GO_Biological_Process_2021

protein localization to membrane raft

positive regulation of synapse maturation (GO:0090129)

bone resorption (GO:0045453)

regulation of synapse maturation (GO:0090128)

insulin-like growth factor receptor signaling pathway (GO:0048009)

positive regulation of endoplasmic reticulum unfolded protein response (GO:1900103)

negative regulation of adenylate cyclase activity (GO:0007194)

negative regulation of cyclase activity (GO:0031280)

ncRNA transcription (GO:0098781)

zygotic determination of anterior/posterior axis, embryo (GO:0007354)

vascular endothelial growth factor receptor-2 signaling pathway (GO:0036324)

transcription initiation from RNA polymerase II promoter (GO:0006367)

thorax and anterior abdomen determination (GO:0007356)

response to morphine (GO:0043278)

regulation of sodium:proton antiporter activity (GO:0032415)

regulation of respiratory gaseous exchange by nervous system process (GO:0002087)

regulation of heart growth (GO:0060420)

regulation of caveolin-mediated endocytosis (GO:2001286)

protein sialylation (GO:1990743)

postsynaptic density protein 95 clustering (GO:0097119)

positive regulation of transcription from RNA polymerase II promoter involved in heart development (GO:1901228)

positive regulation of protein localization to synapse (GO:1902474)

neuroinflammatory response (GO:0150076)

negative regulation of PERK-mediated unfolded protein response (GO:1903898)

late endosome to Golgi transport (GO:0034499)

immature B cell differentiation (GO:0002327)

endothelial cell apoptotic process (GO:0072577)

diphosphoinositol polyphosphate metabolic process (GO:0071543)

diaphragm development (GO:0060539)

diadenosine pentaphosphate metabolic process (GO:1901906)

diadenosine pentaphosphate catabolic process (GO:1901907)

diadenosine hexaphosphate metabolic process (GO:1901908)

diadenosine hexaphosphate catabolic process (GO:1901909)

cyclic-GMP-AMP transmembrane import across plasma membrane (GO:0140361)

cerebellar granule cell differentiation (GO:0021707)

adenosine 5'-(hexahydrogen pentaphosphate) metabolic process (GO:1901910)

adenosine 5'-(hexahydrogen pentaphosphate) catabolic process (GO:1901911)

Term (y-axis)

Enrichment log(combined score) (x-axis)

0   2   4   6

GO_Cellular_Component_2021

secretory vesicle (GO:0099503)

phosphatidylinositol 3–kinase complex, class I (GO:0097651)

flotillin complex (GO:0016600)

transcription factor TFIIIC complex (GO:0000127)

symmetric synapse (GO:0032280)

integral component of presynaptic membrane (GO:0099056)

integral component of postsynaptic membrane (GO:0099055)

hemidesmosome (GO:0030056)

G protein–coupled receptor dimeric complex (GO:0038037)

intrinsic component of the cytoplasmic side of the plasma membrane (GO:0031235)

integral component of synaptic membrane (GO:0099699)

inhibitory synapse (GO:0060077)

Term

0　　　　　　　　2　　　　　　　　4

Enrichment log(combined score)

GO_Molecular_Function_2021

protein kinase C activity (GO:0004697)

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

endopolyphosphatase activity (GO:0000298)

diphosphoinositol−polyphosphate diphosphatase activity (GO:0008486)

bis(5'−adenosyl)−pentaphosphatase activity (GO:0034432)

bis(5'−adenosyl)−hexaphosphatase activity (GO:0034431)

ErbB−3 class receptor binding (GO:0043125)

primary miRNA binding (GO:0070878)

neurotrophin TRKA receptor binding (GO:0005168)

neurotrophin TRK receptor binding (GO:0005167)

alpha−N−acetylneuraminate alpha−2,8−sialyltransferase activity (GO:0003828)

Term

0   2   4

Enrichment log(combined score)