

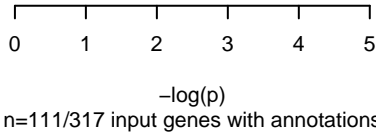
GO:BP  
Elav\_Nvec\_vc1.1\_XM\_001629958.3

fraction genes in fg and expected value

negative regulation of phospholipid bios... GO:0071072  
regulation of chemokine (C–C motif) liga... GO:0071649  
regulation of ubiquitin protein ligase a... GO:1904666  
peptide transport GO:0015833  
mitochondrial fusion GO:0008053  
response to superoxide GO:0000303  
embryo implantation GO:0007566  
transferrin transport GO:0033572  
molybdopterin cofactor biosynthetic proc... GO:0032324  
establishment of protein localization to... GO:0061951  
purine ribonucleoside metabolic process GO:0046128  
regulation of protein localization to pl... GO:1903076  
GTP metabolic process GO:0046039  
negative regulation of phosphatase activ... GO:0010923  
regulation of vesicle-mediated transport GO:0060627  
positive regulation of endocytic recycli... GO:2001137  
regulation of activated T cell prolifera... GO:0046006  
protein transport GO:0015031  
guanosine-containing compound metabolic ... GO:1901068  
retrograde vesicle-mediated transport, G... GO:0006890  
positive regulation of insulin secretion GO:0032024  
response to immobilization stress GO:0035902  
regulation of mitochondrial fusion GO:0010635  
negative regulation of receptor internal... GO:0002091  
positive regulation of ubiquitin protein... GO:1904668  
positive regulation of protein transport GO:0051222  
process utilizing autophagic mechanism GO:0061919  
autophagy GO:0006914  
positive regulation of NF–kappaB transcr... GO:0051092  
regulation of lipid kinase activity GO:0043550

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p=1.7E–03	n=2
p=3.3E–03	n=3
p=3.7E–03	n=28
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p=4.7E–03	n=3
p=4.7E–03	n=3
p=4.7E–03	n=3
p=4.9E–03	n=2
p=5.3E–03	n=4
p=5.3E–03	n=4
p=6.5E–03	n=4
p=6.6E–03	n=3
p=7.9E–03	n=4
p=8.6E–03	n=14
p=9.5E–03	n=2
p=9.5E–03	n=2
p=1.2E–02	n=28
p=1.4E–02	n=3
p=1.5E–02	n=4
p=1.5E–02	n=4
p=1.5E–02	n=2
p=1.5E–02	n=2
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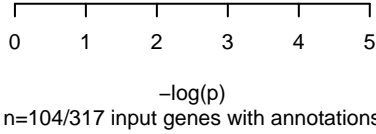
GO:MF  
Elav\_Nvec\_vc1.1\_XM\_001629958.3

fraction genes in fg and expected value

carbon–oxygen lyase activity GO:0016835  
neurexin family protein binding GO:0042043  
nucleoside–triphosphatase activity GO:0017111  
hydro–lyase activity GO:0016836  
pyrophosphatase activity GO:0016462  
hydrolase activity, acting on acid anhyd... GO:0016817  
hydrolase activity, acting on acid anhyd... GO:0016818  
GDP binding GO:0019003  
protein phosphatase inhibitor activity GO:0004864  
sulfurtransferase activity GO:0016783  
protein phosphatase regulator activity GO:0019888  
phosphatidylinositol–3,5–bisphosphate bi... GO:0080025  
O–methyltransferase activity GO:0008171  
carbohydrate derivative binding GO:0097367  
phosphatase inhibitor activity GO:0019212  
carbohydrate kinase activity GO:0019200  
anion binding GO:0043168  
ATP–dependent activity GO:0140657  
purine ribonucleoside triphosphate bindi... GO:0035639  
GTP binding GO:0005525  
phosphatase regulator activity GO:0019208  
supercoiled DNA binding GO:0097100  
transmembrane receptor protein phosphata... GO:0019198  
importin–alpha family protein binding GO:0061676  
oxidative DNA demethylase activity GO:0035516  
interleukin–5 receptor binding GO:0005137  
3–hydroxyacyl–CoA dehydratase activity GO:0018812  
carboxyl–O–methyltransferase activity GO:0010340  
N–acetylglucosamine–1–phosphodiester alp... GO:0003944  
oleic acid binding GO:0070538

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p=5.6E–03	n=2
p=1.2E–02	n=14
p=1.3E–02	n=3
p=1.7E–02	n=14
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p=1.7E–02	n=14
p=1.7E–02	n=3
p=1.8E–02	n=2
p=1.8E–02	n=2
p=2.5E–02	n=3
p=2.5E–02	n=2
p=2.5E–02	n=2
p=2.9E–02	n=14
p=3.5E–02	n=2
p=3.5E–02	n=2
p=3.5E–02	n=20
p=3.7E–02	n=10
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GO:CC  
Elav\_Nvec\_vc1.1\_XM\_001629958.3

fraction genes in fg and expected value

vacuolar proton–transporting V–type ATPa... GO:0000221  
cytosol GO:0005829  
cytoplasmic side of rough endoplasmic re... GO:0098556  
lysosomal membrane GO:0005765  
somatodendritic compartment GO:0036477  
neuronal cell body GO:0043025  
protein phosphatase type 1 complex GO:0000164  
cell body GO:0044297  
mitochondrial outer membrane GO:0005741  
organelle outer membrane GO:0031968  
outer membrane GO:0019867  
lytic vacuole membrane GO:0098852  
plasma membrane proton–transporting V–ty... GO:0033181  
protein serine/threonine phosphatase com... GO:0008287  
male germ cell nucleus GO:0001673  
phosphatase complex GO:1903293  
plasma membrane region GO:0098590  
cell projection GO:0042995  
Ric1–Rgp1 guanyl–nucleotide exchange fac... GO:0034066  
cytoplasmic side of dendritic spine plas... GO:1990780  
interleukin–5 receptor complex GO:0005895  
bub1–bub3 complex GO:1990298  
NF–kappaB complex GO:0071159  
integral component of lysosomal membrane GO:1905103  
plus–end kinesin complex GO:0005873  
RNA nuclear export complex GO:0042565  
Dsl1/NZR complex GO:0070939  
insulin–responsive compartment GO:0032593  
mitotic checkpoint complex GO:0033597  
6–phosphofructokinase complex GO:0005945

p=5.1E–03	n=2
p=9.0E–03	n=58
p=9.9E–03	n=2
p=1.4E–02	n=6
p=1.4E–02	n=17
p=1.5E–02	n=13
p=1.6E–02	n=2
p=1.6E–02	n=14
p=1.9E–02	n=5
p=2.2E–02	n=5
p=2.2E–02	n=5
p=2.2E–02	n=6
p=2.3E–02	n=2
p=2.7E–02	n=3
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p=4.1E–02	n=28
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