GO:BP
Elav_Nvec_vc1.1_XM_001632368.2

fraction genes in fg and expected valu...

Term	p	n	fg	bg
cellular response to glucagon stimulus GO:0071377	p=9.4E−05	n=3	fg=0.08	bg=0.00
negative regulation of cAMP−dependent pr... GO:2000480	p=2.0E−04	n=2	fg=0.05	bg=0.00
positive regulation of meiotic cell cycl... GO:1904146	p=6.0E−04	n=2	fg=0.05	bg=0.00
activation of protein kinase A activity GO:0034199	p=1.2E−03	n=2	fg=0.05	bg=0.00
response to antipsychotic drug GO:0097332	p=1.2E−03	n=2	fg=0.05	bg=0.00
response to clozapine GO:0097338	p=1.2E−03	n=2	fg=0.05	bg=0.00
brain segmentation GO:0035284	p=2.9E−03	n=2	fg=0.05	bg=0.00
cellular response to dexamethasone stimu... GO:0071549	p=2.9E−03	n=2	fg=0.05	bg=0.00
positive regulation of oocyte maturation GO:1900195	p=4.1E−03	n=2	fg=0.05	bg=0.00
O−glycan processing GO:0016266	p=4.1E−03	n=2	fg=0.05	bg=0.00
renal water homeostasis GO:0003091	p=4.1E−03	n=2	fg=0.05	bg=0.00
mitochondrial cytochrome c oxidase assem... GO:0033617	p=4.1E−03	n=2	fg=0.05	bg=0.00
alcohol biosynthetic process GO:0046165	p=7.1E−03	n=3	fg=0.08	bg=0.01
cellular response to xenobiotic stimulus GO:0071466	p=7.1E−03	n=3	fg=0.08	bg=0.01
positive regulation of oocyte developmen... GO:0060282	p=1.0E−02	n=2	fg=0.05	bg=0.00
polyol biosynthetic process GO:0046173	p=1.0E−02	n=2	fg=0.05	bg=0.00
positive regulation of oogenesis GO:1905881	p=1.4E−02	n=2	fg=0.05	bg=0.00
Malpighian tubule tip cell differentiati... GO:0061382	p=1.4E−02	n=1	fg=0.03	bg=0.00
imaginal disc lineage restriction GO:0035161	p=1.4E−02	n=1	fg=0.03	bg=0.00
negative regulation of cardiac muscle ce... GO:0060044	p=1.4E−02	n=1	fg=0.03	bg=0.00
regulation of acrosome reaction GO:0060046	p=1.4E−02	n=1	fg=0.03	bg=0.00
lipoxygenase pathway GO:0019372	p=1.4E−02	n=1	fg=0.03	bg=0.00
S−adenosyl−L−methionine transmembrane tr... GO:1901962	p=1.4E−02	n=1	fg=0.03	bg=0.00
calcium ion transmembrane transport via ... GO:0090676	p=1.4E−02	n=1	fg=0.03	bg=0.00
regulation of Notch signaling pathway in... GO:1902366	p=1.4E−02	n=1	fg=0.03	bg=0.00
negative regulation of Notch signaling p... GO:1902367	p=1.4E−02	n=1	fg=0.03	bg=0.00
dorsal/ventral lineage restriction, imag... GO:0007451	p=1.4E−02	n=1	fg=0.03	bg=0.00
Notch signaling pathway involved in somi... GO:1902359	p=1.4E−02	n=1	fg=0.03	bg=0.00
S−adenosyl−L−methionine transport GO:0015805	p=1.4E−02	n=1	fg=0.03	bg=0.00
positive regulation of acrosome reaction GO:2000344	p=1.4E−02	n=1	fg=0.03	bg=0.00

−log(p) (axis: 0 1 2 3 4 5)
fraction (axis: 0.0 0.2 0.4 0.6 0.8 1.0)

n=39/145 input genes with annotations

GO:MF
Elav_Nvec_vc1.1_XM_001632368.2

fraction genes in fg and expected valu...

Term	p	n	fg	bg
beta−2 adrenergic receptor binding GO:0031698	p=1.9E−04	n=2	fg=0.06	bg=0.00
cAMP−dependent protein kinase inhibitor ... GO:0004862	p=5.6E−04	n=2	fg=0.06	bg=0.00
cAMP binding GO:0030552	p=1.1E−03	n=2	fg=0.06	bg=0.00
protein kinase A catalytic subunit bindi... GO:0034236	p=1.1E−03	n=2	fg=0.06	bg=0.00
acetylglucosaminyltransferase activity GO:0008375	p=7.9E−03	n=2	fg=0.06	bg=0.00
15−hydroxyprostaglandin dehydrogenase (N... GO:0016404	p=1.4E−02	n=1	fg=0.03	bg=0.00
DNA insertion or deletion binding GO:0032135	p=1.4E−02	n=1	fg=0.03	bg=0.00
voltage−gated calcium channel activity i... GO:0086056	p=1.4E−02	n=1	fg=0.03	bg=0.00
voltage−gated calcium channel activity i... GO:0086059	p=1.4E−02	n=1	fg=0.03	bg=0.00
(alpha−N−acetylneuraminyl−2,3−beta−galac... GO:0047290	p=1.4E−02	n=1	fg=0.03	bg=0.00
heteroduplex DNA loop binding GO:0000404	p=1.4E−02	n=1	fg=0.03	bg=0.00
double−strand/single−strand DNA junction... GO:0000406	p=1.4E−02	n=1	fg=0.03	bg=0.00
poly(ADP−ribose) glycohydrolase activity GO:0004649	p=1.4E−02	n=1	fg=0.03	bg=0.00
O−fucosylpeptide 3−beta−N−acetylglucosam... GO:0033829	p=1.4E−02	n=1	fg=0.03	bg=0.00
juvenile hormone epoxide hydrolase activ... GO:0008096	p=1.4E−02	n=1	fg=0.03	bg=0.00
cis−stilbene−oxide hydrolase activity GO:0033961	p=1.4E−02	n=1	fg=0.03	bg=0.00
centromeric DNA binding GO:0019237	p=1.4E−02	n=1	fg=0.03	bg=0.00
sialyltransferase activity GO:0008373	p=1.4E−02	n=1	fg=0.03	bg=0.00
beta−1,3−galactosyl−O−glycosyl−glycoprot... GO:0047223	p=1.4E−02	n=1	fg=0.03	bg=0.00
prostaglandin E receptor activity GO:0004957	p=1.4E−02	n=1	fg=0.03	bg=0.00
voltage−gated calcium channel activity GO:0086007	p=1.4E−02	n=1	fg=0.03	bg=0.00
non−tyrosine kinase fibroblast growth fa... GO:0001571	p=1.4E−02	n=1	fg=0.03	bg=0.00
S−adenosyl−L−methionine transmembrane tr... GO:0000095	p=1.4E−02	n=1	fg=0.03	bg=0.00
alpha−N−acetylgalactosaminide alpha−2,6−... GO:0001665	p=1.4E−02	n=1	fg=0.03	bg=0.00
Y−form DNA binding GO:0000403	p=2.8E−02	n=1	fg=0.03	bg=0.00
NAD+ binding GO:0070403	p=2.8E−02	n=1	fg=0.03	bg=0.00
mismatched DNA binding GO:0030983	p=2.8E−02	n=1	fg=0.03	bg=0.00
protein tag GO:0031386	p=2.8E−02	n=1	fg=0.03	bg=0.00
low voltage−gated calcium channel activi... GO:0008332	p=2.8E−02	n=1	fg=0.03	bg=0.00
gamma−butyrobetaine dioxygenase activity GO:0008336	p=2.8E−02	n=1	fg=0.03	bg=0.00

−log(p) (axis: 0 1 2 3 4 5)
fraction (axis: 0.0 0.2 0.4 0.6 0.8 1.0)

n=33/145 input genes with annotations

GO:CC
Elav_Nvec_vc1.1_XM_001632368.2

fraction genes in fg and expected valu...

Term	p	n	fg	bg
cAMP−dependent protein kinase complex GO:0005952	p=5.4E−04	n=2	fg=0.05	bg=0.00
nucleotide−activated protein kinase comp... GO:0031588	p=1.1E−03	n=2	fg=0.05	bg=0.00
germinal vesicle GO:0042585	p=3.7E−03	n=2	fg=0.05	bg=0.00
dendritic spine GO:0043197	p=5.0E−03	n=4	fg=0.11	bg=0.02
sarcolemma GO:0042383	p=5.5E−03	n=3	fg=0.08	bg=0.01
plasma membrane raft GO:0044853	p=7.5E−03	n=3	fg=0.08	bg=0.01
T−tubule GO:0030315	p=1.3E−02	n=2	fg=0.05	bg=0.00
MutSbeta complex GO:0032302	p=1.4E−02	n=1	fg=0.03	bg=0.00
mitochondrial proton−transporting ATP sy... GO:2000276	p=1.4E−02	n=1	fg=0.03	bg=0.00
proton−transporting ATP synthase complex... GO:0045263	p=1.4E−02	n=1	fg=0.03	bg=0.00
proton−transporting ATP synthase, centra... GO:0045269	p=1.4E−02	n=1	fg=0.03	bg=0.00
mitochondrial proton−transporting ATP sy... GO:0005756	p=1.4E−02	n=1	fg=0.03	bg=0.00
ciliary base GO:0097546	p=1.5E−02	n=2	fg=0.05	bg=0.01
cytosolic ribosome GO:0022626	p=2.4E−02	n=3	fg=0.08	bg=0.02
mitochondrion GO:0005739	p=2.6E−02	n=10	fg=0.27	bg=0.14
mitochondrial proton−transporting ATP sy... GO:0000275	p=2.7E−02	n=1	fg=0.03	bg=0.00
proton−transporting ATP synthase complex... GO:0045261	p=2.7E−02	n=1	fg=0.03	bg=0.00
growth cone filopodium GO:1990812	p=2.7E−02	n=1	fg=0.03	bg=0.00
proton−transporting ATP synthase complex GO:0045259	p=2.7E−02	n=1	fg=0.03	bg=0.00
pleated septate junction GO:0005919	p=2.7E−02	n=1	fg=0.03	bg=0.00
mitochondrial proton−transporting ATP sy... GO:0005753	p=2.7E−02	n=1	fg=0.03	bg=0.00
dendritic shaft GO:0043198	p=3.6E−02	n=2	fg=0.05	bg=0.01
mismatch repair complex GO:0032300	p=4.1E−02	n=1	fg=0.03	bg=0.00
proton−transporting two−sector ATPase co... GO:0033177	p=4.1E−02	n=1	fg=0.03	bg=0.00
phagophore assembly site membrane GO:0034045	p=4.1E−02	n=1	fg=0.03	bg=0.00
ESC/E(Z) complex GO:0035098	p=4.1E−02	n=1	fg=0.03	bg=0.00
ribosomal subunit GO:0044391	p=4.9E−02	n=3	fg=0.08	bg=0.02
cytosolic large ribosomal subunit GO:0022625	p=5.2E−02	n=2	fg=0.05	bg=0.01
growth cone lamellipodium GO:1990761	p=5.4E−02	n=1	fg=0.03	bg=0.00
chromatoid body GO:0033391	p=5.4E−02	n=1	fg=0.03	bg=0.00

−log(p) (axis: 0 1 2 3 4 5)
fraction (axis: 0.0 0.2 0.4 0.6 0.8 1.0)

n=37/145 input genes with annotations