

GO_Biological_Process_2021

Term

morphogenesis of an epithelial sheet

(GO:0002011)

ventricular cardiac muscle cell

differentiation (GO:0055012)

tight junction organization (GO:0120193)

secondary heart field specification

(GO:0003130)

rescue of stalled ribosome (GO:0072344)

renal tubule development (GO:0061326)

regulation of snRNA transcription by RNA

polymerase II (GO:1905380)

regulation of skeletal muscle tissue

development (GO:0048641)

regulation of protein monoubiquitination

(GO:1902525)

regulation of platelet-derived growth factor

receptor-coupled signaling pathway (GO:2000586)

oligomerization domain containing signaling

pathway (GO:0070424)

regulation of centrosome formation

(GO:0002634)

positive regulation of protein

monoubiquitination (GO:1902527)

positive regulation of bicellular tight

junction assembly (GO:1903348)

negative regulation of vascular endothelial

cell proliferation (GO:1905563)

negative regulation of smooth muscle cell

apoptotic process (GO:0034302)

negative regulation of macrophage

differentiation (GO:0045650)

negative regulation of hydrogen peroxide

metabolic process (GO:0010727)

mammary gland duct morphogenesis

(GO:0060603)

kidney morphogenesis (GO:0060993)

heart field specification (GO:0003128)

cellular response to antibiotic (GO:0071236)

aggresome assembly (GO:0070842)

0

2

4

6

Enrichment log(combined score)

GO_Cellular_Component_2021

Term

PCAF complex (GO:0000125)

apicolateral plasma membrane (GO:0016327)

PTW/PP1 phosphatase complex (GO:0072357)

protein serine/threonine phosphatase complex
(GO:0008287)

STAGA complex (GO:0030914)

Sin3 complex (GO:0016580)

SAGA complex (GO:0000124)

CD40 receptor complex (GO:0035631)

U2-type catalytic step 1 spliceosome
(GO:0071006)

Swr1 complex (GO:0000812)

Set1C/COMPASS complex (GO:0048188)

0

2

4

Enrichment log(combined score)

GO_Molecular_Function_2021

Term

minor groove of adenine–thymine–rich DNA
binding (GO:0003680)

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

lipid kinase activity (GO:0001727)

cAMP–dependent protein kinase activity
(GO:0004691)

DNA secondary structure binding (GO:0000217)

supercoiled DNA binding (GO:0097100)

cyclic nucleotide–dependent protein kinase
activity (GO:0004690)

SUMO–specific protease activity (GO:0016929)

sphingosine N–acyltransferase activity
(GO:0050291)

serine–type exopeptidase activity
(GO:0070008)

peroxisome proliferator activated receptor
binding (GO:0042975)

N6–methyladenosine–containing RNA binding
(GO:1990247)

0

2

4

6

Enrichment log(combined score)