074074	0.003739039
GO:0006515	protein quality control for misfolded or incompletely syn	up	protein quality control for misfolded or incompletely synthesized protei	BP	12	11	0	0.004096566
GO:0006091	generation of precursor metabolites and energy	up	generation of precursor metabolites and energy (GO:0006091)	BP	178	158	0.107594937	0.004738542
GO:0009062	fatty acid catabolic process	up	fatty acid catabolic process (GO:0009062)	BP	44	42	0.095238095	0.005542812
GO:1904293	negative regulation of ERAD pathway	up	negative regulation of ERAD pathway (GO:1904293)	BP	10	10	0.1	0.005831587
GO:0090200	positive regulation of release of cytochrome c from mitoc	up	positive regulation of release of cytochrome c from mitochondria (GO:00	BP	19	17	0.176470588	0.006272061
GO:0046031	ADP metabolic process	up	ADP metabolic process (GO:0046031)	BP	51	49	0.12244898	0.006837061
GO:0006778	porphyrin-containing compound metabolic process	up	porphyrin-containing compound metabolic process (GO:0006778)	BP	22	19	0.157894737	0.007573141
GO:0051186	cofactor metabolic process	up	cofactor metabolic process (GO:0051186)	BP	195	185	0.091891892	0.009453259
GO:0007006	mitochondrial membrane organization	up	mitochondrial membrane organization (GO:0007006)	BP	47	45	0.044444444	0.00976694

D90 to Birth

Up Regulated

Class	**GO ID**	**GO Description**	**Direction of c**	**GO Description and ID**	**Class**	**Size**	**Size in data**	**% in data**	**FDR.adj.pval**
CELLULAR COMPONENT									
	GO:0005746	mitochondrial respiratory chain	up	mitochondrial respiratory chain (GO:0005746)	CC	41	28	0.142857143	4.44089E-16
	GO:0005747	mitochondrial respiratory chain complex I	up	mitochondrial respiratory chain complex I (GO:0005747)	CC	33	27	0.148148148	4.44089E-16
	GO:0030964	NADH dehydrogenase complex	up	NADH dehydrogenase complex (GO:0030964)	CC	33	27	0.148148148	4.44089E-16
	GO:0045271	respiratory chain complex I	up	respiratory chain complex I (GO:0045271)	CC	33	27	0.148148148	4.44089E-16
	GO:0070469	respiratory chain	up	respiratory chain (GO:0070469)	CC	48	30	0.133333333	4.44089E-16
	GO:0098798	mitochondrial protein complex	up	mitochondrial protein complex (GO:0098798)	CC	72	54	0.111111111	4.44089E-16
	GO:0098800	inner mitochondrial membrane protein complex	up	inner mitochondrial membrane protein complex (GO:0098800)	CC	61	45	0.111111111	4.44089E-16
	GO:0098803	respiratory chain complex	up	respiratory chain complex (GO:0098803)	CC	44	29	0.137931034	4.44089E-16
	GO:1990204	oxidoreductase complex	up	oxidoreductase complex (GO:1990204)	CC	60	49	0.12244898	2.62652E-10

	GO:0044455	mitochondrial membrane part	up	mitochondrial membrane part (GO:0044455)	CC	104	82	0.085365854	3.02011E-10
	GO:0000313	organellar ribosome	up	organellar ribosome (GO:0000313)	CC	27	25	0.04	1.56161E-08
	GO:0005761	mitochondrial ribosome	up	mitochondrial ribosome (GO:0005761)	CC	27	25	0.04	1.56161E-08
	GO:0005753	mitochondrial proton-transporting ATP synthase comple	up	mitochondrial proton-transporting ATP synthase complex (GO:0005753)	CC	11	8	0.125	3.11366E-08
	GO:0045259	proton-transporting ATP synthase complex	up	proton-transporting ATP synthase complex (GO:0045259)	CC	13	10	0.1	2.43583E-07
	GO:0005840	ribosome	up	ribosome (GO:0005840)	CC	114	109	0.055045872	2.63892E-07
	GO:0015934	large ribosomal subunit	up	large ribosomal subunit (GO:0015934)	CC	33	30	0.1	2.66004E-07
	GO:0005759	mitochondrial matrix	up	mitochondrial matrix (GO:0005759)	CC	113	107	0.08411215	8.47702E-07
	GO:0044391	ribosomal subunit	up	ribosomal subunit (GO:0044391)	CC	63	59	0.06779661	2.33002E-06
	GO:0031304	intrinsic component of mitochondrial inner membrane	up	intrinsic component of mitochondrial inner membrane (GO:0031304)	CC	16	13	0.076923077	1.50823E-05
	GO:0031305	integral component of mitochondrial inner membrane	up	integral component of mitochondrial inner membrane (GO:0031305)	CC	16	13	0.076923077	1.50823E-05
	GO:0022625	cytosolic large ribosomal subunit	up	cytosolic large ribosomal subunit (GO:0022625)	CC	21	21	0.095238095	2.04843E-05
	GO:0005838	proteasome regulatory particle	up	proteasome regulatory particle (GO:0005838)	CC	12	12	0.166666667	4.43961E-05
	GO:0000502	proteasome complex	up	proteasome complex (GO:0000502)	CC	44	43	0.093023256	0.000103807
	GO:1905369	endopeptidase complex	up	endopeptidase complex (GO:1905369)	CC	44	43	0.093023256	0.000103807
	GO:0022624	proteasome accessory complex	up	proteasome accessory complex (GO:0022624)	CC	18	18	0.111111111	0.000113522
	GO:0005865	striated muscle thin filament	up	striated muscle thin filament (GO:0005865)	CC	11	11	0.363636364	0.000133477
	GO:0033177	proton-transporting two-sector ATPase complex, proton-	up	proton-transporting two-sector ATPase complex, proton-transporting do	CC	16	14	0.071428571	0.000407298
	GO:0030684	preribosome	up	preribosome (GO:0030684)	CC	13	12	0.166666667	0.000552842
	GO:0005852	eukaryotic translation initiation factor 3 complex	up	eukaryotic translation initiation factor 3 complex (GO:0005852)	CC	12	12	0.083333333	0.000643312
	GO:1905368	peptidase complex	up	peptidase complex (GO:1905368)	CC	51	50	0.1	0.002315559
	GO:0036379	myofilament	up	myofilament (GO:0036379)	CC	13	13	0.307692308	0.002440226
	GO:0009295	nucleoid	up	nucleoid (GO:0009295)	CC	35	32	0.15625	0.002752763
	GO:0042645	mitochondrial nucleoid	up	mitochondrial nucleoid (GO:0042645)	CC	35	32	0.15625	0.002752763
	GO:0032592	integral component of mitochondrial membrane	up	integral component of mitochondrial membrane (GO:0032592)	CC	35	32	0.03125	0.004040716
	GO:0098573	intrinsic component of mitochondrial membrane	up	intrinsic component of mitochondrial membrane (GO:0098573)	CC	35	32	0.03125	0.004040716
	GO:0022626	cytosolic ribosome	up	cytosolic ribosome (GO:0022626)	CC	42	40	0.05	0.004309291

D90 to Birth

Up Regulated

Clas	GO ID	GO Description	Direction of c	GO Description and ID	Class	Size	Size in data	% in data	FDR.adj.pval
MOLECULAR FUNCTION									
	GO:0008137	NADH dehydrogenase (ubiquinone) activity	up	NADH dehydrogenase (ubiquinone) activity (GO:0008137)	MF	18	11	0.272727273	7.72982E-15
	GO:0050136	NADH dehydrogenase (quinone) activity	up	NADH dehydrogenase (quinone) activity (GO:0050136)	MF	18	11	0.272727273	7.72982E-15
	GO:0003954	NADH dehydrogenase activity	up	NADH dehydrogenase activity (GO:0003954)	MF	19	12	0.25	1.01411E-14
	GO:0016655	oxidoreductase activity, acting on NAD(P)H, quinone or si	up	oxidoreductase activity, acting on NAD(P)H, quinone or similar compoun	MF	22	15	0.2	4.42639E-11
	GO:0003735	structural constituent of ribosome	up	structural constituent of ribosome (GO:0003735)	MF	87	84	0.05952381	2.93613E-07
	GO:0009055	electron transfer activity	up	electron transfer activity (GO:0009055)	MF	37	19	0.105263158	1.83643E-06
	GO:0004806	triglyceride lipase activity	up	triglyceride lipase activity (GO:0004806)	MF	12	11	0.181818182	3.69698E-06
	GO:0016651	oxidoreductase activity, acting on NAD(P)H	up	oxidoreductase activity, acting on NAD(P)H (GO:0016651)	MF	50	41	0.146341463	1.41064E-05
	GO:0051536	iron-sulfur cluster binding	up	iron-sulfur cluster binding (GO:0051536)	MF	32	31	0.193548387	4.76504E-05
	GO:0051540	metal cluster binding	up	metal cluster binding (GO:0051540)	MF	32	31	0.193548387	4.76504E-05
	GO:0008135	translation factor activity, RNA binding	up	translation factor activity, RNA binding (GO:0008135)	MF	50	47	0.127659574	8.44584E-05
	GO:0051537	2 iron, 2 sulfur cluster binding	up	2 iron, 2 sulfur cluster binding (GO:0051537)	MF	10	9	0.111111111	0.000387343
	GO:0051287	NAD binding	up	NAD binding (GO:0051287)	MF	33	33	0.242424242	0.003923734
	GO:0003743	translation initiation factor activity	up	translation initiation factor activity (GO:0003743)	MF	34	33	0.060606061	0.005151006
	GO:0019843	rRNA binding	up	rRNA binding (GO:0019843)	MF	15	15	0	0.007583441