GO:BP
Elav_Nvec_vc1.1_XM_001638492.3

fraction genes in fg and expected val

Term	p-value	n		fg	bg
regulation of cholesterol biosynthetic p... GO:0045540	p=2.7E−04	n=4		fg=0.04	bg=0.00
leukotriene metabolic process GO:0006691	p=1.3E−03	n=2		fg=0.02	bg=0.00
response to cadmium ion GO:0046686	p=3.1E−03	n=4		fg=0.04	bg=0.01
regulation of platelet aggregation GO:0090330	p=3.7E−03	n=2		fg=0.02	bg=0.00
female pregnancy GO:0007565	p=4.2E−03	n=5		fg=0.05	bg=0.01
cellular response to hydrogen peroxide GO:0070301	p=6.7E−03	n=4		fg=0.04	bg=0.01
epithelial cell migration, open tracheal... GO:0007427	p=7.2E−03	n=2		fg=0.02	bg=0.00
response to mercury ion GO:0046689	p=7.2E−03	n=2		fg=0.02	bg=0.00
skeletal muscle organ development GO:0060538	p=9.4E−03	n=6		fg=0.06	bg=0.02
cyclic nucleotide metabolic process GO:0009187	p=9.6E−03	n=3		fg=0.03	bg=0.00
cyclic nucleotide biosynthetic process GO:0009190	p=1.2E−02	n=2		fg=0.02	bg=0.00
negative regulation of Rho protein signa... GO:0035024	p=1.2E−02	n=2		fg=0.02	bg=0.00
cyclic purine nucleotide metabolic proce... GO:0052652	p=1.2E−02	n=2		fg=0.02	bg=0.00
response to testosterone GO:0033574	p=1.2E−02	n=3		fg=0.03	bg=0.01
response to ketone GO:1901654	p=1.6E−02	n=6		fg=0.06	bg=0.02
response to lipid GO:0033993	p=1.6E−02	n=12		fg=0.12	bg=0.06
purine ribonucleotide catabolic process GO:0009154	p=1.7E−02	n=2		fg=0.02	bg=0.00
formation of animal organ boundary GO:0010160	p=1.7E−02	n=2		fg=0.02	bg=0.00
response to fructose GO:0009750	p=1.7E−02	n=2		fg=0.02	bg=0.00
hemidesmosome assembly GO:0031581	p=1.7E−02	n=2		fg=0.02	bg=0.00
positive regulation of triglyceride bios... GO:0010867	p=1.7E−02	n=2		fg=0.02	bg=0.00
brown fat cell differentiation GO:0050873	p=1.7E−02	n=2		fg=0.02	bg=0.00
positive regulation of T cell proliferat... GO:0042102	p=1.7E−02	n=2		fg=0.02	bg=0.00
skeletal muscle tissue development GO:0007519	p=1.9E−02	n=5		fg=0.05	bg=0.02
response to organonitrogen compound GO:0010243	p=2.0E−02	n=16		fg=0.17	bg=0.10
fatty acid derivative metabolic process GO:1901568	p=2.1E−02	n=3		fg=0.03	bg=0.01
regulation of T cell proliferation GO:0042129	p=2.1E−02	n=3		fg=0.03	bg=0.01
ribonucleotide catabolic process GO:0009261	p=2.3E−02	n=2		fg=0.02	bg=0.00
cellular response to angiotensin GO:1904385	p=2.3E−02	n=2		fg=0.02	bg=0.00
multicellular organismal movement GO:0050879	p=2.3E−02	n=2		fg=0.02	bg=0.00

−log(p)
n=96/314 input genes with annotations

fraction

GO:MF
Elav_Nvec_vc1.1_XM_001638492.3

fraction genes in fg and expected valu

Term	p-value	n		fg	bg
magnesium ion binding GO:0000287	p=2.2E−03	n=7		fg=0.08	bg=0.02
transferase activity GO:0016740	p=1.4E−02	n=26		fg=0.31	bg=0.20
tRNA (guanine) methyltransferase activit... GO:0016423	p=1.7E−02	n=2		fg=0.02	bg=0.00
gamma−tubulin binding GO:0043015	p=1.7E−02	n=2		fg=0.02	bg=0.00
MAP kinase kinase activity GO:0004708	p=1.7E−02	n=2		fg=0.02	bg=0.00
protein tyrosine/serine/threonine phosph... GO:0008138	p=2.3E−02	n=2		fg=0.02	bg=0.00
ATP binding GO:0005524	p=2.6E−02	n=8		fg=0.10	bg=0.04
G−protein alpha−subunit binding GO:0001965	p=3.0E−02	n=2		fg=0.02	bg=0.00
Hsp90 protein binding GO:0051879	p=3.2E−02	n=3		fg=0.04	bg=0.01
steroid hydroxylase activity GO:0008395	p=3.5E−02	n=1		fg=0.01	bg=0.00
insulin−like growth factor I binding GO:0031994	p=3.5E−02	n=1		fg=0.01	bg=0.00
dopamine binding GO:0035240	p=3.5E−02	n=1		fg=0.01	bg=0.00
1−alpha,25−dihydroxyvitamin D3 24−hydrox... GO:0030342	p=3.5E−02	n=1		fg=0.01	bg=0.00
vitamin D3 25−hydroxylase activity GO:0030343	p=3.5E−02	n=1		fg=0.01	bg=0.00
3R−hydroxyacyl−CoA dehydratase activity GO:0080023	p=3.5E−02	n=1		fg=0.01	bg=0.00
cholesterol 26−hydroxylase activity GO:0031073	p=3.5E−02	n=1		fg=0.01	bg=0.00
25−hydroxycholecalciferol−24−hydroxylase... GO:0008403	p=3.5E−02	n=1		fg=0.01	bg=0.00
oxidoreductase activity, acting on paire... GO:0016709	p=3.5E−02	n=1		fg=0.01	bg=0.00
pre−miRNA binding GO:0070883	p=3.5E−02	n=1		fg=0.01	bg=0.00
all−trans−retinol binding GO:1904768	p=3.5E−02	n=1		fg=0.01	bg=0.00
carbohydrate:cation symporter activity GO:0005402	p=3.5E−02	n=1		fg=0.01	bg=0.00
carbohydrate:proton symporter activity GO:0005351	p=3.5E−02	n=1		fg=0.01	bg=0.00
all−trans retinal 3,4−desaturase activit... GO:0061896	p=3.5E−02	n=1		fg=0.01	bg=0.00
all−trans retinal 3,4−desaturase activit... GO:0061897	p=3.5E−02	n=1		fg=0.01	bg=0.00
N−acetylglucosamine kinase activity GO:0045127	p=3.5E−02	n=1		fg=0.01	bg=0.00
all−trans retinoic acid 3,4−desaturase a... GO:0061898	p=3.5E−02	n=1		fg=0.01	bg=0.00
11−cis−retinal 3,4−desaturase activity GO:0061899	p=3.5E−02	n=1		fg=0.01	bg=0.00
glucose transmembrane transporter activi... GO:0005355	p=3.5E−02	n=1		fg=0.01	bg=0.00
arginine kinase activity GO:0004054	p=3.5E−02	n=1		fg=0.01	bg=0.00
N−acylmannosamine kinase activity GO:0009384	p=3.5E−02	n=1		fg=0.01	bg=0.00

−log(p)
n=84/314 input genes with annotations

fraction

GO:CC
Elav_Nvec_vc1.1_XM_001638492.3

fraction genes in fg and expected valu

Term	p-value	n		fg	bg
MMXD complex GO:0071817	p=3.7E−03	n=2		fg=0.02	bg=0.00
CIA complex GO:0097361	p=3.7E−03	n=2		fg=0.02	bg=0.00
mitotic spindle GO:0072686	p=1.0E−02	n=5		fg=0.05	bg=0.01
MCM complex GO:0042555	p=1.7E−02	n=2		fg=0.02	bg=0.00
male germ cell nucleus GO:0001673	p=2.3E−02	n=2		fg=0.02	bg=0.00
ubiquitin ligase complex GO:0000151	p=2.6E−02	n=7		fg=0.07	bg=0.03
spindle GO:0005819	p=3.4E−02	n=9		fg=0.09	bg=0.03
transverse filament GO:0000802	p=3.6E−02	n=1		fg=0.01	bg=0.00
integrin alpha3−beta1 complex GO:0034667	p=3.6E−02	n=1		fg=0.01	bg=0.00
integrin alpha6−beta4 complex GO:0034676	p=3.6E−02	n=1		fg=0.01	bg=0.00
integrin alpha7−beta1 complex GO:0034677	p=3.6E−02	n=1		fg=0.01	bg=0.00
Nem1−Spo7 phosphatase complex GO:0071595	p=3.6E−02	n=1		fg=0.01	bg=0.00
immunoglobulin complex GO:0019814	p=3.6E−02	n=1		fg=0.01	bg=0.00
B cell receptor complex GO:0019815	p=3.6E−02	n=1		fg=0.01	bg=0.00
nuclear RNA export factor complex GO:0042272	p=3.6E−02	n=1		fg=0.01	bg=0.00
RNA nuclear export complex GO:0042565	p=3.6E−02	n=1		fg=0.01	bg=0.00
MKS complex GO:0036038	p=3.8E−02	n=2		fg=0.02	bg=0.00
heterochromatin GO:0000792	p=5.1E−02	n=3		fg=0.03	bg=0.01
nuclear body GO:0016604	p=6.3E−02	n=10		fg=0.10	bg=0.06
receptor complex GO:0043235	p=6.4E−02	n=4		fg=0.04	bg=0.02
female germline ring canal GO:0035324	p=7.0E−02	n=1		fg=0.01	bg=0.00
nuclear stress granule GO:0097165	p=7.0E−02	n=1		fg=0.01	bg=0.00
VCP−NPL4−UFD1 AAA ATPase complex GO:0034098	p=7.0E−02	n=1		fg=0.01	bg=0.00
T cell receptor complex GO:0042101	p=7.0E−02	n=1		fg=0.01	bg=0.00
Lewy body GO:0097413	p=7.0E−02	n=1		fg=0.01	bg=0.00
box H/ACA telomerase RNP complex GO:0090661	p=7.0E−02	n=1		fg=0.01	bg=0.00
nucleocytoplasmic transport complex GO:0031074	p=7.0E−02	n=1		fg=0.01	bg=0.00
box H/ACA snoRNP complex GO:0031429	p=7.0E−02	n=1		fg=0.01	bg=0.00
box H/ACA RNP complex GO:0072588	p=7.0E−02	n=1		fg=0.01	bg=0.00
box H/ACA scaRNP complex GO:0072589	p=7.0E−02	n=1		fg=0.01	bg=0.00

−log(p)
n=96/314 input genes with annotations

fraction