

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

peptidyl-serine phosphorylation, GO:0018105
cilium assembly, GO:0060271
protein dephosphorylation, GO:0006470
cell projection organization, GO:0030030
negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, GO:0051436
centriole, GO:0005814
vesicle, GO:0031982
regulation of catalytic activity, GO:0050790
ciliary basal body, GO:0036064
activation of MAPK activity, GO:0000187
stimulatory C-type lectin receptor signaling pathway, GO:0002223
positive regulation of canonical Wnt signaling pathway, GO:0090263
peptidyl-threonine phosphorylation, GO:0018107
cytoskeleton organization, GO:0007010
cell cortex, GO:0005938
protein serine/threonine phosphatase activity, GO:0004722
growth cone, GO:0030426
cerebral cortex development, GO:0021987
non-motile cilium assembly, GO:1905515
transcription initiation from RNA polymerase I promoter, GO:0006361
spindle assembly, GO:0051225
transcription elongation from RNA polymerase I promoter, GO:0006362
termination of RNA polymerase I transcription, GO:0006363
SCF ubiquitin ligase complex, GO:0019005
negative regulation of protein binding, GO:0032091
intraciliary transport involved in cilium assembly, GO:0035735
positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway, GO:1900740
negative regulation of catalytic activity, GO:0043086
regulation of circadian rhythm, GO:0042752
circadian regulation of gene expression, GO:0032922
microtubule associated complex, GO:0005875
structural constituent of cytoskeleton, GO:0005200
intercellular bridge, GO:0045171
neuron migration, GO:0001764
apical part of cell, GO:0045177
ciliary transition zone, GO:0035869
regulation of cell adhesion, GO:0030155
potassium channel regulator activity, GO:0015459
protein serine/threonine/tyrosine kinase activity, GO:0004712
positive regulation of intracellular protein transport, GO:0090316
regulation of heart rate by cardiac conduction, GO:0086091
animal organ regeneration, GO:0031100
RNA polymerase II carboxy-terminal domain kinase activity, GO:0008353
cell leading edge, GO:0031252
melanosome transport, GO:0032402
phosphoprotein binding, GO:0051219
neuron projection morphogenesis, GO:0048812
ciliary base, GO:0097546
cellular response to nerve growth factor stimulus, GO:1990090
negative regulation of phosphatase activity, GO:0010923
hippo signaling, GO:0035329
cellular response to cAMP, GO:0071320
response to radiation, GO:0009314
voltage-gated potassium channel complex, GO:0008076
protein localization to centrosome, GO:0071539
substantia nigra development, GO:0021762
regulation of cytokinesis, GO:0032465
cytoplasmic microtubule organization, GO:0031122
dynein intermediate chain binding, GO:0045505
protein phosphatase 2A binding, GO:0051721
microtubule-based process, GO:0007017
positive regulation of proteolysis, GO:0045862
WW domain binding, GO:0050699
regulation of proteasomal protein catabolic process, GO:0061136
centriolar satellite, GO:0034451
hippocampus development, GO:0021766
protein phosphatase inhibitor activity, GO:0004864
oocyte maturation, GO:0001556
cellular protein localization, GO:0034613
stereocilium, GO:0032420
negative regulation of protein serine/threonine kinase activity, GO:0071901
protein kinase A regulatory subunit binding, GO:0034237
intraciliary retrograde transport, GO:0035721
regulation of nitric-oxide synthase activity, GO:0050999
ATP-dependent microtubule motor activity, GO:0008574
gamma-tubulin binding, GO:0043015
cyclin-dependent protein serine/threonine kinase regulator activity, GO:0016538
cullin-RING ubiquitin ligase complex, GO:0031461
negative regulation of NF-kappaB import into nucleus, GO:0042347
establishment of cell polarity, GO:0030010
dynein light intermediate chain binding, GO:0051959
centriole replication, GO:0007099
regulation of cellular protein localization, GO:1903827
positive regulation of cyclin-dependent protein serine/threonine kinase activity, GO:0045737
positive regulation of protein export from nucleus, GO:0046827
photoreceptor connecting cilium, GO:0032391
holo TFIIF complex, GO:0005675
signal transduction in response to DNA damage, GO:0042770
XY body, GO:0001741
regulation of embryonic development, GO:0045995
positive regulation of programmed cell death, GO:0043068
establishment of protein localization to membrane, GO:0090150
tau-protein kinase activity, GO:0050321
histone H2A monoubiquitination, GO:0035518
plasma membrane raft, GO:0044853
negative regulation of epithelial cell proliferation, GO:0050680
maintenance of protein location in nucleus, GO:0051457
cytoskeleton-dependent intracellular transport, GO:0030705
positive regulation of gene silencing by miRNA, GO:2000637
dynamin family protein polymerization involved in mitochondrial fission, GO:0003374
cellular response to epinephrine stimulus, GO:0071872
positive regulation of cell cycle, GO:0045787
patched binding, GO:0005113
cation binding, GO:0043169
regulation of protein metabolic process, GO:0051246
regulation of synaptic vesicle exocytosis, GO:2000300
MKS complex, GO:0036038
protein localization to Golgi apparatus, GO:0034067
synaptic vesicle transport, GO:0048489
regulation of I-kappaB kinase/NF-kappaB signaling, GO:0043122
pericentriolar material, GO:0000242
negative regulation of ryanodine-sensitive calcium-release channel activity, GO:0060315
RNA polymerase II transcriptional preinitiation complex assembly, GO:0051123
response to reactive oxygen species, GO:0000302
calcium channel inhibitor activity, GO:0019855
natural killer cell mediated cytotoxicity, GO:0042267
regulation of Golgi organization, GO:1903358
positive regulation of gluconeogenesis, GO:0045722
positive regulation of phosphorylation of RNA polymerase II C-terminal domain, GO:1901409
negative regulation of phosphorylation, GO:0042326
protein phosphatase type 1 complex, GO:0000164
response to corticosterone, GO:0051412
regulation of mitotic spindle organization, GO:0060236
regulation of cardiac muscle contraction, GO:0055117
motile cilium assembly, GO:0044458
Golgi cisterna, GO:0031985
glycerophospholipid biosynthetic process, GO:0046474
negative regulation of kinase activity, GO:0033673
transcription factor activity, GO:0001075
cAMP-dependent protein kinase activity, GO:0004691
cellular response to UV-B, GO:0071493
dynein light chain binding, GO:0045503
negative regulation of smoothened signaling pathway, GO:0045879
cellular response to leptin stimulus, GO:0044320
regulation of ryanodine-sensitive calcium-release channel activity, GO:0060314
thioesterase binding, GO:0031996
positive regulation of acrosome reaction, GO:2000344
stem cell proliferation, GO:0072089
ion channel inhibitor activity, GO:0008200
G-protein coupled receptor internalization, GO:0002031
transport along microtubule, GO:0010970
bone trabecula formation, GO:0060346
cochlea development, GO:0090102
transmission of nerve impulse, GO:0019226
negative regulation of neurogenesis, GO:0050768
membrane repolarization during cardiac muscle cell action potential, GO:0086013
alpha-catenin binding, GO:0045294
sensory perception of light stimulus, GO:0050953
cyclin-dependent protein serine/threonine kinase inhibitor activity, GO:0004861
negative regulation of cyclin-dependent protein serine/threonine kinase activity, GO:0045736
protein kinase A catalytic subunit binding, GO:0034236
embryonic camera-type eye development, GO:0031076
positive regulation of Ras protein signal transduction, GO:0046579
interleukin-1-mediated signaling pathway, GO:0070498
activation of protein kinase A activity, GO:0034199