

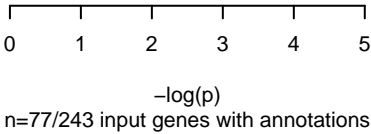
GO:BP
Elav_Nvec_vc1.1_XM_032378928.2

fraction genes in fg and expected value

negative regulation of response to gamma...	GO:2001229
anterior neuropore closure	GO:0021506
specification of segmental identity, abd...	GO:0007385
mitochondrial translation	GO:0032543
long-chain fatty acid catabolic process	GO:0042758
positive regulation of membrane tubulati...	GO:1903527
embryonic body morphogenesis	GO:0010172
monovalent inorganic anion homeostasis	GO:0055083
in utero embryonic development	GO:0001701
cell fate specification	GO:0001708
anatomical structure maturation	GO:0071695
regulation of stem cell population maint...	GO:2000036
basement membrane organization	GO:0071711
pyrimidine ribonucleotide biosynthetic p...	GO:0009220
forebrain neuron fate commitment	GO:0021877
response to chemical	GO:0042221
molting cycle process	GO:0022404
response to peptide	GO:1901652
cAMP metabolic process	GO:0046058
nucleobase-containing small molecule int...	GO:0015949
blastocyst formation	GO:0001825
Notch receptor processing	GO:0007220
branch elongation of an epithelium	GO:0060602
regulation of extracellular matrix disas...	GO:0010715
pyrimidine ribonucleoside biosynthetic p...	GO:0046132
pyrimidine nucleoside biosynthetic proce...	GO:0046134
syncytial blastoderm mitotic cell cycle	GO:0035186
divalent inorganic anion homeostasis	GO:0072505
trivalent inorganic anion homeostasis	GO:0072506
lens morphogenesis in camera-type eye	GO:0002089

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p=2.5E-03	n=4
p=5.2E-03	n=3
p=6.5E-03	n=7
p=6.5E-03	n=6
p=7.2E-03	n=8
p=7.6E-03	n=2
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p=7.6E-03	n=2
p=7.9E-03	n=34
p=8.5E-03	n=4
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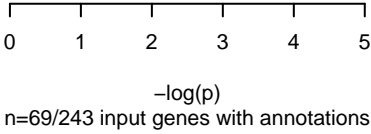
GO:MF
Elav_Nvec_vc1.1_XM_032378928.2

fraction genes in fg and expected value

ATPase-coupled cation transmembrane tran...	GO:0019829
ATPase-coupled ion transmembrane transpo...	GO:0042625
cysteine-type endopeptidase regulator ac...	GO:0043028
rRNA binding	GO:0019843
G-protein alpha-subunit binding	GO:0001965
structural constituent of ribosome	GO:0003735
poly(U) RNA binding	GO:0008266
nicotinate-nucleotide adenyllyltransferas...	GO:0004515
glutathione-disulfide reductase (NADPH) ...	GO:0004362
tRNA-intron endonuclease activity	GO:0000213
TFIIIF-class transcription factor complex...	GO:0001096
beta-1 adrenergic receptor binding	GO:0031697
carbohydrate:cation symporter activity	GO:0005402
carbohydrate:proton symporter activity	GO:0005351
glucose transmembrane transporter activi...	GO:0005355
5'-deoxyribose-5-phosphate lyase activit...	GO:0051575
endoribonuclease activity, producing 3'----	GO:0016892
proton-transporting ATP synthase activit...	GO:0046933
CTP synthase activity	GO:0003883
P-type calcium transporter activity invo...	GO:0086039
dystroglycan binding	GO:0002162
nicotinamide-nucleotide adenyllyltransfer...	GO:0000309
selenodiglutathione-disulfide reductase ...	GO:0098622
polypeptide N-acetylgalactosaminyltransf...	GO:0004653
lutropin-choriogonadotropic hormone rece...	GO:0031775
D-glucose transmembrane transporter acti...	GO:0055056
phosphomannomutase activity	GO:0004615
glutathione disulfide oxidoreductase act...	GO:0015038
MHC class I protein binding	GO:0042288
orotidine-5'-phosphate decarboxylase act...	GO:0004590

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GO:CC
Elav_Nvec_vc1.1_XM_032378928.2

fraction genes in fg and expected value

intercalary heterochromatin	GO:0005725
PRC1 complex	GO:0035102
mitochondrial large ribosomal subunit	GO:0005762
organelle subcompartment	GO:0031984
cell periphery	GO:0071944
excitatory synapse	GO:0060076
Golgi apparatus	GO:0005794
transcription regulator complex	GO:0005667
coated vesicle	GO:0030135
Golgi apparatus subcompartment	GO:0098791
calcium channel complex	GO:0034704
Golgi cisterna membrane	GO:0032580
COPI-coated vesicle	GO:0030137
endoplasmic reticulum-Golgi intermediate...	GO:0005793
Golgi-associated vesicle	GO:0005798
chromaffin granule	GO:0042583
chromaffin granule membrane	GO:0042584
mitochondrial proton-transporting ATP sy...	GO:0005754
cortical microtubule	GO:0055028
centrosomal corona	GO:0031592
cation-transporting ATPase complex	GO:0090533
cortical microtubule cytoskeleton	GO:0030981
calcium ion-transporting ATPase complex	GO:0090534
cortical microtubule plus-end	GO:1903754
tRNA-intron endonuclease complex	GO:0000214
AP-3 adaptor complex	GO:0030123
luminal side of Golgi membrane	GO:0098547
platelet dense tubular network	GO:0031094
platelet dense tubular network membrane	GO:0031095
ribbon synapse	GO:0097470

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p=1.8E-02	n=15
p=1.9E-02	n=7
p=2.0E-02	n=5
p=2.3E-02	n=10
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