

GO_Biological_Process_2021

Term

spliceosomal conformational changes to
generate catalytic conformation (GO:0000393)

nuclear retention of pre-mRNA at the site of
transcription (GO:0071033)

regulation of protein lipidation
(GO:1903059)

negative regulation of ERAD pathway
(GO:1904293)

glycolipid transport (GO:0046836)

aminophospholipid transport (GO:0015917)

SRP-dependent cotranslational protein
targeting to membrane (GO:0006614)

self proteolysis (GO:0097264)

response to hepatocyte growth factor
(GO:0035728)

pre-replicative complex assembly involved in
nuclear cell cycle DNA replication
(GO:0006267)

postsynapse organization (GO:0099173)

cellular response to hepatocyte growth
factor stimulus (GO:0035729)

0

2

4

6

Enrichment log(combined score)

GO_Cellular_Component_2021

Term

polysomal ribosome (GO:0042788)

spermatoproteasome complex (GO:1990111)

endolysosome lumen (GO:0036021)

ribosome (GO:0005840)

rough endoplasmic reticulum membrane
(GO:0030867)

CMG complex (GO:0071162)

cytosolic small ribosomal subunit
(GO:0022627)

cytoplasmic side of endoplasmic reticulum
membrane (GO:0098554)

small ribosomal subunit (GO:0015935)

RNA polymerase II, core complex (GO:0005665)

COPII vesicle coat (GO:0030127)

0

2

4

6

Enrichment log(combined score)

GO_Molecular_Function_2021

Term

ganglioside binding (GO:0035594)

1,4- α -oligoglucan phosphorylase activity
(GO:0004645)

aminophospholipid flippase activity
(GO:0015247)

bile acid binding (GO:0032052)

monocarboxylic acid binding (GO:0033293)

protein serine/threonine phosphatase
inhibitor activity (GO:0004865)

AMP binding (GO:0016208)

3'-5' DNA helicase activity (GO:0043138)

single-stranded DNA helicase activity
(GO:0017116)

pyridoxal phosphate binding (GO:0030170)

0

2

4

6

Enrichment log(combined score)