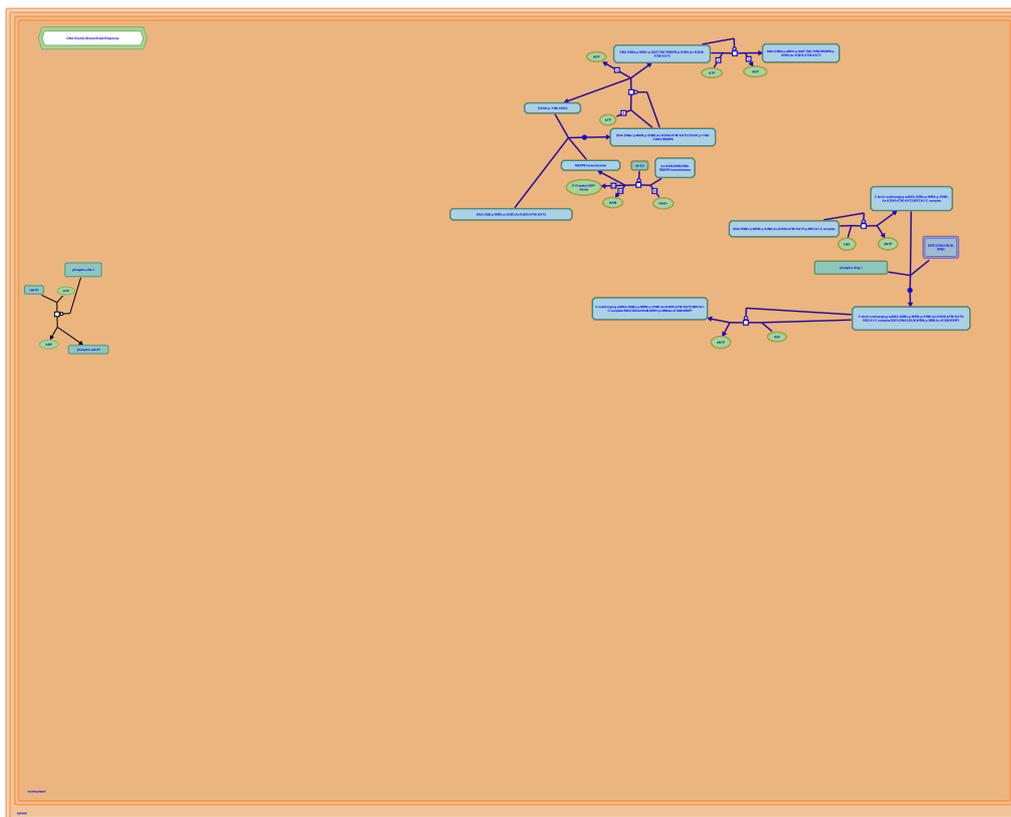


# Processing of DNA double-strand break ends



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.

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: 73

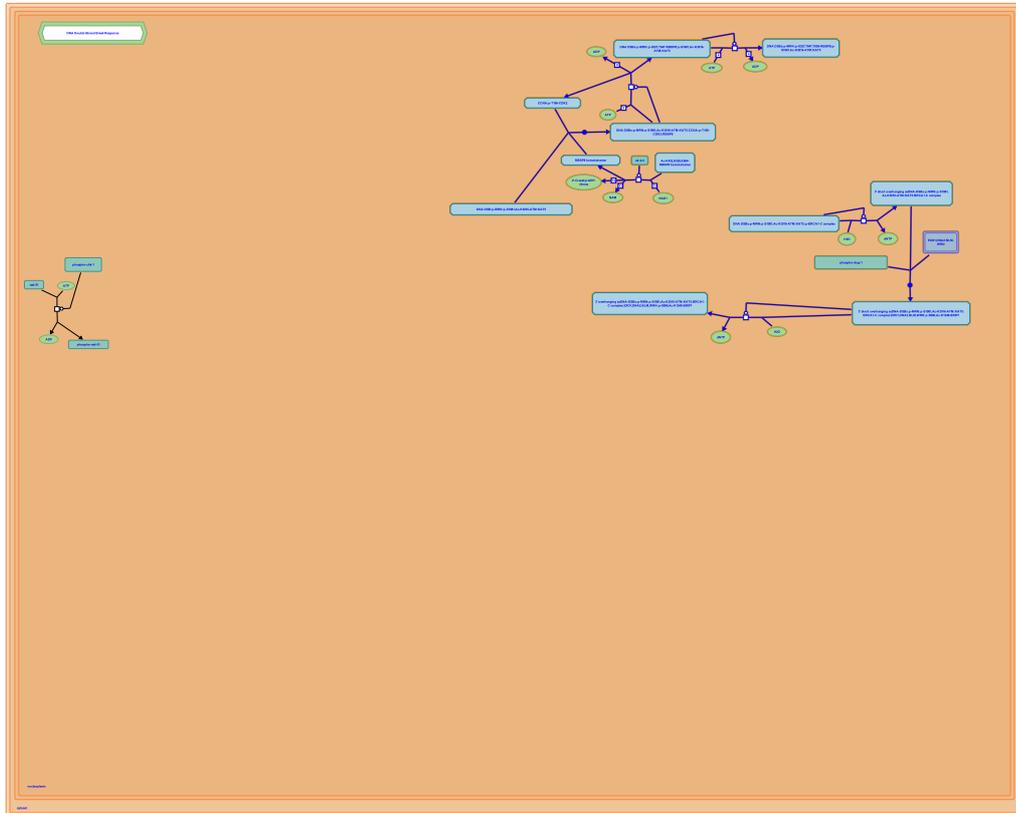
This document contains 1 pathway and 7 reactions ([see Table of Contents](#))

## Processing of DNA double-strand break ends ↗

**Stable identifier:** R-CEL-5693607

**Compartments:** nucleoplasm

**Inferred from:** [Processing of DNA double-strand break ends \(Homo sapiens\)](#)



reactome

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>

## SIRT6 deacetylates RBBP8 ↗

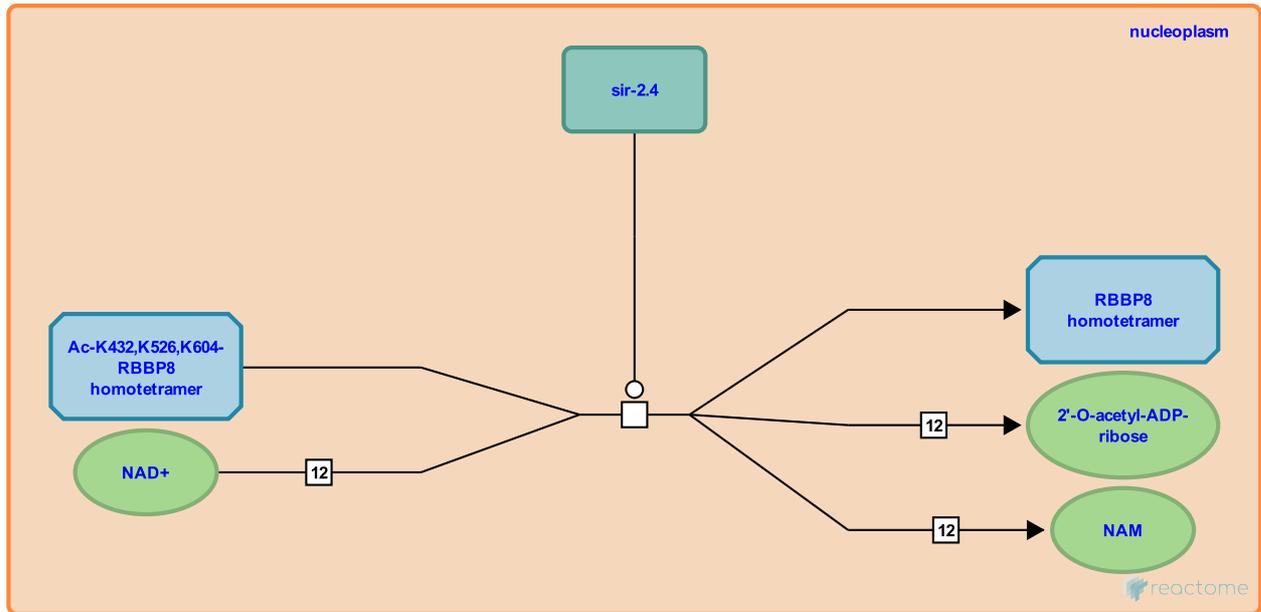
**Location:** Processing of DNA double-strand break ends

**Stable identifier:** R-CEL-5685953

**Type:** transition

**Compartments:** nucleoplasm

**Inferred from:** SIRT6 deacetylates RBBP8 (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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**Followed by:** [MRN complex binds CDK2 and RBBP8](#)

## MRN complex binds CDK2 and RBBP8 ↗

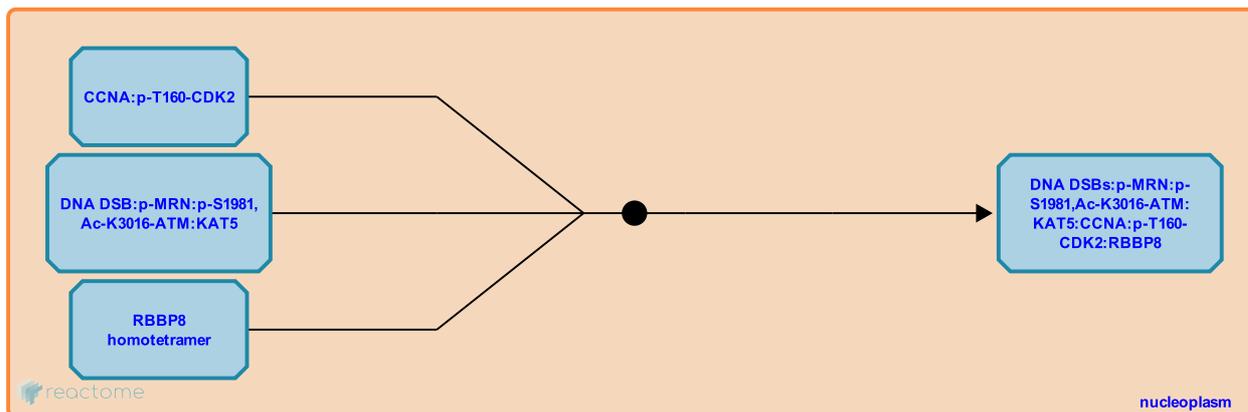
**Location:** [Processing of DNA double-strand break ends](#)

**Stable identifier:** R-CEL-5684081

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** [MRN complex binds CDK2 and RBBP8 \(Homo sapiens\)](#)



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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**Preceded by:** [SIRT6 deacetylates RBBP8](#)

**Followed by:** [CDK2 phosphorylates RBBP8](#)

## CDK2 phosphorylates RBBP8 ↗

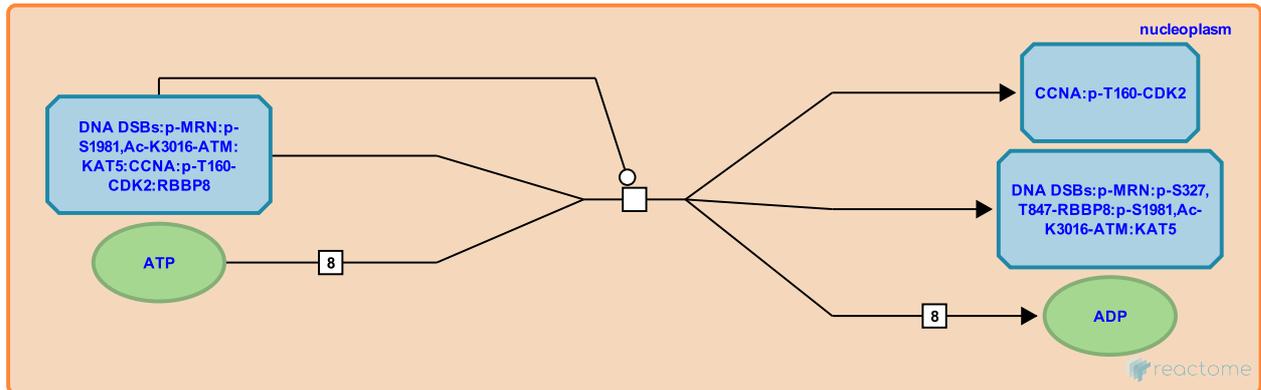
**Location:** [Processing of DNA double-strand break ends](#)

**Stable identifier:** R-CEL-5684096

**Type:** transition

**Compartments:** nucleoplasm

**Inferred from:** [CDK2 phosphorylates RBBP8 \(Homo sapiens\)](#)



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

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**Preceded by:** [MRN complex binds CDK2 and RBBP8](#)

**Followed by:** [ATM phosphorylates RBBP8](#)

## ATM phosphorylates RBBP8 ↗

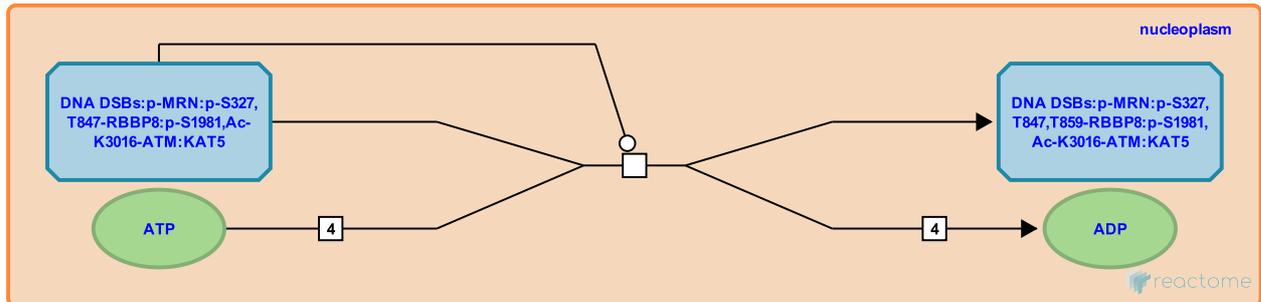
**Location:** [Processing of DNA double-strand break ends](#)

**Stable identifier:** R-CEL-5684140

**Type:** transition

**Compartments:** nucleoplasm

**Inferred from:** [ATM phosphorylates RBBP8 \(Homo sapiens\)](#)



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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**Preceded by:** [CDK2 phosphorylates RBBP8](#)

## Initial resection of double-strand break ends ↗

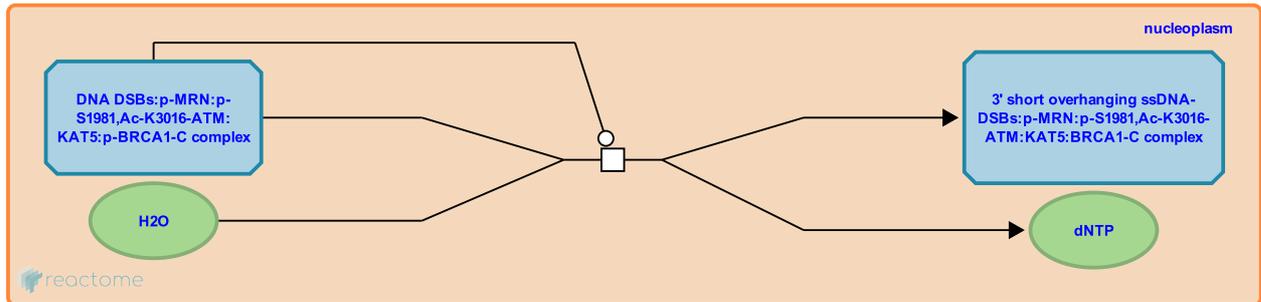
**Location:** [Processing of DNA double-strand break ends](#)

**Stable identifier:** R-CEL-5693608

**Type:** transition

**Compartments:** nucleoplasm

**Inferred from:** [Initial resection of double-strand break ends \(Homo sapiens\)](#)



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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**Followed by:** [EXO1 or DNA2 in complex with BLM or WRN binds initially resected DNA DSBs along with BRIP1 recruitment](#)

## EXO1 or DNA2 in complex with BLM or WRN binds initially resected DNA DSBs along with BRIP1 recruitment ↗

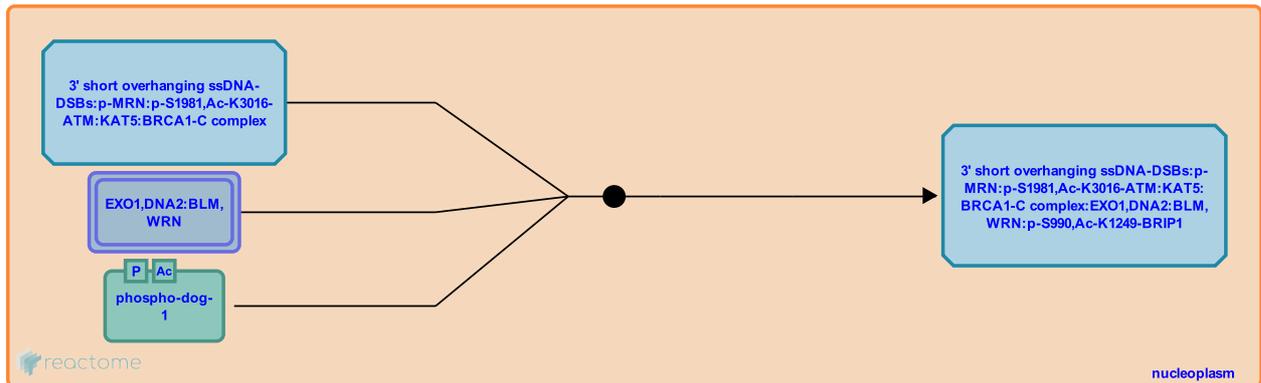
**Location:** [Processing of DNA double-strand break ends](#)

**Stable identifier:** R-CEL-5685985

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** [EXO1 or DNA2 in complex with BLM or WRN binds initially resected DNA DSBs along with BRIP1 recruitment \(Homo sapiens\)](#)



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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**Preceded by:** [Initial resection of double-strand break ends](#)

**Followed by:** [Long-range resection of DNA DSBs by EXO1 or DNA2](#)

## Long-range resection of DNA DSBs by EXO1 or DNA2 ↗

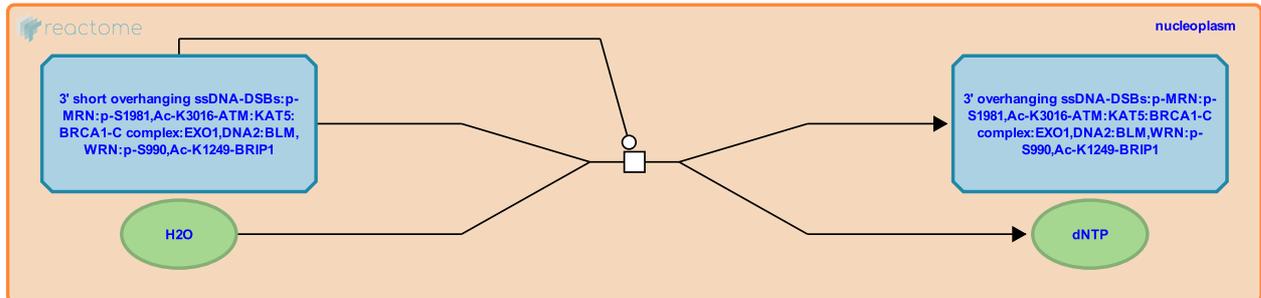
**Location:** [Processing of DNA double-strand break ends](#)

**Stable identifier:** R-CEL-5685994

**Type:** transition

**Compartments:** nucleoplasm

**Inferred from:** [Long-range resection of DNA DSBs by EXO1 or DNA2 \(Homo sapiens\)](#)



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:** [EXO1 or DNA2 in complex with BLM or WRN binds initially resected DNA DSBs along with BRIP1 recruitment](#)

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