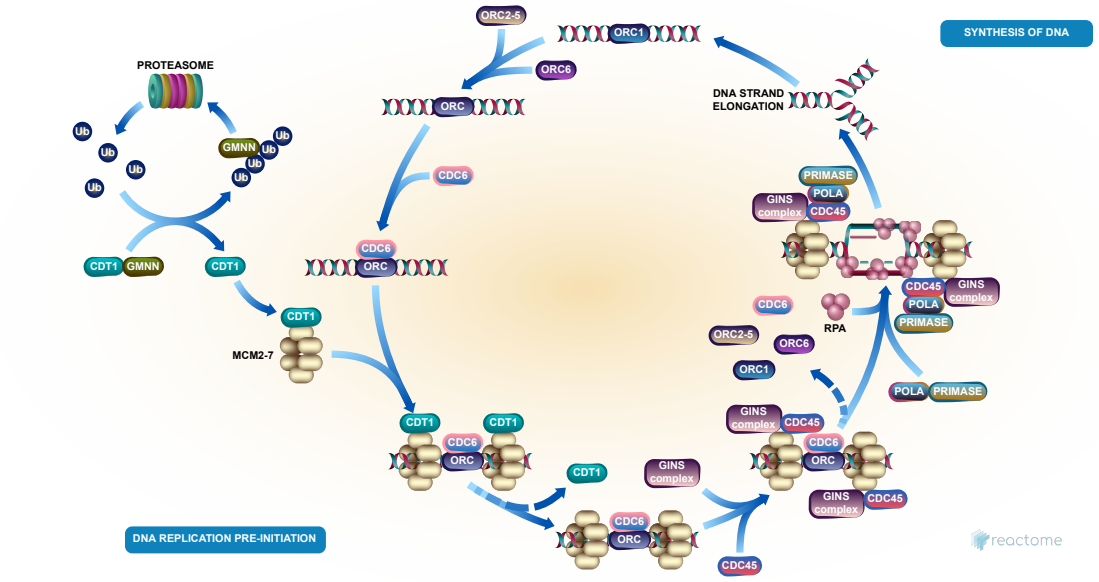
DNA Replication



Aladjem, M., Bambara, RA., Borowiec, JA., Catlett, M., D'Eustachio, P., Davey, MJ., Forsburg, SL., Joshi-Tope, G., Mendez, J., Nickerson, E., O'Donnell, M., Tom, S., Tye, BK.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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.

02/05/2024

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. ↗

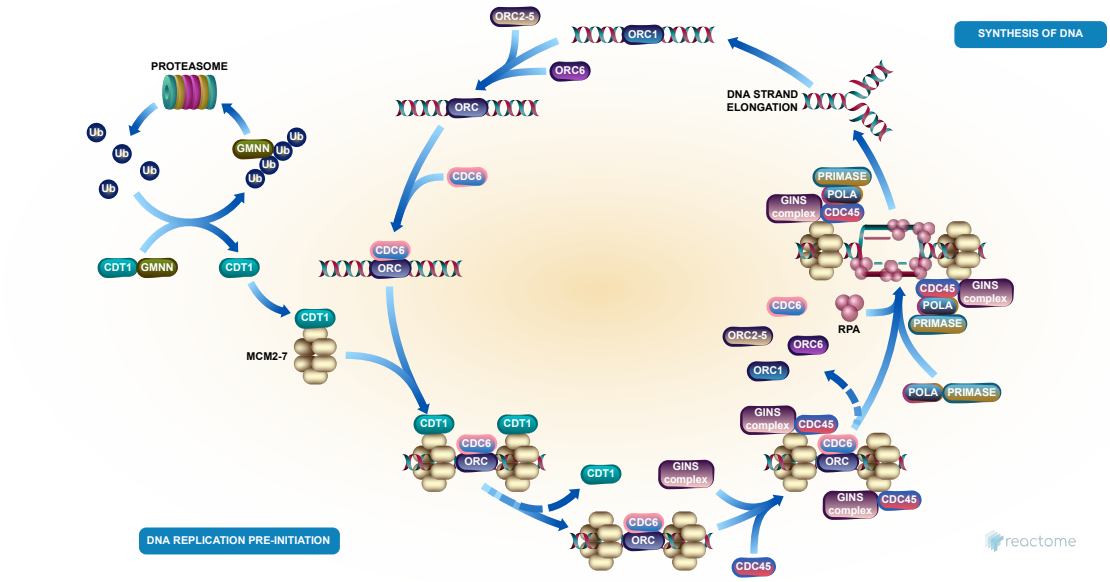
Reactome database release: 88

This document contains 3 pathways (see Table of Contents)

DNA Replication ↗

Stable identifier: R-HSA-69306

Compartments: nucleoplasm, cytosol



Studies in the past decade have suggested that the basic mechanism of DNA replication initiation is conserved in all kingdoms of life. Initiation in unicellular eukaryotes, in particular Saccharomyces cerevisiae (budding yeast), is well understood, and has served as a model for studies of DNA replication initiation in multicellular eukaryotes, including humans. In general terms, the first step of initiation is the binding of the replication initiator to the origin of replication. The replicative helicase is then assembled onto the origin, usually by a helicase assembly factor. Either shortly before or shortly after helicase assembly, some local unwinding of the origin of replication occurs in a region rich in adenine and thymine bases (often termed a DNA unwinding element, DUE). The unwound region provides the substrate for primer synthesis and initiation of DNA replication. The best-defined eukaryotic origins are those of S. cerevisiae, which have well-conserved sequence elements for initiator binding, DNA unwinding and binding of accessory proteins. In multicellular eukaryotes, unlike S. cerevisiae, these loci appear not to be defined by the presence of a DNA sequence motif. Indeed, choice of replication origins in a multicellular eukaryote may vary with developmental stage and tissue type. In cell-free models of metazoan DNA replication, such as the one provided by Xenopus egg extracts, there are only limited DNA sequence specificity requirements for replication initiation (Kelly & Brown 2000; Bell & Dutta 2002; Marahrens & Stillman 1992; Cimbora & Groudine 2001; Mahbubani et al 1992, Hyrien & Mechali 1993).

Literature references

Marahrens, Y., Stillman, B. (1992). A yeast chromosomal origin of DNA replication defined by multiple functional elements. *Science, 255*, 817-23. ↗

Brown, GW., Kelly, TJ. (2000). Regulation of chromosome replication. *Annu Rev Biochem, 69*, 829-80. ↗

Bell, SP., Dutta, A. (2002). DNA replication in eukaryotic cells. *Annu Rev Biochem, 71*, 333-74. ↗

Hyrien, O., Méchali, M. (1993). Chromosomal replication initiates and terminates at random sequences but at regular intervals in the ribosomal DNA of Xenopus early embryos. *EMBO J, 12*, 4511-20. ↗

Elder, JK., Blow, JJ., Mahbubani, HM., Paull, T. (1992). DNA replication initiates at multiple sites on plasmid DNA in Xenopus egg extracts. *Nucleic Acids Res, 20*, 1457-62. ↗

Editions

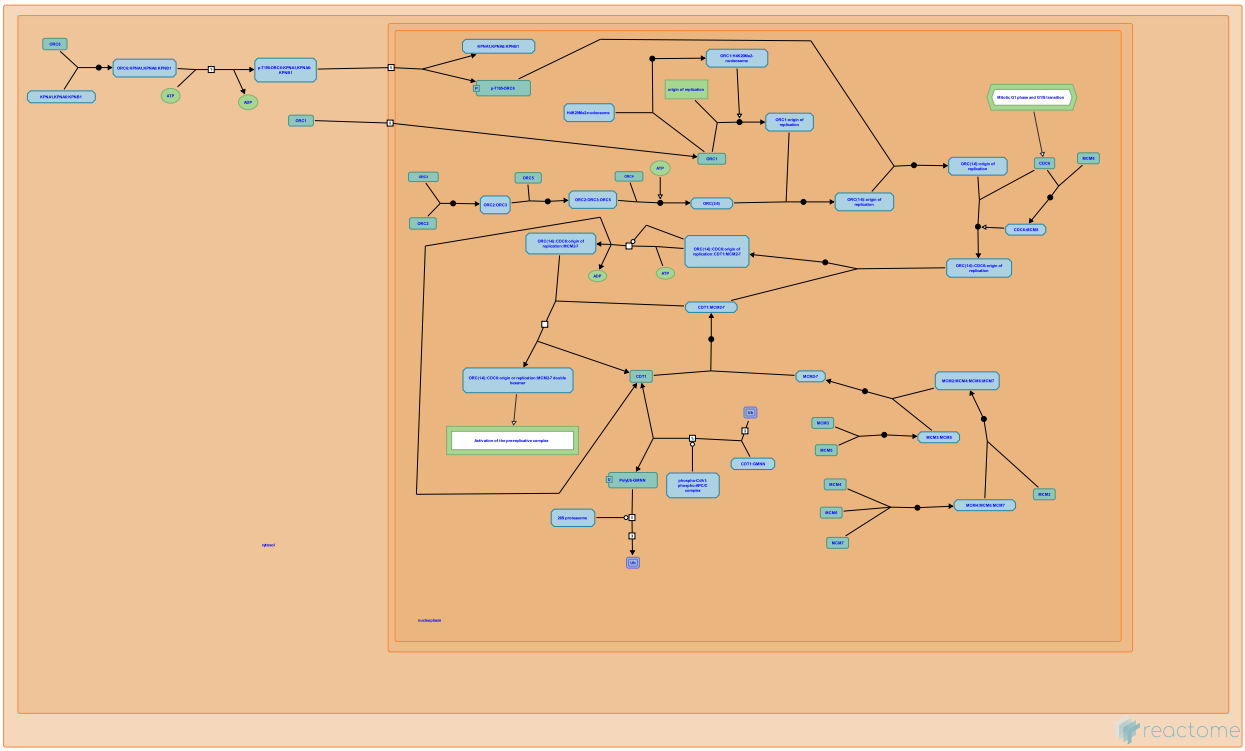
2003-01-06	Authored	Bambara, RA., Davey, MJ., O'Donnell, M., Tye, BK., Tom, S., Catlett, M. et al.
2005-09-07	Revised	Tye, BK., Aladjem, M., Borowiec, JA., Mendez, J.
2024-03-06	Reviewed	Mendez, J., Aladjem, M.
2024-03-06	Edited	Nickerson, E., D'Eustachio, P., Joshi-Tope, G.

DNA Replication Pre-Initiation ↗

Location: DNA Replication

Stable identifier: R-HSA-69002

Compartments: nucleoplasm, cytosol



Although, DNA replication occurs in the S phase of the cell cycle, the formation of the DNA replication pre-initiation complex begins during G1 phase.

Editions

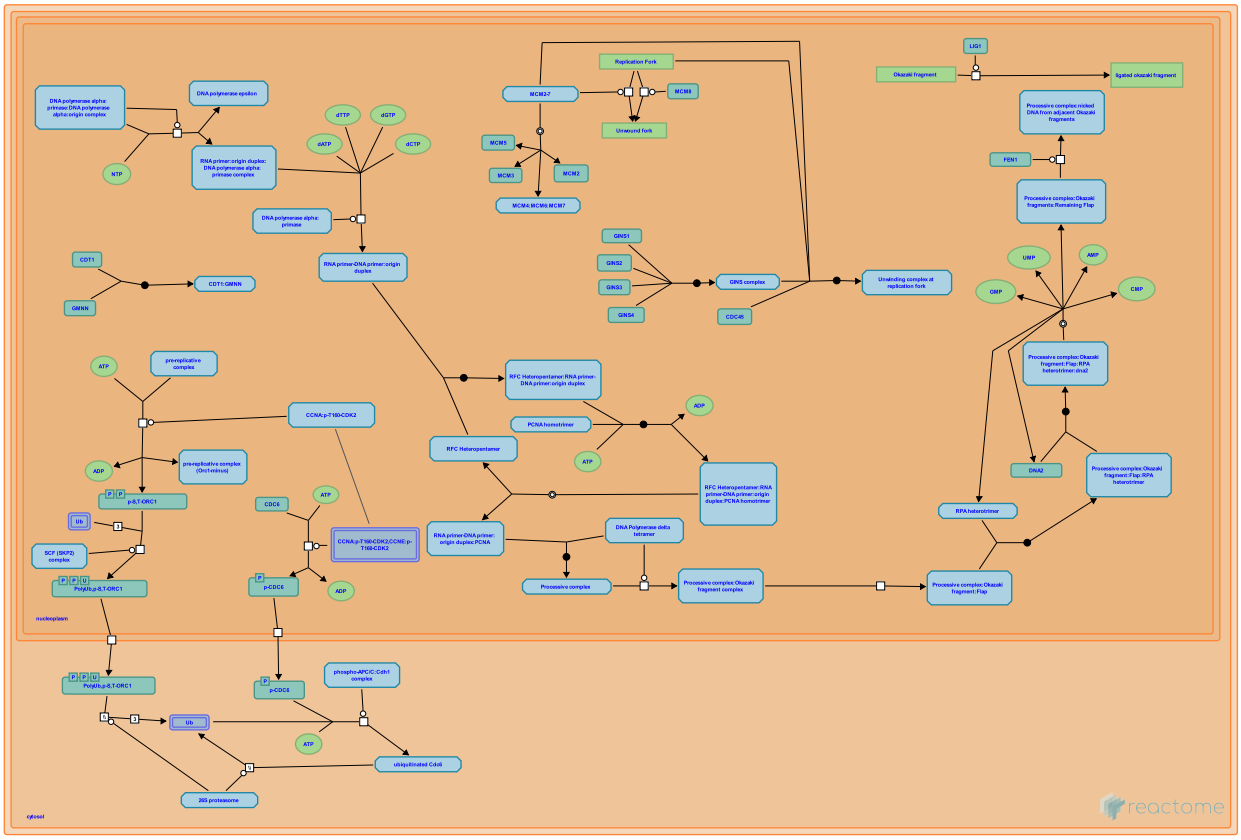
2006-03-17	Authored	Davey, MJ., O'Donnell, M., Tye, BK.
2024-03-06	Edited	Joshi-Tope, G.

Synthesis of DNA ↗

Location: DNA Replication

Stable identifier: R-HSA-69239

Compartments: nucleoplasm, cytosol



The actual synthesis of DNA occurs in the S phase of the cell cycle. This includes the initiation of DNA replication, when the first nucleotide of the new strand is laid down during the synthesis of the primer. The DNA replication preinitiation events begin in late M or early G1 phase.

Table of Contents