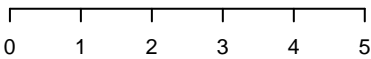


GO:BP
Elav_Nvec_vc1.1_XM_001637155.3

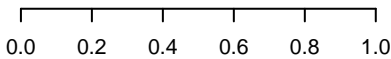
fraction genes in fg and expected value

regulation of synaptic assembly at neuro...	GO:0008582	p=1.4E-03	n=7
regulation of oskar mRNA translation	GO:0046011	p=2.1E-03	n=2
regulation of deacetylase activity	GO:0150065	p=2.1E-03	n=2
determination of digestive tract left/ri...	GO:0071907	p=2.1E-03	n=2
regulation of cell differentiation	GO:0045595	p=2.5E-03	n=24
response to amine	GO:0014075	p=2.9E-03	n=3
salivary gland morphogenesis	GO:0007435	p=5.8E-03	n=5
negative regulation of cilium assembly	GO:1902018	p=6.2E-03	n=2
regulation of histone deacetylation	GO:0031063	p=6.2E-03	n=2
negative regulation of axon regeneration	GO:0048681	p=6.2E-03	n=2
protein localization to cell cortex	GO:0072697	p=6.2E-03	n=2
positive regulation of long-term synapti...	GO:1900454	p=6.2E-03	n=2
proximal/distal axis specification	GO:0009946	p=6.2E-03	n=2
intracellular transport	GO:0046907	p=6.2E-03	n=27
negative regulation of synapse assembly	GO:0051964	p=6.4E-03	n=4
response to bronchodilator	GO:0097366	p=6.6E-03	n=3
regulation of dendritic spine morphogene...	GO:0061001	p=6.6E-03	n=3
positive regulation of supramolecular fi...	GO:1902905	p=8.0E-03	n=5
intracellular estrogen receptor signalin...	GO:0030520	p=9.1E-03	n=3
signaling	GO:0023052	p=1.1E-02	n=47
behavior	GO:0007610	p=1.1E-02	n=20
positive regulation of organelle assembl...	GO:1902117	p=1.2E-02	n=4
regulation of endocytic recycling	GO:2001135	p=1.2E-02	n=2
lipid export from cell	GO:0140353	p=1.2E-02	n=2
response to immobilization stress	GO:0035902	p=1.2E-02	n=2
positive regulation of establishment of ...	GO:1903749	p=1.2E-02	n=2
presynaptic active zone organization	GO:1990709	p=1.2E-02	n=2
neuroblast migration	GO:0097402	p=1.2E-02	n=2
regulation of transport	GO:0051049	p=1.2E-02	n=22
positive regulation of cytoskeleton orga...	GO:0051495	p=1.2E-02	n=5



-log(p)
n=84/228 input genes with annotations

fg=0.08	bg=0.02
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fg=0.02	bg=0.00
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fg=0.04	bg=0.00
fg=0.06	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.32	bg=0.20
fg=0.05	bg=0.01
fg=0.04	bg=0.01
fg=0.04	bg=0.01
fg=0.06	bg=0.02
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fg=0.02	bg=0.00
fg=0.02	bg=0.00
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fg=0.26	bg=0.16
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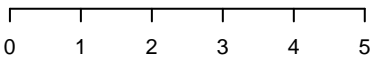


fraction

GO:MF
Elav_Nvec_vc1.1_XM_001637155.3

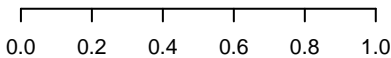
fraction genes in fg and expected value

protein phosphatase 1 binding	GO:0008157	p=2.2E-04	n=4
mitogen-activated protein kinase binding	GO:0051019	p=6.2E-04	n=4
transcription factor binding	GO:0008134	p=5.0E-03	n=12
actin binding	GO:0003779	p=1.4E-02	n=5
protein phosphatase regulator activity	GO:0019888	p=1.8E-02	n=3
cation channel activity	GO:0005261	p=1.8E-02	n=6
MAP kinase activity	GO:0004707	p=1.8E-02	n=2
kinesin binding	GO:0019894	p=2.2E-02	n=3
RNA polymerase II-specific DNA-binding t...	GO:0061629	p=2.4E-02	n=5
phospholipid binding	GO:0005543	p=2.5E-02	n=7
phosphatase regulator activity	GO:0019208	p=2.6E-02	n=3
lipid binding	GO:0008289	p=2.8E-02	n=8
DNA-binding transcription factor binding	GO:0140297	p=3.3E-02	n=5
nuclear estrogen receptor binding	GO:0030331	p=3.6E-02	n=2
potassium ion transmembrane transporter ...	GO:0015079	p=3.7E-02	n=3
protein kinase binding	GO:0019901	p=3.8E-02	n=13
metal ion transmembrane transporter acti...	GO:0046873	p=4.1E-02	n=6
histone deacetylase binding	GO:0042826	p=4.3E-02	n=3
transcription coactivator activity	GO:0003713	p=4.4E-02	n=6
type I transforming growth factor beta r...	GO:0034713	p=4.5E-02	n=1
lipoate synthase activity	GO:0016992	p=4.5E-02	n=1
histone deacetylase regulator activity	GO:0035033	p=4.5E-02	n=1
insulin-like growth factor-activated rec...	GO:0005010	p=4.5E-02	n=1
pre-mRNA 5'-splice site binding	GO:0030627	p=4.5E-02	n=1
glycogen binding	GO:2001069	p=4.5E-02	n=1
myosin II binding	GO:0045159	p=4.5E-02	n=1
transmembrane receptor protein phosphata...	GO:0019198	p=4.5E-02	n=1
polypeptide N-acetylgalactosaminy/transf...	GO:0004653	p=4.5E-02	n=1
insulin-like growth factor II binding	GO:0031995	p=4.5E-02	n=1
transmembrane receptor protein tyrosine ...	GO:0005001	p=4.5E-02	n=1



-log(p)
n=71/228 input genes with annotations

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fg=0.03	bg=0.00
fg=0.04	bg=0.01
fg=0.07	bg=0.02
fg=0.10	bg=0.04
fg=0.04	bg=0.01
fg=0.11	bg=0.05
fg=0.07	bg=0.03
fg=0.03	bg=0.00
fg=0.04	bg=0.01
fg=0.18	bg=0.08
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fg=0.08	bg=0.04
fg=0.01	bg=0.00
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fg=0.01	bg=0.00
fg=0.01	bg=0.00
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fg=0.01	bg=0.00

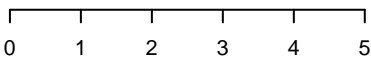


fraction

GO:CC
Elav_Nvec_vc1.1_XM_001637155.3

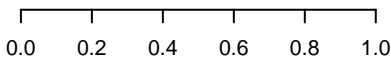
fraction genes in fg and expected value

endolysosome membrane	GO:0036020	p=6.1E-03	n=2
cytoplasmic region	GO:0099568	p=9.8E-03	n=10
neuronal cell body	GO:0043025	p=1.1E-02	n=12
perikaryon	GO:0043204	p=1.4E-02	n=4
cell cortex	GO:0005938	p=1.8E-02	n=8
midbody	GO:0030496	p=1.9E-02	n=4
protein phosphatase type 1 complex	GO:0000164	p=1.9E-02	n=2
cortical actin cytoskeleton	GO:0030864	p=1.9E-02	n=3
cell body	GO:0044297	p=2.0E-02	n=12
cell periphery	GO:0071944	p=2.1E-02	n=33
cell junction	GO:0030054	p=2.4E-02	n=18
axon	GO:0030424	p=2.4E-02	n=12
plasma membrane	GO:0005886	p=2.5E-02	n=31
plasma membrane region	GO:0098590	p=2.6E-02	n=14
dendrite membrane	GO:0032590	p=2.8E-02	n=2
Cajal body	GO:0015030	p=2.8E-02	n=2
cortical cytoskeleton	GO:0030863	p=2.8E-02	n=3
synapse	GO:0045202	p=2.9E-02	n=14
dendrite	GO:0030425	p=3.2E-02	n=11
dendritic tree	GO:0097447	p=3.2E-02	n=11
membrane	GO:0016020	p=3.3E-02	n=48
apicolateral plasma membrane	GO:0016327	p=3.8E-02	n=2
asymmetric synapse	GO:0032279	p=4.4E-02	n=5
katanin complex	GO:0008352	p=4.6E-02	n=1
integrin alpha9-beta1 complex	GO:0034679	p=4.6E-02	n=1
keratin filament	GO:0045095	p=4.6E-02	n=1
spectrosome	GO:0045170	p=4.6E-02	n=1
integral component of lysosomal membrane	GO:1905103	p=4.6E-02	n=1
core-binding factor complex	GO:0016513	p=4.6E-02	n=1
ciliary transition fiber	GO:0097539	p=4.6E-02	n=1



-log(p)
n=83/228 input genes with annotations

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fg=0.02	bg=0.00
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fg=0.14	bg=0.08
fg=0.40	bg=0.29
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fg=0.37	bg=0.27
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fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.04	bg=0.01
fg=0.17	bg=0.10
fg=0.13	bg=0.07
fg=0.13	bg=0.07
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fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00



fraction