

chromosome, GO:0000775

- nuclear envelope, GO:0005635
- midbody, GO:0030496
- sister chromatid cohesion, GO:0007062
- kinetochore, GO:0000776
- spindle pole, GO:0000922
- condensed chromosome kinetochore, GO:0000777
- nuclear pore, GO:0005643
- microtubule cytoskeleton, GO:0015630
- chromosome segregation, GO:0007059
- ciliary basal body docking, GO:0097711
- mitotic cell cycle, GO:0000278
- protein sumoylation, GO:0016925
- regulation of gene silencing by miRNA, GO:0060964
- regulation of G2/M transition of mitotic cell cycle, GO:0010389
- antigen processing and presentation of exogenous peptide antigen via MHC class II, GO:0019886
- retrograde vesicle-mediated transport, GO:0006890
- microtubule-based movement, GO:0007018
- microtubule cytoskeleton organization, GO:0000226
- intracellular transport of virus, GO:0075733
- host cell, GO:0043657
- mitotic spindle, GO:0072686
- microtubule motor activity, GO:0003777
- protein import into nucleus, GO:0006606
- mitotic nuclear envelope disassembly, GO:0007077
- spindle microtubule, GO:0005876
- mitotic metaphase plate congression, GO:0007080
- nuclear chromosome, GO:0000228
- regulation of glycolytic process, GO:0006110
- kinesin complex, GO:0005871
- tRNA export from nucleus, GO:0006409
- regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, GO:0051439
- protein serine/threonine phosphatase activity, GO:0004722
- cleavage furrow, GO:0032154
- CENP-A containing nucleosome assembly, GO:0034080
- mitotic spindle organization, GO:0007052
- cytokinesis, GO:0000910
- protein phosphatase regulator activity, GO:0019888
- nuclear heterochromatin, GO:0005720
- positive regulation of protein kinase activity, GO:0045860
- anaphase-promoting complex, GO:0005680
- motor activity, GO:0003774
- heterochromatin, GO:0000792
- DNA methylation, GO:0006306
- cytoplasmic dynein complex, GO:0005868
- inactivation of MAPK activity, GO:0000188
- spindle organization, GO:0007051
- mitotic sister chromatid segregation, GO:0000070
- mitotic spindle assembly, GO:0090307
- protein serine/threonine/tyrosine kinase activity, GO:0004712
- regulation of mitotic nuclear division, GO:0007088
- nuclear periphery, GO:0034399
- pericentric heterochromatin, GO:0005721
- establishment or maintenance of cell polarity, GO:0007163
- synaptonemal complex, GO:0000795
- spindle midzone, GO:0051233
- microtubule associated complex, GO:0005875
- nucleocytoplasmic transporter activity, GO:0005487
- mitotic spindle assembly checkpoint, GO:0007094
- microtubule plus-end, GO:0035371
- microtubule bundle formation, GO:0001578
- nuclear nucleosome, GO:0000788
- ceramide metabolic process, GO:0006672
- microtubule anchoring, GO:0034453
- beta-tubulin binding, GO:0048487
- histone lysine methylation, GO:0034968
- mitotic spindle pole, GO:0097431
- dynein complex, GO:0030286
- cytoplasmic microtubule, GO:0005881
- microtubule plus-end binding, GO:0051010
- cohesin complex, GO:0008278
- centrosome localization, GO:0051642
- resolution of meiotic recombination intermediates, GO:0000712
- methylation-dependent chromatin silencing, GO:0006346
- microtubule nucleation, GO:0007020
- kinetochore assembly, GO:0051382
- condensed chromosome, GO:0000779
- microtubule organizing center organization, GO:0031023
- chromocenter, GO:0010369
- male meiosis I, GO:0007141
- histone methyltransferase activity, GO:0042054
- establishment of mitotic spindle orientation, GO:0000132
- metaphase plate congression, GO:0051310
- structural constituent of nuclear pore, GO:0017056
- regulation of Wnt signaling pathway, GO:0030111
- regulation of gene expression by genetic imprinting, GO:0006349
- condensed nuclear chromosome, GO:0000780
- regulation of exit from mitosis, GO:0007096
- pronucleus, GO:0045120
- dynein complex binding, GO:0070840
- negative regulation of NIK/NF-kappaB signaling, GO:1901223
- protein localization to chromatin, GO:0071168
- ciliary transition fiber, GO:0097539
- meiotic chromosome segregation, GO:0045132
- Fanconi anaemia nuclear complex, GO:0043240
- cellular protein complex localization, GO:0034629
- condensed chromosome outer kinetochore, GO:0000940
- synaptonemal complex assembly, GO:0007130
- XY body, GO:0001741
- centrosome duplication, GO:0051298
- regulation of chromosome segregation, GO:0051983
- negative regulation of stress fiber assembly, GO:0051497
- positive regulation of gene silencing by miRNA, GO:2000637
- regulation of protein heterodimerization activity, GO:0043497
- regulation of attachment of spindle microtubules to kinetochore, GO:0051988
- sequence-specific mRNA binding, GO:1990825
- vesicle transport along microtubule, GO:0047496
- protein localization to nucleolus, GO:1902570
- histone demethylase activity (H3-K9 specific), GO:0032454
- protein localization to microtubule, GO:0035372
- regulation of cell differentiation, GO:0045595
- mitotic recombination, GO:0006312
- microtubule polymerization, GO:0046785
- regulation of epithelial to mesenchymal transition, GO:0010717
- nBAF complex, GO:0071565
- mitotic spindle midzone assembly, GO:0051256
- PTW/PP1 phosphatase complex, GO:0072357
- gamma-tubulin complex, GO:0000930