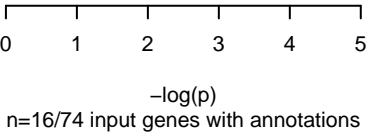


GO:BP  
Elav\_Nvec\_vc1.1\_XM\_001626717.3

fraction genes in fg and expected value

endocrine system development	GO:0035270	p=2.5E-03	n=3
activation of phospholipase C activity	GO:0007202	p=4.2E-03	n=2
cell-cell signaling	GO:0007267	p=4.4E-03	n=8
chordate embryonic development	GO:0043009	p=5.8E-03	n=5
epidermal growth factor receptor signali...	GO:0007173	p=6.8E-03	n=3
positive regulation of calcium ion trans...	GO:0010524	p=8.3E-03	n=2
regulation of neuroblast proliferation	GO:1902692	p=8.3E-03	n=2
cell cycle phase transition	GO:0044770	p=1.1E-02	n=4
secretion	GO:0046903	p=1.2E-02	n=7
pituitary gland development	GO:0021983	p=1.3E-02	n=2
signal release	GO:0023061	p=1.4E-02	n=5
stem cell proliferation	GO:0072089	p=1.4E-02	n=3
signal release from synapse	GO:0099643	p=1.4E-02	n=3
in utero embryonic development	GO:0001701	p=1.4E-02	n=3
neurotransmitter secretion	GO:0007269	p=1.4E-02	n=3
forebrain development	GO:0030900	p=1.6E-02	n=4
positive regulation of biological proces...	GO:0048518	p=1.6E-02	n=13
response to magnesium ion	GO:0032026	p=2.0E-02	n=2
positive regulation of receptor-mediated...	GO:0048260	p=2.0E-02	n=2
neural tube formation	GO:0001841	p=2.0E-02	n=2
blood vessel morphogenesis	GO:0048514	p=2.0E-02	n=3
synaptic signaling	GO:0099536	p=2.2E-02	n=5
trans-synaptic signaling	GO:0099537	p=2.2E-02	n=5
anterograde trans-synaptic signaling	GO:0098916	p=2.2E-02	n=5
chemical synaptic transmission	GO:0007268	p=2.2E-02	n=5
secretion by cell	GO:0032940	p=2.6E-02	n=6
regulation of secretion	GO:0051046	p=2.7E-02	n=5
regulation of neurotransmitter secretion	GO:0046928	p=2.7E-02	n=2
epithelial cell apoptotic process	GO:1904019	p=2.7E-02	n=2
regulation of neurotransmitter transport	GO:0051588	p=2.7E-02	n=2

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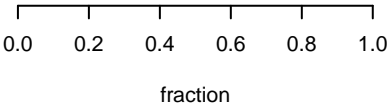
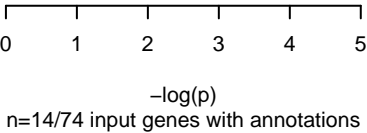


GO:MF  
Elav\_Nvec\_vc1.1\_XM\_001626717.3

fraction genes in fg and expected value

phosphotyrosine residue binding	GO:0001784	p=7.9E-03	n=2
voltage-gated cation channel activity	GO:0022843	p=1.3E-02	n=3
amyloid-beta binding	GO:0001540	p=1.3E-02	n=2
voltage-gated channel activity	GO:0022832	p=1.6E-02	n=3
voltage-gated ion channel activity	GO:0005244	p=1.6E-02	n=3
phosphatidylinositol biphosphate bindin...	GO:1902936	p=1.9E-02	n=2
phosphatidylinositol-4,5-bisphosphate bi...	GO:0005546	p=1.9E-02	n=2
signaling receptor binding	GO:0005102	p=2.4E-02	n=5
outward rectifier potassium channel acti...	GO:0015271	p=2.6E-02	n=2
protein-containing complex binding	GO:0044877	p=2.9E-02	n=4
SH2 domain binding	GO:0042169	p=3.8E-02	n=1
lipoprotein particle receptor binding	GO:0070325	p=3.8E-02	n=1
low-density lipoprotein particle recepto...	GO:0050750	p=3.8E-02	n=1
deubiquitinase activity	GO:0101005	p=3.8E-02	n=1
phospholipase binding	GO:0043274	p=3.8E-02	n=1
vinculin binding	GO:0017166	p=3.8E-02	n=1
phosphatidylinositol phospholipase C act...	GO:0004435	p=3.8E-02	n=1
cysteine-type deubiquitinase activity	GO:0004843	p=3.8E-02	n=1
intracellular sodium activated potassium...	GO:0005228	p=3.8E-02	n=1
ubiquitin-like protein peptidase activit...	GO:0019783	p=3.8E-02	n=1
neurotrophin receptor binding	GO:0005165	p=3.8E-02	n=1
neurotrophin TRK receptor binding	GO:0005167	p=3.8E-02	n=1
neurotrophin TRKA receptor binding	GO:0005168	p=3.8E-02	n=1
insulin receptor binding	GO:0005158	p=3.8E-02	n=1
voltage-gated potassium channel activity	GO:0005249	p=4.2E-02	n=2
phosphatidylinositol phosphate binding	GO:1901981	p=5.2E-02	n=2
peptide binding	GO:0042277	p=5.2E-02	n=2
amide binding	GO:0033218	p=5.2E-02	n=2
transcription coregulator activity	GO:0003712	p=6.3E-02	n=3
cation channel activity	GO:0005261	p=7.0E-02	n=3

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GO:CC  
Elav\_Nvec\_vc1.1\_XM\_001626717.3

fraction genes in fg and expected value

ruffle	GO:0001726	p=1.7E-03	n=3
clathrin-coated vesicle	GO:0030136	p=3.8E-03	n=3
cell-cell junction	GO:0005911	p=6.7E-03	n=4
Golgi trans cisterna	GO:0000138	p=8.5E-03	n=2
cation channel complex	GO:0034703	p=1.8E-02	n=3
transporter complex	GO:1990351	p=2.1E-02	n=3
transmembrane transporter complex	GO:1902495	p=2.1E-02	n=3
ion channel complex	GO:0034702	p=2.1E-02	n=3
basolateral plasma membrane	GO:0016323	p=2.5E-02	n=3
basal plasma membrane	GO:0009925	p=2.5E-02	n=3
cytoskeleton	GO:0005856	p=3.1E-02	n=5
voltage-gated potassium channel complex	GO:0008076	p=3.6E-02	n=2
potassium channel complex	GO:0034705	p=3.6E-02	n=2
neuron spine	GO:0044309	p=3.9E-02	n=3
dendritic spine	GO:0043197	p=3.9E-02	n=3
basal part of cell	GO:0045178	p=3.9E-02	n=3
extrinsic component of Golgi membrane	GO:0090498	p=4.0E-02	n=1
COP9 signalosome	GO:0008180	p=4.0E-02	n=1
cell projection	GO:0042995	p=4.8E-02	n=9
plasma membrane bounded cell projection	GO:0120025	p=4.8E-02	n=9
plasma membrane protein complex	GO:0098797	p=5.0E-02	n=3
adherens junction	GO:0005912	p=5.6E-02	n=2
lamellipodium	GO:0030027	p=5.6E-02	n=2
neuron projection	GO:0043005	p=5.8E-02	n=6
cytoplasmic side of plasma membrane	GO:0009898	p=6.6E-02	n=2
polymeric cytoskeletal fiber	GO:0099513	p=6.6E-02	n=2
cytosolic region	GO:0099522	p=7.8E-02	n=1
postsynaptic cytosol	GO:0099524	p=7.8E-02	n=1
transcription elongation factor complex	GO:0008023	p=7.8E-02	n=1
intermediate filament	GO:0005882	p=7.8E-02	n=1

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