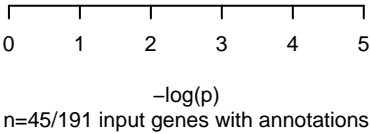


GO:BP
Ncol_Nvec_vc1.1_XM_001629572.3

fraction genes in fg and expected value

response to metal ion	GO:0010038	p=1.1E-03	n=7
protein localization to microtubule	GO:0035372	p=3.5E-03	n=2
negative regulation of synaptic vesicle ...	GO:1902804	p=3.5E-03	n=2
regulation of cell shape	GO:0008360	p=5.0E-03	n=4
nephron tubule epithelial cell different...	GO:0072160	p=5.7E-03	n=2
regulation of NMDA receptor activity	GO:2000310	p=5.7E-03	n=2
embryo development ending in birth or eg...	GO:0009792	p=6.1E-03	n=11
positive regulation of protein polymeriz...	GO:0032273	p=7.6E-03	n=3
cellular chloride ion homeostasis	GO:0030644	p=8.5E-03	n=2
regulation of glutamate receptor signali...	GO:1900449	p=8.5E-03	n=2
brain development	GO:0007420	p=9.4E-03	n=9
cellular component morphogenesis	GO:0032989	p=1.0E-02	n=12
metencephalon development	GO:0022037	p=1.1E-02	n=3
cerebellum development	GO:0021549	p=1.1E-02	n=3
metal ion transport	GO:0030001	p=1.1E-02	n=8
anterior head development	GO:0097065	p=1.2E-02	n=2
cellular response to fluid shear stress	GO:0071498	p=1.2E-02	n=2
membrane organization	GO:0061024	p=1.3E-02	n=9
regulation of protein tyrosine kinase ac...	GO:0061097	p=1.4E-02	n=3
cell morphogenesis involved in different...	GO:0000904	p=1.5E-02	n=10
anterograde axonal transport	GO:0008089	p=1.5E-02	n=2
response to copper ion	GO:0046688	p=1.5E-02	n=2
protein insertion into mitochondrial mem...	GO:0051204	p=1.5E-02	n=2
negative regulation of potassium ion tra...	GO:0043267	p=1.5E-02	n=2
positive regulation of gliogenesis	GO:0014015	p=1.5E-02	n=2
neuronal signal transduction	GO:0023041	p=1.5E-02	n=2
labyrinthine layer development	GO:0060711	p=1.5E-02	n=2
response to fluid shear stress	GO:0034405	p=1.5E-02	n=2
placenta development	GO:0001890	p=1.6E-02	n=3
inorganic cation transmembrane transport	GO:0098662	p=1.7E-02	n=7

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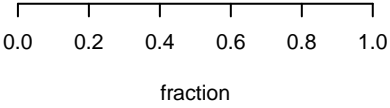
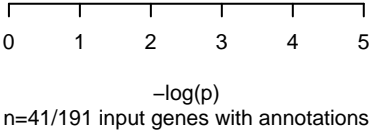


GO:MF
Ncol_Nvec_vc1.1_XM_001629572.3

fraction genes in fg and expected value

phosphatidylinositol 3-kinase binding	GO:0043548	p=6.2E-03	n=2
hydrolase activity, acting on carbon-nit...	GO:0016811	p=7.0E-03	n=3
voltage-gated cation channel activity	GO:0022843	p=9.9E-03	n=3
primary active transmembrane transporter...	GO:0015399	p=1.2E-02	n=4
protein lysine deacetylase activity	GO:0033558	p=1.3E-02	n=2
histone deacetylase activity	GO:0004407	p=1.3E-02	n=2
cytoskeletal protein binding	GO:0008092	p=1.3E-02	n=8
deacetylase activity	GO:0019213	p=1.6E-02	n=2
active transmembrane transporter activit...	GO:0022804	p=1.7E-02	n=5
amide transmembrane transporter activity	GO:0042887	p=2.1E-02	n=2
enzyme binding	GO:0019899	p=2.4E-02	n=16
voltage-gated potassium channel activity	GO:0005249	p=2.6E-02	n=2
spermine:oxygen oxidoreductase (spermidi...	GO:0052901	p=2.6E-02	n=1
N1-acetylspermidine:oxygen oxidoreductas...	GO:0052904	p=2.6E-02	n=1
tricarboxylate secondary active transmem...	GO:0005371	p=2.6E-02	n=1
N-acetylglucosaminyl(diphosphodolichol N-...	GO:0004577	p=2.6E-02	n=1
stearoyl-CoA 9-desaturase activity	GO:0004768	p=2.6E-02	n=1
cadmium ion binding	GO:0046870	p=2.6E-02	n=1
L-asparagine transmembrane transporter a...	GO:0015182	p=2.6E-02	n=1
rRNA primary transcript binding	GO:0042134	p=2.6E-02	n=1
L-aspartate transmembrane transporter ac...	GO:0015183	p=2.6E-02	n=1
L-glutamine transmembrane transporter ac...	GO:0015186	p=2.6E-02	n=1
L-glutamate transmembrane transporter ac...	GO:0005313	p=2.6E-02	n=1
acidic amino acid transmembrane transpor...	GO:0015172	p=2.6E-02	n=1
oxidoreductase activity, acting on the C...	GO:0016647	p=2.6E-02	n=1
aminoacyltransferase activity	GO:0016755	p=2.6E-02	n=1
glutathione gamma-glutamylcysteinyltrans...	GO:0016756	p=2.6E-02	n=1
LEM domain binding	GO:0097726	p=2.6E-02	n=1
S100 protein binding	GO:0044548	p=2.6E-02	n=1
3-phosphoinositide-dependent protein kin...	GO:0043423	p=2.6E-02	n=1

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GO:CC
Ncol_Nvec_vc1.1_XM_001629572.3

fraction genes in fg and expected value

ficolin-1-rich granule membrane	GO:0101003	p=7.8E-03	n=2
transporter complex	GO:1990351	p=1.4E-02	n=4
cell leading edge	GO:0031252	p=1.7E-02	n=5
melanosome	GO:0042470	p=1.8E-02	n=2
endoplasmic reticulum-Golgi intermediate...	GO:0033116	p=1.8E-02	n=2
histone deacetylase complex	GO:0000118	p=2.2E-02	n=2
cleavage furrow	GO:0032154	p=2.2E-02	n=2
pigment granule	GO:0048770	p=2.2E-02	n=2
cell junction	GO:0030054	p=2.3E-02	n=11
Sin3 complex	GO:0016580	p=2.4E-02	n=1
NMDA selective glutamate receptor comple...	GO:0017146	p=2.4E-02	n=1
endocytic vesicle lumen	GO:0071682	p=2.4E-02	n=1
neuron projection terminus	GO:0044306	p=2.7E-02	n=4
presynapse	GO:0098793	p=2.7E-02	n=6
neuronal cell body	GO:0043025	p=2.7E-02	n=7
perinuclear region of cytoplasm	GO:0048471	p=3.3E-02	n=7
transport vesicle membrane	GO:0030658	p=3.5E-02	n=3
transcription repressor complex	GO:0017053	p=3.6E-02	n=2
intercalated disc	GO:0014704	p=3.6E-02	n=2
cell body	GO:0044297	p=3.9E-02	n=7
cell-cell junction	GO:0005911	p=4.2E-02	n=5
anchoring junction	GO:0070161	p=4.2E-02	n=5
endoplasmic reticulum membrane	GO:0005789	p=4.2E-02	n=7
nuclear outer membrane-endoplasmic retic...	GO:0042175	p=4.5E-02	n=7
growth cone filopodium	GO:1990812	p=4.7E-02	n=1
type Ib terminal bouton	GO:0061176	p=4.7E-02	n=1
type Is terminal bouton	GO:0061177	p=4.7E-02	n=1
ionotropic glutamate receptor complex	GO:0008328	p=4.7E-02	n=1
glutamate-cysteine ligase complex	GO:0017109	p=4.7E-02	n=1
phagophore assembly site membrane	GO:0034045	p=4.7E-02	n=1

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