Term	−log(p)	n	fg	bg
calcium−dependent activation of synaptic... GO:0099502	p=1.1E−17	n=18	fg=0.02	bg=0.00
negative regulation of transcription by ... GO:0000122	p=4.6E−13	n=76	fg=0.11	bg=0.04
positive regulation of transcription by ... GO:0045944	p=1.2E−12	n=88	fg=0.12	bg=0.05
calcium ion−regulated exocytosis of neur... GO:0048791	p=3.5E−11	n=18	fg=0.02	bg=0.00
spontaneous neurotransmitter secretion GO:0061669	p=9.4E−10	n=8	fg=0.01	bg=0.00
negative regulation of CD4−positive, alp... GO:0043371	p=4.2E−09	n=10	fg=0.01	bg=0.00
negative regulation of transcription fro... GO:1990441	p=4.3E−09	n=6	fg=0.01	bg=0.00
regulation of calcium−dependent activati... GO:0150037	p=5.7E−09	n=7	fg=0.01	bg=0.00
positive regulation of peptidyl−serine p... GO:0033138	p=9.1E−09	n=14	fg=0.02	bg=0.00
dopamine receptor signaling pathway GO:0007212	p=2.2E−08	n=18	fg=0.02	bg=0.00
positive regulation of NAD(P)H oxidase a... GO:0033864	p=3.5E−08	n=7	fg=0.01	bg=0.00
cellular response to hydroperoxide GO:0071447	p=3.5E−08	n=7	fg=0.01	bg=0.00
G protein−coupled receptor internalizati... GO:0002031	p=6.7E−08	n=6	fg=0.01	bg=0.00
negative regulation of CREB transcriptio... GO:0032792	p=1.3E−07	n=6	fg=0.01	bg=0.00
positive regulation of CD8−positive, alp... GO:0043378	p=1.3E−07	n=6	fg=0.01	bg=0.00
positive regulation of type B pancreatic... GO:1904692	p=1.3E−07	n=6	fg=0.01	bg=0.00
luteinization GO:0001553	p=1.4E−07	n=10	fg=0.01	bg=0.00
thymus development GO:0048538	p=2.6E−07	n=13	fg=0.02	bg=0.00
positive regulation of metanephric glome... GO:0072300	p=3.0E−07	n=4	fg=0.01	bg=0.00
negative regulation of mesenchymal cell ... GO:0072305	p=3.0E−07	n=4	fg=0.01	bg=0.00
positive regulation of response to drug GO:2001025	p=3.0E−07	n=4	fg=0.01	bg=0.00
metanephric mesenchymal cell differentia... GO:0072162	p=3.0E−07	n=4	fg=0.01	bg=0.00
zinc ion import into synaptic vesicle GO:0099180	p=3.0E−07	n=4	fg=0.01	bg=0.00
vestibulocochlear nerve formation GO:0021650	p=3.0E−07	n=4	fg=0.01	bg=0.00
positive regulation of mesenchymal to ep... GO:0072108	p=3.0E−07	n=4	fg=0.01	bg=0.00
optic nerve structural organization GO:0021633	p=3.0E−07	n=4	fg=0.01	bg=0.00
calcium ion regulated lysosome exocytosi... GO:1990927	p=3.0E−07	n=4	fg=0.01	bg=0.00
ureter maturation GO:0035799	p=3.0E−07	n=4	fg=0.01	bg=0.00
negative regulation of apoptotic process... GO:1900215	p=3.0E−07	n=4	fg=0.01	bg=0.00
negative regulation of apoptotic process... GO:1900218	p=3.0E−07	n=4	fg=0.01	bg=0.00
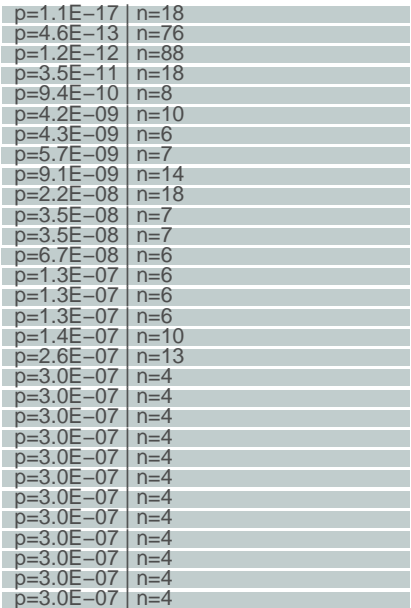
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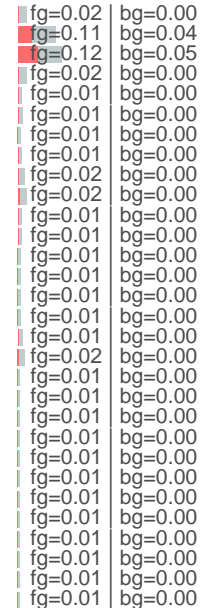
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Term	−log(p)	n	fg	bg
RNA polymerase II cis−regulatory region ... GO:0000978	p=6.5E−24	n=72	fg=0.10	bg=0.02
DNA−binding transcription activator acti... GO:0001228	p=2.1E−13	n=37	fg=0.05	bg=0.01
metal ion binding GO:0046872	p=2.3E−13	n=239	fg=0.33	bg=0.20
high voltage−gated calcium channel activ... GO:0008331	p=1.1E−10	n=8	fg=0.01	bg=0.00
G−protein beta/gamma−subunit complex bin... GO:0031683	p=1.4E−09	n=11	fg=0.02	bg=0.00
syntaxin−1 binding GO:0017075	p=1.6E−09	n=17	fg=0.02	bg=0.00
calcium−dependent phospholipid binding GO:0005544	p=2.1E−09	n=14	fg=0.02	bg=0.00
G protein−coupled serotonin receptor bin... GO:0031821	p=2.8E−09	n=7	fg=0.01	bg=0.00
voltage−gated calcium channel activity i... GO:0099626	p=3.3E−08	n=6	fg=0.01	bg=0.00
3',5'−cyclic−AMP phosphodiesterase activ... GO:0004115	p=4.8E−08	n=8	fg=0.01	bg=0.00
transcription corepressor activity GO:0003714	p=5.0E−08	n=24	fg=0.03	bg=0.01
protein phosphatase 1 binding GO:0008157	p=9.4E−08	n=10	fg=0.01	bg=0.00
histone deacetylase binding GO:0042826	p=2.2E−07	n=20	fg=0.03	bg=0.01
calcium− and calmodulin−responsive adeny... GO:0008294	p=3.1E−07	n=4	fg=0.01	bg=0.00
alpha−2B adrenergic receptor binding GO:0031695	p=3.1E−07	n=4	fg=0.01	bg=0.00
alpha−2C adrenergic receptor binding GO:0031696	p=3.1E−07	n=4	fg=0.01	bg=0.00
DNA−binding transcription factor activit... GO:0000981	p=6.5E−07	n=67	fg=0.09	bg=0.02
neurexin family protein binding GO:0042043	p=1.5E−06	n=4	fg=0.01	bg=0.00
protein tyrosine phosphatase activity GO:0004725	p=1.6E−06	n=15	fg=0.02	bg=0.00
syntaxin−3 binding GO:0030348	p=1.6E−06	n=5	fg=0.01	bg=0.00
spectrin binding GO:0030507	p=1.7E−06	n=12	fg=0.02	bg=0.00
phosphatidylserine binding GO:0001786	p=3.2E−06	n=10	fg=0.01	bg=0.00
DNA−binding transcription repressor acti... GO:0001227	p=3.2E−06	n=18	fg=0.02	bg=0.01
SNARE binding GO:0000149	p=4.9E−06	n=36	fg=0.05	bg=0.01
TFIIB−class transcription factor binding GO:0001093	p=4.9E−06	n=6	fg=0.01	bg=0.00
GTPase activating protein binding GO:0032794	p=5.3E−06	n=8	fg=0.01	bg=0.00
1−phosphatidylinositol−3−kinase regulato... GO:0046935	p=6.7E−06	n=6	fg=0.01	bg=0.00
cAMP response element binding protein bi... GO:0008140	p=9.1E−06	n=6	fg=0.01	bg=0.00
calmodulin binding GO:0005516	p=9.2E−06	n=19	fg=0.03	bg=0.01
GTPase activity GO:0003924	p=9.3E−06	n=36	fg=0.05	bg=0.02
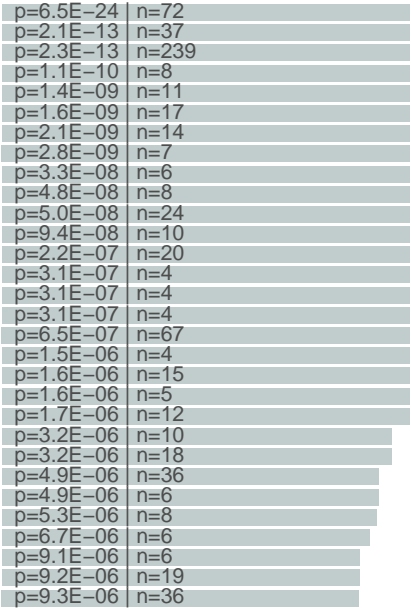
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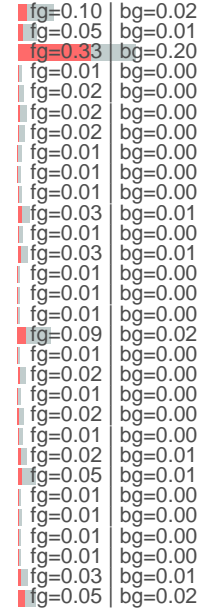
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Term	−log(p)	n	fg	bg
heterotrimeric G−protein complex GO:0005834	p=1.7E−18	n=17	fg=0.02	bg=0.00
hippocampal mossy fiber to CA3 synapse GO:0098686	p=4.2E−12	n=17	fg=0.02	bg=0.00
plasma membrane GO:0005886	p=3.5E−10	n=289	fg=0.40	bg=0.25
voltage−gated calcium channel complex GO:0005891	p=4.7E−10	n=9	fg=0.01	bg=0.00
core−binding factor complex GO:0016513	p=4.4E−09	n=6	fg=0.01	bg=0.00
synaptic vesicle GO:0008021	p=1.6E−08	n=45	fg=0.06	bg=0.02
protein phosphatase type 1 complex GO:0000164	p=4.7E−08	n=8	fg=0.01	bg=0.00
dense core granule GO:0031045	p=6.1E−08	n=13	fg=0.02	bg=0.00
transcription factor AP−1 complex GO:0035976	p=3.0E−07	n=4	fg=0.01	bg=0.00
acetylcholine−gated channel complex GO:0005892	p=3.0E−07	n=4	fg=0.01	bg=0.00
extrinsic component of neuronal dense co... GO:0098674	p=3.0E−07	n=4	fg=0.01	bg=0.00
beta−catenin−TCF7L2 complex GO:0070369	p=3.0E−07	n=4	fg=0.01	bg=0.00
axon terminus GO:0043679	p=1.1E−06	n=23	fg=0.03	bg=0.01
exocytic vesicle GO:0070382	p=1.7E−06	n=53	fg=0.07	bg=0.03
glutamatergic synapse GO:0098978	p=1.8E−06	n=57	fg=0.08	bg=0.04
presynaptic active zone membrane GO:0048787	p=1.9E−06	n=12	fg=0.02	bg=0.00
zymogen granule GO:0042588	p=5.0E−06	n=9	fg=0.01	bg=0.00
neuron projection terminus GO:0044306	p=1.1E−05	n=31	fg=0.04	bg=0.01
extrinsic component of presynaptic membr... GO:0098888	p=1.8E−05	n=7	fg=0.01	bg=0.00
cytoskeleton of presynaptic active zone GO:0048788	p=2.0E−05	n=4	fg=0.01	bg=0.00
early phagosome GO:0032009	p=2.0E−05	n=4	fg=0.01	bg=0.00
presynaptic cytosol GO:0099523	p=2.1E−05	n=11	fg=0.02	bg=0.00
photoreceptor inner segment GO:0001917	p=3.3E−05	n=9	fg=0.01	bg=0.00
SNARE complex GO:0031201	p=3.7E−05	n=12	fg=0.02	bg=0.00
insulin−responsive compartment GO:0032593	p=4.3E−05	n=7	fg=0.01	bg=0.00
perikaryon GO:0043204	p=6.5E−05	n=17	fg=0.02	bg=0.01
microvillus membrane GO:0031528	p=8.7E−05	n=4	fg=0.01	bg=0.00
dendrite GO:0030425	p=8.9E−05	n=60	fg=0.08	bg=0.04
voltage−gated potassium channel complex GO:0008076	p=1.7E−04	n=6	fg=0.01	bg=0.00
endosome GO:0005768	p=3.3E−04	n=73	fg=0.10	bg=0.06
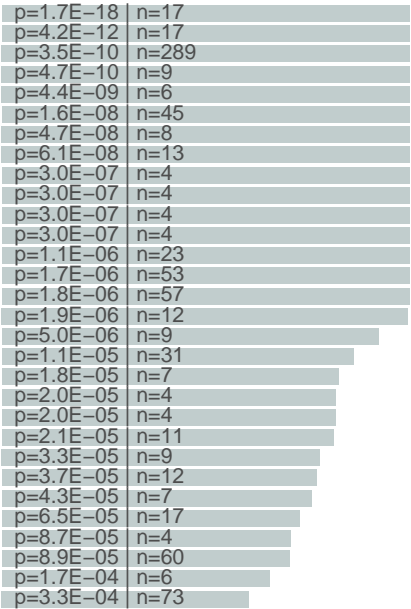
−log(p)
n=727/1256 input genes with annotations

fraction