

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: 74

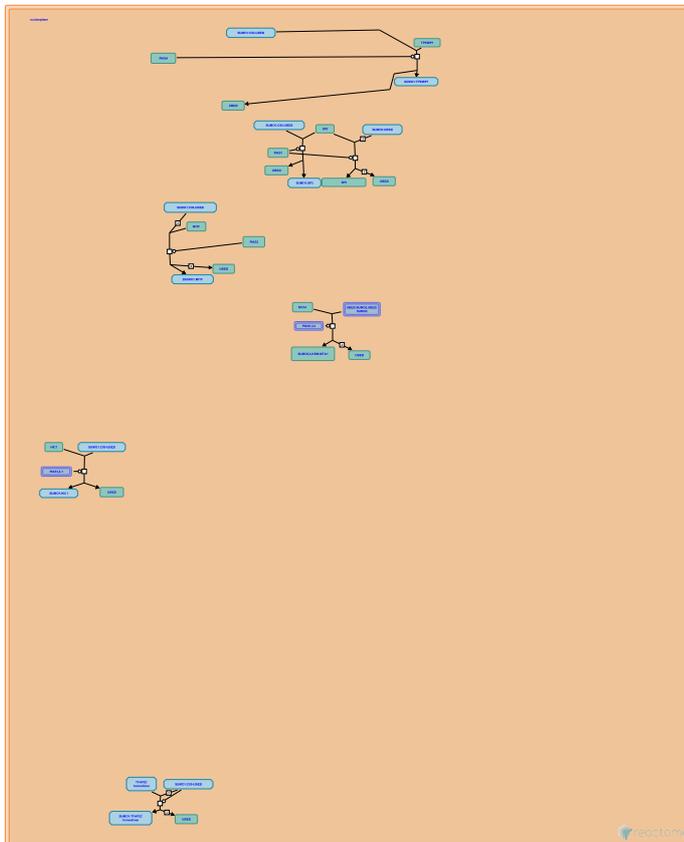
This document contains 1 pathway and 7 reactions ([see Table of Contents](#))

SUMOylation of transcription factors ↗

Stable identifier: R-SSC-3232118

Compartments: nucleoplasm

Inferred from: [SUMOylation of transcription factors \(Homo sapiens\)](#)



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>

PIAS3 SUMOylates MITF with SUMO1 ↗

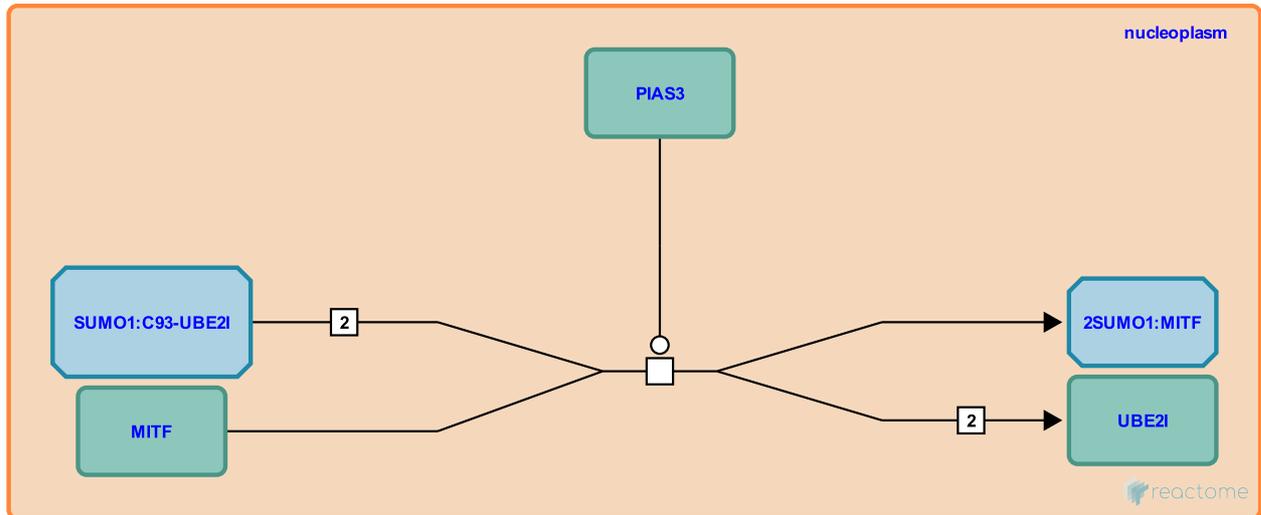
Location: [SUMOylation of transcription factors](#)

Stable identifier: R-SSC-3232162

Type: transition

Compartments: nucleoplasm

Inferred from: [PIAS3 SUMOylates MITF 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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PIAS1,3,4 SUMOylate MTA1 with SUMO2,3 ↗

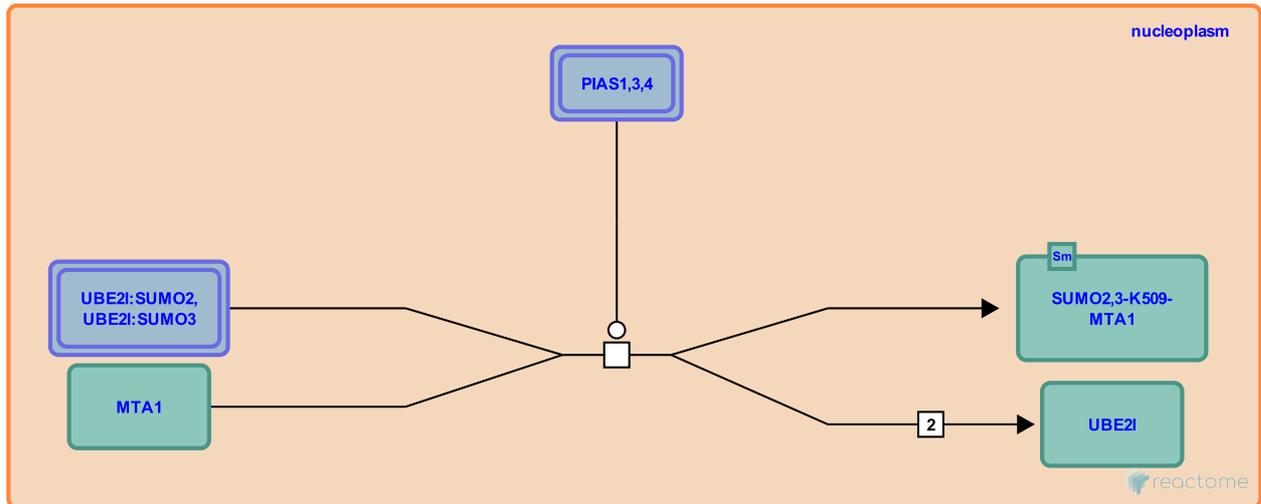
Location: SUMOylation of transcription factors

Stable identifier: R-SSC-3465545

Type: transition

Compartments: nucleoplasm

Inferred from: PIAS1,3,4 SUMOylate MTA1 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 SUMOylates SP3 with SUMO1 ↗

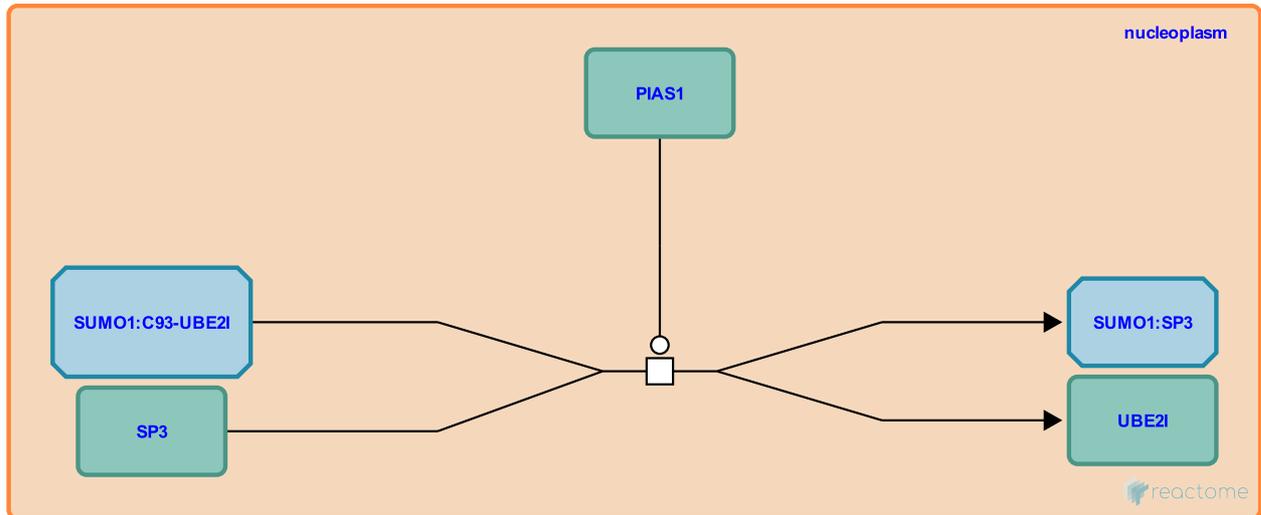
Location: [SUMOylation of transcription factors](#)

Stable identifier: R-SSC-3247493

Type: transition

Compartments: nucleoplasm

Inferred from: [PIAS1 SUMOylates SP3 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 SUMOylates SP3 with SUMO2 ↗

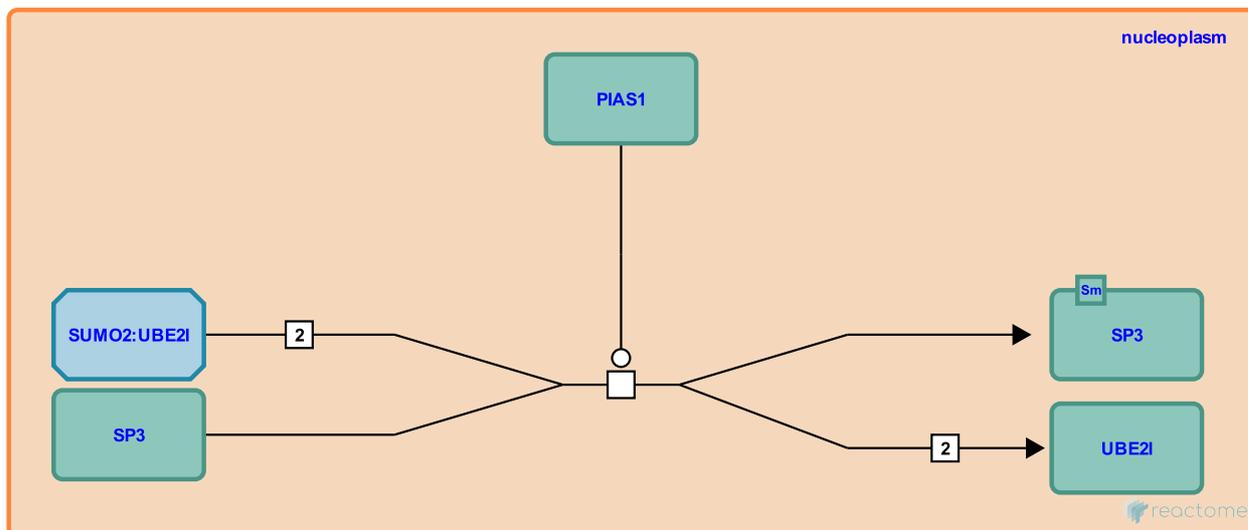
Location: [SUMOylation of transcription factors](#)

Stable identifier: R-SSC-6804468

Type: transition

Compartments: nucleoplasm

Inferred from: [PIAS1 SUMOylates SP3 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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PIAS4 SUMOylates TP53BP1 with SUMO1 [↗](#)

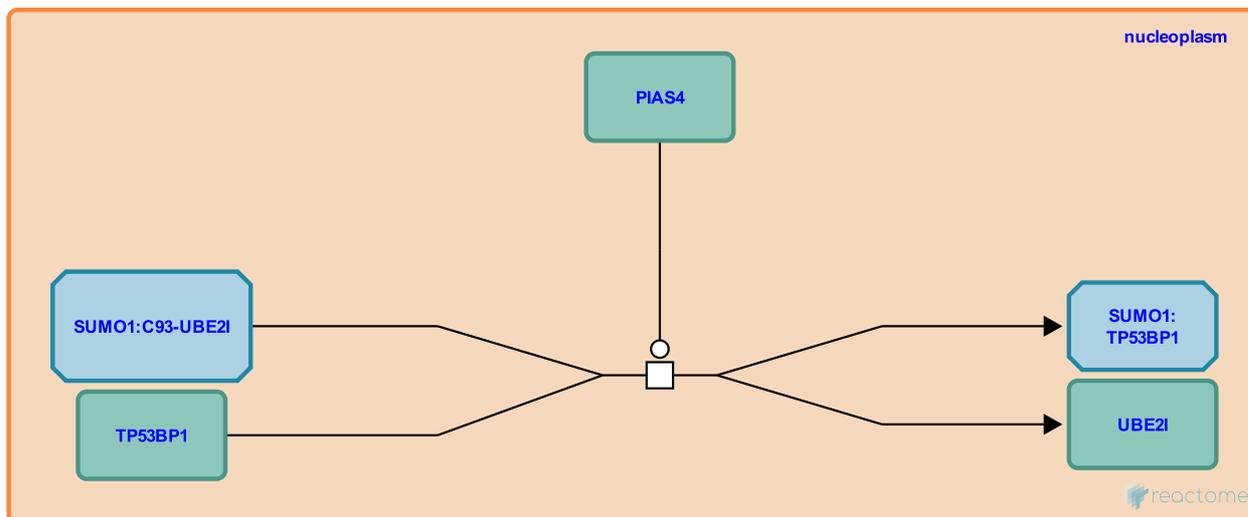
Location: [SUMOylation of transcription factors](#)

Stable identifier: R-SSC-2997723

Type: transition

Compartments: nucleoplasm

Inferred from: [PIAS4 SUMOylates TP53BP1 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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PIAS1,2-1 SUMOylate HIC1 with SUMO1 ↗

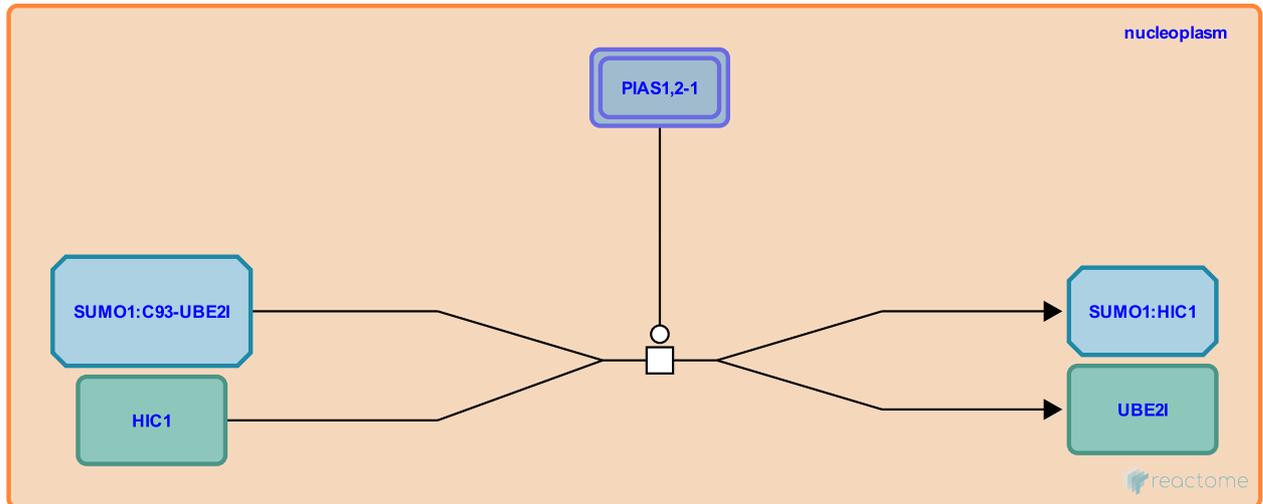
Location: SUMOylation of transcription factors

Stable identifier: R-SSC-4090281

Type: transition

Compartments: nucleoplasm

Inferred from: PIAS1,2-1 SUMOylate HIC1 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 TFAP2C with SUMO1 ↗

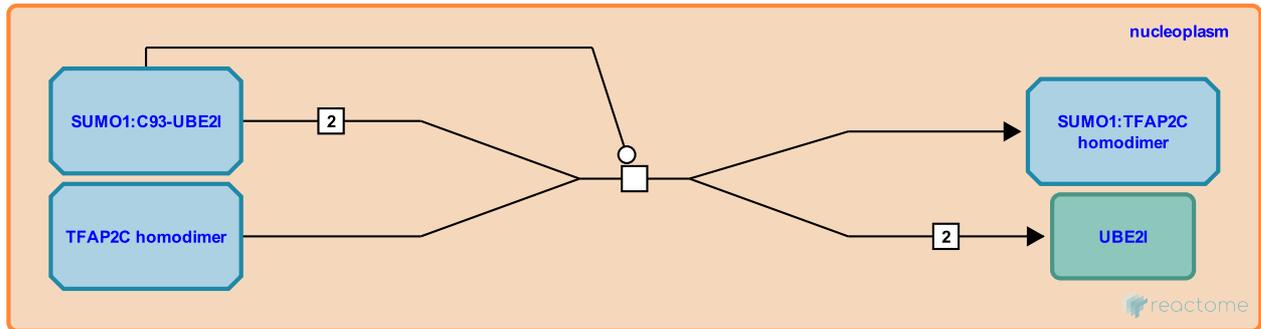
Location: [SUMOylation of transcription factors](#)

Stable identifier: R-SSC-3234094

Type: transition

Compartments: nucleoplasm

Inferred from: [SUMOylation of TFAP2C 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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