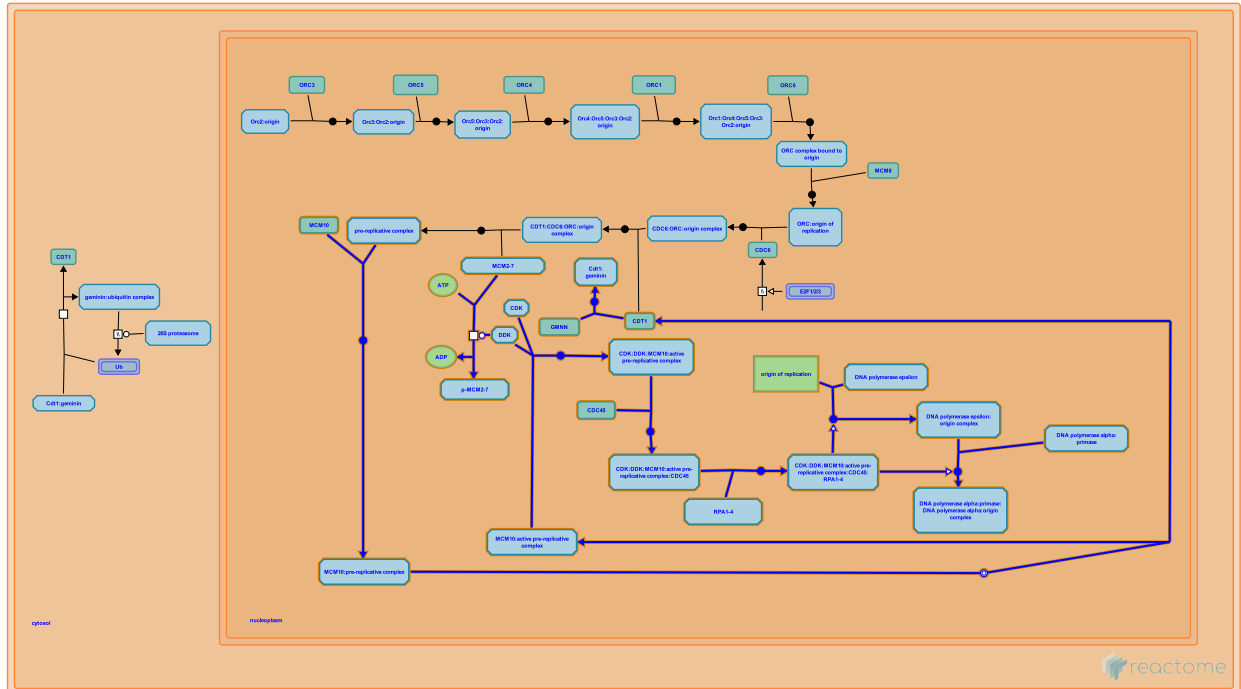


Activation of the pre-replicative complex



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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://creativecommons.org/licenses/by/4.0/).

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: 70

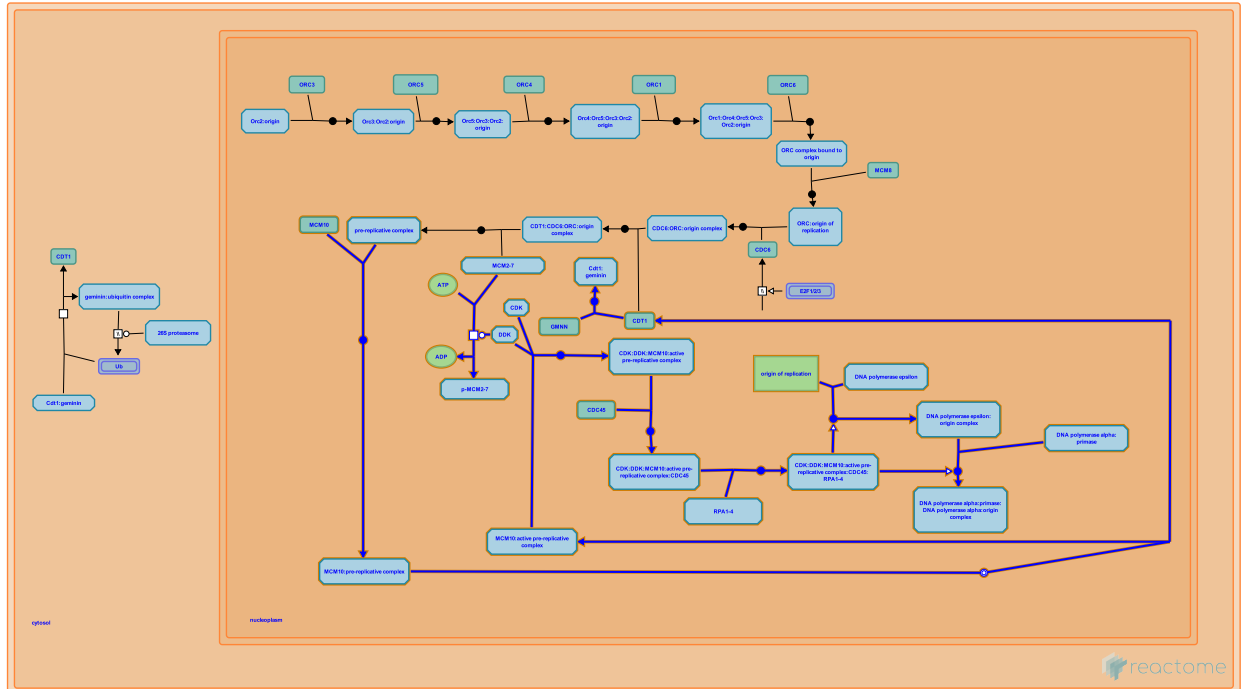
This document contains 1 pathway and 9 reactions ([see Table of Contents](#))

Activation of the pre-replicative complex ↗

Stable identifier: R-RNO-68962

Compartments: nucleoplasm

Inferred from: Activation of the pre-replicative complex (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Mcm10 associates with the pre-replicative complex, stabilizing Mcm2-7 ↗

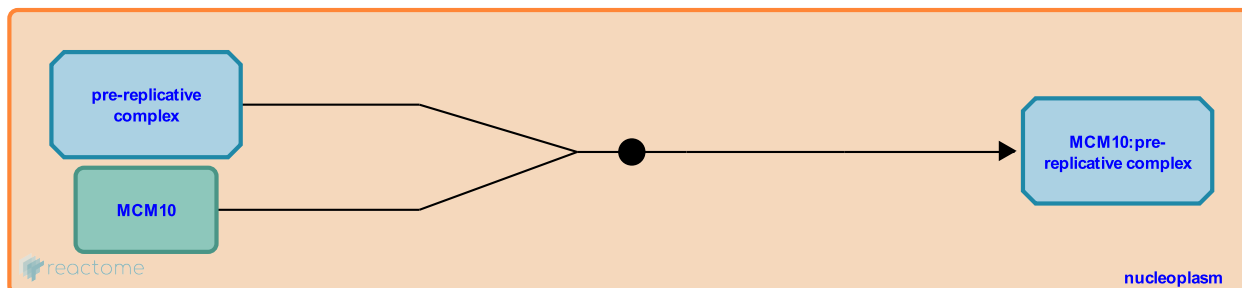
Location: [Activation of the pre-replicative complex](#)

Stable identifier: R-RNO-68919

Type: binding

Compartments: nucleoplasm

Inferred from: [Mcm10 associates with the pre-replicative complex, stabilizing Mcm2-7 \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Followed by: [Cdt1 is displaced from the pre-replicative complex.](#)

Cdt1 is displaced from the pre-replicative complex. ↗

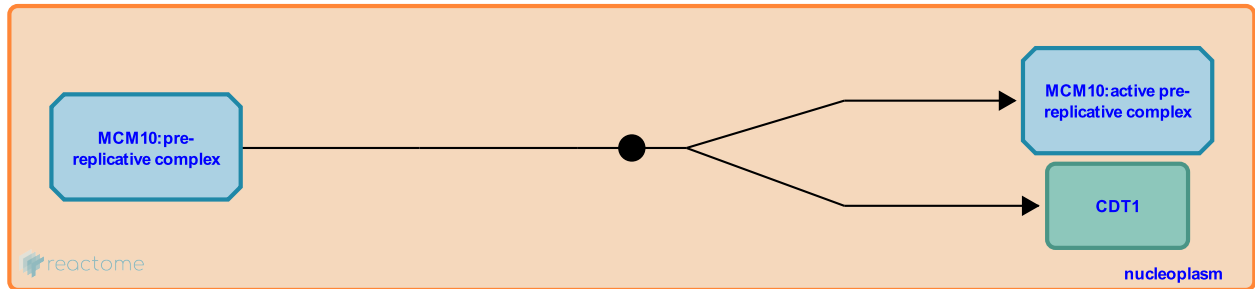
Location: [Activation of the pre-replicative complex](#)

Stable identifier: R-RNO-68940

Type: dissociation

Compartments: nucleoplasm

Inferred from: [Cdt1 is displaced from the pre-replicative complex. \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [Mcm10 associates with the pre-replicative complex, stabilizing Mcm2-7](#)

Followed by: [Cdt1 associates with geminin, CDK and DDK associate with the Mcm10:pre-replicative complex](#)

Cdt1 associates with geminin ↗

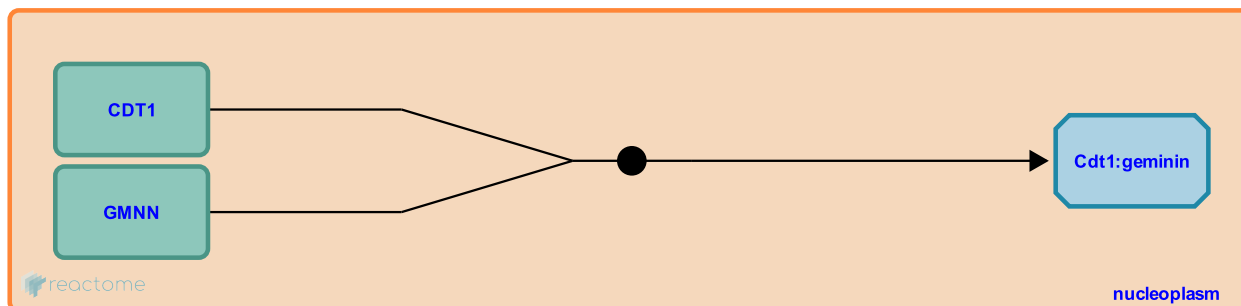
Location: [Activation of the pre-replicative complex](#)

Stable identifier: R-RNO-69299

Type: binding

Compartments: nucleoplasm

Inferred from: [Cdt1 associates with geminin \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [Cdt1 is displaced from the pre-replicative complex.](#)

CDK and DDK associate with the Mcm10:pre-replicative complex ↗

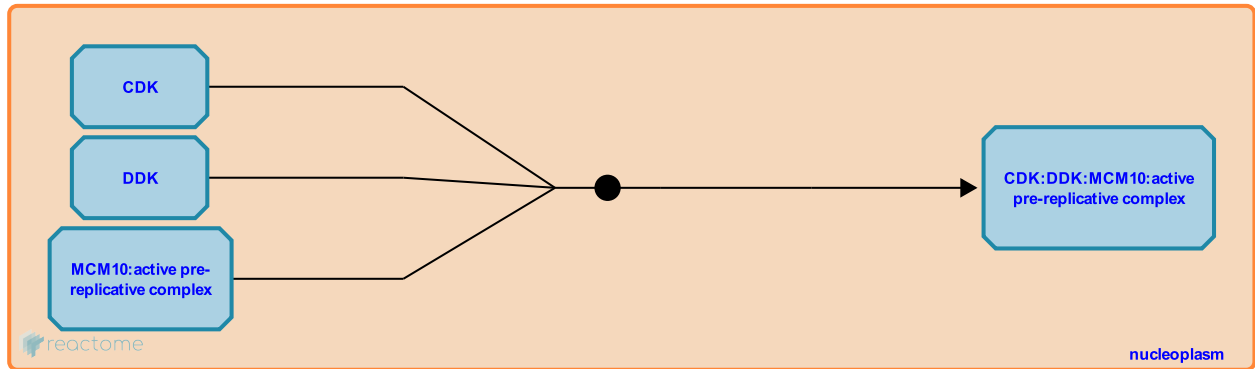
Location: [Activation of the pre-replicative complex](#)

Stable identifier: R-RNO-68918

Type: binding

Compartments: nucleoplasm

Inferred from: [CDK and DDK associate with the Mcm10:pre-replicative complex \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [Cdt1 is displaced from the pre-replicative complex.](#)

Followed by: [Mcm2-7 is phosphorylated by DDK, Cdc45 associates with the pre-replicative complex at the origin](#)

Mcm2-7 is phosphorylated by DDK ↗

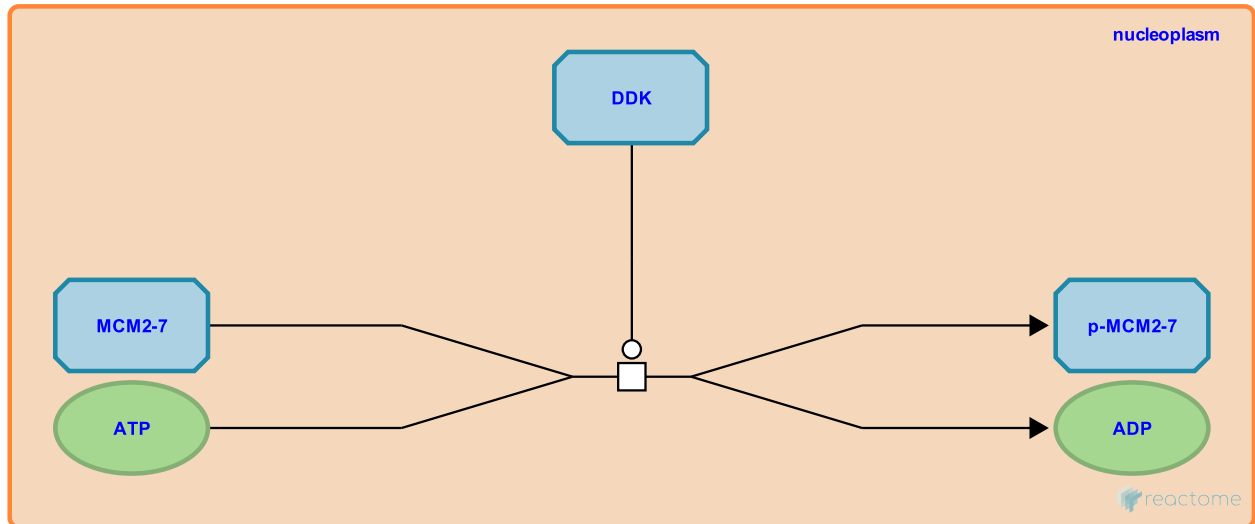
Location: [Activation of the pre-replicative complex](#)

Stable identifier: R-RNO-68954

Type: transition

Compartments: nucleoplasm

Inferred from: [Mcm2-7 is phosphorylated by DDK \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [CDK and DDK associate with the Mcm10:pre-replicative complex](#)

Cdc45 associates with the pre-replicative complex at the origin ↗

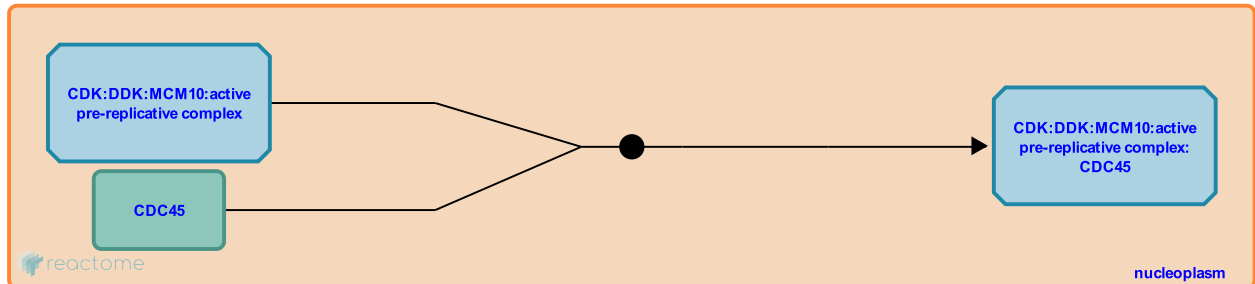
Location: [Activation of the pre-replicative complex](#)

Stable identifier: R-RNO-68917

Type: binding

Compartments: nucleoplasm

Inferred from: [Cdc45 associates with the pre-replicative complex at the origin \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [CDK and DDK associate with the Mcm10:pre-replicative complex](#)

Followed by: [DNA Replication Factor A \(RPA\) associates with the pre-replicative complex at the origin](#)

DNA Replication Factor A (RPA) associates with the pre-replicative complex at the origin ↗

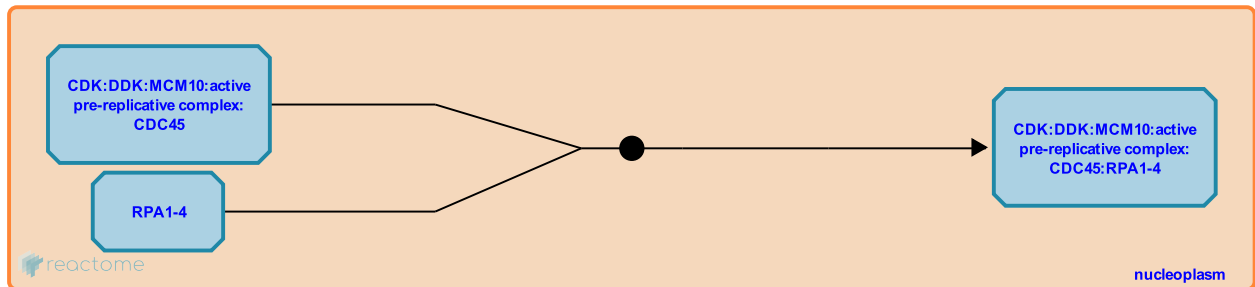
Location: [Activation of the pre-replicative complex](#)

Stable identifier: R-RNO-68916

Type: binding

Compartments: nucleoplasm

Inferred from: [DNA Replication Factor A \(RPA\) associates with the pre-replicative complex at the origin \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [Cdc45 associates with the pre-replicative complex at the origin](#)

Followed by: [DNA polymerase alpha:primase binds at the origin](#), [DNA polymerase epsilon binds at the origin](#)

DNA polymerase alpha:primase binds at the origin ↗

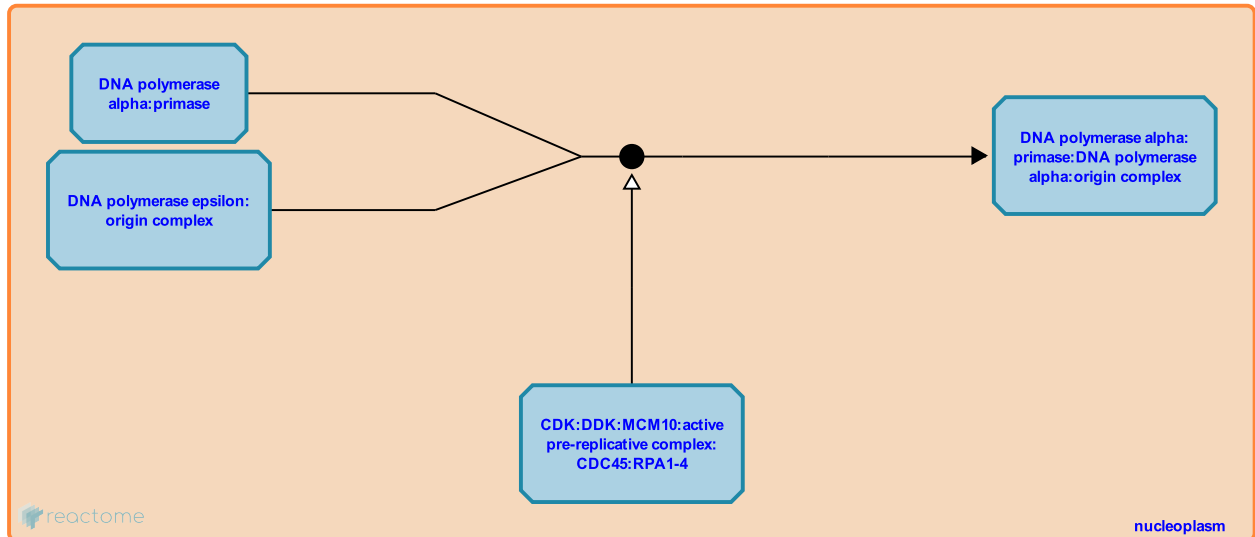
Location: [Activation of the pre-replicative complex](#)

Stable identifier: R-RNO-68914

Type: binding

Compartments: nucleoplasm

Inferred from: [DNA polymerase alpha:primase binds at the origin \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [DNA Replication Factor A \(RPA\) associates with the pre-replicative complex at the origin, DNA polymerase epsilon binds at the origin](#)

DNA polymerase epsilon binds at the origin ↗

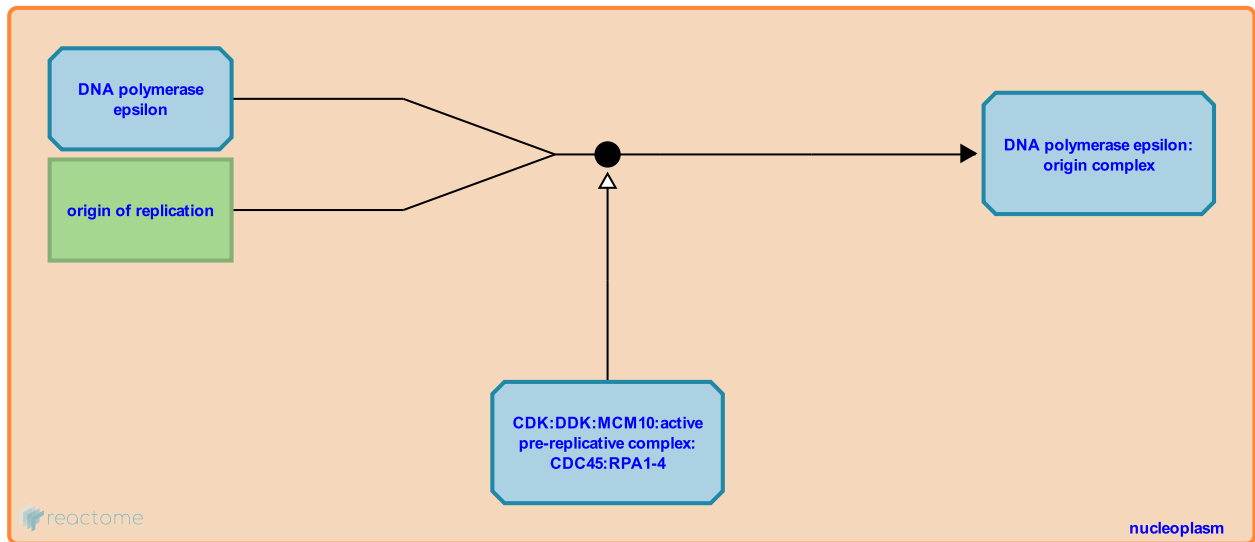
Location: [Activation of the pre-replicative complex](#)

Stable identifier: R-RNO-68960

Type: binding

Compartments: nucleoplasm

Inferred from: [DNA polymerase epsilon binds at the origin \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [DNA Replication Factor A \(RPA\) associates with the pre-replicative complex at the origin](#)

Followed by: [DNA polymerase alpha:primase binds at the origin](#)

Table of Contents

Introduction	1
☰ Activation of the pre-replicative complex	2
↳ Mcm10 associates with the pre-replicative complex, stabilizing Mcm2-7	3
↳ Cdt1 is displaced from the pre-replicative complex.	4
↳ Cdt1 associates with geminin	5
↳ CDK and DDK associate with the Mcm10:pre-replicative complex	6
↳ Mcm2-7 is phosphorylated by DDK	7
↳ Cdc45 associates with the pre-replicative complex at the origin	8
↳ DNA Replication Factor A (RPA) associates with the pre-replicative complex at the origin	9
↳ DNA polymerase alpha:primase binds at the origin	10
↳ DNA polymerase epsilon binds at the origin	11
Table of Contents	12