GO:BP
Elav_Nvec_vc1.1_XM_032378021.2

fraction genes in fg and expected value

Term	p	n	fg	bg
neurotransmitter secretion GO:0007269	p=2.0E−03	n=6	fg=0.10	bg=0.02
positive regulation of DNA−templated tra... GO:0032786	p=2.3E−03	n=3	fg=0.05	bg=0.00
negative regulation of neuroblast prolif... GO:0007406	p=2.3E−03	n=3	fg=0.05	bg=0.00
dicarboxylic acid transport GO:0006835	p=2.4E−03	n=4	fg=0.06	bg=0.01
negative regulation of stem cell prolife... GO:2000647	p=2.9E−03	n=3	fg=0.05	bg=0.00
positive regulation of adenylate cyclase... GO:0045762	p=3.1E−03	n=2	fg=0.03	bg=0.00
interleukin−6−mediated signaling pathway GO:0070102	p=3.1E−03	n=2	fg=0.03	bg=0.00
regulation of transcription elongation f... GO:0034243	p=3.7E−03	n=3	fg=0.05	bg=0.01
negative regulation of mRNA metabolic pr... GO:1903312	p=4.5E−03	n=3	fg=0.05	bg=0.01
response to interleukin−6 GO:0070741	p=4.8E−03	n=4	fg=0.06	bg=0.00
sensory perception of mechanical stimulu... GO:0050954	p=4.8E−03	n=6	fg=0.10	bg=0.03
aorta morphogenesis GO:0035909	p=5.1E−03	n=2	fg=0.03	bg=0.00
positive regulation of histone H3−K4 met... GO:0051571	p=5.1E−03	n=2	fg=0.03	bg=0.00
chitin−based larval cuticle pattern form... GO:0035293	p=5.1E−03	n=2	fg=0.03	bg=0.00
regulation of imaginal disc growth GO:0045570	p=5.1E−03	n=2	fg=0.03	bg=0.00
establishment or maintenance of polarity... GO:0016334	p=5.1E−03	n=2	fg=0.03	bg=0.00
regulation of neurotransmitter transport GO:0051588	p=5.3E−03	n=4	fg=0.06	bg=0.01
gamma−aminobutyric acid secretion GO:0014051	p=7.6E−03	n=2	fg=0.03	bg=0.00
sympathetic nervous system development GO:0048485	p=7.6E−03	n=2	fg=0.03	bg=0.00
cellular response to dexamethasone stimu... GO:0071549	p=7.6E−03	n=2	fg=0.03	bg=0.00
monocarboxylic acid transport GO:0015718	p=1.0E−02	n=4	fg=0.06	bg=0.01
negative regulation of lymphocyte activa... GO:0051250	p=1.0E−02	n=3	fg=0.05	bg=0.01
positive regulation of neurotransmitter ... GO:0001956	p=1.0E−02	n=2	fg=0.03	bg=0.00
negative regulation of mRNA catabolic pr... GO:1902373	p=1.0E−02	n=2	fg=0.03	bg=0.00
regulation of catecholamine metabolic pr... GO:0042069	p=1.0E−02	n=2	fg=0.03	bg=0.00
regulation of dopamine metabolic process GO:0042053	p=1.0E−02	n=2	fg=0.03	bg=0.00
chordate embryonic development GO:0043009	p=1.1E−02	n=9	fg=0.14	bg=0.06
organic hydroxy compound metabolic proce... GO:1901615	p=1.1E−02	n=7	fg=0.11	bg=0.04
negative regulation of leukocyte activat... GO:0002695	p=1.2E−02	n=3	fg=0.05	bg=0.01
regulation of cell shape GO:0008360	p=1.2E−02	n=4	fg=0.06	bg=0.01

−log(p) (axis 0 1 2 3 4 5)
fraction (axis 0.0 0.2 0.4 0.6 0.8 1.0)
n=63/224 input genes with annotations

GO:MF
Elav_Nvec_vc1.1_XM_032378021.2

fraction genes in fg and expected value

Term	p	n	fg	bg
ion binding GO:0043167	p=1.0E−03	n=22	fg=0.39	bg=0.20
outward rectifier potassium channel acti... GO:0015271	p=1.5E−02	n=2	fg=0.04	bg=0.00
purine ribonucleoside triphosphate bindi... GO:0035639	p=1.7E−02	n=8	fg=0.14	bg=0.06
cation binding GO:0043169	p=1.8E−02	n=12	fg=0.21	bg=0.11
metal ion binding GO:0046872	p=2.2E−02	n=11	fg=0.19	bg=0.10
lipid transporter activity GO:0005319	p=2.3E−02	n=3	fg=0.05	bg=0.01
anion binding GO:0043168	p=2.4E−02	n=13	fg=0.23	bg=0.13
ferrochelatase activity GO:0004325	p=2.4E−02	n=1	fg=0.02	bg=0.00
myosin II binding GO:0045159	p=2.4E−02	n=1	fg=0.02	bg=0.00
thiamin−triphosphatase activity GO:0050333	p=2.4E−02	n=1	fg=0.02	bg=0.00
beta−galactosidase activity GO:0004565	p=2.4E−02	n=1	fg=0.02	bg=0.00
protein tyrosine phosphatase activity, m... GO:0030946	p=2.4E−02	n=1	fg=0.02	bg=0.00
short−branched−chain−acyl−CoA dehydrogen... GO:0016937	p=2.4E−02	n=1	fg=0.02	bg=0.00
intracellular sodium activated potassium... GO:0005228	p=2.4E−02	n=1	fg=0.02	bg=0.00
DNA end binding GO:0045027	p=2.4E−02	n=1	fg=0.02	bg=0.00
iron−responsive element binding GO:0030350	p=2.4E−02	n=1	fg=0.02	bg=0.00
acid−sensing ion channel activity GO:0044736	p=2.4E−02	n=1	fg=0.02	bg=0.00
DNA topoisomerase type II (double strand... GO:0072586	p=2.4E−02	n=1	fg=0.02	bg=0.00
DNA topoisomerase type II (double strand... GO:0072587	p=2.4E−02	n=1	fg=0.02	bg=0.00
choline dehydrogenase activity GO:0008812	p=2.4E−02	n=1	fg=0.02	bg=0.00
voltage−gated potassium channel activity GO:0005249	p=2.7E−02	n=2	fg=0.04	bg=0.00
carbohydrate derivative binding GO:0097367	p=3.0E−02	n=9	fg=0.16	bg=0.08
ribonucleotide binding GO:0032553	p=3.2E−02	n=8	fg=0.14	bg=0.07
purine ribonucleotide binding GO:0032555	p=3.2E−02	n=8	fg=0.14	bg=0.07
steroid binding GO:0005496	p=3.2E−02	n=2	fg=0.04	bg=0.01
monocarboxylic acid transmembrane transp... GO:0008028	p=3.2E−02	n=2	fg=0.04	bg=0.01
iron ion binding GO:0005506	p=3.7E−02	n=2	fg=0.04	bg=0.01
purine nucleotide binding GO:0017076	p=3.9E−02	n=8	fg=0.14	bg=0.07
PDZ domain binding GO:0030165	p=4.3E−02	n=3	fg=0.05	bg=0.01
ligand−gated sodium channel activity GO:0015280	p=4.8E−02	n=1	fg=0.02	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=57/224 input genes with annotations

GO:CC
Elav_Nvec_vc1.1_XM_032378021.2

fraction genes in fg and expected value

Term	p	n	fg	bg
transcription elongation factor complex GO:0008023	p=5.1E−03	n=3	fg=0.05	bg=0.01
cell cortex GO:0005938	p=7.2E−03	n=7	fg=0.11	bg=0.03
intercellular bridge GO:0045171	p=1.2E−02	n=3	fg=0.05	bg=0.01
cortical actin cytoskeleton GO:0030864	p=1.2E−02	n=3	fg=0.05	bg=0.01
cell−cell junction GO:0005911	p=1.7E−02	n=7	fg=0.11	bg=0.04
anchoring junction GO:0070161	p=1.7E−02	n=7	fg=0.11	bg=0.04
cortical cytoskeleton GO:0030863	p=1.7E−02	n=3	fg=0.05	bg=0.01
voltage−gated potassium channel complex GO:0008076	p=2.3E−02	n=2	fg=0.03	bg=0.00
potassium channel complex GO:0034705	p=2.3E−02	n=2	fg=0.03	bg=0.00
Dsl1/NZR complex GO:0070939	p=2.4E−02	n=1	fg=0.02	bg=0.00
female germline ring canal outer rim GO:0035182	p=2.4E−02	n=1	fg=0.02	bg=0.00
smooth septate junction GO:0005920	p=2.4E−02	n=1	fg=0.02	bg=0.00
plastid GO:0009536	p=2.4E−02	n=1	fg=0.02	bg=0.00
symplast GO:0055044	p=2.4E−02	n=1	fg=0.02	bg=0.00
micropyle GO:0070825	p=2.4E−02	n=1	fg=0.02	bg=0.00
plasmodesma GO:0009506	p=2.4E−02	n=1	fg=0.02	bg=0.00
chloroplast GO:0009507	p=2.4E−02	n=1	fg=0.02	bg=0.00
condensin complex GO:0000796	p=2.4E−02	n=1	fg=0.02	bg=0.00
actin rod GO:0031002	p=2.4E−02	n=1	fg=0.02	bg=0.00
palmitoyltransferase complex GO:0002178	p=2.4E−02	n=1	fg=0.02	bg=0.00
egg chorion GO:0042600	p=2.4E−02	n=1	fg=0.02	bg=0.00
Cdc73/Paf1 complex GO:0016593	p=2.4E−02	n=1	fg=0.02	bg=0.00
apoplast GO:0048046	p=2.4E−02	n=1	fg=0.02	bg=0.00
Dbf4−dependent protein kinase complex GO:0031431	p=2.4E−02	n=1	fg=0.02	bg=0.00
cofilin−actin rod GO:0090732	p=2.4E−02	n=1	fg=0.02	bg=0.00
cell junction GO:0030054	p=3.2E−02	n=13	fg=0.20	bg=0.11
nuclear matrix GO:0016363	p=3.2E−02	n=3	fg=0.05	bg=0.01
growth cone GO:0030426	p=3.4E−02	n=4	fg=0.06	bg=0.02
apical part of cell GO:0045177	p=3.7E−02	n=7	fg=0.11	bg=0.05
transporter complex GO:1990351	p=4.1E−02	n=4	fg=0.06	bg=0.02

−log(p) (axis 0 1 2 3 4 5)
fraction (axis 0.0 0.2 0.4 0.6 0.8 1.0)
n=66/224 input genes with annotations