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glycolytic process, GO:0006110 methylated histone binding, GO:0035064 spindle microtubule, GO:0005876 protein import into nucleus, GO:0006606 mitotic metaphase plate congression, GO:0007080 mitotic spindle organization, GO:0007052 cytokinesis, GO:0000910 positive regulation of telomere maintenance via telomerase, GO:0032212 mitotic sister chromatid segregation, GO:0000070 kinesin complex, GO:0005871 cleavage furrow, GO:0032154 spindle midzone, GO:0051233 protein serine/threonine phosphatase activity, GO:0004722 regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, GO:0051439 protein phosphatase regulator activity, GO:0019888 motor activity, GO:0003774 heterochromatin, GO:0000792 cytoplasmic microtubule, GO:0005881 chromatin organization, GO:0006325 chromosome organization, GO:0051276 positive regulation of telomerase activity, GO:0051973 mitotic spindle assembly, GO:0090307 spindle assembly, GO:0051225 positive regulation of protein kinase activity, GO:0045860 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microtubule plus-end binding, GO:0051010 ceramide metabolic process, GO:0006672 establishment of mitotic spindle orientation, GO:0000132 cellular response to amino acid stimulus, GO:0071230 protein localization to kinetochore, GO:0034501 protein phosphatase type 2A complex, GO:0000159 negative regulation of microtubule depolymerization, GO:0007026 pericentric heterochromatin, GO:0005721 microtubule polymerization, GO:0046785 condensed nuclear chromosome, GO:0000780 spindle pole centrosome, GO:0031616 protein localization to chromatin, GO:0071168 nuclear pore outer ring, GO:0031080 maintenance of DNA methylation, GO:0010216 chromocenter, GO:0010369 synaptonemal complex, GO:0000795 ciliary transition fiber, GO:0097539 nuclear pericentric heterochromatin, GO:0031618 cellular response to heat, GO:0034605 attachment of mitotic spindle microtubules to kinetochore, GO:0051315 centrosome localization, GO:0051642 protein serine/threonine/tyrosine kinase activity, GO:0004712 microtubule anchoring, GO:0034453 chromosome, GO:0000775 regulation of exit from mitosis, GO:0007096 resolution of meiotic recombination intermediates, GO:0000712 histone acetyltransferase activity (H4-K5 specific), GO:0043995 histone acetyltransferase activity (H4-K8 specific), GO:0043996 histone acetyltransferase activity (H4-K16 specific), GO:0046972 mitotic spindle midzone assembly, GO:0051256 SMN complex, GO:0032797 kinetochore assembly, GO:0051382 Fanconi anaemia nuclear complex, GO:0043240 non-motile cilium, GO:0097730 negative regulation of telomere maintenance via telomere lengthening, GO:1904357 microtubule organizing center organization, GO:0031023 central region of growth cone, GO:0090724 chromatin assembly or disassembly, GO:0006333 condensed chromosome, GO:0000779 regulation of attachment of spindle microtubules to kinetochore, GO:0051988 dynactin complex, GO:0005869 condensed chromosome outer kinetochore, GO:0000940 microtubule bundle formation, GO:0001578 mitotic recombination, 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regulation of microtubule-based process, GO:0032886 regulation of mitotic spindle assembly, GO:1901673 cohesin complex, GO:0008278 G-quadruplex RNA binding, GO:0002151 positive regulation of mitotic cell cycle spindle assembly checkpoint, GO:0090267 astral microtubule organization, GO:0030953 establishment of epithelial cell polarity, GO:0090162 synaptonemal complex assembly, GO:0007130 XY body, GO:0001741 positive regulation of epithelial cell migration, GO:0010634 regulation of chromosome segregation, GO:0051983 condensed nuclear chromosome outer kinetochore, GO:0000942 regulation of protein ubiquitination, GO:0031396 histone methyltransferase activity (H3-K9 specific), GO:0046974 chromosome passenger complex, GO:0032133 protein localization to chromosome, GO:0071459 beta-catenin destruction complex assembly, GO:1904885 female pronucleus, GO:0001939 peptidyl-serine dephosphorylation, GO:0070262 negative regulation of chromatin binding, GO:0035562 cellular response to ethanol, GO:0071361 dynein heavy chain binding, GO:0045504 aorta development, GO:0035904 cerebral cortex radially oriented cell migration, GO:0021799 regulation of insulin secretion involved in cellular response to glucose stimulus, GO:0061178 regulation of neurotransmitter secretion, GO:0046928 neuroblast proliferation, GO:0007405 negative regulation of tyrosine phosphorylation of STAT protein, GO:0042532 retrograde axonal transport, GO:0008090 SNARE complex assembly, GO:0035493 regulation of DNA binding, GO:0051101 maintenance of centrosome location, GO:0051661 male pronucleus, GO:0001940 positive regulation of exocytosis, GO:0045921 inhibition of cysteine-type endopeptidase activity involved in apoptotic process, GO:1990001 mitotic nuclear envelope reassembly, GO:0007084 multivesicular body sorting pathway, GO:0071985 positive regulation of gene silencing by miRNA, GO:2000637 negative regulation of epithelial to mesenchymal transition, GO:0010719 vesicle transport along microtubule, GO:0047496 glial cell projection, GO:0097386 centriole-centriole cohesion, GO:0010457 paraxial mesoderm development, GO:0048339 cellular protein complex localization, GO:0034629 regulation of NIK/NF-kappaB signaling, GO:1901222 hyaluronan metabolic process, GO:0030212 cellular response to copper ion, GO:0071280 regulation of ruffle assembly, GO:1900027 microtubule depolymerization, GO:0007019 septin complex, GO:0031105 interaction with symbiont, GO:0051702 mitotic centrosome separation, GO:0007100 histone methyltransferase binding, GO:1990226 regulation of intracellular protein transport, GO:0033157 anchored component of external side of plasma membrane, GO:0031362