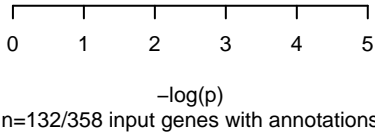


GO:BP
Ncol_Nvec_vc1.1_XM_032372883.2

fraction genes in fg and expected value

regulation of oskar mRNA translation	GO:0046011	p=2.4E-03	n=2
regulation of deacetylase activity	GO:0150065	p=2.4E-03	n=2
determination of digestive tract left/right	GO:0071907	p=2.4E-03	n=2
intracellular estrogen receptor signaling	GO:0030520	p=2.8E-03	n=4
regulation of circadian rhythm	GO:0042752	p=5.3E-03	n=6
autophagosome maturation	GO:0097352	p=6.3E-03	n=4
negative regulation of cellular catabolic process	GO:0031330	p=6.8E-03	n=9
cellular response to nitric oxide	GO:0071732	p=6.9E-03	n=2
response to hydrogen peroxide	GO:0042542	p=7.1E-03	n=6
response to bronchodilator	GO:0097366	p=7.7E-03	n=3
positive regulation of long-term synaptic transmission	GO:1900273	p=7.7E-03	n=3
circadian behavior	GO:0048512	p=9.2E-03	n=6
purine ribonucleoside triphosphate metabolism	GO:0009205	p=9.8E-03	n=9
purine ribonucleoside metabolic process	GO:0046128	p=9.8E-03	n=4
GTP metabolic process	GO:0046039	p=1.1E-02	n=3
neuroblast proliferation	GO:0007405	p=1.1E-02	n=7
regulation of histone deacetylation	GO:0031063	p=1.3E-02	n=2
proximal/distal axis specification	GO:0009946	p=1.3E-02	n=2
magnesium ion homeostasis	GO:0010960	p=1.4E-02	n=3
cellular response to endogenous stimulus	GO:0071495	p=1.4E-02	n=26
stem cell proliferation	GO:0072089	p=1.6E-02	n=8
gene silencing by RNA	GO:0031047	p=1.8E-02	n=5
positive regulation of transporter activity	GO:0032411	p=2.0E-02	n=4
cellular response to hydrogen peroxide	GO:0070301	p=2.0E-02	n=4
macromolecule metabolic process	GO:0043170	p=2.0E-02	n=95
ribonucleoside monophosphate biosynthesis	GO:0009156	p=2.0E-02	n=5
cellular response to starvation	GO:0009267	p=2.1E-02	n=7
regulation of endocytic recycling	GO:2001135	p=2.1E-02	n=2
larval chitin-based cuticle development	GO:0008363	p=2.1E-02	n=2
positive regulation of chemokine production	GO:0032722	p=2.1E-02	n=2

fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.03	bg=0.00
fg=0.05	bg=0.01
fg=0.03	bg=0.01
fg=0.07	bg=0.03
fg=0.02	bg=0.00
fg=0.05	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.05	bg=0.01
fg=0.07	bg=0.03
fg=0.03	bg=0.01
fg=0.02	bg=0.00
fg=0.05	bg=0.02
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.20	bg=0.11
fg=0.06	bg=0.03
fg=0.04	bg=0.01
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.72	bg=0.63
fg=0.04	bg=0.01
fg=0.05	bg=0.02
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00

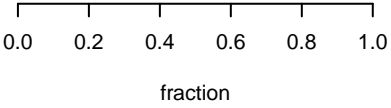
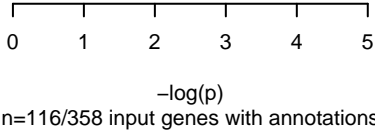


GO:MF
Ncol_Nvec_vc1.1_XM_032372883.2

fraction genes in fg and expected value

mitogen-activated protein kinase binding	GO:0051019	p=2.0E-03	n=4
protein disulfide isomerase activity	GO:0003756	p=2.1E-03	n=3
nuclear estrogen receptor binding	GO:0030331	p=2.8E-03	n=4
kinesin binding	GO:0019894	p=7.9E-03	n=4
potassium channel activity	GO:0005267	p=9.8E-03	n=4
protein phosphatase 1 binding	GO:0008157	p=1.1E-02	n=3
protein dimerization activity	GO:0046983	p=1.2E-02	n=24
ligand-gated cation channel activity	GO:0099094	p=1.4E-02	n=4
hormone receptor binding	GO:0051427	p=1.7E-02	n=6
oxidoreductase activity, acting on a sulfur compound	GO:0016667	p=1.7E-02	n=4
ion gated channel activity	GO:0022839	p=1.8E-02	n=7
disordered domain specific binding	GO:0097718	p=1.8E-02	n=3
gated channel activity	GO:0022836	p=2.1E-02	n=7
GTPase binding	GO:0051020	p=2.1E-02	n=12
sulfurtransferase activity	GO:0016783	p=2.2E-02	n=2
nuclear androgen receptor binding	GO:0050681	p=2.3E-02	n=3
intracellular ligand-gated ion channel activity	GO:0005217	p=2.3E-02	n=3
ammonium ion binding	GO:0070405	p=2.3E-02	n=3
protein homodimerization activity	GO:0042803	p=2.7E-02	n=18
disulfide oxidoreductase activity	GO:0015036	p=2.8E-02	n=3
transcription coregulator activity	GO:0003712	p=2.9E-02	n=11
cation channel activity	GO:0005261	p=2.9E-02	n=10
voltage-gated potassium channel activity	GO:0086090	p=3.1E-02	n=2
voltage-gated potassium channel activity	GO:0086087	p=3.1E-02	n=2
voltage-gated potassium channel activity	GO:0086089	p=3.1E-02	n=2
delayed rectifier potassium channel activity	GO:0005251	p=3.1E-02	n=2
intracellular cyclic nucleotide activate	GO:0005221	p=3.1E-02	n=2
MAP kinase kinase activity	GO:0004708	p=3.1E-02	n=2
voltage-gated potassium channel activity	GO:0086008	p=3.1E-02	n=2
cyclic nucleotide-gated ion channel activity	GO:0043855	p=3.1E-02	n=2

fg=0.03	bg=0.01
fg=0.03	bg=0.00
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.03	bg=0.00
fg=0.21	bg=0.13
fg=0.03	bg=0.01
fg=0.05	bg=0.02
fg=0.03	bg=0.01
fg=0.06	bg=0.02
fg=0.03	bg=0.01
fg=0.06	bg=0.02
fg=0.10	bg=0.05
fg=0.02	bg=0.00
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.16	bg=0.10
fg=0.03	bg=0.01
fg=0.09	bg=0.05
fg=0.09	bg=0.03
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00



GO:CC
Ncol_Nvec_vc1.1_XM_032372883.2

fraction genes in fg and expected value

midbody	GO:0030496	p=1.0E-03	n=8
perikaryon	GO:0043204	p=5.0E-03	n=5
late endosome	GO:0005770	p=6.1E-03	n=8
endolysosome membrane	GO:0036020	p=6.8E-03	n=2
cation channel complex	GO:0034703	p=7.2E-03	n=5
cell surface	GO:0009986	p=1.6E-02	n=10
mediator complex	GO:0016592	p=1.8E-02	n=3
dendritic shaft	GO:0043198	p=2.0E-02	n=4
proximal dendrite	GO:1990635	p=2.1E-02	n=2
membrane microdomain	GO:0098857	p=2.3E-02	n=8
membrane raft	GO:0045121	p=2.3E-02	n=8
intracellular canaliculus	GO:0046691	p=3.1E-02	n=2
juxtaparanode region of axon	GO:0044224	p=3.1E-02	n=2
nuclear envelope	GO:0005635	p=3.4E-02	n=11
transferase complex, transferring phosphorus	GO:0061695	p=3.8E-02	n=8
cytosolic large ribosomal subunit	GO:0022625	p=3.9E-02	n=4
microvillus membrane	GO:0031528	p=4.2E-02	n=2
aminoacyl-tRNA synthetase multienzyme complex	GO:0017101	p=4.2E-02	n=2
rhabdomere microvillus	GO:0035996	p=4.9E-02	n=1
rhabdomere microvillus membrane	GO:0035997	p=4.9E-02	n=1
Shu complex	GO:0097196	p=4.9E-02	n=1
core-binding factor complex	GO:0016513	p=4.9E-02	n=1
postsynaptic actin cytoskeleton	GO:0098871	p=4.9E-02	n=1
cytoskeleton of presynaptic active zone	GO:0048788	p=4.9E-02	n=1
integral component of lysosomal membrane	GO:1905103	p=4.9E-02	n=1
presynaptic active zone cytoplasmic component	GO:0098831	p=4.9E-02	n=1
RNA nuclear export complex	GO:0042565	p=4.9E-02	n=1
Holliday junction resolvase complex	GO:0048476	p=4.9E-02	n=1
smooth septate junction	GO:0005920	p=4.9E-02	n=1
proton-transporting ATP synthase, catalytic	GO:0045267	p=4.9E-02	n=1

fg=0.06	bg=0.02
fg=0.04	bg=0.01
fg=0.06	bg=0.02
fg=0.02	bg=0.00
fg=0.04	bg=0.01
fg=0.08	bg=0.04
fg=0.02	bg=0.00
fg=0.03	bg=0.01
fg=0.02	bg=0.00
fg=0.06	bg=0.03
fg=0.06	bg=0.03
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.08	bg=0.05
fg=0.06	bg=0.03
fg=0.03	bg=0.01
fg=0.02	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00

