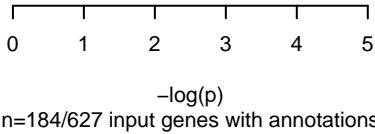


GO:BP
Elav_Nvec_vc1.1_XM_032387218.2

fraction genes in fg and expected value

regulation of phospholipid metabolic pro...	GO:1903725	p=1.5E-03	n=6
cellular response to nerve growth factor...	GO:1990090	p=1.5E-03	n=6
regulation of phosphate transport	GO:0010966	p=3.8E-03	n=3
triglyceride catabolic process	GO:0019433	p=3.8E-03	n=3
neuromuscular process controlling balanc...	GO:0050885	p=4.8E-03	n=6
blood vessel endothelial cell migration	GO:0043534	p=4.8E-03	n=6
regulation of GTPase activity	GO:0043087	p=6.4E-03	n=13
pH reduction	GO:0045851	p=6.6E-03	n=5
regulation of morphogenesis of a branchi...	GO:0060688	p=8.6E-03	n=4
angiogenesis	GO:0001525	p=8.7E-03	n=10
sequestering of triglyceride	GO:0030730	p=8.8E-03	n=3
positive regulation of vascular endothel...	GO:1905564	p=8.8E-03	n=3
negative regulation of Rho protein signa...	GO:0035024	p=8.8E-03	n=3
secretory granule localization	GO:0032252	p=8.8E-03	n=3
mRNA stabilization	GO:0048255	p=8.8E-03	n=3
glycolytic process	GO:0006096	p=9.5E-03	n=5
establishment of organelle localization	GO:0051656	p=9.6E-03	n=21
response to stimulus	GO:0050896	p=1.0E-02	n=125
negative regulation of triglyceride meta...	GO:0090209	p=1.0E-02	n=2
sodium-dependent phosphate transport	GO:0044341	p=1.0E-02	n=2
negative regulation of sequestering of t...	GO:0010891	p=1.0E-02	n=2
regulation of triglyceride catabolic pro...	GO:0010896	p=1.0E-02	n=2
aldosterone metabolic process	GO:0032341	p=1.0E-02	n=2
positive regulation of p38MAPK cascade	GO:1900745	p=1.0E-02	n=2
glucose catabolic process to pyruvate	GO:0061718	p=1.0E-02	n=2
mineralocorticoid metabolic process	GO:0008212	p=1.0E-02	n=2
C21-steroid hormone metabolic process	GO:0008207	p=1.0E-02	n=2
positive regulation of sodium-dependent ...	GO:2000120	p=1.0E-02	n=2
regulation of sodium-dependent phosphate...	GO:2000118	p=1.0E-02	n=2
glycolytic process through glucose-6-pho...	GO:0061620	p=1.0E-02	n=2

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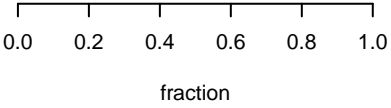
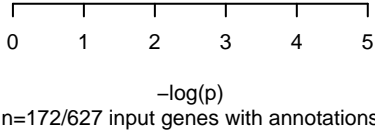


GO:MF
Elav_Nvec_vc1.1_XM_032387218.2

fraction genes in fg and expected value

GTPase regulator activity	GO:0030695	p=4.7E-03	n=16
telomerase RNA binding	GO:0070034	p=1.2E-02	n=2
N4-(beta-N-acetylglucosaminyl)-L-asparag...	GO:0003948	p=1.2E-02	n=2
GTPase binding	GO:0051020	p=1.5E-02	n=19
GTPase activator activity	GO:0005096	p=2.0E-02	n=9
phospholipid binding	GO:0005543	p=2.1E-02	n=13
double-stranded RNA binding	GO:0003725	p=2.4E-02	n=4
potassium ion transmembrane transporter ...	GO:0015079	p=2.9E-02	n=5
miRNA binding	GO:0035198	p=3.2E-02	n=2
intramolecular transferase activity	GO:0016866	p=3.2E-02	n=2
WW domain binding	GO:0050699	p=3.2E-02	n=2
peroxidase activity	GO:0004601	p=3.2E-02	n=2
triglyceride lipase activity	GO:0004806	p=3.2E-02	n=2
phosphoric diester hydrolase activity	GO:0008081	p=3.7E-02	n=5
small GTPase binding	GO:0031267	p=3.7E-02	n=15
phosphatidylinositol-4-phosphate binding	GO:0070273	p=4.6E-02	n=3
N-acyltransferase activity	GO:0016410	p=4.6E-02	n=3
Notch binding	GO:0005112	p=4.6E-02	n=3
potassium channel activity	GO:0005267	p=5.5E-02	n=4
kinesin binding	GO:0019894	p=5.5E-02	n=4
lipid binding	GO:0008289	p=5.6E-02	n=14
cyclin-dependent protein kinase activity	GO:0097472	p=6.0E-02	n=2
oxidoreductase activity, acting on perox...	GO:0016684	p=6.0E-02	n=2
cyclin-dependent protein serine/threonin...	GO:0004693	p=6.0E-02	n=2
GTPase inhibitor activity	GO:0005095	p=6.0E-02	n=2
regulatory RNA binding	GO:0061980	p=6.0E-02	n=2
tachykinin receptor activity	GO:0004995	p=6.0E-02	n=2
snRNA binding	GO:0017069	p=6.0E-02	n=2
translation repressor activity	GO:0030371	p=6.0E-02	n=2
phosphatidic acid binding	GO:0070300	p=6.0E-02	n=2

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GO:CC
Elav_Nvec_vc1.1_XM_032387218.2

fraction genes in fg and expected value

caveola	GO:0005901	p=4.8E-04	n=7
cytoplasmic side of apical plasma membra...	GO:0098592	p=3.7E-03	n=3
cell-substrate junction	GO:0030055	p=6.3E-03	n=6
recycling endosome membrane	GO:0055038	p=8.3E-03	n=4
lipid droplet	GO:0005811	p=8.5E-03	n=6
extrinsic component of endoplasmic retic...	GO:0042406	p=1.0E-02	n=2
cytoplasmic region	GO:0099568	p=1.1E-02	n=17
microvillus	GO:0005902	p=2.2E-02	n=5
nuclear matrix	GO:0016363	p=2.2E-02	n=5
lysosome	GO:0005764	p=2.6E-02	n=16
EARP complex	GO:1990745	p=2.8E-02	n=2
spot adherens junction	GO:0005914	p=2.8E-02	n=2
axon cytoplasm	GO:1904115	p=2.8E-02	n=2
GARP complex	GO:0000938	p=2.8E-02	n=2
cell cortex	GO:0005938	p=3.0E-02	n=13
Z disc	GO:0030018	p=3.3E-02	n=6
nuclear speck	GO:0016607	p=3.7E-02	n=11
lytic vacuole	GO:0000323	p=3.7E-02	n=16
proton-transporting two-sector ATPase co...	GO:0016469	p=3.8E-02	n=3
proton-transporting V-type ATPase comple...	GO:0033176	p=3.8E-02	n=3
I band	GO:0031674	p=4.0E-02	n=6
vacuolar membrane	GO:0005774	p=4.1E-02	n=11
adherens junction	GO:0005912	p=4.1E-02	n=8
perikaryon	GO:0043204	p=5.2E-02	n=5
zonula adherens	GO:0005915	p=5.3E-02	n=2
subsynaptic reticulum	GO:0071212	p=5.3E-02	n=2
endonuclease complex	GO:1905348	p=5.3E-02	n=2
microvillus membrane	GO:0031528	p=5.3E-02	n=2
cytoplasmic dynein complex	GO:0005868	p=5.3E-02	n=2
organellar large ribosomal subunit	GO:0000315	p=5.3E-02	n=2

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