

Supplementary 1 Go Ontology Enrichment Analysis

GO biological process complete		Homo sapiens - REFLIST (20814)	upload_1 (22)	upload_1 (expected)	upload_1 (fold Enrichment)	upload_1 (P-value)	-log (p-value)
Biological process	regulation of cell proliferation (GO:0042127)	1501	15	1.59	9.45	6.40E-09	8.19
	negative regulation of cell differentiation (GO:0045596)	599	11	0.63	17.37	4.87E-08	7.31
	positive regulation of cell proliferation (GO:0008284)	826	12	0.87	13.74	5.61E-08	7.25
	positive regulation of cellular process (GO:0048522)	4728	20	5	4	1.57E-07	6.8
	positive regulation of macromolecule metabolic process (GO:0010604)	2891	17	3.06	5.56	2.87E-07	6.54
	generation of neurons (GO:0048699)	1629	14	1.72	8.13	4.66E-07	6.33
	cell surface receptor signaling pathway (GO:0007166)	2470	16	2.61	6.13	4.68E-07	6.33
	negative regulation of cellular process (GO:0048523)	4246	19	4.49	4.23	5.09E-07	6.29
	tissue morphogenesis (GO:0048729)	556	10	0.59	17.02	7.35E-07	6.13
	regulation of multicellular organismal development (GO:2000026)	1698	14	1.79	7.8	8.10E-07	6.09
	neurogenesis (GO:0022008)	1707	14	1.8	7.76	8.70E-07	6.06
	negative regulation of developmental process (GO:0051093)	799	11	0.84	13.03	1.05E-06	5.98
	morphogenesis of an epithelium (GO:0002009)	419	9	0.44	20.32	1.76E-06	5.75
	regulation of developmental process (GO:0050793)	2236	15	2.36	6.35	1.96E-06	5.71
	negative regulation of biological process (GO:0048519)	4624	19	4.89	3.89	2.41E-06	5.62
	positive regulation of biological process (GO:0048518)	5476	20	5.79	3.46	2.70E-06	5.57
	regulation of cell differentiation (GO:0045595)	1492	13	1.58	8.24	2.92E-06	5.53
	epithelial tube morphogenesis (GO:0060562)	296	8	0.31	25.57	3.69E-06	5.43
	cellular response to stimulus (GO:0051716)	6613	21	6.99	3	4.41E-06	5.36
	anatomical structure morphogenesis (GO:0009653)	2415	15	2.55	5.88	5.85E-06	5.23
	positive regulation of metabolic process (GO:0009893)	3595	17	3.8	4.47	9.68E-06	5.01
	tube morphogenesis (GO:0035239)	335	8	0.35	22.59	9.71E-06	5.01
	positive regulation of gene expression (GO:0010628)	1730	13	1.83	7.11	1.80E-05	4.74
	signal transduction (GO:0007165)	5174	19	5.47	3.47	1.85E-05	4.73
	regulation of multicellular organismal process (GO:0051239)	2631	15	2.78	5.39	1.96E-05	4.71
	cell development (GO:0048468)	1742	13	1.84	7.06	1.96E-05	4.71
	tube development (GO:0035295)	564	9	0.6	15.1	2.35E-05	4.63
	cell morphogenesis involved in differentiation (GO:0000904)	854	10	0.9	11.08	4.58E-05	4.34
	positive regulation of developmental process (GO:0051094)	1150	11	1.22	9.05	4.82E-05	4.32

nervous system development (GO:0007399)	2355	14	2.49	5.62	6.10E-05	4.21
cell differentiation (GO:0030154)	3423	16	3.62	4.42	6.44E-05	4.19
single organism signaling (GO:0044700)	5561	19	5.88	3.23	6.79E-05	4.17
signaling (GO:0023052)	5564	19	5.88	3.23	6.86E-05	4.16
neuron differentiation (GO:0030182)	1208	11	1.28	8.62	8.04E-05	4.09
positive regulation of cellular metabolic process (GO:0031325)	2928	15	3.09	4.85	8.76E-05	4.06
cell communication (GO:0007154)	5650	19	5.97	3.18	9.04E-05	4.04
positive regulation of response to stimulus (GO:0048584)	2027	13	2.14	6.07	1.24E-04	3.91
nephron tubule development (GO:0072080)	75	5	0.08	63.07	1.25E-04	3.9
epithelium development (GO:0060429)	969	10	1.02	9.76	1.52E-04	3.82
renal tubule development (GO:0061326)	78	5	0.08	60.65	1.52E-04	3.82
cellular developmental process (GO:0048869)	3635	16	3.84	4.16	1.57E-04	3.8
cell morphogenesis involved in neuron differentiation (GO:0048667)	716	9	0.76	11.89	1.84E-04	3.74
neuron development (GO:0048666)	1024	10	1.08	9.24	2.56E-04	3.59
response to stimulus (GO:0050896)	8117	21	8.58	2.45	2.94E-04	3.53
regulation of response to stimulus (GO:0048583)	3823	16	4.04	3.96	3.32E-04	3.48
nephron epithelium development (GO:0072009)	93	5	0.1	50.87	3.63E-04	3.44
regulation of cell aging (GO:0090342)	33	4	0.03	> 100	3.73E-04	3.43
stem cell differentiation (GO:0048863)	196	6	0.21	28.96	3.77E-04	3.42
positive regulation of multicellular organismal process (GO:0051240)	1416	11	1.5	7.35	4.15E-04	3.38
regulation of signal transduction (GO:0009966)	2740	14	2.9	4.83	4.35E-04	3.36
positive regulation of nucleic acid-templated transcription (GO:1903508)	1428	11	1.51	7.29	4.52E-04	3.34
positive regulation of transcription, DNA-templated (GO:0045893)	1428	11	1.51	7.29	4.52E-04	3.34
response to external stimulus (GO:0009605)	2261	13	2.39	5.44	4.63E-04	3.33
positive regulation of RNA biosynthetic process (GO:1902680)	1456	11	1.54	7.15	5.52E-04	3.26
regulation of molecular function (GO:0065009)	2832	14	2.99	4.68	6.65E-04	3.18
animal organ development (GO:0048513)	2833	14	2.99	4.68	6.68E-04	3.18
positive regulation of RNA metabolic process (GO:0051254)	1497	11	1.58	6.95	7.34E-04	3.13
multicellular organism development (GO:0007275)	4737	17	5.01	3.4	7.66E-04	3.12
negative regulation of apoptotic process (GO:0043066)	855	9	0.9	9.96	8.39E-04	3.08
cell morphogenesis (GO:0000902)	1164	10	1.23	8.13	8.55E-04	3.07

regulation of localization (GO:0032879)	2390	13	2.53	5.15	9.00E-04	3.05
negative regulation of programmed cell death (GO:0043069)	865	9	0.91	9.84	9.26E-04	3.03
single-multicellular organism process (GO:0044707)	5587	18	5.91	3.05	9.79E-04	3.01
nephron development (GO:0072006)	115	5	0.12	41.13	1.03E-03	2.99
cell fate commitment (GO:0045165)	235	6	0.25	24.16	1.09E-03	2.96
system development (GO:0048731)	4147	16	4.38	3.65	1.10E-03	2.96
tissue development (GO:0009888)	1562	11	1.65	6.66	1.13E-03	2.95
columnar/cuboidal epithelial cell differentiation (GO:0002065)	118	5	0.12	40.09	1.17E-03	2.93
regulation of cell death (GO:0010941)	1574	11	1.66	6.61	1.22E-03	2.91
multicellular organismal process (GO:0032501)	6615	19	6.99	2.72	1.51E-03	2.82
cellular component morphogenesis (GO:0032989)	1240	10	1.31	7.63	1.54E-03	2.81
kidney epithelium development (GO:0072073)	125	5	0.13	37.84	1.56E-03	2.81
response to virus (GO:0009615)	251	6	0.27	22.62	1.60E-03	2.8
negative regulation of cell death (GO:0060548)	928	9	0.98	9.18	1.68E-03	2.77
glomerulus development (GO:0032835)	49	4	0.05	77.23	1.79E-03	2.75
regulation of neurogenesis (GO:0050767)	669	8	0.71	11.31	2.00E-03	2.7
regulation of signaling (GO:0023051)	3089	14	3.27	4.29	2.02E-03	2.69
branching morphogenesis of an epithelial tube (GO:0048754)	132	5	0.14	35.84	2.04E-03	2.69
axonogenesis (GO:0007409)	672	8	0.71	11.26	2.07E-03	2.68
positive regulation of macromolecule biosynthetic process (GO:0010557)	1668	11	1.76	6.24	2.21E-03	2.66
brain development (GO:0007420)	682	8	0.72	11.1	2.32E-03	2.63
regulation of cell communication (GO:0010646)	3127	14	3.31	4.24	2.36E-03	2.63
regulation of cellular process (GO:0050794)	10542	22	11.14	1.97	2.61E-03	2.58
mesenchymal cell differentiation (GO:0048762)	139	5	0.15	34.03	2.63E-03	2.58
negative regulation of multicellular organismal process (GO:0051241)	981	9	1.04	8.68	2.69E-03	2.57
axon development (GO:0061564)	697	8	0.74	10.86	2.74E-03	2.56
positive regulation of nucleobase-containing compound metabolic process (GO:0045935)	1725	11	1.82	6.03	3.10E-03	2.51
regulation of primary metabolic process (GO:0080090)	5997	18	6.34	2.84	3.17E-03	2.5
regulation of macromolecule metabolic process (GO:0060255)	6005	18	6.35	2.84	3.24E-03	2.49
regulation of metabolic process (GO:0019222)	6911	19	7.3	2.6	3.26E-03	2.49
anatomical structure development (GO:0048856)	5200	17	5.5	3.09	3.27E-03	2.49

positive regulation of transcription from RNA polymerase II promoter (GO:0045944)	1010	9	1.07	8.43	3.43E-03	2.46
head development (GO:0060322)	720	8	0.76	10.51	3.50E-03	2.46
leukocyte differentiation (GO:0002521)	293	6	0.31	19.37	3.95E-03	2.4
regulation of developmental growth (GO:0048638)	293	6	0.31	19.37	3.95E-03	2.4
regulation of cellular metabolic process (GO:0031323)	6100	18	6.45	2.79	4.19E-03	2.38
regulation of protein modification process (GO:0031399)	1781	11	1.88	5.84	4.28E-03	2.37
cell division (GO:0051301)	496	7	0.52	13.35	4.48E-03	2.35
neuron projection morphogenesis (GO:0048812)	745	8	0.79	10.16	4.53E-03	2.34
positive regulation of cellular biosynthetic process (GO:0031328)	1796	11	1.9	5.79	4.66E-03	2.33
positive regulation of developmental growth (GO:0048639)	157	5	0.17	30.13	4.77E-03	2.32
negative regulation of cell development (GO:0010721)	304	6	0.32	18.67	4.89E-03	2.31
regulation of nervous system development (GO:0051960)	755	8	0.8	10.02	5.00E-03	2.3
morphogenesis of a branching epithelium (GO:0061138)	160	5	0.17	29.57	5.23E-03	2.28
positive regulation of nitrogen compound metabolic process (GO:0051173)	1818	11	1.92	5.72	5.26E-03	2.28
positive regulation of biosynthetic process (GO:0009891)	1827	11	1.93	5.7	5.53E-03	2.26
hemopoiesis (GO:0030097)	515	7	0.54	12.86	5.76E-03	2.24
single-organism developmental process (GO:0044767)	5414	17	5.72	2.97	6.08E-03	2.22
negative regulation of ossification (GO:0030279)	67	4	0.07	56.48	6.19E-03	2.21
neuroepithelial cell differentiation (GO:0060563)	67	4	0.07	56.48	6.19E-03	2.21
positive regulation of signal transduction (GO:0009967)	1452	10	1.53	6.52	6.65E-03	2.18
negative regulation of cell aging (GO:0090344)	17	3	0.02	> 100	6.84E-03	2.16
morphogenesis of a branching structure (GO:0001763)	171	5	0.18	27.66	7.24E-03	2.14
negative regulation of neuron death (GO:1901215)	171	5	0.18	27.66	7.24E-03	2.14
regulation of apoptotic process (GO:0042981)	1470	10	1.55	6.44	7.45E-03	2.13
developmental process (GO:0032502)	5502	17	5.82	2.92	7.79E-03	2.11
regulation of biological process (GO:0050789)	11094	22	11.73	1.88	8.03E-03	2.1
morphogenesis of an endothelium (GO:0003159)	18	3	0.02	> 100	8.12E-03	2.09
regulation of programmed cell death (GO:0043067)	1485	10	1.57	6.37	8.18E-03	2.09
regulation of ossification (GO:0030278)	176	5	0.19	26.88	8.33E-03	2.08
regulation of neuron differentiation (GO:0045664)	555	7	0.59	11.93	9.47E-03	2.02
core promoter binding (GO:0001047)	153	6	0.16	37.1	2.88E-05	4.54

Molecular function	protein domain specific binding (GO:0019904)	610	8	0.64	12.41	3.26E-04	3.49
	transcription factor binding (GO:0008134)	547	7	0.58	12.11	2.83E-03	2.55
	transcription regulatory region DNA binding (GO:0044212)	803	8	0.85	9.43	2.61E-03	2.58
	regulatory region DNA binding (GO:0000975)	807	8	0.85	9.38	2.71E-03	2.57
	regulatory region nucleic acid binding (GO:0001067)	808	8	0.85	9.37	2.74E-03	2.56
	sequence-specific DNA binding (GO:0043565)	1143	8	1.21	6.62	3.57E-02	1.45
	protein binding (GO:0005515)	10761	22	11.37	1.93	1.35E-03	2.87
