GO:BP
Ncol_Nvec_vc1.1_XM_001625437.3

fraction genes in fg and expected valu

Term	p	n	fg	bg
lymphangiogenesis GO:0001946	p=1.3E−03	n=5	fg=0.01	bg=0.00
cellular response to cadmium ion GO:0071276	p=1.4E−03	n=6	fg=0.01	bg=0.00
regulation of erythrocyte differentiatio... GO:0045646	p=2.3E−03	n=7	fg=0.02	bg=0.01
response to manganese ion GO:0010042	p=2.9E−03	n=5	fg=0.01	bg=0.00
positive regulation of angiogenesis GO:0045766	p=3.1E−03	n=10	fg=0.02	bg=0.01
regulation of hemoglobin biosynthetic pr... GO:0046984	p=3.5E−03	n=3	fg=0.01	bg=0.00
regulation of prostaglandin biosynthetic... GO:0031392	p=3.5E−03	n=3	fg=0.01	bg=0.00
primitive erythrocyte differentiation GO:0060319	p=3.5E−03	n=3	fg=0.01	bg=0.00
central nervous system development GO:0007417	p=3.5E−03	n=54	fg=0.13	bg=0.09
protein phosphorylation GO:0006468	p=3.6E−03	n=71	fg=0.17	bg=0.13
positive regulation of cellular biosynth... GO:0031328	p=4.1E−03	n=77	fg=0.19	bg=0.14
cardiac septum morphogenesis GO:0060411	p=4.2E−03	n=8	fg=0.02	bg=0.01
regulation of establishment of protein l... GO:1903747	p=4.8E−03	n=6	fg=0.01	bg=0.00
regulation of blood pressure GO:0008217	p=5.8E−03	n=10	fg=0.02	bg=0.01
regulation of translation in response to... GO:0043555	p=5.8E−03	n=5	fg=0.01	bg=0.00
zinc ion transport GO:0006829	p=6.0E−03	n=4	fg=0.01	bg=0.00
zinc ion homeostasis GO:0055069	p=6.0E−03	n=4	fg=0.01	bg=0.00
neuron projection arborization GO:0140058	p=6.0E−03	n=4	fg=0.01	bg=0.00
positive regulation of cell migration in... GO:0090050	p=6.0E−03	n=4	fg=0.01	bg=0.00
negative regulation of apoptotic process GO:0043066	p=6.7E−03	n=41	fg=0.10	bg=0.07
regulation of mitotic cell cycle GO:0007346	p=7.3E−03	n=41	fg=0.10	bg=0.07
kidney morphogenesis GO:0060993	p=7.6E−03	n=10	fg=0.02	bg=0.01
artery morphogenesis GO:0048844	p=7.8E−03	n=6	fg=0.01	bg=0.00
ventricular septum development GO:0003281	p=8.5E−03	n=7	fg=0.02	bg=0.01
somatic stem cell population maintenance GO:0035019	p=8.6E−03	n=8	fg=0.02	bg=0.01
positive regulation of ERK1 and ERK2 cas... GO:0070374	p=8.6E−03	n=8	fg=0.02	bg=0.01
microtubule bundle formation GO:0001578	p=8.9E−03	n=11	fg=0.03	bg=0.01
positive regulation of purine nucleotide... GO:1900373	p=1.0E−02	n=5	fg=0.01	bg=0.00
positive regulation of nucleotide biosyn... GO:0030810	p=1.0E−02	n=5	fg=0.01	bg=0.00
thymus development GO:0048538	p=1.0E−02	n=5	fg=0.01	bg=0.00

x-axis (left): 0 1 2 3 4 5 — −log(p)
n=409/1446 input genes with annotations

x-axis (right): 0.0 0.2 0.4 0.6 0.8 1.0 — fraction

GO:MF
Ncol_Nvec_vc1.1_XM_001625437.3

fraction genes in fg and expected valu

Term	p	n	fg	bg
epoxide hydrolase activity GO:0004301	p=3.5E−03	n=3	fg=0.01	bg=0.00
protein serine/threonine kinase activity GO:0004674	p=4.6E−03	n=25	fg=0.07	bg=0.04
transcription cis−regulatory region bind... GO:0000976	p=7.5E−03	n=27	fg=0.07	bg=0.05
core promoter sequence−specific DNA bind... GO:0001046	p=1.2E−02	n=7	fg=0.02	bg=0.01
zinc ion transmembrane transporter activ... GO:0005385	p=1.2E−02	n=3	fg=0.01	bg=0.00
chloride channel regulator activity GO:0017081	p=1.3E−02	n=4	fg=0.01	bg=0.00
tubulin binding GO:0015631	p=1.4E−02	n=20	fg=0.06	bg=0.03
ATP binding GO:0005524	p=1.5E−02	n=24	fg=0.07	bg=0.04
small molecule binding GO:0036094	p=1.6E−02	n=50	fg=0.14	bg=0.10
ATPase regulator activity GO:0060590	p=1.8E−02	n=6	fg=0.02	bg=0.01
adenyl nucleotide binding GO:0030554	p=1.9E−02	n=27	fg=0.07	bg=0.05
nucleotide binding GO:0000166	p=1.9E−02	n=40	fg=0.11	bg=0.08
nucleoside phosphate binding GO:1901265	p=1.9E−02	n=40	fg=0.11	bg=0.08
nuclear receptor binding GO:0016922	p=2.2E−02	n=11	fg=0.03	bg=0.02
Notch binding GO:0005112	p=2.2E−02	n=4	fg=0.01	bg=0.00
RNA polymerase II−specific DNA−binding t... GO:0061629	p=2.3E−02	n=14	fg=0.04	bg=0.02
gamma−glutamylcyclotransferase activity GO:0003839	p=2.3E−02	n=2	fg=0.01	bg=0.00
armadillo repeat domain binding GO:0070016	p=2.3E−02	n=2	fg=0.01	bg=0.00
DNA binding, bending GO:0008301	p=2.3E−02	n=2	fg=0.01	bg=0.00
calcium−induced calcium release activity GO:0048763	p=2.3E−02	n=2	fg=0.01	bg=0.00
thiopurine S−methyltransferase activity GO:0008119	p=2.3E−02	n=2	fg=0.01	bg=0.00
L−malate dehydrogenase activity GO:0030060	p=2.3E−02	n=2	fg=0.01	bg=0.00
guanylyltransferase activity GO:0070568	p=2.3E−02	n=2	fg=0.01	bg=0.00
general transcription initiation factor ... GO:0140223	p=2.3E−02	n=2	fg=0.01	bg=0.00
adenyl ribonucleotide binding GO:0032559	p=2.5E−02	n=26	fg=0.07	bg=0.05
ion channel regulator activity GO:0099106	p=2.5E−02	n=10	fg=0.03	bg=0.01
S−adenosyl−L−methionine binding GO:1904047	p=2.7E−02	n=3	fg=0.01	bg=0.00
toxic substance binding GO:0015643	p=2.7E−02	n=3	fg=0.01	bg=0.00
cis−regulatory region sequence−specific ... GO:0000987	p=2.8E−02	n=18	fg=0.05	bg=0.03
RNA polymerase II cis−regulatory region ... GO:0000978	p=2.8E−02	n=18	fg=0.05	bg=0.03

x-axis (left): 0 1 2 3 4 5 — −log(p)
n=360/1446 input genes with annotations

x-axis (right): 0.0 0.2 0.4 0.6 0.8 1.0 — fraction

GO:CC
Ncol_Nvec_vc1.1_XM_001625437.3

fraction genes in fg and expected valu

Term	p	n	fg	bg
Flemming body GO:0090543	p=3.5E−03	n=3	fg=0.01	bg=0.00
spindle pole GO:0000922	p=4.7E−03	n=13	fg=0.03	bg=0.01
rough endoplasmic reticulum membrane GO:0030867	p=6.2E−03	n=4	fg=0.01	bg=0.00
ISWI−type complex GO:0031010	p=6.2E−03	n=4	fg=0.01	bg=0.00
cell body GO:0044297	p=1.1E−02	n=39	fg=0.09	bg=0.07
neuronal cell body GO:0043025	p=1.5E−02	n=35	fg=0.08	bg=0.06
spindle GO:0005819	p=1.8E−02	n=27	fg=0.07	bg=0.03
cytoskeleton GO:0005856	p=2.1E−02	n=80	fg=0.19	bg=0.15
mitotic spindle GO:0072686	p=2.2E−02	n=11	fg=0.03	bg=0.01
actomyosin contractile ring GO:0005826	p=2.3E−02	n=2	fg=0.00	bg=0.00
GAIT complex GO:0097452	p=2.3E−02	n=2	fg=0.00	bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102	p=2.3E−02	n=2	fg=0.00	bg=0.00
transcription factor AP−1 complex GO:0035976	p=2.3E−02	n=2	fg=0.00	bg=0.00
Parkin−FBXW7−Cul1 ubiquitin ligase compl... GO:1990452	p=2.3E−02	n=2	fg=0.00	bg=0.00
eukaryotic translation elongation factor... GO:0005853	p=2.3E−02	n=2	fg=0.00	bg=0.00
somatodendritic compartment GO:0036477	p=2.8E−02	n=46	fg=0.11	bg=0.09
MKS complex GO:0036038	p=3.6E−02	n=4	fg=0.01	bg=0.00
integral component of Golgi membrane GO:0030173	p=3.6E−02	n=5	fg=0.01	bg=0.00
midbody GO:0030496	p=3.7E−02	n=14	fg=0.03	bg=0.02
methyltransferase complex GO:0034708	p=4.4E−02	n=9	fg=0.02	bg=0.01
vacuolar lumen GO:0005775	p=4.4E−02	n=9	fg=0.02	bg=0.01
cell projection GO:0042995	p=6.1E−02	n=86	fg=0.21	bg=0.18
ESC/E(Z) complex GO:0035098	p=6.3E−02	n=2	fg=0.00	bg=0.00
RNA N6−methyladenosine methyltransferase... GO:0036396	p=6.3E−02	n=2	fg=0.00	bg=0.00
mRNA editing complex GO:0045293	p=6.3E−02	n=2	fg=0.00	bg=0.00
CHRAC GO:0008623	p=6.3E−02	n=2	fg=0.00	bg=0.00
FAR/SIN/STRIPAK complex GO:0090443	p=6.3E−02	n=2	fg=0.00	bg=0.00
NURF complex GO:0016589	p=6.3E−02	n=2	fg=0.00	bg=0.00
acetylcholine−gated channel complex GO:0005892	p=6.3E−02	n=2	fg=0.00	bg=0.00
eukaryotic translation initiation factor... GO:0005850	p=6.3E−02	n=2	fg=0.00	bg=0.00

x-axis (left): 0 1 2 3 4 5 — −log(p)
n=412/1446 input genes with annotations

x-axis (right): 0.0 0.2 0.4 0.6 0.8 1.0 — fraction