

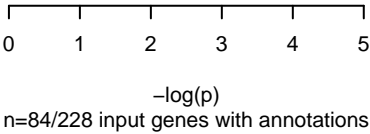
GO:BP
Elav_Nvec_vc1.1_XM_001639002.3

fraction genes in fg and expected value

regulation of synaptic assembly at neuro... GO:0008582
regulation of oskar mRNA translation GO:0046011
regulation of deacetylase activity GO:0150065
determination of digestive tract left/ri... GO:0071907
regulation of cell differentiation GO:0045595
response to amine GO:0014075
salivary gland morphogenesis GO:0007435
negative regulation of cilium assembly GO:1902018
regulation of histone deacetylation GO:0031063
negative regulation of axon regeneration GO:0048681
protein localization to cell cortex GO:0072697
positive regulation of long-term synapti... GO:1900454
proximal/distal axis specification GO:0009946
intracellular transport GO:0046907
negative regulation of synapse assembly GO:0051964
response to bronchodilator GO:0097366
regulation of dendritic spine morphogene... GO:0061001
positive regulation of supramolecular fi... GO:1902905
intracellular estrogen receptor signalin... GO:0030520
signaling GO:0023052
behavior GO:0007610
positive regulation of organelle assembl... GO:1902117
regulation of endocytic recycling GO:2001135
lipid export from cell GO:0140353
response to immobilization stress GO:0035902
positive regulation of establishment of ... GO:1903749
presynaptic active zone organization GO:1990709
neuroblast migration GO:0097402
regulation of transport GO:0051049
positive regulation of cytoskeleton orga... GO:0051495

p=1.4E-03	n=7
p=2.1E-03	n=2
p=2.1E-03	n=2
p=2.1E-03	n=2
p=2.5E-03	n=24
p=2.9E-03	n=3
p=5.8E-03	n=5
p=6.2E-03	n=2
p=6.2E-03	n=2
p=6.2E-03	n=2
p=6.2E-03	n=2
p=6.2E-03	n=2
p=6.2E-03	n=2
p=6.2E-03	n=2
p=6.2E-03	n=27
p=6.4E-03	n=4
p=6.6E-03	n=3
p=6.6E-03	n=3
p=8.0E-03	n=5
p=9.1E-03	n=3
p=1.1E-02	n=47
p=1.1E-02	n=20
p=1.2E-02	n=4
p=1.2E-02	n=2
p=1.2E-02	n=2
p=1.2E-02	n=2
p=1.2E-02	n=2
p=1.2E-02	n=2
p=1.2E-02	n=2
p=1.2E-02	n=22
p=1.2E-02	n=5

fg=0.08	bg=0.02
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.29	bg=0.16
fg=0.04	bg=0.00
fg=0.06	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.32	bg=0.20
fg=0.05	bg=0.01
fg=0.04	bg=0.01
fg=0.04	bg=0.01
fg=0.06	bg=0.02
fg=0.04	bg=0.01
fg=0.56	bg=0.40
fg=0.24	bg=0.14
fg=0.05	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.26	bg=0.16
fg=0.06	bg=0.02



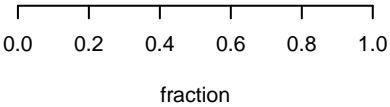
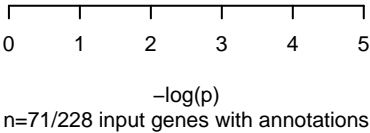
GO:MF
Elav_Nvec_vc1.1_XM_001639002.3

fraction genes in fg and expected value

protein phosphatase 1 binding GO:0008157
mitogen-activated protein kinase binding GO:0051019
transcription factor binding GO:0008134
actin binding GO:0003779
protein phosphatase regulator activity GO:0019888
cation channel activity GO:0005261
MAP kinase activity GO:0004707
kinesin binding GO:0019894
RNA polymerase II-specific DNA-binding t... GO:0061629
phospholipid binding GO:0005543
phosphatase regulator activity GO:0019208
lipid binding GO:0008289
DNA-binding transcription factor binding GO:0140297
nuclear estrogen receptor binding GO:0030331
potassium ion transmembrane transporter ... GO:0015079
protein kinase binding GO:0019901
metal ion transmembrane transporter acti... GO:0046873
histone deacetylase binding GO:0042826
transcription coactivator activity GO:0003713
type I transforming growth factor beta r... GO:0034713
lipoate synthase activity GO:0016992
histone deacetylase regulator activity GO:0035033
insulin-like growth factor-activated rec... GO:0005010
pre-mRNA 5'-splice site binding GO:0030627
glycogen binding GO:2001069
myosin II binding GO:0045159
transmembrane receptor protein phosphata... GO:0019198
polypeptide N-acetylgalactosaminy/transf... GO:0004653
insulin-like growth factor II binding GO:0031995
transmembrane receptor protein tyrosine ... GO:0005001

p=2.2E-04	n=4
p=6.2E-04	n=4
p=5.0E-03	n=12
p=1.4E-02	n=5
p=1.8E-02	n=3
p=1.8E-02	n=6
p=1.8E-02	n=2
p=2.2E-02	n=3
p=2.4E-02	n=5
p=2.5E-02	n=7
p=2.6E-02	n=3
p=2.8E-02	n=8
p=3.3E-02	n=5
p=3.6E-02	n=2
p=3.7E-02	n=3
p=3.8E-02	n=13
p=4.1E-02	n=6
p=4.3E-02	n=3
p=4.4E-02	n=6
p=4.5E-02	n=1
p=4.5E-02	n=1
p=4.5E-02	n=1
p=4.5E-02	n=1
p=4.5E-02	n=1
p=4.5E-02	n=1
p=4.5E-02	n=1
p=4.5E-02	n=1
p=4.5E-02	n=1
p=4.5E-02	n=1
p=4.5E-02	n=1

fg=0.06	bg=0.01
fg=0.06	bg=0.01
fg=0.17	bg=0.07
fg=0.07	bg=0.02
fg=0.04	bg=0.01
fg=0.08	bg=0.03
fg=0.03	bg=0.00
fg=0.04	bg=0.01
fg=0.07	bg=0.02
fg=0.10	bg=0.04
fg=0.04	bg=0.01
fg=0.11	bg=0.05
fg=0.07	bg=0.03
fg=0.03	bg=0.00
fg=0.04	bg=0.01
fg=0.18	bg=0.08
fg=0.08	bg=0.04
fg=0.04	bg=0.01
fg=0.08	bg=0.04
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00



GO:CC
Elav_Nvec_vc1.1_XM_001639002.3

fraction genes in fg and expected value

endolysosome membrane GO:0036020
cytoplasmic region GO:0099568
neuronal cell body GO:0043025
perikaryon GO:0043204
cell cortex GO:0005938
midbody GO:0030496
protein phosphatase type 1 complex GO:0000164
cortical actin cytoskeleton GO:0030864
cell body GO:0044297
cell periphery GO:0071944
cell junction GO:0030054
axon GO:0030424
plasma membrane GO:0005886
plasma membrane region GO:0098590
dendrite membrane GO:0032590
Cajal body GO:0015030
cortical cytoskeleton GO:0030863
synapse GO:0045202
dendrite GO:0030425
dendritic tree GO:0097447
membrane GO:0016020
apicolateral plasma membrane GO:0016327
asymmetric synapse GO:0032279
katanin complex GO:0008352
integrin alpha9-beta1 complex GO:0034679
keratin filament GO:0045095
spectrosome GO:0045170
integral component of lysosomal membrane GO:1905103
core-binding factor complex GO:0016513
ciliary transition fiber GO:0097539

p=6.1E-03	n=2
p=9.8E-03	n=10
p=1.1E-02	n=12
p=1.4E-02	n=4
p=1.8E-02	n=8
p=1.9E-02	n=4
p=1.9E-02	n=2
p=1.9E-02	n=3
p=2.0E-02	n=12
p=2.1E-02	n=33
p=2.4E-02	n=18
p=2.4E-02	n=12
p=2.5E-02	n=31
p=2.6E-02	n=14
p=2.8E-02	n=2
p=2.8E-02	n=2
p=2.8E-02	n=3
p=2.9E-02	n=14
p=3.2E-02	n=11
p=3.2E-02	n=11
p=3.3E-02	n=48
p=3.8E-02	n=2
p=4.4E-02	n=5
p=4.6E-02	n=1
p=4.6E-02	n=1
p=4.6E-02	n=1
p=4.6E-02	n=1
p=4.6E-02	n=1
p=4.6E-02	n=1
p=4.6E-02	n=1

fg=0.02	bg=0.00
fg=0.12	bg=0.05
fg=0.14	bg=0.07
fg=0.05	bg=0.01
fg=0.10	bg=0.04
fg=0.05	bg=0.01
fg=0.02	bg=0.00
fg=0.04	bg=0.01
fg=0.14	bg=0.08
fg=0.40	bg=0.29
fg=0.22	bg=0.13
fg=0.14	bg=0.08
fg=0.37	bg=0.27
fg=0.17	bg=0.10
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.04	bg=0.01
fg=0.17	bg=0.10
fg=0.13	bg=0.07
fg=0.13	bg=0.07
fg=0.58	bg=0.46
fg=0.02	bg=0.00
fg=0.06	bg=0.02
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00

