

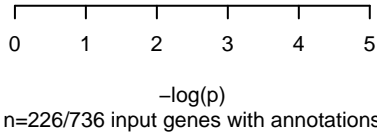
GO:BP
Elav_Nvec_vc1.1_XM_001634132.3

fraction genes in fg and expected value

tyrosine catabolic process	GO:0006572
response to amino acid	GO:0043200
NADH regeneration	GO:0006735
positive regulation of neurotransmitter ...	GO:0001956
blood vessel endothelial cell migration	GO:0043534
establishment of vesicle localization	GO:0051650
primitive hemopoiesis	GO:0060215
L-phenylalanine catabolic process	GO:0006559
sphingomyelin metabolic process	GO:0006684
motor neuron axon guidance	GO:0008045
positive regulation of hydrolase activit...	GO:0051345
triglyceride biosynthetic process	GO:0019432
regulation of protein secretion	GO:0050708
epithelial structure maintenance	GO:0010669
head involution	GO:0008258
negative regulation of angiogenesis	GO:0016525
heart development	GO:0007507
vulval development	GO:0040025
macropinocytosis	GO:0044351
negative regulation of Rac protein signa...	GO:0035021
negative regulation of Rho protein signa...	GO:0035024
positive regulation of cAMP-mediated sig...	GO:0043950
response to acidic pH	GO:0010447
cellular response to decreased oxygen le...	GO:0036294
regulation of catabolic process	GO:0009894
glucose catabolic process	GO:0006007
positive regulation of cytolysis	GO:0045919
negative regulation of sequestering of t...	GO:0010891
nephric duct formation	GO:0072179
plasma membrane raft assembly	GO:0044854

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p=2.2E-03	n=3
p=2.5E-03	n=6
p=2.8E-03	n=22
p=2.9E-03	n=5
p=3.3E-03	n=16
p=4.3E-03	n=4
p=4.3E-03	n=4
p=4.3E-03	n=4
p=4.4E-03	n=21
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p=5.3E-03	n=10
p=6.2E-03	n=35
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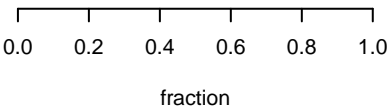
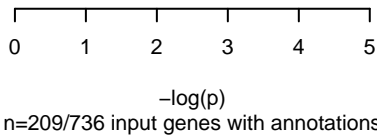
GO:MF
Elav_Nvec_vc1.1_XM_001634132.3

fraction genes in fg and expected value

carboxylic acid binding	GO:0031406
amino acid binding	GO:0016597
signaling receptor binding	GO:0005102
GTPase regulator activity	GO:0030695
nucleoside diphosphate kinase activity	GO:0004550
epinephrine binding	GO:0051379
xenobiotic transmembrane transporter act...	GO:0042910
ATP-dependent protein binding	GO:0043008
calcium channel inhibitor activity	GO:0019855
voltage-gated potassium channel activity	GO:0005249
GTPase activator activity	GO:0005096
disordered domain specific binding	GO:0097718
phospholipid binding	GO:0005543
oxidoreductase activity, acting on singl...	GO:0016702
oxidoreductase activity, acting on the C...	GO:0016899
MHC protein binding	GO:0042287
phosphoenolpyruvate carboxykinase activi...	GO:0004611
phosphoenolpyruvate carboxykinase (GTP) ...	GO:0004613
inosine kinase activity	GO:0008906
outward rectifier potassium channel acti...	GO:0015271
quaternary ammonium group binding	GO:0050997
protein-disulfide reductase (NAD(P)) act...	GO:0047134
oxidoreductase activity, acting on singl...	GO:0016701
receptor-receptor interaction	GO:0090722
phosphatidylethanolamine binding	GO:0008429
FAD binding	GO:0071949
lactate dehydrogenase activity	GO:0004457
DNA binding domain binding	GO:0050692
WW domain binding	GO:0050699
mRNA methyltransferase activity	GO:0008174

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p=1.7E-02	n=4
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p=2.2E-02	n=2
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GO:CC
Elav_Nvec_vc1.1_XM_001634132.3

fraction genes in fg and expected value

sperm fibrous sheath	GO:0035686
cell leading edge	GO:0031252
voltage-gated potassium channel complex	GO:0008076
Gtr1-Gtr2 GTPase complex	GO:1990131
collagen and cuticulin-based cuticle ext...	GO:0060102
axon cytoplasm	GO:1904115
caveola	GO:0005901
presynapse	GO:0098793
nuclear membrane	GO:0031965
integral component of endoplasmic reticu...	GO:0030176
presynaptic active zone membrane	GO:0048787
synaptic vesicle	GO:0008021
intrinsic component of endoplasmic retic...	GO:0031227
caspase complex	GO:0008303
EARP complex	GO:1990745
oligosaccharyltransferase complex	GO:0008250
beta-catenin-TCF complex	GO:1990907
GPI-anchor transamidase complex	GO:0042765
GARP complex	GO:0000938
vesicle tethering complex	GO:0099023
cytoplasmic dynein complex	GO:0005868
lamellipodium	GO:0030027
integral component of presynaptic membra...	GO:0099056
integral component of synaptic membrane	GO:0099699
intrinsic component of synaptic membrane	GO:0099240
intrinsic component of presynaptic membr...	GO:0098889
plasma membrane raft	GO:0044853
exocytic vesicle	GO:0070382
cell periphery	GO:0071944
subsynaptic reticulum	GO:0071212

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p=6.1E-03	n=16
p=7.1E-03	n=4
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p=7.2E-03	n=2
p=1.0E-02	n=3
p=1.1E-02	n=6
p=1.3E-02	n=18
p=1.4E-02	n=11
p=1.4E-02	n=10
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