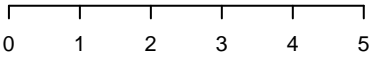


GO:BP
Elav_Nvec_vc1.1_XM_032373618.2

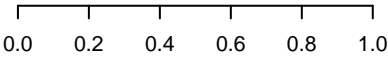
fraction genes in fg and expected value

endocrine system development	GO:0035270	p=1.6E-03	n=4
Wnt signaling pathway	GO:0016055	p=1.6E-03	n=6
protein acylation	GO:0043543	p=2.2E-03	n=5
transforming growth factor beta receptor...	GO:0007179	p=2.6E-03	n=4
embryonic morphogenesis	GO:0048598	p=3.4E-03	n=9
epithelial structure maintenance	GO:0010669	p=5.6E-03	n=2
protein localization to synapse	GO:0035418	p=5.6E-03	n=2
atrioventricular valve development	GO:0003171	p=5.6E-03	n=2
hormone-mediated signaling pathway	GO:0009755	p=6.2E-03	n=4
negative regulation of DNA-binding trans...	GO:0043433	p=6.8E-03	n=3
regulation of cellular macromolecule bio...	GO:2000112	p=7.7E-03	n=16
positive regulation of protein metabolic...	GO:0051247	p=8.1E-03	n=10
regulation of cell cycle process	GO:0010564	p=9.1E-03	n=7
positive regulation of transcription by ...	GO:0045944	p=9.7E-03	n=9
mitotic cell cycle phase transition	GO:0044772	p=9.9E-03	n=5
spinal cord development	GO:0021510	p=1.1E-02	n=3
negative regulation of cellular process	GO:0048523	p=1.1E-02	n=21
central nervous system development	GO:0007417	p=1.2E-02	n=10
protein localization to nucleus	GO:0034504	p=1.2E-02	n=4
protein acetylation	GO:0006473	p=1.2E-02	n=4
regulation of Wnt signaling pathway	GO:0030111	p=1.2E-02	n=4
peptidyl-lysine acetylation	GO:0018394	p=1.2E-02	n=4
positive regulation of gene expression	GO:0010628	p=1.4E-02	n=12
negative regulation of developmental pro...	GO:0051093	p=1.5E-02	n=8
regulation of RNA metabolic process	GO:0051252	p=1.5E-02	n=18
regulation of cell cycle phase transitio...	GO:1901987	p=1.5E-02	n=5
positive regulation of cell cycle	GO:0045787	p=1.5E-02	n=5
regulation of mitotic cell cycle	GO:0007346	p=1.6E-02	n=6
gastrulation	GO:0007369	p=1.6E-02	n=4
negative regulation of synapse organizat...	GO:1905809	p=1.6E-02	n=2



-log(p)
n=31/125 input genes with annotations

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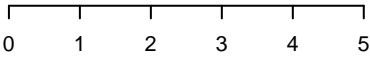


fraction

GO:MF
Elav_Nvec_vc1.1_XM_032373618.2

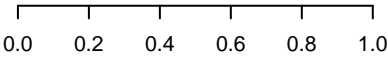
fraction genes in fg and expected value

transcription regulator activity	GO:0140110	p=1.4E-02	n=11
transcription regulatory region nucleic ...	GO:0001067	p=1.7E-02	n=7
transcription coregulator binding	GO:0001221	p=2.0E-02	n=2
Wnt-protein binding	GO:0017147	p=2.0E-02	n=2
mitogen-activated protein kinase binding	GO:0051019	p=2.3E-02	n=3
phosphoprotein binding	GO:0051219	p=2.4E-02	n=4
transcription coactivator activity	GO:0003713	p=3.5E-02	n=10
nucleic acid binding	GO:0003676	p=3.8E-02	n=2
mitogen-activated protein kinase kinase ...	GO:0031434	p=4.2E-02	n=6
transcription cis-regulatory region bind...	GO:0000976	p=4.5E-02	n=9
DNA-binding transcription factor activit...	GO:0003700	p=4.6E-02	n=8
DNA binding	GO:0003677	p=4.7E-02	n=13
organic cyclic compound binding	GO:0097159	p=4.9E-02	n=6
sequence-specific double-stranded DNA bi...	GO:1990837	p=5.0E-02	n=5
transcription coregulator activity	GO:0003712	p=5.6E-02	n=6
double-stranded DNA binding	GO:0003690	p=6.0E-02	n=2
protein phosphorylated amino acid bindin...	GO:0045309	p=6.0E-02	n=2
transmembrane transporter binding	GO:0044325	p=6.0E-02	n=2
voltage-gated calcium channel activity	GO:0005245	p=7.2E-02	n=9
protein dimerization activity	GO:0046983	p=7.6E-02	n=12
heterocyclic compound binding	GO:1901363	p=7.9E-02	n=4
cis-regulatory region sequence-specific ...	GO:0000987	p=7.9E-02	n=4
RNA polymerase II cis-regulatory region ...	GO:0000978	p=8.0E-02	n=6
sequence-specific DNA binding	GO:0043565	p=8.5E-02	n=2
adrenergic receptor binding	GO:0031690	p=8.5E-02	n=2
hormone receptor binding	GO:0051427	p=8.5E-02	n=1
V2 vasopressin receptor binding	GO:0031896	p=8.5E-02	n=1
epidermal growth factor receptor binding	GO:0005154	p=8.5E-02	n=1
mRNA 3'-UTR AU-rich region binding	GO:0035925	p=8.5E-02	n=1
opsin binding	GO:0002046	p=8.5E-02	n=1



-log(p)
n=31/125 input genes with annotations

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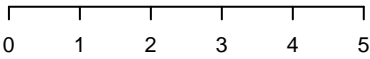


fraction

GO:CC
Elav_Nvec_vc1.1_XM_032373618.2

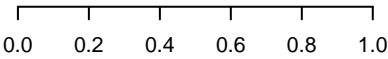
fraction genes in fg and expected value

sensory dendrite	GO:0071683	p=1.6E-02	n=2
cytoskeleton	GO:0005856	p=2.1E-02	n=8
ciliary base	GO:0097546	p=3.1E-02	n=2
ciliary basal body	GO:0036064	p=3.1E-02	n=2
cell cortex	GO:0005938	p=3.4E-02	n=4
cytoplasmic region	GO:0099568	p=4.1E-02	n=4
nucleus	GO:0005634	p=5.3E-02	n=19
non-motile cilium	GO:0097730	p=7.1E-02	n=2
Cajal body	GO:0015030	p=7.7E-02	n=1
striated muscle thin filament	GO:0005865	p=7.7E-02	n=1
actin filament	GO:0005884	p=7.7E-02	n=1
peptidase complex	GO:1905368	p=7.7E-02	n=1
clathrin-coated pit	GO:0005905	p=7.7E-02	n=1
pseudopodium	GO:0031143	p=7.7E-02	n=1
filopodium membrane	GO:0031527	p=7.7E-02	n=1
membrane coat	GO:0030117	p=7.7E-02	n=1
clathrin coat	GO:0030118	p=7.7E-02	n=1
clathrin coat of coated pit	GO:0030132	p=7.7E-02	n=1
polysomal ribosome	GO:0042788	p=7.7E-02	n=1
XY body	GO:0001741	p=7.7E-02	n=1
SAGA-type complex	GO:0070461	p=7.7E-02	n=1
coated membrane	GO:0048475	p=7.7E-02	n=1
filamentous actin	GO:0031941	p=7.7E-02	n=1
polycystin complex	GO:0002133	p=7.7E-02	n=1
PML body	GO:0016605	p=7.7E-02	n=1
myofilament	GO:0036379	p=7.7E-02	n=1
SAGA complex	GO:0000124	p=7.7E-02	n=1
mitochondrial membrane	GO:0031966	p=8.5E-02	n=3
actin cytoskeleton	GO:0015629	p=8.5E-02	n=3
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-log(p)
n=31/125 input genes with annotations

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fraction