

# GO\_Biological\_Process\_2021

Term

negative regulation of mRNA splicing, via  
spliceosome (GO:0048025)

negative regulation of mRNA processing  
(GO:0050686)

ubiquitin-independent protein catabolic  
process via the multivesicular body sorting  
pathway (GO:0090611)

regulation of snRNA transcription by RNA  
polymerase II (GO:1905380)

regulation of maintenance of mitotic sister  
chromatid cohesion (GO:0034182)

protein localization to site of  
double-strand break (GO:1990166)

positive regulation of maintenance of sister  
chromatid cohesion (GO:0034093)

positive regulation of maintenance of  
mitotic sister chromatid cohesion  
(GO:0034184)

negative regulation of posttranscriptional  
gene silencing (GO:0060149)

negative regulation of metalloproteinase  
activity (GO:1905049)

negative regulation of gene silencing by RNA  
(GO:0060967)

mRNA cleavage (GO:0006379)

intracellular distribution of mitochondria  
(GO:0048312)

glutathione transport (GO:0034635)

0

2

4

Enrichment log(combined score)

# GO\_Cellular\_Component\_2021

Term

postsynaptic recycling endosome (GO:0098837)

anaphase-promoting complex (GO:0005680)

NSL complex (GO:0044545)

MICOS complex (GO:0061617)

nuclear inclusion body (GO:0042405)

0

1

2

3

4

5

Enrichment log(combined score)

# GO\_Molecular\_Function\_2021

Term

nuclear import signal receptor activity  
(GO:0061608)

supercoiled DNA binding (GO:0097100)

protein carboxyl O-methyltransferase  
activity (GO:0051998)

threonine-type peptidase activity  
(GO:0070003)

serine-type exopeptidase activity  
(GO:0070008)

3',5'-cyclic-GMP phosphodiesterase activity  
(GO:0047555)

3-hydroxyacyl-CoA dehydrogenase activity  
(GO:0003857)

0

1

2

3

4

5

Enrichment log(combined score)