GO:BP
Elav_Nvec_vc1.1_XM_032364561.2

fraction genes in fg and expected valu...

Term	p-value	n	fg	bg
establishment of epithelial cell apical/... GO:0045198	p=5.0E−04	n=2	fg=0.08	bg=0.00
embryonic hemopoiesis GO:0035162	p=5.3E−04	n=3	fg=0.12	bg=0.01
positive regulation of intracellular sig... GO:1902533	p=7.3E−04	n=7	fg=0.29	bg=0.07
negative regulation of endothelial cell ... GO:2000352	p=9.9E−04	n=2	fg=0.08	bg=0.00
homophilic cell adhesion via plasma memb... GO:0007156	p=9.9E−04	n=2	fg=0.08	bg=0.00
mesenchymal to epithelial transition GO:0060231	p=9.9E−04	n=2	fg=0.08	bg=0.00
central nervous system neuron developmen... GO:0021954	p=1.0E−03	n=3	fg=0.12	bg=0.01
cochlea development GO:0090102	p=1.0E−03	n=3	fg=0.12	bg=0.01
negative regulation of inflammatory resp... GO:0050728	p=1.0E−03	n=3	fg=0.12	bg=0.01
gland development GO:0048732	p=1.4E−03	n=6	fg=0.25	bg=0.05
ommatidial rotation GO:0016318	p=1.6E−03	n=2	fg=0.08	bg=0.00
positive regulation of muscle cell apopt... GO:0010661	p=1.6E−03	n=2	fg=0.08	bg=0.00
regulation of epithelial tube formation GO:1905276	p=1.6E−03	n=2	fg=0.08	bg=0.00
establishment of imaginal disc−derived w... GO:0001737	p=1.6E−03	n=2	fg=0.08	bg=0.00
brain development GO:0007420	p=2.4E−03	n=7	fg=0.29	bg=0.08
positive regulation of protein−containin... GO:0043243	p=2.4E−03	n=2	fg=0.08	bg=0.00
branched−chain amino acid catabolic proc... GO:0009083	p=2.4E−03	n=2	fg=0.08	bg=0.00
animal organ maturation GO:0048799	p=2.4E−03	n=2	fg=0.08	bg=0.00
positive regulation of G protein−coupled... GO:0045745	p=2.4E−03	n=2	fg=0.08	bg=0.00
brown fat cell differentiation GO:0050873	p=2.4E−03	n=2	fg=0.08	bg=0.00
regulation of tube length, open tracheal... GO:0035159	p=3.4E−03	n=2	fg=0.08	bg=0.00
heart valve morphogenesis GO:0003179	p=3.4E−03	n=2	fg=0.08	bg=0.00
nephron tubule development GO:0072080	p=3.4E−03	n=3	fg=0.12	bg=0.01
heart morphogenesis GO:0003007	p=4.2E−03	n=4	fg=0.17	bg=0.03
cellular response to BMP stimulus GO:0071773	p=4.3E−03	n=3	fg=0.12	bg=0.01
fatty acid beta−oxidation GO:0006635	p=4.5E−03	n=2	fg=0.08	bg=0.00
regulation of cardiac muscle cell differ... GO:2000725	p=4.5E−03	n=2	fg=0.08	bg=0.00
regulation of angiogenesis GO:0045765	p=4.8E−03	n=3	fg=0.12	bg=0.01
renal tubule morphogenesis GO:0061333	p=4.8E−03	n=3	fg=0.12	bg=0.01
negative regulation of vasculature devel... GO:1901343	p=5.7E−03	n=2	fg=0.08	bg=0.01

−log(p): 0 1 2 3 4 5
n=24/91 input genes with annotations

fraction: 0.0 0.2 0.4 0.6 0.8 1.0

GO:MF
Elav_Nvec_vc1.1_XM_032364561.2

fraction genes in fg and expected valu...

Term	p-value	n	fg	bg
amyloid−beta binding GO:0001540	p=9.3E−03	n=2	fg=0.09	bg=0.01
ammonium ion binding GO:0070405	p=1.1E−02	n=2	fg=0.09	bg=0.01
beta1−adrenergic receptor activity GO:0004940	p=1.4E−02	n=1	fg=0.05	bg=0.00
C−acyltransferase activity GO:0016408	p=1.4E−02	n=1	fg=0.05	bg=0.00
beta2−adrenergic receptor activity GO:0004941	p=1.4E−02	n=1	fg=0.05	bg=0.00
testosterone 17−beta−dehydrogenase (NADP... GO:0047045	p=1.4E−02	n=1	fg=0.05	bg=0.00
steroid dehydrogenase activity GO:0016229	p=1.4E−02	n=1	fg=0.05	bg=0.00
acetyl−CoA C−acetyltransferase activity GO:0003985	p=1.4E−02	n=1	fg=0.05	bg=0.00
beta−adrenergic receptor activity GO:0004939	p=1.4E−02	n=1	fg=0.05	bg=0.00
acetyl−CoA C−acyltransferase activity GO:0003988	p=1.4E−02	n=1	fg=0.05	bg=0.00
C−acetyltransferase activity GO:0016453	p=1.4E−02	n=1	fg=0.05	bg=0.00
dopamine binding GO:0035240	p=1.4E−02	n=1	fg=0.05	bg=0.00
ribokinase activity GO:0004747	p=1.4E−02	n=1	fg=0.05	bg=0.00
phosphatidylcholine transporter activity GO:0008525	p=1.4E−02	n=1	fg=0.05	bg=0.00
estradiol 17−beta−dehydrogenase activity GO:0004303	p=1.4E−02	n=1	fg=0.05	bg=0.00
alpha−galactosidase activity GO:0004557	p=1.4E−02	n=1	fg=0.05	bg=0.00
steroid dehydrogenase activity, acting o... GO:0033764	p=1.4E−02	n=1	fg=0.05	bg=0.00
alpha−N−acetylgalactosaminidase activity GO:0008456	p=1.4E−02	n=1	fg=0.05	bg=0.00
interleukin−2 receptor binding GO:0005134	p=1.4E−02	n=1	fg=0.05	bg=0.00
[3−methyl−2−oxobutanoate dehydrogenase (... GO:0047323	p=1.4E−02	n=1	fg=0.05	bg=0.00
bradykinin receptor binding GO:0031711	p=1.4E−02	n=1	fg=0.05	bg=0.00
B2 bradykinin receptor binding GO:0031713	p=1.4E−02	n=1	fg=0.05	bg=0.00
long−chain fatty acid transporter activi... GO:0005324	p=1.4E−02	n=1	fg=0.05	bg=0.00
protein homodimerization activity GO:0042803	p=1.7E−02	n=6	fg=0.27	bg=0.10
protein dimerization activity GO:0046983	p=1.7E−02	n=7	fg=0.32	bg=0.13
identical protein binding GO:0042802	p=2.1E−02	n=8	fg=0.36	bg=0.17
translation regulator activity, nucleic ... GO:0090079	p=2.4E−02	n=2	fg=0.09	bg=0.01
alpha−2A adrenergic receptor binding GO:0031694	p=2.8E−02	n=1	fg=0.05	bg=0.00
adrenergic receptor activity GO:0004935	p=2.8E−02	n=1	fg=0.05	bg=0.00
phosphatidic acid transfer activity GO:1990050	p=2.8E−02	n=1	fg=0.05	bg=0.00

−log(p): 0 1 2 3 4 5
n=22/91 input genes with annotations

fraction: 0.0 0.2 0.4 0.6 0.8 1.0

GO:CC
Elav_Nvec_vc1.1_XM_032364561.2

fraction genes in fg and expected valu...

Term	p-value	n	fg	bg
mitochondrial alpha−ketoglutarate dehydr... GO:0005947	p=1.3E−02	n=1	fg=0.04	bg=0.00
dihydrolipoyl dehydrogenase complex GO:0045240	p=1.3E−02	n=1	fg=0.04	bg=0.00
clathrin−coated vesicle membrane GO:0030665	p=1.5E−02	n=2	fg=0.09	bg=0.01
Seh1−associated complex GO:0035859	p=2.5E−02	n=1	fg=0.04	bg=0.00
Wnt signalosome GO:1990909	p=2.5E−02	n=1	fg=0.04	bg=0.00
mitochondrial tricarboxylic acid cycle e... GO:0030062	p=2.5E−02	n=1	fg=0.04	bg=0.00
growth cone filopodium GO:1990812	p=2.5E−02	n=1	fg=0.04	bg=0.00
GATOR2 complex GO:0061700	p=2.5E−02	n=1	fg=0.04	bg=0.00
tricarboxylic acid cycle enzyme complex GO:0045239	p=2.5E−02	n=1	fg=0.04	bg=0.00
peroxisome GO:0005777	p=2.8E−02	n=2	fg=0.09	bg=0.01
microbody GO:0042579	p=2.8E−02	n=2	fg=0.09	bg=0.01
coated vesicle membrane GO:0030662	p=3.6E−02	n=2	fg=0.09	bg=0.01
intrinsic component of mitochondrial out... GO:0031306	p=3.8E−02	n=1	fg=0.04	bg=0.00
integral component of mitochondrial oute... GO:0031307	p=3.8E−02	n=1	fg=0.04	bg=0.00
smooth endoplasmic reticulum cisterna GO:0120082	p=3.8E−02	n=1	fg=0.04	bg=0.00
growth cone lamellipodium GO:1990761	p=3.8E−02	n=1	fg=0.04	bg=0.00
endoplasmic reticulum cisternal network GO:0071781	p=3.8E−02	n=1	fg=0.04	bg=0.00
intercalary heterochromatin GO:0005725	p=3.8E−02	n=1	fg=0.04	bg=0.00
subrhabdomeral cisterna GO:0016029	p=3.8E−02	n=1	fg=0.04	bg=0.00
Cul4A−RING E3 ubiquitin ligase complex GO:0031464	p=3.8E−02	n=1	fg=0.04	bg=0.00
PRC1 complex GO:0035102	p=3.8E−02	n=1	fg=0.04	bg=0.00
integral component of peroxisomal membra... GO:0005779	p=5.0E−02	n=1	fg=0.04	bg=0.00
intrinsic component of peroxisomal membr... GO:0031231	p=5.0E−02	n=1	fg=0.04	bg=0.00
eukaryotic translation initiation factor... GO:0005851	p=5.0E−02	n=1	fg=0.04	bg=0.00
clathrin−coated vesicle GO:0030136	p=6.1E−02	n=2	fg=0.09	bg=0.02
synapse GO:0045202	p=6.9E−02	n=5	fg=0.22	bg=0.10
integral component of membrane GO:0016021	p=7.0E−02	n=7	fg=0.30	bg=0.16
postsynapse GO:0098794	p=7.1E−02	n=3	fg=0.13	bg=0.04
clathrin−coated endocytic vesicle membra... GO:0030669	p=7.4E−02	n=1	fg=0.04	bg=0.00
peroxisomal membrane GO:0005778	p=7.4E−02	n=1	fg=0.04	bg=0.00

−log(p): 0 1 2 3 4 5
n=23/91 input genes with annotations

fraction: 0.0 0.2 0.4 0.6 0.8 1.0