

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

protein ubiquitination involved in ubiquitin-dependent protein catabolic process, GO:0042787
myelin sheath, GO:0043209
cilium assembly, GO:0060271
cell projection organization, GO:0030030
anaphase-promoting complex-dependent catabolic process, GO:0031145
centriole, GO:0005814
negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, GO:0051436
regulation of cell cycle, GO:0051726
positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition, GO:0051437
stimulatory C-type lectin receptor signaling pathway, GO:0002223
SCF-dependent proteasomal ubiquitin-dependent protein catabolic process, GO:0031146
ciliary basal body, GO:0036064
NIK/NF-kappaB signaling, GO:0038061
cell cycle arrest, GO:0007050
vesicle, GO:0031982
protein dephosphorylation, GO:0006470
negative regulation of G2/M transition of mitotic cell cycle, GO:0010972
regulation of catalytic activity, GO:0050790
positive regulation of canonical Wnt signaling pathway, GO:0090263
activation of MAPK activity, GO:0000187
cell cortex, GO:0005938
positive regulation of proteasomal ubiquitin-dependent protein catabolic process, GO:0032436
cytoskeleton organization, GO:0007010
termination of RNA polymerase I transcription, GO:0006363
global genome nucleotide-excision repair, GO:0070911
intercellular bridge, GO:0045171
peptidyl-threonine phosphorylation, GO:0018107
negative regulation of type I interferon production, GO:0032480
transcription elongation from RNA polymerase I promoter, GO:0006362
cellular response to organic cyclic compound, GO:0071407
JNK cascade, GO:0007254
negative regulation of catalytic activity, GO:0043086
SCF ubiquitin ligase complex, GO:0019005
TRIF-dependent toll-like receptor signaling pathway, GO:0035666
nucleotide-excision repair, GO:0000717
transforming growth factor beta receptor signaling pathway, GO:0007179
apical part of cell, GO:0045177
cell leading edge, GO:0031252
regulation of circadian rhythm, GO:0042752
viral life cycle, GO:0019058
regulation of tumor necrosis factor-mediated signaling pathway, GO:0010803
negative regulation of phosphatase activity, GO:0010923
intraciliary transport involved in cilium assembly, GO:0035735
protein destabilization, GO:0031648
negative regulation of protein binding, GO:0032091
regulation of cell adhesion, GO:0030155
non-motile cilium assembly, GO:1905515
cyclin-dependent protein serine/threonine kinase activity, GO:0004693
tubulin binding, GO:0015631
regulation of cytokinesis, GO:0032465
negative regulation of transforming growth factor beta receptor signaling pathway, GO:0030512
centriolar satellite, GO:0034451
cerebral cortex development, GO:0021987
circadian regulation of gene expression, GO:0032922
potassium channel regulator activity, GO:0015459
protein phosphatase inhibitor activity, GO:0004864
animal organ regeneration, GO:0031100
positive regulation of mitotic cell cycle, GO:0045931
cellular iron ion homeostasis, GO:0006879
Golgi stack, GO:0005795
cytoplasmic microtubule organization, GO:0031122
ciliary transition zone, GO:0035869
establishment of cell polarity, GO:0030010
voltage-gated potassium channel complex, GO:0008076
protein targeting, GO:0006605
protein secretion, GO:0009306
positive regulation of intracellular protein transport, GO:0090316
structural constituent of cytoskeleton, GO:0005200
pericentriolar material, GO:0000242
positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway, GO:1900740
ciliary base, GO:0097546
dynein light intermediate chain binding, GO:0051959
intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator, GO:0042771
gamma-tubulin binding, GO:0043015
positive regulation of proteolysis, GO:0045862
positive regulation of cyclin-dependent protein serine/threonine kinase activity, GO:0045737
photoreceptor connecting cilium, GO:0032391
neuron migration, GO:0001764
dynein light chain binding, GO:0045503
endocytic vesicle membrane, GO:0030666
regulation of proteasomal protein catabolic process, GO:0061136
response to radiation, GO:0009314
substantia nigra development, GO:0021762
protein localization to centrosome, GO:0071539
centriole replication, GO:0007099
positive regulation of MAP kinase activity, GO:0043406
positive regulation of smooth muscle cell proliferation, GO:0048661
regulation of canonical Wnt signaling pathway, GO:0060828
neuron projection morphogenesis, GO:0048812
RNA polymerase II carboxy-terminal domain kinase activity, GO:0008353
cellular response to drug, GO:0035690
regulation of mitotic spindle organization, GO:0060236
hippo signaling, GO:0035329
cellular response to X-ray, GO:0071481
cAMP-dependent protein kinase activity, GO:0004691
regulation of nitric-oxide synthase activity, GO:0050999
MHC class I protein binding, GO:0042288
regulation of cellular protein localization, GO:1903827
cellular response to cAMP, GO:0071320
positive regulation of ubiquitin protein ligase activity, GO:1904668
tau-protein kinase activity, GO:0050321
cytoskeleton-dependent intracellular transport, GO:0030705
negative regulation of protein serine/threonine kinase activity, GO:0071901
dynein intermediate chain binding, GO:0045505
microtubule-based process, GO:0007017
negative regulation of NF-kappaB import into nucleus, GO:0042347
ATP-dependent microtubule motor activity, GO:0008574
regulation of proteasomal ubiquitin-dependent protein catabolic process, GO:0032434
melanosome transport, GO:0032402
cyclin-dependent protein serine/threonine kinase regulator activity, GO:0016538
positive regulation of RNA polymerase II transcriptional preinitiation complex assembly, GO:0045899
regulation of microtubule cytoskeleton organization, GO:0070507
negative regulation of cyclin-dependent protein serine/threonine kinase activity, GO:0045736
regulation of heart rate by cardiac conduction, GO:0086091
protein import into mitochondrial outer membrane, GO:0045040
glycogen granule, GO:0042587
positive regulation of protein export from nucleus, GO:0046827
generation of neurons, GO:0048699
cellular protein localization, GO:0034613
acrosomal vesicle, GO:0001669
protein phosphatase 2A binding, GO:0051721
trophoblast giant cell differentiation, GO:0060707
natural killer cell mediated cytotoxicity, GO:0042267
positive regulation of microtubule polymerization, GO:0031116
regulation of bicellular tight junction assembly, GO:2000810
renal water homeostasis, GO:0003091
positive regulation of nitric oxide biosynthetic process, GO:0045429
regulation of ryanodine-sensitive calcium-release channel activity, GO:0060314
intrinsic apoptotic signaling pathway in response to oxidative stress, GO:0008631
maintenance of protein location in nucleus, GO:0051457
negative regulation of epithelial cell proliferation, GO:0050680
activation of protein kinase A activity, GO:0034199
stereocilium, GO:0032420
HAUS complex, GO:0070652
membrane repolarization during cardiac muscle cell action potential, GO:0086013
protein polyglutamylation, GO:0018095
establishment of protein localization to membrane, GO:0090150
positive regulation of extrinsic apoptotic signaling pathway in absence of ligand, GO:2001241
photoreceptor inner segment, GO:0001917
regulation of protein complex assembly, GO:0043254
MHC class II protein complex binding, GO:0023026
response to glucagon, GO:0033762
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negative regulation of smoothened signaling pathway involved in dorsal/ventral neural tube patterning, GO:1901621
regulation of protein transport, GO:0051223
high-density lipoprotein particle assembly, GO:0034380
growth, GO:0040007
phosphatidylinositol 3-kinase regulatory subunit binding, GO:0036312
negative regulation of protein tyrosine kinase activity, GO:0061099
spectrin binding, GO:0030507
holo TFIIH complex, GO:0005675
cell cortex region, GO:0099738
intraciliary retrograde transport, GO:0035721
cellular response to glucagon stimulus, GO:0071377
protein kinase A regulatory subunit binding, GO:0034237
regulation of glucose metabolic process, GO:0010906
response to arsenic-containing substance, GO:0046685
neuron projection extension, GO:1990138
cochlea development, GO:0090102
transcription factor activity, GO:0001075
negative regulation of phosphoprotein phosphatase activity, GO:0032515
regulation of glycogen biosynthetic process, GO:0005979
oocyte maturation, GO:0001556
negative regulation of microtubule polymerization, GO:0031115
regulation of I-kappaB kinase/NF-kappaB signaling, GO:0043122
transport along microtubule, GO:0010970
regulation of protein processing, GO:0070613
cellular response to UV-B, GO:0071493
protein tyrosine kinase binding, GO:1990782
Golgi cisterna, GO:0031985
signal transduction in response to DNA damage, GO:0042770
macropinocytosis, GO:0044351
cyclin-dependent protein serine/threonine kinase inhibitor activity, GO:0004861
peptidyl-threonine dephosphorylation, GO:0035970
phosphatase regulator activity, GO:0019208
TPR domain binding, GO:0030911
WW domain binding, GO:0050699
cellular response to extracellular stimulus, GO:0031668
cellular protein catabolic process, GO:0044257
thioesterase binding, GO:0031996
protein kinase A catalytic subunit binding, GO:0034236
tissue regeneration, GO:0042246
dynamin family protein polymerization involved in mitochondrial fission, GO:0003374
regulation of potassium ion transmembrane transporter activity, GO:1901016
positive regulation of protein polyubiquitination, GO:1902916
mitochondrion transport along microtubule, GO:0047497
interleukin-1-mediated signaling pathway, GO:0070498
anterior/posterior axis specification, GO:0009948
cell projection membrane, GO:0031253
negative regulation of ryanodine-sensitive calcium-release channel activity, GO:0060315
wound healing, GO:0035313
ubiquitin-like protein ligase binding, GO:0044389
response to corticosterone, GO:0051412
response to osmotic stress, GO:0006970
G-protein beta/gamma-subunit complex binding, GO:0031683
regulation of synaptic vesicle exocytosis, GO:2000300
branching involved in mammary gland duct morphogenesis, GO:0060444
regulation of centriole replication, GO:0046599
microtubule anchoring at centrosome, GO:0034454
meiotic spindle organization, GO:0000212
positive regulation of mRNA 3'-end processing, GO:0031442
negative regulation of phosphorylation, GO:0042326
negative regulation of neurogenesis, GO:0050768
positive regulation of lamellipodium assembly, GO:0010592