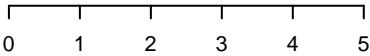


GO:BP  
Elav\_Nvec\_vc1.1\_XM\_032385647.2

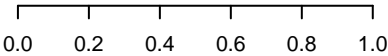
fraction genes in fg and expected value

histone biotinylation	GO:0071110	p=1.4E-03	n=2
peptidyl-lysine biotinylation	GO:0018054	p=1.4E-03	n=2
negative regulation of apoptotic signalin...	GO:2001234	p=3.5E-03	n=6
response to hydrostatic pressure	GO:0051599	p=4.1E-03	n=2
calcium ion export across plasma membran...	GO:1990034	p=4.1E-03	n=2
mitotic cell cycle checkpoint signaling	GO:0007093	p=5.6E-03	n=4
flagellated sperm motility	GO:0030317	p=5.6E-03	n=4
negative regulation of G1/S transition o...	GO:2000134	p=6.7E-03	n=3
endosome to lysosome transport	GO:0008333	p=6.7E-03	n=3
response to hermaphrodite contact	GO:0034606	p=7.9E-03	n=2
metanephric ascending thin limb developm...	GO:0072218	p=7.9E-03	n=2
metanephric distal tubule development	GO:0072235	p=7.9E-03	n=2
atrioventricular valve development	GO:0003171	p=7.9E-03	n=2
epithelial cell migration, open tracheal...	GO:0007427	p=7.9E-03	n=2
cilium assembly	GO:0060271	p=8.6E-03	n=8
pituitary gland development	GO:0021983	p=8.7E-03	n=3
DNA damage checkpoint signaling	GO:0000077	p=9.3E-03	n=4
regulation of neurotransmitter levels	GO:0001505	p=1.0E-02	n=8
negative regulation of extrinsic apoptot...	GO:2001237	p=1.1E-02	n=3
response to UV	GO:0009411	p=1.3E-02	n=4
serotonin metabolic process	GO:0042428	p=1.3E-02	n=2
peroxisomal membrane transport	GO:0015919	p=1.3E-02	n=2
negative regulation of extrinsic apoptot...	GO:1902042	p=1.3E-02	n=2
mitotic DNA damage checkpoint signaling	GO:0044773	p=1.4E-02	n=3
microtubule cytoskeleton organization	GO:0000226	p=1.5E-02	n=10
vacuole organization	GO:0007033	p=1.5E-02	n=5
mitotic DNA integrity checkpoint signali...	GO:0044774	p=1.7E-02	n=3
regulation of cAMP-dependent protein kin...	GO:2000479	p=1.9E-02	n=2
mitotic G1 DNA damage checkpoint signali...	GO:0031571	p=1.9E-02	n=2
negative regulation of calcium ion trans...	GO:1901020	p=1.9E-02	n=2



-log(p)  
n=68/290 input genes with annotations

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fg=0.03	bg=0.00

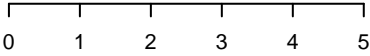


fraction

GO:MF  
Elav\_Nvec\_vc1.1\_XM\_032385647.2

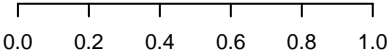
fraction genes in fg and expected value

cAMP binding	GO:0030552	p=7.2E-03	n=2
kinase inhibitor activity	GO:0019210	p=1.2E-02	n=3
protein kinase inhibitor activity	GO:0004860	p=1.2E-02	n=3
protein kinase regulator activity	GO:0019887	p=1.6E-02	n=4
transcription coactivator activity	GO:0003713	p=1.7E-02	n=6
kinase regulator activity	GO:0019207	p=2.3E-02	n=4
protein serine/threonine kinase inhibito...	GO:0030291	p=2.4E-02	n=2
phosphoprotein binding	GO:0051219	p=2.8E-02	n=3
DNA-binding transcription factor activit...	GO:0000981	p=3.3E-02	n=8
long-chain fatty acid transporter activi...	GO:0005324	p=3.6E-02	n=1
protein kinase C inhibitor activity	GO:0008426	p=3.6E-02	n=1
HLH domain binding	GO:0043398	p=3.6E-02	n=1
biotin-protein ligase activity	GO:0018271	p=3.6E-02	n=1
growth hormone-releasing hormone recepto...	GO:0016520	p=3.6E-02	n=1
ATPase-coupled inorganic anion transmemb...	GO:0043225	p=3.6E-02	n=1
muscle alpha-actinin binding	GO:0051371	p=3.6E-02	n=1
fibronectin binding	GO:0001968	p=3.6E-02	n=1
microtubule-severing ATPase activity	GO:0008568	p=3.6E-02	n=1
neuregulin binding	GO:0038132	p=3.6E-02	n=1
insulin-like growth factor I binding	GO:0031994	p=3.6E-02	n=1
MRF binding	GO:0043426	p=3.6E-02	n=1
phosphoserine residue binding	GO:0050815	p=3.6E-02	n=1
calmodulin-activated 3',5'-cyclic-GMP ph...	GO:0048101	p=3.6E-02	n=1
biotin binding	GO:0009374	p=3.6E-02	n=1
calmodulin-activated dual specificity 3'...	GO:0004117	p=3.6E-02	n=1
dihydrouridine synthase activity	GO:0106413	p=3.6E-02	n=1
interferon binding	GO:0019961	p=3.6E-02	n=1
telomeric repeat-containing RNA binding	GO:0061752	p=3.6E-02	n=1
interferon-gamma binding	GO:0019964	p=3.6E-02	n=1
tRNA dihydrouridine synthase activity	GO:0017150	p=3.6E-02	n=1



-log(p)  
n=57/290 input genes with annotations

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fg=0.14	bg=0.07
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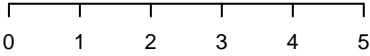


fraction

GO:CC  
Elav\_Nvec\_vc1.1\_XM\_032385647.2

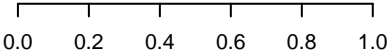
fraction genes in fg and expected value

cilium	GO:0005929	p=4.8E-03	n=13
lateral plasma membrane	GO:0016328	p=6.5E-03	n=3
Set1C/COMPASS complex	GO:0048188	p=7.7E-03	n=2
motile cilium	GO:0031514	p=9.3E-03	n=5
sperm principal piece	GO:0097228	p=1.3E-02	n=2
microbody membrane	GO:0031903	p=1.8E-02	n=2
peroxisomal membrane	GO:0005778	p=1.8E-02	n=2
PML body	GO:0016605	p=2.5E-02	n=2
ciliary plasm	GO:0097014	p=2.7E-02	n=3
axoneme	GO:0005930	p=2.7E-02	n=3
microtubule cytoskeleton	GO:0015630	p=2.9E-02	n=12
rhabdomere	GO:0016028	p=3.3E-02	n=2
sperm flagellum	GO:0036126	p=3.5E-02	n=3
transcription factor TFIIC complex	GO:0000127	p=3.7E-02	n=1
integrin alpha3-beta1 complex	GO:0034667	p=3.7E-02	n=1
CORVET complex	GO:0033263	p=3.7E-02	n=1
integrin alpha6-beta4 complex	GO:0034676	p=3.7E-02	n=1
integrin alpha7-beta1 complex	GO:0034677	p=3.7E-02	n=1
core-binding factor complex	GO:0016513	p=3.7E-02	n=1
outer dynein arm	GO:0036157	p=3.7E-02	n=1
RNA polymerase III transcription regulat...	GO:0090576	p=3.7E-02	n=1
FHF complex	GO:0070695	p=3.7E-02	n=1
ESCRT-0 complex	GO:0033565	p=3.7E-02	n=1
postsynaptic endosome	GO:0098845	p=3.7E-02	n=1
sperm cytoplasmic droplet	GO:0097598	p=3.7E-02	n=1
postsynaptic recycling endosome	GO:0098837	p=3.7E-02	n=1
polycystin complex	GO:0002133	p=3.7E-02	n=1
sarcolemma	GO:0042383	p=4.0E-02	n=3
9+2 motile cilium	GO:0097729	p=4.0E-02	n=3
neuronal cell body	GO:0043025	p=4.1E-02	n=9



-log(p)  
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fg=0.04	bg=0.01
fg=0.04	bg=0.01
fg=0.13	bg=0.07



fraction