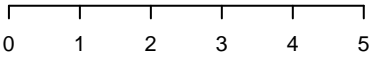


GO:BP  
Elav\_Nvec\_vc1.1\_XM\_032375459.2

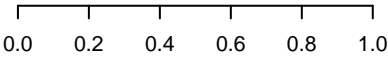
fraction genes in fg and expected value

substrate-dependent cell migration	GO:0006929	p=1.2E-03	n=3
positive regulation of histone H3-K9 met...	GO:0051574	p=2.5E-03	n=2
regulation of mitotic cell cycle DNA rep...	GO:1903463	p=4.9E-03	n=2
diacylglycerol metabolic process	GO:0046339	p=8.0E-03	n=2
chemotaxis	GO:0006935	p=8.2E-03	n=10
macromolecule biosynthetic process	GO:0009059	p=9.2E-03	n=38
cilium organization	GO:0044782	p=9.7E-03	n=9
axon guidance	GO:0007411	p=1.1E-02	n=8
cellular macromolecule biosynthetic proc...	GO:0034645	p=1.1E-02	n=37
response to leukemia inhibitory factor	GO:1990823	p=1.2E-02	n=4
cellular response to leukemia inhibitory...	GO:1990830	p=1.2E-02	n=4
cranial nerve formation	GO:0021603	p=1.2E-02	n=2
regulation of cytoplasmic translation	GO:2000765	p=1.2E-02	n=2
neuron projection guidance	GO:0097485	p=1.2E-02	n=8
response to peptide	GO:1901652	p=1.3E-02	n=9
ciliary basal body-plasma membrane docki...	GO:0097711	p=1.5E-02	n=4
response to axon injury	GO:0048678	p=1.5E-02	n=4
animal organ maturation	GO:0048799	p=1.6E-02	n=2
axonogenesis	GO:0007409	p=1.7E-02	n=10
plasma membrane bounded cell projection ...	GO:0120031	p=1.9E-02	n=10
axon development	GO:0061564	p=2.3E-02	n=10
cell projection assembly	GO:0030031	p=2.4E-02	n=10
cellular response to peptide	GO:1901653	p=2.4E-02	n=7
cilium assembly	GO:0060271	p=2.4E-02	n=8
positive regulation of neuron projection...	GO:0070572	p=2.7E-02	n=2
positive regulation of axon regeneration	GO:0048680	p=2.7E-02	n=2
negative regulation of mRNA processing	GO:0050686	p=2.7E-02	n=2
lens fiber cell differentiation	GO:0070306	p=2.7E-02	n=2
detection of light stimulus involved in ...	GO:0050962	p=2.7E-02	n=2
detection of light stimulus involved in ...	GO:0050908	p=2.7E-02	n=2



-log(p)  
n=79/278 input genes with annotations

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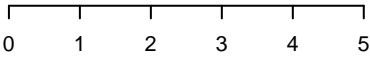


fraction

GO:MF  
Elav\_Nvec\_vc1.1\_XM\_032375459.2

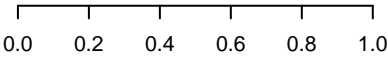
fraction genes in fg and expected value

mRNA regulatory element binding translat...	GO:0000900	p=2.5E-03	n=2
tau-protein kinase activity	GO:0050321	p=5.0E-03	n=2
insulin receptor binding	GO:0005158	p=1.6E-02	n=2
protein tyrosine kinase activity	GO:0004713	p=2.2E-02	n=3
poly(U) RNA binding	GO:0008266	p=2.7E-02	n=2
guanyl-nucleotide exchange factor activi...	GO:0005085	p=2.9E-02	n=4
D-glucose transmembrane transporter acti...	GO:0055056	p=2.9E-02	n=1
alanine-oxo-acid transaminase activity	GO:0047635	p=2.9E-02	n=1
carbohydrate:proton symporter activity	GO:0005351	p=2.9E-02	n=1
glucose transmembrane transporter activi...	GO:0005355	p=2.9E-02	n=1
polypeptide N-acetylgalactosaminyltransf...	GO:0004653	p=2.9E-02	n=1
nickel cation binding	GO:0016151	p=2.9E-02	n=1
angiostatin binding	GO:0043532	p=2.9E-02	n=1
carbohydrate:cation symporter activity	GO:0005402	p=2.9E-02	n=1
phosphopantetheine-dependent carrier act...	GO:0140414	p=2.9E-02	n=1
proton-transporting ATP synthase activit...	GO:0046933	p=2.9E-02	n=1
phosphomannomutase activity	GO:0004615	p=2.9E-02	n=1
prosthetic group binding	GO:0051192	p=2.9E-02	n=1
carbohydrate transmembrane transporter a...	GO:0015144	p=2.9E-02	n=1
monosaccharide transmembrane transporter...	GO:0015145	p=2.9E-02	n=1
hexose transmembrane transporter activit...	GO:0015149	p=2.9E-02	n=1
phosphopantetheine binding	GO:0031177	p=2.9E-02	n=1
phenanthrene-epoxide hydrolase activity	GO:0019118	p=2.9E-02	n=1
phenanthrene-9,10-epoxide hydrolase acti...	GO:0019119	p=2.9E-02	n=1
phosphatidylserine decarboxylase activit...	GO:0004609	p=2.9E-02	n=1
MHC class I protein binding	GO:0042288	p=2.9E-02	n=1
ACP phosphopantetheine attachment site b...	GO:0044620	p=2.9E-02	n=1
L-alanine:2-oxoglutarate aminotransferas...	GO:0004021	p=2.9E-02	n=1
sugar transmembrane transporter activity	GO:0051119	p=2.9E-02	n=1
acyl binding	GO:0000035	p=2.9E-02	n=1



-log(p)  
n=70/278 input genes with annotations

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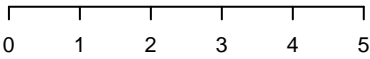


fraction

GO:CC  
Elav\_Nvec\_vc1.1\_XM\_032375459.2

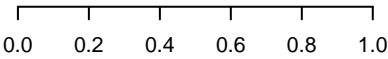
fraction genes in fg and expected value

presynaptic active zone	GO:0048786	p=3.9E-03	n=4
intracellular membrane-bounded organelle	GO:0043231	p=6.2E-03	n=70
transcription factor TFTC complex	GO:0033276	p=1.2E-02	n=2
voltage-gated calcium channel complex	GO:0005891	p=1.2E-02	n=2
excitatory synapse	GO:0060076	p=1.6E-02	n=2
membrane-bounded organelle	GO:0043227	p=1.8E-02	n=74
nuclear body	GO:0016604	p=1.9E-02	n=10
vesicle coat	GO:0030120	p=2.1E-02	n=2
SAGA-type complex	GO:0070461	p=2.1E-02	n=2
calcium channel complex	GO:0034704	p=2.7E-02	n=2
COPI-coated vesicle	GO:0030137	p=2.7E-02	n=2
ACF complex	GO:0016590	p=2.9E-02	n=1
chromaffin granule	GO:0042583	p=2.9E-02	n=1
chromaffin granule membrane	GO:0042584	p=2.9E-02	n=1
mitochondrial proton-transporting ATP sy...	GO:0005754	p=2.9E-02	n=1
L-type voltage-gated calcium channel com...	GO:1990454	p=2.9E-02	n=1
polytene chromosome band	GO:0005704	p=2.9E-02	n=1
Ric1-Rgp1 guanyl-nucleotide exchange fac...	GO:0034066	p=2.9E-02	n=1
proton-transporting ATP synthase, cataly...	GO:0045267	p=2.9E-02	n=1
polysomal ribosome	GO:0042788	p=3.3E-02	n=2
RNA polymerase II transcription regulato...	GO:0090575	p=3.3E-02	n=4
mitochondrial protein-containing complex	GO:0098798	p=3.5E-02	n=5
organellar large ribosomal subunit	GO:0000315	p=3.9E-02	n=2
mitochondrial large ribosomal subunit	GO:0005762	p=3.9E-02	n=2
Cajal body	GO:0015030	p=3.9E-02	n=2
mitochondrial inner membrane	GO:0005743	p=4.0E-02	n=7
sarcolemma	GO:0042383	p=4.3E-02	n=3
nucleus	GO:0005634	p=5.1E-02	n=47
ribosome	GO:0005840	p=5.2E-02	n=5
T-tubule	GO:0030315	p=5.3E-02	n=2



-log(p)  
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fraction