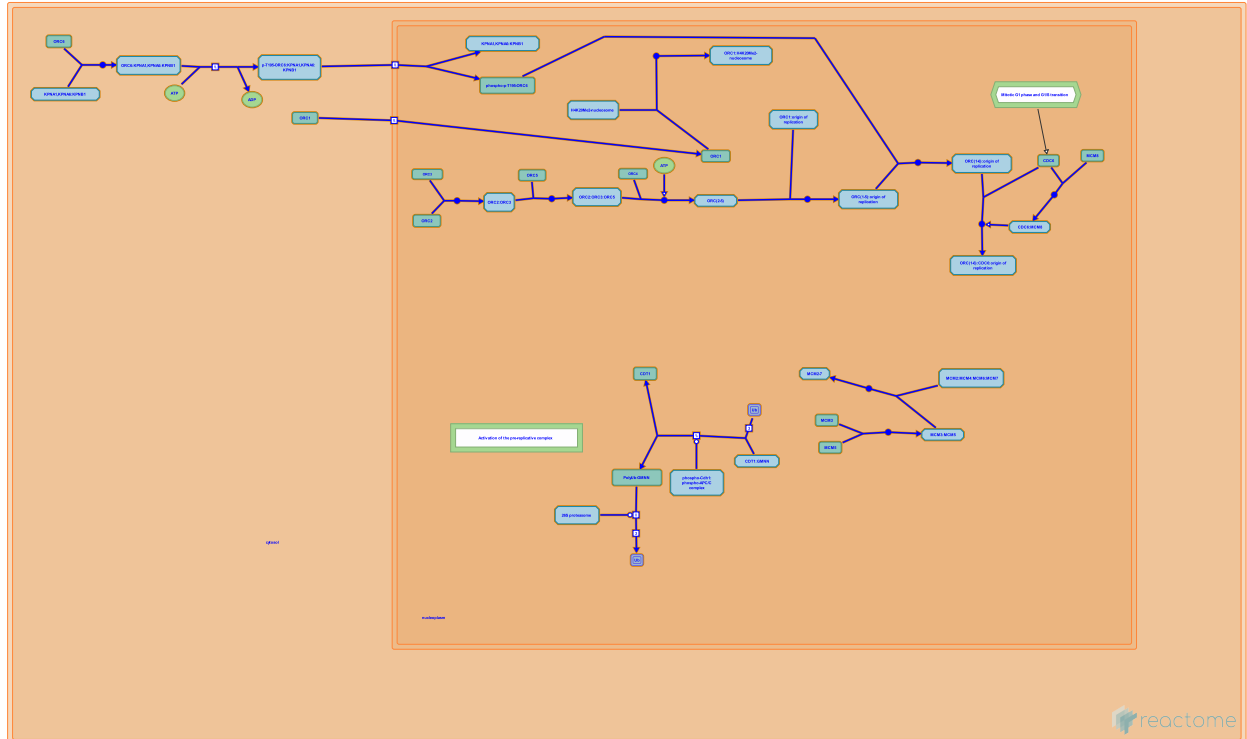


# Assembly of the pre-replicative complex



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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](https://reactome.org/textbook/).

18/05/2024

## 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

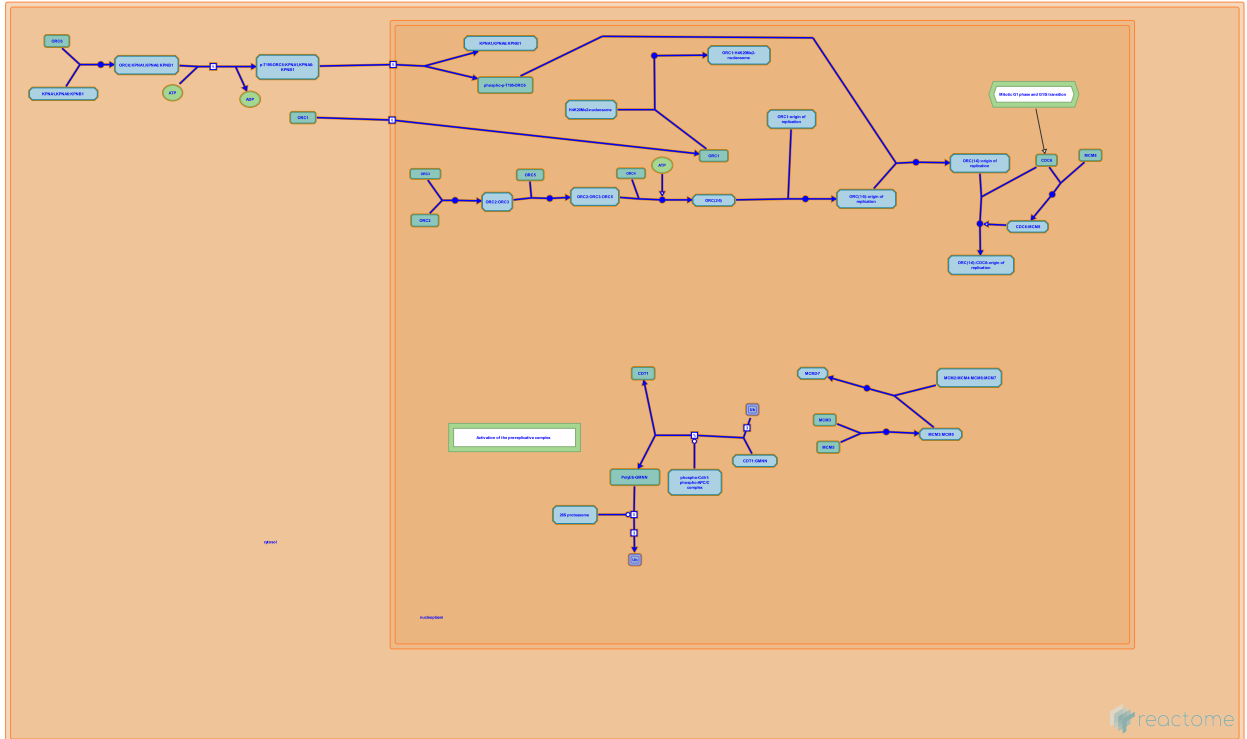
This document contains 3 pathways and 4 reactions ([see Table of Contents](#))

## Assembly of the pre-replicative complex ↗

**Stable identifier:** R-GGA-68867

**Compartment:** cytosol, nucleoplasm

**Inferred from:** Assembly 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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

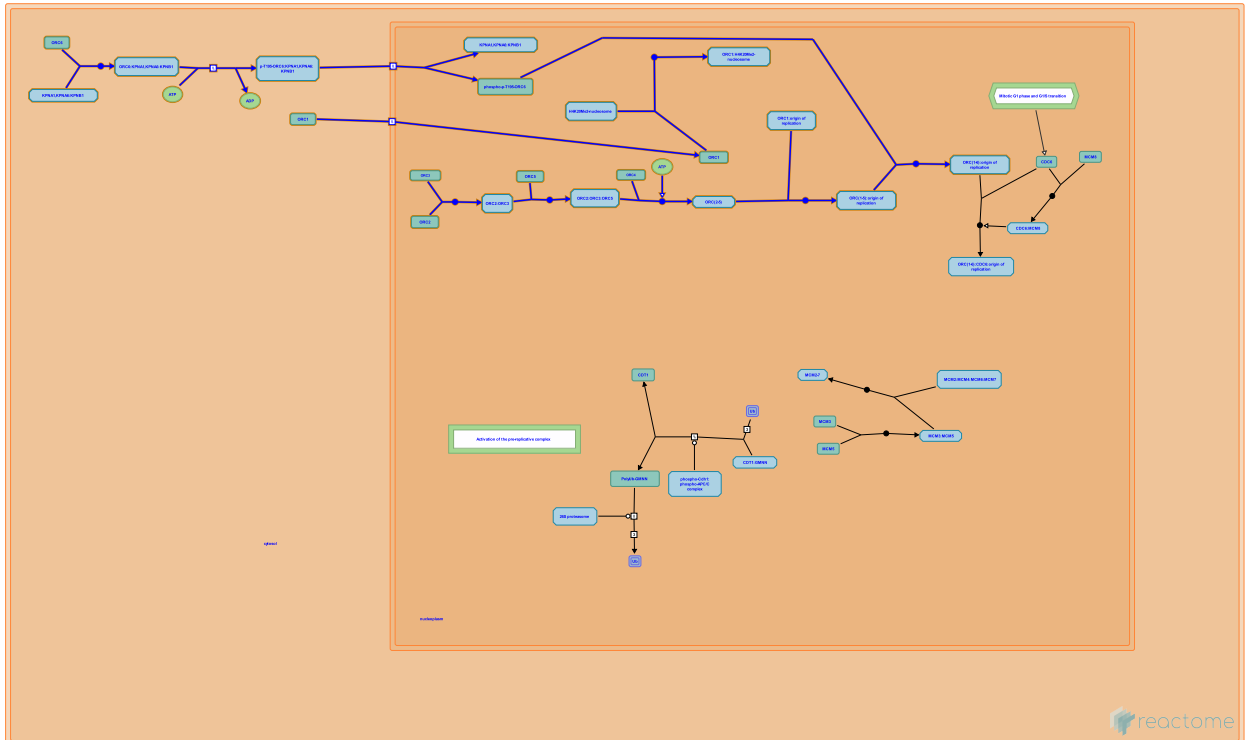
## Assembly of the ORC complex at the origin of replication ↗

**Location:** Assembly of the pre-replicative complex

**Stable identifier:** R-GGA-68616

**Compartments:** nucleoplasm

**Inferred from:** Assembly of the ORC complex at the origin of replication (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.

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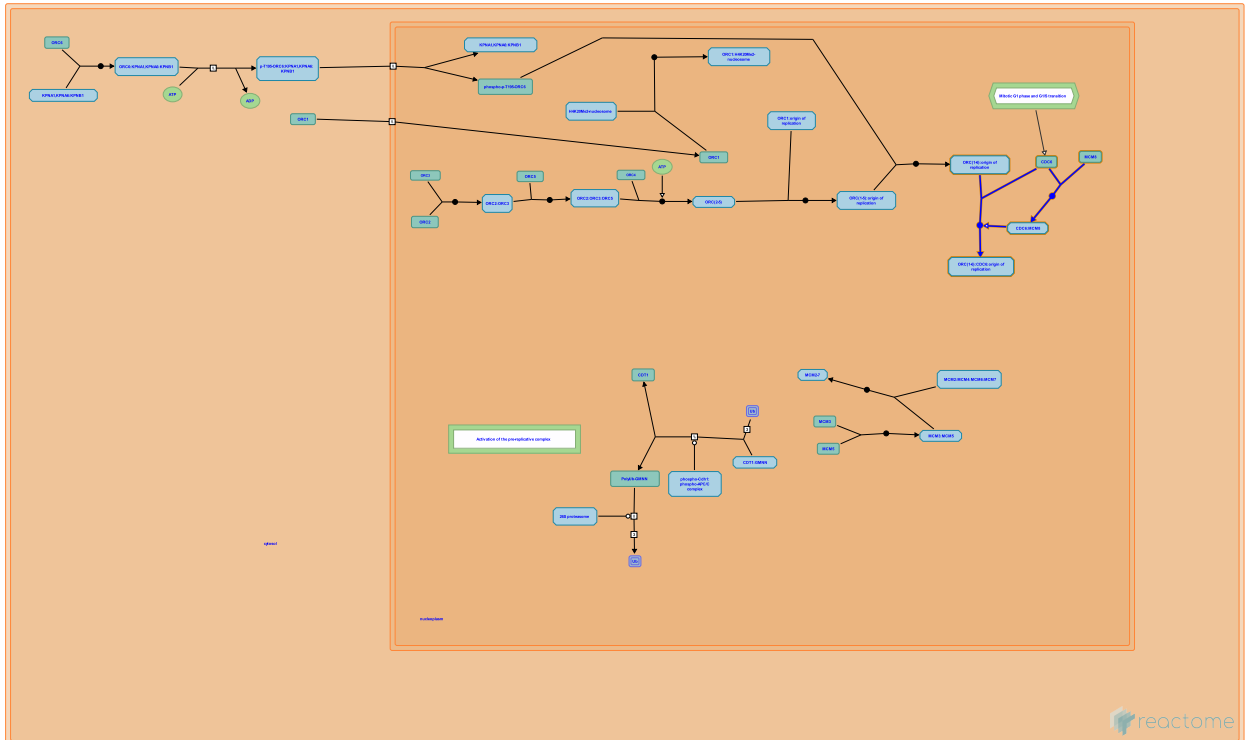
## CDC6 association with the ORC:origin complex ↗

**Location:** Assembly of the pre-replicative complex

**Stable identifier:** R-GGA-68689

**Compartments:** nucleoplasm

**Inferred from:** CDC6 association with the ORC:origin 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.

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## MCM3 binds MCM5 ↗

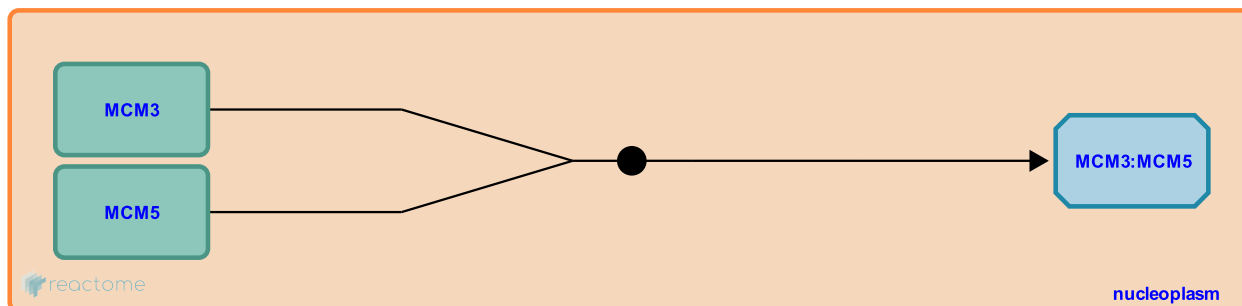
**Location:** [Assembly of the pre-replicative complex](#)

**Stable identifier:** R-GGA-9757256

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** [MCM3 binds MCM5 \(Homo sapiens\)](#)



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.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Followed by:** [Formation of MCM2-7 complex](#)

## Formation of MCM2-7 complex ↗

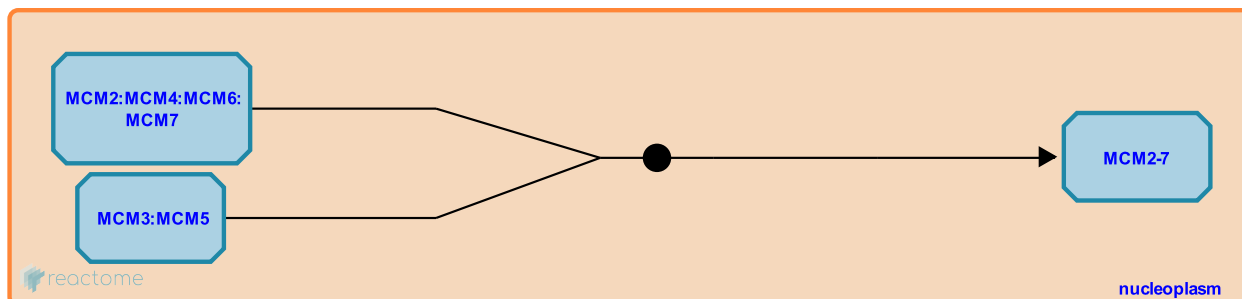
**Location:** [Assembly of the pre-replicative complex](#)

**Stable identifier:** R-GGA-9749253

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** [Formation of MCM2-7 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.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [MCM3 binds MCM5](#)

## The geminin component of geminin:Cdt1 complexes is ubiquitinated, releasing Cdt1



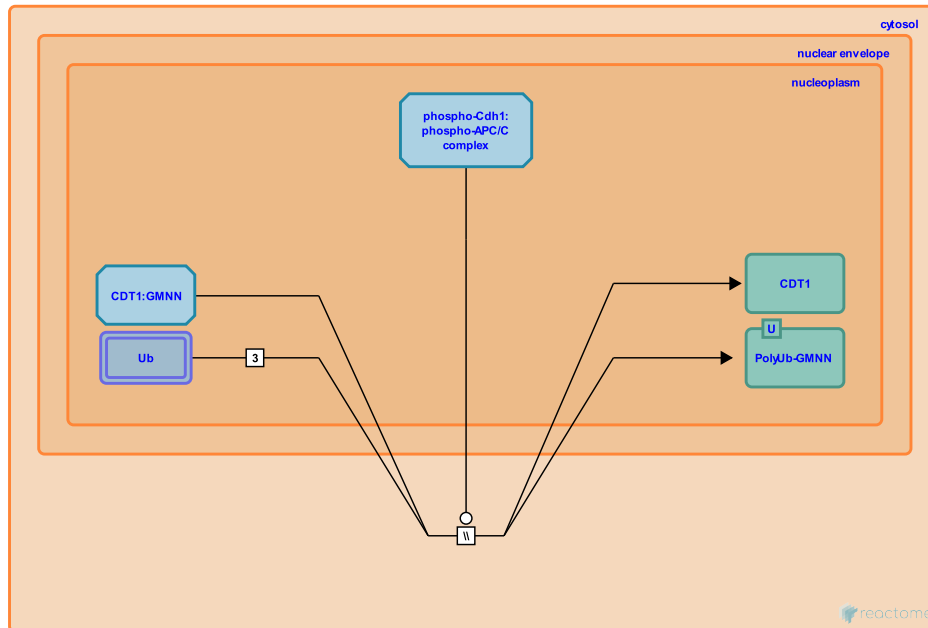
**Location:** Assembly of the pre-replicative complex

**Stable identifier:** R-GGA-68712

**Type:** omitted

**Compartments:** cytosol

**Inferred from:** The geminin component of geminin:Cdt1 complexes is ubiquitinated, releasing Cdt1 (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Followed by:** Ubiquitinated geminin is degraded by the proteasome



## Ubiquitinated geminin is degraded by the proteasome ↗

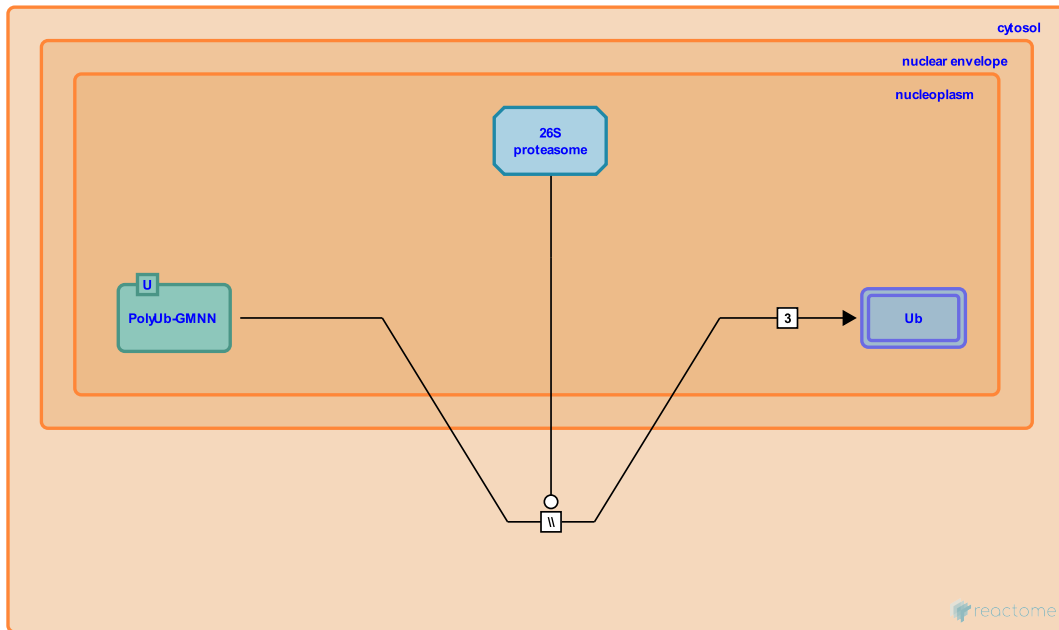
**Location:** [Assembly of the pre-replicative complex](#)

**Stable identifier:** R-GGA-68825

**Type:** omitted

**Compartments:** cytosol

**Inferred from:** [Ubiquitinated geminin is degraded by the proteasome \(Homo sapiens\)](#)



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.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [The geminin component of geminin:Cdt1 complexes is ubiquitinated, releasing Cdt1](#)

# Table of Contents

Introduction	1
☒ Assembly of the pre-replicative complex	2
☒ Assembly of the ORC complex at the origin of replication	3
☒ CDC6 association with the ORC:origin complex	4
☞ MCM3 binds MCM5	5
☞ Formation of MCM2-7 complex	6
☞ The geminin component of geminin:Cdt1 complexes is ubiquitinated, releasing Cdt1	7
☞ Ubiquitinated geminin is degraded by the proteasome	8
Table of Contents	9