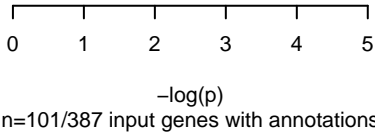


GO:BP
Ncol_Nvec_vc1.1_XM_001629572.3

fraction genes in fg and expected value

regulation of cation transmembrane trans...	GO:1904062	p=8.2E-04	n=8
sprouting angiogenesis	GO:0002040	p=1.0E-03	n=4
regulation of response to drug	GO:2001023	p=1.3E-03	n=5
negative regulation of intrinsic apoptot...	GO:1903751	p=1.4E-03	n=2
L-alanine transport	GO:0015808	p=1.4E-03	n=2
regulation of ubiquitin protein ligase a...	GO:1904666	p=2.5E-03	n=3
cellular response to fluid shear stress	GO:0071498	p=2.5E-03	n=3
negative regulation of cytosolic calcium...	GO:0051481	p=3.0E-03	n=4
neuronal signal transduction	GO:0023041	p=3.6E-03	n=3
regulation of viral genome replication	GO:0045069	p=4.6E-03	n=4
negative regulation of potassium ion tra...	GO:0043267	p=5.0E-03	n=3
dopamine transport	GO:0015872	p=5.0E-03	n=3
regulation of reactive oxygen species bi...	GO:1903426	p=5.6E-03	n=4
positive regulation of protein modificat...	GO:1903322	p=5.9E-03	n=6
cerebellum morphogenesis	GO:0021587	p=6.7E-03	n=3
magnesium ion homeostasis	GO:0010960	p=6.7E-03	n=3
chemical synaptic transmission	GO:0007268	p=7.1E-03	n=13
negative regulation of synaptic vesicle ...	GO:1902804	p=7.9E-03	n=2
melanotic encapsulation of foreign targe...	GO:0035011	p=7.9E-03	n=2
response to lithium ion	GO:0010226	p=7.9E-03	n=2
protein localization to microtubule	GO:0035372	p=7.9E-03	n=2
serine family amino acid catabolic proce...	GO:0009071	p=7.9E-03	n=2
aromatic amino acid transport	GO:0015801	p=7.9E-03	n=2
regulation of glycoprotein metabolic pro...	GO:1903018	p=7.9E-03	n=2
DNA methylation or demethylation	GO:0044728	p=8.0E-03	n=4
cell-cell junction organization	GO:0045216	p=8.1E-03	n=6
positive regulation of telomerase activi...	GO:0051973	p=8.7E-03	n=3
cellular component morphogenesis	GO:0032989	p=8.8E-03	n=20
protein modification by small protein co...	GO:0032446	p=1.1E-02	n=14
cell morphogenesis	GO:0000902	p=1.1E-02	n=19

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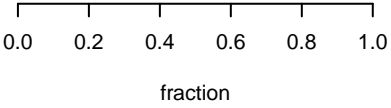
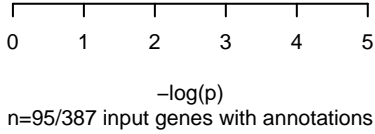


GO:MF
Ncol_Nvec_vc1.1_XM_001629572.3

fraction genes in fg and expected value

L-alanine transmembrane transporter acti...	GO:0015180	p=1.6E-03	n=2
beta-aspartyl-peptidase activity	GO:0008798	p=1.6E-03	n=2
transcription corepressor activity	GO:0003714	p=3.0E-03	n=6
oxidoreductase activity, acting on paire...	GO:0016705	p=5.9E-03	n=4
histone deacetylase activity	GO:0004407	p=6.1E-03	n=3
voltage-gated potassium channel activity	GO:0005249	p=8.2E-03	n=3
aromatic amino acid transmembrane transp...	GO:0015173	p=9.1E-03	n=2
enzyme binding	GO:0019899	p=1.1E-02	n=31
iron ion binding	GO:0005506	p=1.3E-02	n=3
alkali metal ion binding	GO:0031420	p=1.5E-02	n=2
RNA binding	GO:0003723	p=1.5E-02	n=17
2-oxoglutarate-dependent dioxygenase act...	GO:0016706	p=2.0E-02	n=3
voltage-gated potassium channel activity...	GO:0086090	p=2.1E-02	n=2
voltage-gated potassium channel activity...	GO:0086087	p=2.1E-02	n=2
phosphatidylinositol 3-kinase binding	GO:0043548	p=2.1E-02	n=2
voltage-gated potassium channel activity...	GO:0086089	p=2.1E-02	n=2
delayed rectifier potassium channel acti...	GO:0005251	p=2.1E-02	n=2
intracellular cyclic nucleotide activate...	GO:0005221	p=2.1E-02	n=2
voltage-gated potassium channel activity...	GO:0086008	p=2.1E-02	n=2
cyclic nucleotide-gated ion channel acti...	GO:0043855	p=2.1E-02	n=2
kinesin binding	GO:0019894	p=2.8E-02	n=3
MAP kinase activity	GO:0004707	p=2.9E-02	n=2
ferrous iron binding	GO:0008198	p=2.9E-02	n=2
potassium channel inhibitor activity	GO:0019870	p=2.9E-02	n=2
primary active transmembrane transporter...	GO:0015399	p=2.9E-02	n=5
dioxygenase activity	GO:0051213	p=3.3E-02	n=3
outward rectifier potassium channel acti...	GO:0015271	p=3.8E-02	n=2
vitamin B6 binding	GO:0070279	p=3.8E-02	n=2
pyridoxal phosphate binding	GO:0030170	p=3.8E-02	n=2
active transmembrane transporter activit...	GO:0022804	p=3.9E-02	n=7

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GO:CC
Ncol_Nvec_vc1.1_XM_001629572.3

fraction genes in fg and expected value

transcription repressor complex	GO:0017053	p=3.6E-03	n=4
cytoplasmic ribonucleoprotein granule	GO:0036464	p=5.4E-03	n=7
Z disc	GO:0030018	p=7.5E-03	n=5
histone deacetylase complex	GO:0000118	p=1.1E-02	n=3
neuron spine	GO:0044309	p=1.1E-02	n=6
dendritic spine	GO:0043197	p=1.1E-02	n=6
U4/U6 x U5 tri-snRNP complex	GO:0046540	p=1.3E-02	n=2
cell body	GO:0044297	p=1.4E-02	n=13
neuronal cell body	GO:0043025	p=1.4E-02	n=12
intercalated disc	GO:0014704	p=1.6E-02	n=3
intracellular canaliculus	GO:0046691	p=1.8E-02	n=2
juxtaparanode region of axon	GO:0044224	p=1.8E-02	n=2
spliceosomal tri-snRNP complex	GO:0097526	p=1.8E-02	n=2
rough endoplasmic reticulum membrane	GO:0030867	p=1.8E-02	n=2
P granule	GO:0043186	p=1.9E-02	n=3
pole plasm	GO:0045495	p=2.3E-02	n=3
neuronal cell body membrane	GO:0032809	p=2.3E-02	n=3
germ plasm	GO:0060293	p=2.3E-02	n=3
cell leading edge	GO:0031252	p=2.4E-02	n=8
cell-cell contact zone	GO:0044291	p=2.7E-02	n=3
cell body membrane	GO:0044298	p=2.7E-02	n=3
Golgi apparatus	GO:0005794	p=2.8E-02	n=18
ribonucleoprotein complex	GO:1990904	p=2.8E-02	n=15
main axon	GO:0044304	p=3.1E-02	n=3
presynaptic membrane	GO:0042734	p=3.2E-02	n=4
ficolin-1-rich granule membrane	GO:0101003	p=3.3E-02	n=2
integral component of postsynaptic membr...	GO:0099055	p=3.3E-02	n=2
intrinsic component of postsynaptic memb...	GO:0098936	p=3.3E-02	n=2
U5 snRNP	GO:0005682	p=3.3E-02	n=2
paranode region of axon	GO:0033270	p=3.3E-02	n=2

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