GO:BP
Elav_Nvec_vc1.1_XM_032385373.2

fraction genes in fg and expected value

ammonium transmembrane transport GO:0072488	p=6.7E−04 | n=4	fg=0.03 | bg=0.00
pH reduction GO:0045851	p=8.6E−04 | n=5	fg=0.03 | bg=0.01
vacuolar acidification GO:0007035	p=2.8E−03 | n=4	fg=0.03 | bg=0.00
endothelial cell morphogenesis GO:0001886	p=3.4E−03 | n=2	fg=0.01 | bg=0.00
positive regulation of Ras protein signa... GO:0046579	p=4.0E−03 | n=4	fg=0.03 | bg=0.00
multicellular organism growth GO:0035264	p=5.2E−03 | n=11	fg=0.07 | bg=0.03
secondary alcohol biosynthetic process GO:1902653	p=5.4E−03 | n=4	fg=0.03 | bg=0.00
regulation of anatomical structure size GO:0090066	p=5.5E−03 | n=19	fg=0.12 | bg=0.06
androgen receptor signaling pathway GO:0030521	p=7.3E−03 | n=4	fg=0.03 | bg=0.01
sterol biosynthetic process GO:0016126	p=7.3E−03 | n=4	fg=0.03 | bg=0.01
negative regulation of ion transmembrane... GO:0032413	p=7.3E−03 | n=4	fg=0.03 | bg=0.01
larval development GO:0002164	p=7.5E−03 | n=16	fg=0.10 | bg=0.05
T cell proliferation GO:0042098	p=7.7E−03 | n=5	fg=0.03 | bg=0.01
regulation of cardiac muscle contraction... GO:0010882	p=9.0E−03 | n=3	fg=0.02 | bg=0.00
sarcoplasmic reticulum calcium ion trans... GO:0070296	p=9.0E−03 | n=3	fg=0.02 | bg=0.00
axon regeneration GO:0031103	p=9.4E−03 | n=5	fg=0.03 | bg=0.01
immunological synapse formation GO:0001771	p=9.9E−03 | n=2	fg=0.01 | bg=0.00
ribosomal large subunit export from nucl... GO:0000055	p=9.9E−03 | n=2	fg=0.01 | bg=0.00
negative gravitaxis GO:0048060	p=9.9E−03 | n=2	fg=0.01 | bg=0.00
cellular response to 2,3,7,8−tetrachloro... GO:1904613	p=9.9E−03 | n=2	fg=0.01 | bg=0.00
microvillus assembly GO:0030033	p=9.9E−03 | n=2	fg=0.01 | bg=0.00
diet induced thermogenesis GO:0002024	p=9.9E−03 | n=2	fg=0.01 | bg=0.00
retina vasculature morphogenesis in came... GO:0061299	p=9.9E−03 | n=2	fg=0.01 | bg=0.00
morphogenesis of an epithelium GO:0002009	p=1.0E−02 | n=24	fg=0.15 | bg=0.09
microtubule−based transport GO:0099111	p=1.1E−02 | n=8	fg=0.05 | bg=0.02
embryonic hemopoiesis GO:0035162	p=1.2E−02 | n=4	fg=0.03 | bg=0.01
pinocytosis GO:0006907	p=1.3E−02 | n=3	fg=0.02 | bg=0.00
cellular response to salt stress GO:0071472	p=1.3E−02 | n=3	fg=0.02 | bg=0.00
negative regulation of protein transport GO:0051224	p=1.3E−02 | n=7	fg=0.04 | bg=0.02
regulation of ATP−dependent activity GO:0043462	p=1.4E−02 | n=5	fg=0.03 | bg=0.01

```
0   1   2   3   4   5            0.0  0.2  0.4  0.6  0.8  1.0
        −log(p)                            fraction
n=159/537 input genes with annotations
```

GO:MF
Elav_Nvec_vc1.1_XM_032385373.2

fraction genes in fg and expected value

ammonium transmembrane transporter activ... GO:0008519	p=6.8E−04 | n=4	fg=0.03 | bg=0.00
protein domain specific binding GO:0019904	p=1.9E−03 | n=22	fg=0.16 | bg=0.08
eukaryotic initiation factor 4E binding GO:0008190	p=3.5E−03 | n=2	fg=0.01 | bg=0.00
D3 dopamine receptor binding GO:0031750	p=3.5E−03 | n=2	fg=0.01 | bg=0.00
D4 dopamine receptor binding GO:0031751	p=3.5E−03 | n=2	fg=0.01 | bg=0.00
peroxidase activity GO:0004601	p=3.5E−03 | n=3	fg=0.02 | bg=0.00
cyclin binding GO:0030332	p=5.9E−03 | n=3	fg=0.02 | bg=0.00
snRNA binding GO:0017069	p=9.1E−03 | n=3	fg=0.02 | bg=0.00
D2 dopamine receptor binding GO:0031749	p=1.0E−02 | n=2	fg=0.01 | bg=0.00
cation:chloride symporter activity GO:0015377	p=1.0E−02 | n=2	fg=0.01 | bg=0.00
potassium:chloride symporter activity GO:0015379	p=1.0E−02 | n=2	fg=0.01 | bg=0.00
anion:cation symporter activity GO:0015296	p=1.0E−02 | n=2	fg=0.01 | bg=0.00
S100 protein binding GO:0044548	p=1.0E−02 | n=2	fg=0.01 | bg=0.00
U2 snRNA binding GO:0030620	p=1.0E−02 | n=2	fg=0.01 | bg=0.00
signaling receptor binding GO:0005102	p=1.4E−02 | n=24	fg=0.17 | bg=0.10
cAMP binding GO:0030552	p=1.9E−02 | n=2	fg=0.01 | bg=0.00
protein kinase A catalytic subunit bindi... GO:0034236	p=1.9E−02 | n=2	fg=0.01 | bg=0.00
WW domain binding GO:0050699	p=1.9E−02 | n=2	fg=0.01 | bg=0.00
xylosyltransferase activity GO:0042285	p=1.9E−02 | n=2	fg=0.01 | bg=0.00
glutathione peroxidase activity GO:0004602	p=1.9E−02 | n=2	fg=0.01 | bg=0.00
UDP−xylosyltransferase activity GO:0035252	p=1.9E−02 | n=2	fg=0.01 | bg=0.00
phosphatidylinositol−4−phosphate binding GO:0070273	p=3.0E−02 | n=3	fg=0.02 | bg=0.01
pentosyltransferase activity GO:0016763	p=3.0E−02 | n=3	fg=0.02 | bg=0.01
cyclic nucleotide binding GO:0030551	p=3.1E−02 | n=2	fg=0.01 | bg=0.00
AP−2 adaptor complex binding GO:0035612	p=3.1E−02 | n=2	fg=0.01 | bg=0.00
phosphatidylinositol−5−phosphate binding GO:0010314	p=3.1E−02 | n=2	fg=0.01 | bg=0.00
phospholipid binding GO:0005543	p=3.2E−02 | n=10	fg=0.07 | bg=0.04
RNA polymerase II−specific DNA−binding t... GO:0061629	p=3.4E−02 | n=7	fg=0.05 | bg=0.02
nuclear androgen receptor binding GO:0050681	p=3.7E−02 | n=3	fg=0.02 | bg=0.01
inorganic anion transmembrane transporte... GO:0015103	p=4.2E−02 | n=5	fg=0.04 | bg=0.01

```
0   1   2   3   4   5            0.0  0.2  0.4  0.6  0.8  1.0
        −log(p)                            fraction
n=140/537 input genes with annotations
```

GO:CC
Elav_Nvec_vc1.1_XM_032385373.2

fraction genes in fg and expected value

brush border GO:0005903	p=6.1E−04 | n=8	fg=0.05 | bg=0.01
perinuclear region of cytoplasm GO:0048471	p=7.0E−04 | n=21	fg=0.14 | bg=0.06
DNA polymerase III complex GO:0009360	p=3.3E−03 | n=2	fg=0.01 | bg=0.00
ruffle GO:0001726	p=5.1E−03 | n=6	fg=0.04 | bg=0.01
stereocilium GO:0032420	p=6.6E−03 | n=4	fg=0.03 | bg=0.01
filopodium GO:0030175	p=6.9E−03 | n=5	fg=0.03 | bg=0.01
extrinsic component of plasma membrane GO:0019897	p=7.2E−03 | n=6	fg=0.04 | bg=0.01
muscle cell projection membrane GO:0036195	p=9.5E−03 | n=2	fg=0.01 | bg=0.00
extracellular vesicle GO:1903561	p=1.0E−02 | n=5	fg=0.03 | bg=0.01
extracellular membrane−bounded organelle GO:0065010	p=1.0E−02 | n=5	fg=0.03 | bg=0.01
extracellular organelle GO:0043230	p=1.0E−02 | n=5	fg=0.03 | bg=0.01
dendrite GO:0030425	p=1.1E−02 | n=17	fg=0.11 | bg=0.06
midbody GO:0030496	p=1.1E−02 | n=7	fg=0.05 | bg=0.02
dendritic tree GO:0097447	p=1.2E−02 | n=17	fg=0.11 | bg=0.06
vesicle GO:0031982	p=1.4E−02 | n=36	fg=0.23 | bg=0.16
intracellular vesicle GO:0097708	p=1.8E−02 | n=34	fg=0.22 | bg=0.15
cytoplasmic vesicle GO:0031410	p=1.8E−02 | n=34	fg=0.22 | bg=0.15
manchette GO:0002177	p=1.8E−02 | n=2	fg=0.01 | bg=0.00
basal part of cell GO:0045178	p=1.9E−02 | n=9	fg=0.06 | bg=0.03
somatodendritic compartment GO:0036477	p=2.1E−02 | n=21	fg=0.14 | bg=0.09
cytoplasmic side of membrane GO:0098562	p=2.4E−02 | n=8	fg=0.05 | bg=0.02
basolateral plasma membrane GO:0016323	p=2.4E−02 | n=8	fg=0.05 | bg=0.02
basal plasma membrane GO:0009925	p=2.4E−02 | n=8	fg=0.05 | bg=0.02
growth cone GO:0030426	p=2.5E−02 | n=7	fg=0.05 | bg=0.02
lysosomal lumen GO:0043202	p=2.5E−02 | n=4	fg=0.03 | bg=0.01
cell body GO:0044297	p=2.6E−02 | n=17	fg=0.11 | bg=0.07
distal axon GO:0150034	p=2.8E−02 | n=11	fg=0.07 | bg=0.04
microvillus GO:0005902	p=2.9E−02 | n=4	fg=0.03 | bg=0.01
extrinsic component of cytoplasmic side ... GO:0031234	p=2.9E−02 | n=4	fg=0.03 | bg=0.01
guanyl−nucleotide exchange factor comple... GO:0032045	p=2.9E−02 | n=2	fg=0.01 | bg=0.00

```
0   1   2   3   4   5            0.0  0.2  0.4  0.6  0.8  1.0
        −log(p)                            fraction
n=155/537 input genes with annotations
```