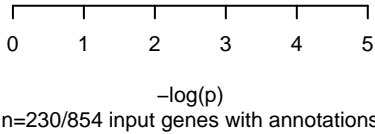


GO:BP
Elav_Nvec_vc1.1_XM_048732912.1

fraction genes in fg and expected value

ommochrome biosynthetic process	GO:0006727	p=2.0E-03	n=3
organelle localization	GO:0051640	p=2.5E-03	n=33
negative regulation of exocytosis	GO:0045920	p=2.6E-03	n=5
muscle organ development	GO:0007517	p=3.0E-03	n=17
somatic stem cell population maintenance	GO:0035019	p=3.0E-03	n=7
negative regulation of microtubule polym...	GO:0031111	p=3.1E-03	n=6
multicellular organismal homeostasis	GO:0048871	p=4.3E-03	n=15
positive regulation of cell maturation	GO:1903431	p=4.6E-03	n=5
regulation of cyclin-dependent protein k...	GO:1904029	p=4.6E-03	n=5
mitotic DNA damage checkpoint signaling	GO:0044773	p=4.8E-03	n=6
negative regulation of supramolecular fi...	GO:1902904	p=5.3E-03	n=8
regulation of G2/M transition of mitotic...	GO:0010389	p=5.7E-03	n=10
negative regulation of DNA metabolic pro...	GO:0051053	p=6.3E-03	n=7
germarium-derived oocyte differentiation	GO:0030706	p=6.5E-03	n=4
heart valve morphogenesis	GO:0003179	p=6.5E-03	n=4
regulation of cyclase activity	GO:0031279	p=6.5E-03	n=4
axonogenesis	GO:0007409	p=6.8E-03	n=26
ether metabolic process	GO:0018904	p=7.3E-03	n=3
atrioventricular valve development	GO:0003171	p=7.3E-03	n=3
regulation of protein targeting to mitoc...	GO:1903214	p=7.3E-03	n=3
cardiac right ventricle morphogenesis	GO:0003215	p=7.3E-03	n=3
ventricular septum morphogenesis	GO:0060412	p=7.6E-03	n=5
dosage compensation	GO:0007549	p=7.6E-03	n=5
negative regulation of G1/S transition o...	GO:2000134	p=7.6E-03	n=5
positive regulation of GTPase activity	GO:0043547	p=8.7E-03	n=13
cellular protein modification process	GO:0006464	p=9.6E-03	n=91
metal ion homeostasis	GO:0055065	p=9.8E-03	n=21
regulation of ATP-dependent activity	GO:0043462	p=1.0E-02	n=6
cochlea development	GO:0090102	p=1.0E-02	n=6
regulation of calcium ion transport	GO:0051924	p=1.0E-02	n=11

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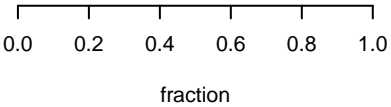
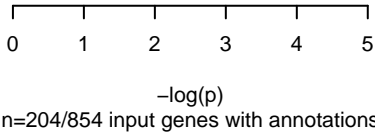


GO:MF
Elav_Nvec_vc1.1_XM_048732912.1

fraction genes in fg and expected value

protein serine/threonine kinase activity	GO:0004674	p=8.1E-04	n=18
nuclear receptor binding	GO:0016922	p=2.5E-03	n=9
nucleoside-triphosphatase regulator acti...	GO:0060589	p=3.7E-03	n=20
hormone receptor binding	GO:0051427	p=7.8E-03	n=9
calcium-induced calcium release activity	GO:0048763	p=1.6E-02	n=2
armadillo repeat domain binding	GO:0070016	p=1.6E-02	n=2
lipid phosphatase activity	GO:0042577	p=1.6E-02	n=2
LIM domain binding	GO:0030274	p=1.6E-02	n=2
ABC-type transporter activity	GO:0140359	p=1.7E-02	n=3
phospholipase binding	GO:0043274	p=1.7E-02	n=3
small GTPase binding	GO:0031267	p=2.0E-02	n=18
GTPase regulator activity	GO:0030695	p=2.4E-02	n=16
ion channel regulator activity	GO:0099106	p=2.6E-02	n=7
phosphoprotein binding	GO:0051219	p=2.6E-02	n=6
channel regulator activity	GO:0016247	p=4.0E-02	n=7
tubulin binding	GO:0015631	p=4.0E-02	n=12
transmembrane receptor protein kinase ac...	GO:0019199	p=4.2E-02	n=4
ATPase regulator activity	GO:0060590	p=4.2E-02	n=4
hydrolase activity, acting on glycosyl b...	GO:0016798	p=4.2E-02	n=6
GTPase binding	GO:0051020	p=4.2E-02	n=20
ATP binding	GO:0005524	p=4.4E-02	n=14
oxidoreductase activity, acting on the a...	GO:0016620	p=4.5E-02	n=2
ATPase-coupled lipid transmembrane trans...	GO:0034040	p=4.5E-02	n=2
receptor-receptor interaction	GO:0090722	p=4.5E-02	n=2
organic hydroxy compound transmembrane t...	GO:1901618	p=4.5E-02	n=2
DNA N-glycosylase activity	GO:0019104	p=4.5E-02	n=2
fibroblast growth factor-activated recep...	GO:0005007	p=4.5E-02	n=2
hydrolase activity, hydrolyzing N-glycos...	GO:0016799	p=4.5E-02	n=2
nuclear glucocorticoid receptor binding	GO:0035259	p=4.5E-02	n=2
heparin binding	GO:0008201	p=4.9E-02	n=3

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GO:CC
Elav_Nvec_vc1.1_XM_048732912.1

fraction genes in fg and expected value

neuronal cell body	GO:0043025	p=1.2E-03	n=28
dendrite	GO:0030425	p=7.3E-03	n=26
Parkin-FBXW7-Cul1 ubiquitin ligase compl...	GO:1990452	p=1.5E-02	n=2
axon	GO:0030424	p=2.1E-02	n=26
nuclear speck	GO:0016607	p=3.3E-02	n=13
plasma membrane raft	GO:0044853	p=3.7E-02	n=6
lateral plasma membrane	GO:0016328	p=3.8E-02	n=4
cytoplasm	GO:0005737	p=3.9E-02	n=190
caveola	GO:0005901	p=3.9E-02	n=5
integral component of cytoplasmic side o...	GO:0071458	p=4.2E-02	n=2
inaD signaling complex	GO:0016027	p=4.2E-02	n=2
aster	GO:0005818	p=4.2E-02	n=2
spindle pole centrosome	GO:0031616	p=4.2E-02	n=2
distal axon	GO:0150034	p=4.5E-02	n=16
calcium channel complex	GO:0034704	p=4.5E-02	n=3
P-body	GO:0000932	p=5.0E-02	n=5
cytosol	GO:0005829	p=5.4E-02	n=99
membrane raft	GO:0045121	p=5.6E-02	n=11
membrane microdomain	GO:0098857	p=5.6E-02	n=11
intracellular anatomical structure	GO:0005622	p=5.8E-02	n=217
vesicle	GO:0031982	p=5.9E-02	n=52
growth cone	GO:0030426	p=5.9E-02	n=9
cytoskeleton	GO:0005856	p=6.1E-02	n=40
transferase complex	GO:1990234	p=6.5E-02	n=24
rhabdomere	GO:0016028	p=6.6E-02	n=3
spindle pole	GO:0000922	p=6.8E-02	n=6
membrane	GO:0016020	p=7.1E-02	n=115
methyltransferase complex	GO:0034708	p=7.7E-02	n=5
lipid droplet	GO:0005811	p=7.7E-02	n=5
site of polarized growth	GO:0030427	p=7.7E-02	n=9

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