SUMOylation of DNA damage response and repair proteins

22/04/2021

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.

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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

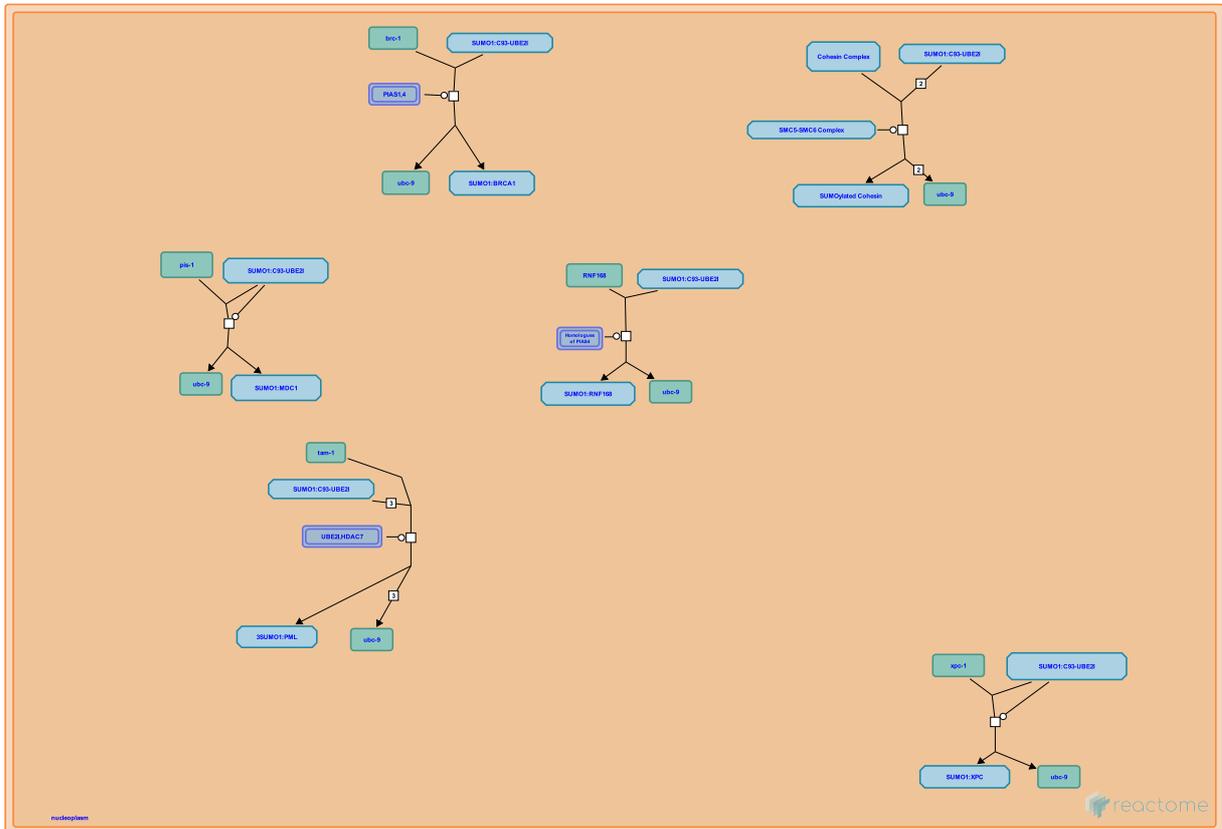This document contains 1 pathway and 6 reactions (see Table of Contents)

SUMOylation of DNA damage response and repair proteins ↗

Stable identifier: R-CEL-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
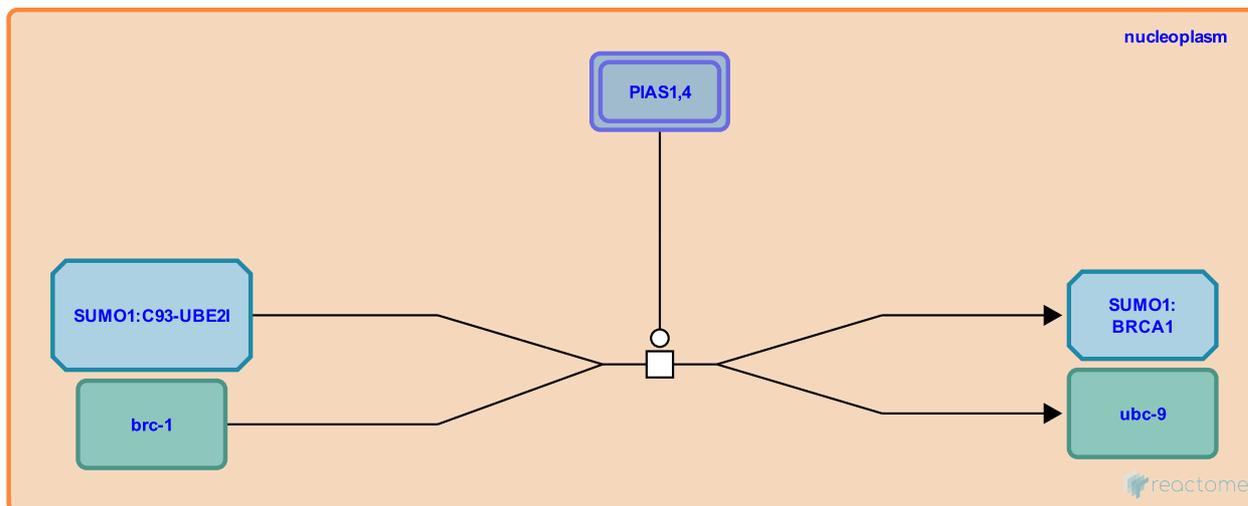
PIAS1,4 SUMOylates BRCA1 with SUMO1 ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-CEL-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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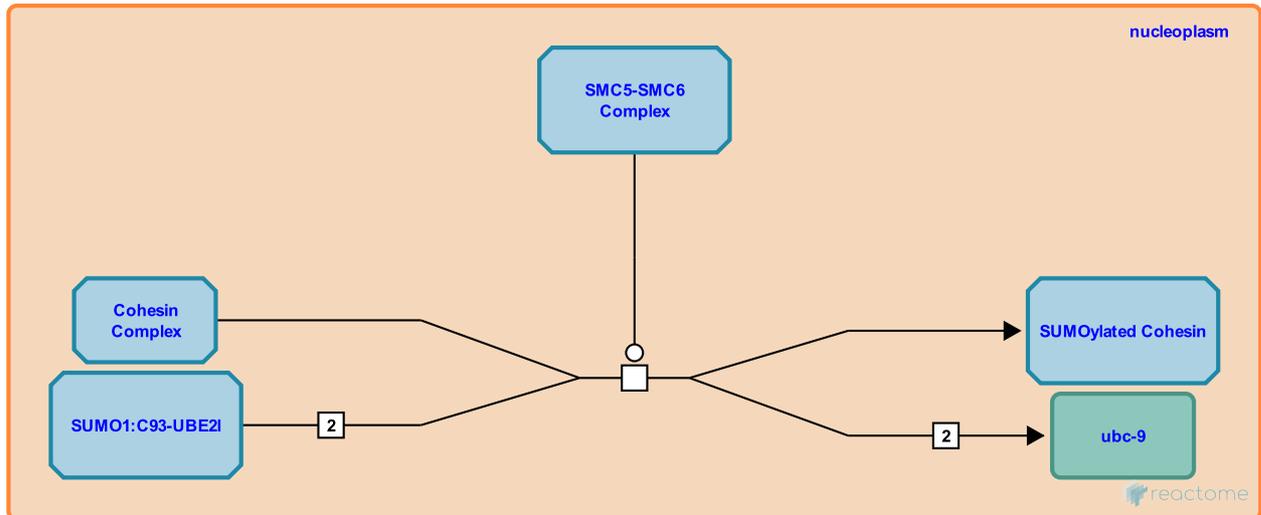**SMC5-SMC6 Complex SUMOylates Cohesin with SUMO1** ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-CEL-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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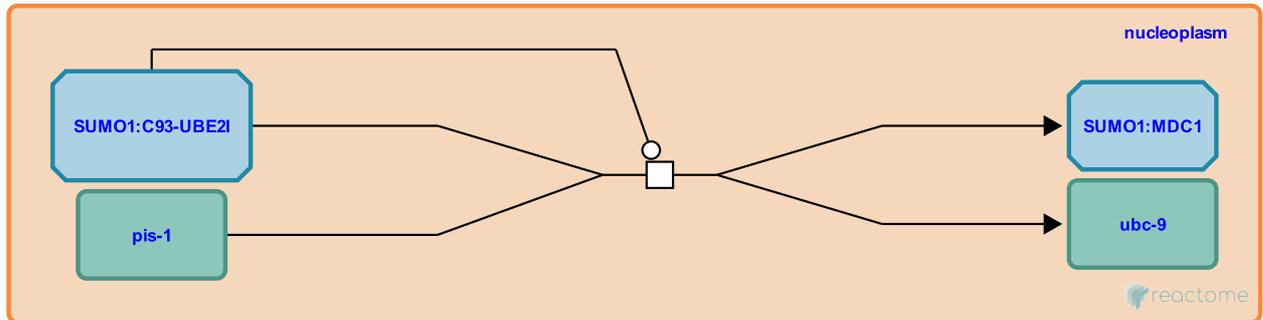
SUMOylation of MDC1 with SUMO1 ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-CEL-4570554

Type: transition

Compartments: nucleoplasm

Inferred from: SUMOylation of MDC1 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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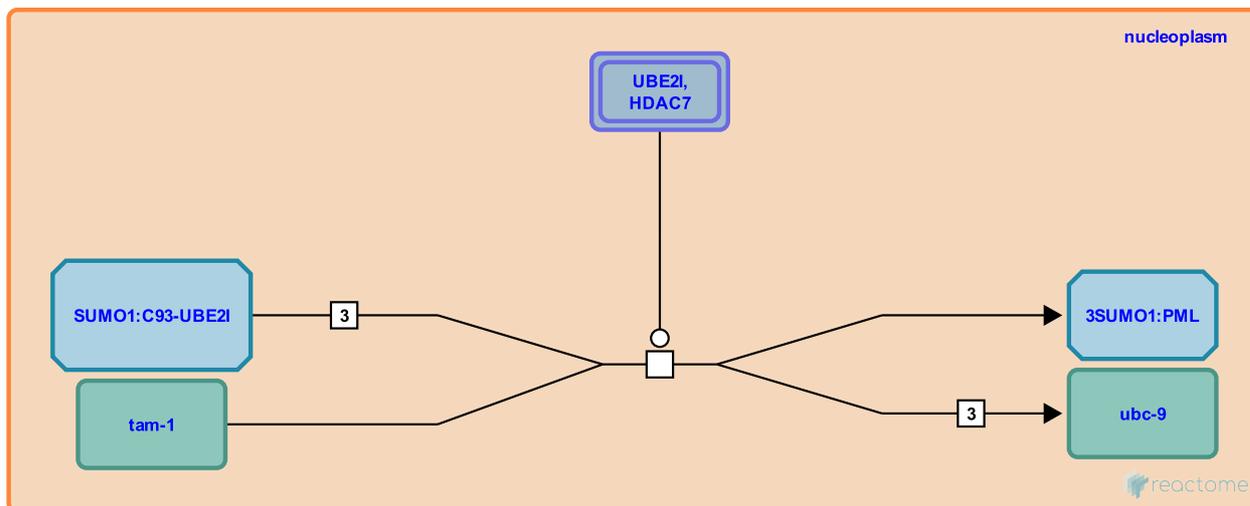
UBE2I, HDAC7 SUMOylate PML with SUMO1 ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-CEL-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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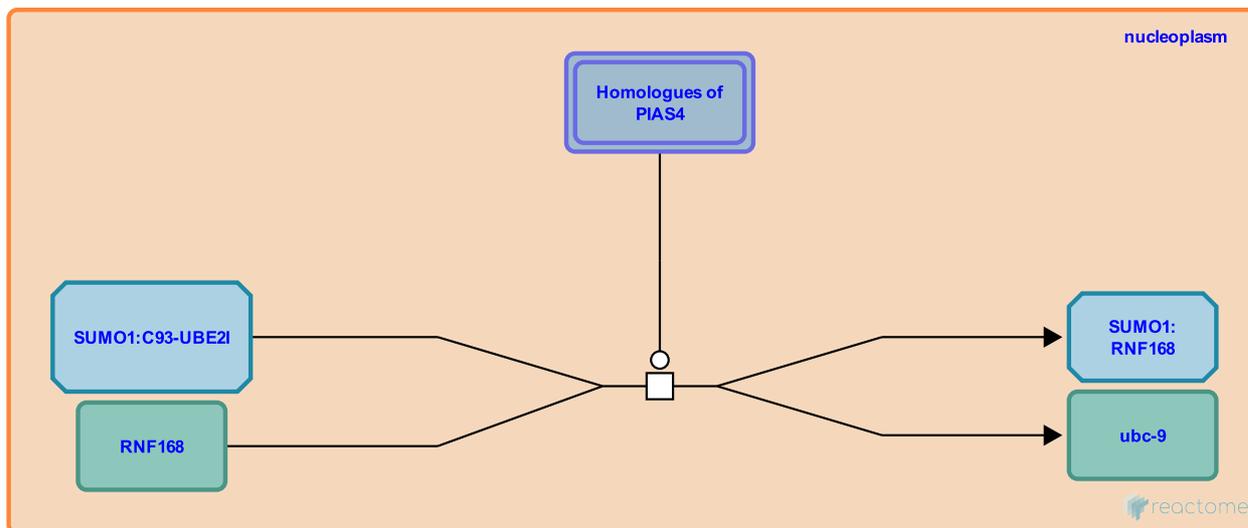# PIAS4 SUMOylates RNF168 with SUMO1 ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-CEL-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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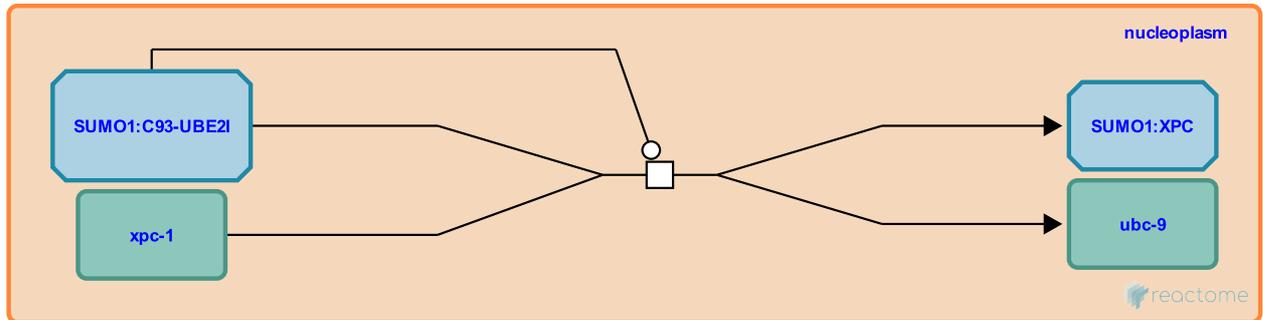
SUMOylation of XPC with SUMO1 ↗

Location: SUMOylation of DNA damage response and repair proteins

Stable identifier: R-CEL-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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