

GO_Biological_Process_2021

Term

positive regulation of posttranscriptional
gene silencing (GO:0060148)

regulation of vascular associated smooth
muscle contraction (GO:0003056)

regulation of retinal ganglion cell axon
guidance (GO:0090259)

regulation of chromosome separation
(GO:1905818)

regulation of DNA topoisomerase
(ATP-hydrolyzing) activity (GO:2000371)

positive regulation of vascular associated
smooth muscle cell apoptotic process
(GO:1905461)

positive regulation of metallopeptidase
activity (GO:1905050)

positive regulation of mast cell activation
involved in immune response (GO:0033008)

positive regulation of axon extension
involved in axon guidance (GO:0048842)

positive regulation of DNA topoisomerase
(ATP-hydrolyzing) activity (GO:2000373)

p38MAPK cascade (GO:0038066)

negative regulation of smooth muscle
contraction (GO:0045986)

lipid transport across blood-brain barrier
(GO:1990379)

dopamine catabolic process (GO:0042420)

0

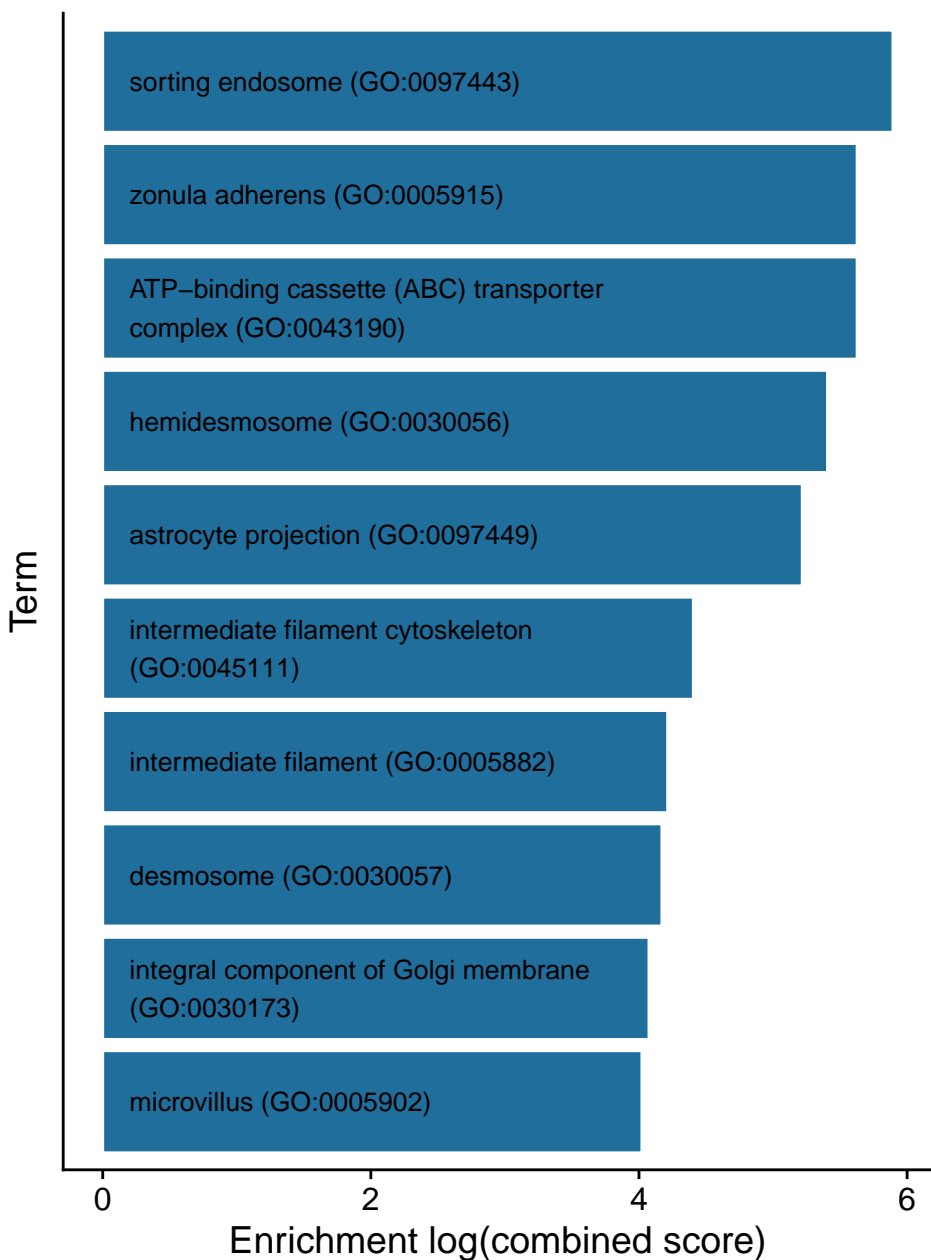
2

4

6

Enrichment log(combined score)

GO_Cellular_Component_2021



GO_Molecular_Function_2021

Term

phosphatidylserine flippase activity
(GO:0140346)

glial cell-derived neurotrophic factor
receptor activity (GO:0016167)

primary miRNA binding (GO:0070878)

phosphatidylethanolamine flippase activity
(GO:0090555)

oncostatin-M receptor activity (GO:0004924)

leukemia inhibitory factor receptor activity
(GO:0004923)

chitinase activity (GO:0004568)

G protein-coupled serotonin receptor binding
(GO:0031821)

vascular endothelial growth factor-activated
receptor activity (GO:0005021)

phospholipid scramblase activity
(GO:0017128)

mannosyl-oligosaccharide mannosidase
activity (GO:0015924)

mannosyl-oligosaccharide
1,2- α -mannosidase activity (GO:0004571)

aminophospholipid flippase activity
(GO:0015247)

0

2

4

6

Enrichment log(combined score)