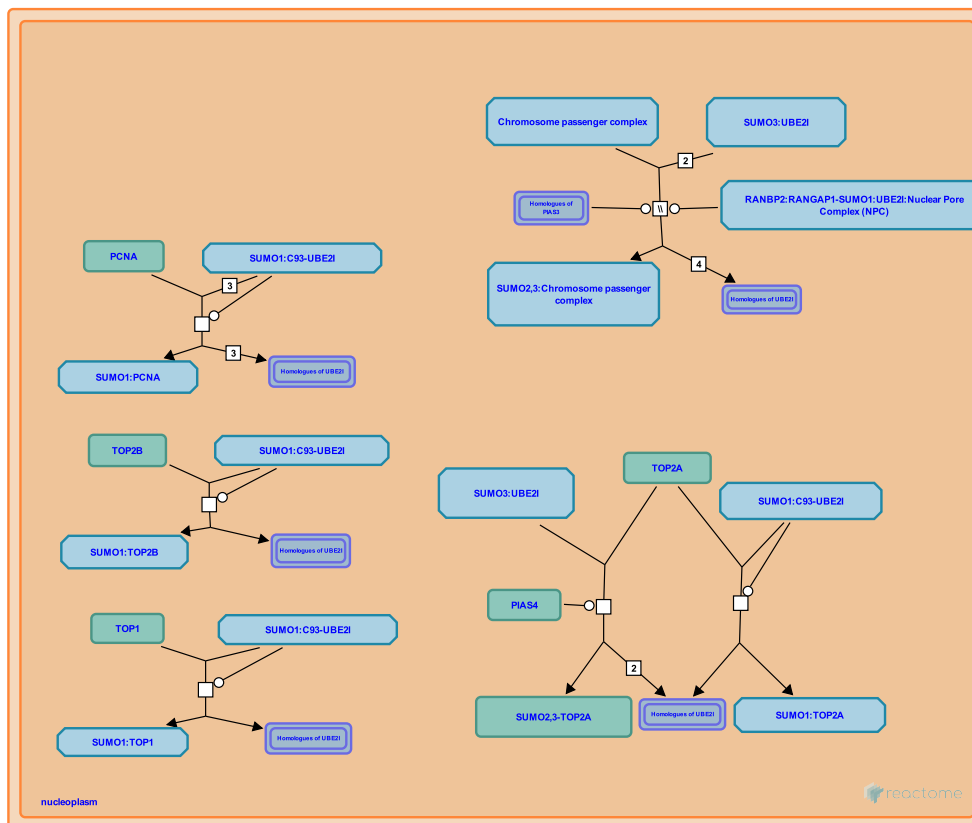


SUMOylation of DNA replication proteins



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

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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

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- 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

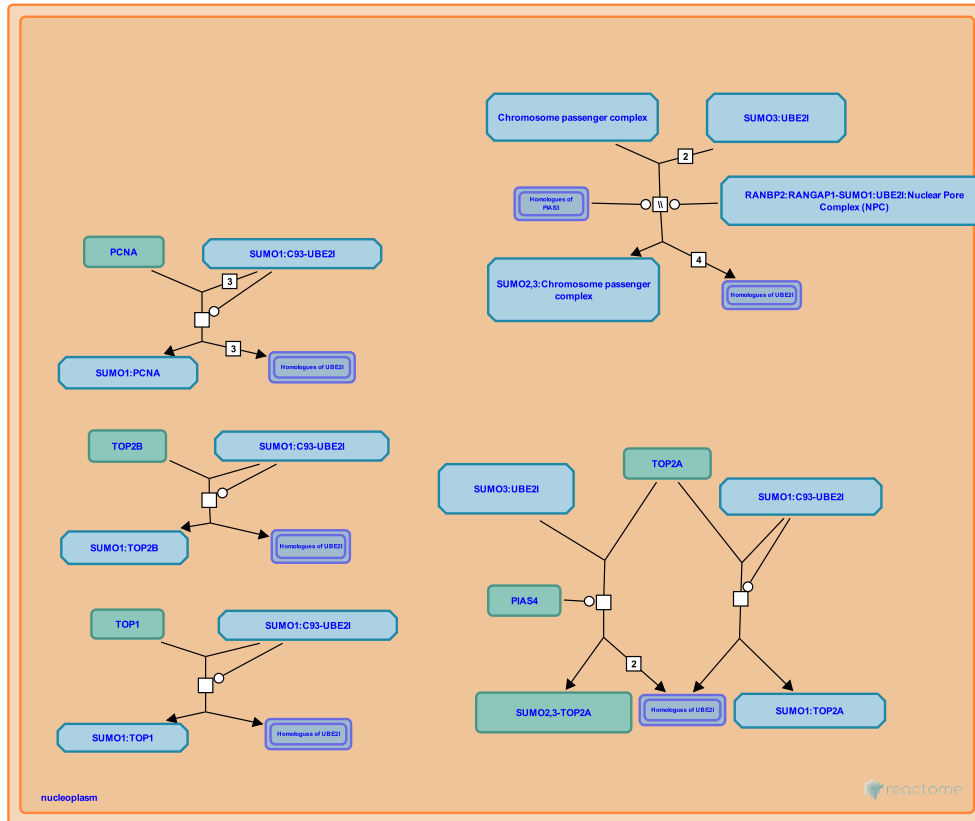
This document contains 1 pathway and 6 reactions ([see Table of Contents](#))

SUMOylation of DNA replication proteins ↗

Stable identifier: R-DRE-4615885

Compartments: nucleoplasm

Inferred from: SUMOylation of DNA replication proteins (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>

RANBP2 SUMOylates CDCA8 (Borealin) and PIAS3 SUMOylates AURKB (Aurora-B) ↗

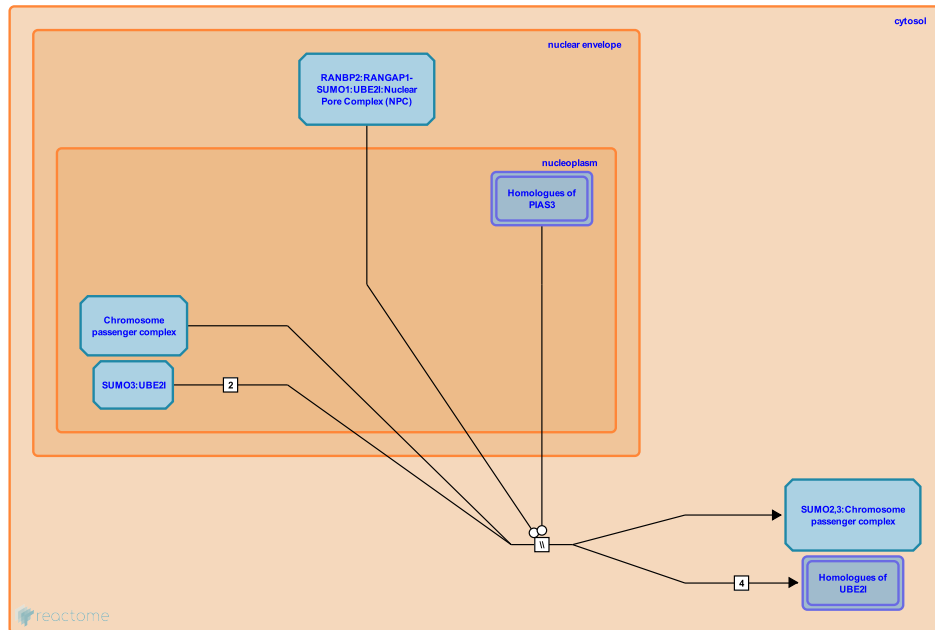
Location: [SUMOylation of DNA replication proteins](#)

Stable identifier: R-DRE-4655355

Type: omitted

Compartments: cytosol, nucleoplasm

Inferred from: [RANBP2 SUMOylates CDCA8 \(Borealin\) and PIAS3 SUMOylates AURKB \(Aurora-B\) \(Homo sapiens\)](#)



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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SUMOylation of PCNA with SUMO1 ↗

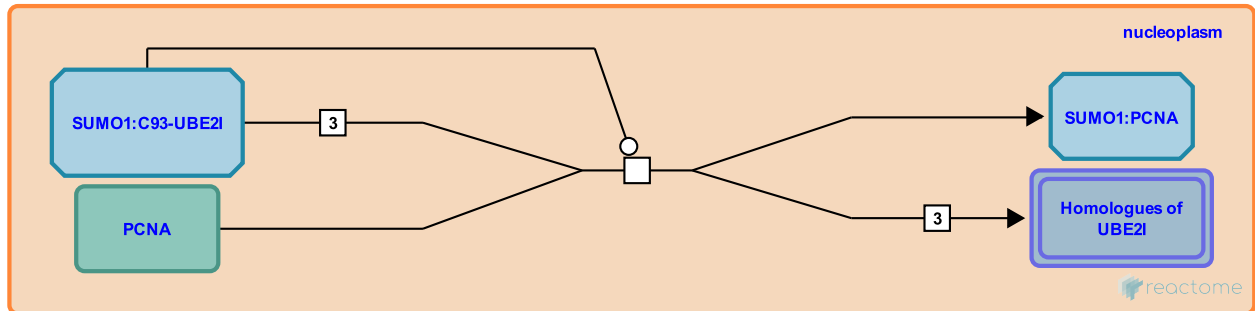
Location: [SUMOylation of DNA replication proteins](#)

Stable identifier: R-DRE-4615910

Type: transition

Compartments: nucleoplasm

Inferred from: [SUMOylation of PCNA with SUMO1 \(Homo sapiens\)](#)



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>

SUMOylation of TOP1 with SUMO1 [↗](#)

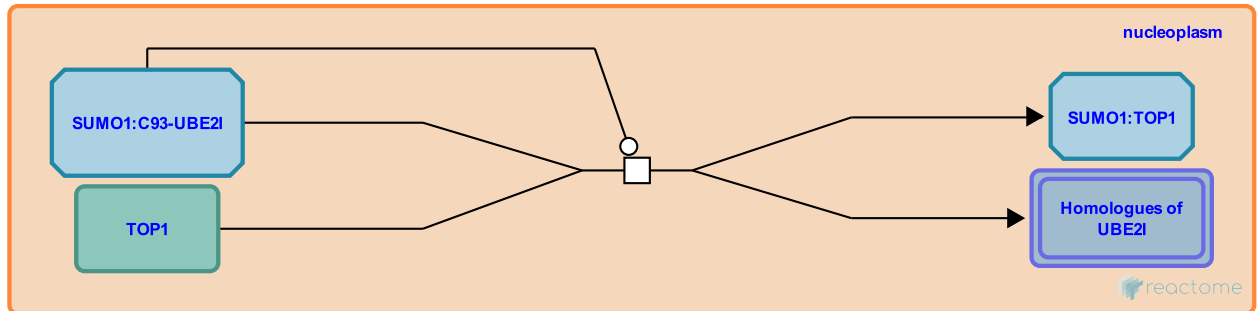
Location: [SUMOylation of DNA replication proteins](#)

Stable identifier: R-DRE-4641362

Type: transition

Compartments: nucleoplasm

Inferred from: [SUMOylation of TOP1 with SUMO1 \(Homo sapiens\)](#)



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>

SUMOylation of TOP2A with SUMO1 ↗

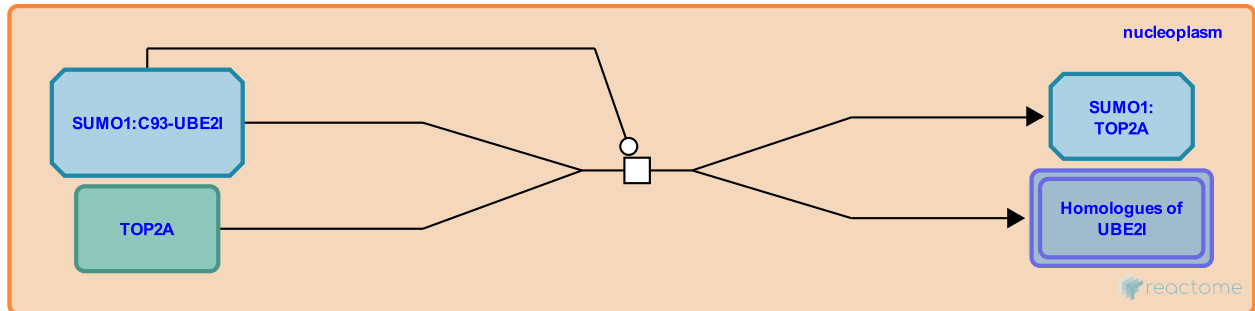
Location: [SUMOylation of DNA replication proteins](#)

Stable identifier: R-DRE-4641342

Type: transition

Compartments: nucleoplasm

Inferred from: [SUMOylation of TOP2A with SUMO1 \(Homo sapiens\)](#)



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>

PIAS4 SUMOylates TOP2A with SUMO2,3 ↗

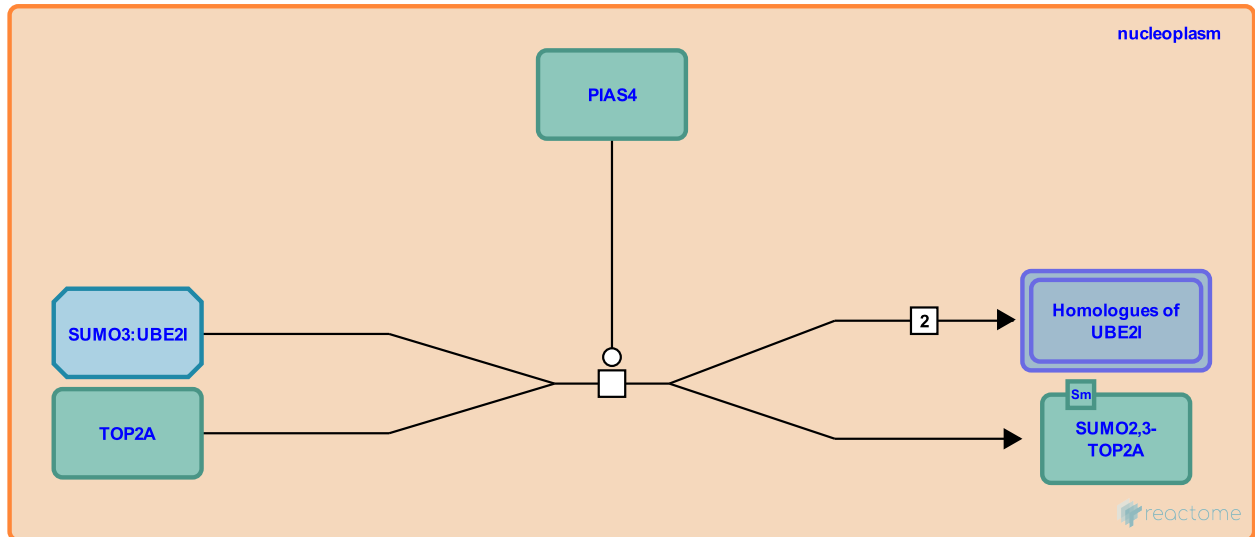
Location: [SUMOylation of DNA replication proteins](#)

Stable identifier: R-DRE-4641350

Type: transition

Compartments: nucleoplasm

Inferred from: [PIAS4 SUMOylates TOP2A with SUMO2,3 \(Homo sapiens\)](#)



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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SUMOylation of TOP2B with SUMO1 ↗

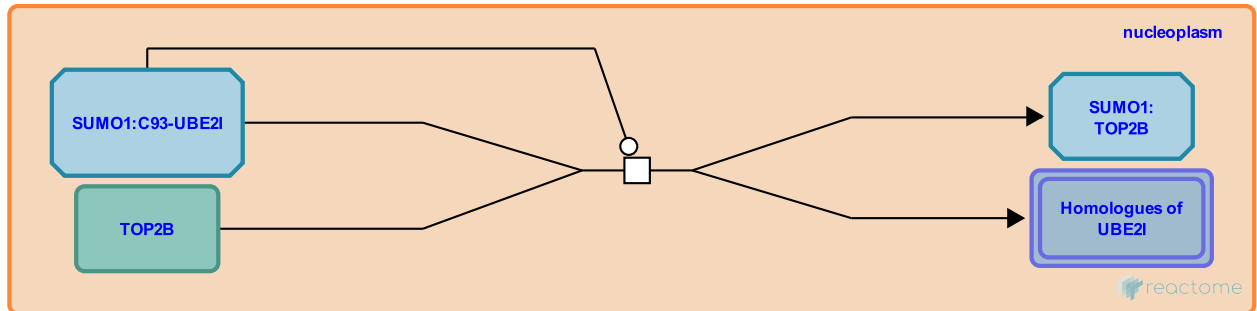
Location: [SUMOylation of DNA replication proteins](#)

Stable identifier: R-DRE-4641345

Type: transition

Compartments: nucleoplasm

Inferred from: [SUMOylation of TOP2B with SUMO1 \(Homo sapiens\)](#)



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>

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