```
kinetochore, GO:0000776
                                        midbody, GO:0030496
                                        sister chromatid cohesion, GO:0007062
                                       nuclear envelope, GO:0005635
                                        condensed chromosome kinetochore, GO:0000777
                                        spindle pole, GO:0000922
                                       mitotic cell cycle, GO:0000278
                                       ciliary basal body docking, GO:0097711
                                        nuclear pore, GO:0005643
                                        regulation of gene silencing by miRNA, GO:0060964
                                        protein sumoylation, GO:0016925
                                        chromosome segregation, GO:0007059
                                       microtubule cytoskeleton, GO:0015630
                                        regulation of G2/M transition of mitotic cell cycle, GO:0010389
                                        positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition, GO:0051437
                                        anaphase-promoting complex-dependent catabolic process, GO:0031145
                                        antigen processing and presentation of exogenous peptide antigen via MHC class II, GO:0019886
                                       host cell, GO:0043657
                                       microtubule cytoskeleton organization, GO:0000226
                                        methylated histone binding, GO:0035064
                                        intracellular transport of virus, GO:0075733
                                        nuclear chromosome, GO:0000228
                                        mitotic spindle, GO:0072686
                                        mitotic nuclear envelope disassembly, GO:0007077
                                        motor activity, GO:0003774
                                        mitotic spindle organization, GO:0007052
                                        positive regulation of telomerase activity, GO:0051973
                                        microtubule-based movement, GO:0007018
                                        tRNA export from nucleus, GO:0006409
                                        regulation of glycolytic process, GO:0006110
                                        protein import into nucleus, GO:0006606
                                        microtubule motor activity, GO:0003777
                                        positive regulation of telomere maintenance via telomerase, GO:0032212
                                        kinesin complex, GO:0005871
                                        mitotic spindle assembly, GO:0090307
                                       mitotic sister chromatid segregation, GO:0000070
                                       CENP-A containing nucleosome assembly, GO:0034080
                                        protein phosphatase regulator activity, GO:0019888
                                        cytokinesis, GO:0000910
                                        spindle organization, GO:0007051
                                        cytoplasmic microtubule, GO:0005881
                                        spindle microtubule, GO:0005876
                                        cleavage furrow, GO:0032154
                                        nuclear heterochromatin, GO:0005720
                                        mitotic metaphase plate congression, GO:0007080
                                       vesicle transport along microtubule, GO:0047496
                                        regulation of mitotic nuclear division, GO:0007088
                                        protein phosphatase type 2A complex, GO:0000159
                                        mitotic cytokinesis, GO:0000281
                                        heterochromatin, GO:0000792
                                        cytoplasmic dynein complex, GO:0005868
                                        positive regulation of protein kinase activity, GO:0045860
                                        dynein complex, GO:0030286
                                       beta-tubulin binding, GO:0048487
                                       mitotic spindle assembly checkpoint, GO:0007094
                                        synaptonemal complex, GO:0000795
                                        kinetochore assembly, GO:0051382
                                        microtubule nucleation, GO:0007020
                                       mitotic spindle pole, GO:0097431
                                        microtubule anchoring, GO:0034453
                                       microtubule plus-end, GO:0035371
                                        nuclear periphery, GO:0034399
                                        pericentric heterochromatin, GO:0005721
                                        nucleocytoplasmic transporter activity, GO:0005487
                                        cellular response to cadmium ion, GO:0071276
                                        Fanconi anaemia nuclear complex, GO:0043240
                                        positive regulation of telomere capping, GO:1904355
                                       structural constituent of nuclear pore, GO:0017056
                                        tubulin binding, GO:0015631
                                        establishment of mitotic spindle orientation, GO:0000132
                                        anaphase-promoting complex, GO:0005680
                                        microtubule bundle formation, GO:0001578
                                        centrosome localization, GO:0051642
                                        male meiosis I, GO:0007141
                                        mitotic recombination, GO:0006312
                                        establishment or maintenance of cell polarity, GO:0007163
                                        exit from mitosis, GO:0010458
                                       inactivation of MAPK activity, GO:0000188
                                        regulation of epithelial to mesenchymal transition, GO:0010717
                                       vesicle targeting, GO:0006903
                                        DNA methylation, GO:0006306
                                       condensed nuclear chromosome, GO:0000780
                                        condensed chromosome, GO:0000779
                                       regulation of attachment of spindle microtubules to kinetochore, GO:0051988
                                       regulation of chromosome segregation, GO:0051983
                                       microtubule plus-end binding, GO:0051010
                                       dynein complex binding, GO:0070840
                                        ceramide metabolic process, GO:0006672
chromosome, GO:0000775
                                        centrosome duplication, GO:0051298
                                        regulation of fibroblast migration, GO:0010762
                                        retrograde axonal transport, GO:0008090
                                        synaptonemal complex assembly, GO:0007130
                                        resolution of meiotic recombination intermediates, GO:0000712
                                        cellular response to X-ray, GO:0071481
                                        nuclear stress granule, GO:0097165
                                        cellular response to interferon-alpha, GO:0035457
                                        positive regulation of isotype switching, GO:0045830
                                        condensed chromosome outer kinetochore, GO:0000940
                                       spindle midzone, GO:0051233
                                        spindle pole centrosome, GO:0031616
                                        establishment of epithelial cell polarity, GO:0090162
                                        nuclear lamina, GO:0005652
                                        protein localization to nucleolus, GO:1902570
                                        negative regulation of establishment of protein localization to plasma membrane, GO:0090005
                                       negative regulation of focal adhesion assembly, GO:0051895
                                        negative regulation of substrate adhesion-dependent cell spreading, GO:1900025
                                        regulation of gene expression, GO:0040029
                                       attachment of spindle microtubules to kinetochore, GO:0008608
                                        microtubule organizing center organization, GO:0031023
                                        regulation of microtubule-based process, GO:0032886
                                        positive regulation of epithelial cell migration, GO:0010634
                                       positive regulation of TORC1 signaling, GO:1904263
                                        sequence-specific mRNA binding, GO:1990825
                                        histone methyltransferase activity, GO:0042054
                                        positive regulation of non-motile cilium assembly, GO:1902857
                                        maintenance of centrosome location, GO:0051661
                                        kinetochore microtubule, GO:0005828
                                        positive regulation of ubiquitin protein ligase activity, GO:1904668
                                       negative regulation of inclusion body assembly, GO:0090084
                                        mitotic nuclear envelope reassembly, GO:0007084
                                       negative regulation of tyrosine phosphorylation of STAT protein, GO:0042532
                                       multivesicular body sorting pathway, GO:0071985
                                        meiotic chromosome segregation, GO:0045132
                                       regulation of mitotic spindle assembly, GO:1901673
                                       HOPS complex, GO:0030897
                                        mitotic spindle midzone assembly, GO:0051256
                                        regulation of vesicle-mediated transport, GO:0060627
                                        positive regulation of mitotic cell cycle spindle assembly checkpoint, GO:0090267
                                        astral microtubule organization, GO:0030953
                                        cellular response to heat, GO:0034605
                                        histone modification, GO:0016570
                                        nuclear pericentric heterochromatin, GO:0031618
                                        regulation of protein heterodimerization activity, GO:0043497
                                        gamma-tubulin complex, GO:0000930
                                        ventricular system development, GO:0021591
                                        pericentric heterochromatin assembly, GO:0031508
                                       nuclear envelope disassembly, GO:0051081
                                        regulation of microtubule motor activity, GO:2000574
                                        positive regulation of protein localization to nucleolus, GO:1904751
                                        cellular protein complex localization, GO:0034629
                                        peptidyl-serine dephosphorylation, GO:0070262
                                        centriole-centriole cohesion, GO:0010457
                                        regulation of osteoclast differentiation, GO:0045670
                                        GATOR2 complex, GO:0061700
                                        positive regulation of cytokinesis, GO:0032467
                                        abscission, GO:0009838
                                        maintenance of DNA methylation, GO:0010216
                                        centromeric DNA binding, GO:0019237
                                        nucleosome positioning, GO:0016584
                                        negative regulation of voltage-gated calcium channel activity, GO:1901386
                                        macromolecular complex binding, GO:0044877
                                        ciliary transition fiber, GO:0097539
                                        beta-catenin destruction complex, GO:0030877
                                        axon terminus, GO:0043679
                                        SUMO binding, GO:0032183
                                        dystroglycan binding, GO:0002162
                                        cleavage furrow formation, GO:0036089
                                        chromocenter, GO:0010369
                                        histone methyltransferase activity (H3-K9 specific), GO:0046974
                                        protein localization to chromosome, GO:0071459
                                        positive regulation of ATP-dependent microtubule motor activity, GO:2000582
                                        central nervous system neuron axonogenesis, GO:0021955
                                        protein localization to microtubule, GO:0035372
                                        regulation of NIK/NF-kappaB signaling, GO:1901222
                                        regulation of histone acetylation, GO:0035065
                                        urogenital system development, GO:0001655
                                        regulation of DNA binding, GO:0051101
                                        mitotic centrosome separation, GO:0007100
                                        mitotic spindle midzone, GO:1990023
                                        regulation of cell differentiation, GO:0045595
                                        GABA receptor binding, GO:0050811
                                        positive regulation of exocytosis, GO:0045921
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response to peptide, GO:1901652

chromatin assembly or disassembly, GO:0006333

negative regulation of chromatin binding, GO:0035562

negative regulation of microtubule depolymerization, GO:0007026