

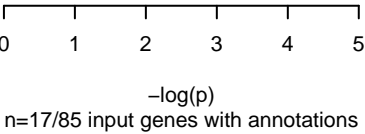
GO:BP
Elav_Nvec_vc1.1_XM_032367573.2

fraction genes in fg and expected value

lysine transport	GO:0015819
calcium ion import across plasma membran...	GO:0098703
cell junction maintenance	GO:0034331
positive regulation of cAMP-dependent pr...	GO:2000481
regulation of adenylate cyclase-activati...	GO:0106070
actin cortical patch localization	GO:0051666
late endosome to vacuole transport	GO:0045324
adenylate cyclase-activating adrenergic ...	GO:0071880
regulation of sodium ion transport	GO:0002028
cerebellar Purkinje cell differentiation	GO:0021702
embryonic morphogenesis	GO:0048598
modulation of chemical synaptic transmis...	GO:0050804
biomineral tissue development	GO:0031214
regulation of calcineurin-NFAT signaling...	GO:0070884
negative regulation of microtubule depol...	GO:0007026
negative regulation of wound healing	GO:0061045
positive regulation of embryonic develop...	GO:0040019
nephron tubule epithelial cell different...	GO:0072160
regulation of the force of heart contrac...	GO:0002026
positive regulation of cellular componen...	GO:0051130
regulation of cAMP-mediated signaling	GO:0043949
glomerulus development	GO:0032835
positive regulation of synaptic transmis...	GO:0050806
gastrulation	GO:0007369
cell morphogenesis involved in neuron di...	GO:0048667
regulation of transcription by RNA polym...	GO:0006357
positive regulation of organelle organiz...	GO:0010638
transcription by RNA polymerase II	GO:0006366
neuromuscular process	GO:0050905
body fluid secretion	GO:0007589

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p=4.8E-03	n=2
p=6.3E-03	n=6
p=6.8E-03	n=5
p=8.1E-03	n=3
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p=1.7E-02	n=6
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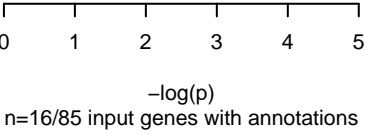
GO:MF
Elav_Nvec_vc1.1_XM_032367573.2

fraction genes in fg and expected value

actin binding	GO:0003779
microtubule binding	GO:0008017
protein phosphatase binding	GO:0019903
glutamate receptor binding	GO:0035254
actin filament binding	GO:0051015
phosphatase binding	GO:0019902
organic cyclic compound binding	GO:0097159
PDZ domain binding	GO:0030165
calcium-dependent ATPase activity	GO:0030899
nitric-oxide synthase binding	GO:0050998
dopamine binding	GO:0035240
poly(U) RNA binding	GO:0008266
ankyrin binding	GO:0030506
dystroglycan binding	GO:0002162
intracellular sodium activated potassium...	GO:0005228
nitric-oxide synthase regulator activity	GO:0030235
protein phosphatase 2A binding	GO:0051721
nitric-oxide synthase inhibitor activity	GO:0036487
poly-pyrimidine tract binding	GO:0008187
beta1-adrenergic receptor activity	GO:0004940
beta2-adrenergic receptor activity	GO:0004941
bradykinin receptor binding	GO:0031711
B2 bradykinin receptor binding	GO:0031713
racemase and epimerase activity	GO:0016854
racemase and epimerase activity, acting ...	GO:0016857
mRNA 3'-UTR AU-rich region binding	GO:0035925
kinetochore binding	GO:0043515
chondroitin-glucuronate 5-epimerase acti...	GO:0047757
beta-adrenergic receptor activity	GO:0004939
double-stranded RNA binding	GO:0003725

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GO:CC
Elav_Nvec_vc1.1_XM_032367573.2

fraction genes in fg and expected value

cell tip	GO:0051286
fungus-type vacuole membrane	GO:0000329
cortical cytoskeleton	GO:0030863
cell division site	GO:0032153
sarcolemma	GO:0042383
caveola	GO:0005901
ruffle	GO:0001726
cytoplasmic region	GO:0099568
axon	GO:0030424
microtubule plus-end	GO:0035371
dendritic spine membrane	GO:0032591
cortical microtubule plus-end	GO:1903754
Cajal body	GO:0015030
cytoplasmic microtubule plus-end	GO:1904511
postsynaptic specialization membrane	GO:0099634
polysomal ribosome	GO:0042788
centrosomal corona	GO:0031592
cortical microtubule	GO:0055028
kinetochore	GO:0000776
spindle microtubule	GO:0005876
cortical microtubule cytoskeleton	GO:0030981
spectrin	GO:0008091
kinetochore microtubule	GO:0005828
NELF complex	GO:0032021
spectrosome	GO:0045170
sperm principal piece	GO:0097228
postsynaptic density membrane	GO:0098839
supramolecular complex	GO:0099080
plasma membrane raft	GO:0044853
cytoplasmic side of plasma membrane	GO:0009898

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p=4.3E-02	n=5
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