

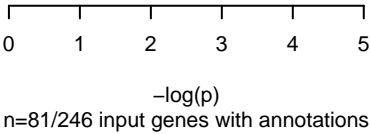
GO:BP
Elav_Nvec_vc1.1_XM_048719424.1

fraction genes in fg and expected value

regulation of mitochondrial outer membra... GO:1901028
establishment or maintenance of cytoskel... GO:0003380
negative regulation of sequestering of t... GO:0010891
regulation of cell communication by elec... GO:0010649
cellular response to exogenous dsRNA GO:0071360
plasma membrane raft assembly GO:0044854
mesectoderm development GO:0048383
negative regulation of mitochondrion org... GO:0010823
positive regulation of multicellular org... GO:0040018
cell surface receptor signaling pathway GO:0007166
negative regulation of transport GO:0051051
regulation of cytosolic calcium ion conc... GO:0051480
chemical synaptic transmission GO:0007268
neuron projection morphogenesis GO:0048812
phosphatidylserine metabolic process GO:0006658
positive regulation of interferon-gamma ... GO:0032729
regulation of myosin II filament organiz... GO:0043519
positive regulation of protein sumoylati... GO:0033235
regulation of heart rate by cardiac cond... GO:0086091
cardiac muscle cell membrane repolarizat... GO:0099622
regulation of membrane repolarization GO:0060306
gastrulation involving germ band extensi... GO:0010004
regulation of potassium ion transmembran... GO:1901016
regulation of intracellular signal trans... GO:1902531
positive regulation of mitochondrion org... GO:0010822
positive regulation of signal transducti... GO:0009967
regulation of immune effector process GO:0002697
action potential GO:0001508
regulation of immune response GO:0050776
movement of cell or subcellular componen... GO:0006928

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p=4.5E-03	n=7
p=4.8E-03	n=13
p=5.1E-03	n=16
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p=6.4E-03	n=20
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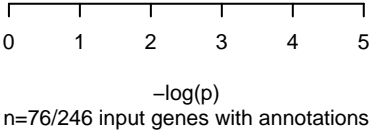
GO:MF
Elav_Nvec_vc1.1_XM_048719424.1

fraction genes in fg and expected value

phosphatidylcholine binding GO:0031210
spectrin binding GO:0030507
calcium channel regulator activity GO:0005246
histone deacetylase binding GO:0042826
phosphatidylethanolamine binding GO:0008429
potassium channel regulator activity GO:0015459
ammonium ion binding GO:0070405
phosphatidylserine binding GO:0001786
G-protein beta/gamma-subunit complex bin... GO:0031683
BH domain binding GO:0051400
ATPase-coupled ion transmembrane transpo... GO:0042625
structural constituent of cytoskeleton GO:0005200
transmembrane transporter binding GO:0044325
histone deacetylase activity GO:0004407
protein-disulfide reductase (NAD(P)) act... GO:0047134
protein lysine deacetylase activity GO:0033558
oxidoreductase activity, acting on a sul... GO:0016668
signaling receptor binding GO:0005102
nucleoside-triphosphatase activity GO:0017111
1-phosphatidylinositol-3-phosphate 4-kin... GO:0052811
MHC protein complex binding GO:0023023
MHC class Ib protein complex binding GO:0023025
diacylglycerol binding GO:0019992
lysophosphatidic acid binding GO:0035727
MHC class Ib protein binding GO:0023029
phosphatidylinositol phosphate kinase ac... GO:0016307
1-phosphatidylinositol-4-phosphate 5-kin... GO:0016308
1-phosphatidylinositol-5-phosphate 4-kin... GO:0016309
BH2 domain binding GO:0051433
MHC class Ib protein binding, via antige... GO:0023030

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p=8.8E-03	n=4
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p=1.3E-02	n=3
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GO:CC
Elav_Nvec_vc1.1_XM_048719424.1

fraction genes in fg and expected value

heterotrimeric G-protein complex GO:0005834
vacuolar proton-transporting V-type ATPa... GO:0000221
FAR/SIN/STRIPAK complex GO:0090443
clathrin-coated pit GO:0005905
recycling endosome membrane GO:0055038
Z disc GO:0030018
I band GO:0031674
sarcoplasm GO:0016528
sarcoplasmic reticulum GO:0016529
plasma membrane proton-transporting V-ty... GO:0033181
membrane raft GO:0045121
membrane microdomain GO:0098857
plasma membrane bounded cell projection GO:0120025
plasma membrane protein complex GO:0098797
cell projection GO:0042995
early endosome GO:0005769
caveola GO:0005901
cell-cell contact zone GO:0044291
paranode region of axon GO:0033270
asymmetric synapse GO:0032279
supramolecular fiber GO:0099512
supramolecular polymer GO:0099081
supramolecular complex GO:0099080
postsynaptic membrane GO:0045211
microtubule associated complex GO:0005875
neuron to neuron synapse GO:0098984
DNA ligase III-XRCC1 complex GO:0070421
cell trailing edge GO:0031254
tRNA-intron endonuclease complex GO:0000214
collagen and cuticulin-based cuticle ext... GO:0060102

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p=2.2E-02	n=4
p=2.5E-02	n=4
p=2.6E-02	n=2
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p=2.6E-02	n=2
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p=2.7E-02	n=6
p=2.9E-02	n=23
p=2.9E-02	n=9
p=3.0E-02	n=23
p=3.0E-02	n=7
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