

protein ubiquitination involved in ubiquitin-dependent protein catabolic process, GO:0042787
cell projection organization, GO:0030030
peptidyl-serine phosphorylation, GO:0018105
centriole, GO:0005814
ciliary basal body, GO:0036064
myelin sheath, GO:0043209
negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, GO:0051436
positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition, GO:0051437
protein dephosphorylation, GO:0006470
positive regulation of canonical Wnt signaling pathway, GO:0090263
stimulatory C-type lectin receptor signaling pathway, GO:0002223
SCF-dependent proteasomal ubiquitin-dependent protein catabolic process, GO:0031146
NIK/NF-kappaB signaling, GO:0038061
endosomal transport, GO:0016197
vesicle, GO:0031982
cell cortex, GO:0005938
negative regulation of G2/M transition of mitotic cell cycle, GO:0010972
activation of MAPK activity, GO:0000187
rhythmic process, GO:0048511
protein serine/threonine phosphatase activity, GO:0004722
peptidyl-threonine phosphorylation, GO:0018107
JNK cascade, GO:0007254
I-kappaB kinase/NF-kappaB signaling, GO:0007249
SCF ubiquitin ligase complex, GO:0019005
cytoskeleton organization, GO:0007010
7-methylguanosine mRNA capping, GO:0006370
transforming growth factor beta receptor signaling pathway, GO:0007179
cerebral cortex development, GO:0021987
intraciliary transport involved in cilium assembly, GO:0035735
spindle assembly, GO:0051225
global genome nucleotide-excision repair, GO:0070911
cell leading edge, GO:0031252
non-motile cilium assembly, GO:1905515
tubulin binding, GO:0015631
stress-activated MAPK cascade, GO:0051403
apical part of cell, GO:0045177
neuron migration, GO:0001764
cellular response to organic cyclic compound, GO:0071407
negative regulation of type I interferon production, GO:0032480
cytoplasmic microtubule organization, GO:0031122
nucleotide-binding oligomerization domain containing signaling pathway, GO:0070423
centriolar satellite, GO:0034451
viral life cycle, GO:0019058
cyclin-dependent protein serine/threonine kinase activity, GO:0004693
transcription elongation from RNA polymerase I promoter, GO:0006362
regulation of tumor necrosis factor-mediated signaling pathway, GO:0010803
transcription initiation from RNA polymerase I promoter, GO:0006361
intercellular bridge, GO:0045171
intrinsic apoptotic signaling pathway, GO:0097193
regulation of circadian rhythm, GO:0042752
termination of RNA polymerase I transcription, GO:0006363
positive regulation of intracellular protein transport, GO:0090316
positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway, GO:1900740
cellular iron ion homeostasis, GO:0006879
ciliary base, GO:0097546
neuron projection morphogenesis, GO:0048812
negative regulation of epidermal growth factor receptor signaling pathway, GO:0042059
protein destabilization, GO:0031648
photoreceptor connecting cilium, GO:0032391
response to toxic substance, GO:0009636
cellular response to nerve growth factor stimulus, GO:1990090
hippo signaling, GO:0035329
regulation of cytokinesis, GO:0032465
voltage-gated potassium channel complex, GO:0008076
negative regulation of transforming growth factor beta receptor signaling pathway, GO:0030512
endocytic vesicle membrane, GO:0030666
regulation of protein binding, GO:0043393
dynein light intermediate chain binding, GO:0051959
Golgi stack, GO:0005795
pericentriolar material, GO:0000242
substantia nigra development, GO:0021762
positive regulation of cell cycle, GO:0045787
ciliary transition zone, GO:0035869
non-membrane spanning protein tyrosine kinase activity, GO:0004715
negative regulation of phosphatase activity, GO:0010923
positive regulation of microtubule polymerization, GO:0031116
microtubule-based process, GO:0007017
dynein intermediate chain binding, GO:0045505
structural constituent of cytoskeleton, GO:0005200
regulation of cell adhesion, GO:0030155
circadian regulation of gene expression, GO:0032922
positive regulation of protein export from nucleus, GO:0046827
protein localization to centrosome, GO:0071539
response to radiation, GO:0009314
dynein light chain binding, GO:0045503
positive regulation of proteolysis, GO:0045862
stereocilium, GO:0032420
gamma-tubulin binding, GO:0043015
regulation of mitotic spindle organization, GO:0060236
cyclin-dependent protein serine/threonine kinase regulator activity, GO:0016538
hippocampus development, GO:0021766
establishment of cell polarity, GO:0030010
positive regulation of mitotic cell cycle, GO:0045931
positive regulation of cyclin-dependent protein serine/threonine kinase activity, GO:0045737
centriole replication, GO:0007099
spectrin binding, GO:0030507
protein phosphatase 2A binding, GO:0051721
natural killer cell mediated cytotoxicity, GO:0042267
HAUS complex, GO:0070652
negative regulation of protein serine/threonine kinase activity, GO:0071901
protein secretion, GO:0009306
intraciliary retrograde transport, GO:0035721
cell cortex region, GO:0099738
negative regulation of cyclin-dependent protein serine/threonine kinase activity, GO:0045736
potassium channel regulator activity, GO:0015459
cellular protein localization, GO:0034613
protein phosphatase inhibitor activity, GO:0004864
ATP-dependent microtubule motor activity, GO:0008574
cellular response to extracellular stimulus, GO:0031668
animal organ regeneration, GO:0031100
WW domain binding, GO:0050699
cytoskeleton-dependent intracellular transport, GO:0030705
MHC class I protein binding, GO:0042288
peptidyl-threonine dephosphorylation, GO:0035970
positive regulation of ubiquitin protein ligase activity, GO:1904668
regulation of canonical Wnt signaling pathway, GO:0060828
regulation of protein metabolic process, GO:0051246
cullin-RING ubiquitin ligase complex, GO:0031461
histone H2A monoubiquitination, GO:0035518
positive regulation of cilium assembly, GO:0045724
protein methyltransferase activity, GO:0008276
regulation of proteasomal protein catabolic process, GO:0061136
oocyte maturation, GO:0001556
establishment of protein localization to membrane, GO:0090150
cellular response to cAMP, GO:0071320
regulation of glycogen biosynthetic process, GO:0005979
RNA polymerase II carboxy-terminal domain kinase activity, GO:0008353
protein localization to organelle, GO:0033365
negative regulation of ryanodine-sensitive calcium-release channel activity, GO:0060315
regulation of centriole replication, GO:0046599
melanosome transport, GO:0032402
hematopoietic stem cell proliferation, GO:0071425
positive regulation of RNA polymerase II transcriptional preinitiation complex assembly, GO:0045899
regulation of proteasomal ubiquitin-dependent protein catabolic process, GO:0032434
regulation of bicellular tight junction assembly, GO:2000810
tau-protein kinase activity, GO:0050321
endocytic vesicle lumen, GO:0071682
response to corticosterone, GO:0051412
Golgi ribbon formation, GO:0090161
response to reactive oxygen species, GO:0000302
histone demethylase activity (H3-K36 specific), GO:0051864
histone H3-K36 demethylation, GO:0070544
regulation of protein transport, GO:0051223
response to arsenic-containing substance, GO:0046685
photoreceptor inner segment, GO:0001917
positive regulation of nitric oxide biosynthetic process, GO:0045429
negative regulation of microtubule polymerization, GO:0031115
stress granule assembly, GO:0034063
regulation of nitric-oxide synthase activity, GO:0050999
cell projection membrane, GO:0031253
COP1-coated vesicle, GO:0030137
protein localization to Golgi apparatus, GO:0034067
regulation of cytosolic calcium ion concentration, GO:0051480
cAMP-dependent protein kinase complex, GO:0005952
negative regulation of phosphoprotein phosphatase activity, GO:0032515
regulation of cellular protein localization, GO:1903827
cation binding, GO:0043169
regulation of I-kappaB kinase/NF-kappaB signaling, GO:0043122
transport along microtubule, GO:0010970
polar microtubule, GO:0005827
G-protein coupled acetylcholine receptor signaling pathway, GO:0007213
regulation of heart rate by cardiac conduction, GO:0086091
negative regulation of NF-kappaB import into nucleus, GO:0042347
cellular process, GO:0009987
Golgi cisterna, GO:0031985
dynactin binding, GO:0034452
negative regulation of kinase activity, GO:0033673
ubiquitin-like protein ligase binding, GO:0044389
activation of protein kinase A activity, GO:0034199
regulation of microvillus length, GO:0032532
regulation of Ras protein signal transduction, GO:0046578
regulation of ryanodine-sensitive calcium-release channel activity, GO:0060314
MKS complex, GO:0036038
regulation of cell cycle arrest, GO:0071156
mitochondrion transport along microtubule, GO:0047497
negative regulation of hippo signaling, GO:0035331
cochlea development, GO:0090102
positive regulation of dendritic spine morphogenesis, GO:0061003
cellular response to leptin stimulus, GO:0044320
glycerophospholipid biosynthetic process, GO:0046474
negative regulation of protein tyrosine kinase activity, GO:0061099
renal water homeostasis, GO:0003091
auditory receptor cell differentiation, GO:0042491
cellular response to parathyroid hormone stimulus, GO:0071374
protein phosphatase type 1 complex, GO:0000164
cilium organization, GO:0044782
stem cell division, GO:0017145
holo TFIIF complex, GO:0005675
tube formation, GO:0035148
mammary gland epithelial cell differentiation, GO:0060644
motile cilium assembly, GO:0044458
negative regulation of phosphorylation, GO:0042326
response to osmotic stress, GO:0006970
phosphatidylinositol 3-kinase regulatory subunit binding, GO:0036312
positive regulation of programmed cell death, GO:0043068
regulation of actin polymerization or depolymerization, GO:0008064
stem cell proliferation, GO:0072089
contractile fiber, GO:0043292
phospholipase C activity, GO:0004629
cyclin-dependent protein serine/threonine kinase inhibitor activity, GO:0004861
regulation of synaptic vesicle exocytosis, GO:2000300
synaptic vesicle transport, GO:0048489
auditory receptor cell development, GO:0060117
cerebral cortex neuron differentiation, GO:0021895
cellular response to glucagon stimulus, GO:0071377
phospholipase binding, GO:0043274
GTPase activating protein binding, GO:0032794
positive regulation of neural precursor cell proliferation, GO:2000179

G2/M transition of mitotic cell cycle, GO:0000086