GO:BP
Ncol_Nvec_v1g241767

fraction genes in fg and expected valu

Term	p-value	n	fg	bg
tRNA aminoacylation for protein translat... GO:0006418	p=3.5E−04	n=5	fg=0.04	bg=0.01
plasma membrane to endosome transport GO:0048227	p=1.0E−03	n=3	fg=0.02	bg=0.00
mitochondrion localization GO:0051646	p=1.7E−03	n=5	fg=0.04	bg=0.01
histone H4−K16 acetylation GO:0043984	p=2.0E−03	n=3	fg=0.02	bg=0.00
positive regulation of T cell mediated c... GO:0001916	p=2.3E−03	n=2	fg=0.02	bg=0.00
response to manganese−induced endoplasmi... GO:1990737	p=2.3E−03	n=2	fg=0.02	bg=0.00
DNA synthesis involved in DNA repair GO:0000731	p=2.7E−03	n=5	fg=0.04	bg=0.01
protein monoubiquitination GO:0006513	p=3.4E−03	n=5	fg=0.04	bg=0.01
regulation of translational initiation i... GO:0043558	p=3.4E−03	n=3	fg=0.02	bg=0.00
regulation of hematopoietic stem cell di... GO:1902036	p=3.6E−03	n=4	fg=0.03	bg=0.01
protein autoubiquitination GO:0051865	p=5.0E−03	n=5	fg=0.04	bg=0.01
mannosylation GO:0097502	p=5.2E−03	n=3	fg=0.02	bg=0.00
PERK−mediated unfolded protein response GO:0036499	p=5.2E−03	n=3	fg=0.02	bg=0.00
regulation of viral life cycle GO:1903900	p=6.0E−03	n=5	fg=0.04	bg=0.01
regulation of dendritic spine developmen... GO:0060998	p=6.1E−03	n=4	fg=0.03	bg=0.01
vesicle−mediated transport to the plasma... GO:0098876	p=6.7E−03	n=7	fg=0.05	bg=0.02
protein localization to nucleolus GO:1902570	p=6.8E−03	n=2	fg=0.02	bg=0.00
regulation of IRE1−mediated unfolded pro... GO:1903894	p=6.8E−03	n=2	fg=0.02	bg=0.00
L−serine transport GO:0015825	p=6.8E−03	n=2	fg=0.02	bg=0.00
aminoacyl−tRNA metabolism involved in tr... GO:0106074	p=6.8E−03	n=2	fg=0.02	bg=0.00
negative regulation of translational ini... GO:0032057	p=6.8E−03	n=2	fg=0.02	bg=0.00
regulation of neurotransmitter secretion GO:0046928	p=7.2E−03	n=5	fg=0.04	bg=0.01
regulation of hemocyte proliferation GO:0035206	p=7.6E−03	n=3	fg=0.02	bg=0.00
histone H2A ubiquitination GO:0033522	p=7.6E−03	n=3	fg=0.02	bg=0.00
response to topologically incorrect prot... GO:0035966	p=8.1E−03	n=11	fg=0.08	bg=0.02
neuron remodeling GO:0016322	p=8.5E−03	n=5	fg=0.04	bg=0.01
base−excision repair GO:0006284	p=9.5E−03	n=4	fg=0.03	bg=0.01
multicellular organism aging GO:0010259	p=1.0E−02	n=11	fg=0.08	bg=0.04
endosome transport via multivesicular bo... GO:0032509	p=1.0E−02	n=3	fg=0.02	bg=0.00
regulation of viral genome replication GO:0045069	p=1.2E−02	n=4	fg=0.03	bg=0.01
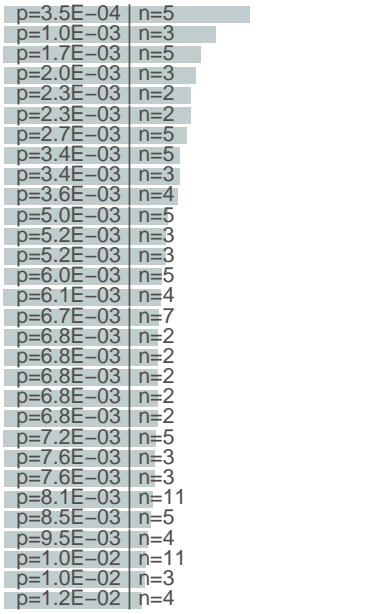
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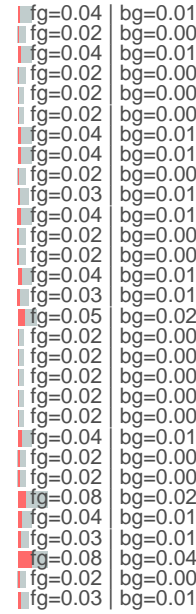
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GO:MF
Ncol_Nvec_v1g241767

fraction genes in fg and expected valu

Term	p-value	n	fg	bg
aminoacyl−tRNA ligase activity GO:0004812	p=2.0E−03	n=4	fg=0.03	bg=0.01
translation release factor activity GO:0003747	p=2.4E−03	n=2	fg=0.02	bg=0.00
glycolipid mannosyltransferase activity GO:0004376	p=2.4E−03	n=2	fg=0.02	bg=0.00
four−way junction DNA binding GO:0000400	p=2.4E−03	n=2	fg=0.02	bg=0.00
translation initiation factor activity GO:0003743	p=6.3E−03	n=4	fg=0.03	bg=0.01
cAMP response element binding GO:0035497	p=6.9E−03	n=2	fg=0.02	bg=0.00
L−serine transmembrane transporter activ... GO:0015194	p=6.9E−03	n=2	fg=0.02	bg=0.00
aminoacyl−tRNA editing activity GO:0002161	p=6.9E−03	n=2	fg=0.02	bg=0.00
G−quadruplex DNA binding GO:0051880	p=6.9E−03	n=2	fg=0.02	bg=0.00
ubiquitin binding GO:0043130	p=9.8E−03	n=4	fg=0.03	bg=0.01
acetyltransferase activity GO:0016407	p=9.8E−03	n=4	fg=0.03	bg=0.01
purine ribonucleoside triphosphate bindi... GO:0035639	p=1.7E−02	n=13	fg=0.11	bg=0.06
GDP binding GO:0019003	p=2.3E−02	n=3	fg=0.03	bg=0.01
ribonucleotide binding GO:0032553	p=4.0E−02	n=13	fg=0.11	bg=0.07
purine ribonucleotide binding GO:0032555	p=4.0E−02	n=13	fg=0.11	bg=0.07
UDP−glycosyltransferase activity GO:0008194	p=4.0E−02	n=4	fg=0.03	bg=0.01
translation regulator activity GO:0045182	p=4.2E−02	n=9	fg=0.08	bg=0.01
sulfur amino acid transmembrane transpor... GO:0000099	p=4.3E−02	n=2	fg=0.02	bg=0.00
damaged DNA binding GO:0003684	p=4.7E−02	n=3	fg=0.03	bg=0.01
3'−flap−structured DNA binding GO:0070337	p=4.9E−02	n=1	fg=0.01	bg=0.00
macrophage migration inhibitory factor b... GO:0035718	p=4.9E−02	n=1	fg=0.01	bg=0.00
phosphatidylserine decarboxylase activit... GO:0004609	p=4.9E−02	n=1	fg=0.01	bg=0.00
branched−chain amino acid transmembrane ... GO:0015658	p=4.9E−02	n=1	fg=0.01	bg=0.00
importin−alpha family protein binding GO:0061676	p=4.9E−02	n=1	fg=0.01	bg=0.00
phospholipase D activator activity GO:1990583	p=4.9E−02	n=1	fg=0.01	bg=0.00
ubiquitin−like protein−specific endopept... GO:0070137	p=4.9E−02	n=1	fg=0.01	bg=0.00
SUMO−specific endopeptidase activity GO:0070139	p=4.9E−02	n=1	fg=0.01	bg=0.00
MHC protein complex binding GO:0023023	p=4.9E−02	n=1	fg=0.01	bg=0.00
glutamate−5−semialdehyde dehydrogenase a... GO:0004350	p=4.9E−02	n=1	fg=0.01	bg=0.00
MHC class Ib protein complex binding GO:0023025	p=4.9E−02	n=1	fg=0.01	bg=0.00
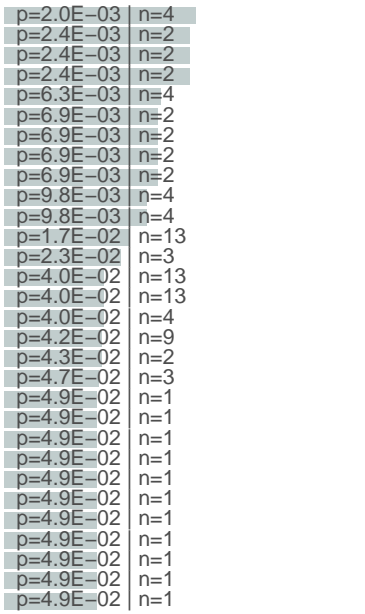
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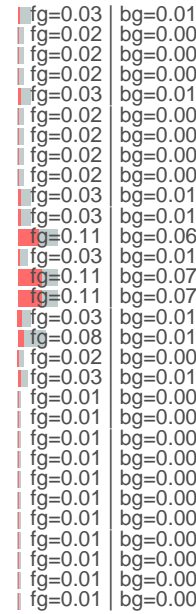
fraction

GO:CC
Ncol_Nvec_v1g241767

fraction genes in fg and expected valu

Term	p-value	n	fg	bg
multi−eIF complex GO:0043614	p=1.2E−04	n=3	fg=0.02	bg=0.00
translation preinitiation complex GO:0070993	p=2.5E−03	n=2	fg=0.01	bg=0.00
eukaryotic translation initiation factor... GO:0005850	p=7.2E−03	n=2	fg=0.01	bg=0.00
endoplasmic reticulum membrane GO:0005789	p=7.9E−03	n=18	fg=0.13	bg=0.07
mitochondrial nucleoid GO:0042645	p=8.2E−03	n=3	fg=0.02	bg=0.00
eukaryotic translation initiation factor... GO:0005852	p=3.3E−02	n=2	fg=0.01	bg=0.00
male germ cell nucleus GO:0001673	p=4.4E−02	n=2	fg=0.01	bg=0.00
aminoacyl−tRNA synthetase multienzyme co... GO:0017101	p=4.4E−02	n=2	fg=0.01	bg=0.00
translation release factor complex GO:0018444	p=5.0E−02	n=1	fg=0.01	bg=0.00
anchored component of synaptic vesicle m... GO:0098993	p=5.0E−02	n=1	fg=0.01	bg=0.00
core−binding factor complex GO:0016513	p=5.0E−02	n=1	fg=0.01	bg=0.00
eukaryotic 43S preinitiation complex GO:0016282	p=5.0E−02	n=1	fg=0.01	bg=0.00
DNA topoisomerase type II (double strand... GO:0009330	p=5.0E−02	n=1	fg=0.01	bg=0.00
endocytic vesicle lumen GO:0071682	p=5.0E−02	n=1	fg=0.01	bg=0.00
RNA nuclear export complex GO:0042565	p=5.0E−02	n=1	fg=0.01	bg=0.00
Holliday junction resolvase complex GO:0048476	p=5.0E−02	n=1	fg=0.01	bg=0.00
eukaryotic 48S preinitiation complex GO:0033290	p=5.0E−02	n=1	fg=0.01	bg=0.00
astrocyte end−foot GO:0097450	p=5.0E−02	n=1	fg=0.01	bg=0.00
glial limiting end−foot GO:0097451	p=5.0E−02	n=1	fg=0.01	bg=0.00
gamma DNA polymerase complex GO:0005760	p=5.0E−02	n=1	fg=0.01	bg=0.00
longitudinal sarcoplasmic reticulum GO:0014801	p=5.0E−02	n=1	fg=0.01	bg=0.00
ribbon synapse GO:0097470	p=5.0E−02	n=1	fg=0.01	bg=0.00
nuclear RNA export factor complex GO:0042272	p=5.0E−02	n=1	fg=0.01	bg=0.00
methionyl glutamyl tRNA synthetase compl... GO:0017102	p=5.0E−02	n=1	fg=0.01	bg=0.00
platelet dense tubular network GO:0031094	p=5.0E−02	n=1	fg=0.01	bg=0.00
platelet dense tubular network membrane GO:0031095	p=5.0E−02	n=1	fg=0.01	bg=0.00
cation−transporting ATPase complex GO:0090533	p=5.0E−02	n=1	fg=0.01	bg=0.00
calcium ion−transporting ATPase complex GO:0090534	p=5.0E−02	n=1	fg=0.01	bg=0.00
synaptic cleft GO:0043083	p=5.0E−02	n=1	fg=0.01	bg=0.00
endodeoxyribonuclease complex GO:1905347	p=5.0E−02	n=1	fg=0.01	bg=0.00
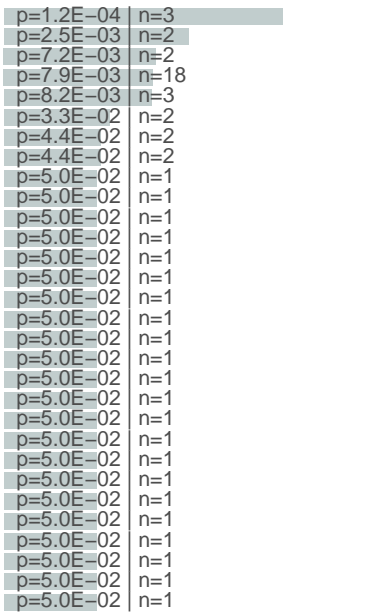
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fraction