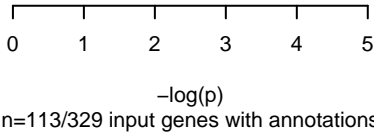


GO:BP  
Elav\_Nvec\_vc1.1\_XM\_032376736.2

fraction genes in fg and expected value

protein autophosphorylation	GO:0046777	p=1.5E-03	n=8
negative regulation of hippo signaling	GO:0035331	p=2.2E-03	n=3
branching involved in open tracheal syst...	GO:0060446	p=5.0E-03	n=3
protein O-linked fucosylation	GO:0036066	p=5.1E-03	n=2
negative regulation of telomere maintena...	GO:0032211	p=5.1E-03	n=2
cardiac ventricle formation	GO:0003211	p=5.1E-03	n=2
compartment pattern specification	GO:0007386	p=5.1E-03	n=2
cardiac myofibril assembly	GO:0055003	p=5.1E-03	n=2
queuosine biosynthetic process	GO:0008616	p=9.9E-03	n=2
N-terminal protein amino acid acetylati...	GO:0006474	p=9.9E-03	n=2
sperm DNA decondensation	GO:0035041	p=9.9E-03	n=2
Notch signaling pathway	GO:0007219	p=1.2E-02	n=8
fucosylation	GO:0036065	p=1.5E-02	n=4
suckling behavior	GO:0001967	p=1.6E-02	n=2
regulation of respiratory gaseous exchan...	GO:0043576	p=1.6E-02	n=2
negative regulation of protein-containin...	GO:0031333	p=1.6E-02	n=4
regulation of neuron apoptotic process	GO:0043523	p=2.2E-02	n=7
larval lymph gland hemopoiesis	GO:0035167	p=2.2E-02	n=3
positive regulation of stress fiber asse...	GO:0051496	p=2.2E-02	n=3
NADPH regeneration	GO:0006740	p=2.3E-02	n=2
muscle cell fate commitment	GO:0042693	p=2.3E-02	n=2
branched-chain amino acid metabolic proc...	GO:0009081	p=2.3E-02	n=2
branched-chain amino acid catabolic proc...	GO:0009083	p=2.3E-02	n=2
negative regulation of calcium ion-depen...	GO:0045955	p=2.3E-02	n=2
positive regulation of transcription by ...	GO:0045944	p=2.6E-02	n=16
embryonic hemopoiesis	GO:0035162	p=2.7E-02	n=3
regulation of actomyosin structure organ...	GO:0110020	p=2.7E-02	n=4
contractile actin filament bundle assemb...	GO:0030038	p=2.7E-02	n=4
stress fiber assembly	GO:0043149	p=2.7E-02	n=4
regulation of Notch signaling pathway	GO:0008593	p=2.8E-02	n=6

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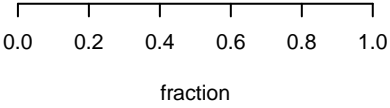
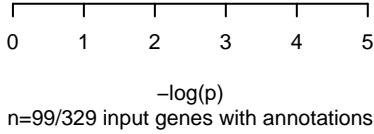


GO:MF  
Elav\_Nvec\_vc1.1\_XM\_032376736.2

fraction genes in fg and expected value

protein serine/threonine kinase activity	GO:0004674	p=5.9E-04	n=12
RNA polymerase II cis-regulatory region ...	GO:0000978	p=3.4E-03	n=9
caspase binding	GO:0089720	p=5.0E-03	n=2
DNA-binding transcription activator acti...	GO:0001228	p=1.1E-02	n=8
DNA-binding transcription activator acti...	GO:0001216	p=1.1E-02	n=8
purine ribonucleoside triphosphate bindi...	GO:0035639	p=1.2E-02	n=12
alpha-(1->3)-fucosyltransferase activity	GO:0046920	p=1.6E-02	n=2
fucosyltransferase activity	GO:0008417	p=1.6E-02	n=2
ATP binding	GO:0005524	p=2.4E-02	n=9
SMAD binding	GO:0046332	p=2.7E-02	n=3
nucleotide binding	GO:0000166	p=2.7E-02	n=14
nucleoside phosphate binding	GO:1901265	p=2.7E-02	n=14
ribonucleotide binding	GO:0032553	p=2.8E-02	n=12
purine ribonucleotide binding	GO:0032555	p=2.8E-02	n=12
kinase binding	GO:0019900	p=2.9E-02	n=13
polynucleotide adenyllyltransferase activ...	GO:0004652	p=3.2E-02	n=2
MAP kinase activity	GO:0004707	p=3.2E-02	n=2
purine nucleotide binding	GO:0017076	p=3.6E-02	n=12
protein kinase binding	GO:0019901	p=3.8E-02	n=12
carbohydrate derivative binding	GO:0097367	p=4.1E-02	n=13
NAD(P)+ transhydrogenase (AB-specific) a...	GO:0008750	p=4.2E-02	n=1
GDP-mannose 4,6-dehydratase activity	GO:0008446	p=4.2E-02	n=1
Rho GDP-dissociation inhibitor binding	GO:0051022	p=4.2E-02	n=1
apolipoprotein receptor binding	GO:0034190	p=4.2E-02	n=1
apolipoprotein A-I receptor binding	GO:0034191	p=4.2E-02	n=1
G-protein beta-subunit binding	GO:0031681	p=4.2E-02	n=1
ribokinase activity	GO:0004747	p=4.2E-02	n=1
RNA uridylyltransferase activity	GO:0050265	p=4.2E-02	n=1
adenylate cyclase activator activity	GO:0010856	p=4.2E-02	n=1
5-phosphoribosyl 1-pyrophosphate pyropho...	GO:0043135	p=4.2E-02	n=1

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GO:CC  
Elav\_Nvec\_vc1.1\_XM\_032376736.2

fraction genes in fg and expected value

FAR/SIN/STRIPAK complex	GO:0090443	p=5.0E-03	n=2
intracellular membrane-bounded organelle	GO:0043231	p=1.3E-02	n=96
intermediate filament	GO:0005882	p=1.6E-02	n=2
nuclear speck	GO:0016607	p=2.1E-02	n=8
membrane-bounded organelle	GO:0043227	p=2.2E-02	n=98
Golgi apparatus	GO:0005794	p=2.3E-02	n=20
preribosome	GO:0030684	p=3.0E-02	n=4
preribosome, small subunit precursor	GO:0036688	p=3.1E-02	n=2
nuclear body	GO:0016604	p=3.6E-02	n=12
vesicle coat	GO:0030120	p=4.1E-02	n=2
ACF complex	GO:0016590	p=4.1E-02	n=1
XPC complex	GO:0071942	p=4.1E-02	n=1
Sec61 translocon complex	GO:0005784	p=4.1E-02	n=1
keratin filament	GO:0045095	p=4.1E-02	n=1
desmosome	GO:0030057	p=4.1E-02	n=1
bleb	GO:0032059	p=4.1E-02	n=1
translocon complex	GO:0071256	p=4.1E-02	n=1
nucleotide-excision repair complex	GO:0000109	p=4.1E-02	n=1
NatB complex	GO:0031416	p=4.1E-02	n=1
sperm individualization complex	GO:0070864	p=4.1E-02	n=1
investment cone	GO:0070865	p=4.1E-02	n=1
Golgi stack	GO:0005795	p=4.3E-02	n=5
Golgi cisterna	GO:0031985	p=4.5E-02	n=4
Golgi cisterna membrane	GO:0032580	p=5.1E-02	n=2
cell cortex region	GO:0099738	p=5.4E-02	n=3
intermediate filament cytoskeleton	GO:0045111	p=7.3E-02	n=2
endocytic vesicle	GO:0030139	p=7.5E-02	n=5
dihydrolipoyl dehydrogenase complex	GO:0045240	p=8.1E-02	n=1
signal peptidase complex	GO:0005787	p=8.1E-02	n=1
vacuolar proton-transporting V-type ATPa...	GO:0000220	p=8.1E-02	n=1

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