GO:BP
Elav_Nvec_vc1.1_XM_001637733.3

fraction genes in fg and expected valu...

pyrimidine nucleotide import into mitoch... GO:1990519	p=2.0E−03	n=2	fg=0.04	bg=0.00
deoxynucleotide transport GO:0030302	p=2.0E−03	n=2	fg=0.04	bg=0.00
negative regulation of lymphocyte mediat... GO:0002707	p=2.0E−03	n=2	fg=0.04	bg=0.00
regulation of collagen biosynthetic proc... GO:0032965	p=4.0E−03	n=2	fg=0.04	bg=0.00
mitochondrial transcription GO:0006390	p=4.0E−03	n=2	fg=0.04	bg=0.00
regulation of androgen receptor signalin... GO:0060765	p=4.0E−03	n=2	fg=0.04	bg=0.00
response to acidic pH GO:0010447	p=6.5E−03	n=2	fg=0.04	bg=0.00
cellular homeostasis GO:0019725	p=7.7E−03	n=10	fg=0.21	bg=0.09
regulation of pole plasm oskar mRNA loca... GO:0007317	p=9.6E−03	n=2	fg=0.04	bg=0.00
regulation of embryonic pattern specific... GO:1902875	p=9.6E−03	n=2	fg=0.04	bg=0.00
regulation of oogenesis GO:1905879	p=1.3E−02	n=3	fg=0.06	bg=0.01
synaptic vesicle priming GO:0016082	p=1.3E−02	n=2	fg=0.04	bg=0.00
cytokinesis GO:0000910	p=1.5E−02	n=4	fg=0.08	bg=0.02
negative regulation of mitotic cell cycl... GO:1901991	p=1.7E−02	n=3	fg=0.06	bg=0.01
regulation of post−embryonic development GO:0048580	p=1.7E−02	n=3	fg=0.06	bg=0.01
positive regulation of vulval developmen... GO:0040026	p=1.7E−02	n=2	fg=0.04	bg=0.00
negative regulation of apoptotic signali... GO:2001234	p=2.1E−02	n=4	fg=0.08	bg=0.02
morphogenesis of follicular epithelium GO:0016333	p=2.2E−02	n=2	fg=0.04	bg=0.01
oocyte karyosome formation GO:0030717	p=2.2E−02	n=2	fg=0.04	bg=0.01
mitochondrion distribution GO:0048311	p=2.2E−02	n=2	fg=0.04	bg=0.01
karyosome formation GO:0061988	p=2.2E−02	n=2	fg=0.04	bg=0.01
cellular chemical homeostasis GO:0055082	p=2.3E−02	n=8	fg=0.17	bg=0.07
regulation of synaptic vesicle membrane ... GO:1901632	p=2.6E−02	n=1	fg=0.02	bg=0.00
kidney smooth muscle tissue development GO:0072194	p=2.6E−02	n=1	fg=0.02	bg=0.00
translocation of molecules into host GO:0044417	p=2.6E−02	n=1	fg=0.02	bg=0.00
maternal determination of dorsal/ventral... GO:0008070	p=2.6E−02	n=1	fg=0.02	bg=0.00
detection of chemical stimulus involved ... GO:0001581	p=2.6E−02	n=1	fg=0.02	bg=0.00
response to oscillatory fluid shear stre... GO:0097702	p=2.6E−02	n=1	fg=0.02	bg=0.00
cellular response to oscillatory fluid s... GO:0097704	p=2.6E−02	n=1	fg=0.02	bg=0.00
dosage compensation by hypoactivation of... GO:0042464	p=2.6E−02	n=1	fg=0.02	bg=0.00

0 1 2 3 4 5

−log(p)
n=48/153 input genes with annotations

0.0 0.2 0.4 0.6 0.8 1.0

fraction

GO:MF
Elav_Nvec_vc1.1_XM_001637733.3

fraction genes in fg and expected valu...

cysteine−type endopeptidase inhibitor ac... GO:0004869	p=1.8E−03	n=2	fg=0.05	bg=0.00
pyrimidine nucleotide transmembrane tran... GO:0015218	p=1.8E−03	n=2	fg=0.05	bg=0.00
ADP binding GO:0043531	p=1.6E−02	n=2	fg=0.05	bg=0.01
methionine adenosyltransferase regulator... GO:0048270	p=2.5E−02	n=1	fg=0.03	bg=0.00
phosphoglycerate kinase activity GO:0004618	p=2.5E−02	n=1	fg=0.03	bg=0.00
L−asparagine transmembrane transporter a... GO:0015182	p=2.5E−02	n=1	fg=0.03	bg=0.00
L−aspartate transmembrane transporter ac... GO:0015183	p=2.5E−02	n=1	fg=0.03	bg=0.00
L−glutamine transmembrane transporter ac... GO:0015186	p=2.5E−02	n=1	fg=0.03	bg=0.00
HLH domain binding GO:0043398	p=2.5E−02	n=1	fg=0.03	bg=0.00
phosphopantothenate−−cysteine ligase act... GO:0004632	p=2.5E−02	n=1	fg=0.03	bg=0.00
L−glutamate transmembrane transporter ac... GO:0005313	p=2.5E−02	n=1	fg=0.03	bg=0.00
platelet activating factor receptor bind... GO:0031859	p=2.5E−02	n=1	fg=0.03	bg=0.00
acidic amino acid transmembrane transpor... GO:0015172	p=2.5E−02	n=1	fg=0.03	bg=0.00
follicle−stimulating hormone receptor bi... GO:0031762	p=2.5E−02	n=1	fg=0.03	bg=0.00
muscle alpha−actinin binding GO:0051371	p=2.5E−02	n=1	fg=0.03	bg=0.00
ecdysis−triggering hormone receptor acti... GO:0042654	p=2.5E−02	n=1	fg=0.03	bg=0.00
type 2A serotonin receptor binding GO:0031826	p=2.5E−02	n=1	fg=0.03	bg=0.00
phosphatidylserine decarboxylase activit... GO:0004609	p=2.5E−02	n=1	fg=0.03	bg=0.00
opsin binding GO:0002046	p=2.5E−02	n=1	fg=0.03	bg=0.00
branched−chain amino acid transmembrane ... GO:0015658	p=2.5E−02	n=1	fg=0.03	bg=0.00
phosphatidylcholine transporter activity GO:0008525	p=2.5E−02	n=1	fg=0.03	bg=0.00
alpha−1A adrenergic receptor binding GO:0031691	p=2.5E−02	n=1	fg=0.03	bg=0.00
ankyrin repeat binding GO:0071532	p=2.5E−02	n=1	fg=0.03	bg=0.00
methionine transmembrane transporter act... GO:0043865	p=2.5E−02	n=1	fg=0.03	bg=0.00
L−leucine transmembrane transporter acti... GO:0015190	p=2.5E−02	n=1	fg=0.03	bg=0.00
L−methionine transmembrane transporter a... GO:0015191	p=2.5E−02	n=1	fg=0.03	bg=0.00
V2 vasopressin receptor binding GO:0031896	p=2.5E−02	n=1	fg=0.03	bg=0.00
ATP binding GO:0005524	p=2.5E−02	n=5	fg=0.12	bg=0.04
purine ribonucleoside triphosphate bindi... GO:0035639	p=2.6E−02	n=6	fg=0.15	bg=0.06
phosphatidylinositol binding GO:0035091	p=2.6E−02	n=4	fg=0.10	bg=0.03

0 1 2 3 4 5

−log(p)
n=40/153 input genes with annotations

0.0 0.2 0.4 0.6 0.8 1.0

fraction

GO:CC
Elav_Nvec_vc1.1_XM_001637733.3

fraction genes in fg and expected valu...

Set1C/COMPASS complex GO:0048188	p=3.8E−03	n=2	fg=0.04	bg=0.00
organelle membrane GO:0031090	p=2.0E−02	n=19	fg=0.40	bg=0.26
clathrin−coated pit GO:0005905	p=2.1E−02	n=2	fg=0.04	bg=0.00
THO complex part of transcription export... GO:0000445	p=2.6E−02	n=1	fg=0.02	bg=0.00
extrinsic component of presynaptic activ... GO:0098891	p=2.6E−02	n=1	fg=0.02	bg=0.00
transcription export complex GO:0000346	p=2.6E−02	n=1	fg=0.02	bg=0.00
THO complex GO:0000347	p=2.6E−02	n=1	fg=0.02	bg=0.00
extrinsic component of synaptic membrane GO:0099243	p=2.6E−02	n=1	fg=0.02	bg=0.00
CHRAC GO:0008623	p=2.6E−02	n=1	fg=0.02	bg=0.00
extrinsic component of presynaptic membr... GO:0098888	p=2.6E−02	n=1	fg=0.02	bg=0.00
anchored component of synaptic vesicle m... GO:0098993	p=2.6E−02	n=1	fg=0.02	bg=0.00
ACF complex GO:0016590	p=2.6E−02	n=1	fg=0.02	bg=0.00
methionine adenosyltransferase complex GO:0048269	p=2.6E−02	n=1	fg=0.02	bg=0.00
polycystin complex GO:0002133	p=2.6E−02	n=1	fg=0.02	bg=0.00
synaptic membrane GO:0097060	p=2.7E−02	n=4	fg=0.09	bg=0.02
mitochondrial inner membrane GO:0005743	p=2.8E−02	n=5	fg=0.11	bg=0.04
endocytic vesicle GO:0030139	p=3.2E−02	n=4	fg=0.09	bg=0.03
plasma membrane region GO:0098590	p=3.3E−02	n=9	fg=0.19	bg=0.10
P granule GO:0043186	p=3.7E−02	n=2	fg=0.04	bg=0.01
organelle inner membrane GO:0019866	p=4.0E−02	n=5	fg=0.11	bg=0.04
germ plasm GO:0060293	p=4.3E−02	n=2	fg=0.04	bg=0.01
pole plasm GO:0045495	p=4.3E−02	n=2	fg=0.04	bg=0.01
myelin sheath GO:0043209	p=4.4E−02	n=3	fg=0.06	bg=0.02
NURF complex GO:0016589	p=5.1E−02	n=1	fg=0.02	bg=0.00
PTW/PP1 phosphatase complex GO:0072357	p=5.1E−02	n=1	fg=0.02	bg=0.00
mitochondrial crista GO:0030061	p=5.1E−02	n=1	fg=0.02	bg=0.00
RSF complex GO:0031213	p=5.1E−02	n=1	fg=0.02	bg=0.00
pyruvate dehydrogenase (lipoamide) phosp... GO:0045253	p=5.1E−02	n=1	fg=0.02	bg=0.00
mitochondrial pyruvate dehydrogenase (li... GO:0019910	p=5.1E−02	n=1	fg=0.02	bg=0.00
organelle subcompartment GO:0031984	p=6.2E−02	n=11	fg=0.23	bg=0.14

0 1 2 3 4 5

−log(p)
n=47/153 input genes with annotations

0.0 0.2 0.4 0.6 0.8 1.0

fraction