GO with down regulated genes												
Category	Term	Genes	Count	List Total	Pop Hits	Pop Total	P-Value	Benjamini	Fold Enrichment	Bonferroni	FDR	Fisher Exact
GOTERM_BP_DIRECT	negative regulation of apoptotic process	4%	47	870	543	19512	2.41E-05	0.0532	1.94	0.0897	0.0531	0.0000115
GOTERM_BP_DIRECT	negative regulation of cell population proliferation	4%	41	870	450	19512	2.72E-05	0.0532	2.04	0.101	0.0531	0.0000125
GOTERM_BP_DIRECT	endochondral ossification	1%	9	870	32	19512	6.07E-05	0.079	6.31	0.211	0.0789	0.00000742
GOTERM_BP_DIRECT	kidney development	2%	19	870	149	19512	0.000115	0.0906	2.86	0.363	0.0904	0.0000363
GOTERM_BP_DIRECT	regulation of cell population proliferation	2%	23	870	204	19512	0.000118	0.0906	2.53	0.37	0.0904	0.0000426
GOTERM_BP_DIRECT	osteoblast differentiation	2%	18	870	138	19512	0.000139	0.0906	2.93	0.419	0.0904	0.0000426
GOTERM_BP_DIRECT	negative regulation of cell cycle	1%	11	870	59	19512	0.000252	0.126	4.18	0.626	0.126	0.0000511
GOTERM_BP_DIRECT	developmental growth	1%	8	870	30	19512	0.000281	0.126	5.98	0.666	0.126	0.0000369
GOTERM_BP_DIRECT	negative regulation of fat cell differentiation	1%	11	870	60	19512	0.00029	0.126	4.11	0.678	0.126	0.0000601
GOTERM_BP_DIRECT	response to ischemia	1%	11	870	65	19512	0.000564	0.22	3.80	0.89	0.22	0.000128
GOTERM_BP_DIRECT	positive regulation of cell migration	2%	27	870	300	19512	0.000958	0.33	2.02	0.976	0.33	0.000444
GOTERM_BP_DIRECT	amino acid biosynthetic process	1%	7	870	27	19512	0.00102	0.33	5.81	0.981	0.33	0.000139
GOTERM_BP_DIRECT	response to toxic substance	1%	12	870	84	19512	0.00122	0.367	3.20	0.992	0.367	0.000336
GOTERM_BP_DIRECT	positive regulation of miRNA transcription	1%	10	870	61	19512	0.00143	0.399	3.68	0.996	0.399	0.000337
GOTERM_BP_DIRECT	ossification	1%	14	870	113	19512	0.00156	0.405	2.78	0.998	0.405	0.000502
GOTERM_BP_DIRECT	response to steroid hormone	1%	7	870	30	19512	0.00182	0.444	5.23	0.999	0.443	0.000283
GOTERM_BP_DIRECT	cellular response to glucagon stimulus	0%	5	870	13	19512	0.00202	0.461	8.63	1.00e+0	0.46	0.000166
GOTERM_BP_DIRECT	positive regulation of angiogenesis	2%	17	870	160	19512	0.00213	0.461	2.38	1.00e+0	0.46	0.000812
GOTERM_BP_DIRECT	regulation of small GTPase mediated signal transduction	1%	14	870	121	19512	0.00288	0.556	2.59	1.00e+0	0.556	0.000999
GOTERM_BP_DIRECT	positive regulation of gene expression	3%	38	870	515	19512	0.00302	0.556	1.65	1.00e+0	0.556	0.00171
GOTERM_BP_DIRECT	positive regulation of endothelial cell migration	1%	10	870	68	19512	0.00309	0.556	3.30	1.00e+0	0.556	0.00082
GOTERM_BP_DIRECT	negative regulation of transcription by RNA polymerase II	6%	66	870	1034	19512	0.00315	0.556	1.43	1.00e+0	0.556	0.00216
GOTERM_BP_DIRECT	phosphatidylinositol phosphate biosynthetic process	1%	8	870	45	19512	0.00351	0.556	3.99	1.00e+0	0.556	0.000751
GOTERM_BP_DIRECT	bone morphogenesis	1%	7	870	34	19512	0.00354	0.556	4.62	1.00e+0	0.556	0.00064
GOTERM_BP_DIRECT	negative regulation of chondrocyte differentiation	1%	6	870	24	19512	0.00363	0.556	5.61	1.00e+0	0.556	0.000521
GOTERM_BP_DIRECT	skeletal system development	1%	16	870	154	19512	0.00371	0.556	2.33	1.00e+0	0.556	0.00145
GOTERM_BP_DIRECT	gene expression	2%	24	870	282	19512	0.00402	0.559	1.91	1.00e+0	0.558	0.00192
GOTERM_BP_DIRECT	post-embryonic development	1%	11	870	84	19512	0.00408	0.559	2.94	1.00e+0	0.558	0.00123
GOTERM_BP_DIRECT	negative regulation of gene expression	3%	28	870	351	19512	0.00427	0.559	1.79	1.00e+0	0.558	0.00223
GOTERM_BP_DIRECT	endoplasmic reticulum unfolded protein response	1%	9	870	59	19512	0.00444	0.559	3.42	1.00e+0	0.558	0.00113
GOTERM_BP_DIRECT	negative regulation of protein ubiquitination	1%	9	870	59	19512	0.00444	0.559	3.42	1.00e+0	0.558	0.00113
GOTERM_BP_DIRECT	tRNA aminoacylation for protein translation	1%	7	870	36	19512	0.00476	0.58	4.36	1.00e+0	0.579	0.000919
GOTERM_BP_DIRECT	proximal/distal pattern formation	1%	6	870	26	19512	0.00522	0.593	5.18	1.00e+0	0.592	0.000826
GOTERM_BP_DIRECT	negative regulation of fibroblast proliferation	1%	7	870	37	19512	0.00547	0.593	4.24	1.00e+0	0.592	0.00109
GOTERM_BP_DIRECT	positive regulation of intrinsic apoptotic signaling pathway	1%	7	870	37	19512	0.00547	0.593	4.24	1.00e+0	0.592	0.00109
GOTERM_BP_DIRECT	mammary gland development	1%	7	870	37	19512	0.00547	0.593	4.24	1.00e+0	0.592	0.00109
GOTERM_BP_DIRECT	cellular response to epidermal growth factor stimulus	1%	8	870	49	19512	0.0057	0.601	3.66	1.00e+0	0.6	0.00134
GOTERM_BP_DIRECT	response to oxidative stress	1%	15	870	148	19512	0.0064	0.657	2.27	1.00e+0	0.656	0.00256
GOTERM_BP_DIRECT	response to hypoxia	2%	17	870	181	19512	0.0071	0.69	2.11	1.00e+0	0.689	0.00309
GOTERM_BP_DIRECT	positive regulation of protein-containing complex assembly	1%	8	870	51	19512	0.00711	0.69	3.52	1.00e+0	0.689	0.00175
GOTERM_BP_DIRECT	phosphate-containing compound metabolic process	1%	6	870	28	19512	0.00725	0.69	4.81	1.00e+0	0.689	0.00125
GOTERM_BP_DIRECT	canonical Wnt signaling pathway	1%	12	870	106	19512	0.00759	0.705	2.54	1.00e+0	0.704	0.00269
GOTERM_BP_DIRECT	cellular response to glucose starvation	1%	8	870	52	19512	0.00791	0.711	3.45	1.00e+0	0.71	0.00199
GOTERM_BP_DIRECT	chondrocyte differentiation	1%	9	870	65	19512	0.00801	0.711	3.11	1.00e+0	0.71	0.00227
GOTERM_BP_DIRECT	L-serine metabolic process	0%	4	870	10	19512	0.00835	0.724	8.97	1.00e+0	0.723	0.000664
GOTERM_BP_DIRECT	negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	0%	5	870	19	19512	0.00887	0.737	5.90	1.00e+0	0.736	0.0012
GOTERM_BP_DIRECT	phosphatidylinositol 3-kinase/protein kinase B signal transduction	1%	11	870	94	19512	0.009	0.737	2.62	1.00e+0	0.736	0.00307
GOTERM_BP_DIRECT	positive regulation of osteoblast differentiation	1%	10	870	80	19512	0.00907	0.737	2.80	1.00e+0	0.736	0.00288
GOTERM_BP_DIRECT	homocysteine metabolic process	0%	4	870	11	19512	0.0111	0.841	8.16	1.00e+0	0.839	0.00101
GOTERM_BP_DIRECT	response to caloric restriction	0%	4	870	11	19512	0.0111	0.841	8.16	1.00e+0	0.839	0.00101
GOTERM_BP_DIRECT	proline transport	0%	4	870	11	19512	0.0111	0.841	8.16	1.00e+0	0.839	0.00101
GOTERM_BP_DIRECT	endothelial cell-cell adhesion	0%	3	870	4	19512	0.0112	0.841	16.82	1.00e+0	0.839	0.000342
GOTERM_BP_DIRECT	cellular response to ionizing radiation	1%	7	870	43	19512	0.0114	0.843	3.65	1.00e+0	0.842	0.00271
GOTERM_BP_DIRECT	positive regulation of nitric oxide biosynthetic process	1%	7	870	44	19512	0.0128	0.923	3.57	1.00e+0	0.922	0.0031
GOTERM_BP_DIRECT	in utero embryonic development	2%	21	870	262	19512	0.0137	0.964	1.80	1.00e+0	0.963	0.00708
GOTERM_BP_DIRECT	bone mineralization	1%	8	870	58	19512	0.0141	0.964	3.09	1.00e+0	0.963	0.00402
GOTERM_BP_DIRECT	heart development	2%	22	870	280	19512	0.0142	0.964	1.76	1.00e+0	0.963	0.00746
GOTERM_BP_DIRECT	collagen biosynthetic process	0%	4	870	12	19512	0.0143	0.964	7.48	1.00e+0	0.963	0.00146
GOTERM_BP_DIRECT	fibroblast growth factor receptor signaling pathway	1%	8	870	59	19512	0.0155	0.987	3.04	1.00e+0	0.986	0.00447
GOTERM_BP_DIRECT	cellular senescence	1%	8	870	59	19512	0.0155	0.987	3.04	1.00e+0	0.986	0.00447
GOTERM_BP_DIRECT	reactive oxygen species metabolic process	1%	7	870	46	19512	0.0157	0.987	3.41	1.00e+0	0.986	0.00401
GOTERM_BP_DIRECT	response to retinoic acid	1%	7	870	46	19512	0.0157	0.987	3.41	1.00e+0	0.986	0.00401
GOTERM_BP_DIRECT	protein export from nucleus	1%	6	870	34	19512	0.0165	0.987	3.96	1.00e+0	0.986	0.00356
GOTERM_BP_DIRECT	embryonic digit morphogenesis	1%	8	870	60	19512	0.0168	0.987	2.99	1.00e+0	0.986	0.00496
GOTERM_BP_DIRECT	endothelial cell migration	1%	7	870	47	19512	0.0174	0.987	3.34	1.00e+0	0.986	0.00453
GOTERM_BP_DIRECT	regulation of cell cycle	2%	21	870	269	19512	0.0178	0.987	1.75	1.00e+0	0.986	0.00943
GOTERM_BP_DIRECT	tRNA aminoacylation	0%	4	870	13	19512	0.018	0.987	6.90	1.00e+0	0.986	0.00203
GOTERM_BP_DIRECT	cellular response to epinephrine stimulus	0%	4	870	13	19512	0.018	0.987	6.90	1.00e+0	0.986	0.00203
GOTERM_BP_DIRECT	negative regulation of multicellular organism growth	0%	4	870	13	19512	0.018	0.987	6.90	1.00e+0	0.986	0.00203
GOTERM_BP_DIRECT	positive regulation of epithelial tube formation	0%	3	870	5	19512	0.0181	0.987	13.46	1.00e+0	0.986	0.000826
GOTERM_BP_DIRECT	cerebral cortex radial glia-guided migration	0%	3	870	5	19512	0.0181	0.987	13.46	1.00e+0	0.986	0.000826
GOTERM_BP_DIRECT	regulation of mitotic cell cycle	1%	9	870	75	19512	0.0182	0.987	2.69	1.00e+0	0.986	0.00602
GOTERM_BP_DIRECT	placenta development	1%	7	870	48	19512	0.0191	1.00e+0	3.27	1.00e+0	0.999	0.0051
GOTERM_BP_DIRECT	hematopoietic progenitor cell differentiation	1%	9	870	76	19512	0.0196	1.00e+0	2.66	1.00e+0	0.999	0.00656
GOTERM_BP_DIRECT	Wnt signaling pathway	2%	19	870	237	19512	0.0196	1.00e+0	1.80	1.00e+0	0.999	0.0101
GOTERM_BP_DIRECT	nitric oxide biosynthetic process	0%	5	870	24	19512	0.0204	1.00e+0	4.67	1.00e+0	0.999	0.00365
GOTERM_BP_DIRECT	ventricular septum development	1%	6	870	36	19512	0.0208	1.00e+0	3.74	1.00e+0	0.999	0.00478
GOTERM_BP_DIRECT	response to testosterone	1%	6	870	36	19512	0.0208	1.00e+0	3.74	1.00e+0	0.999	0.00478
GOTERM_BP_DIRECT	cellular response to glucose stimulus	1%	9	870	77	19512	0.021	1.00e+0	2.62	1.00e+0	0.999	0.00714
GOTERM_BP_DIRECT	angiogenesis	2%	22	870	292	19512	0.0215	1.00e+0	1.69	1.00e+0	0.999	0.0118
GOTERM_BP_DIRECT	negative regulation of ferroptosis	0%	4	870	14	19512	0.0222	1.00e+0	6.41	1.00e+0	0.999	0.00274
GOTERM_BP_DIRECT	locomotor rhythm	0%	4	870	14	19512	0.0222	1.00e+0	6.41	1.00e+0	0.999	0.00274
GOTERM_BP_DIRECT	response to unfolded protein	1%	9	870	78	19512	0.0225	1.00e+0	2.59	1.00e+0	0.999	0.00777
GOTERM_BP_DIRECT	positive regulation of MAPK cascade	2%	18	870	224	19512	0.023	1.00e+0	1.80	1.00e+0	0.999	0.0117
GOTERM_BP_DIRECT	positive regulation of blood vessel endothelial cell migration	1%	7	870	50	19512	0.023	1.00e+0	3.14	1.00e+0	0.999	0.00641
GOTERM_BP_DIRECT	integrated stress response signaling	0%	5	870	25	19512	0.0234	1.00e+0	4.49	1.00e+0	0.999	0.0044
GOTERM_BP_DIRECT	negative regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	1%	9	870	79	19512	0.0241	1.00e+0	2.56	1.00e+0	0.999	0.00843
GOTERM_BP_DIRECT	collagen fibril organization	1%	8	870	65	19512	0.0251	1.00e+0	2.76	1.00e+0	0.999	0.00806
GOTERM_BP_DIRECT	positive regulation of apoptotic process	2%	24	870	333	19512	0.0254	1.00e+0	1.62	1.00e+0	0.999	0.0146
GOTERM_BP_DIRECT	response to axon injury	1%	6	870	38	19512	0.0257	1.00e+0	3.54	1.00e+0	0.999	0.00629
GOTERM_BP_DIRECT	negative regulation of cell migration	1%	16	870	193	19512	0.0261	1.00e+0	1.86	1.00e+0	0.999	0.0128
GOTERM_BP_DIRECT	tryptophan transport	0%	3	870	6	19512	0.0264	1.00e+0	11.21	1.00e+0	0.999	0.0016
GOTERM_BP_DIRECT	regulation of heme biosynthetic process	0%	3	870	6	19512	0.0264	1.00e+0	11.21	1.00e+0	0.999	0.0016
GOTERM_BP_DIRECT	L-serine biosynthetic process	0%	3	870	6	19512	0.0264	1.00e+0	11.21	1.00e+0	0.999	0.0016
GOTERM_BP_DIRECT	cysteine metabolic process	0%	3	870	6	19512	0.0264	1.00e+0	11.21	1.00e+0	0.999	0.0016
GOTERM_BP_DIRECT	GDF15-GFRAL signaling pathway	0%	3	870	6	19512	0.0264	1.00e+0	11.21	1.00e+0	0.999	0.0016
GOTERM_BP_DIRECT	regulation of neuron apoptotic process	0%	5	870	26	19512	0.0268	1.00e+0	4.31	1.00e+0	0.999	0.00525
GOTERM_BP_DIRECT	response to hyperoxia	0%	4	870	15	19512	0.0268	1.00e+0	5.98	1.00e+0	0.999	0.00361
GOTERM_BP_DIRECT	inner ear morphogenesis	1%	8	870	66	19512	0.0271	1.00e+0	2.72	1.00e+0	0.999	0.00883
GOTERM_BP_DIRECT	T cell receptor signaling pathway	1%	12	870	128	19512	0.0278	1.00e+0	2.10	1.00e+0	0.999	0.012
GOTERM_BP_DIRECT	response to starvation	1%	6	870	39	19512	0.0285	1.00e+0	3.45	1.00e+0	0.999	0.00716
GOTERM_BP_DIRECT	intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	1%	6	870	39	19512	0.0285	1.00e+0	3.45	1.00e+0	0.999	0.00716
GOTERM_BP_DIRECT	negative regulation of transforming growth factor beta receptor signaling pathway	1%	12	870	129	19512	0.0292	1.00e+0	2.09	1.00e+0	0.999	0.0127
GOTERM_BP_DIRECT	cellular response to oxidative stress	1%	11	870	113	19512	0.0293	1.00e+0	2.18	1.00e+0	0.999	0.0121
GOTERM_BP_DIRECT	epithelial cell differentiation	1%	11	870	114	19512	0.0309	1.00e+0	2.16	1.00e+0	0.999	0.0129
GOTERM_BP_DIRECT	angiotensin-activated signaling pathway	0%	4	870	16	19512	0.0319	1.00e+0	5.61	1.00e+0	0.999	0.00465
GOTERM_BP_DIRECT	response to insulin	1%	9	870	84	19512	0.0333	1.00e+0	2.40	1.00e+0	0.999	0.0124
GOTERM_BP_DIRECT	response to mechanical stimulus	1%	8	870	69	19512	0.0335	1.00e+0	2.60	1.00e+0	0.999	0.0114
GOTERM_BP_DIRECT	cell migration	2%	22	870	306	19512	0.0336	1.00e+0	1.61	1.00e+0	0.999	0.0192
GOTERM_BP_DIRECT	positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	2%	17	870	217	19512	0.0338	1.00e+0	1.76	1.00e+0	0.999	0.0176

GOTERM_BP_DIRECT	hormone metabolic process	0%	5	870	28	19512	0.0342	1.00e+0	4.00	1.00e+0	0.999	0.00728
GOTERM_BP_DIRECT	hippo signaling	0%	5	870	28	19512	0.0342	1.00e+0	4.00	1.00e+0	0.999	0.00728
GOTERM_BP_DIRECT	intracellular protein localization	1%	16	870	200	19512	0.0343	1.00e+0	1.79	1.00e+0	0.999	0.0175
GOTERM_BP_DIRECT	mitochondrion organization	1%	12	870	133	19512	0.0354	1.00e+0	2.02	1.00e+0	0.999	0.0159
GOTERM_BP_DIRECT	cellular response to iron ion	0%	3	870	7	19512	0.0358	1.00e+0	9.61	1.00e+0	0.999	0.0027
GOTERM_BP_DIRECT	regulation of DNA damage response, signal transduction by p53 class mediator	0%	3	870	7	19512	0.0358	1.00e+0	9.61	1.00e+0	0.999	0.0027
GOTERM_BP_DIRECT	enucleate erythrocyte differentiation	0%	3	870	7	19512	0.0358	1.00e+0	9.61	1.00e+0	0.999	0.0027
GOTERM_BP_DIRECT	muscle tissue development	0%	3	870	7	19512	0.0358	1.00e+0	9.61	1.00e+0	0.999	0.0027
GOTERM_BP_DIRECT	cellular response to transforming growth factor beta stimulus	1%	8	870	70	19512	0.0358	1.00e+0	2.56	1.00e+0	0.999	0.0124
GOTERM_BP_DIRECT	enzyme-linked receptor protein signaling pathway	0%	4	870	17	19512	0.0375	1.00e+0	5.28	1.00e+0	0.999	0.00587
GOTERM_BP_DIRECT	rhythmic process	1%	13	870	151	19512	0.0376	1.00e+0	1.93	1.00e+0	0.999	0.0177
GOTERM_BP_DIRECT	response to hydrogen peroxide	1%	6	870	42	19512	0.0378	1.00e+0	3.20	1.00e+0	0.999	0.0103
GOTERM_BP_DIRECT	regulation of developmental process	1%	6	870	42	19512	0.0378	1.00e+0	3.20	1.00e+0	0.999	0.0103
GOTERM_BP_DIRECT	multicellular organismal-level iron ion homeostasis	0%	5	870	29	19512	0.0383	1.00e+0	3.87	1.00e+0	0.999	0.00848
GOTERM_BP_DIRECT	positive regulation of ubiquitin-dependent protein catabolic process	0%	5	870	29	19512	0.0383	1.00e+0	3.87	1.00e+0	0.999	0.00848
GOTERM_BP_DIRECT	negative regulation of myoblast differentiation	0%	5	870	29	19512	0.0383	1.00e+0	3.87	1.00e+0	0.999	0.00848
GOTERM_BP_DIRECT	blood vessel development	1%	8	870	71	19512	0.0383	1.00e+0	2.53	1.00e+0	0.999	0.0135
GOTERM_BP_DIRECT	roof of mouth development	1%	8	870	71	19512	0.0383	1.00e+0	2.53	1.00e+0	0.999	0.0135
GOTERM_BP_DIRECT	positive regulation of DNA-templated transcription	4%	47	870	791	19512	0.0396	1.00e+0	1.33	1.00e+0	0.999	0.0279
GOTERM_BP_DIRECT	inner ear development	1%	7	870	57	19512	0.0405	1.00e+0	2.75	1.00e+0	0.999	0.013
GOTERM_BP_DIRECT	positive regulation of SMAD protein signal transduction	1%	6	870	43	19512	0.0412	1.00e+0	3.13	1.00e+0	0.999	0.0115
GOTERM_BP_DIRECT	positive regulation of bone mineralization	1%	6	870	43	19512	0.0412	1.00e+0	3.13	1.00e+0	0.999	0.0115
GOTERM_BP_DIRECT	protein stabilization	2%	19	870	259	19512	0.0423	1.00e+0	1.65	1.00e+0	0.999	0.0234
GOTERM_BP_DIRECT	sensory perception of sound	1%	14	870	171	19512	0.0425	1.00e+0	1.84	1.00e+0	0.999	0.0211
GOTERM_BP_DIRECT	chondrocyte proliferation	0%	4	870	18	19512	0.0436	1.00e+0	4.98	1.00e+0	0.999	0.00728
GOTERM_BP_DIRECT	viral release from host cell	0%	4	870	18	19512	0.0436	1.00e+0	4.98	1.00e+0	0.999	0.00728
GOTERM_BP_DIRECT	positive regulation of intracellular signal transduction	1%	6	870	44	19512	0.0449	1.00e+0	3.06	1.00e+0	0.999	0.0128
GOTERM_BP_DIRECT	cell redox homeostasis	1%	6	870	44	19512	0.0449	1.00e+0	3.06	1.00e+0	0.999	0.0128
GOTERM_BP_DIRECT	positive regulation of cell cycle	1%	6	870	44	19512	0.0449	1.00e+0	3.06	1.00e+0	0.999	0.0128
GOTERM_BP_DIRECT	positive regulation of epithelial cell proliferation	1%	8	870	74	19512	0.0463	1.00e+0	2.42	1.00e+0	0.999	0.017
GOTERM_BP_DIRECT	negative regulation of canonical Wnt signaling pathway	1%	13	870	156	19512	0.0463	1.00e+0	1.87	1.00e+0	0.999	0.0225
GOTERM_BP_DIRECT	odontoblast differentiation	0%	3	870	8	19512	0.0464	1.00e+0	8.41	1.00e+0	0.999	0.00418
GOTERM_BP_DIRECT	caveola assembly	0%	3	870	8	19512	0.0464	1.00e+0	8.41	1.00e+0	0.999	0.00418
GOTERM_BP_DIRECT	bone trabecula formation	0%	3	870	8	19512	0.0464	1.00e+0	8.41	1.00e+0	0.999	0.00418
GOTERM_BP_DIRECT	positive regulation of chromatin binding	0%	3	870	8	19512	0.0464	1.00e+0	8.41	1.00e+0	0.999	0.00418
GOTERM_BP_DIRECT	positive regulation of skeletal muscle acetylcholine-gated channel clustering	0%	3	870	8	19512	0.0464	1.00e+0	8.41	1.00e+0	0.999	0.00418
GOTERM_BP_DIRECT	pericardium development	0%	3	870	8	19512	0.0464	1.00e+0	8.41	1.00e+0	0.999	0.00418
GOTERM_BP_DIRECT	protein localization to ciliary transition zone	0%	3	870	8	19512	0.0464	1.00e+0	8.41	1.00e+0	0.999	0.00418
GOTERM_BP_DIRECT	positive regulation of sprouting angiogenesis	0%	5	870	31	19512	0.0473	1.00e+0	3.62	1.00e+0	0.999	0.0113
GOTERM_BP_DIRECT	cellular response to hypoxia	1%	12	870	140	19512	0.0484	1.00e+0	1.92	1.00e+0	0.999	0.0228
GOTERM_BP_DIRECT	establishment or maintenance of cell polarity	1%	6	870	45	19512	0.0487	1.00e+0	2.99	1.00e+0	0.999	0.0143
GOTERM_BP_DIRECT	intracellular potassium ion homeostasis	0%	4	870	19	19512	0.0501	1.00e+0	4.72	1.00e+0	0.999	0.0089
GOTERM_BP_DIRECT	negative regulation of reactive oxygen species metabolic process	0%	4	870	19	19512	0.0501	1.00e+0	4.72	1.00e+0	0.999	0.0089
GOTERM_BP_DIRECT	hippocampus development	1%	8	870	76	19512	0.0522	1.00e+0	2.36	1.00e+0	0.999	0.0197
GOTERM_BP_DIRECT	post-transcriptional regulation of gene expression	0%	5	870	32	19512	0.0523	1.00e+0	3.50	1.00e+0	0.999	0.0129
GOTERM_BP_DIRECT	positive regulation of macroautophagy	0%	5	870	32	19512	0.0523	1.00e+0	3.50	1.00e+0	0.999	0.0129
GOTERM_BP_DIRECT	transforming growth factor beta receptor signaling pathway	1%	10	870	109	19512	0.0543	1.00e+0	2.06	1.00e+0	0.999	0.0237
GOTERM_BP_DIRECT	intrinsic apoptotic signaling pathway	1%	6	870	47	19512	0.0569	1.00e+0	2.86	1.00e+0	0.999	0.0175
GOTERM_BP_DIRECT	white fat cell differentiation	0%	4	870	20	19512	0.0571	1.00e+0	4.49	1.00e+0	0.999	0.0107
GOTERM_BP_DIRECT	osteoblast development	0%	4	870	20	19512	0.0571	1.00e+0	4.49	1.00e+0	0.999	0.0107
GOTERM_BP_DIRECT	fibroblast migration	0%	4	870	20	19512	0.0571	1.00e+0	4.49	1.00e+0	0.999	0.0107
GOTERM_BP_DIRECT	embryonic forelimb morphogenesis	0%	5	870	33	19512	0.0575	1.00e+0	3.40	1.00e+0	0.999	0.0147
GOTERM_BP_DIRECT	common myeloid progenitor cell proliferation	0%	3	870	9	19512	0.0579	1.00e+0	7.48	1.00e+0	0.999	0.00606
GOTERM_BP_DIRECT	regulation of cell communication by electrical coupling involved in cardiac conduction	0%	3	870	9	19512	0.0579	1.00e+0	7.48	1.00e+0	0.999	0.00606
GOTERM_BP_DIRECT	regulation of lipid storage	0%	3	870	9	19512	0.0579	1.00e+0	7.48	1.00e+0	0.999	0.00606
GOTERM_BP_DIRECT	cAMP catabolic process	0%	3	870	9	19512	0.0579	1.00e+0	7.48	1.00e+0	0.999	0.00606
GOTERM_BP_DIRECT	neuroblast proliferation	1%	6	870	48	19512	0.0613	1.00e+0	2.80	1.00e+0	0.999	0.0192
GOTERM_BP_DIRECT	cellular response to growth factor stimulus	1%	8	870	79	19512	0.0619	1.00e+0	2.27	1.00e+0	0.999	0.0243
GOTERM_BP_DIRECT	negative regulation of signal transduction	1%	8	870	79	19512	0.0619	1.00e+0	2.27	1.00e+0	0.999	0.0243
GOTERM_BP_DIRECT	regulation of protein ubiquitination	0%	4	870	21	19512	0.0645	1.00e+0	4.27	1.00e+0	0.999	0.0128
GOTERM_BP_DIRECT	response to antibiotic	0%	4	870	21	19512	0.0645	1.00e+0	4.27	1.00e+0	0.999	0.0128
GOTERM_BP_DIRECT	apoptotic process	4%	46	870	800	19512	0.0646	1.00e+0	1.29	1.00e+0	0.999	0.0471
GOTERM_BP_DIRECT	regulation of transcription by RNA polymerase II	8%	87	870	1643	19512	0.0659	1.00e+0	1.19	1.00e+0	0.999	0.0513
GOTERM_BP_DIRECT	skeletal muscle cell differentiation	1%	6	870	49	19512	0.0659	1.00e+0	2.75	1.00e+0	0.999	0.0211
GOTERM_BP_DIRECT	biomineral tissue development	0%	5	870	35	19512	0.0687	1.00e+0	3.20	1.00e+0	0.999	0.0186
GOTERM_BP_DIRECT	positive regulation of neuron apoptotic process	1%	7	870	65	19512	0.0689	1.00e+0	2.42	1.00e+0	0.999	0.0253
GOTERM_BP_DIRECT	regulation of cell growth	1%	8	870	81	19512	0.069	1.00e+0	2.22	1.00e+0	0.999	0.0277
GOTERM_BP_DIRECT	membrane repolarization during cardiac muscle cell action potential	0%	3	870	10	19512	0.0703	1.00e+0	6.73	1.00e+0	0.999	0.00838
GOTERM_BP_DIRECT	mesenchyme development	0%	3	870	10	19512	0.0703	1.00e+0	6.73	1.00e+0	0.999	0.00838
GOTERM_BP_DIRECT	cardiac muscle cell contraction	0%	3	870	10	19512	0.0703	1.00e+0	6.73	1.00e+0	0.999	0.00838
GOTERM_BP_DIRECT	endochondral bone growth	0%	3	870	10	19512	0.0703	1.00e+0	6.73	1.00e+0	0.999	0.00838
GOTERM_BP_DIRECT	superoxide metabolic process	0%	4	870	22	19512	0.0723	1.00e+0	4.08	1.00e+0	0.999	0.0151
GOTERM_BP_DIRECT	positive regulation of chondrocyte differentiation	0%	4	870	22	19512	0.0723	1.00e+0	4.08	1.00e+0	0.999	0.0151
GOTERM_BP_DIRECT	female pregnancy	1%	8	870	82	19512	0.0726	1.00e+0	2.19	1.00e+0	0.999	0.0296
GOTERM_BP_DIRECT	response to xenobiotic stimulus	2%	18	870	260	19512	0.0741	1.00e+0	1.55	1.00e+0	0.999	0.0438
GOTERM_BP_DIRECT	regulation of multicellular organismal process	0%	5	870	36	19512	0.0746	1.00e+0	3.11	1.00e+0	0.999	0.0209
GOTERM_BP_DIRECT	negative regulation of smoothened signaling pathway	0%	5	870	36	19512	0.0746	1.00e+0	3.11	1.00e+0	0.999	0.0209
GOTERM_BP_DIRECT	regulation of mitochondrial membrane potential	0%	5	870	36	19512	0.0746	1.00e+0	3.11	1.00e+0	0.999	0.0209
GOTERM_BP_DIRECT	response to estrogen	1%	6	870	51	19512	0.0756	1.00e+0	2.64	1.00e+0	0.999	0.0252
GOTERM_BP_DIRECT	embryonic morphogenesis	0%	4	870	23	19512	0.0805	1.00e+0	3.90	1.00e+0	0.999	0.0177
GOTERM_BP_DIRECT	carbohydrate derivative metabolic process	0%	4	870	23	19512	0.0805	1.00e+0	3.90	1.00e+0	0.999	0.0177
GOTERM_BP_DIRECT	regulation of transforming growth factor beta receptor signaling pathway	0%	4	870	23	19512	0.0805	1.00e+0	3.90	1.00e+0	0.999	0.0177
GOTERM_BP_DIRECT	positive regulation of autophagosome assembly	0%	4	870	23	19512	0.0805	1.00e+0	3.90	1.00e+0	0.999	0.0177
GOTERM_BP_DIRECT	male gonad development	1%	10	870	118	19512	0.0807	1.00e+0	1.90	1.00e+0	0.999	0.0381
GOTERM_BP_DIRECT	aortic valve morphogenesis	0%	5	870	37	19512	0.0809	1.00e+0	3.03	1.00e+0	0.999	0.0233
GOTERM_BP_DIRECT	negative regulation of cardiac muscle cell apoptotic process	0%	5	870	37	19512	0.0809	1.00e+0	3.03	1.00e+0	0.999	0.0233
GOTERM_BP_DIRECT	blood vessel diameter maintenance	0%	5	870	37	19512	0.0809	1.00e+0	3.03	1.00e+0	0.999	0.0233
GOTERM_BP_DIRECT	positive regulation of cell migration involved in sprouting angiogenesis	0%	5	870	37	19512	0.0809	1.00e+0	3.03	1.00e+0	0.999	0.0233
GOTERM_BP_DIRECT	cilium assembly	2%	17	870	244	19512	0.0815	1.00e+0	1.56	1.00e+0	0.999	0.0463
GOTERM_BP_DIRECT	cellular response to amino acid starvation	1%	7	870	68	19512	0.0818	1.00e+0	2.31	1.00e+0	0.999	0.0314
GOTERM_BP_DIRECT	cellular response to amino acid stimulus	1%	7	870	68	19512	0.0818	1.00e+0	2.31	1.00e+0	0.999	0.0314
GOTERM_BP_DIRECT	protein-containing complex assembly	1%	12	870	154	19512	0.0832	1.00e+0	1.75	1.00e+0	0.999	0.043
GOTERM_BP_DIRECT	mitral valve morphogenesis	0%	3	870	11	19512	0.0835	1.00e+0	6.12	1.00e+0	0.999	0.0111
GOTERM_BP_DIRECT	thymocyte apoptotic process	0%	3	870	11	19512	0.0835	1.00e+0	6.12	1.00e+0	0.999	0.0111
GOTERM_BP_DIRECT	determination of left/right asymmetry in lateral mesoderm	0%	3	870	11	19512	0.0835	1.00e+0	6.12	1.00e+0	0.999	0.0111
GOTERM_BP_DIRECT	branching involved in mammary gland duct morphogenesis	0%	3	870	11	19512	0.0835	1.00e+0	6.12	1.00e+0	0.999	0.0111
GOTERM_BP_DIRECT	positive regulation of peroxisome proliferator activated receptor signaling pathway	0%	3	870	11	19512	0.0835	1.00e+0	6.12	1.00e+0	0.999	0.0111
GOTERM_BP_DIRECT	cell activation	0%	3	870	11	19512	0.0835	1.00e+0	6.12	1.00e+0	0.999	0.0111
GOTERM_BP_DIRECT	neural tube formation	0%	3	870	11	19512	0.0835	1.00e+0	6.12	1.00e+0	0.999	0.0111
GOTERM_BP_DIRECT	PERK-mediated unfolded protein response	0%	3	870	11	19512	0.0835	1.00e+0	6.12	1.00e+0	0.999	0.0111
GOTERM_BP_DIRECT	positive regulation of vascular permeability	0%	3	870	11	19512	0.0835	1.00e+0	6.12	1.00e+0	0.999	0.0111
GOTERM_BP_DIRECT	apoptotic signaling pathway	1%	8	870	85	19512	0.0844	1.00e+0	2.11	1.00e+0	0.999	0.0356
GOTERM_BP_DIRECT	cell adhesion	4%	39	870	677	19512	0.086	1.00e+0	1.29	1.00e+0	0.999	0.0613
GOTERM_BP_DIRECT	response to activity	1%	6	870	53	19512	0.0861	1.00e+0	2.54	1.00e+0	0.999	0.0299
GOTERM_BP_DIRECT	positive regulation of G1/S transition of mitotic cell cycle	1%	6	870	53	19512	0.0861	1.00e+0	2.54	1.00e+0	0.999	0.0299
GOTERM_BP_DIRECT	lymph circulation	0%	2	870	2	19512	0.0871	1.00e+0	22.43	1.00e+0	0.999	0.00199
GOTERM_BP_DIRECT	pre-miRNA export from nucleus	0%	2	870	2	19512	0.0871	1.00e+0	22.43	1.00e+0	0.999	0.00199
GOTERM_BP_DIRECT	regulation of endodeoxyribonuclease activity	0%	2	870	2	19512	0.0871	1.00e+0	22.43	1.00e+0	0.999	0.00199
GOTERM_BP_DIRECT	response to forskolin	0%	2	870	2	19512	0.0871	1.00e+0	22.43	1.00e+0	0.999	0.00199

GOTERM_BP_DIRECT	corticosterone secretion	0%	2	870	2	19512	0.0871	1.00e+0	22.43	1.00e+0	0.999	0.00199
GOTERM_BP_DIRECT	L-tryptophan transmembrane transport	0%	2	870	2	19512	0.0871	1.00e+0	22.43	1.00e+0	0.999	0.00199
GOTERM_BP_DIRECT	detoxification of nitrogen compound	0%	2	870	2	19512	0.0871	1.00e+0	22.43	1.00e+0	0.999	0.00199
GOTERM_BP_DIRECT	follicle-stimulating hormone secretion	0%	2	870	2	19512	0.0871	1.00e+0	22.43	1.00e+0	0.999	0.00199
GOTERM_BP_DIRECT	DNA replication preinitiation complex assembly	0%	2	870	2	19512	0.0871	1.00e+0	22.43	1.00e+0	0.999	0.00199
GOTERM_BP_DIRECT	negative regulation of programmed necrotic cell death	0%	2	870	2	19512	0.0871	1.00e+0	22.43	1.00e+0	0.999	0.00199
GOTERM_BP_DIRECT	regulation of mitochondrial DNA metabolic process	0%	2	870	2	19512	0.0871	1.00e+0	22.43	1.00e+0	0.999	0.00199
GOTERM_BP_DIRECT	negative regulation of relaxation of cardiac muscle	0%	2	870	2	19512	0.0871	1.00e+0	22.43	1.00e+0	0.999	0.00199
GOTERM_BP_DIRECT	negative regulation of DNA-templated DNA replication	0%	2	870	2	19512	0.0871	1.00e+0	22.43	1.00e+0	0.999	0.00199
GOTERM_BP_DIRECT	negative regulation of endothelial cell apoptotic process	0%	5	870	38	19512	0.0874	1.00e+0	2.95	1.00e+0	0.999	0.0258
GOTERM_BP_DIRECT	phosphatidylinositol metabolic process	0%	5	870	38	19512	0.0874	1.00e+0	2.95	1.00e+0	0.999	0.0258
GOTERM_BP_DIRECT	Notch signaling pathway	1%	10	870	120	19512	0.0875	1.00e+0	1.87	1.00e+0	0.999	0.042
GOTERM_BP_DIRECT	positive regulation of cell differentiation	1%	8	870	86	19512	0.0886	1.00e+0	2.09	1.00e+0	0.999	0.0378
GOTERM_BP_DIRECT	uterus development	0%	4	870	24	19512	0.089	1.00e+0	3.74	1.00e+0	0.999	0.0205
GOTERM_BP_DIRECT	embryo development ending in birth or egg hatching	0%	4	870	24	19512	0.089	1.00e+0	3.74	1.00e+0	0.999	0.0205
GOTERM_BP_DIRECT	regulation of proteasomal protein catabolic process	0%	4	870	24	19512	0.089	1.00e+0	3.74	1.00e+0	0.999	0.0205
GOTERM_BP_DIRECT	negative regulation of keratinocyte proliferation	0%	4	870	24	19512	0.089	1.00e+0	3.74	1.00e+0	0.999	0.0205
GOTERM_BP_DIRECT	phosphatidylinositol-mediated signaling	0%	4	870	24	19512	0.089	1.00e+0	3.74	1.00e+0	0.999	0.0205
GOTERM_BP_DIRECT	cell population proliferation	2%	18	870	267	19512	0.0893	1.00e+0	1.51	1.00e+0	0.999	0.0542
GOTERM_BP_DIRECT	negative regulation of cell growth	1%	10	870	121	19512	0.091	1.00e+0	1.85	1.00e+0	0.999	0.0441
GOTERM_BP_DIRECT	transcription by RNA polymerase II	2%	18	870	268	19512	0.0926	1.00e+0	1.51	1.00e+0	0.999	0.0561
GOTERM_BP_DIRECT	regulation of cytosolic calcium ion concentration	0%	5	870	39	19512	0.0941	1.00e+0	2.88	1.00e+0	0.999	0.0286
GOTERM_BP_DIRECT	lipid metabolic process	4%	47	870	847	19512	0.0954	1.00e+0	1.24	1.00e+0	0.999	0.0709
GOTERM_BP_DIRECT	cellular response to hydrogen peroxide	1%	7	870	71	19512	0.0961	1.00e+0	2.21	1.00e+0	0.999	0.0385
GOTERM_BP_DIRECT	system development	1%	8	870	88	19512	0.0972	1.00e+0	2.04	1.00e+0	0.999	0.0424
GOTERM_BP_DIRECT	stem cell proliferation	1%	6	870	55	19512	0.0973	1.00e+0	2.45	1.00e+0	0.999	0.035
GOTERM_BP_DIRECT	glycosaminoglycan metabolic process	0%	3	870	12	19512	0.0973	1.00e+0	5.61	1.00e+0	0.999	0.0144
GOTERM_BP_DIRECT	ER overload response	0%	3	870	12	19512	0.0973	1.00e+0	5.61	1.00e+0	0.999	0.0144
GOTERM_BP_DIRECT	cellular response to electrical stimulus	0%	3	870	12	19512	0.0973	1.00e+0	5.61	1.00e+0	0.999	0.0144
GOTERM_BP_DIRECT	negative regulation of axonogenesis	0%	3	870	12	19512	0.0973	1.00e+0	5.61	1.00e+0	0.999	0.0144
GOTERM_BP_DIRECT	cerebellar Purkinje cell layer development	0%	3	870	12	19512	0.0973	1.00e+0	5.61	1.00e+0	0.999	0.0144
GOTERM_BP_DIRECT	osteoblast proliferation	0%	3	870	12	19512	0.0973	1.00e+0	5.61	1.00e+0	0.999	0.0144
GOTERM_BP_DIRECT	myoblast proliferation	0%	3	870	12	19512	0.0973	1.00e+0	5.61	1.00e+0	0.999	0.0144
GOTERM_BP_DIRECT	response to selenium ion	0%	3	870	12	19512	0.0973	1.00e+0	5.61	1.00e+0	0.999	0.0144
GOTERM_BP_DIRECT	negative regulation of intrinsic apoptotic signaling pathway	0%	4	870	25	19512	0.098	1.00e+0	3.59	1.00e+0	0.999	0.0235
GOTERM_BP_DIRECT	release of cytochrome c from mitochondria	0%	4	870	25	19512	0.098	1.00e+0	3.59	1.00e+0	0.999	0.0235
GOTERM_BP_DIRECT	regulation of protein metabolic process	0%	4	870	25	19512	0.098	1.00e+0	3.59	1.00e+0	0.999	0.0235
GOTERM_BP_DIRECT	central nervous system development	1%	12	870	159	19512	0.0986	1.00e+0	1.69	1.00e+0	0.999	0.0526

GO with upregulated genes												
Category	Term	Genes	Count	List Total	Pop Hits	Pop Total	P-Value	Benjamini	Fold Enrich	Bonferroni	FDR	Fisher Exact
GOTERM_BP_DIRECT	RNA processing	5%	44	720	601	19512	2.74E-05	0.0896	1.98	0.0857	0.0896	1.31E-05
GOTERM_BP_DIRECT	connective tissue replacement involved in inflammatory response wound healing	0%	4	720	5	19512	0.000471	0.537	21.68	0.786	0.537	8.93E-06
GOTERM_BP_DIRECT	intracellular signal transduction	4%	35	720	501	19512	0.000492	0.537	1.89	0.8	0.537	0.000246
GOTERM_BP_DIRECT	response to muscle activity	1%	7	720	30	19512	0.000683	0.559	6.32	0.893	0.559	8.77E-05
GOTERM_BP_DIRECT	semaphorin-plexin signaling pathway	1%	8	720	45	19512	0.0012	0.691	4.82	0.98	0.691	0.000212
GOTERM_BP_DIRECT	angiogenesis	3%	23	720	292	19512	0.00127	0.691	2.13	0.984	0.691	0.000552
GOTERM_BP_DIRECT	protein phosphorylation	2%	21	720	261	19512	0.00168	0.788	2.18	0.996	0.788	0.000719
GOTERM_BP_DIRECT	activation of GTPase activity	1%	6	720	26	19512	0.00231	0.947	6.25	0.999	0.947	0.000302
GOTERM_BP_DIRECT	positive regulation of transcription by RNA polymerase II	8%	66	720	1243	19512	0.00278	0.949	1.44	1.00e+0	0.949	0.00182
GOTERM_BP_DIRECT	neutrophil activation	1%	5	720	17	19512	0.00297	0.949	7.97	1.00e+0	0.949	0.000288
GOTERM_BP_DIRECT	response to xenobiotic stimulus	2%	20	720	260	19512	0.00369	0.949	2.08	1.00e+0	0.949	0.00164
GOTERM_BP_DIRECT	glucose homeostasis	2%	13	720	135	19512	0.00425	0.949	2.61	1.00e+0	0.949	0.00148
GOTERM_BP_DIRECT	positive regulation of interleukin-6 production	1%	11	720	103	19512	0.00469	0.949	2.89	1.00e+0	0.949	0.00146
GOTERM_BP_DIRECT	interleukin-17-mediated signaling pathway	0%	4	720	10	19512	0.00492	0.949	10.84	1.00e+0	0.949	0.000323
GOTERM_BP_DIRECT	inflammatory response	4%	30	720	474	19512	0.00554	0.949	1.72	1.00e+0	0.949	0.00302
GOTERM_BP_DIRECT	monoatomic ion transport	5%	39	720	672	19512	0.00617	0.949	1.57	1.00e+0	0.949	0.0036
GOTERM_BP_DIRECT	positive regulation of apoptotic process	3%	23	720	333	19512	0.00622	0.949	1.87	1.00e+0	0.949	0.00309
GOTERM_BP_DIRECT	positive regulation of inflammatory response	1%	12	720	125	19512	0.00652	0.949	2.60	1.00e+0	0.949	0.00228
GOTERM_BP_DIRECT	negative regulation of platelet aggregation	0%	4	720	11	19512	0.00659	0.949	9.85	1.00e+0	0.949	0.000493
GOTERM_BP_DIRECT	negative regulation of catalytic activity	0%	4	720	11	19512	0.00659	0.949	9.85	1.00e+0	0.949	0.000493
GOTERM_BP_DIRECT	positive regulation of canonical NF-kappaB signal transduction	2%	18	720	236	19512	0.0067	0.949	2.07	1.00e+0	0.949	0.003
GOTERM_BP_DIRECT	cellular response to vascular endothelial growth factor stimulus	1%	6	720	33	19512	0.00676	0.949	4.93	1.00e+0	0.949	0.00117
GOTERM_BP_DIRECT	positive regulation of macromolecule metabolic process	1%	6	720	33	19512	0.00676	0.949	4.93	1.00e+0	0.949	0.00117
GOTERM_BP_DIRECT	positive regulation of miRNA transcription	1%	8	720	61	19512	0.00695	0.949	3.55	1.00e+0	0.949	0.00173
GOTERM_BP_DIRECT	triglyceride biosynthetic process	1%	5	720	22	19512	0.00788	0.999	6.16	1.00e+0	0.999	0.00105
GOTERM_BP_DIRECT	response to virus	1%	12	720	129	19512	0.00821	0.999	2.52	1.00e+0	0.999	0.00296
GOTERM_BP_DIRECT	skin morphogenesis	0%	4	720	12	19512	0.00854	0.999	9.03	1.00e+0	0.999	0.000718
GOTERM_BP_DIRECT	negative regulation of cardiac muscle hypertrophy in response to stress	0%	4	720	12	19512	0.00854	0.999	9.03	1.00e+0	0.999	0.000718
GOTERM_BP_DIRECT	SMAD protein signal transduction	1%	5	720	23	19512	0.00926	1.00e+0	5.89	1.00e+0	1.00e+0	0.00131
GOTERM_BP_DIRECT	positive regulation of ERK1 and ERK2 cascade	2%	16	720	207	19512	0.00995	1.00e+0	2.09	1.00e+0	1.00e+0	0.00438
GOTERM_BP_DIRECT	positive regulation of glycolytic process	1%	5	720	24	19512	0.0108	1.00e+0	5.65	1.00e+0	1.00e+0	0.0016
GOTERM_BP_DIRECT	response to immobilization stress	1%	5	720	24	19512	0.0108	1.00e+0	5.65	1.00e+0	1.00e+0	0.0016
GOTERM_BP_DIRECT	positive regulation of phagocytosis, engulfment	0%	4	720	13	19512	0.0108	1.00e+0	8.34	1.00e+0	1.00e+0	0.00101
GOTERM_BP_DIRECT	T-helper 17 type immune response	0%	3	720	5	19512	0.0126	1.00e+0	16.26	1.00e+0	1.00e+0	0.000473
GOTERM_BP_DIRECT	negative regulation of inflammatory response	2%	13	720	156	19512	0.0129	1.00e+0	2.26	1.00e+0	1.00e+0	0.00523
GOTERM_BP_DIRECT	embryonic skeletal system morphogenesis	1%	7	720	53	19512	0.0129	1.00e+0	3.58	1.00e+0	1.00e+0	0.00319
GOTERM_BP_DIRECT	CDP-diacylglycerol biosynthetic process	0%	4	720	14	19512	0.0134	1.00e+0	7.74	1.00e+0	1.00e+0	0.00137
GOTERM_BP_DIRECT	positive regulation of smooth muscle cell differentiation	0%	4	720	14	19512	0.0134	1.00e+0	7.74	1.00e+0	1.00e+0	0.00137
GOTERM_BP_DIRECT	cytoskeleton-dependent intracellular transport	0%	4	720	14	19512	0.0134	1.00e+0	7.74	1.00e+0	1.00e+0	0.00137
GOTERM_BP_DIRECT	negative regulation of ERK1 and ERK2 cascade	1%	9	720	86	19512	0.0139	1.00e+0	2.84	1.00e+0	1.00e+0	0.00441
GOTERM_BP_DIRECT	lung morphogenesis	1%	5	720	26	19512	0.0143	1.00e+0	5.21	1.00e+0	1.00e+0	0.00233
GOTERM_BP_DIRECT	negative regulation of Ras protein signal transduction	1%	5	720	26	19512	0.0143	1.00e+0	5.21	1.00e+0	1.00e+0	0.00233
GOTERM_BP_DIRECT	positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	2%	16	720	217	19512	0.0148	1.00e+0	2.00	1.00e+0	1.00e+0	0.00683
GOTERM_BP_DIRECT	monoatomic anion transmembrane transport	1%	6	720	40	19512	0.0152	1.00e+0	4.07	1.00e+0	1.00e+0	0.00325
GOTERM_BP_DIRECT	transforming growth factor beta receptor superfamily signaling pathway	0%	4	720	15	19512	0.0163	1.00e+0	7.23	1.00e+0	1.00e+0	0.00181
GOTERM_BP_DIRECT	retina vasculature development in camera-type eye	0%	4	720	15	19512	0.0163	1.00e+0	7.23	1.00e+0	1.00e+0	0.00181
GOTERM_BP_DIRECT	positive regulation of fatty acid biosynthetic process	0%	4	720	15	19512	0.0163	1.00e+0	7.23	1.00e+0	1.00e+0	0.00181
GOTERM_BP_DIRECT	epithelial structure maintenance	0%	4	720	15	19512	0.0163	1.00e+0	7.23	1.00e+0	1.00e+0	0.00181
GOTERM_BP_DIRECT	regulation of glucose metabolic process	1%	5	720	27	19512	0.0163	1.00e+0	5.02	1.00e+0	1.00e+0	0.00277
GOTERM_BP_DIRECT	negative regulation of proteolysis	1%	5	720	27	19512	0.0163	1.00e+0	5.02	1.00e+0	1.00e+0	0.00277
GOTERM_BP_DIRECT	negative regulation of cell population proliferation	3%	27	720	450	19512	0.0165	1.00e+0	1.63	1.00e+0	1.00e+0	0.00936
GOTERM_BP_DIRECT	response to cytokine	1%	7	720	56	19512	0.0167	1.00e+0	3.39	1.00e+0	1.00e+0	0.00436
GOTERM_BP_DIRECT	cell surface receptor protein tyrosine kinase signaling pathway	1%	11	720	125	19512	0.0173	1.00e+0	2.38	1.00e+0	1.00e+0	0.00659
GOTERM_BP_DIRECT	positive regulation of lipid metabolic process	0%	3	720	6	19512	0.0184	1.00e+0	13.55	1.00e+0	1.00e+0	0.000921
GOTERM_BP_DIRECT	interleukin-1-mediated signaling pathway	1%	5	720	28	19512	0.0185	1.00e+0	4.84	1.00e+0	1.00e+0	0.00327
GOTERM_BP_DIRECT	MyD88-dependent toll-like receptor signaling pathway	0%	4	720	16	19512	0.0195	1.00e+0	6.78	1.00e+0	1.00e+0	0.00235
GOTERM_BP_DIRECT	positive regulation of SMAD protein signal transduction	1%	6	720	43	19512	0.0203	1.00e+0	3.78	1.00e+0	1.00e+0	0.00471
GOTERM_BP_DIRECT	regulation of exocytosis	1%	5	720	29	19512	0.0209	1.00e+0	4.67	1.00e+0	1.00e+0	0.00384
GOTERM_BP_DIRECT	animal organ regeneration	1%	5	720	29	19512	0.0209	1.00e+0	4.67	1.00e+0	1.00e+0	0.00384
GOTERM_BP_DIRECT	type I interferon-mediated signaling pathway	1%	7	720	60	19512	0.0228	1.00e+0	3.16	1.00e+0	1.00e+0	0.0064
GOTERM_BP_DIRECT	intracellular glucose homeostasis	1%	5	720	30	19512	0.0234	1.00e+0	4.52	1.00e+0	1.00e+0	0.00447
GOTERM_BP_DIRECT	innate immune response	4%	34	720	621	19512	0.0238	1.00e+0	1.48	1.00e+0	1.00e+0	0.0144
GOTERM_BP_DIRECT	connective tissue development	0%	3	720	7	19512	0.0252	1.00e+0	11.61	1.00e+0	1.00e+0	0.00157
GOTERM_BP_DIRECT	negative regulation of plasminogen activation	0%	3	720	7	19512	0.0252	1.00e+0	11.61	1.00e+0	1.00e+0	0.00157
GOTERM_BP_DIRECT	lipid modification	0%	3	720	7	19512	0.0252	1.00e+0	11.61	1.00e+0	1.00e+0	0.00157
GOTERM_BP_DIRECT	glandular epithelial cell maturation	0%	3	720	7	19512	0.0252	1.00e+0	11.61	1.00e+0	1.00e+0	0.00157
GOTERM_BP_DIRECT	negative regulation of response to endoplasmic reticulum stress	0%	3	720	7	19512	0.0252	1.00e+0	11.61	1.00e+0	1.00e+0	0.00157
GOTERM_BP_DIRECT	cellular response to growth factor stimulus	1%	8	720	79	19512	0.0263	1.00e+0	2.74	1.00e+0	1.00e+0	0.00861
GOTERM_BP_DIRECT	cytokine-mediated signaling pathway	1%	12	720	153	19512	0.0263	1.00e+0	2.13	1.00e+0	1.00e+0	0.0113
GOTERM_BP_DIRECT	negative regulation of collagen biosynthetic process	0%	4	720	18	19512	0.0269	1.00e+0	6.02	1.00e+0	1.00e+0	0.00372
GOTERM_BP_DIRECT	receptor-mediated endocytosis	1%	8	720	80	19512	0.028	1.00e+0	2.71	1.00e+0	1.00e+0	0.00926
GOTERM_BP_DIRECT	neural crest cell migration	1%	6	720	47	19512	0.0287	1.00e+0	3.46	1.00e+0	1.00e+0	0.00732
GOTERM_BP_DIRECT	viral protein processing	1%	5	720	32	19512	0.029	1.00e+0	4.23	1.00e+0	1.00e+0	0.00594
GOTERM_BP_DIRECT	protein localization to plasma membrane	1%	12	720	156	19512	0.0298	1.00e+0	2.08	1.00e+0	1.00e+0	0.013
GOTERM_BP_DIRECT	positive regulation of cell migration	2%	19	720	300	19512	0.0299	1.00e+0	1.72	1.00e+0	1.00e+0	0.0162
GOTERM_BP_DIRECT	exocytosis	1%	11	720	137	19512	0.0304	1.00e+0	2.18	1.00e+0	1.00e+0	0.0127
GOTERM_BP_DIRECT	long-chain fatty-acyl-CoA biosynthetic process	0%	4	720	19	19512	0.0311	1.00e+0	5.71	1.00e+0	1.00e+0	0.00458
GOTERM_BP_DIRECT	muscle structure development	0%	4	720	19	19512	0.0311	1.00e+0	5.71	1.00e+0	1.00e+0	0.00458
GOTERM_BP_DIRECT	axon guidance	2%	14	720	198	19512	0.0321	1.00e+0	1.92	1.00e+0	1.00e+0	0.0154
GOTERM_BP_DIRECT	negative regulation of MAPK cascade	1%	7	720	65	19512	0.0322	1.00e+0	2.92	1.00e+0	1.00e+0	0.00986
GOTERM_BP_DIRECT	negative regulation of type II interferon-mediated signaling pathway	0%	3	720	8	19512	0.0328	1.00e+0	10.16	1.00e+0	1.00e+0	0.00244
GOTERM_BP_DIRECT	regulation of D-glucose import	0%	3	720	8	19512	0.0328	1.00e+0	10.16	1.00e+0	1.00e+0	0.00244
GOTERM_BP_DIRECT	Notch signaling pathway	1%	10	720	120	19512	0.0334	1.00e+0	2.26	1.00e+0	1.00e+0	0.0134
GOTERM_BP_DIRECT	positive regulation of chemokine production	1%	6	720	49	19512	0.0336	1.00e+0	3.32	1.00e+0	1.00e+0	0.00896
GOTERM_BP_DIRECT	cell migration	2%	19	720	306	19512	0.0346	1.00e+0	1.68	1.00e+0	1.00e+0	0.0191
GOTERM_BP_DIRECT	platelet-derived growth factor receptor signaling pathway	1%	5	720	34	19512	0.0353	1.00e+0	3.99	1.00e+0	1.00e+0	0.00773
GOTERM_BP_DIRECT	non-canonical NF-kappaB signal transduction	1%	5	720	34	19512	0.0353	1.00e+0	3.99	1.00e+0	1.00e+0	0.00773
GOTERM_BP_DIRECT	positive regulation of superoxide anion generation	0%	4	720	20	19512	0.0356	1.00e+0	5.42	1.00e+0	1.00e+0	0.00556
GOTERM_BP_DIRECT	monocyte differentiation	0%	4	720	20	19512	0.0356	1.00e+0	5.42	1.00e+0	1.00e+0	0.00556
GOTERM_BP_DIRECT	positive regulation of lipid biosynthetic process	0%	4	720	20	19512	0.0356	1.00e+0	5.42	1.00e+0	1.00e+0	0.00556
GOTERM_BP_DIRECT	regulation of actin cytoskeleton organization	1%	9	720	105	19512	0.0402	1.00e+0	2.32	1.00e+0	1.00e+0	0.0156
GOTERM_BP_DIRECT	positive regulation of DNA-templated transcription	5%	40	720	791	19512	0.0404	1.00e+0	1.37	1.00e+0	1.00e+0	0.0277
GOTERM_BP_DIRECT	positive regulation of chemotaxis	0%	4	720	21	19512	0.0404	1.00e+0	5.16	1.00e+0	1.00e+0	0.00667
GOTERM_BP_DIRECT	anterograde axonal protein transport	0%	3	720	9	19512	0.0411	1.00e+0	9.03	1.00e+0	1.00e+0	0.00356
GOTERM_BP_DIRECT	negative regulation of platelet activation	0%	3	720	9	19512	0.0411	1.00e+0	9.03	1.00e+0	1.00e+0	0.00356
GOTERM_BP_DIRECT	bone marrow development	0%	3	720	9	19512	0.0411	1.00e+0	9.03	1.00e+0	1.00e+0	0.00356
GOTERM_BP_DIRECT	hexose metabolic process	0%	3	720	9	19512	0.0411	1.00e+0	9.03	1.00e+0	1.00e+0	0.00356
GOTERM_BP_DIRECT	regulation of cell cycle	2%	17	720	269	19512	0.0416	1.00e+0	1.71	1.00e+0	1.00e+0	0.0224

GOTERM_BP_DIRECT	MAPK cascade	1%	11	720	145	19512	0.0422	1.00e+0	2.06	1.00e+0	1.00e+0	0.0187
GOTERM_BP_DIRECT	regulation of multicellular organismal process	1%	5	720	36	19512	0.0424	1.00e+0	3.76	1.00e+0	1.00e+0	0.00986
GOTERM_BP_DIRECT	establishment of endothelial barrier	0%	4	720	22	19512	0.0456	1.00e+0	4.93	1.00e+0	1.00e+0	0.00791
GOTERM_BP_DIRECT	lipid metabolic process	5%	42	720	847	19512	0.0461	1.00e+0	1.34	1.00e+0	1.00e+0	0.0321
GOTERM_BP_DIRECT	aortic valve morphogenesis	1%	5	720	37	19512	0.0462	1.00e+0	3.66	1.00e+0	1.00e+0	0.0111
GOTERM_BP_DIRECT	blood vessel development	1%	7	720	71	19512	0.0466	1.00e+0	2.67	1.00e+0	1.00e+0	0.0156
GOTERM_BP_DIRECT	vasodilation	1%	6	720	54	19512	0.0481	1.00e+0	3.01	1.00e+0	1.00e+0	0.0142
GOTERM_BP_DIRECT	transforming growth factor beta receptor signaling pathway	1%	9	720	109	19512	0.0483	1.00e+0	2.24	1.00e+0	1.00e+0	0.0195
GOTERM_BP_DIRECT	endothelial cell chemotaxis	0%	3	720	10	19512	0.0501	1.00e+0	8.13	1.00e+0	1.00e+0	0.00494
GOTERM_BP_DIRECT	cell-cell junction maintenance	0%	3	720	10	19512	0.0501	1.00e+0	8.13	1.00e+0	1.00e+0	0.00494
GOTERM_BP_DIRECT	salivary gland morphogenesis	0%	3	720	10	19512	0.0501	1.00e+0	8.13	1.00e+0	1.00e+0	0.00494
GOTERM_BP_DIRECT	post-translational protein modification	1%	5	720	38	19512	0.0502	1.00e+0	3.57	1.00e+0	1.00e+0	0.0124
GOTERM_BP_DIRECT	carbohydrate derivative metabolic process	0%	4	720	23	19512	0.051	1.00e+0	4.71	1.00e+0	1.00e+0	0.00931
GOTERM_BP_DIRECT	defense response to virus	2%	16	720	256	19512	0.0535	1.00e+0	1.69	1.00e+0	1.00e+0	0.0285
GOTERM_BP_DIRECT	positive regulation of epithelial cell migration	1%	5	720	39	19512	0.0544	1.00e+0	3.47	1.00e+0	1.00e+0	0.0138
GOTERM_BP_DIRECT	cell adhesion mediated by integrin	1%	5	720	39	19512	0.0544	1.00e+0	3.47	1.00e+0	1.00e+0	0.0138
GOTERM_BP_DIRECT	intracellular receptor signaling pathway	1%	5	720	39	19512	0.0544	1.00e+0	3.47	1.00e+0	1.00e+0	0.0138
GOTERM_BP_DIRECT	glycolytic process	1%	6	720	56	19512	0.0548	1.00e+0	2.90	1.00e+0	1.00e+0	0.0168
GOTERM_BP_DIRECT	heart development	2%	17	720	280	19512	0.0556	1.00e+0	1.65	1.00e+0	1.00e+0	0.031
GOTERM_BP_DIRECT	positive regulation of peptidyl-tyrosine phosphorylation	0%	4	720	24	19512	0.0568	1.00e+0	4.52	1.00e+0	1.00e+0	0.0108
GOTERM_BP_DIRECT	positive regulation of megakaryocyte differentiation	0%	3	720	11	19512	0.0598	1.00e+0	7.39	1.00e+0	1.00e+0	0.00661
GOTERM_BP_DIRECT	regulation of cell cycle phase transition	0%	3	720	11	19512	0.0598	1.00e+0	7.39	1.00e+0	1.00e+0	0.00661
GOTERM_BP_DIRECT	establishment of blood-brain barrier	0%	3	720	11	19512	0.0598	1.00e+0	7.39	1.00e+0	1.00e+0	0.00661
GOTERM_BP_DIRECT	ganglioside biosynthetic process	0%	3	720	11	19512	0.0598	1.00e+0	7.39	1.00e+0	1.00e+0	0.00661
GOTERM_BP_DIRECT	transferrin transport	0%	3	720	11	19512	0.0598	1.00e+0	7.39	1.00e+0	1.00e+0	0.00661
GOTERM_BP_DIRECT	neuroendocrine cell differentiation	0%	3	720	11	19512	0.0598	1.00e+0	7.39	1.00e+0	1.00e+0	0.00661
GOTERM_BP_DIRECT	dendritic spine maintenance	0%	3	720	11	19512	0.0598	1.00e+0	7.39	1.00e+0	1.00e+0	0.00661
GOTERM_BP_DIRECT	neutrophil mediated immunity	0%	3	720	11	19512	0.0598	1.00e+0	7.39	1.00e+0	1.00e+0	0.00661
GOTERM_BP_DIRECT	regulation of blood coagulation	0%	3	720	11	19512	0.0598	1.00e+0	7.39	1.00e+0	1.00e+0	0.00661
GOTERM_BP_DIRECT	regulation of gene expression	3%	23	720	419	19512	0.0616	1.00e+0	1.49	1.00e+0	1.00e+0	0.0384
GOTERM_BP_DIRECT	sodium ion transmembrane transport	1%	10	720	135	19512	0.0621	1.00e+0	2.01	1.00e+0	1.00e+0	0.028
GOTERM_BP_DIRECT	positive regulation of tumor necrosis factor production	1%	9	720	115	19512	0.0624	1.00e+0	2.12	1.00e+0	1.00e+0	0.0265
GOTERM_BP_DIRECT	integrated stress response signaling	0%	4	720	25	19512	0.0628	1.00e+0	4.34	1.00e+0	1.00e+0	0.0125
GOTERM_BP_DIRECT	positive regulation of gluconeogenesis	0%	4	720	25	19512	0.0628	1.00e+0	4.34	1.00e+0	1.00e+0	0.0125
GOTERM_BP_DIRECT	regulation of epithelial cell proliferation	0%	4	720	25	19512	0.0628	1.00e+0	4.34	1.00e+0	1.00e+0	0.0125
GOTERM_BP_DIRECT	negative chemotaxis	1%	5	720	41	19512	0.0632	1.00e+0	3.30	1.00e+0	1.00e+0	0.0169
GOTERM_BP_DIRECT	phospholipid biosynthetic process	1%	6	720	59	19512	0.0658	1.00e+0	2.76	1.00e+0	1.00e+0	0.0212
GOTERM_BP_DIRECT	synaptic vesicle endocytosis	1%	5	720	42	19512	0.0679	1.00e+0	3.23	1.00e+0	1.00e+0	0.0186
GOTERM_BP_DIRECT	positive regulation of collagen biosynthetic process	0%	4	720	26	19512	0.0691	1.00e+0	4.17	1.00e+0	1.00e+0	0.0144
GOTERM_BP_DIRECT	cell-substrate adhesion	0%	4	720	26	19512	0.0691	1.00e+0	4.17	1.00e+0	1.00e+0	0.0144
GOTERM_BP_DIRECT	microtubule nucleation	0%	4	720	26	19512	0.0691	1.00e+0	4.17	1.00e+0	1.00e+0	0.0144
GOTERM_BP_DIRECT	regulation of toll-like receptor signaling pathway	0%	3	720	12	19512	0.0701	1.00e+0	6.77	1.00e+0	1.00e+0	0.00858
GOTERM_BP_DIRECT	collagen-activated tyrosine kinase receptor signaling pathway	0%	3	720	12	19512	0.0701	1.00e+0	6.77	1.00e+0	1.00e+0	0.00858
GOTERM_BP_DIRECT	positive regulation of cytokine-mediated signaling pathway	0%	3	720	12	19512	0.0701	1.00e+0	6.77	1.00e+0	1.00e+0	0.00858
GOTERM_BP_DIRECT	positive regulation of MAPK cascade	2%	14	720	224	19512	0.0717	1.00e+0	1.69	1.00e+0	1.00e+0	0.0387
GOTERM_BP_DIRECT	negative regulation of Kit signaling pathway	0%	2	720	2	19512	0.0723	1.00e+0	27.10	1.00e+0	1.00e+0	0.00136
GOTERM_BP_DIRECT	positive regulation of long-chain fatty acid import across plasma membrane	0%	2	720	2	19512	0.0723	1.00e+0	27.10	1.00e+0	1.00e+0	0.00136
GOTERM_BP_DIRECT	respiratory basal cell differentiation	0%	2	720	2	19512	0.0723	1.00e+0	27.10	1.00e+0	1.00e+0	0.00136
GOTERM_BP_DIRECT	regulation of glucocorticoid metabolic process	0%	2	720	2	19512	0.0723	1.00e+0	27.10	1.00e+0	1.00e+0	0.00136
GOTERM_BP_DIRECT	olfactory learning	0%	2	720	2	19512	0.0723	1.00e+0	27.10	1.00e+0	1.00e+0	0.00136
GOTERM_BP_DIRECT	protein deamination	0%	2	720	2	19512	0.0723	1.00e+0	27.10	1.00e+0	1.00e+0	0.00136
GOTERM_BP_DIRECT	protein autophosphorylation	1%	9	720	119	19512	0.073	1.00e+0	2.05	1.00e+0	1.00e+0	0.0321
GOTERM_BP_DIRECT	cell-cell adhesion	2%	14	720	225	19512	0.074	1.00e+0	1.69	1.00e+0	1.00e+0	0.0398
GOTERM_BP_DIRECT	cellular response to hypoxia	1%	10	720	140	19512	0.0744	1.00e+0	1.94	1.00e+0	1.00e+0	0.0348
GOTERM_BP_DIRECT	positive regulation of interleukin-17 production	0%	4	720	27	19512	0.0757	1.00e+0	4.01	1.00e+0	1.00e+0	0.0164
GOTERM_BP_DIRECT	ATP biosynthetic process	0%	4	720	27	19512	0.0757	1.00e+0	4.01	1.00e+0	1.00e+0	0.0164
GOTERM_BP_DIRECT	protein polyubiquitination	1%	11	720	162	19512	0.0771	1.00e+0	1.84	1.00e+0	1.00e+0	0.038
GOTERM_BP_DIRECT	regulation of glycolytic process	0%	3	720	13	19512	0.0809	1.00e+0	6.25	1.00e+0	1.00e+0	0.0108
GOTERM_BP_DIRECT	regulation of resting membrane potential	0%	3	720	13	19512	0.0809	1.00e+0	6.25	1.00e+0	1.00e+0	0.0108
GOTERM_BP_DIRECT	phosphate ion transmembrane transport	0%	3	720	13	19512	0.0809	1.00e+0	6.25	1.00e+0	1.00e+0	0.0108
GOTERM_BP_DIRECT	protein acetylation	0%	3	720	13	19512	0.0809	1.00e+0	6.25	1.00e+0	1.00e+0	0.0108
GOTERM_BP_DIRECT	negative regulation of neural precursor cell proliferation	0%	3	720	13	19512	0.0809	1.00e+0	6.25	1.00e+0	1.00e+0	0.0108
GOTERM_BP_DIRECT	response to muramyl dipeptide	0%	3	720	13	19512	0.0809	1.00e+0	6.25	1.00e+0	1.00e+0	0.0108
GOTERM_BP_DIRECT	response to lipopolysaccharide	1%	11	720	164	19512	0.0822	1.00e+0	1.82	1.00e+0	1.00e+0	0.041
GOTERM_BP_DIRECT	negative regulation of ossification	0%	4	720	28	19512	0.0826	1.00e+0	3.87	1.00e+0	1.00e+0	0.0186
GOTERM_BP_DIRECT	regulation of intracellular signal transduction	1%	5	720	45	19512	0.0831	1.00e+0	3.01	1.00e+0	1.00e+0	0.0244
GOTERM_BP_DIRECT	monoatomic ion transmembrane transport	3%	22	720	413	19512	0.0865	1.00e+0	1.44	1.00e+0	1.00e+0	0.0553
GOTERM_BP_DIRECT	negative regulation of viral genome replication	1%	5	720	46	19512	0.0885	1.00e+0	2.95	1.00e+0	1.00e+0	0.0266
GOTERM_BP_DIRECT	positive regulation of JNK cascade	1%	8	720	104	19512	0.0895	1.00e+0	2.08	1.00e+0	1.00e+0	0.0385
GOTERM_BP_DIRECT	negative regulation of miRNA transcription	0%	4	720	29	19512	0.0897	1.00e+0	3.74	1.00e+0	1.00e+0	0.021
GOTERM_BP_DIRECT	positive regulation of mitotic nuclear division	0%	4	720	29	19512	0.0897	1.00e+0	3.74	1.00e+0	1.00e+0	0.021
GOTERM_BP_DIRECT	cell differentiation	6%	50	720	1094	19512	0.0913	1.00e+0	1.24	1.00e+0	1.00e+0	0.0693
GOTERM_BP_DIRECT	receptor recycling	0%	3	720	14	19512	0.0921	1.00e+0	5.81	1.00e+0	1.00e+0	0.0134
GOTERM_BP_DIRECT	positive regulation of triglyceride biosynthetic process	0%	3	720	14	19512	0.0921	1.00e+0	5.81	1.00e+0	1.00e+0	0.0134
GOTERM_BP_DIRECT	mesodermal cell differentiation	0%	3	720	14	19512	0.0921	1.00e+0	5.81	1.00e+0	1.00e+0	0.0134
GOTERM_BP_DIRECT	transport across blood-brain barrier	1%	7	720	85	19512	0.0935	1.00e+0	2.23	1.00e+0	1.00e+0	0.0375
GOTERM_BP_DIRECT	cytoplasmic microtubule organization	1%	5	720	47	19512	0.0941	1.00e+0	2.88	1.00e+0	1.00e+0	0.0289
GOTERM_BP_DIRECT	cell-cell junction organization	0%	4	720	30	19512	0.0971	1.00e+0	3.61	1.00e+0	1.00e+0	0.0235
GOTERM_BP_DIRECT	establishment or maintenance of epithelial cell apical/basal polarity	0%	4	720	30	19512	0.0971	1.00e+0	3.61	1.00e+0	1.00e+0	0.0235
GOTERM_BP_DIRECT	positive regulation of Rho protein signal transduction	0%	4	720	30	19512	0.0971	1.00e+0	3.61	1.00e+0	1.00e+0	0.0235
GOTERM_BP_DIRECT	peptidyl-serine phosphorylation	1%	5	720	48	19512	0.0998	1.00e+0	2.82	1.00e+0	1.00e+0	0.0313