GO:BP
Elav_Nvec_v1g244929

fraction genes in fg and expected valu...

neuron projection development GO:0031175	p=5.0E−04 | n=21	fg=0.28 | bg=0.13
chemical synaptic transmission GO:0007268	p=8.7E−04 | n=14	fg=0.18 | bg=0.07
extracellular matrix organization GO:0030198	p=9.8E−04 | n=6	fg=0.08 | bg=0.02
establishment or maintenance of cytoskel... GO:0003380	p=1.7E−03 | n=2	fg=0.03 | bg=0.00
positive regulation of myotube different... GO:0010831	p=1.7E−03 | n=2	fg=0.03 | bg=0.00
optic vesicle morphogenesis GO:0003404	p=1.7E−03 | n=2	fg=0.03 | bg=0.00
positive regulation of myoblast fusion GO:1901741	p=1.7E−03 | n=2	fg=0.03 | bg=0.00
cellular response to exogenous dsRNA GO:0071360	p=1.7E−03 | n=2	fg=0.03 | bg=0.00
plasma membrane raft assembly GO:0044854	p=1.7E−03 | n=2	fg=0.03 | bg=0.00
lens induction in camera−type eye GO:0060235	p=1.7E−03 | n=2	fg=0.03 | bg=0.00
heterotypic cell−cell adhesion GO:0034113	p=1.7E−03 | n=2	fg=0.03 | bg=0.00
mesectoderm development GO:0048383	p=1.7E−03 | n=2	fg=0.03 | bg=0.00
body morphogenesis GO:0010171	p=2.1E−03 | n=5	fg=0.07 | bg=0.01
regulation of intracellular estrogen rec... GO:0033146	p=2.2E−03 | n=3	fg=0.04 | bg=0.00
positive regulation of T cell activation GO:0050870	p=4.5E−03 | n=4	fg=0.05 | bg=0.01
regulation of triglyceride biosynthetic ... GO:0010866	p=5.1E−03 | n=2	fg=0.03 | bg=0.00
positive regulation of interferon−gamma ... GO:0032729	p=5.1E−03 | n=2	fg=0.03 | bg=0.00
regulation of myosin II filament organiz... GO:0043519	p=5.1E−03 | n=2	fg=0.03 | bg=0.00
positive regulation of growth GO:0045927	p=7.6E−03 | n=9	fg=0.12 | bg=0.05
synaptic vesicle cycle GO:0099504	p=7.8E−03 | n=6	fg=0.08 | bg=0.02
regulation of Ras protein signal transdu... GO:0046578	p=8.2E−03 | n=5	fg=0.07 | bg=0.02
nematode larval development GO:0002119	p=8.2E−03 | n=8	fg=0.11 | bg=0.04
necroptotic process GO:0070266	p=9.8E−03 | n=2	fg=0.03 | bg=0.00
negative regulation of mitochondrial fus... GO:0010637	p=9.8E−03 | n=2	fg=0.03 | bg=0.00
regulation of activin receptor signaling... GO:0032925	p=9.8E−03 | n=2	fg=0.03 | bg=0.00
regulation of protein−containing complex... GO:0043244	p=9.9E−03 | n=4	fg=0.05 | bg=0.01
regulation of cell differentiation GO:0045595	p=1.0E−02 | n=22	fg=0.29 | bg=0.16
regulation of developmental process GO:0050793	p=1.1E−02 | n=30	fg=0.39 | bg=0.24
regulation of protein localization GO:0032880	p=1.2E−02 | n=14	fg=0.18 | bg=0.10
cell morphogenesis GO:0000902	p=1.2E−02 | n=17	fg=0.22 | bg=0.13
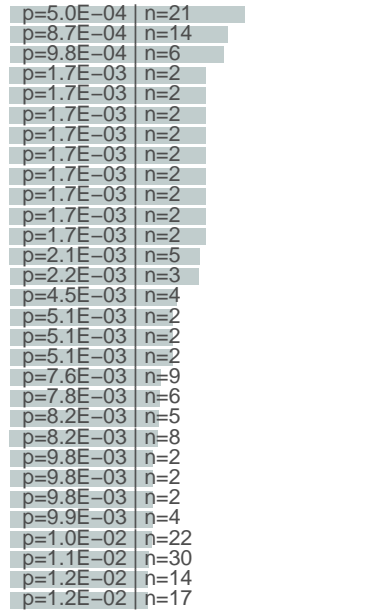
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n=76/227 input genes with annotations

fraction

GO:MF
Elav_Nvec_v1g244929

fraction genes in fg and expected valu...

phosphatidylcholine binding GO:0031210	p=2.5E−03 | n=3	fg=0.04 | bg=0.00
ligase activity, forming phosphoric este... GO:0016886	p=5.6E−03 | n=2	fg=0.03 | bg=0.00
microtubule binding GO:0008017	p=9.8E−03 | n=6	fg=0.09 | bg=0.03
phosphatidylethanolamine binding GO:0008429	p=1.1E−02 | n=2	fg=0.03 | bg=0.00
ammonium ion binding GO:0070405	p=1.3E−02 | n=3	fg=0.04 | bg=0.01
BH domain binding GO:0051400	p=1.8E−02 | n=2	fg=0.03 | bg=0.00
AP−2 adaptor complex binding GO:0035612	p=1.8E−02 | n=2	fg=0.03 | bg=0.00
enzyme inhibitor activity GO:0004857	p=2.3E−02 | n=5	fg=0.07 | bg=0.02
signaling receptor binding GO:0005102	p=2.4E−02 | n=13	fg=0.19 | bg=0.10
galactosyltransferase activity GO:0008378	p=2.5E−02 | n=2	fg=0.03 | bg=0.00
UDP−galactosyltransferase activity GO:0035250	p=2.5E−02 | n=2	fg=0.03 | bg=0.00
beta−1,3−galactosyltransferase activity GO:0048531	p=2.5E−02 | n=2	fg=0.03 | bg=0.00
UDP−galactose:beta−N−acetylglucosamine b... GO:0008499	p=2.5E−02 | n=2	fg=0.03 | bg=0.00
spectrin binding GO:0030507	p=3.5E−02 | n=2	fg=0.03 | bg=0.00
potassium ion transmembrane transporter ... GO:0015079	p=3.6E−02 | n=3	fg=0.04 | bg=0.01
1−phosphatidylinositol−3−phosphate 4−kin... GO:0052811	p=4.4E−02 | n=1	fg=0.01 | bg=0.00
pseudophosphatase activity GO:0001691	p=4.4E−02 | n=1	fg=0.01 | bg=0.00
MHC protein complex binding GO:0023023	p=4.4E−02 | n=1	fg=0.01 | bg=0.00
MHC class Ib protein complex binding GO:0023025	p=4.4E−02 | n=1	fg=0.01 | bg=0.00
diacylglycerol binding GO:0019992	p=4.4E−02 | n=1	fg=0.01 | bg=0.00
MHC class Ib protein binding GO:0023029	p=4.4E−02 | n=1	fg=0.01 | bg=0.00
phosphatidylinositol phosphate kinase ac... GO:0016307	p=4.4E−02 | n=1	fg=0.01 | bg=0.00
1−phosphatidylinositol−4−phosphate 5−kin... GO:0016308	p=4.4E−02 | n=1	fg=0.01 | bg=0.00
phosphatidylinositol 3−kinase catalytic ... GO:0036313	p=4.4E−02 | n=1	fg=0.01 | bg=0.00
1−phosphatidylinositol−5−phosphate 4−kin... GO:0016309	p=4.4E−02 | n=1	fg=0.01 | bg=0.00
RNA polymerase III core binding GO:0000994	p=4.4E−02 | n=1	fg=0.01 | bg=0.00
BH2 domain binding GO:0051433	p=4.4E−02 | n=1	fg=0.01 | bg=0.00
ribokinase activity GO:0004747	p=4.4E−02 | n=1	fg=0.01 | bg=0.00
insulin−like growth factor I binding GO:0031994	p=4.4E−02 | n=1	fg=0.01 | bg=0.00
MHC class Ib protein binding, via antige... GO:0023030	p=4.4E−02 | n=1	fg=0.01 | bg=0.00
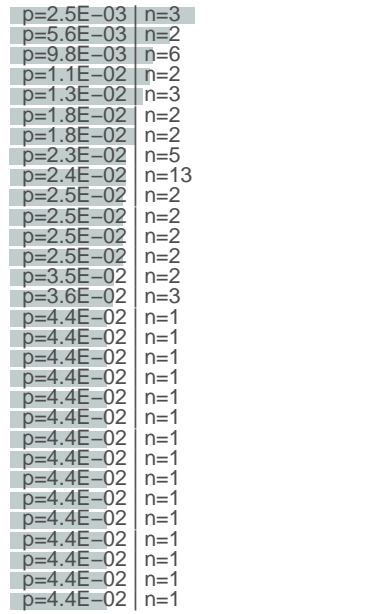
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n=70/227 input genes with annotations

fraction

GO:CC
Elav_Nvec_v1g244929

fraction genes in fg and expected valu...

photoreceptor outer segment membrane GO:0042622	p=1.7E−03 | n=2	fg=0.03 | bg=0.00
plasma membrane protein complex GO:0098797	p=3.3E−03 | n=8	fg=0.11 | bg=0.03
axon GO:0030424	p=4.2E−03 | n=13	fg=0.17 | bg=0.08
cell leading edge GO:0031252	p=4.5E−03 | n=8	fg=0.11 | bg=0.04
clathrin−coated pit GO:0005905	p=4.8E−03 | n=3	fg=0.04 | bg=0.00
postsynaptic membrane GO:0045211	p=6.8E−03 | n=5	fg=0.07 | bg=0.02
extrinsic component of plasma membrane GO:0019897	p=9.5E−03 | n=4	fg=0.05 | bg=0.01
transcription elongation factor complex GO:0008023	p=1.1E−02 | n=3	fg=0.04 | bg=0.01
cytoplasmic side of membrane GO:0098562	p=1.1E−02 | n=6	fg=0.08 | bg=0.03
somatodendritic compartment GO:0036477	p=1.3E−02 | n=14	fg=0.19 | bg=0.10
cell junction GO:0030054	p=1.6E−02 | n=20	fg=0.27 | bg=0.13
side of membrane GO:0098552	p=1.7E−02 | n=7	fg=0.09 | bg=0.04
anchoring junction GO:0070161	p=1.8E−02 | n=8	fg=0.11 | bg=0.05
cell−cell junction GO:0005911	p=1.8E−02 | n=8	fg=0.11 | bg=0.05
neuronal cell body membrane GO:0032809	p=1.8E−02 | n=3	fg=0.04 | bg=0.01
presynapse GO:0098793	p=1.9E−02 | n=9	fg=0.12 | bg=0.05
synaptic membrane GO:0097060	p=1.9E−02 | n=8	fg=0.11 | bg=0.02
distal axon GO:0150034	p=1.9E−02 | n=8	fg=0.11 | bg=0.05
extrinsic component of cytoplasmic side ... GO:0031234	p=2.2E−02 | n=3	fg=0.04 | bg=0.01
cell body membrane GO:0044298	p=2.2E−02 | n=3	fg=0.04 | bg=0.01
cell body GO:0044297	p=2.3E−02 | n=11	fg=0.15 | bg=0.08
heterotrimeric G−protein complex GO:0005834	p=2.3E−02 | n=2	fg=0.03 | bg=0.00
dendrite membrane GO:0032590	p=2.3E−02 | n=2	fg=0.03 | bg=0.00
GTPase complex GO:1905360	p=2.3E−02 | n=2	fg=0.03 | bg=0.00
growth cone GO:0030426	p=2.5E−02 | n=5	fg=0.07 | bg=0.02
caveola GO:0005901	p=2.6E−02 | n=3	fg=0.04 | bg=0.01
mitochondrial outer membrane GO:0005741	p=2.6E−02 | n=4	fg=0.05 | bg=0.02
cytoplasmic side of plasma membrane GO:0009898	p=2.8E−02 | n=5	fg=0.07 | bg=0.02
synapse GO:0045202	p=2.8E−02 | n=16	fg=0.21 | bg=0.10
organelle outer membrane GO:0031968	p=2.9E−02 | n=4	fg=0.05 | bg=0.02
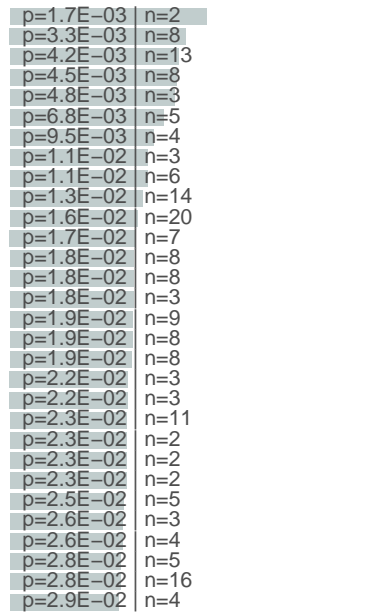
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n=75/227 input genes with annotations

fraction