GO_Biological_Process_2021

positive regulation of nucleotide-binding oligomerization domain containing signaling pathway (GO:0070426)

regulation of nucleotide-binding oligomerization domain containing 2 signaling pathway (GO:0070432)

negative regulation of erythrocyte differentiation (GO:0045647)

heat acclimation (GO:0010286)

cellular heat acclimation (GO:0070370)

positive regulation of microtubule nucleation (GO:0090063)

negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway (GO:1902236)

cellular response to unfolded protein (GO:0034620)

positive regulation of tumor necrosis factor-mediated signaling pathway (GO:1903265)

regulation of microtubule nucleation (GO:0010968)

negative regulation of transcription from RNA polymerase II promoter in response to stress (GO:0097201)

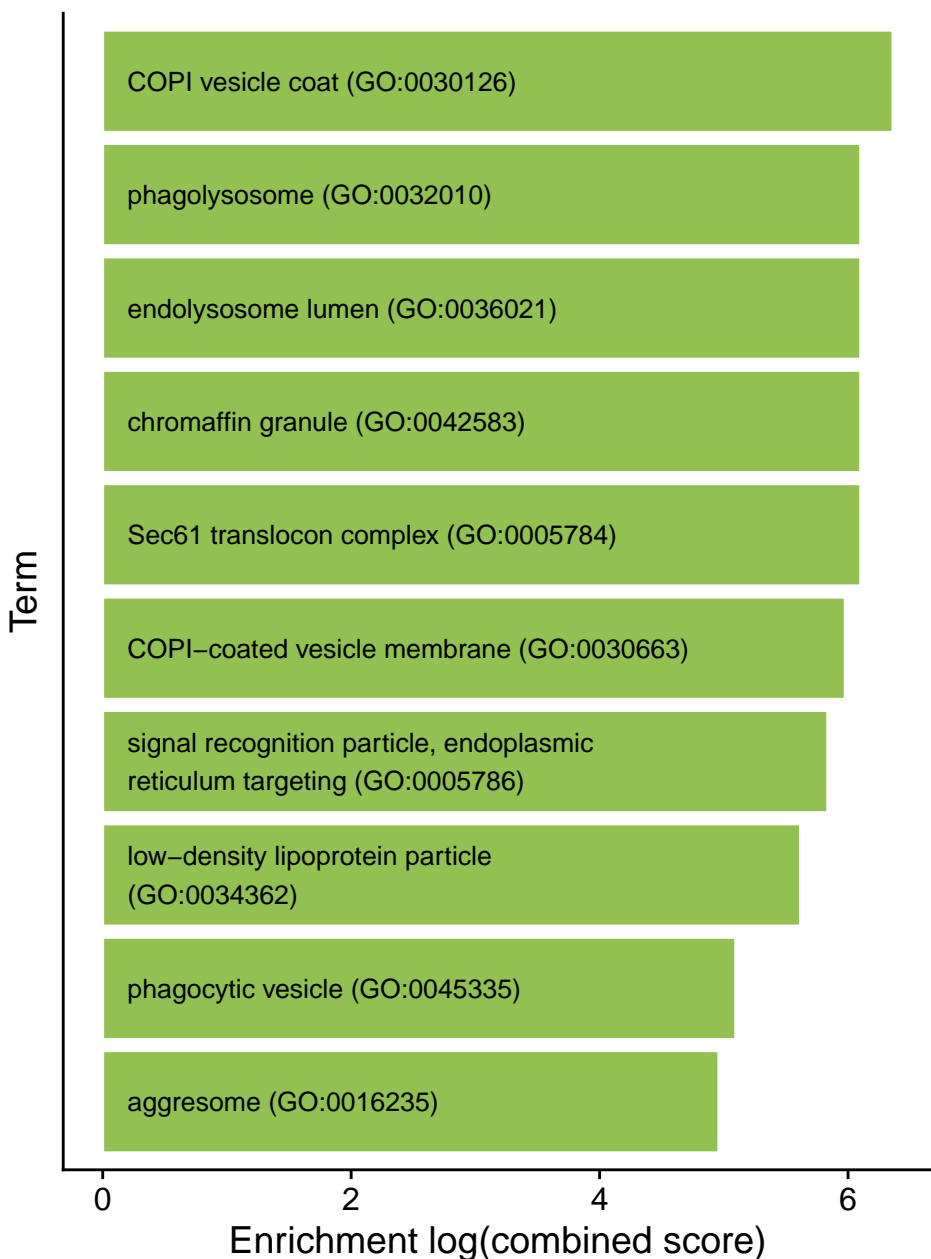negative regulation of inclusion body assembly (GO:0090084)

Term

Enrichment log(combined score)

GO_Cellular_Component_2021

COPI vesicle coat (GO:0030126)

phagolysosome (GO:0032010)

endolysosome lumen (GO:0036021)

chromaffin granule (GO:0042583)

Sec61 translocon complex (GO:0005784)

COPI−coated vesicle membrane (GO:0030663)

signal recognition particle, endoplasmic
reticulum targeting (GO:0005786)

low−density lipoprotein particle
(GO:0034362)

phagocytic vesicle (GO:0045335)

aggresome (GO:0016235)

Term

Enrichment log(combined score)

GO_Molecular_Function_2021

C3HC4–type RING finger domain binding (GO:0055131)

sequence–specific single stranded DNA binding (GO:0098847)

procollagen–proline 4–dioxygenase activity (GO:0004656)

peptidoglycan immune receptor activity (GO:0016019)

apolipoprotein A–I binding (GO:0034186)

TPR domain binding (GO:0030911)

L–ornithine transmembrane transporter activity (GO:0000064)

L–lysine transmembrane transporter activity (GO:0015189)

L–histidine transmembrane transporter activity (GO:0005290)

L–arginine transmembrane transporter activity (GO:0061459)

Term

Enrichment log(combined score)

0   2   4   6