

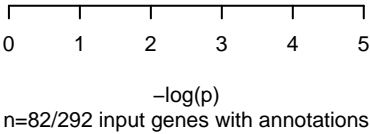
GO:BP
Elav_Nvec_vc1.1_XM_032372264.2

fraction genes in fg and expected value

neural retina development	GO:0003407
cardiac conduction	GO:0061337
phosphatidylglycerol acyl-chain remodeli...	GO:0036148
positive regulation of defense response	GO:0031349
renal water homeostasis	GO:0003091
cellular response to parathyroid hormone...	GO:0071374
cellular response to glucagon stimulus	GO:0071377
learning or memory	GO:0007611
hippocampus development	GO:0021766
sensory perception of chemical stimulus	GO:0007606
response to retinoic acid	GO:0032526
nematode larval development	GO:0002119
positive regulation of lipid transport	GO:0032370
retina morphogenesis in camera-type eye	GO:0060042
cellular cation homeostasis	GO:0030003
neuron migration	GO:0001764
positive regulation of cell cycle proces...	GO:0090068
axon development	GO:0061564
regulation of cell cycle G1/S phase tran...	GO:1902806
cell fate determination	GO:0001709
regulation of mitotic cell cycle phase t...	GO:1901990
cellular response to epinephrine stimulu...	GO:0071872
positive regulation of peroxisome prolifer...	GO:0035360
negative regulation of endothelial cell ...	GO:0001937
cardiac ventricle formation	GO:0003211
negative regulation of appetite	GO:0032099
activation of protein kinase A activity	GO:0034199
regulation of protein binding	GO:0043393
muscle system process	GO:0003012
feeding behavior	GO:0007631

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p=2.5E-03	n=6
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p=2.7E-03	n=3
p=2.7E-03	n=3
p=3.4E-03	n=11
p=3.6E-03	n=5
p=3.6E-03	n=5
p=3.6E-03	n=5
p=3.8E-03	n=9
p=4.2E-03	n=3
p=4.2E-03	n=3
p=4.3E-03	n=11
p=4.6E-03	n=6
p=4.9E-03	n=7
p=5.1E-03	n=13
p=5.2E-03	n=5
p=5.2E-03	n=5
p=5.7E-03	n=8
p=5.9E-03	n=2
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p=7.0E-03	n=6

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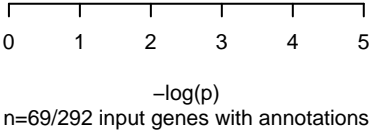
GO:MF
Elav_Nvec_vc1.1_XM_032372264.2

fraction genes in fg and expected value

ATPase-coupled ion transmembrane transpo...	GO:0042625
protein kinase A regulatory subunit bind...	GO:0034237
protein domain specific binding	GO:0019904
P-type calcium transporter activity	GO:0005388
tumor necrosis factor receptor binding	GO:0005164
WW domain binding	GO:0050699
voltage-gated potassium channel activity	GO:0005249
acetylcholine receptor binding	GO:0033130
lipid transporter activity	GO:0005319
signaling receptor binding	GO:0005102
phospholipid transporter activity	GO:0005548
signaling adaptor activity	GO:0035591
ephrin receptor binding	GO:0046875
protein phosphatase 2B binding	GO:0030346
leak channel activity	GO:0022840
potassium ion leak channel activity	GO:0022841
narrow pore channel activity	GO:0022842
Wnt-protein binding	GO:0017147
lipid transfer activity	GO:0120013
mRNA binding	GO:0003729
carbohydrate derivative binding	GO:0097367
ubiquitin protein ligase binding	GO:0031625
SMAD binding	GO:0046332
lipoprotein particle receptor binding	GO:0070325
G-protein alpha-subunit binding	GO:0001965
peptidase activator activity	GO:0016504
HMG box domain binding	GO:0071837
beta-tubulin binding	GO:0048487
low-density lipoprotein particle recepto...	GO:0050750
ubiquitin-like protein ligase binding	GO:0044389

p=1.7E-03	n=4
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p=2.5E-03	n=16
p=5.4E-03	n=2
p=5.4E-03	n=2
p=5.4E-03	n=2
p=7.5E-03	n=3
p=1.1E-02	n=2
p=1.3E-02	n=4
p=1.5E-02	n=15
p=1.6E-02	n=3
p=1.6E-02	n=3
p=1.7E-02	n=2
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p=1.7E-02	n=2
p=1.7E-02	n=2
p=1.7E-02	n=6
p=1.8E-02	n=11
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p=2.5E-02	n=2
p=2.9E-02	n=7

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GO:CC
Elav_Nvec_vc1.1_XM_032372264.2

fraction genes in fg and expected value

dendritic spine	GO:0043197
growth cone filopodium	GO:1990812
plasma membrane	GO:0005886
secretory granule membrane	GO:0030667
nucleotide-activated protein kinase comp...	GO:0031588
cAMP-dependent protein kinase complex	GO:0005952
growth cone lamellipodium	GO:1990761
stress fiber	GO:0001725
plasma membrane region	GO:0098590
germinal vesicle	GO:0042585
plasma membrane raft	GO:0044853
intrinsic component of membrane	GO:0031224
neuromuscular junction	GO:0031594
integral component of plasma membrane	GO:0005887
integral component of membrane	GO:0016021
female germ cell nucleus	GO:0001674
intrinsic component of plasma membrane	GO:0031226
acrosomal vesicle	GO:0001669
centriolar satellite	GO:0034451
membrane raft	GO:0045121
membrane microdomain	GO:0098857
Golgi apparatus	GO:0005794
main axon	GO:0044304
intermediate filament cytoskeleton	GO:0045111
precatalytic spliceosome	GO:0071011
postsynaptic membrane	GO:0045211
dendritic shaft	GO:0043198
ACF complex	GO:0016590
cell trailing edge	GO:0031254
amyloid-beta complex	GO:0106003

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p=1.9E-03	n=2
p=3.5E-03	n=37
p=5.5E-03	n=6
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p=5.6E-03	n=2
p=5.6E-03	n=2
p=5.8E-03	n=3
p=8.3E-03	n=15
p=1.1E-02	n=2
p=1.2E-02	n=4
p=1.3E-02	n=22
p=1.3E-02	n=5
p=1.4E-02	n=12
p=1.5E-02	n=21
p=1.8E-02	n=2
p=2.4E-02	n=12
p=2.6E-02	n=2
p=2.6E-02	n=2
p=2.7E-02	n=6
p=2.7E-02	n=6
p=2.9E-02	n=17
p=3.1E-02	n=3
p=3.5E-02	n=2
p=3.5E-02	n=2
p=4.1E-02	n=4
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