

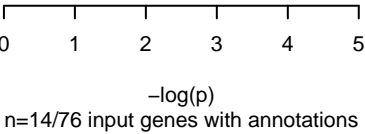
GO:BP
Elav_Nvec_vc1.1_XM_032373619.2

fraction genes in fg and expected value

cellular response to glucagon stimulus	GO:0071377
positive regulation of oocyte maturation	GO:1900195
wound healing	GO:0042060
multicellular organismal water homeostas...	GO:0050891
water homeostasis	GO:0030104
renal water homeostasis	GO:0003091
regulation of oocyte development	GO:0060281
positive regulation of oocyte developmen...	GO:0060282
positive regulation of oogenesis	GO:1905881
regulation of oogenesis	GO:1905879
memory	GO:0007613
regulation of body fluid levels	GO:0050878
cell development	GO:0048468
neuron development	GO:0048666
gamete generation	GO:0007276
negative regulation of vasoconstriction	GO:0045906
pericardium development	GO:0060039
regulation of terminal button organizati...	GO:2000331
regulation of motor neuron apoptotic pro...	GO:2000671
negative regulation of motor neuron apop...	GO:2000672
presynapse organization	GO:0099172
regulation of presynapse organization	GO:0099174
maintenance of protein location in plasm...	GO:0072660
calcium-dependent cell-matrix adhesion	GO:0016340
maintenance of protein location in membr...	GO:0072658
calcium-dependent cell-cell adhesion via...	GO:0016339
maternal determination of dorsal/ventral...	GO:0008070
negative regulation of vascular associat...	GO:1904694
response to forskolin	GO:1904321
cellular response to forskolin	GO:1904322

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p=9.7E-03	n=4
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p=1.5E-02	n=2
p=1.9E-02	n=3
p=2.6E-02	n=3
p=3.0E-02	n=9
p=3.1E-02	n=6
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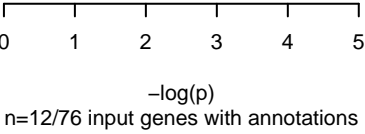
GO:MF
Elav_Nvec_vc1.1_XM_032373619.2

fraction genes in fg and expected value

protein kinase A binding	GO:0051018
cAMP-dependent protein kinase regulator ...	GO:0008603
protein serine/threonine kinase inhibito...	GO:0030291
fucosyltransferase activity	GO:0008417
protein kinase A catalytic subunit bindi...	GO:0034236
alpha-(1->3)-fucosyltransferase activity	GO:0046920
glucosylceramidase activity	GO:0004348
extracellular matrix binding	GO:0050840
calcium- and calmodulin-responsive adeny...	GO:0008294
cAMP-dependent protein kinase inhibitor ...	GO:0004862
translation factor activity, RNA binding	GO:0008135
beta-2 adrenergic receptor binding	GO:0031698
ubiquitin-protein transferase activator ...	GO:0097027
laminin binding	GO:0043236
ubiquitin-protein transferase regulator ...	GO:0055106
beta-glucosidase activity	GO:0008422
kinase binding	GO:0019900
protein kinase binding	GO:0019901
ubiquitin protein ligase binding	GO:0031625
ubiquitin-like protein ligase binding	GO:0044389
glucosidase activity	GO:0015926
ribosome binding	GO:0043022
protein kinase A regulatory subunit bind...	GO:0034237
adenylate cyclase activity	GO:0004016
protein phosphatase 2B binding	GO:0030346
beta-tubulin binding	GO:0048487
adenylate cyclase binding	GO:0008179
translation regulator activity	GO:0045182
mRNA regulatory element binding translat...	GO:0000900
ribonucleoprotein complex binding	GO:0043021

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p=4.5E-02	n=4
p=6.4E-02	n=2
p=6.4E-02	n=2
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GO:CC
Elav_Nvec_vc1.1_XM_032373619.2

fraction genes in fg and expected value

mitochondrial inner membrane	GO:0005743
organelle inner membrane	GO:0019866
mitochondrial crista	GO:0030061
microvillus membrane	GO:0031528
integrin alpha9-beta1 complex	GO:0034679
integrin complex	GO:0008305
protein complex involved in cell adhesio...	GO:0098636
messenger ribonucleoprotein complex	GO:1990124
envelope	GO:0031975
organelle envelope	GO:0031967
heterochromatin	GO:0000792
nucleotide-activated protein kinase comp...	GO:0031588
female germ cell nucleus	GO:0001674
cAMP-dependent protein kinase complex	GO:0005952
germinal vesicle	GO:0042585
intercalary heterochromatin	GO:0005725
mitochondrial membrane	GO:0031966
mitochondrial envelope	GO:0005740
plasma membrane region	GO:0098590
germ cell nucleus	GO:0043073
nuclear ubiquitin ligase complex	GO:0000152
PRC1 complex	GO:0035102
plasma membrane signaling receptor compl...	GO:0098802
microvillus	GO:0005902
protein kinase complex	GO:1902911
guanylate cyclase complex, soluble	GO:0008074
T-tubule	GO:0030315
ciliary base	GO:0097546
membrane	GO:0016020
membrane raft	GO:0045121

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p=3.0E-02	n=1
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p=4.4E-02	n=3
p=5.9E-02	n=1
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p=5.9E-02	n=1
p=6.1E-02	n=2
p=7.8E-02	n=2
p=8.3E-02	n=4
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