

Genes GENES - GO Biological Process Annotations

Used notations:

- **List Hits** - the number of genes annotated by the considered GO Biological Process category or annotation cluster within the analyzed list of target genes
- **List Total** - the number of genes within the analyzed list of target genes having at least one GO Biological Process annotation
- **Population Hits** - the number of genes, available on the entire microarray, annotated by the considered GO Biological Process category or annotation cluster
- **Population Total** - the number of genes available on the entire microarray and having at least one GO Biological Process annotation
- **P-value** - the significance p-value of the gene enrichment of the considered GO Biological Process category or annotation cluster, calculated with a unilateral Fisher exact test

Terms

Rank	ID	Term	List Hits	List Total	Population Hits	Population Total	P-value	Genes ID's	Genes Names
1	GO:0010467	gene expression	50	471	407	14200	7.93e-16		PRP8 pre-mRNA processing factor 8 homolog (S. cerevisiae)
2	GO:0044267	cellular protein metabolic process	46	471	283	14200	1.86e-19		defender against cell death 1
3	GO:0016032	viral reproduction	40	471	333	14200	1.5e-12		adaptor-related protein complex 2, beta 1 subunit
4	GO:0006412	translation	36	471	254	14200	1.43e-13		eukaryotic translation initiation factor 1
5	GO:0006810	transport	34	471	569	14200	6.75e-04		solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15
6	GO:0006414	translational elongation	26	471	93	14200	1.76e-17		eukaryotic translation elongation factor 1 gamma
7	GO:0031018	endocrine pancreas development	25	471	116	14200	5.49e-14		hairy and enhancer of split 1, (Drosophila)
8	GO:0022904	respiratory electron transport chain	24	471	97	14200	6.49e-15		ATP synthase, H ⁺ transporting, mitochondrial Fo complex, subunit d
9	GO:0006415	translational termination	24	471	86	14200	3.26e-16		ribosomal protein SA
10	GO:0019058	viral infectious cycle	24	471	91	14200	1.34e-15		ribosomal protein SA
11	GO:0019083	viral transcription	24	471	82	14200	9.68e-17		ribosomal protein SA
		cellular nitrogen							

12	GO:0034641	compound metabolic process	19	471	194	14200	2.49e-05		solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15
13	GO:0008380	RNA splicing	19	471	270	14200	1.71e-03		breast carcinoma amplified sequence 2
14	GO:0044419	interspecies interaction between organisms	19	471	307	14200	6.93e-03		reticulon 3
15	GO:0006457	protein folding	19	471	183	14200	1.08e-05		crystallin, alpha B
16	GO:0000278	mitotic cell cycle	17	471	308	14200	2.82e-02		centrin, EF-hand protein, 2
17	GO:0016192	vesicle-mediated transport	16	471	175	14200	2.39e-04		reticulon 3
18	GO:0016070	RNA metabolic process	16	471	158	14200	7.21e-05		eukaryotic translation initiation factor 4B
19	GO:0006916	anti-apoptosis	15	471	191	14200	1.78e-03		Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2
20	GO:0000398	nuclear mRNA splicing, via spliceosome	15	471	166	14200	4.21e-04		synaptotagmin binding, cytoplasmic RNA interacting protein
21	GO:0006979	response to oxidative stress	14	471	105	14200	9.32e-06		peroxiredoxin 3
22	GO:0048011	nerve growth factor receptor signaling pathway	14	471	214	14200	1.21e-02		adenylate cyclase 9
23	GO:0018279	protein N-linked glycosylation via asparagine	14	471	88	14200	1.09e-06		defender against cell death 1
24	GO:0043687	post-translational protein modification	14	471	123	14200	5.69e-05		defender against cell death 1
25	GO:0016071	mRNA metabolic process	14	471	121	14200	4.74e-05		eukaryotic translation initiation factor 4B
26	GO:0030168	platelet activation	14	471	232	14200	2.29e-02		fibronectin 1
27	GO:0016044	cellular membrane organization	13	471	92	14200	1.02e-05		clathrin, heavy chain (Hc)
28	GO:0001666	response to hypoxia	12	471	150	14200	4.26e-03		CD24 molecule
29	GO:0042981	regulation of apoptosis	12	471	182	14200	1.83e-02		nucleotide-binding oligomerization domain containing 1
		cell redox					2.08e-		peroxiredoxin 3

30	GO:0045454	homeostasis	12	471	68	14200	06		
31	GO:0006986	response to unfolded protein	12	471	52	14200	9.52e-08		activating transcription factor 6
32	GO:0006184	GTP catabolic process	12	471	141	14200	2.57e-03		GNAS complex locus
33	GO:0006413	translational initiation	11	471	41	14200	6.11e-08		eukaryotic translation initiation factor 1
34	GO:0006200	ATP catabolic process	11	471	74	14200	3.01e-05		ATP synthase, H ⁺ transporting, mitochondrial Fo complex, subunit d
35	GO:0000082	G1/S transition of mitotic cell cycle	11	471	135	14200	5.3e-03		G1 to S phase transition 1
36	GO:0006091	generation of precursor metabolites and energy	10	471	57	14200	1.56e-05		cytochrome c oxidase subunit VIa polypeptide 1
37	GO:0015992	proton transport	10	471	43	14200	1.05e-06		nicotinamide nucleotide transhydrogenase
38	GO:0000075	cell cycle checkpoint	9	471	129	14200	2.79e-02		damage-specific DNA binding protein 1, 127kDa
39	GO:0001525	angiogenesis	9	471	137	14200	3.88e-02		endothelial PAS domain protein 1
40	GO:0002576	platelet degranulation	9	471	79	14200	1.18e-03		fibronectin 1
41	GO:0006364	rRNA processing	8	471	89	14200	9.33e-03		Shwachman-Bodian-Diamond syndrome
42	GO:0000084	S phase of mitotic cell cycle	8	471	111	14200	3.13e-02		proteasome (prosome, macropain) subunit, alpha type, 3
43	GO:0000216	M/G1 transition of mitotic cell cycle	8	471	79	14200	4.59e-03		proteasome (prosome, macropain) subunit, alpha type, 3
44	GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	8	471	61	14200	8.68e-04		proteasome (prosome, macropain) subunit, alpha type, 3
45	GO:0031145	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein	8	471	80	14200	4.95e-03		proteasome (prosome, macropain) subunit, alpha type, 3

		catabolic process							
46	GO:0051436	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	8	471	65	14200	1.33e-03		proteasome (prosome, macropain) subunit, alpha type, 3
47	GO:0051437	positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	8	471	71	14200	2.35e-03		proteasome (prosome, macropain) subunit, alpha type, 3
48	GO:0051439	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	8	471	75	14200	3.33e-03		proteasome (prosome, macropain) subunit, alpha type, 3
49	GO:0043627	response to estrogen stimulus	7	471	56	14200	2.4e-03		CD24 molecule
50	GO:0042776	mitochondrial ATP synthesis coupled proton transport	7	471	15	14200	2.16e-07		ATP synthase, H ⁺ transporting, mitochondrial Fo complex, subunit d
51	GO:0006112	energy reserve metabolic process	7	471	100	14200	4.84e-02		adenylate cyclase 9
52	GO:0007173	epidermal growth factor receptor signaling pathway	7	471	75	14200	1.2e-02		clathrin, heavy chain (Hc)
53	GO:0006521	regulation of cellular amino acid metabolic process	7	471	51	14200	1.38e-03		NAD(P)H dehydrogenase, quinone 1
54	GO:0042446	hormone biosynthetic process	7	471	63	14200	4.7e-03		deiodinase, iodothyronine, type I
55	GO:0006879	cellular iron ion homeostasis	7	471	64	14200	5.13e-03		ferritin, light polypeptide
56	GO:0006334	nucleosome assembly	7	471	99	14200	4.63e-02		H1 histone family, member 0
57	GO:0006446	regulation of translational initiation	6	471	26	14200	1.69e-04		eukaryotic translation initiation factor 1
58	GO:0051092	positive regulation of NF-kappaB transcription factor activity	6	471	77	14200	4.24e-02		nucleotide-binding oligomerization domain containing 1

59	GO:0042744	hydrogen peroxide catabolic process	6	471	19	14200	2.42e-05		peroxiredoxin 3
60	GO:0006892	post-Golgi vesicle-mediated transport	6	471	41	14200	2.16e-03		clathrin, heavy chain (Hc)
61	GO:0042059	negative regulation of epidermal growth factor receptor signaling pathway	6	471	33	14200	6.67e-04		clathrin, heavy chain (Hc)
62	GO:0009408	response to heat	6	471	50	14200	5.95e-03		crystallin, alpha B
63	GO:0006613	cotranslational protein targeting to membrane	6	471	9	14200	9.96e-08		ADP-ribosylation factor-like 6 interacting protein 1
64	GO:0043434	response to peptide hormone stimulus	6	471	60	14200	1.42e-02		glycine amidinotransferase (L-arginine:glycine amidinotransferase)
65	GO:0006120	mitochondrial electron transport, NADH to ubiquinone	6	471	43	14200	2.77e-03		NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa
66	GO:0006754	ATP biosynthetic process	6	471	54	14200	8.66e-03		ATPase, Na ⁺ /K ⁺ transporting, alpha 1 polypeptide
67	GO:0015991	ATP hydrolysis coupled proton transport	6	471	30	14200	3.89e-04		ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle
68	GO:0042274	ribosomal small subunit biogenesis	6	471	12	14200	1.01e-06		ribosomal protein S6
69	GO:0042787	protein ubiquitination involved in ubiquitin-dependent protein catabolic process	5	471	45	14200	1.61e-02		HECT, UBA and WWE domain containing 1
70	GO:0030521	androgen receptor signaling pathway	5	471	41	14200	1.1e-02		peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
71	GO:0030433	ER-associated protein catabolic process	5	471	32	14200	3.77e-03		osteosarcoma amplified 9, endoplasmic reticulum lectin
72	GO:0030968	endoplasmic reticulum unfolded protein response	5	471	22	14200	6.48e-04		activating transcription factor 6
73	GO:0001657	ureteric bud development	5	471	40	14200	9.93e-03		nephronectin

74	GO:0016197	endosome transport	5	471	50	14200	2.45e-02	chromatin modifying protein 2A
75	GO:0006469	negative regulation of protein kinase activity	5	471	48	14200	2.09e-02	cysteine-rich PAK1 inhibitor
76	GO:0006662	glycerol ether metabolic process	5	471	14	14200	6.14e-05	protein disulfide isomerase family A, member 3
77	GO:0051603	proteolysis involved in cellular protein catabolic process	5	471	26	14200	1.45e-03	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
78	GO:0043408	regulation of MAPKKK cascade	4	471	11	14200	3.28e-04	CD24 molecule
79	GO:0033572	transferrin transport	4	471	30	14200	1.65e-02	clathrin, heavy chain (Hc)
80	GO:0050690	regulation of defense response to virus by virus	4	471	28	14200	1.3e-02	adaptor-related protein complex 2, beta 1 subunit
81	GO:0006099	tricarboxylic acid cycle	4	471	24	14200	7.49e-03	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)
82	GO:0009306	protein secretion	4	471	16	14200	1.58e-03	GNAS complex locus
83	GO:0006749	glutathione metabolic process	4	471	25	14200	8.69e-03	glutathione peroxidase 3 (plasma)
84	GO:0045665	negative regulation of neuron differentiation	4	471	36	14200	3.05e-02	hairy and enhancer of split 1, (Drosophila)
85	GO:0021766	hippocampus development	4	471	28	14200	1.3e-02	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
86	GO:0008344	adult locomotory behavior	4	471	29	14200	1.47e-02	amyloid beta (A4) precursor protein
87	GO:0006090	pyruvate metabolic process	4	471	21	14200	4.57e-03	lactate dehydrogenase B
88	GO:0032480	negative regulation of type I interferon production	4	471	30	14200	1.65e-02	poly(rC) binding protein 2
89	GO:0007249	I-kappaB kinase/NF-kappaB cascade	4	471	35	14200	2.78e-02	protein tyrosine phosphatase-like A domain containing 1
90	GO:0043085	positive regulation of catalytic activity	4	471	42	14200	4.96e-02	presenilin enhancer 2 homolog (C. elegans)

91	GO:0001541	ovarian follicle development	4	471	41	14200	4.61e-02		B-cell CLL/lymphoma 2
92	GO:0045787	positive regulation of cell cycle	3	471	22	14200	3.5e-02		Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2
93	GO:0006378	mRNA polyadenylation	3	471	14	14200	1e-02		poly(A) polymerase alpha
94	GO:0051881	regulation of mitochondrial membrane potential	3	471	10	14200	3.66e-03		peroxiredoxin 3
95	GO:0006621	protein retention in ER lumen	3	471	9	14200	2.62e-03		osteosarcoma amplified 9, endoplasmic reticulum lectin
96	GO:0001824	blastocyst development	3	471	16	14200	1.47e-02		defender against cell death 1
97	GO:0045931	positive regulation of mitotic cell cycle	3	471	22	14200	3.5e-02		ubiquitin specific peptidase 22
98	GO:0035116	embryonic hindlimb morphogenesis	3	471	22	14200	3.5e-02		dicer 1, ribonuclease type III
99	GO:0048812	neuron projection morphogenesis	3	471	22	14200	3.5e-02		dicer 1, ribonuclease type III
100	GO:0051412	response to corticosterone stimulus	3	471	19	14200	2.37e-02		glutathione peroxidase 3 (plasma)
101	GO:0006309	DNA fragmentation involved in apoptotic nuclear change	3	471	23	14200	3.92e-02		H1 histone family, member 0
102	GO:0060334	regulation of interferon-gamma-mediated signaling pathway	3	471	16	14200	1.47e-02		heat shock protein 90kDa alpha (cytosolic), class B member 1
103	GO:0045599	negative regulation of fat cell differentiation	3	471	21	14200	3.09e-02		inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
104	GO:0006878	cellular copper ion homeostasis	3	471	10	14200	3.66e-03		amyloid beta (A4) precursor protein
105	GO:0051894	positive regulation of focal adhesion assembly	3	471	7	14200	1.15e-03		kinase insert domain receptor (a type III receptor tyrosine kinase)
106	GO:0000028	ribosomal small subunit assembly	3	471	6	14200	6.73e-04		ribosomal protein SA

107	GO:0002026	regulation of the force of heart contraction	3	471	17	14200	1.74e-02	ATPase, Na+/K+ transporting, alpha 1 polypeptide
108	GO:0006119	oxidative phosphorylation	3	471	9	14200	2.62e-03	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1
109	GO:0032880	regulation of protein localization	3	471	23	14200	3.92e-02	solute carrier family 26, member 4
110	GO:0006614	SRP-dependent cotranslational protein targeting to membrane	3	471	6	14200	6.73e-04	signal recognition particle 14kDa (homologous Alu RNA binding protein)
111	GO:0030856	regulation of epithelial cell differentiation	2	471	7	14200	2.06e-02	CD24 molecule
112	GO:0016574	histone ubiquitination	2	471	8	14200	2.69e-02	HECT, UBA and WWE domain containing 1
113	GO:0070934	CRD-mediated mRNA stabilization	2	471	5	14200	1.03e-02	synaptotagmin binding, cytoplasmic RNA interacting protein
114	GO:0030643	cellular phosphate ion homeostasis	2	471	6	14200	1.51e-02	solute carrier family 34 (sodium phosphate), member 2
115	GO:0048205	COPI coating of Golgi vesicle	2	471	10	14200	4.14e-02	coatamer protein complex, subunit alpha
116	GO:0006584	catecholamine metabolic process	2	471	10	14200	4.14e-02	myotrophin
117	GO:0006590	thyroid hormone generation	2	471	6	14200	1.51e-02	deiodinase, iodothyronine, type I
118	GO:0042403	thyroid hormone metabolic process	2	471	5	14200	1.03e-02	deiodinase, iodothyronine, type II
119	GO:0006554	lysine catabolic process	2	471	8	14200	2.69e-02	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)
120	GO:0033962	cytoplasmic mRNA processing body assembly	2	471	5	14200	1.03e-02	dynein, cytoplasmic 1, heavy chain 1
121	GO:0007097	nuclear migration	2	471	5	14200	1.03e-02	spectrin repeat containing, nuclear envelope 2
122	GO:0046689	response to mercury ion	2	471	9	14200	3.39e-02	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
123	GO:0006002	fructose 6-phosphate metabolic process	2	471	7	14200	2.06e-02	glutamine--fructose-6-phosphate transaminase 1
124	GO:0006984	ER-nucleus signaling pathway	2	471	3	14200	3.22e-03	cysteine-rich PAK1 inhibitor

125	GO:0051493	regulation of cytoskeleton organization	2	471	7	14200	2.06e-02		cysteine-rich PAK1 inhibitor
126	GO:0006122	mitochondrial electron transport, ubiquinol to cytochrome c	2	471	4	14200	6.3e-03		ubiquinol-cytochrome c reductase, complex III subunit X
127	GO:0007028	cytoplasm organization	2	471	2	14200	1.1e-03		transcription factor CP2-like 1
128	GO:0045047	protein targeting to ER	2	471	4	14200	6.3e-03		Sec61 alpha 1 subunit (<i>S. cerevisiae</i>)
129	GO:0048667	cell morphogenesis involved in neuron differentiation	2	471	5	14200	1.03e-02		hexosaminidase A (alpha polypeptide)
130	GO:0006559	L-phenylalanine catabolic process	2	471	9	14200	3.39e-02		homogentisate 1,2-dioxygenase
131	GO:0042026	protein refolding	2	471	7	14200	2.06e-02		heat shock 70kDa protein 1B
132	GO:0006983	ER overload response	2	471	9	14200	3.39e-02		heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
133	GO:0021895	cerebral cortex neuron differentiation	2	471	7	14200	2.06e-02		inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
134	GO:0047496	vesicle transport along microtubule	2	471	7	14200	2.06e-02		kinesin family member 5B
135	GO:0000447	endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	2	471	4	14200	6.3e-03		ribosomal protein SA
136	GO:0000461	endonucleolytic cleavage to generate mature 3'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	2	471	2	14200	1.1e-03		ribosomal protein SA
137	GO:0006089	lactate metabolic	2	471	3	14200	3.22e-		lactate dehydrogenase B

		process					03		
138	GO:0044262	cellular carbohydrate metabolic process	2	471	10	14200	4.14e-02		lactate dehydrogenase B
139	GO:0042359	vitamin D metabolic process	2	471	10	14200	4.14e-02		low density lipoprotein receptor-related protein 2
140	GO:0045056	transcytosis	2	471	5	14200	1.03e-02		low density lipoprotein receptor-related protein 2
141	GO:0021794	thalamus development	2	471	8	14200	2.69e-02		low density lipoprotein receptor-related protein 6
142	GO:0051593	response to folic acid	2	471	9	14200	3.39e-02		low density lipoprotein receptor-related protein 6
143	GO:0001880	Mullerian duct regression	2	471	4	14200	6.3e-03		SMAD family member 9
144	GO:0015986	ATP synthesis coupled proton transport	2	471	9	14200	3.39e-02		ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit pseudogene 2
145	GO:0045822	negative regulation of heart contraction	2	471	6	14200	1.51e-02		ATPase, Na+/K+ transporting, alpha 1 polypeptide
146	GO:0006596	polyamine biosynthetic process	2	471	6	14200	1.51e-02		ornithine decarboxylase antizyme 1
147	GO:0006172	ADP biosynthetic process	2	471	4	14200	6.3e-03		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle
148	GO:0000132	establishment of mitotic spindle orientation	2	471	8	14200	2.69e-02		platelet-activating factor acetylhydrolase 1b, regulatory subunit 1 (45kDa)
149	GO:0019226	transmission of nerve impulse	2	471	9	14200	3.39e-02		platelet-activating factor acetylhydrolase 1b, regulatory subunit 1 (45kDa)
150	GO:0043496	regulation of protein homodimerization activity	2	471	8	14200	2.69e-02		pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha
151	GO:0042273	ribosomal large subunit biogenesis	2	471	10	14200	4.14e-02		Shwachman-Bodian-Diamond syndrome
152	GO:0016601	Rac protein signal transduction	2	471	9	14200	3.39e-02		protein tyrosine phosphatase-like A domain containing 1
153	GO:0015705	iodide transport	2	471	4	14200	6.3e-03		solute carrier family 26, member 4
154	GO:0006098	pentose-phosphate shunt	2	471	11	14200	4.95e-02		phosphogluconate dehydrogenase
		regulation of							

155	GO:0043666	phosphoprotein phosphatase activity	2	471	11	14200	4.95e-02		protein phosphatase 6, regulatory subunit 3
156	GO:0060736	prostate gland growth	2	471	7	14200	2.06e-02		prosaposin
157	GO:0002326	B cell lineage commitment	2	471	4	14200	6.3e-03		recombination activating gene 2
158	GO:0002360	T cell lineage commitment	2	471	4	14200	6.3e-03		recombination activating gene 2
159	GO:0031000	response to caffeine	2	471	8	14200	2.69e-02		B-cell CLL/lymphoma 2
160	GO:0016925	protein sumoylation	2	471	11	14200	4.95e-02		SMT3 suppressor of mif two 3 homolog 2 (<i>S. cerevisiae</i>)
161	GO:0051208	sequestering of calcium ion	2	471	3	14200	3.22e-03		heat shock protein 90kDa beta (Grp94), member 1
162	GO:0032597	B cell receptor transport into membrane raft	1	471	1	14200	3.32e-02		CD24 molecule
163	GO:0032600	chemokine receptor transport out of membrane raft	1	471	1	14200	3.32e-02		CD24 molecule
164	GO:0032913	negative regulation of transforming growth factor-beta3 production	1	471	1	14200	3.32e-02		CD24 molecule
165	GO:0035360	positive regulation of peroxisome proliferator activated receptor signaling pathway	1	471	1	14200	3.32e-02		Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2
166	GO:0042228	interleukin-8 biosynthetic process	1	471	1	14200	3.32e-02		nucleotide-binding oligomerization domain containing 1
167	GO:0048199	vesicle targeting, to, from or within Golgi	1	471	1	14200	3.32e-02		transmembrane emp24-like trafficking protein 10 (yeast)
168	GO:0070267	oncosis	1	471	1	14200	3.32e-02		transmembrane protein 123
169	GO:0071352	cellular response to interleukin-2	1	471	1	14200	3.32e-02		carboxypeptidase D
170	GO:0008039	synaptic target recognition	1	471	1	14200	3.32e-02		dynein, light chain, LC8-type 2
		epithelial cell							

171	GO:0060690	differentiation involved in salivary gland development	1	471	1	14200	3.32e-02		catenin (cadherin-associated protein), delta 1
172	GO:0060761	negative regulation of response to cytokine stimulus	1	471	1	14200	3.32e-02		amino-terminal enhancer of split
173	GO:0006990	positive regulation of transcription from RNA polymerase II promoter involved in unfolded protein response	1	471	1	14200	3.32e-02		activating transcription factor 6
174	GO:0032290	peripheral nervous system myelin formation	1	471	1	14200	3.32e-02		dicer 1, ribonuclease type III
175	GO:0040032	post-embryonic body morphogenesis	1	471	1	14200	3.32e-02		GNAS complex locus
176	GO:0042340	keratan sulfate catabolic process	1	471	1	14200	3.32e-02		glucosamine (N-acetyl)-6-sulfatase
177	GO:0010988	regulation of low-density lipoprotein particle clearance	1	471	1	14200	3.32e-02		heterogeneous nuclear ribonucleoprotein K
178	GO:0061106	negative regulation of stomach neuroendocrine cell differentiation	1	471	1	14200	3.32e-02		hairy and enhancer of split 1, (Drosophila)
179	GO:0021589	cerebellum structural organization	1	471	1	14200	3.32e-02		heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
180	GO:0060904	regulation of protein folding in endoplasmic reticulum	1	471	1	14200	3.32e-02		heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
181	GO:0048669	collateral sprouting in absence of injury	1	471	1	14200	3.32e-02		amyloid beta (A4) precursor protein
182	GO:0090275	negative regulation of somatostatin secretion	1	471	1	14200	3.32e-02		insulin receptor substrate 1
		neural crest					3.32e-		low density lipoprotein receptor-related protein 6

183	GO:0014029	formation	1	471	1	14200	02		
184	GO:0060284	regulation of cell development	1	471	1	14200	3.32e-02		low density lipoprotein receptor-related protein 6
185	GO:0061310	canonical Wnt receptor signaling pathway involved in cardiac neural crest cell differentiation involved in heart development	1	471	1	14200	3.32e-02		low density lipoprotein receptor-related protein 6
186	GO:0061324	canonical Wnt receptor signaling pathway involved in positive regulation of cardiac outflow tract cell proliferation	1	471	1	14200	3.32e-02		low density lipoprotein receptor-related protein 6
187	GO:2000055	positive regulation of Wnt receptor signaling pathway involved in dorsal/ventral axis specification	1	471	1	14200	3.32e-02		low density lipoprotein receptor-related protein 6
188	GO:2000149	negative regulation of planar cell polarity pathway involved in ventricular septum morphogenesis	1	471	1	14200	3.32e-02		low density lipoprotein receptor-related protein 6
189	GO:2000151	negative regulation of planar cell polarity pathway involved in cardiac muscle tissue morphogenesis	1	471	1	14200	3.32e-02		low density lipoprotein receptor-related protein 6
190	GO:2000162	negative regulation of planar cell polarity pathway involved in cardiac right atrium morphogenesis	1	471	1	14200	3.32e-02		low density lipoprotein receptor-related protein 6

191	GO:2000164	negative regulation of planar cell polarity pathway involved in outflow tract morphogenesis	1	471	1	14200	3.32e-02		low density lipoprotein receptor-related protein 6
192	GO:2000166	negative regulation of planar cell polarity pathway involved in pericardium morphogenesis	1	471	1	14200	3.32e-02		low density lipoprotein receptor-related protein 6
193	GO:2000168	negative regulation of planar cell polarity pathway involved in neural tube closure	1	471	1	14200	3.32e-02		low density lipoprotein receptor-related protein 6
194	GO:0015700	arsenite transport	1	471	1	14200	3.32e-02		arsA arsenite transporter, ATP-binding, homolog 1 (bacterial)
195	GO:0031947	negative regulation of glucocorticoid biosynthetic process	1	471	1	14200	3.32e-02		ATPase, Na+/K+ transporting, alpha 1 polypeptide
196	GO:0045989	positive regulation of striated muscle contraction	1	471	1	14200	3.32e-02		ATPase, Na+/K+ transporting, alpha 1 polypeptide
197	GO:0070417	cellular response to cold	1	471	1	14200	3.32e-02		nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha
198	GO:0060409	positive regulation of acetylcholine metabolic process	1	471	1	14200	3.32e-02		phosphatidylethanolamine binding protein 1
199	GO:0021540	corpus callosum morphogenesis	1	471	1	14200	3.32e-02		platelet-activating factor acetylhydrolase 1b, regulatory subunit 1 (45kDa)
200	GO:0046469	platelet activating factor metabolic process	1	471	1	14200	3.32e-02		platelet-activating factor acetylhydrolase 1b, regulatory subunit 1 (45kDa)
201	GO:0051660	establishment of centrosome localization	1	471	1	14200	3.32e-02		platelet-activating factor acetylhydrolase 1b, regulatory subunit 1 (45kDa)
202	GO:0006933	negative regulation of cell adhesion involved	1	471	1	14200	3.32e-		ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide

		in substrate-bound cell migration					02		
203	GO:0007387	anterior compartment pattern formation	1	471	1	14200	3.32e-02		pre-B-cell leukemia homeobox 3
204	GO:0007388	posterior compartment specification	1	471	1	14200	3.32e-02		pre-B-cell leukemia homeobox 3
205	GO:0015698	inorganic anion transport	1	471	1	14200	3.32e-02		solute carrier family 26, member 4
206	GO:0050904	diapedesis	1	471	1	14200	3.32e-02		platelet/endothelial cell adhesion molecule
207	GO:0033986	response to methanol	1	471	1	14200	3.32e-02		serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1
208	GO:0046687	response to chromate	1	471	1	14200	3.32e-02		serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1
209	GO:0031087	deadenylation-independent decapping of nuclear-transcribed mRNA	1	471	1	14200	3.32e-02		proline-rich nuclear receptor coactivator 2
210	GO:0045844	positive regulation of striated muscle tissue development	1	471	1	14200	3.32e-02		MKL/myocardin-like 2
211	GO:2000272	negative regulation of receptor activity	1	471	1	14200	3.32e-02		protein tyrosine phosphatase, receptor type, J
212	GO:0002358	B cell homeostatic proliferation	1	471	1	14200	3.32e-02		recombination activating gene 2
213	GO:0006582	melanin metabolic process	1	471	1	14200	3.32e-02		B-cell CLL/lymphoma 2
214	GO:0006808	regulation of nitrogen utilization	1	471	1	14200	3.32e-02		B-cell CLL/lymphoma 2
215	GO:0014042	positive regulation of neuron maturation	1	471	1	14200	3.32e-02		B-cell CLL/lymphoma 2
216	GO:0021747	cochlear nucleus development	1	471	1	14200	3.32e-02		B-cell CLL/lymphoma 2
		negative							

217	GO:0032848	regulation of cellular pH reduction	1	471	1	14200	3.32e-02		B-cell CLL/lymphoma 2
218	GO:0043375	CD8-positive, alpha-beta T cell lineage commitment	1	471	1	14200	3.32e-02		B-cell CLL/lymphoma 2
219	GO:0048087	positive regulation of developmental pigmentation	1	471	1	14200	3.32e-02		B-cell CLL/lymphoma 2
220	GO:0048743	positive regulation of skeletal muscle fiber development	1	471	1	14200	3.32e-02		B-cell CLL/lymphoma 2
221	GO:0048753	pigment granule organization	1	471	1	14200	3.32e-02		B-cell CLL/lymphoma 2
222	GO:0015669	gas transport	1	471	1	14200	3.32e-02		ribosomal protein S19
223	GO:0003272	endocardial cushion formation	1	471	1	14200	3.32e-02		bone morphogenetic protein receptor, type IA
224	GO:0021998	neural plate mediolateral regionalization	1	471	1	14200	3.32e-02		bone morphogenetic protein receptor, type IA
225	GO:0048352	paraxial mesoderm structural organization	1	471	1	14200	3.32e-02		bone morphogenetic protein receptor, type IA
226	GO:0048378	regulation of lateral mesodermal cell fate specification	1	471	1	14200	3.32e-02		bone morphogenetic protein receptor, type IA
227	GO:0015732	prostaglandin transport	1	471	1	14200	3.32e-02		solute carrier organic anion transporter family, member 2A1
228	GO:0032287	peripheral nervous system myelin maintenance	1	471	1	14200	3.32e-02		superoxide dismutase 1, soluble
229	GO:0035037	sperm entry	1	471	1	14200	3.32e-02		ubiquitin protein ligase E3A
230	GO:0001885	endothelial cell development	1	471	1	14200	3.32e-02		vascular endothelial zinc finger 1
231	GO:0007174	epidermal growth factor ligand processing	1	471	1	14200	3.32e-02		RAB7A, member RAS oncogene family
		regulation of myeloid					3.32e-		

232	GO:0002761	leukocyte differentiation	1	471	1	14200	02		Nedd4 family interacting protein 1
233	GO:0002502	peptide antigen assembly with MHC class I protein complex	1	471	1	14200	3.32e-02		calreticulin
234	GO:0042990	regulation of transcription factor import into nucleus	1	471	1	14200	3.32e-02		membrane-bound transcription factor peptidase, site 1
235	GO:0010983	positive regulation of high-density lipoprotein particle clearance	1	471	1	14200	3.32e-02		lipase, endothelial
236	GO:0050746	regulation of lipoprotein metabolic process	1	471	1	14200	3.32e-02		lipase, endothelial
237	GO:0030497	fatty acid elongation	1	471	1	14200	3.32e-02		trans-2,3-enoyl-CoA reductase

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