

chromosome, GO:0000775

kinetochore, GO:0000776  
midbody, GO:0030496  
spindle pole, GO:0000922  
sister chromatid cohesion, GO:0007062  
nuclear envelope, GO:0005635  
condensed chromosome kinetochore, GO:0000777  
viral transcription, GO:0019083  
mitotic cell cycle, GO:0000278  
mRNA transport, GO:0051028  
ciliary basal body docking, GO:0097711  
microtubule cytoskeleton, GO:0015630  
regulation of gene silencing by miRNA, GO:0060964  
chromosome segregation, GO:0007059  
nuclear pore, GO:0005643  
anaphase-promoting complex-dependent catabolic process, GO:0031145  
regulation of G2/M transition of mitotic cell cycle, GO:0010389  
nuclear matrix, GO:0016363  
protein sumoylation, GO:0016925  
retrograde vesicle-mediated transport, GO:0006890  
host cell, GO:0043657  
intracellular transport of virus, GO:0075733  
mitotic nuclear envelope disassembly, GO:0007077  
methylated histone binding, GO:0035064  
microtubule cytoskeleton organization, GO:0000226  
tRNA export from nucleus, GO:0006409  
antigen processing and presentation of exogenous peptide antigen via MHC class II, GO:0019886  
protein import into nucleus, GO:0006606  
cytokinesis, GO:0000910  
regulation of glycolytic process, GO:0006110  
CENP-A containing nucleosome assembly, GO:0034080  
mitotic spindle, GO:0072686  
microtubule-based movement, GO:0007018  
mitotic spindle assembly, GO:0090307  
centrosome cycle, GO:0007098  
positive regulation of telomere maintenance via telomerase, GO:0032212  
mitotic spindle organization, GO:0007052  
microtubule motor activity, GO:0003777  
mitotic metaphase plate congression, GO:0007080  
nuclear chromosome, GO:0000228  
positive regulation of telomerase activity, GO:0051973  
motor activity, GO:0003774  
spindle microtubule, GO:0005876  
kinesin complex, GO:0005871  
heterochromatin, GO:0000792  
protein phosphatase regulator activity, GO:0019888  
cellular response to heat, GO:0034605  
cytoplasmic dynein complex, GO:0005868  
regulation of mitotic nuclear division, GO:0007088  
structural constituent of nuclear pore, GO:0017056  
cellular response to cadmium ion, GO:0071276  
mitotic sister chromatid segregation, GO:0000070  
cytoplasmic microtubule, GO:0005881  
microtubule nucleation, GO:0007020  
nucleocytoplasmic transporter activity, GO:0005487  
microtubule bundle formation, GO:0001578  
anaphase-promoting complex, GO:0005680  
mitotic spindle pole, GO:0097431  
cleavage furrow, GO:0032154  
dynein complex, GO:0030286  
nuclear heterochromatin, GO:0005720  
nuclear periphery, GO:0034399  
microtubule plus-end, GO:0035371  
protein serine/threonine/tyrosine kinase activity, GO:0004712  
microtubule associated complex, GO:0005875  
establishment of mitotic spindle orientation, GO:0000132  
spindle midzone, GO:0051233  
mitotic spindle assembly checkpoint, GO:0007094  
dynein complex binding, GO:0070840  
Fanconi anaemia nuclear complex, GO:0043240  
spindle organization, GO:0007051  
protein phosphatase type 2A complex, GO:0000159  
DNA methylation, GO:0006306  
cytoplasmic ribonucleoprotein granule, GO:0036464  
pericentric heterochromatin, GO:0005721  
positive regulation of protein kinase activity, GO:0045860  
centrosome duplication, GO:0051298  
spindle pole centrosome, GO:0031616  
chromocenter, GO:0010369  
regulation of mitotic spindle assembly, GO:1901673  
histone lysine methylation, GO:0034968  
microtubule organizing center organization, GO:0031023  
regulation of cell differentiation, GO:0045595  
ciliary transition fiber, GO:0097539  
histone methyltransferase activity, GO:0042054  
regulation of exit from mitosis, GO:0007096  
pronucleus, GO:0045120  
inactivation of MAPK activity, GO:0000188  
microtubule polymerization, GO:0046785  
positive regulation of cytokinesis, GO:0032467  
cellular response to copper ion, GO:0071280  
centrosome localization, GO:0051642  
positive regulation of response to DNA damage stimulus, GO:2001022  
regulation of histone acetylation, GO:0035065  
synaptonemal complex, GO:0000795  
gamma-tubulin complex, GO:0000930  
regulation of chromosome segregation, GO:0051983  
establishment or maintenance of cell polarity, GO:0007163  
regulation of Wnt signaling pathway, GO:0030111  
HOPS complex, GO:0030897  
positive regulation of gene silencing by miRNA, GO:2000637  
chromatin assembly or disassembly, GO:0006333  
negative regulation of establishment of protein localization to plasma membrane, GO:0090005  
microtubule anchoring, GO:0034453  
ceramide metabolic process, GO:0006672  
macromolecular complex binding, GO:0044877  
protein localization to chromatin, GO:0071168  
kinetochore microtubule, GO:0005828  
regulation of protein complex assembly, GO:0043254  
non-motile cilium, GO:0097730  
positive regulation of non-motile cilium assembly, GO:1902857  
regulation of protein ubiquitination, GO:0031396  
astral microtubule organization, GO:0030953  
negative regulation of tyrosine phosphorylation of STAT protein, GO:0042532  
mitotic nuclear envelope reassembly, GO:0007084  
vesicle transport along microtubule, GO:0047496  
microtubule plus-end binding, GO:0051010  
condensed nuclear chromosome, GO:0000780  
kinetochore assembly, GO:0051382  
translation repressor activity, GO:0030371  
nucleosome positioning, GO:0016584  
positive regulation of TORC1 signaling, GO:1904263  
condensed chromosome outer kinetochore, GO:0000940  
male meiosis I, GO:0007141  
ventricular system development, GO:0021591  
negative regulation of translational initiation, GO:0045947  
retrograde axonal transport, GO:0008090  
condensed chromosome, GO:0000779  
sequence-specific mRNA binding, GO:1990825  
polysomal ribosome, GO:0042788  
nuclear lamina, GO:0005652  
maintenance of DNA methylation, GO:0010216  
positive regulation of telomere capping, GO:1904355  
positive regulation of isotype switching, GO:0045830  
centriole-centriole cohesion, GO:0010457  
lamin binding, GO:0005521  
protein phosphatase 1 binding, GO:0008157  
GATOR2 complex, GO:0061700  
regulation of fibroblast migration, GO:0010762  
G-quadruplex RNA binding, GO:0002151  
positive regulation of mitotic cell cycle spindle assembly checkpoint, GO:0090267  
regulation of microtubule cytoskeleton organization, GO:0070507  
attachment of spindle microtubules to kinetochore, GO:0008608  
microtubule depolymerization, GO:0007019  
negative regulation of inclusion body assembly, GO:0090084  
nuclear pericentric heterochromatin, GO:0031618  
SUMO binding, GO:0032183  
metaphase plate congression, GO:0051310  
exit from mitosis, GO:0010458  
regulation of cohesin loading, GO:0071922  
protein poly-ADP-ribosylation, GO:0070212  
positive regulation of epithelial cell migration, GO:0010634  
nuclear stress granule, GO:0097165  
regulation of attachment of spindle microtubules to kinetochore, GO:0051988  
negative regulation of substrate adhesion-dependent cell spreading, GO:1900025  
RNA stem-loop binding, GO:0035613  
regulation of microtubule-based process, GO:0032886  
PTW/PPI phosphatase complex, GO:0072357  
cleavage furrow formation, GO:0036089  
cohesin complex, GO:0008278  
protein ADP-ribosylation, GO:0006471  
hepatocyte apoptotic process, GO:0097284  
male pronucleus, GO:0001940  
regulation of insulin secretion involved in cellular response to glucose stimulus, GO:0061178  
paraxial mesoderm development, GO:0048339  
cellular protein complex localization, GO:0034629  
negative regulation of chromatin binding, GO:0035562  
dynactin complex, GO:0005869  
positive regulation of proteasomal protein catabolic process, GO:1901800  
glutamate receptor signaling pathway, GO:0007215  
regulation of microtubule polymerization or depolymerization, GO:0031110  
mitotic spindle midzone, GO:1990023  
GABA receptor binding, GO:0050811  
synaptonemal complex assembly, GO:0007130  
acrosome assembly, GO:0001675  
histone H3-K9 demethylation, GO:0033169  
vesicle targeting, GO:0006903  
regulation of mitotic cell cycle phase transition, GO:1901990  
RNA strand annealing activity, GO:0033592  
beta-catenin destruction complex assembly, GO:1904885  
female pronucleus, GO:0001939  
euchromatin, GO:0000791  
regulation of NIK/NF-kappaB signaling, GO:1901222  
abscission, GO:0009838  
maintenance of centrosome location, GO:0051661  
regulation of DNA binding, GO:0051101  
meiotic chromosome segregation, GO:0045132  
centromeric DNA binding, GO:0019237  
leucine zipper domain binding, GO:0043522  
cellular response to peptide hormone stimulus, GO:0071375  
negative regulation of B cell apoptotic process, GO:0002903