GO:BP
Ncol_Nvec_vc1.1_XM_001624046.3

fraction genes in fg and expected val

Term	p-value	n	fg	bg
positive regulation of inclusion body as... GO:0090261	p=6.0E−04	n=2	fg=0.04	bg=0.00
response to increased oxygen levels GO:0036296	p=2.7E−03	n=3	fg=0.07	bg=0.01
regulation of photoreceptor cell differe... GO:0046532	p=2.7E−03	n=3	fg=0.07	bg=0.01
imaginal disc morphogenesis GO:0007560	p=3.1E−03	n=7	fg=0.16	bg=0.04
cellular response to arsenic−containing ... GO:0071243	p=3.5E−03	n=2	fg=0.04	bg=0.00
adherens junction maintenance GO:0034334	p=3.5E−03	n=2	fg=0.04	bg=0.00
C4−dicarboxylate transport GO:0015740	p=5.7E−03	n=2	fg=0.04	bg=0.00
motor neuron axon guidance GO:0008045	p=6.4E−03	n=3	fg=0.07	bg=0.01
response to antibiotic GO:0046677	p=1.0E−02	n=6	fg=0.13	bg=0.04
imaginal disc−derived leg morphogenesis GO:0007480	p=1.1E−02	n=3	fg=0.07	bg=0.01
leg disc morphogenesis GO:0007478	p=1.1E−02	n=3	fg=0.07	bg=0.01
leg disc development GO:0035218	p=1.1E−02	n=3	fg=0.07	bg=0.01
anterior head development GO:0097065	p=1.2E−02	n=2	fg=0.04	bg=0.00
positive regulation of execution phase o... GO:1900119	p=1.2E−02	n=2	fg=0.04	bg=0.00
positive regulation of photoreceptor cel... GO:0046534	p=1.2E−02	n=2	fg=0.04	bg=0.00
cellular response to metal ion GO:0071248	p=1.2E−02	n=4	fg=0.09	bg=0.02
response to hyperoxia GO:0055093	p=1.5E−02	n=2	fg=0.04	bg=0.01
regulation of vasoconstriction GO:0019229	p=1.6E−02	n=3	fg=0.07	bg=0.01
post−embryonic appendage morphogenesis GO:0035120	p=1.8E−02	n=5	fg=0.11	bg=0.03
imaginal disc−derived appendage morphoge... GO:0035114	p=1.8E−02	n=5	fg=0.11	bg=0.03
imaginal disc−derived appendage developm... GO:0048737	p=1.9E−02	n=5	fg=0.11	bg=0.04
cellular response to cadmium ion GO:0071276	p=1.9E−02	n=2	fg=0.04	bg=0.00
vasoconstriction GO:0042310	p=2.0E−02	n=3	fg=0.07	bg=0.01
cellular response to inorganic substance GO:0071241	p=2.2E−02	n=4	fg=0.09	bg=0.02
cellular response to organonitrogen comp... GO:0071417	p=2.3E−02	n=7	fg=0.16	bg=0.06
serine family amino acid metabolic proce... GO:0009069	p=2.4E−02	n=2	fg=0.04	bg=0.01
magnesium ion homeostasis GO:0010960	p=2.4E−02	n=2	fg=0.04	bg=0.01
positive regulation of cell cycle G1/S p... GO:1902808	p=2.4E−02	n=2	fg=0.04	bg=0.01
cellular response to glucocorticoid stim... GO:0071385	p=2.4E−02	n=2	fg=0.04	bg=0.01
cellular response to cAMP GO:0071320	p=2.4E−02	n=2	fg=0.04	bg=0.01

−log(p)

n=45/150 input genes with annotations

fraction

GO:MF
Ncol_Nvec_vc1.1_XM_001624046.3

fraction genes in fg and expected valu

Term	p-value	n	fg	bg
copper ion binding GO:0005507	p=1.7E−02	n=2	fg=0.05	bg=0.01
intracellular ligand−gated ion channel a... GO:0005217	p=2.1E−02	n=2	fg=0.05	bg=0.01
tRNA (guanine−N1−)−methyltransferase act... GO:0009019	p=2.3E−02	n=1	fg=0.03	bg=0.00
succinate transmembrane transporter acti... GO:0015141	p=2.3E−02	n=1	fg=0.03	bg=0.00
citrate transmembrane transporter activi... GO:0015137	p=2.3E−02	n=1	fg=0.03	bg=0.00
N−acetylglucosamine−1−phosphodiester alp... GO:0003944	p=2.3E−02	n=1	fg=0.03	bg=0.00
ecdysone binding GO:0035100	p=2.3E−02	n=1	fg=0.03	bg=0.00
nucleocytoplasmic carrier activity GO:0140142	p=2.3E−02	n=1	fg=0.03	bg=0.00
nuclear export signal receptor activity GO:0005049	p=2.3E−02	n=1	fg=0.03	bg=0.00
phorbol ester receptor activity GO:0001565	p=2.3E−02	n=1	fg=0.03	bg=0.00
translation elongation factor binding GO:0061770	p=2.3E−02	n=1	fg=0.03	bg=0.00
protein self−association GO:0043621	p=2.5E−02	n=2	fg=0.05	bg=0.01
heat shock protein binding GO:0031072	p=3.9E−02	n=3	fg=0.08	bg=0.02
ligand−gated cation channel activity GO:0099094	p=4.6E−02	n=2	fg=0.05	bg=0.01
STAT family protein binding GO:0097677	p=4.6E−02	n=1	fg=0.03	bg=0.00
dipeptidyl−peptidase activity GO:0008239	p=4.6E−02	n=1	fg=0.03	bg=0.00
store−operated calcium channel activity GO:0015279	p=4.6E−02	n=1	fg=0.03	bg=0.00
exogenous protein binding GO:0140272	p=4.6E−02	n=1	fg=0.03	bg=0.00
tricarboxylic acid transmembrane transpo... GO:0015142	p=4.6E−02	n=1	fg=0.03	bg=0.00
N4−(beta−N−acetylglucosaminyl)−L−asparag... GO:0003948	p=4.6E−02	n=1	fg=0.03	bg=0.00
cystathionine beta−synthase activity GO:0004122	p=4.6E−02	n=1	fg=0.03	bg=0.00
cysteine synthase activity GO:0004124	p=4.6E−02	n=1	fg=0.03	bg=0.00
pyruvate transmembrane transporter activ... GO:0050833	p=4.6E−02	n=1	fg=0.03	bg=0.00
C4−dicarboxylate transmembrane transport... GO:0015556	p=4.6E−02	n=1	fg=0.03	bg=0.00
tRNA (guanine) methyltransferase activit... GO:0016423	p=4.6E−02	n=1	fg=0.03	bg=0.00
calcium−induced calcium release activity GO:0048763	p=4.6E−02	n=1	fg=0.03	bg=0.00
sequence−specific single stranded DNA bi... GO:0098847	p=4.6E−02	n=1	fg=0.03	bg=0.00
UDP−galactose transmembrane transporter ... GO:0005459	p=4.6E−02	n=1	fg=0.03	bg=0.00
virus receptor activity GO:0001618	p=4.6E−02	n=1	fg=0.03	bg=0.00
hydrolase activity, acting on carbon−nit... GO:0016811	p=5.1E−02	n=2	fg=0.05	bg=0.01

−log(p)

n=37/150 input genes with annotations

fraction

GO:CC
Ncol_Nvec_vc1.1_XM_001624046.3

fraction genes in fg and expected valu

Term	p-value	n	fg	bg
katanin complex GO:0008352	p=2.6E−02	n=1	fg=0.02	bg=0.00
Lsm1−7−Pat1 complex GO:1990726	p=2.6E−02	n=1	fg=0.02	bg=0.00
Sin3 complex GO:0016580	p=2.6E−02	n=1	fg=0.02	bg=0.00
sarcoplasmic reticulum membrane GO:0033017	p=5.1E−02	n=1	fg=0.02	bg=0.00
cytosolic aryl hydrocarbon receptor comp... GO:0034752	p=5.1E−02	n=1	fg=0.02	bg=0.00
mRNA cap binding complex GO:0005845	p=5.1E−02	n=1	fg=0.02	bg=0.00
BLOC−1 complex GO:0031083	p=5.1E−02	n=1	fg=0.02	bg=0.00
nuclear stress granule GO:0097165	p=5.1E−02	n=1	fg=0.02	bg=0.00
kinetochore GO:0000776	p=6.3E−02	n=2	fg=0.04	bg=0.01
Sin3−type complex GO:0070822	p=7.6E−02	n=1	fg=0.02	bg=0.00
RNA cap binding complex GO:0034518	p=7.6E−02	n=1	fg=0.02	bg=0.00
nuclear aryl hydrocarbon receptor comple... GO:0034753	p=7.6E−02	n=1	fg=0.02	bg=0.00
BLOC complex GO:0031082	p=7.6E−02	n=1	fg=0.02	bg=0.00
cortical endoplasmic reticulum GO:0032541	p=1.0E−01	n=1	fg=0.02	bg=0.00
aryl hydrocarbon receptor complex GO:0034751	p=1.0E−01	n=1	fg=0.02	bg=0.00
intercellular canaliculus GO:0046581	p=1.0E−01	n=6	fg=0.02	bg=0.00
condensed chromosome, centromeric region GO:0000779	p=1.0E−01	n=2	fg=0.04	bg=0.01
midbody GO:0030496	p=1.2E−01	n=2	fg=0.04	bg=0.01
juxtaparanode region of axon GO:0044224	p=1.2E−01	n=1	fg=0.02	bg=0.00
intracellular canaliculus GO:0046691	p=1.2E−01	n=1	fg=0.02	bg=0.00
messenger ribonucleoprotein complex GO:1990124	p=1.2E−01	n=1	fg=0.02	bg=0.00
mitotic spindle pole GO:0097431	p=1.2E−01	n=1	fg=0.02	bg=0.00
spindle pole GO:0000922	p=1.3E−01	n=2	fg=0.04	bg=0.01
sarcoplasmic reticulum GO:0016529	p=1.5E−01	n=1	fg=0.02	bg=0.00
dynactin complex GO:0005869	p=1.5E−01	n=1	fg=0.02	bg=0.00
pronucleus GO:0045120	p=1.5E−01	n=1	fg=0.02	bg=0.00
plasma membrane proton−transporting V−ty... GO:0033181	p=1.5E−01	n=1	fg=0.02	bg=0.00
sarcoplasm GO:0016528	p=1.5E−01	n=1	fg=0.02	bg=0.00
supramolecular complex GO:0099080	p=1.5E−01	n=6	fg=0.13	bg=0.08
chromosome, centromeric region GO:0000775	p=1.6E−01	n=2	fg=0.04	bg=0.02

−log(p)

n=47/150 input genes with annotations

fraction