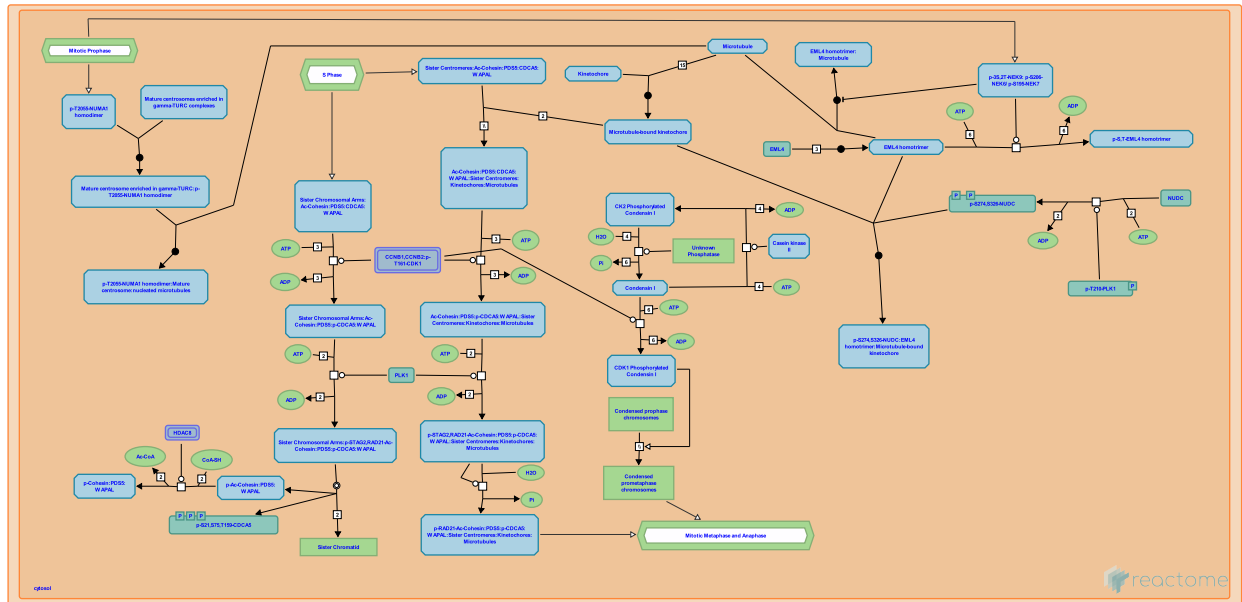


Mitotic Prometaphase



Bechstedt, S., Cheeseman, IM., D'Eustachio, P., Fry, AM., Gillespie, ME., Lucken, KJ., Matthews, L., Merdes, A., O'Regan, L., Orlic-Milacic, M., Tanno, Y., Watanabe, Y., Zhang, N.

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Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

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Literature references

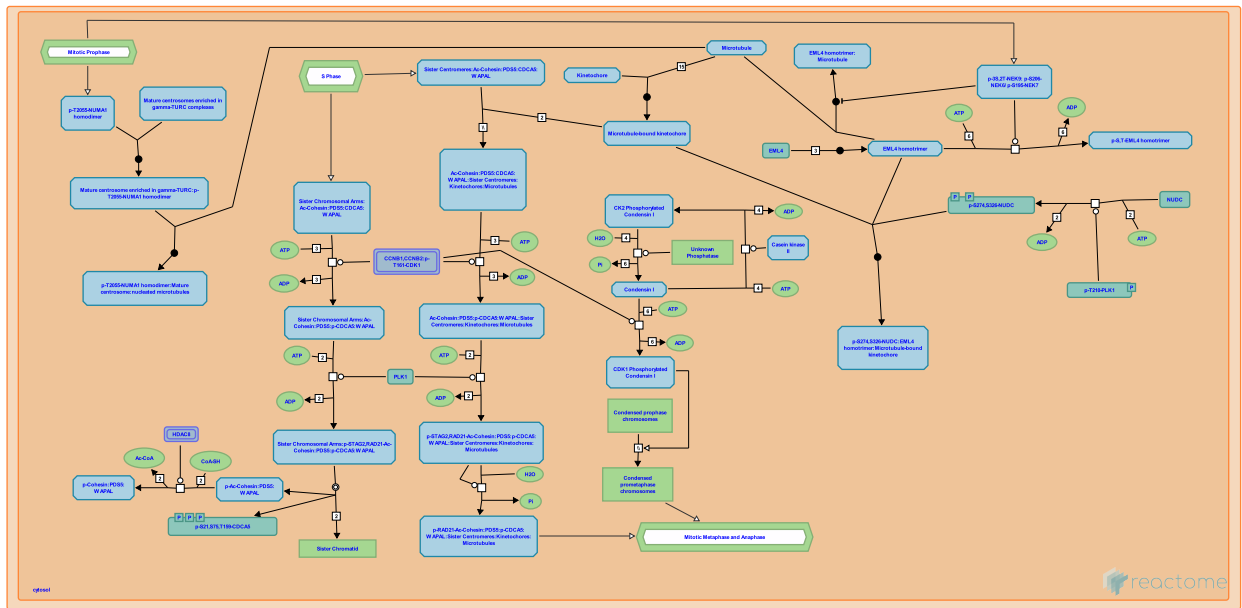
- Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*, 18, 142. [↗](#)
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
- Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res*, 46, D649-D655. [↗](#)
- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, 14, e1005968. [↗](#)

Reactome database release: 80

This document contains 5 pathways and 1 reaction ([see Table of Contents](#))

Mitotic Prometaphase ➤

Stable identifier: R-HSA-68877



The dissolution of the nuclear membrane marks the beginning of the prometaphase. Kinetochores are created when proteins attach to the centromeres. Microtubules then attach at the kinetochores, and the chromosomes begin to move to the metaphase plate.

Kinetochores capture of astral microtubules ↗

Location: [Mitotic Prometaphase](#)

Stable identifier: R-HSA-375302