GO:BP
gc029

fraction genes in fg and expected valu

sucrose transport GO:0015770	p=3.7E−13	n=9
regulation of oligodendrocyte differenti... GO:0048713	p=8.5E−12	n=11
positive regulation of fatty acid biosyn... GO:0045723	p=1.0E−10	n=9
positive regulation of glucose metabolic... GO:0010907	p=5.0E−09	n=9
regulation of skeletal muscle contractio... GO:0100001	p=7.2E−08	n=5
negative regulation of cellular extravas... GO:0002692	p=1.2E−07	n=3
negative regulation of macrophage migrat... GO:1905522	p=1.2E−07	n=3
negative regulation of blood vessel remo... GO:0060313	p=1.2E−07	n=3
choline transport GO:0015871	p=2.6E−07	n=5
neuropeptide catabolic process GO:0010813	p=4.5E−07	n=5
neuromuscular process controlling balanc... GO:0050885	p=1.3E−06	n=7
membrane depolarization during action po... GO:0086010	p=2.1E−06	n=5
negative regulation of neutrophil degran... GO:0043314	p=2.4E−06	n=3
negative regulation of respiratory burst GO:0060268	p=2.7E−06	n=4
regulation of long−term neuronal synapti... GO:0048169	p=4.2E−06	n=5
calcium activated phosphatidylcholine sc... GO:0061590	p=6.7E−06	n=3
calcium activated galactosylceramide scr... GO:0061591	p=6.7E−06	n=3
calcium activated phosphatidylserine scr... GO:0061589	p=6.7E−06	n=3
SMAD protein signal transduction GO:0060395	p=7.7E−06	n=7
positive regulation of blood pressure GO:0045777	p=1.3E−05	n=6
cholecystokinin signaling pathway GO:0038188	p=2.5E−05	n=2
positive regulation of somatostatin secr... GO:0090274	p=2.5E−05	n=2
estrous cycle GO:0044849	p=2.5E−05	n=2
regulation of postsynaptic neurotransmit... GO:0098962	p=4.3E−05	n=3
negative regulation of cold−induced ther... GO:0120163	p=1.1E−04	n=5
dihydrobiopterin metabolic process GO:0051066	p=1.5E−04	n=2
diacylglycerol catabolic process GO:0046340	p=1.5E−04	n=2
positive regulation of blood−brain barri... GO:1905605	p=1.5E−04	n=2
positive regulation of behavioral fear r... GO:2000987	p=1.5E−04	n=2
neuronal action potential GO:0019228	p=1.6E−04	n=5
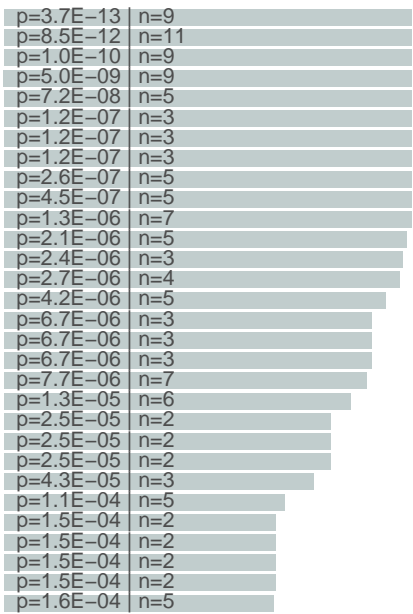
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−log(p)

n=154/399 input genes with annotations

fraction

GO:MF
gc029

fraction genes in fg and expected valu

sucrose:proton symporter activity GO:0008506	p=1.8E−12	n=9
hormone−sensitive lipase activity GO:0033878	p=7.3E−06	n=3
voltage−gated sodium channel activity GO:0005248	p=2.1E−05	n=5
cholecystokinin receptor activity GO:0004951	p=2.6E−05	n=2
type B gastrin/cholecystokinin receptor ... GO:0031741	p=2.6E−05	n=2
gastrin receptor activity GO:0015054	p=2.6E−05	n=2
pyrimidine−nucleoside phosphorylase acti... GO:0016154	p=7.8E−05	n=2
AP−2 adaptor complex binding GO:0035612	p=1.4E−04	n=3
GTP cyclohydrolase I activity GO:0003934	p=1.6E−04	n=2
1,3−diacylglycerol acylhydrolase activit... GO:0102258	p=1.6E−04	n=2
1,2−diacylglycerol acylhydrolase activit... GO:0102259	p=1.6E−04	n=2
retinyl−palmitate esterase activity GO:0050253	p=1.6E−04	n=2
intracellular calcium activated chloride... GO:0005229	p=2.5E−04	n=3
metalloaminopeptidase activity GO:0070006	p=3.9E−04	n=5
thymidine phosphorylase activity GO:0009032	p=5.4E−04	n=2
sterol esterase activity GO:0004771	p=7.2E−04	n=2
1,4−alpha−oligoglucan phosphorylase acti... GO:0004645	p=1.4E−03	n=2
glutathione synthase activity GO:0004363	p=1.7E−03	n=2
PDZ domain binding GO:0030165	p=1.8E−03	n=5
phospholipid scramblase activity GO:0017128	p=1.9E−03	n=3
triglyceride lipase activity GO:0004806	p=2.1E−03	n=3
voltage−gated ion channel activity GO:0005244	p=2.1E−03	n=5
acylglycerol lipase activity GO:0047372	p=2.3E−03	n=3
guanyl−nucleotide exchange factor activi... GO:0005085	p=2.4E−03	n=7
rRNA primary transcript binding GO:0042134	p=2.6E−03	n=2
mitogen−activated protein kinase binding GO:0051019	p=4.2E−03	n=3
phosphatidylserine binding GO:0001786	p=4.8E−03	n=3
amide binding GO:0033218	p=5.1E−03	n=15
thyroid hormone transmembrane transporte... GO:0015349	p=5.4E−03	n=3
platelet−derived growth factor receptor ... GO:0005161	p=5.6E−03	n=2
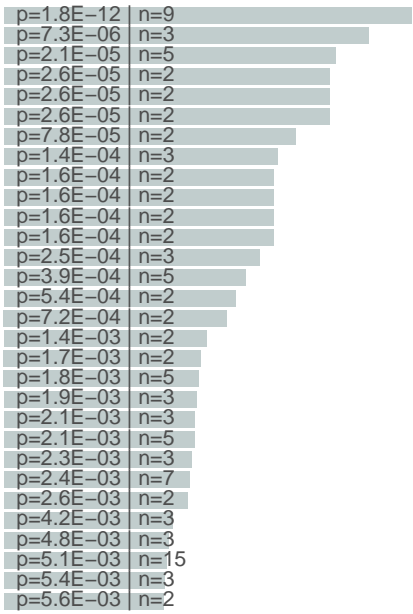
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−log(p)

n=157/399 input genes with annotations

fraction

GO:CC
gc029

fraction genes in fg and expected valu

voltage−gated sodium channel complex GO:0001518	p=6.2E−07	n=5
insulin−responsive compartment GO:0032593	p=1.9E−06	n=5
cholinergic synapse GO:0098981	p=6.7E−06	n=3
clathrin−sculpted glutamate transport ve... GO:0060203	p=4.3E−05	n=3
plasma membrane GO:0005886	p=9.1E−05	n=66
postsynaptic density, intracellular comp... GO:0099092	p=7.8E−04	n=3
presynaptic active zone membrane GO:0048787	p=1.2E−03	n=4
axon GO:0030424	p=2.0E−03	n=15
lipid droplet GO:0005811	p=2.8E−03	n=5
basal part of cell GO:0045178	p=6.0E−03	n=9
B−WICH complex GO:0110016	p=6.4E−03	n=2
exocytic vesicle GO:0070382	p=6.9E−03	n=10
AIM2 inflammasome complex GO:0097169	p=1.0E−02	n=1
IPAF inflammasome complex GO:0072557	p=1.0E−02	n=1
neuronal cell body membrane GO:0032809	p=1.1E−02	n=2
cell body membrane GO:0044298	p=1.1E−02	n=2
microvillus GO:0005902	p=1.3E−02	n=4
caveola GO:0005901	p=1.4E−02	n=4
autophagosome membrane GO:0000421	p=1.7E−02	n=3
mitochondrial DNA−directed RNA polymeras... GO:0034245	p=2.0E−02	n=1
glutamatergic synapse GO:0098978	p=2.4E−02	n=12
ATF1−ATF4 transcription factor complex GO:1990590	p=2.5E−02	n=1
ATF4−CREB1 transcription factor complex GO:1990589	p=2.5E−02	n=1
cell surface GO:0009986	p=2.6E−02	n=12
plasma membrane raft GO:0044853	p=2.8E−02	n=4
phagolysosome membrane GO:0061474	p=3.0E−02	n=1
cytolytic granule membrane GO:0101004	p=3.0E−02	n=1
phagolysosome GO:0032010	p=3.0E−02	n=1
neuronal cell body GO:0043025	p=3.4E−02	n=12
filamentous actin GO:0031941	p=3.4E−02	n=2
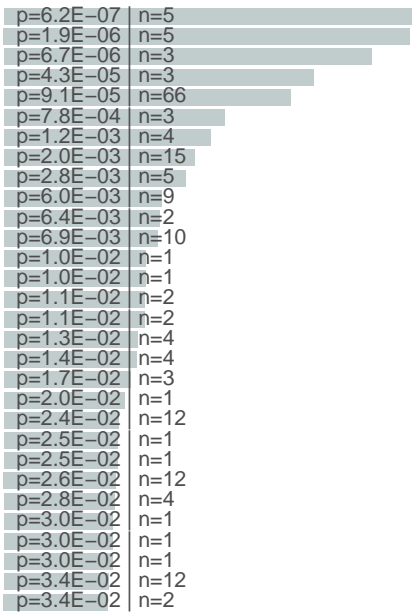
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−log(p)

n=155/399 input genes with annotations

fraction