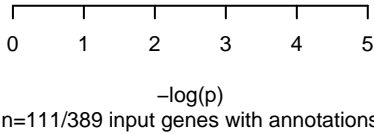


GO:BP  
Elav\_Nvec\_vc1.1\_XM\_032379457.2

fraction genes in fg and expected value

positive regulation of calcium ion trans...	GO:1904879	p=1.7E-03	n=2
error-free translesion synthesis	GO:0070987	p=3.3E-03	n=3
mismatch repair	GO:0006298	p=3.3E-03	n=3
synaptic vesicle cycle	GO:0099504	p=3.8E-03	n=7
positive regulation of translational ini...	GO:0045948	p=4.7E-03	n=3
nucleotide-excision repair, preincision ...	GO:0006293	p=4.7E-03	n=3
actin filament severing	GO:0051014	p=4.9E-03	n=2
negative regulation of miRNA-mediated ge...	GO:0060965	p=4.9E-03	n=2
positive regulation of actin filament de...	GO:0030836	p=4.9E-03	n=2
regulation of barbed-end actin filament ...	GO:2000812	p=4.9E-03	n=2
response to iron(III) ion	GO:0010041	p=4.9E-03	n=2
striated muscle cell development	GO:0055002	p=4.9E-03	n=5
base-excision repair	GO:0006284	p=5.3E-03	n=4
interstrand cross-link repair	GO:0036297	p=8.8E-03	n=3
T cell receptor signaling pathway	GO:0050852	p=9.4E-03	n=4
cellular response to insulin-like growth...	GO:1990314	p=9.5E-03	n=2
negative regulation of centrosome duplic...	GO:0010826	p=9.5E-03	n=2
positive regulation of anoikis	GO:2000210	p=9.5E-03	n=2
proton-transporting two-sector ATPase co...	GO:0070071	p=9.5E-03	n=2
lamellipodium assembly	GO:0030032	p=1.1E-02	n=4
response to endoplasmic reticulum stress	GO:0034976	p=1.1E-02	n=9
nucleotide-excision repair, preincision ...	GO:0006294	p=1.1E-02	n=3
positive regulation of lamellipodium org...	GO:1902745	p=1.1E-02	n=3
protein exit from endoplasmic reticulum	GO:0032527	p=1.4E-02	n=3
centrosome separation	GO:0051299	p=1.4E-02	n=3
nucleobase-containing small molecule met...	GO:0055086	p=1.5E-02	n=15
purine ribonucleoside monophosphate meta...	GO:0009167	p=1.5E-02	n=7
endoplasmic reticulum mannose trimming	GO:1904380	p=1.5E-02	n=2
purine nucleoside monophosphate metaboli...	GO:0009126	p=1.6E-02	n=7
DNA recombination	GO:0006310	p=1.6E-02	n=7



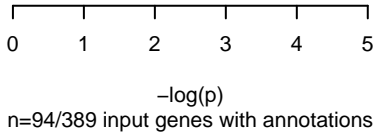
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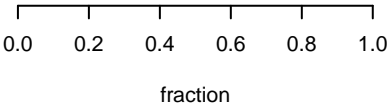
GO:MF  
Elav\_Nvec\_vc1.1\_XM\_032379457.2

fraction genes in fg and expected value

P-type proton-exporting transporter acti...	GO:0008553	p=1.6E-03	n=2
damaged DNA binding	GO:0003684	p=3.7E-03	n=4
translation factor activity, RNA binding	GO:0008135	p=4.2E-03	n=5
mRNA regulatory element binding translat...	GO:0000900	p=4.6E-03	n=2
single-stranded DNA binding	GO:0003697	p=4.9E-03	n=5
zinc ion binding	GO:0008270	p=5.0E-03	n=10
glucose binding	GO:0005536	p=8.9E-03	n=2
tau-protein kinase activity	GO:0050321	p=8.9E-03	n=2
ATP hydrolysis activity	GO:0016887	p=9.8E-03	n=10
SNAP receptor activity	GO:0005484	p=1.3E-02	n=3
ephrin receptor binding	GO:0046875	p=1.4E-02	n=2
NF-kappaB binding	GO:0051059	p=1.4E-02	n=2
deoxyribonuclease activity	GO:0004536	p=1.6E-02	n=3
proton-transporting ATPase activity, rot...	GO:0046961	p=2.1E-02	n=2
ATPase activity, coupled to transmembran...	GO:0044769	p=2.1E-02	n=2
ATPase-coupled ion transmembrane transpo...	GO:0042625	p=2.3E-02	n=3
translation initiation factor activity	GO:0003743	p=2.3E-02	n=3
ribonucleoprotein complex binding	GO:0043021	p=2.6E-02	n=5
oxidoreduction-driven active transmembra...	GO:0015453	p=2.8E-02	n=3
ribosomal small subunit binding	GO:0043024	p=2.9E-02	n=2
calcium channel activity	GO:0005262	p=3.2E-02	n=4
molecular carrier activity	GO:0140104	p=3.7E-02	n=2
GTPase activity	GO:0003924	p=3.9E-02	n=5
ATP-dependent DNA/DNA annealing activity	GO:0036310	p=4.0E-02	n=1
myosin VI binding	GO:0070853	p=4.0E-02	n=1
myosin VI heavy chain binding	GO:0070854	p=4.0E-02	n=1
glutaminase activity	GO:0004359	p=4.0E-02	n=1
misfolded RNA binding	GO:0034336	p=4.0E-02	n=1
P-type divalent copper transporter activ...	GO:0043682	p=4.0E-02	n=1
galactose binding	GO:0005534	p=4.0E-02	n=1



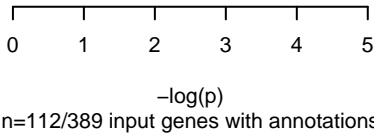
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GO:CC  
Elav\_Nvec\_vc1.1\_XM\_032379457.2

fraction genes in fg and expected value

phagocytic vesicle membrane	GO:0030670	p=4.9E-03	n=3
DNA replication factor A complex	GO:0005662	p=5.0E-03	n=2
Smc5-Smc6 complex	GO:0030915	p=5.0E-03	n=2
synaptic vesicle	GO:0008021	p=7.5E-03	n=7
trans-Golgi network membrane	GO:0032588	p=9.2E-03	n=5
endoplasmic reticulum quality control co...	GO:0044322	p=9.7E-03	n=2
synaptic vesicle membrane	GO:0030672	p=1.3E-02	n=4
integral component of synaptic vesicle m...	GO:0030285	p=1.5E-02	n=3
smooth endoplasmic reticulum	GO:0005790	p=1.5E-02	n=3
exocytic vesicle membrane	GO:0099501	p=1.6E-02	n=4
zymogen granule	GO:0042588	p=1.6E-02	n=2
dendrite cytoplasm	GO:0032839	p=1.6E-02	n=2
transport vesicle membrane	GO:0030658	p=1.7E-02	n=5
intrinsic component of synaptic vesicle ...	GO:0098563	p=1.8E-02	n=3
ribonucleoprotein complex	GO:1990904	p=1.8E-02	n=17
distal axon	GO:0150034	p=2.2E-02	n=9
Derlin-1 retrotranslocation complex	GO:0036513	p=2.3E-02	n=2
voltage-gated calcium channel complex	GO:0005891	p=2.3E-02	n=2
organelle membrane contact site	GO:0044232	p=2.3E-02	n=2
ribosome	GO:0005840	p=2.4E-02	n=7
SNARE complex	GO:0031201	p=2.6E-02	n=3
polymeric cytoskeletal fiber	GO:0099513	p=2.8E-02	n=7
vacuolar proton-transporting V-type ATPa...	GO:0016471	p=3.1E-02	n=2
plasma membrane bounded cell projection	GO:0120025	p=3.5E-02	n=28
brush border membrane	GO:0031526	p=3.6E-02	n=3
neuron projection	GO:0043005	p=3.7E-02	n=20
cell projection	GO:0042995	p=3.7E-02	n=28
dendritic tree	GO:0097447	p=3.8E-02	n=12
membrane protein complex	GO:0098796	p=4.0E-02	n=14
proton-transporting V-type ATPase comple...	GO:0033176	p=4.1E-02	n=2



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