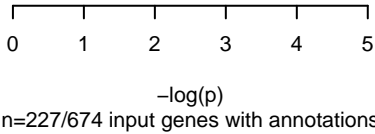


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Elav_Nvec_vc1.1_XM_048728399.1

fraction genes in fg and expected value

sulfate transport	GO:0008272	p=2.2E-03	n=3
leukocyte migration	GO:0050900	p=4.8E-03	n=9
nephron tubule epithelial cell different...	GO:0072160	p=5.2E-03	n=3
microtubule cytoskeleton organization in...	GO:1902850	p=6.7E-03	n=12
positive regulation of cardiac muscle ti...	GO:0055025	p=6.8E-03	n=4
photoreactive repair	GO:0000719	p=7.0E-03	n=2
nephric duct formation	GO:0072179	p=7.0E-03	n=2
negative regulation of viral transcripti...	GO:0032897	p=7.0E-03	n=2
phosphatidylcholine catabolic process	GO:0034638	p=7.0E-03	n=2
base-excision repair, gap-filling	GO:0006287	p=7.0E-03	n=2
negative regulation of fat cell prolifer...	GO:0070345	p=7.0E-03	n=2
nuclear export	GO:0051168	p=8.6E-03	n=12
negative regulation of adherens junction...	GO:1903392	p=9.7E-03	n=3
positive regulation of cardiac muscle ce...	GO:0060045	p=9.7E-03	n=3
regulation of organelle assembly	GO:1902115	p=1.1E-02	n=11
cellular protein localization	GO:0034613	p=1.2E-02	n=52
cellular macromolecule localization	GO:0070727	p=1.2E-02	n=53
catabolic process	GO:0009056	p=1.4E-02	n=63
protein K48-linked ubiquitination	GO:0070936	p=1.4E-02	n=5
secretory granule organization	GO:0033363	p=1.4E-02	n=4
leukocyte chemotaxis	GO:0030595	p=1.4E-02	n=4
protein K11-linked ubiquitination	GO:0070979	p=1.4E-02	n=4
protein localization to membrane	GO:0072657	p=1.4E-02	n=20
regulation of protein homodimerization a...	GO:0043496	p=1.6E-02	n=3
mitotic spindle organization	GO:0007052	p=1.6E-02	n=9
cortical cytoskeleton organization	GO:0030865	p=1.8E-02	n=6
centrosome separation	GO:0051299	p=1.9E-02	n=4
positive regulation of dephosphorylation	GO:0035306	p=1.9E-02	n=4
regulation of cell migration	GO:0030334	p=1.9E-02	n=20
type 2 immune response	GO:0042092	p=2.0E-02	n=2



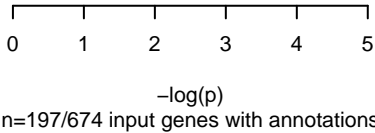
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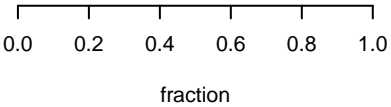
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Elav_Nvec_vc1.1_XM_048728399.1

fraction genes in fg and expected value

dicarboxylic acid transmembrane transpor...	GO:0005310	p=2.5E-03	n=4
GTPase activity	GO:0003924	p=5.0E-03	n=10
calcium-independent phospholipase A2 act...	GO:0047499	p=6.9E-03	n=2
lipid phosphatase activity	GO:0042577	p=6.9E-03	n=2
ubiquitin-like protein binding	GO:0032182	p=9.3E-03	n=6
deoxyribodipyrimidine photo-lyase activi...	GO:0003904	p=1.9E-02	n=2
sulfate transmembrane transporter activi...	GO:0015116	p=1.9E-02	n=2
oxalate transmembrane transporter activi...	GO:0019531	p=1.9E-02	n=2
1-acylglycerophosphocholine O-acyltransf...	GO:0047184	p=1.9E-02	n=2
formate transmembrane transporter activi...	GO:0015499	p=1.9E-02	n=2
ether hydrolase activity	GO:0016803	p=1.9E-02	n=2
epoxide hydrolase activity	GO:0004301	p=1.9E-02	n=2
DNA photolyase activity	GO:0003913	p=1.9E-02	n=2
small GTPase binding	GO:0031267	p=2.6E-02	n=15
sulfur compound transmembrane transporte...	GO:1901682	p=3.0E-02	n=4
GTPase binding	GO:0051020	p=3.5E-02	n=17
oxidoreductase activity, acting on a sul...	GO:0016670	p=3.7E-02	n=2
C2H2 zinc finger domain binding	GO:0070742	p=3.7E-02	n=2
hydrolase activity, acting on ether bond...	GO:0016801	p=3.7E-02	n=2
poly-pyrimidine tract binding	GO:0008187	p=4.4E-02	n=3
O-acyltransferase activity	GO:0008374	p=4.4E-02	n=3
GTPase activating protein binding	GO:0032794	p=4.4E-02	n=3
catalytic activity, acting on a tRNA	GO:0140101	p=4.5E-02	n=6
organic anion transmembrane transporter ...	GO:0008514	p=4.9E-02	n=7
ubiquitin binding	GO:0043130	p=5.6E-02	n=4
general transcription initiation factor ...	GO:0140296	p=5.6E-02	n=4
JUN kinase binding	GO:0008432	p=5.8E-02	n=2
G-protein beta/gamma-subunit complex bin...	GO:0031683	p=5.8E-02	n=2
protein kinase A regulatory subunit bind...	GO:0034237	p=5.8E-02	n=2
molecular adaptor activity	GO:0060090	p=6.7E-02	n=9



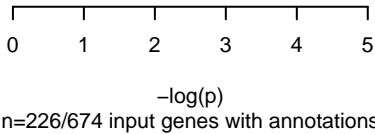
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GO:CC
Elav_Nvec_vc1.1_XM_048728399.1

fraction genes in fg and expected value

gamma-tubulin complex	GO:0000930	p=7.0E-03	n=2
mitotic spindle midzone	GO:1990023	p=9.6E-03	n=3
spindle pole	GO:0000922	p=1.6E-02	n=8
SAGA-type complex	GO:0070461	p=2.4E-02	n=3
Golgi medial cisterna	GO:0005797	p=3.1E-02	n=4
nuclear pore	GO:0005643	p=3.2E-02	n=5
subapical complex	GO:0035003	p=3.7E-02	n=2
SAGA complex	GO:0000124	p=3.7E-02	n=2
COPI-coated vesicle membrane	GO:0030663	p=3.7E-02	n=2
Golgi stack	GO:0005795	p=3.8E-02	n=8
perinuclear region of cytoplasm	GO:0048471	p=5.2E-02	n=21
fibrillar center	GO:0001650	p=5.2E-02	n=6
transcription repressor complex	GO:0017053	p=5.8E-02	n=4
mitotic spindle pole	GO:0097431	p=5.8E-02	n=3
neuron projection cytoplasm	GO:0120111	p=5.8E-02	n=3
guanyl-nucleotide exchange factor comple...	GO:0032045	p=5.9E-02	n=2
nuclear proteasome complex	GO:0031595	p=5.9E-02	n=2
phagophore assembly site	GO:0000407	p=5.9E-02	n=2
Golgi cis cisterna	GO:0000137	p=5.9E-02	n=2
cytoplasmic side of apical plasma membra...	GO:0098592	p=5.9E-02	n=2
cytosol	GO:0005829	p=6.3E-02	n=102
cis-Golgi network	GO:0005801	p=6.8E-02	n=4
polytene chromosome puff	GO:0005703	p=7.2E-02	n=3
Golgi trans cisterna	GO:0000138	p=7.2E-02	n=3
intracellular membrane-bounded organelle	GO:0043231	p=7.7E-02	n=183
intercellular bridge	GO:0045171	p=8.0E-02	n=4
mitochondrial intermembrane space	GO:0005758	p=8.0E-02	n=4
cortical actin cytoskeleton	GO:0030864	p=8.0E-02	n=4
membrane-bounded organelle	GO:0043227	p=8.2E-02	n=189
postsynapse of neuromuscular junction	GO:0098975	p=8.4E-02	n=2



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