

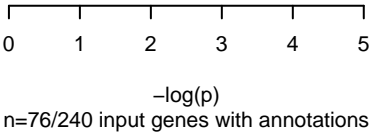
GO:BP
Elav_Nvec_vc1.1_XM_032373497.2

fraction genes in fg and expected value

Golgi ribbon formation	GO:0090161
maternal process involved in female preg...	GO:0060135
3'-UTR-mediated mRNA destabilization	GO:0061158
purine nucleobase biosynthetic process	GO:0009113
'de novo' IMP biosynthetic process	GO:0006189
regulation of miRNA metabolic process	GO:2000628
relaxation of cardiac muscle	GO:0055119
negative regulation of neurogenesis	GO:0050768
cell migration in hindbrain	GO:0021535
positive regulation of autophagy	GO:0010508
modulation by host of symbiont process	GO:0051851
sperm axoneme assembly	GO:0007288
sperm flagellum assembly	GO:0120316
peptidyl-lysine dimethylation	GO:0018027
positive regulation of macroautophagy	GO:0016239
biological process involved in interacti...	GO:0051702
positive regulation of response to exter...	GO:0032103
negative regulation of T cell proliferat...	GO:0042130
intrinsic apoptotic signaling pathway in...	GO:0042771
regulation of cardiac muscle cell apopto...	GO:0010665
negative regulation of neuron differenti...	GO:0045665
in utero embryonic development	GO:0001701
phosphatidylinositol dephosphorylation	GO:0046856
negative regulation of mononuclear cell ...	GO:0032945
attachment of spindle microtubules to ki...	GO:0008608
modulation by host of symbiont transcrip...	GO:0052472
negative regulation of leukocyte prolife...	GO:0070664
negative regulation of lymphocyte prolif...	GO:0050672
modulation by host of viral transcriptio...	GO:0043921
negative regulation by host of viral tra...	GO:0043922

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p=2.2E-03	n=3
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p=4.5E-03	n=2
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p=4.5E-03	n=2
p=7.4E-03	n=2
p=7.9E-03	n=7
p=1.1E-02	n=2
p=1.3E-02	n=4
p=1.3E-02	n=3
p=1.5E-02	n=2
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p=1.5E-02	n=2
p=1.5E-02	n=3
p=1.5E-02	n=3
p=1.5E-02	n=6
p=2.0E-02	n=2
p=2.0E-02	n=2
p=2.0E-02	n=2
p=2.2E-02	n=5
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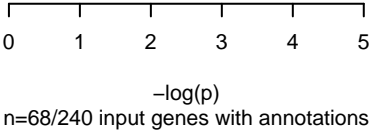
GO:MF
Elav_Nvec_vc1.1_XM_032373497.2

fraction genes in fg and expected value

RNA stem-loop binding	GO:0035613
phosphatidylinositol-4,5-bisphosphate ph...	GO:0106019
cyclosporin A binding	GO:0016018
symporter activity	GO:0015293
ubiquitin-like protein ligase activity	GO:0061659
ubiquitin protein ligase activity	GO:0061630
DNA-binding transcription factor activit...	GO:0000981
mRNA binding	GO:0003729
amidophosphoribosyltransferase activity	GO:0004044
phosphoribosylaminoimidazole carboxylase...	GO:0004638
phosphoribosylaminoimidazolesuccinocarbo...	GO:0004639
semaphorin receptor binding	GO:0030215
methotrexate transmembrane transporter a...	GO:0015350
MAP kinase kinase kinase kinase activity	GO:0008349
protein-L-isoaspartate (D-aspartate) O-m...	GO:0004719
carboxyl-O-methyltransferase activity	GO:0010340
beta-1,3-galactosyl-O-glycosyl-glycoprot...	GO:0047223
hedgehog receptor activity	GO:0008158
protein carboxyl O-methyltransferase act...	GO:0051998
phosphatidylinositol-4,5-bisphosphate 4-...	GO:0034597
dolichyl-phosphate beta-glucosyltransfer...	GO:0004581
cis-trans isomerase activity	GO:0016859
peptidyl-prolyl cis-trans isomerase acti...	GO:0003755
calmodulin binding	GO:0005516
amide transmembrane transporter activity	GO:0042887
DNA-binding transcription factor activit...	GO:0003700
SNAP receptor activity	GO:0005484
organic acid transmembrane transporter a...	GO:0005342
carboxylic acid transmembrane transporte...	GO:0046943
xenobiotic transmembrane transporter act...	GO:0042910

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p=1.1E-02	n=2
p=1.4E-02	n=3
p=1.6E-02	n=6
p=1.6E-02	n=6
p=1.6E-02	n=9
p=1.9E-02	n=6
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GO:CC
Elav_Nvec_vc1.1_XM_032373497.2

fraction genes in fg and expected value

trans-Golgi network	GO:0005802
Prp19 complex	GO:0000974
cytoplasmic ubiquitin ligase complex	GO:0000153
U2-type catalytic step 2 spliceosome	GO:0071007
Golgi-associated vesicle	GO:0005798
catalytic step 2 spliceosome	GO:0071013
polytene chromosome band	GO:0005704
DNA ligase III-XRCC1 complex	GO:0070421
sarcoplasmic reticulum lumen	GO:0033018
condensed nuclear chromosome	GO:0000794
phagocytic vesicle	GO:0045335
cytoplasmic stress granule	GO:0010494
Golgi trans cisterna	GO:0000138
mediator complex	GO:0016592
integral component of Golgi membrane	GO:0030173
6-phosphofructo-2-kinase/fructose-2,6-bi...	GO:0043540
growth cone filopodium	GO:1990812
SMAD protein complex	GO:0071141
axonemal central apparatus	GO:1990716
nuclear SCF ubiquitin ligase complex	GO:0043224
Cul7-RING ubiquitin ligase complex	GO:0031467
post-mRNA release spliceosomal complex	GO:0071014
t-UTP complex	GO:0034455
trans-Golgi network membrane	GO:0032588
fibrillar center	GO:0001650
COPII-coated ER to Golgi transport vesic...	GO:0030134
intrinsic component of Golgi membrane	GO:0031228
supramolecular complex	GO:0099080
coated vesicle	GO:0030135
brush border	GO:0005903

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p=1.4E-02	n=2
p=1.9E-02	n=2
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p=2.6E-02	n=3
p=2.7E-02	n=1
p=2.7E-02	n=1
p=2.7E-02	n=1
p=2.9E-02	n=3
p=3.3E-02	n=3
p=4.1E-02	n=2
p=4.1E-02	n=2
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p=4.8E-02	n=2
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