

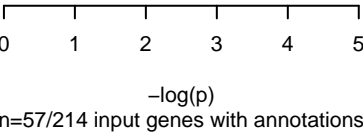
GO:BP
Elav_Nvec_vc1.1_XM_001636163.3

fraction genes in fg and expected value

response to mechanical stimulus	GO:0009612
detection of endogenous stimulus	GO:0009726
cellular response to external stimulus	GO:0071496
response to hydrostatic pressure	GO:0051599
positive regulation of cholesterol trans...	GO:0032376
pallium development	GO:0021543
positive regulation of protein serine/th...	GO:0071902
learning	GO:0007612
regulation of actin filament polymerizat...	GO:0030833
response to inorganic substance	GO:0010035
negative regulation of transport	GO:0051051
response to anesthetic	GO:0072347
presynaptic active zone organization	GO:1990709
metanephric ascending thin limb developm...	GO:0072218
metanephric distal tubule development	GO:0072235
positive regulation of cholesterol metab...	GO:0090205
foam cell differentiation	GO:0090077
central nervous system development	GO:0007417
cell morphogenesis involved in neuron di...	GO:0048667
alpha-amino acid biosynthetic process	GO:1901607
cholesterol homeostasis	GO:0042632
regulation of multicellular organismal d...	GO:2000026
detection of external stimulus	GO:0009581
positive regulation of cellular componen...	GO:0051130
negative regulation of cytosolic calcium...	GO:0051481
negative regulation of developmental pro...	GO:0051093
neuron projection morphogenesis	GO:0048812
negative regulation of hydrogen peroxide...	GO:1903206
positive regulation of necrotic cell dea...	GO:0010940
intracellular cholesterol transport	GO:0032367

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p=9.7E-04	n=2
p=1.4E-03	n=8
p=2.9E-03	n=2
p=2.9E-03	n=2
p=2.9E-03	n=6
p=3.2E-03	n=6
p=4.0E-03	n=6
p=4.2E-03	n=4
p=4.3E-03	n=13
p=4.9E-03	n=8
p=5.0E-03	n=4
p=5.6E-03	n=2
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p=5.6E-03	n=2
p=5.6E-03	n=2
p=6.2E-03	n=16
p=6.5E-03	n=12
p=6.7E-03	n=3
p=6.7E-03	n=3
p=7.4E-03	n=19
p=8.1E-03	n=5
p=8.3E-03	n=14
p=8.4E-03	n=3
p=8.7E-03	n=11
p=8.9E-03	n=12
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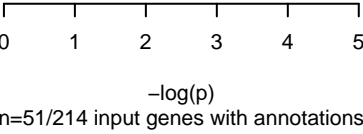
GO:MF
Elav_Nvec_vc1.1_XM_001636163.3

fraction genes in fg and expected value

signaling receptor complex adaptor activ...	GO:0030159
phospholipid binding	GO:0005543
cytoskeletal protein binding	GO:0008092
clathrin binding	GO:0030276
oxidoreductase activity, acting on the C...	GO:0016646
calcium ion binding	GO:0005509
transaminase activity	GO:0008483
JUN kinase binding	GO:0008432
BH domain binding	GO:0051400
AP-2 adaptor complex binding	GO:0035612
transmembrane transporter binding	GO:0044325
cholesterol binding	GO:0015485
mitogen-activated protein kinase kinase ...	GO:0031434
outward rectifier potassium channel acti...	GO:0015271
sterol binding	GO:0032934
actinin binding	GO:0042805
steroid binding	GO:0005496
alpha-actinin binding	GO:0051393
protein domain specific binding	GO:0019904
ornithine-oxo-acid transaminase activity	GO:0004587
mitogen-activated protein kinase p38 bin...	GO:0048273
rRNA primary transcript binding	GO:0042134
HLH domain binding	GO:0043398
fibroblast growth factor receptor bindin...	GO:0005104
muscle alpha-actinin binding	GO:0051371
ABC-type sterol transporter activity	GO:0034041
L-tyrosine aminotransferase activity	GO:0070547
L-tyrosine:2-oxoglutarate aminotransfera...	GO:0004838
BH4 domain binding	GO:0051435
pyrroline-5-carboxylate reductase activi...	GO:0004735

p=9.9E-04	n=3
p=4.1E-03	n=7
p=5.5E-03	n=10
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p=5.8E-03	n=2
p=7.0E-03	n=5
p=9.5E-03	n=2
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p=9.5E-03	n=2
p=1.1E-02	n=3
p=1.4E-02	n=2
p=1.4E-02	n=2
p=1.9E-02	n=2
p=1.9E-02	n=2
p=2.5E-02	n=2
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p=2.5E-02	n=2
p=3.1E-02	n=11
p=3.2E-02	n=1
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GO:CC
Elav_Nvec_vc1.1_XM_001636163.3

fraction genes in fg and expected value

neuromuscular junction	GO:0031594
postsynaptic membrane	GO:0045211
dendritic spine membrane	GO:0032591
growth cone lamellipodium	GO:1990761
side of membrane	GO:0098552
presynaptic periaxial zone	GO:0036062
axon	GO:0030424
I band	GO:0031674
neuronal cell body membrane	GO:0032809
neuron to neuron synapse	GO:0098984
cytoplasmic vesicle membrane	GO:0030659
main axon	GO:0044304
vesicle membrane	GO:0012506
cytoplasmic side of membrane	GO:0098562
acrosomal vesicle	GO:0001669
presynaptic active zone	GO:0048786
polytene chromosome puff	GO:0005703
exocytic vesicle membrane	GO:0099501
presynaptic membrane	GO:0042734
fusome	GO:0045169
cell leading edge	GO:0031252
stress fiber	GO:0001725
contractile actin filament bundle	GO:0097517
actin filament bundle	GO:0032432
recycling endosome	GO:0055037
cell periphery	GO:0071944
spectrosome	GO:0045170
spectrin	GO:0008091
interphase microtubule organizing center	GO:0031021
AP-4 adaptor complex	GO:0030124

p=3.5E-04	n=6
p=1.7E-03	n=5
p=2.7E-03	n=2
p=2.7E-03	n=2
p=3.2E-03	n=7
p=5.2E-03	n=2
p=5.5E-03	n=12
p=6.9E-03	n=4
p=7.6E-03	n=3
p=9.5E-03	n=5
p=1.1E-02	n=10
p=1.1E-02	n=3
p=1.2E-02	n=10
p=1.3E-02	n=5
p=1.3E-02	n=2
p=1.6E-02	n=3
p=1.7E-02	n=2
p=2.1E-02	n=3
p=2.2E-02	n=5
p=2.3E-02	n=2
p=2.7E-02	n=8
p=2.9E-02	n=2
p=2.9E-02	n=2
p=2.9E-02	n=2
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