

A

ErmineJ

File Gene Sets Analysis Results Help

Table Tree

Name	Description	Pr...	G...	Run 1 Pval	Run 2 Pval	Run 3 ...
GO:0005830	cytosolic ribosome (sensu Eukaryota)	86	73	10e-013	3.4542e-027	4.1922e-021
GO:0015934	large ribosomal subunit	45	41	10e-013	3.9995e-017	3.8406e-020
GO:0005842	cytosolic large ribosomal subunit (sensu Eukaryota)	42	38	10e-013	2.3241e-017	1.2547e-018
GO:0006414	translational elongation	36	25	10e-013	6.8444e-005	4.296e-008
GO:0042254	ribosome biogenesis and assembly	72	59	10e-013	9.0694e-012	5.6505e-007
GO:0005759	mitochondrial matrix	74	59	10e-013	0.0002	2.9463e-006
GO:0005853	eukaryotic translation elongation factor 1 complex	10	6	0.0026	9.1444e-006	1.1268e-005
GO:0006099	tricarboxylic acid cycle	77	66	10e-013	0.0001	1.1513e-005
GO:0005743	mitochondrial inner membrane	98	81	10e-013	0.0006	1.5366e-005
GO:0009060	aerobic respiration	79	68	10e-013	9.2288e-005	1.7399e-005
GO:0007046	ribosome biogenesis	95	76	10e-013	9.6156e-009	2.4057e-005
GO:0016282	eukaryotic 43S preinitiation complex	45	36	10e-013	3.6316e-013	3.0941e-005
GO:0006818	hydrogen transport	80	64	10e-013	0.0409	4.0164e-005
GO:0016836	hydro-lyase activity	47	38	10e-013	0.0916	4.1168e-005
GO:0016283	eukaryotic 48S initiation complex	34	26	10e-013	2.7066e-011	5.4508e-005
GO:0009206	purine ribonucleoside triphosphate biosynthesis	46	33	10e-013	0.0021	7.6901e-005
GO:0003746	translation elongation factor activity	43	28	0.0003	0.0158	0.0001
GO:0006519	amino acid and derivative metabolism	98	77	10e-013	0.0051	0.0001
GO:0042589	zymogen granule membrane	8	5	0.0058	0.007	0.0001
GO:0016405	CoA-ligase activity	8	5	0.0011	0.014	0.0001
GO:0046146	tetrahydrobiopterin metabolism	5	5	0.001	0.104	0.0001
GO:0016616	oxidoreductase activity, acting on the CH-OH group of donors, NA...	73	63	10e-013	0.009	0.0001
GO:0015935	small ribosomal subunit	41	29	10e-013	1.8884e-009	0.0001
GO:0019866	inner membrane	95	80	10e-013	0.0045	0.0002
GO:0030667	secretory granule membrane	15	9	0.0019	0.0159	0.0002
GO:0019843	rRNA binding	11	9	0.0014	0.0011	0.0002
GO:0015992	protein transport	73	58	10e-013	0.0359	0.0002
GO:0005504	fatty acid binding	23	19	0.0004	0.0166	0.0002
GO:0004112	cyclic-nucleotide phosphodiesterase activity	33	25	10e-013	0.0228	0.0003
GO:0015908	fatty acid transport	6	6	0.0387	0.1196	0.0004
GO:0004705	JUN kinase activity	12	6	0.0069	0.0402	0.0004
GO:0045666	positive regulation of neuron differentiation	9	6	0.0249	0.0088	0.0004
GO:0044271	nitrogen compound biosynthesis	8	6	0.0224	0.0516	0.0004
GO:0003857	3-hydroxyacyl-CoA dehydrogenase activity	7	6	0.0365	0.0461	0.0004
GO:0030323	respiratory tube development	66	33	0.0001	0.0048	0.0004
GO:0045255	hydrogen-translocating F-type ATPase complex	20	16	0.0033	0.0077	0.0006
GO:0050770	regulation of axonogenesis	23	16	0.003	0.0122	0.0006

Done!

B

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all: all

- GO:0003674: molecular_function
- GO:0005575: cellular_component -- 735 probes, 558 genes
 - GO:0005576: extracellular region
 - GO:0005623: cell
 - GO:0000267: cell fraction -- 1240 probes, 888 genes
 - GO:0001917: photoreceptor inner segment
 - GO:0005622: intracellular
 - GO:0005933: bud
 - GO:0009986: cell surface -- 138 probes, 101 genes -- p = 0.734
 - GO:0016020: membrane
 - GO:0030312: external encapsulating structure -- 17 probes, 14 genes -- p = 0.015
 - GO:0030427: site of polarized growth
 - GO:0001411: hyphal tip
 - GO:0030426: growth cone -- 16 probes, 14 genes -- p = 0.002
 - GO:0043332: mating projection tip
 - GO:0030428: cell septum
 - GO:0030496: midbody -- 7 probes, 4 genes
 - GO:0031026: glutamate synthase complex
 - GO:0031252: leading edge -- 76 probes, 54 genes -- p = 0.094
 - GO:0031254: trailing edge
 - GO:0031255: lateral part of mobile cell
 - GO:0031317: tripartite ATP-independent periplasmic transporter complex
 - GO:0042597: periplasmic space
 - GO:0042763: immature spore
 - GO:0042995: cell projection -- 120 probes, 84 genes -- p = 0.018
 - GO:0043025: cell soma -- 7 probes, 6 genes -- p = 0.065
 - GO:0043190: ATP-binding cassette (ABC) transporter complex -- 15 probes, 10 genes -- p = 0.161
 - GO:0045177: apical part of cell -- 78 probes, 59 genes -- p = 0.414
 - GO:0045178: basal part of cell -- 9 probes, 5 genes -- p = 0.314
 - GO:0051286: cell tip
 - GO:0008372: cellular component unknown
 - GO:0019012: virion -- 5 probes, 4 genes
 - GO:0031012: extracellular matrix -- 263 probes, 193 genes
 - GO:0043226: organelle
 - GO:0043234: protein complex -- 1422 probes, 1032 genes
 - GO:0008150: biological_process -- 808 probes, 603 genes

User-defined or modified

Done!