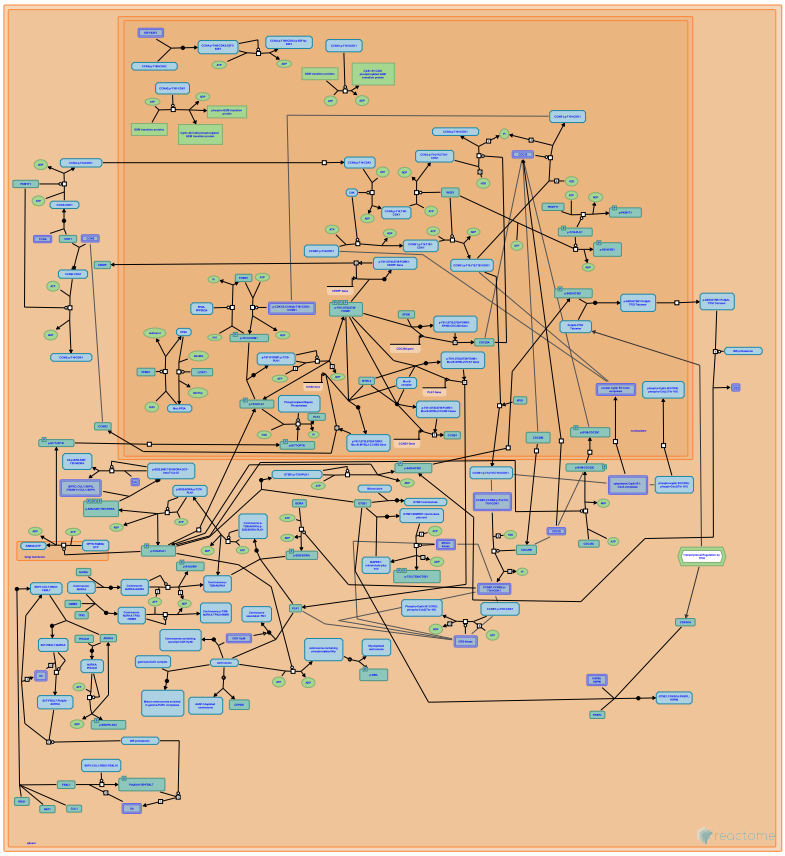
Mitotic G2-G2/M phases



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This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the Reactome Textbook.

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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.
The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

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. ↗

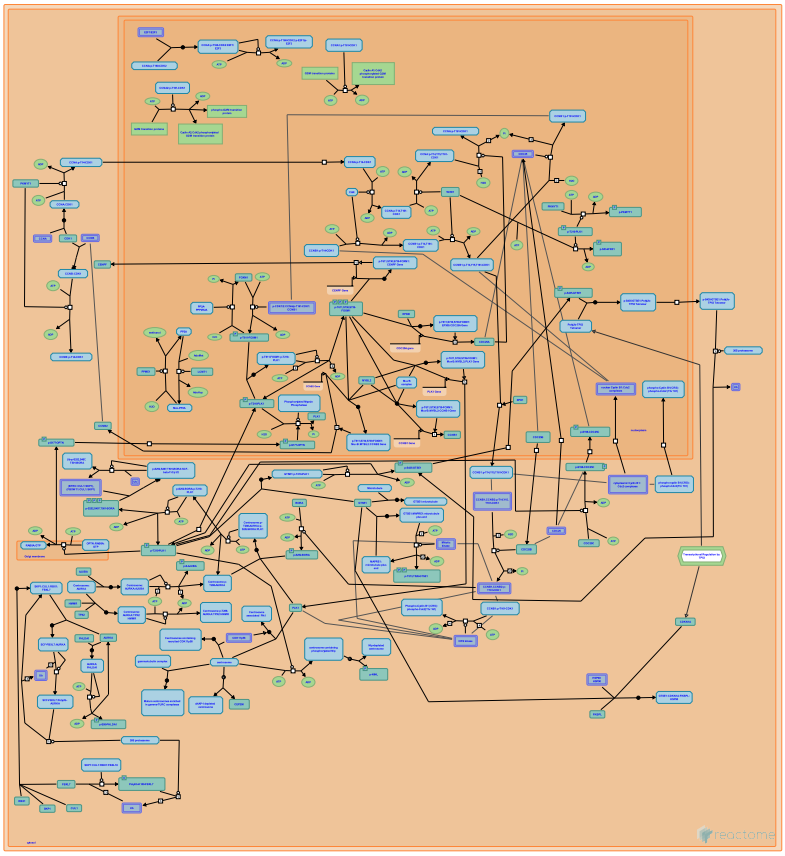
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

Reactome database release: 88

This document contains 3 pathways (see Table of Contents)

Mitotic G2-G2/M phases ↗

Stable identifier: R-HSA-453274



Mitotic G2 (gap 2) phase is the second growth phase during eukaryotic mitotic cell cycle. G2 encompasses the interval between the completion of DNA synthesis and the beginning of mitosis. During G2, the cytoplasmic content of the cell increases. At G2/M transition, duplicated centrosomes mature and separate and CDK1:cyclin B complexes become active, setting the stage for spindle assembly and chromosome condensation that occur in the prophase of mitosis (O'Farrell 2001, Bruinsma et al. 2012, Jiang et al. 2014).

Literature references

O'Farrell, PH. (2001). Triggering the all-or-nothing switch into mitosis. *Trends Cell Biol., 11*, 512-9. ↗

Wang, G., Jiang, Q., Zhang, C. (2014). The role of mitotic kinases in coupling the centrosome cycle with the assembly of the mitotic spindle. *J. Cell. Sci., 127*, 4111-22. ↗

Medema, RH., Raaijmakers, JA., Bruinsma, W. (2012). Switching Polo-like kinase-1 on and off in time and space. *Trends Biochem. Sci., 37*, 534-42. ↗

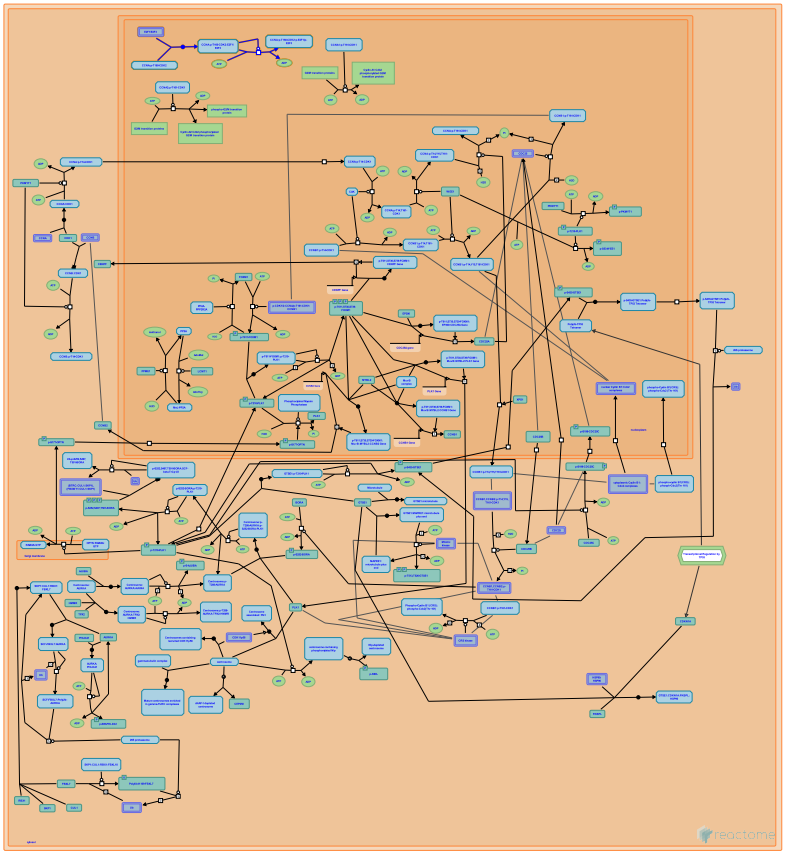
Editions

2017-03-24	Edited	Orlic-Milacic, M.
2018-07-10	Reviewed	Manfredi, JJ.

G2 Phase ↗

Location: Mitotic G2-G2/M phases

Stable identifier: R-HSA-68911



This is one of two 'gap' phases in the standard eukaryotic mitotic cell cycle. It is the interval between the completion of DNA synthesis and the beginning of mitosis. Protein synthesis occurs in this phase, following DNA replication in the S phase. This is the time when the cell stockpiles on the cytoplasmic contents, before mitosis and cytokinesis occur (Mitchison 2003, Kaldis 2016).

Literature references

Mitchison, JM. (2003). Growth during the cell cycle. *Int. Rev. Cytol., 226*, 165-258. ↗

Kaldis, P. (2016). Quo Vadis Cell Growth and Division?. *Front Cell Dev Biol, 4*, 95. ↗

Editions

2017-03-25	Edited	Orlic-Milacic, M.

G2/M Transition ↗

Location: Mitotic G2-G2/M phases

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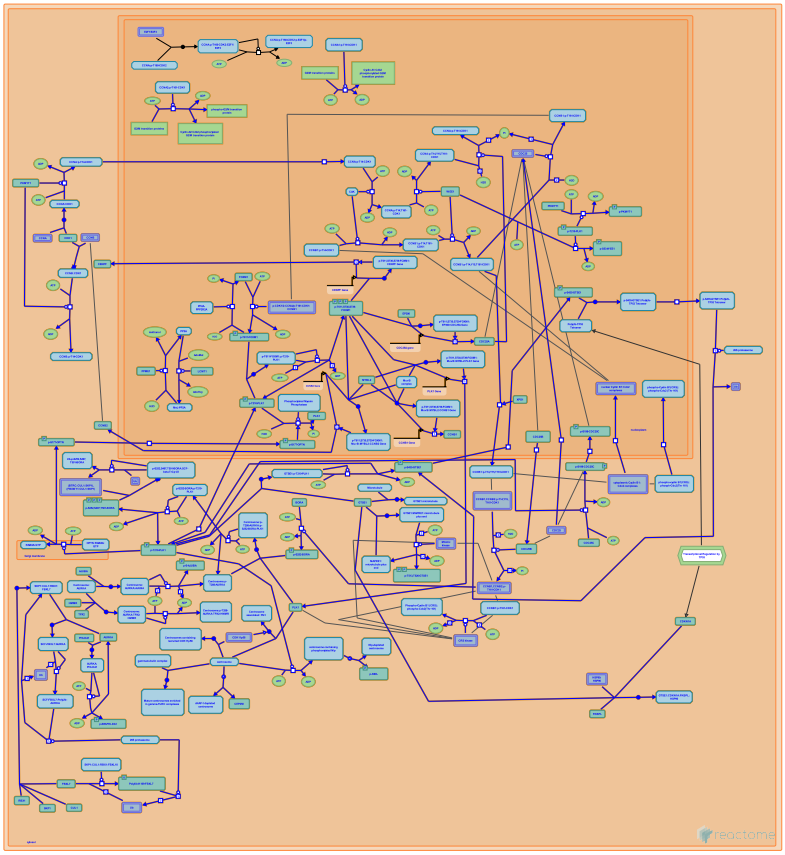

Together with two B-type cyclins, CCNB1 and CCNB2, Cdc2 (CDK1) regulates the transition from G2 into mitosis. CDK1 can also form complexes with Cyclin A (CCNA1 and CCNA3). CDK1 complexes with A and B type cyclins are activated by dephosphorylation of CDK1 threonine residue T14 and tyrosine residue Y15. Cyclin A:CDK1 and Cyclin B:CDK1 complexes phosphorylate several proteins involved in mitotic spindle formation and function, the breakdown of the nuclear envelope, and chromosome condensation that is necessary for the ~2 meters of DNA to be segregated at mitosis (Nigg 1998, Nilsson and Hoffmann 2000, Salaun et al. 2008, Fisher et al. 2012).

Literature references

Nigg, EA. (1998). Polo-like kinases: positive regulators of cell division from start to finish. *Curr. Opin. Cell Biol., 10*, 776-83. ↗

Salaun, P., Rannou, Y., Prigent, C. (2008). Cdk1, Plks, Auroras, and Neks: the mitotic bodyguards. *Adv. Exp. Med. Biol., 617*, 41-56. ↗

Nilsson, I., Hoffmann, I. (2000). Cell cycle regulation by the Cdc25 phosphatase family. *Prog Cell Cycle Res, 4*, 107-14. ↗

Coudreuse, D., Novák, B., Krasinska, L., Fisher, D. (2012). Phosphorylation network dynamics in the control of cell cycle transitions. *J. Cell. Sci., 125*, 4703-11. ↗

Editions

2005-10-10	Reviewed	Lorca, T.
2017-03-25	Edited	Orlic-Milacic, M.

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