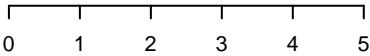


GO:BP
Elav_Nvec_vc1.1_XM_048733866.1

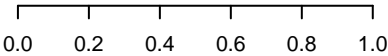
fraction genes in fg and expected value

astrocyte cell migration	GO:0043615	p=1.6E−03	n=2
negative regulation of myofibroblast dif...	GO:1904761	p=1.6E−03	n=2
cellular response to UV	GO:0034644	p=1.8E−03	n=4
germarium–derived egg chamber formation	GO:0007293	p=3.0E−03	n=4
regulation of vasculature development	GO:1901342	p=4.4E−03	n=5
growth hormone receptor signaling pathwa...	GO:0060396	p=4.7E−03	n=2
histone H4–K20 methylation	GO:0034770	p=4.7E−03	n=2
pentose–phosphate shunt	GO:0006098	p=4.7E−03	n=2
signal complex assembly	GO:0007172	p=4.7E−03	n=2
negative regulation of cellular process	GO:0048523	p=4.7E−03	n=40
modification–dependent macromolecule cat...	GO:0043632	p=5.1E−03	n=11
compound eye photoreceptor development	GO:0042051	p=5.9E−03	n=4
positive regulation of translation	GO:0045727	p=7.2E−03	n=4
flagellated sperm motility	GO:0030317	p=7.2E−03	n=4
regulation of nucleobase–containing comp...	GO:0019219	p=8.0E−03	n=29
dosage compensation	GO:0007549	p=8.2E−03	n=3
cellular response to stress	GO:0033554	p=8.2E−03	n=24
nucleolar chromatin organization	GO:1990700	p=9.1E−03	n=2
glyceraldehyde–3–phosphate metabolic pro...	GO:0019682	p=9.1E−03	n=2
histone H2A monoubiquitination	GO:0035518	p=9.1E−03	n=2
cellular response to transforming growth...	GO:0071560	p=1.0E−02	n=5
response to transforming growth factor b...	GO:0071559	p=1.0E−02	n=5
organic cyclic compound biosynthetic pro...	GO:1901362	p=1.0E−02	n=31
heterocycle biosynthetic process	GO:0018130	p=1.2E−02	n=30
aromatic compound biosynthetic process	GO:0019438	p=1.2E−02	n=30
cellular response to oxidative stress	GO:0034599	p=1.2E−02	n=6
ubiquitin–dependent protein catabolic pr...	GO:0006511	p=1.2E−02	n=10
modification–dependent protein catabolic...	GO:0019941	p=1.3E−02	n=10
protein autophosphorylation	GO:0046777	p=1.3E−02	n=5
protein phosphorylation	GO:0006468	p=1.3E−02	n=17



−log(p)
n=73/230 input genes with annotations

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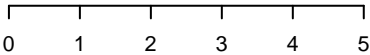


fraction

GO:MF
Elav_Nvec_vc1.1_XM_048733866.1

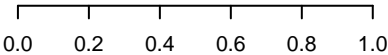
fraction genes in fg and expected value

JUN kinase binding	GO:0008432	p=5.1E−04	n=3
protein serine/threonine kinase activity	GO:0004674	p=2.6E−03	n=8
nuclear androgen receptor binding	GO:0050681	p=3.8E−03	n=3
mRNA regulatory element binding translat...	GO:0000900	p=4.2E−03	n=2
R–SMAD binding	GO:0070412	p=1.3E−02	n=2
SMAD binding	GO:0046332	p=1.4E−02	n=3
poly–pyrimidine tract binding	GO:0008187	p=2.0E−02	n=2
hormone receptor binding	GO:0051427	p=2.3E−02	n=4
DEAD/H–box RNA helicase binding	GO:0017151	p=2.7E−02	n=2
single–stranded RNA binding	GO:0003727	p=3.3E−02	n=3
lysine N–methyltransferase activity	GO:0016278	p=3.5E−02	n=2
Roundabout binding	GO:0048495	p=3.8E−02	n=1
CXCR chemokine receptor binding	GO:0045236	p=3.8E−02	n=1
histone methyltransferase activity (H3–K...	GO:0046976	p=3.8E−02	n=1
BH4 domain binding	GO:0051435	p=3.8E−02	n=1
S100 protein binding	GO:0044548	p=3.8E−02	n=1
glucose–6–phosphate dehydrogenase activi...	GO:0004345	p=3.8E−02	n=1
ribokinase activity	GO:0004747	p=3.8E−02	n=1
neuropilin binding	GO:0038191	p=3.8E−02	n=1
DNA replication origin binding	GO:0003688	p=3.8E−02	n=1
histone H3–tri/di/monomethyl–lysine–4 de...	GO:0034647	p=3.8E−02	n=1
triplex DNA binding	GO:0045142	p=3.8E−02	n=1
open rectifier potassium channel activit...	GO:0005252	p=3.8E−02	n=1
3–phosphoinositide–dependent protein kin...	GO:0043423	p=3.8E−02	n=1
JUN kinase kinase kinase activity	GO:0004706	p=3.8E−02	n=1
phosphoglycerate kinase activity	GO:0004618	p=3.8E−02	n=1
calcium channel inhibitor activity	GO:0019855	p=3.8E−02	n=1
histone kinase activity	GO:0035173	p=3.8E−02	n=1
ribonuclease III activity	GO:0004525	p=3.8E−02	n=1
dynein light intermediate chain binding	GO:0051959	p=3.8E−02	n=1



−log(p)
n=61/230 input genes with annotations

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fraction

GO:CC
Elav_Nvec_vc1.1_XM_048733866.1

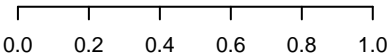
fraction genes in fg and expected value

COPI–coated vesicle	GO:0030137	p=2.0E−03	n=3
focal adhesion	GO:0005925	p=2.5E−03	n=4
stress fiber	GO:0001725	p=4.6E−03	n=3
Sin3–type complex	GO:0070822	p=4.8E−03	n=2
Cul4A–RING E3 ubiquitin ligase complex	GO:0031464	p=4.8E−03	n=2
manchette	GO:0002177	p=4.8E−03	n=2
fibrillar center	GO:0001650	p=6.3E−03	n=4
X chromosome	GO:0000805	p=9.4E−03	n=2
subsynaptic reticulum	GO:0071212	p=9.4E−03	n=2
female germ cell nucleus	GO:0001674	p=1.5E−02	n=2
actin filament	GO:0005884	p=1.5E−02	n=2
adherens junction	GO:0005912	p=2.1E−02	n=5
secondary lysosome	GO:0005767	p=3.0E−02	n=2
cytoplasmic ribonucleoprotein granule	GO:0036464	p=3.1E−02	n=5
nuclear speck	GO:0016607	p=3.5E−02	n=6
germ cell nucleus	GO:0043073	p=3.9E−02	n=2
striated muscle dense body	GO:0055120	p=3.9E−02	n=2
coated membrane	GO:0048475	p=4.0E−02	n=3
membrane coat	GO:0030117	p=4.0E−02	n=3
nucleus	GO:0005634	p=4.0E−02	n=45
ribonucleoprotein granule	GO:0035770	p=4.0E−02	n=5
dihydrolipoyl dehydrogenase complex	GO:0045240	p=4.1E−02	n=1
microprocessor complex	GO:0070877	p=4.1E−02	n=1
piP–body	GO:0071547	p=4.1E−02	n=1
AP–3 adaptor complex	GO:0030123	p=4.1E−02	n=1
NMDA selective glutamate receptor comple...	GO:0017146	p=4.1E−02	n=1
apoptosome	GO:0043293	p=4.1E−02	n=1
neuronal ribonucleoprotein granule	GO:0071598	p=4.1E−02	n=1
autosome	GO:0030849	p=4.1E−02	n=1
ribonuclease III complex	GO:1903095	p=4.1E−02	n=1



−log(p)
n=74/230 input genes with annotations

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fraction