reactome

SUMOylation of DNA damage response and repair proteins

19/04/2021

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: 76

This document contains 1 pathway and 21 reactions (see Table of Contents)

SUMOylation of DNA damage response and repair proteins ↗

Stable identifier: R-RNO-3108214

Compartments: nucleoplasm

Inferred from: SUMOylation of DNA damage response and repair 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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

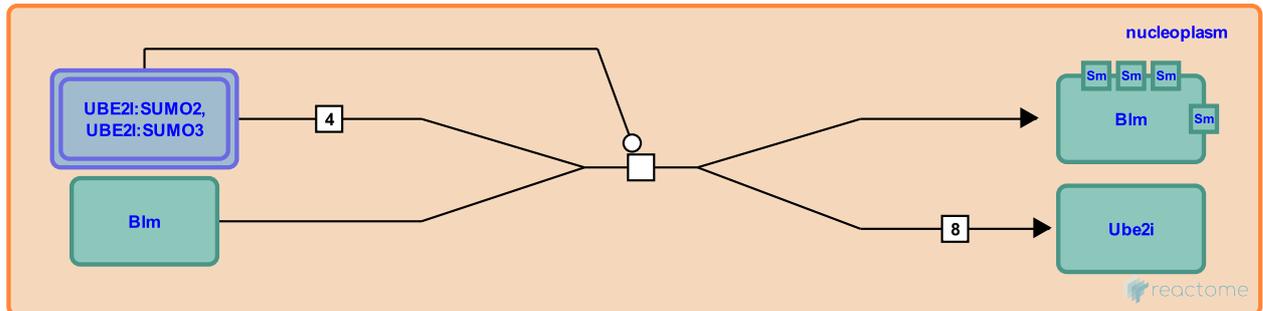## SUMOylation of BLM with SUMO2,3 ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-RNO-4568914

Type: transition

Compartments: nucleoplasm

Inferred from: SUMOylation of BLM 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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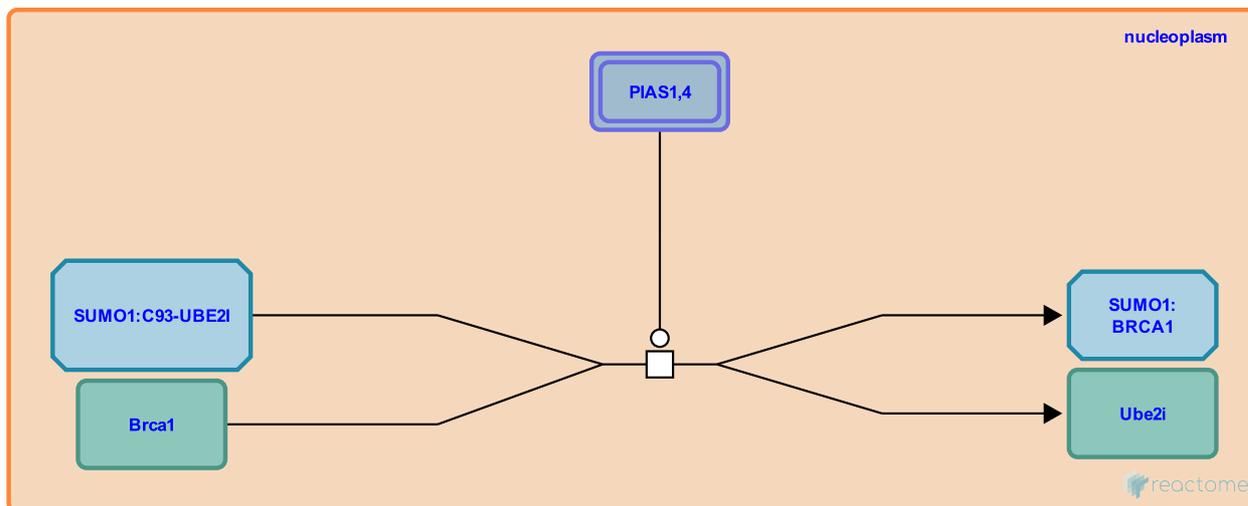
PIAS1,4 SUMOylates BRCA1 with SUMO1 ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-RNO-2997709

Type: transition

Compartments: nucleoplasm

Inferred from: PIAS1,4 SUMOylates BRCA1 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.

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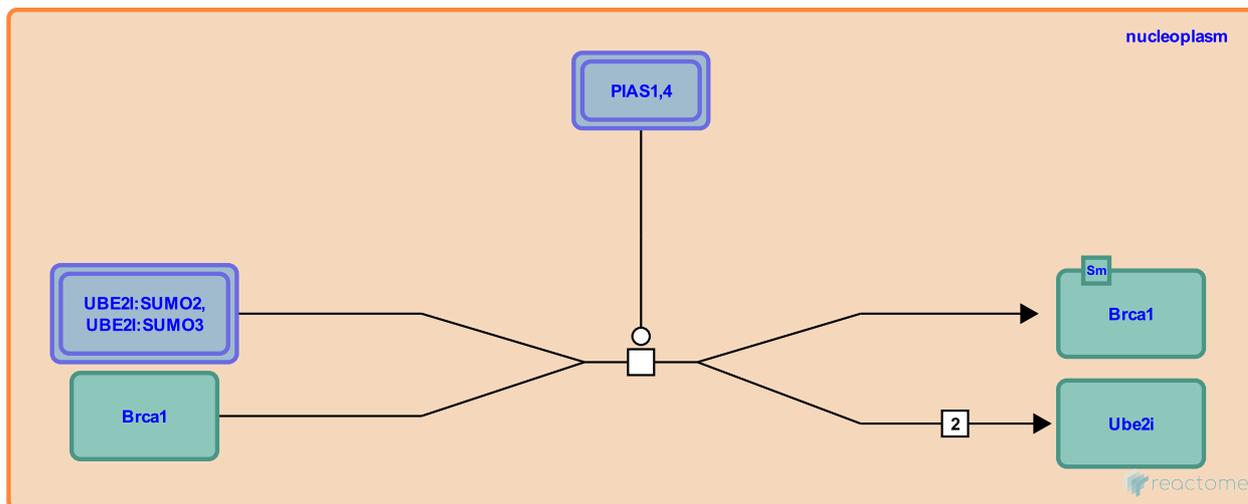# PIAS1,4 SUMOylates BRCA1 with SUMO2,3 ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-RNO-2997616

Type: transition

Compartments: nucleoplasm

Inferred from: PIAS1,4 SUMOylates BRCA1 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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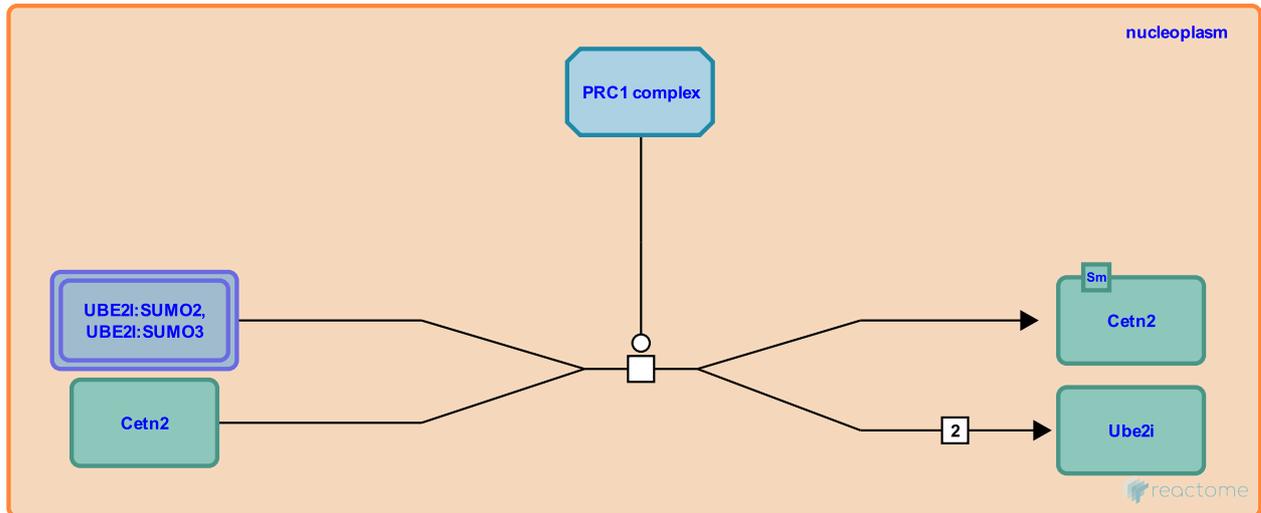# CBX4 (Pc2) SUMOylates CETN2 with SUMO2,3 ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-RNO-4570463

Type: transition

Compartments: nucleoplasm

Inferred from: CBX4 (Pc2) SUMOylates CETN2 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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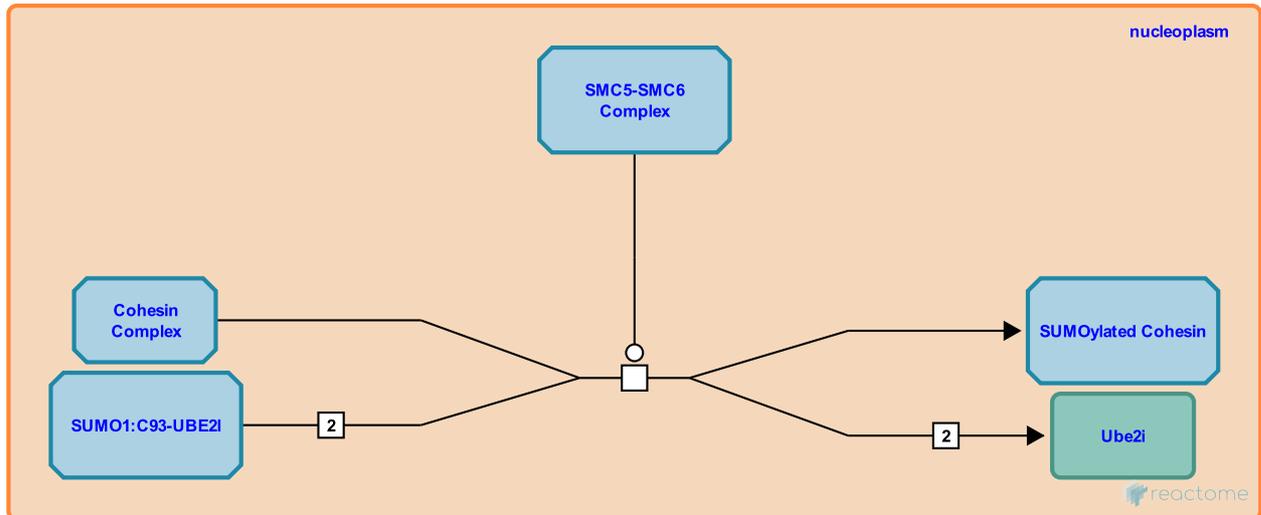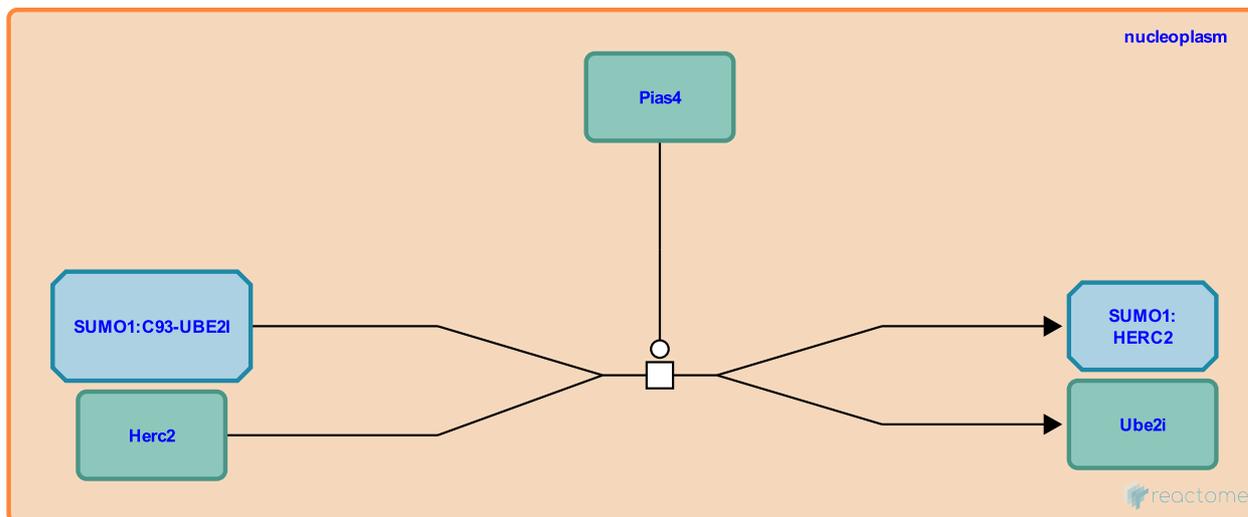**SMC5-SMC6 Complex SUMOylates Cohesin with SUMO1** ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-RNO-3108212

Type: transition

Compartments: nucleoplasm

Inferred from: SMC5-SMC6 Complex SUMOylates Cohesin 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.

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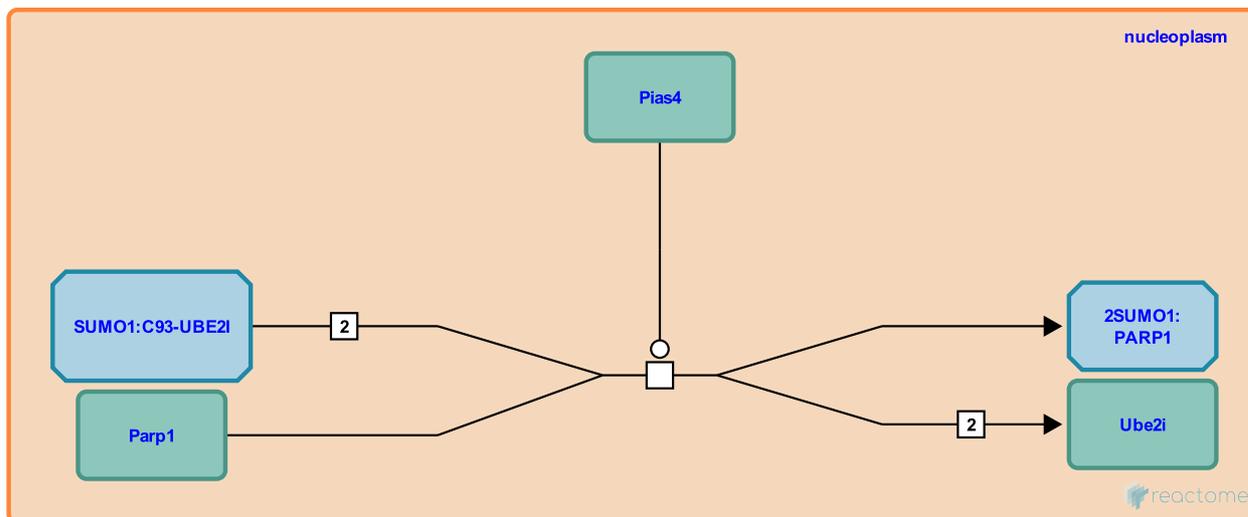
PIAS4 SUMOylates HERC2 with SUMO1 ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-RNO-4551724

Type: transition

Compartments: nucleoplasm

Inferred from: PIAS4 SUMOylates HERC2 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.

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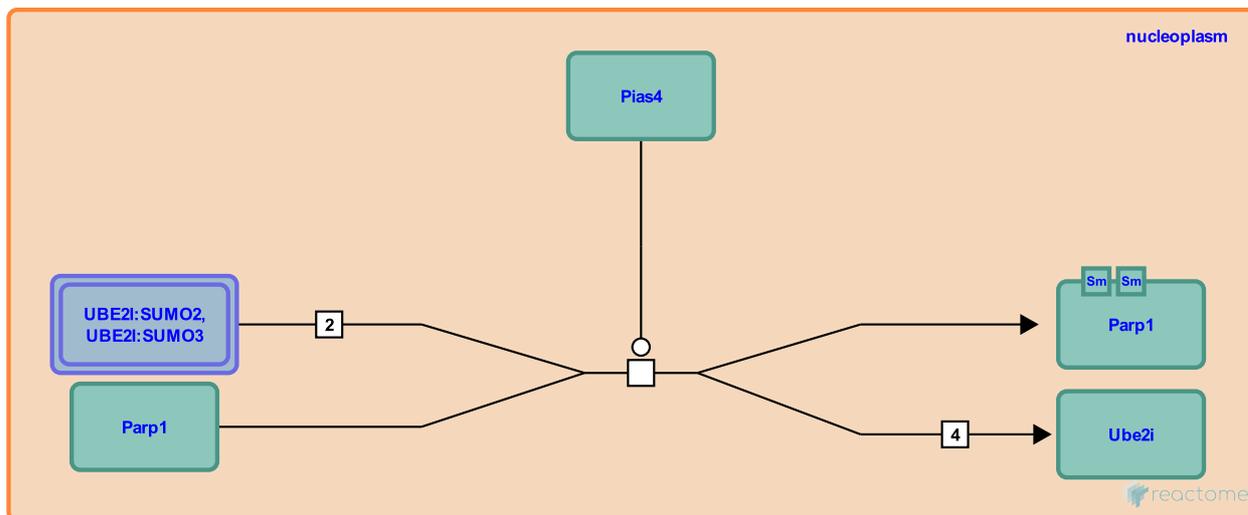
PIAS4 SUMOylates PARP1 with SUMO1 ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-RNO-4551604

Type: transition

Compartments: nucleoplasm

Inferred from: PIAS4 SUMOylates PARP1 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.

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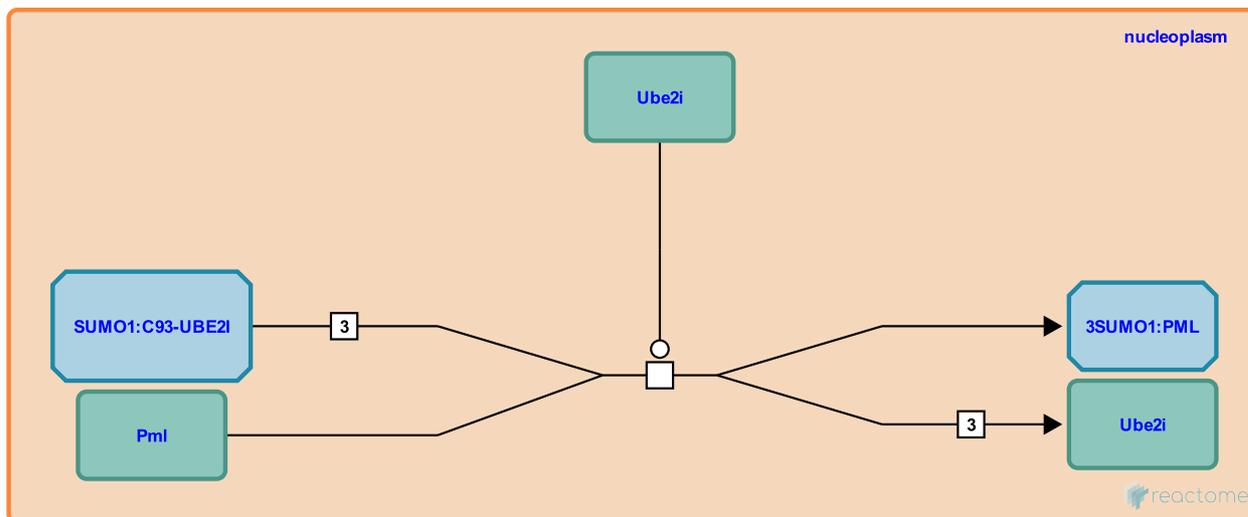
PIAS4 SUMOylates PARP1 with SUMO2,3 ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-RNO-4551768

Type: transition

Compartments: nucleoplasm

Inferred from: PIAS4 SUMOylates PARP1 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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UBE2I, HDAC7 SUMOylate PML with SUMO1 ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-RNO-3000383

Type: transition

Compartments: nucleoplasm

Inferred from: UBE2I, HDAC7 SUMOylate PML 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.

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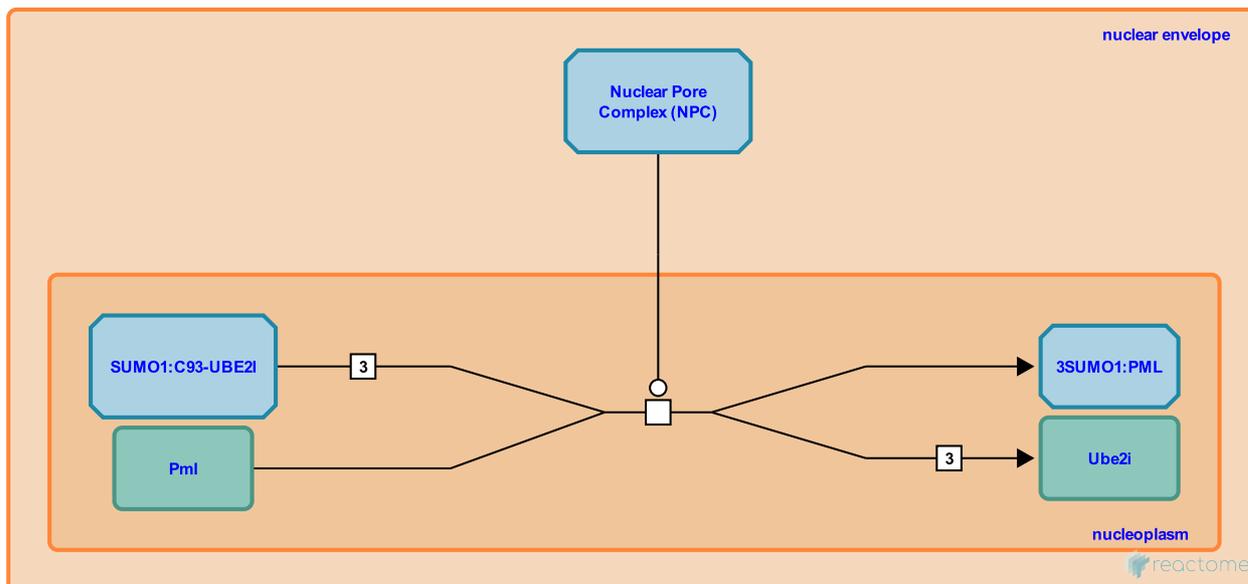# RANBP2 SUMOylates PML with SUMO1 ↗

**Location:** SUMOylation of DNA damage response and repair proteins

Stable identifier: R-RNO-5228508

Type: transition

Compartments: nucleoplasm, nuclear envelope

Inferred from: RANBP2 SUMOylates PML 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.

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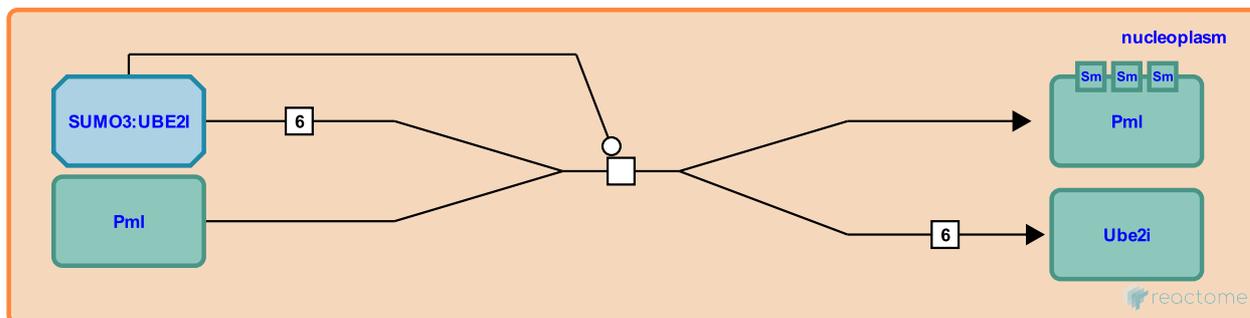
RANBP2 SUMOylates PML with SUMO2 ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-RNO-3000411

Type: transition

Compartments: nucleoplasm, nuclear envelope

Inferred from: RANBP2 SUMOylates PML with SUMO2 (Homo sapiens)
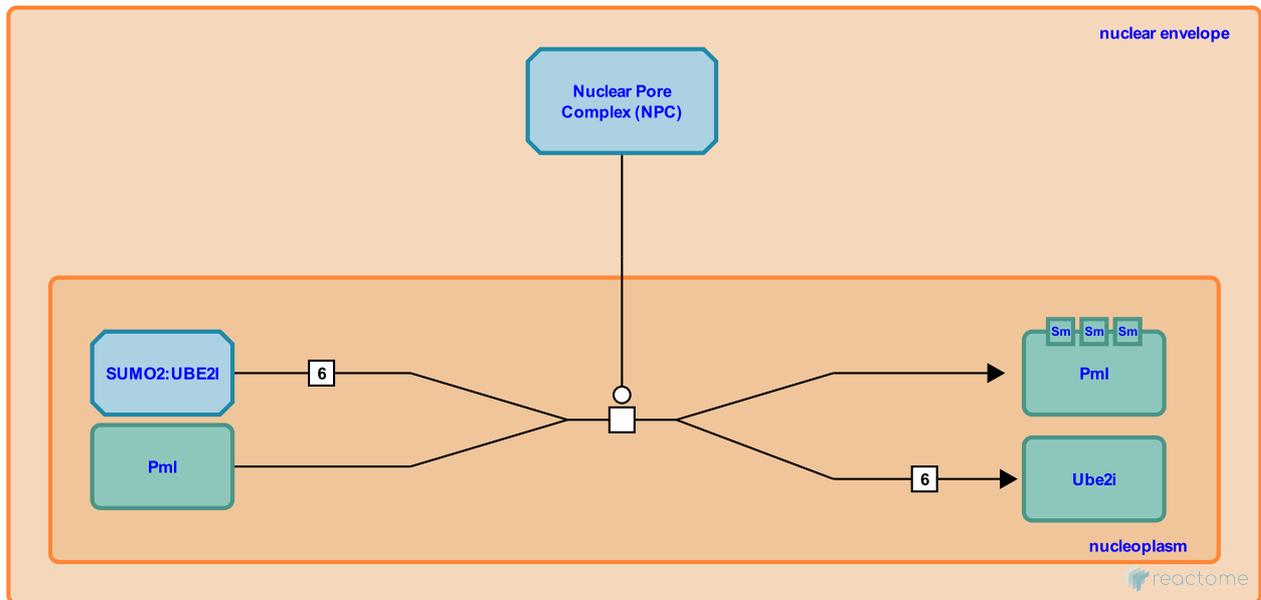
This event has been computationally inferred from an event that has been demonstrated in another species.

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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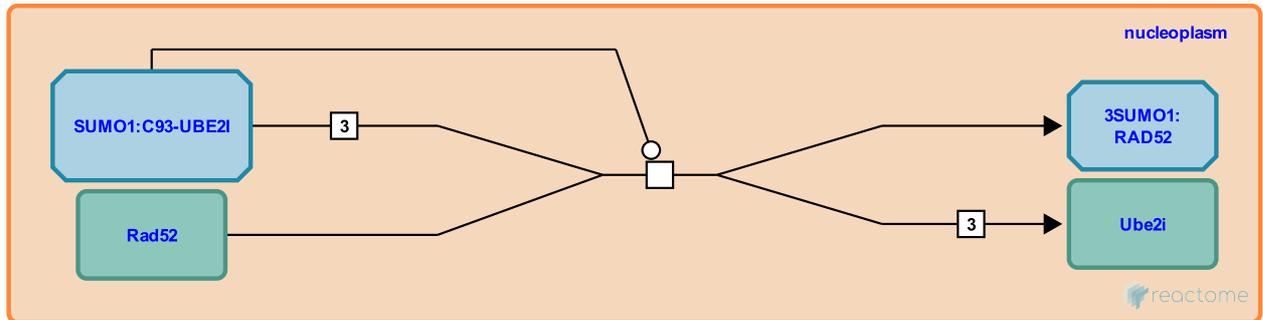
SUMOylation of PML with SUMO3 ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-RNO-3000433

Type: transition

Compartments: nucleoplasm

Inferred from: SUMOylation of PML with SUMO3 (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp
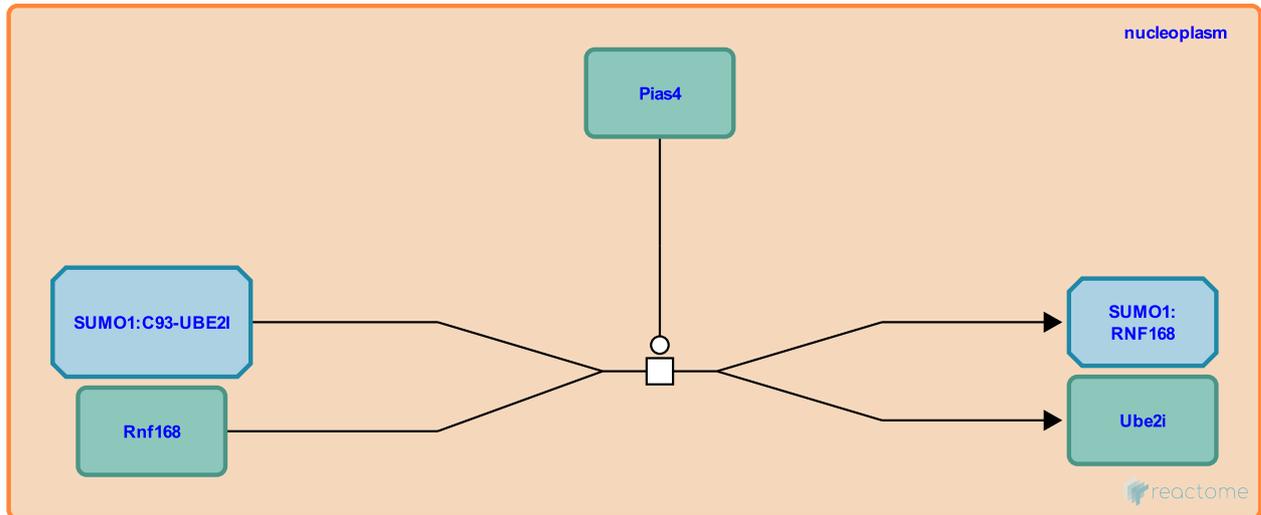
SUMOylation of RAD52 with SUMO1 ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-RNO-4568863

Type: transition

Compartments: nucleoplasm

Inferred from: SUMOylation of RAD52 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.

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PIAS4 SUMOylates RNF168 with SUMO1 ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-RNO-4551661

Type: transition

Compartments: nucleoplasm

Inferred from: PIAS4 SUMOylates RNF168 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.

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SUMOylation of RPA1 (RPA70) with SUMO2,3 ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-RNO-4551616

Type: transition

Compartments: nucleoplasm

Inferred from: SUMOylation of RPA1 (RPA70) with SUMO2,3 (Homo sapiens)
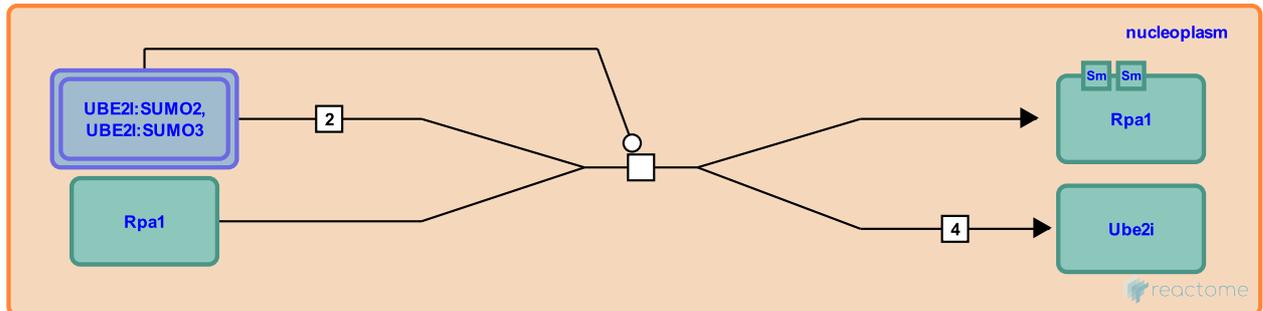
This event has been computationally inferred from an event that has been demonstrated in another species.

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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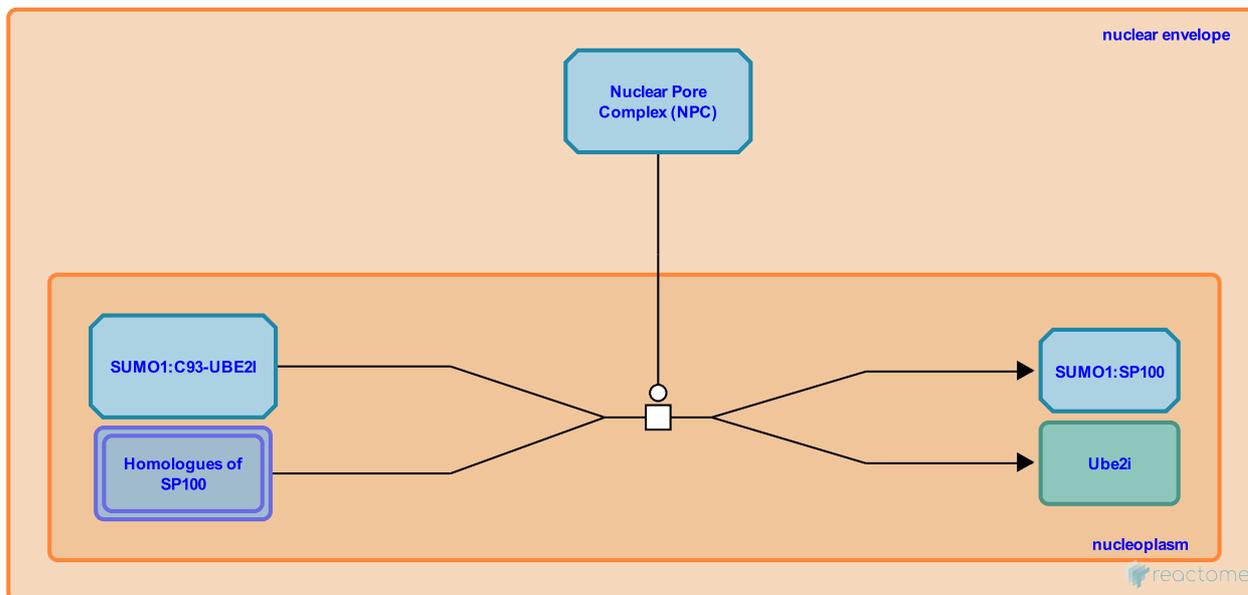
RANBP2 SUMOylates SP100 with SUMO1 ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-RNO-3000399

Type: transition

Compartments: nucleoplasm, nuclear envelope

Inferred from: RANBP2 SUMOylates SP100 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.

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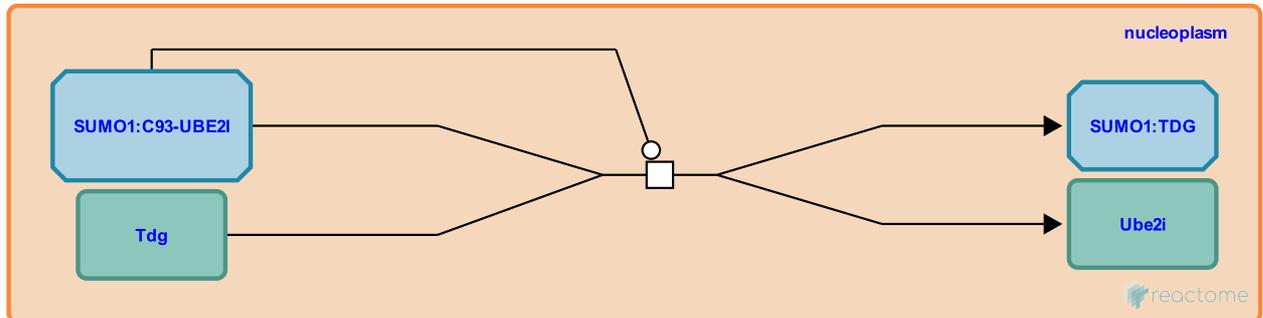
RANBP2 SUMOylates SP100 with SUMO2 ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-RNO-3000348

Type: transition

Compartments: nucleoplasm, nuclear envelope

Inferred from: RANBP2 SUMOylates SP100 with SUMO2 (Homo sapiens)
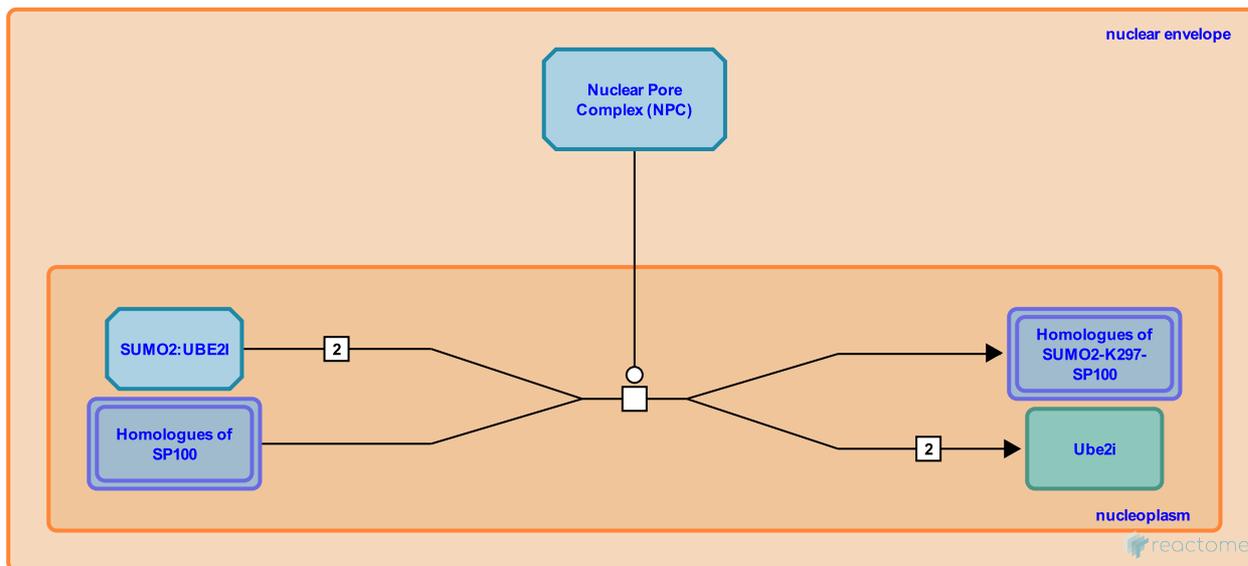
This event has been computationally inferred from an event that has been demonstrated in another species.

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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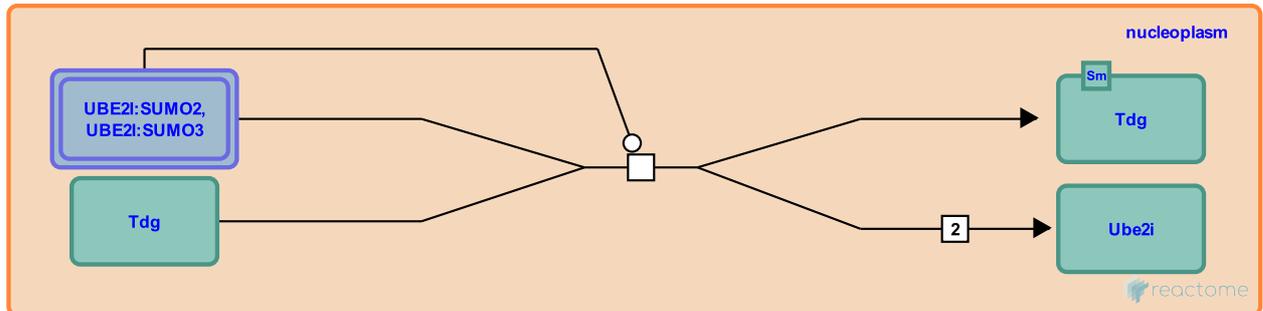
SUMOylation of TDG with SUMO1 ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-RNO-4551648

Type: transition

Compartments: nucleoplasm

Inferred from: SUMOylation of TDG 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.

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SUMOylation of TDG with SUMO2,3 ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-RNO-4551738

Type: transition

Compartments: nucleoplasm

Inferred from: SUMOylation of TDG 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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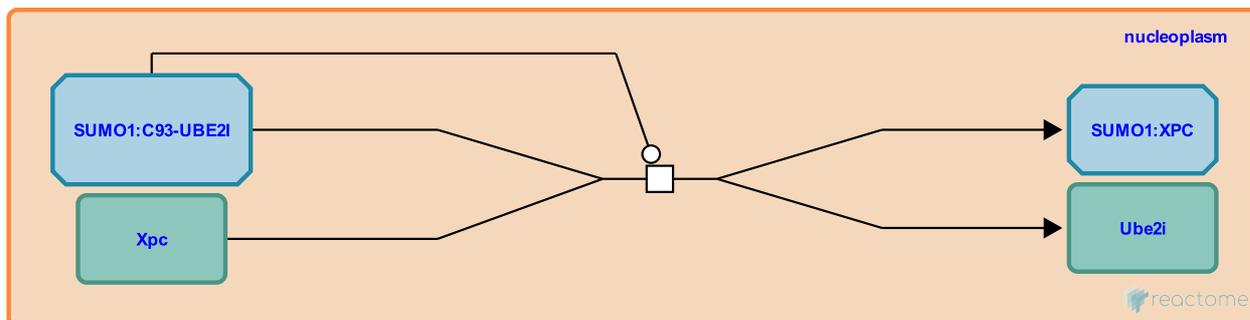
PIAS1,2-1 SUMOylates XRCC4 with SUMO1 ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-RNO-4568848

Type: transition

Compartments: nucleoplasm

Inferred from: PIAS1,2-1 SUMOylates XRCC4 with SUMO1 (Homo sapiens)
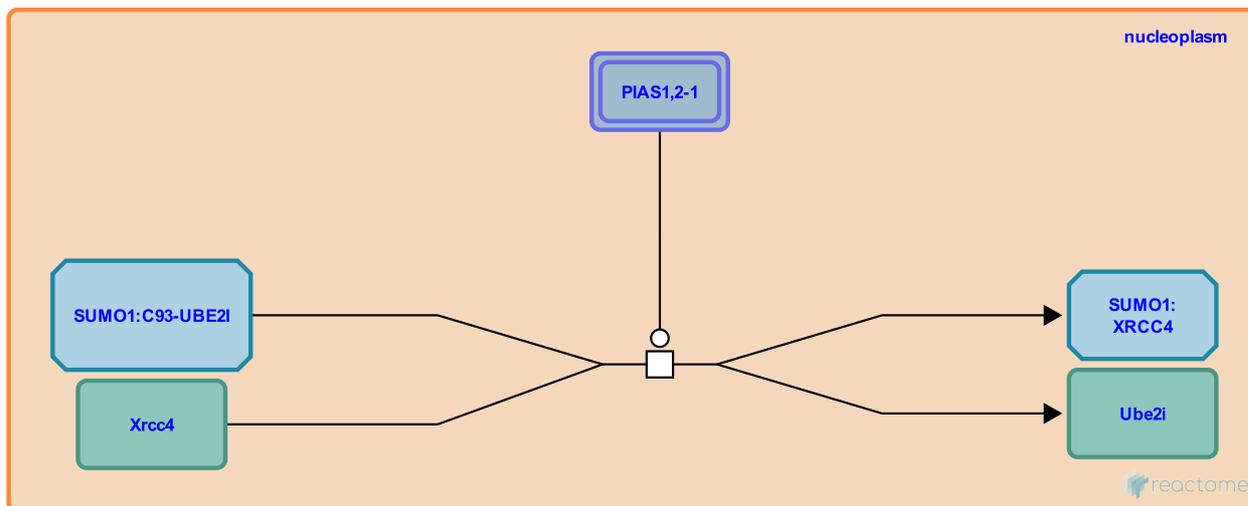
This event has been computationally inferred from an event that has been demonstrated in another species.

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.

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SUMOylation of XPC with SUMO1 ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-RNO-4570528

Type: transition

Compartments: nucleoplasm

Inferred from: SUMOylation of XPC 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.

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