GO:BP
Ncol_Nvec_vc1.1_XM_001634326.3

fraction genes in fg and expected valu

Term	p	n	fg	bg
protein destabilization GO:0031648	p=1.5E−03	n=2	fg=0.09	bg=0.00
positive regulation of telomere maintena... GO:0032206	p=2.2E−03	n=2	fg=0.09	bg=0.00
proteolysis involved in cellular protein... GO:0051603	p=3.6E−03	n=6	fg=0.26	bg=0.07
multicellular organismal signaling GO:0035637	p=5.8E−03	n=3	fg=0.13	bg=0.02
circadian regulation of gene expression GO:0032922	p=6.5E−03	n=2	fg=0.09	bg=0.01
histone deacetylation GO:0016575	p=7.9E−03	n=2	fg=0.09	bg=0.01
secretory granule organization GO:0033363	p=9.4E−03	n=2	fg=0.09	bg=0.01
regulation of sphingolipid biosynthetic ... GO:0090153	p=1.3E−02	n=1	fg=0.04	bg=0.00
positive regulation of sphingolipid bios... GO:0090154	p=1.3E−02	n=1	fg=0.04	bg=0.00
regulation of glucocorticoid receptor si... GO:2000322	p=1.3E−02	n=1	fg=0.04	bg=0.00
negative regulation of glucocorticoid re... GO:2000323	p=1.3E−02	n=1	fg=0.04	bg=0.00
regulation of membrane lipid metabolic p... GO:1905038	p=1.3E−02	n=1	fg=0.04	bg=0.00
regulation of ceramide biosynthetic proc... GO:2000303	p=1.3E−02	n=1	fg=0.04	bg=0.00
positive regulation of ceramide biosynth... GO:2000304	p=1.3E−02	n=1	fg=0.04	bg=0.00
estrogen biosynthetic process GO:0006703	p=1.3E−02	n=1	fg=0.04	bg=0.00
steroid catabolic process GO:0006706	p=1.3E−02	n=1	fg=0.04	bg=0.00
protein localization to nuclear pore GO:0090204	p=1.3E−02	n=1	fg=0.04	bg=0.00
phosphatidylserine acyl−chain remodeling GO:0036150	p=1.3E−02	n=1	fg=0.04	bg=0.00
regulation of type B pancreatic cell dev... GO:2000074	p=1.3E−02	n=1	fg=0.04	bg=0.00
eclosion rhythm GO:0008062	p=1.3E−02	n=1	fg=0.04	bg=0.00
maternal process involved in parturition GO:0060137	p=1.3E−02	n=1	fg=0.04	bg=0.00
circadian regulation of heart rate GO:0003053	p=1.3E−02	n=1	fg=0.04	bg=0.00
common myeloid progenitor cell prolifera... GO:0035726	p=1.3E−02	n=1	fg=0.04	bg=0.00
positive regulation of protein autoubiqu... GO:1902499	p=1.3E−02	n=1	fg=0.04	bg=0.00
response to redox state GO:0051775	p=1.3E−02	n=1	fg=0.04	bg=0.00
fatty acid elongation GO:0030497	p=1.3E−02	n=1	fg=0.04	bg=0.00
histone H3−K9 deacetylation GO:1990619	p=1.3E−02	n=1	fg=0.04	bg=0.00
estrogen metabolic process GO:0008210	p=1.3E−02	n=1	fg=0.04	bg=0.00
protein import into peroxisome membrane GO:0045046	p=1.3E−02	n=1	fg=0.04	bg=0.00
S−adenosylmethionine cycle GO:0033353	p=1.3E−02	n=1	fg=0.04	bg=0.00

−log(p)
n=23/112 input genes with annotations

fraction

GO:MF
Ncol_Nvec_vc1.1_XM_001634326.3

fraction genes in fg and expected valu

Term	p	n	fg	bg
histone deacetylase activity GO:0004407	p=3.7E−03	n=2	fg=0.09	bg=0.00
cysteine−type endopeptidase activity GO:0004197	p=9.3E−03	n=2	fg=0.09	bg=0.01
open rectifier potassium channel activit... GO:0005252	p=1.4E−02	n=1	fg=0.05	bg=0.00
NAD−dependent protein deacetylase activi... GO:0034979	p=1.4E−02	n=1	fg=0.05	bg=0.00
steroid dehydrogenase activity, acting o... GO:0033764	p=1.4E−02	n=1	fg=0.05	bg=0.00
phorbol ester receptor activity GO:0001565	p=1.4E−02	n=1	fg=0.05	bg=0.00
NAD−dependent histone deacetylase activi... GO:0046969	p=1.4E−02	n=1	fg=0.05	bg=0.00
NAD−dependent histone deacetylase activi... GO:0017136	p=1.4E−02	n=1	fg=0.05	bg=0.00
histone deacetylase activity (H3−K9 spec... GO:0032129	p=1.4E−02	n=1	fg=0.05	bg=0.00
S100 protein binding GO:0044548	p=1.4E−02	n=1	fg=0.05	bg=0.00
steroid dehydrogenase activity GO:0016229	p=1.4E−02	n=1	fg=0.05	bg=0.00
testosterone 17−beta−dehydrogenase (NADP... GO:0047045	p=1.4E−02	n=1	fg=0.05	bg=0.00
L−tyrosine aminotransferase activity GO:0070547	p=1.4E−02	n=1	fg=0.05	bg=0.00
L−tyrosine:2−oxoglutarate aminotransfera... GO:0004838	p=1.4E−02	n=1	fg=0.05	bg=0.00
estradiol 17−beta−dehydrogenase activity GO:0004303	p=1.4E−02	n=1	fg=0.05	bg=0.00
NAD+ binding GO:0070403	p=1.4E−02	n=1	fg=0.05	bg=0.00
voltage−gated cation channel activity GO:0022843	p=2.4E−02	n=2	fg=0.09	bg=0.01
oxysterol binding GO:0008142	p=2.8E−02	n=1	fg=0.05	bg=0.00
NAD binding GO:0051287	p=4.1E−02	n=1	fg=0.05	bg=0.00
bHLH transcription factor binding GO:0043425	p=4.1E−02	n=1	fg=0.05	bg=0.00
voltage−gated ion channel activity GO:0005244	p=4.2E−02	n=2	fg=0.09	bg=0.02
voltage−gated channel activity GO:0022832	p=4.2E−02	n=2	fg=0.09	bg=0.02
voltage−gated sodium channel activity GO:0005248	p=5.4E−02	n=1	fg=0.05	bg=0.00
NAD+ ADP−ribosyltransferase activity GO:0003950	p=5.4E−02	n=1	fg=0.05	bg=0.00
sequence−specific DNA binding GO:0043565	p=6.3E−02	n=4	fg=0.18	bg=0.07
transcription corepressor activity GO:0003714	p=6.7E−02	n=2	fg=0.09	bg=0.02
lysophospholipase activity GO:0004622	p=6.7E−02	n=1	fg=0.05	bg=0.00
sodium channel activity GO:0005272	p=6.7E−02	n=1	fg=0.05	bg=0.00
ephrin receptor binding GO:0046875	p=6.7E−02	n=1	fg=0.05	bg=0.00
intramolecular oxidoreductase activity, ... GO:0016864	p=6.7E−02	n=1	fg=0.05	bg=0.00

−log(p)
n=22/112 input genes with annotations

fraction

GO:CC
Ncol_Nvec_vc1.1_XM_001634326.3

fraction genes in fg and expected valu

Term	p	n	fg	bg
protein−lipid complex GO:0032994	p=2.5E−02	n=1	fg=0.04	bg=0.00
cytosol GO:0005829	p=2.6E−02	n=14	fg=0.61	bg=0.39
endoplasmic reticulum subcompartment GO:0098827	p=3.1E−02	n=5	fg=0.22	bg=0.08
NuRD complex GO:0016581	p=3.8E−02	n=1	fg=0.04	bg=0.00
CHD−type complex GO:0090545	p=3.8E−02	n=1	fg=0.04	bg=0.00
muscle cell projection GO:0036194	p=3.8E−02	n=1	fg=0.04	bg=0.00
muscle cell projection membrane GO:0036195	p=3.8E−02	n=1	fg=0.04	bg=0.00
endoplasmic reticulum GO:0005783	p=3.8E−02	n=7	fg=0.30	bg=0.14
cullin−RING ubiquitin ligase complex GO:0031461	p=4.5E−02	n=2	fg=0.09	bg=0.01
cortical endoplasmic reticulum GO:0032541	p=5.0E−02	n=1	fg=0.04	bg=0.00
integral component of peroxisomal membra... GO:0005779	p=5.0E−02	n=1	fg=0.04	bg=0.00
intrinsic component of peroxisomal membr... GO:0031231	p=5.0E−02	n=1	fg=0.04	bg=0.00
specific granule lumen GO:0035580	p=5.0E−02	n=1	fg=0.04	bg=0.00
chromatoid body GO:0033391	p=5.0E−02	n=1	fg=0.04	bg=0.00
Cul3−RING ubiquitin ligase complex GO:0031463	p=6.2E−02	n=1	fg=0.04	bg=0.00
peroxisomal membrane GO:0005778	p=7.4E−02	n=1	fg=0.04	bg=0.00
microbody membrane GO:0031903	p=7.4E−02	n=1	fg=0.04	bg=0.00
cytosolic small ribosomal subunit GO:0022627	p=8.6E−02	n=1	fg=0.04	bg=0.00
endoplasmic reticulum tubular network GO:0071782	p=8.6E−02	n=1	fg=0.04	bg=0.00
endoplasmic reticulum membrane GO:0005789	p=9.4E−02	n=4	fg=0.17	bg=0.08
supramolecular complex GO:0099080	p=9.6E−02	n=4	fg=0.17	bg=0.08
chromosome, telomeric region GO:0000781	p=9.7E−02	n=1	fg=0.04	bg=0.00
fusome GO:0045169	p=9.7E−02	n=1	fg=0.04	bg=0.00
MKS complex GO:0036038	p=9.7E−02	n=1	fg=0.04	bg=0.00
striated muscle dense body GO:0055120	p=9.7E−02	n=1	fg=0.04	bg=0.00
nuclear outer membrane−endoplasmic retic... GO:0042175	p=9.8E−02	n=4	fg=0.17	bg=0.08
cytoplasmic ribonucleoprotein granule GO:0036464	p=1.1E−01	n=2	fg=0.09	bg=0.02
ribonucleoprotein granule GO:0005770	p=1.2E−01	n=2	fg=0.09	bg=0.03
small ribosomal subunit GO:0015935	p=1.2E−01	n=1	fg=0.04	bg=0.01
histone deacetylase complex GO:0000118	p=1.2E−01	n=1	fg=0.04	bg=0.01

−log(p)
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fraction