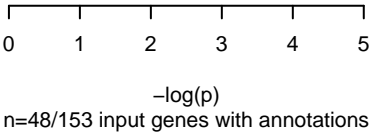


GO:BP
Elav_Nvec_vc1.1_XM_001639164.3

fraction genes in fg and expected value

pyrimidine nucleotide import into mitoch...	GO:1990519	p=2.0E−03	n=2
deoxynucleotide transport	GO:0030302	p=2.0E−03	n=2
negative regulation of lymphocyte mediat...	GO:0002707	p=2.0E−03	n=2
regulation of collagen biosynthetic proc...	GO:0032965	p=4.0E−03	n=2
mitochondrial transcription	GO:0006390	p=4.0E−03	n=2
regulation of androgen receptor signalin...	GO:0060765	p=4.0E−03	n=2
response to acidic pH	GO:0010447	p=6.5E−03	n=2
cellular homeostasis	GO:0019725	p=7.7E−03	n=10
regulation of pole plasm oskar mRNA loca...	GO:0007317	p=9.6E−03	n=2
regulation of embryonic pattern specific...	GO:1902875	p=9.6E−03	n=2
regulation of oogenesis	GO:1905879	p=1.3E−02	n=3
synaptic vesicle priming	GO:0016082	p=1.3E−02	n=2
cytokinesis	GO:0000910	p=1.5E−02	n=4
negative regulation of mitotic cell cycl...	GO:1901991	p=1.7E−02	n=3
regulation of post−embryonic development	GO:0048580	p=1.7E−02	n=3
positive regulation of vulval developmen...	GO:0040026	p=1.7E−02	n=2
negative regulation of apoptotic signali...	GO:2001234	p=2.1E−02	n=4
morphogenesis of follicular epithelium	GO:0016333	p=2.2E−02	n=2
oocyte karyosome formation	GO:0030717	p=2.2E−02	n=2
mitochondrion distribution	GO:0048311	p=2.2E−02	n=2
karyosome formation	GO:0061988	p=2.2E−02	n=2
cellular chemical homeostasis	GO:0055082	p=2.3E−02	n=8
regulation of synaptic vesicle membrane ...	GO:1901632	p=2.6E−02	n=1
kidney smooth muscle tissue development	GO:0072194	p=2.6E−02	n=1
translocation of molecules into host	GO:0044417	p=2.6E−02	n=1
maternal determination of dorsal/ventral...	GO:0008070	p=2.6E−02	n=1
detection of chemical stimulus involved ...	GO:0001581	p=2.6E−02	n=1
response to oscillatory fluid shear stre...	GO:0097702	p=2.6E−02	n=1
cellular response to oscillatory fluid s...	GO:0097704	p=2.6E−02	n=1
dosage compensation by hypoactivation of...	GO:0042464	p=2.6E−02	n=1



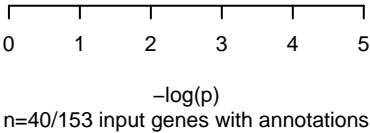
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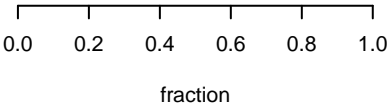
GO:MF
Elav_Nvec_vc1.1_XM_001639164.3

fraction genes in fg and expected value

cysteine−type endopeptidase inhibitor ac...	GO:0004869	p=1.8E−03	n=2
pyrimidine nucleotide transmembrane tran...	GO:0015218	p=1.8E−03	n=2
ADP binding	GO:0043531	p=1.6E−02	n=2
methionine adenosyltransferase regulator...	GO:0048270	p=2.5E−02	n=1
phosphoglycerate kinase activity	GO:0004618	p=2.5E−02	n=1
L−asparagine transmembrane transporter a...	GO:0015182	p=2.5E−02	n=1
L−aspartate transmembrane transporter ac...	GO:0015183	p=2.5E−02	n=1
L−glutamine transmembrane transporter ac...	GO:0015186	p=2.5E−02	n=1
HLH domain binding	GO:0043398	p=2.5E−02	n=1
phosphopantothenate−cysteine ligase act...	GO:0004632	p=2.5E−02	n=1
L−glutamate transmembrane transporter ac...	GO:0005313	p=2.5E−02	n=1
platelet activating factor receptor bind...	GO:0031859	p=2.5E−02	n=1
acidic amino acid transmembrane transpor...	GO:0015172	p=2.5E−02	n=1
follicle−stimulating hormone receptor bi...	GO:0031762	p=2.5E−02	n=1
muscle alpha−actinin binding	GO:0051371	p=2.5E−02	n=1
ecdysis−triggering hormone receptor acti...	GO:0042654	p=2.5E−02	n=1
type 2A serotonin receptor binding	GO:0031826	p=2.5E−02	n=1
phosphatidylserine decarboxylase activit...	GO:0004609	p=2.5E−02	n=1
opsin binding	GO:0002046	p=2.5E−02	n=1
branched−chain amino acid transmembrane ...	GO:0015658	p=2.5E−02	n=1
phosphatidylcholine transporter activity	GO:0008525	p=2.5E−02	n=1
alpha−1A adrenergic receptor binding	GO:0031691	p=2.5E−02	n=1
ankyrin repeat binding	GO:0071532	p=2.5E−02	n=1
methionine transmembrane transporter act...	GO:0043865	p=2.5E−02	n=1
L−leucine transmembrane transporter acti...	GO:0015190	p=2.5E−02	n=1
L−methionine transmembrane transporter a...	GO:0015191	p=2.5E−02	n=1
V2 vasopressin receptor binding	GO:0031896	p=2.5E−02	n=1
ATP binding	GO:0005524	p=2.5E−02	n=5
purine ribonucleoside triphosphate bindi...	GO:0035639	p=2.6E−02	n=6
phosphatidylinositol binding	GO:0035091	p=2.6E−02	n=4



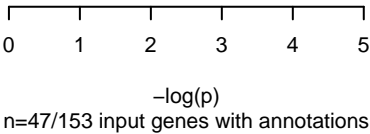
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GO:CC
Elav_Nvec_vc1.1_XM_001639164.3

fraction genes in fg and expected value

Set1C/COMPASS complex	GO:0048188	p=3.8E−03	n=2
organelle membrane	GO:0031090	p=2.0E−02	n=19
clathrin−coated pit	GO:0005905	p=2.1E−02	n=2
THO complex part of transcription export...	GO:0000445	p=2.6E−02	n=1
extrinsic component of presynaptic activ...	GO:0098891	p=2.6E−02	n=1
transcription export complex	GO:0000346	p=2.6E−02	n=1
THO complex	GO:0000347	p=2.6E−02	n=1
extrinsic component of synaptic membrane	GO:0099243	p=2.6E−02	n=1
CHAC	GO:0008623	p=2.6E−02	n=1
extrinsic component of presynaptic membr...	GO:0098888	p=2.6E−02	n=1
anchored component of synaptic vesicle m...	GO:0098993	p=2.6E−02	n=1
ACF complex	GO:0016590	p=2.6E−02	n=1
methionine adenosyltransferase complex	GO:0048269	p=2.6E−02	n=1
polycystin complex	GO:0002133	p=2.6E−02	n=1
synaptic membrane	GO:0097060	p=2.7E−02	n=4
mitochondrial inner membrane	GO:0005743	p=2.8E−02	n=5
endocytic vesicle	GO:0030139	p=3.2E−02	n=4
plasma membrane region	GO:0098590	p=3.3E−02	n=9
P granule	GO:0043186	p=3.7E−02	n=2
organelle inner membrane	GO:0019866	p=4.0E−02	n=5
germ plasm	GO:0060293	p=4.3E−02	n=2
pole plasm	GO:0045495	p=4.3E−02	n=2
myelin sheath	GO:0043209	p=4.4E−02	n=3
NURF complex	GO:0016589	p=5.1E−02	n=1
PTW/PP1 phosphatase complex	GO:0072357	p=5.1E−02	n=1
mitochondrial crista	GO:0030061	p=5.1E−02	n=1
RSF complex	GO:0031213	p=5.1E−02	n=1
pyruvate dehydrogenase (lipoamide) phosp...	GO:0045253	p=5.1E−02	n=1
mitochondrial pyruvate dehydrogenase (li...	GO:0019910	p=5.1E−02	n=1
organelle subcompartment	GO:0031984	p=6.2E−02	n=11



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