Genes GENES - GO Cellular Component Annotations

Used notations:

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

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Terms

Rank	ID	Term	List Hits	List Total	Population Hits	Population Total	P-value	Genes ID's	Genes Names
1	GO:0005737	cytoplasm	184	520	4954	16399	5.65e-03	10075 10209 10238	HECT, UBA and WWE domain containing 1
2	GO:0016020	membrane	146	520	3711	16399	1.86e-03	100128553 100128731 100133941	CTAGE family, member 4
3	GO:0005829	cytosol	120	520	1980	16399	8.28e-13	10040 10392 10398	target of myb1 (chicken)-like 1
4	GO:0005739	mitochondrion	77	520	1313	16399	9.19e-08	10166 10476 10935	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15
5	GO:0005783	endoplasmic reticulum	68	520	952	16399	2.32e-10	10313 10492 10525	reticulon 3
6	GO:0005794	Golgi apparatus	49	520	885	16399	1.04e-04	10040 10090 10313	target of myb1 (chicken)-like 1
7	GO:0005789	endoplasmic reticulum membrane	44	520	610	16399	3.35e-07	10313 11014 11161	reticulon 3
8	GO:0005743	mitochondrial inner membrane	34	520	297	16399	9.32e-11	10166 10476 1337	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15
9	GO:0000139	Golgi membrane	23	520	395	16399	3.9e-03	10090 10313 10610	uronyl-2-sulfotransferase
10	GO:0042470	melanosome	21	520	89	16399	3.95e-13	10972 1213 23193	transmembrane emp24-like trafficking protein 10 (yeast)
11	GO:0009986	cell surface	20	520	264	16399	3.01e-04	100133941 222663 2665	CD24 molecule
12	GO:0005792	microsome	17	520	257	16399	3.54e-03	10492 10972 1314	synaptotagmin binding, cytoplasmic RNA interacting protein
13	GO:0005840	ribosome	17	520	154	16399	8e-06	219927 54460 60488	mitochondrial ribosomal protein L21
14	GO:0005788	endoplasmic reticulum lumen	16	520	97	16399	6.15e-08	10525 10956 23071	hypoxia up-regulated 1

15	GO:0030529	ribonucleoprotein complex	15	520	109	16399	1.76e-06	10492 1655 1938	synaptotagmin binding, cytoplasmic RNA interacting protein
16	GO:0005759	mitochondrial matrix	15	520	198	16399	1.65e-03	1743 3030 3032	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)
17	GO:0005764	lysosome	13	520	168	16399	2.74e-03	10040 11337 157310	target of myb1 (chicken)-like 1
18	GO:0022627	cytosolic small ribosomal subunit	13	520	35	16399	2.2e-11	3921 6189 6193	ribosomal protein SA
19	GO:0010008	endosome membrane	11	520	136	16399	4.04e-03	10040 25849 3920	target of myb1 (chicken)-like 1
20	GO:0070469	respiratory chain	9	520	52	16399	3.3e-05	29796 4694 4700	ubiquinol-cytochrome c reductase, complex III subunit X
21	GO:0005753	mitochondrial proton-transporting ATP synthase complex	7	520	18	16399	7.27e-07	10476 498 506	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit d
22	GO:0071013	catalytic step 2 spliceosome	7	520	80	16399	1.34e-02	10492 10594 1655	synaptotagmin binding, cytoplasmic RNA interacting protein
23	GO:0005747	mitochondrial respiratory chain complex I	7	520	46	16399	5.67e-04	4694 4700 4706	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa
24	GO:0022625	cytosolic large ribosomal subunit	7	520	37	16399	1.39e-04	6124 6128 6142	ribosomal protein L4
25	GO:0005793	ER-Golgi intermediate compartment	6	520	40	16399	1.52e-03	10972 23071 2335	transmembrane emp24-like trafficking protein 10 (yeast)
26	GO:0000786	nucleosome	6	520	64	16399	1.57e-02	3005 3006 3021	H1 histone family, member 0
27	GO:0000502	proteasome complex	6	520	57	16399	9.12e-03	3315 5684 5691	heat shock 27kDa protein 1
28	GO:0016459	myosin complex	5	520	41	16399	9.19e-03	10398 10627 140735	myosin, light chain 9, regulatory
29	GO:0008250	oligosaccharyltransferase complex	5	520	10	16399	6.95e-06	1603 3703 6184	defender against cell death 1
30	GO:0042645	mitochondrial nucleoid	5	520	35	16399	4.65e-03	26073 3030 3032	polymerase (DNA-directed), delta interacting protein 2
31	GO:0005901	caveola	5	520	52	16399	2.4e-02	3667 4040 657	insulin receptor substrate 1
32	GO:0031966	mitochondrial membrane	5	520	58	16399	3.64e-02	4694 4700 4706	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa
33	GO:0005689	U12-type spliceosomal complex	5	520	24	16399	8.11e-04	4904 51639 6633	Y box binding protein 1
34	GO:0005852	eukaryotic translation initiation factor 3 complex	4	520	14	16399	7.76e-04	10480 27335 8663	eukaryotic translation initiation factor 3, subunit M
35	GO:0030133	transport vesicle	4	520	39	16399	3.43e-02	11161 2778 54432	chromosome 14 open reading frame 1
36	GO:0005746	mitochondrial respiratory chain	4	520	14	16399	7.76e-04	1346 1349 23530	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)

37	GO:0030666	endocytic vesicle membrane	4	520	29	16399	1.27e-02	163 7311 7314	adaptor-related protein complex 2, beta 1 subunit
38	GO:0030018	Z disc	4	520	43	16399	4.66e-02	23224 3315 3880	spectrin repeat containing, nuclear envelope 2
39	GO:0000275	mitochondrial proton-transporting ATP synthase complex, catalytic core F(1)	4	520	5	16399	4.87e-06	432369 498 509	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit pseudogene 2
40	GO:0015935	small ribosomal subunit	4	520	17	16399	1.71e-03	6194 6217 6227	ribosomal protein S6
41	GO:0000276	mitochondrial proton-transporting ATP synthase complex, coupling factor F(o)	3	520	8	16399	1.58e-03	10476 515 521	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit d
42	GO:0005868	cytoplasmic dynein complex	3	520	11	16399	4.32e-03	1778 6993 83658	dynein, cytoplasmic 1, heavy chain 1
43	GO:0016529	sarcoplasmic reticulum	3	520	23	16399	3.51e-02	23224 488 811	spectrin repeat containing, nuclear envelope 2
44	GO:0010494	stress granule	3	520	15	16399	1.09e-02	23369 26065 4904	pumilio homolog 2 (Drosophila)
45	GO:0005871	kinesin complex	3	520	17	16399	1.55e-02	3799 5048 7531	kinesin family member 5B
46	GO:0005839	proteasome core complex	3	520	14	16399	8.89e-03	5684 5691 5694	proteasome (prosome, macropain) subunit, alpha type, 3
47	GO:0070937	CRD-mediated mRNA stability complex	2	520	5	16399	9.42e-03	10492 4904	synaptotagmin binding, cytoplasmic RNA interacting protein
48	GO:0071204	histone pre-mRNA 3'end processing complex	2	520	5	16399	9.42e-03	10492 4904	synaptotagmin binding, cytoplasmic RNA interacting protein
49	GO:0016281	eukaryotic translation initiation factor 4F complex	2	520	9	16399	3.12e-02	1975 1982	eukaryotic translation initiation factor 4B
50	GO:0016589	NURF complex	2	520	6	16399	1.38e-02	2186 6594	bromodomain PHD finger transcription factor
51	GO:0045335	phagocytic vesicle	2	520	6	16399	1.38e-02	23673 7879	syntaxin 12
52	GO:0019718	rough microsome	2	520	4	16399	5.77e-03	29927 6184	Sec61 alpha 1 subunit (S. cerevisiae)
53	GO:0016507	fatty acid beta-oxidation multienzyme complex	2	520	2	16399	1e-03	3030 3032	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit
54	GO:0035253	ciliary rootlet	2	520	8	16399	2.48e-02	351 3799	amyloid beta (A4) precursor protein
55	GO:0031088	platelet dense granule membrane	2	520	5	16399	9.42e-03	3708 3920	inositol 1,4,5-trisphosphate receptor, type 1
56	GO:0031095	platelet dense tubular network membrane	2	520	8	16399	2.48e-02	3708 488	inositol 1,4,5-trisphosphate receptor, type 1
57	GO:0043034	costamere	2	520	11	16399	4.57e-02	3880 6385	keratin 19
							4.57e-		

58	GO:0015934	large ribosomal subunit	2	520	11	16399	02	4736 6139	ribosomal protein L10a
59	GO:0033267	axon part	2	520	8	16399	2.48e-02	5048 7531	platelet-activating factor acetylhydrolase 1b, regulatory subunit 1 (45kDa)
60	GO:0016471	vacuolar proton-transporting V-type ATPase complex	2	520	9	16399	3.12e-02	51382 9114	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D
61	GO:0046930	pore complex	2	520	9	16399	3.12e-02	596 7419	B-cell CLL/lymphoma 2
62	GO:0005786	signal recognition particle, endoplasmic reticulum targeting	2	520	6	16399	1.38e-02	6727 6731	signal recognition particle 14kDa (homologous Alu RNA binding protein)
63	GO:0005750	mitochondrial respiratory chain complex III	2	520	6	16399	1.38e-02	7385 7388	ubiquinol-cytochrome c reductase core protein II
64	GO:0033179	proton-transporting V-type ATPase, V0 domain	2	520	6	16399	1.38e-02	8992 9114	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1
65	GO:0000836	Hrd1p ubiquitin ligase complex	1	520	1	16399	3.17e-02	10956	osteosarcoma amplified 9, endoplasmic reticulum lectin
66	GO:0008303	caspase complex	1	520	1	16399	3.17e-02	3309	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
67	GO:0000235	astral microtubule	1	520	1	16399	3.17e-02	5048	platelet-activating factor acetylhydrolase 1b, regulatory subunit 1 (45kDa)
68	GO:0005754	mitochondrial proton-transporting ATP synthase, catalytic core	1	520	1	16399	3.17e-02	506	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide
69	GO:0005895	interleukin-5 receptor complex	1	520	1	16399	3.17e-02	6386	syndecan binding protein (syntenin)
70	GO:0032579	apical lamina of hyaline layer	1	520	1	16399	3.17e-02	7033	trefoil factor 3 (intestinal)

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