

negative regulation of biomineralization (GO:0011515)
 G-protein-coupled receptor particle (GO:0011515)
 metabolic process (GO:0008084)
 catabolic process (GO:0032802)
 acetyl-CoA biosynthetic process (GO:0006085)
 negative regulation of cell division (GO:0051782)
 myelination in hindbrain (GO:0051782)
 nucleoside diphosphate biosynthetic process (GO:0025538)
 cell growth factor (GO:0001156)
 regulation of synaptic vesicle reuptake (GO:0036324)
 protein monoubiquitination (GO:0019041)
 regulation of adenylate cyclase-activating G protein-coupled receptor signaling pathway (GO:0025255)
 protein-coupled receptor signaling pathway (GO:0025255)
 ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway (GO:1990564)
 protein polyubiquitylation (GO:0043328)
 protein K69-linked ubiquitylation (GO:1990592)
 positive regulation of protein ubiquitylation (GO:1990592)
 positive regulation of transcription (GO:0010025)
 posttranscriptional regulation of viral genome replication (GO:0006045)
 negative regulation of cell differentiation (GO:0045578)
 myosin-light-chain-phosphatase activity (GO:0035509)
 L-methionine salvage from methionine (GO:0019509)
 isocitrate metabolic process (GO:0006102)
 His-Purkinje system development (GO:0003164)
 glucuronate catabolic process to xylulose 5-phosphate (GO:0019640)
 glucuronate catabolic process (GO:0006064)
 glomerular visceral epithelial cell differentiation (GO:0005211)
 fatty acid metabolic process (GO:0008084)
 localization of protein localization to vacuole (GO:0072686)
 Purkinje cell differentiation (GO:0021895)
 Purkinje cell differentiation (GO:0021702)
 Purkinje cell differentiation (GO:0021702)
 Purkinje cell differentiation (GO:0021702)

0

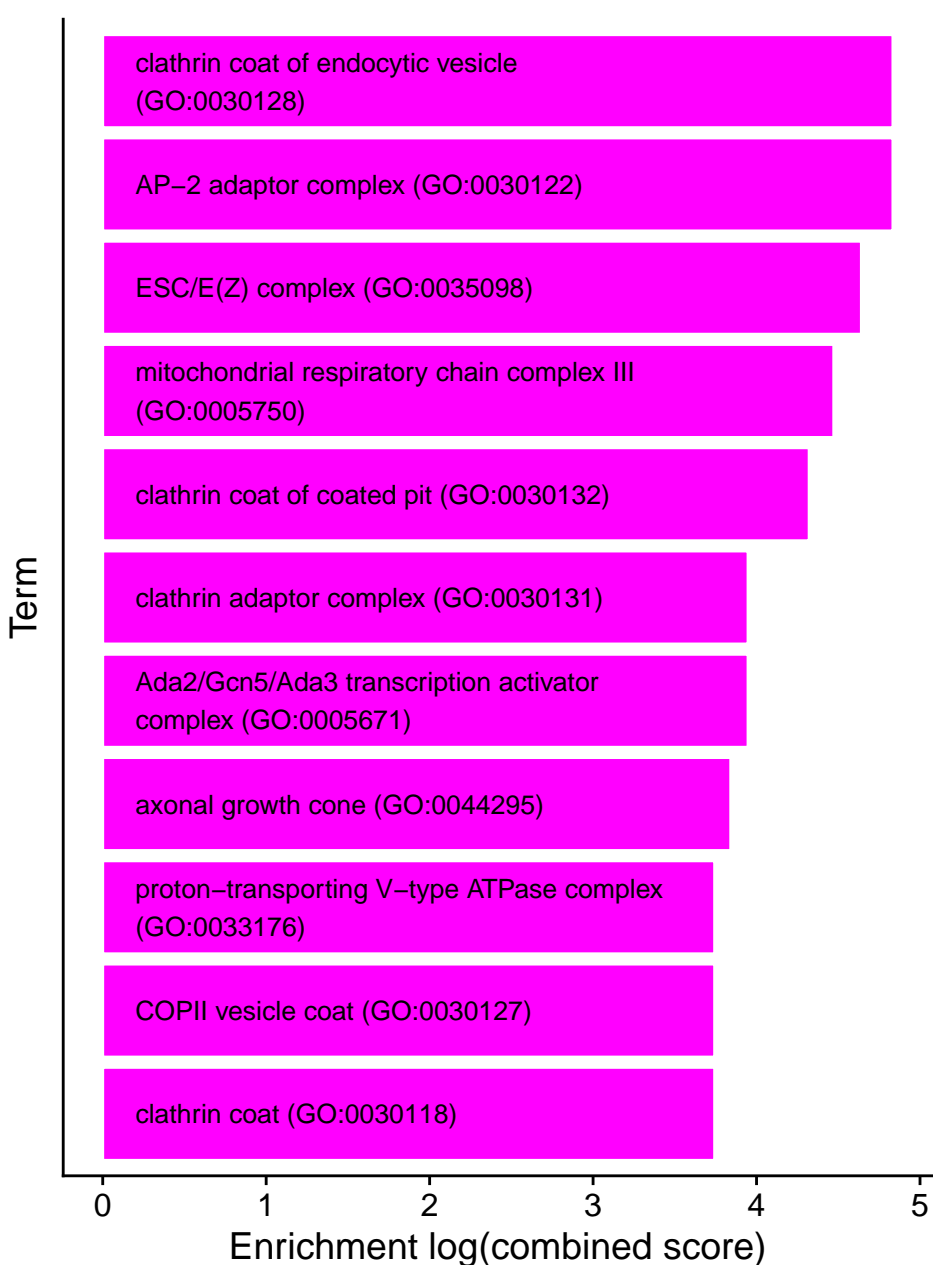
2

4

6

Enrichment log(combined score)

GO_Cellular_Component_2021



GO_Molecular_Function_2021

Term

rDNA binding (GO:0000182)

isocitrate dehydrogenase activity
(GO:0004448)

carbonyl reductase (NADPH) activity
(GO:0004090)

C-acetyltransferase activity (GO:0016453)

alpha-2A adrenergic receptor binding
(GO:0031694)

acetyl-CoA C-acyltransferase activity
(GO:0003988)

oxidoreductase activity, acting on the
aldehyde or oxo group of donors, disulfide
as acceptor (GO:0016624)

aspartic-type endopeptidase inhibitor
activity (GO:0019828)

aminophospholipid flippase activity
(GO:0015247)

calcium-independent phospholipase A2
activity (GO:0047499)

aldehyde-lyase activity (GO:0016832)

0

2

4

Enrichment log(combined score)