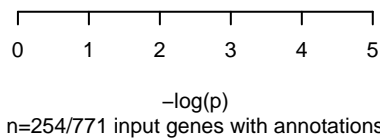


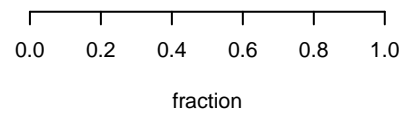
GO:BP  
Elav\_Nvec\_vc1.1\_XM\_001627907.3

fraction genes in fg and expected value

regulation of extrinsic apoptotic signal...	GO:2001239	p=4.8E-03	n=5
potassium ion transmembrane transport	GO:0071805	p=6.4E-03	n=8
cellular response to salt stress	GO:0071472	p=6.6E-03	n=4
head involution	GO:0008258	p=6.6E-03	n=4
meiosis II	GO:0007135	p=6.6E-03	n=4
negative regulation of purine nucleotide...	GO:1900543	p=6.6E-03	n=4
skeletal muscle fiber development	GO:0048741	p=6.6E-03	n=4
ommochrome biosynthetic process	GO:0006727	p=7.1E-03	n=3
regulation of sodium ion transmembrane t...	GO:2000649	p=7.1E-03	n=3
galactosylceramide metabolic process	GO:0006681	p=7.1E-03	n=3
protein maturation by copper ion transfe...	GO:0015680	p=8.8E-03	n=2
disruption of cells of another organism	GO:0044364	p=8.8E-03	n=2
cellular hypotonic response	GO:0071476	p=8.8E-03	n=2
regulation of iron ion transmembrane tra...	GO:0034759	p=8.8E-03	n=2
response to odorant	GO:1990834	p=8.8E-03	n=2
globoside metabolic process	GO:0001575	p=8.8E-03	n=2
negative regulation of cell migration in...	GO:0090051	p=8.8E-03	n=2
killing of cells of another organism	GO:0031640	p=8.8E-03	n=2
lysosomal lumen pH elevation	GO:0035752	p=8.8E-03	n=2
negative regulation of oxidative phospho...	GO:0090324	p=8.8E-03	n=2
pH elevation	GO:0045852	p=8.8E-03	n=2
negative regulation of sprouting angioge...	GO:1903671	p=8.8E-03	n=2
negative regulation of pancreatic juice ...	GO:0090188	p=8.8E-03	n=2
regulation of cilium beat frequency invo...	GO:0060296	p=8.8E-03	n=2
male germ-line sex determination	GO:0019100	p=8.8E-03	n=2
ciliary basal body-plasma membrane docki...	GO:0097711	p=9.5E-03	n=8
regulation of lamellipodium assembly	GO:0010591	p=9.7E-03	n=5
mitotic sister chromatid separation	GO:0051306	p=1.1E-02	n=6
regulation of G2/M transition of mitotic...	GO:0010389	p=1.2E-02	n=10
positive regulation of plasma membrane b...	GO:0120034	p=1.3E-02	n=7



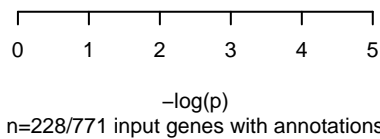
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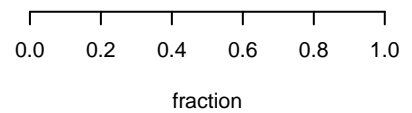
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**Elav\_Nvec\_vc1.1\_XM\_001627907.3**

fraction genes in fg and expected value

translation factor activity, RNA binding	GO:0008135	p=8.2E-04	n=9
calcium-activated potassium channel acti...	GO:0015269	p=7.6E-03	n=3
ribosome binding	GO:0043022	p=7.6E-03	n=5
N4-(beta-N-acetylglucosaminyl)-L-asparag...	GO:0003948	p=9.2E-03	n=2
BH3 domain binding	GO:0051434	p=9.2E-03	n=2
flap-structured DNA binding	GO:0070336	p=9.2E-03	n=2
superoxide dismutase copper chaperone ac...	GO:0016532	p=9.2E-03	n=2
phospholipase binding	GO:0043274	p=2.3E-02	n=3
carbohydrate kinase activity	GO:0019200	p=2.3E-02	n=3
antiporter activity	GO:0015297	p=2.4E-02	n=5
signaling adaptor activity	GO:0035591	p=2.4E-02	n=5
cGMP binding	GO:0030553	p=2.6E-02	n=2
3',5'-cyclic-AMP phosphodiesterase activ...	GO:0004115	p=2.6E-02	n=2
microtubule motor activity	GO:0003777	p=3.0E-02	n=4
DNA-directed 5'-3' RNA polymerase activi...	GO:0003899	p=3.4E-02	n=3
5'-3' RNA polymerase activity	GO:0034062	p=4.8E-02	n=3
RNA polymerase activity	GO:0097747	p=4.8E-02	n=3
dynein light intermediate chain binding	GO:0051959	p=4.9E-02	n=2
palmitoyl--(protein) hydrolase activity	GO:0008474	p=4.9E-02	n=2
5'-3' exonuclease activity	GO:0008409	p=4.9E-02	n=2
palmitoyl hydrolase activity	GO:0098599	p=4.9E-02	n=2
hydrolase activity, acting on ester bond...	GO:0016788	p=5.6E-02	n=22
purine nucleotide binding	GO:0017076	p=6.0E-02	n=22
translation initiation factor activity	GO:0003743	p=6.0E-02	n=4
histone deacetylase activity	GO:0004407	p=6.3E-02	n=3
nucleotide binding	GO:0000166	p=7.0E-02	n=25
nucleoside phosphate binding	GO:1901265	p=7.0E-02	n=25
ribonucleotide binding	GO:0032553	p=7.0E-02	n=21
purine ribonucleotide binding	GO:0032555	p=7.0E-02	n=21
carbohydrate derivative binding	GO:0097367	p=7.4E-02	n=24



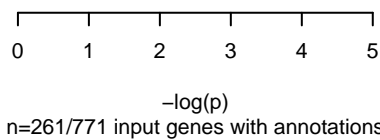
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**GO:CC**  
**Elav\_Nvec\_vc1.1\_XM\_001627907.3**

fraction genes in fg and expected value

intermediate filament cytoskeleton	GO:0045111	p=1.6E-02	n=4
neuron projection cytoplasm	GO:0120111	p=1.6E-02	n=4
lipid droplet	GO:0005811	p=2.3E-02	n=6
presynaptic active zone membrane	GO:0048787	p=2.3E-02	n=3
centriole	GO:0005814	p=2.5E-02	n=7
EARP complex	GO:1990745	p=2.6E-02	n=2
eukaryotic translation initiation factor...	GO:0005850	p=2.6E-02	n=2
GARP complex	GO:0000938	p=2.6E-02	n=2
Bcl-2 family protein complex	GO:0097136	p=2.6E-02	n=2
apical plasma membrane	GO:0016324	p=3.4E-02	n=15
actin filament	GO:0005884	p=3.9E-02	n=4
apical part of cell	GO:0045177	p=4.1E-02	n=19
synaptonemal structure	GO:0099086	p=4.8E-02	n=3
synaptonemal complex	GO:0000795	p=4.8E-02	n=3
RNA polymerase I complex	GO:0005736	p=4.9E-02	n=2
subsynaptic reticulum	GO:0071212	p=4.9E-02	n=2
caveola	GO:0005901	p=6.4E-02	n=5
voltage-gated potassium channel complex	GO:0008076	p=6.4E-02	n=3
potassium channel complex	GO:0034705	p=6.4E-02	n=3
endocytic vesicle membrane	GO:0030666	p=7.5E-02	n=5
dendrite cytoplasm	GO:0032839	p=7.6E-02	n=2
eukaryotic translation initiation factor...	GO:0005851	p=7.6E-02	n=2
RNA polymerase II, core complex	GO:0005665	p=7.6E-02	n=2
intermediate filament	GO:0005882	p=7.6E-02	n=2
sperm fibrous sheath	GO:0035686	p=7.6E-02	n=2
chromosome, centromeric region	GO:0000775	p=7.8E-02	n=8
tertiary granule	GO:0070820	p=8.7E-02	n=5
brush border membrane	GO:0031526	p=8.8E-02	n=4
A band	GO:0031672	p=8.8E-02	n=4
membrane raft	GO:0045121	p=8.9E-02	n=1



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