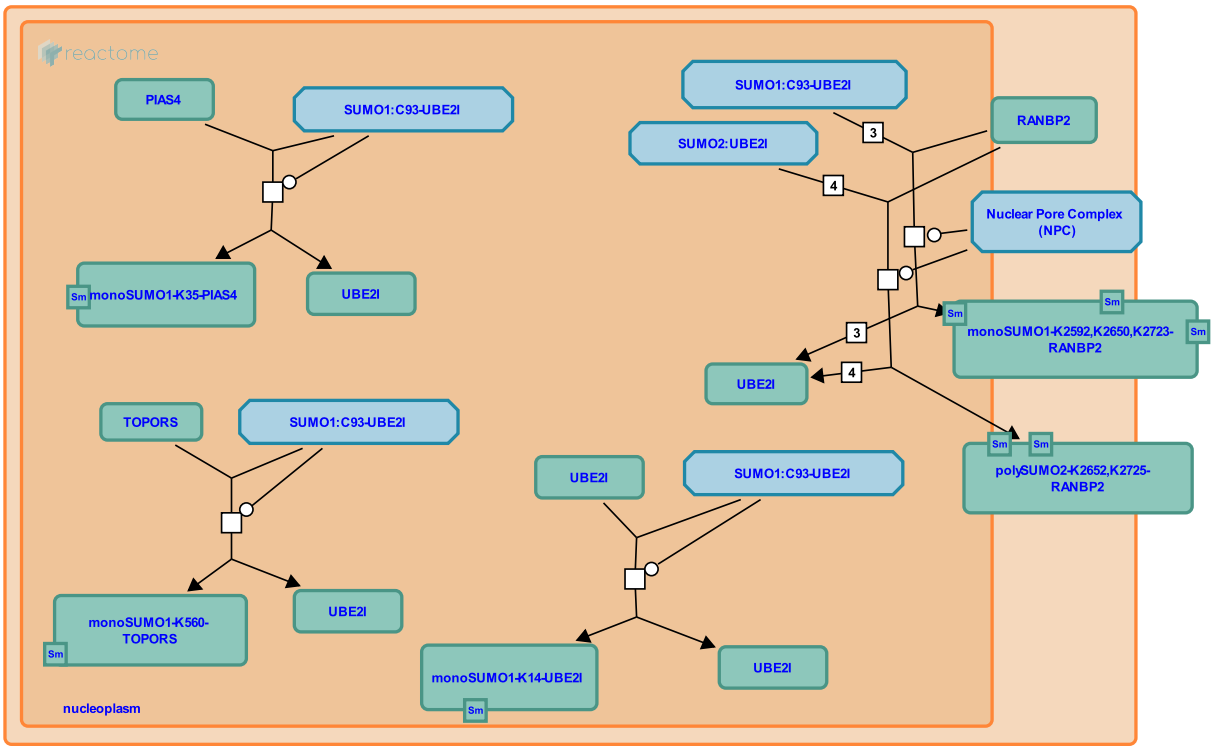
# SUMOylation of SUMOylation proteins

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This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the Reactome Textbook.

26/04/2024

# 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. ↗

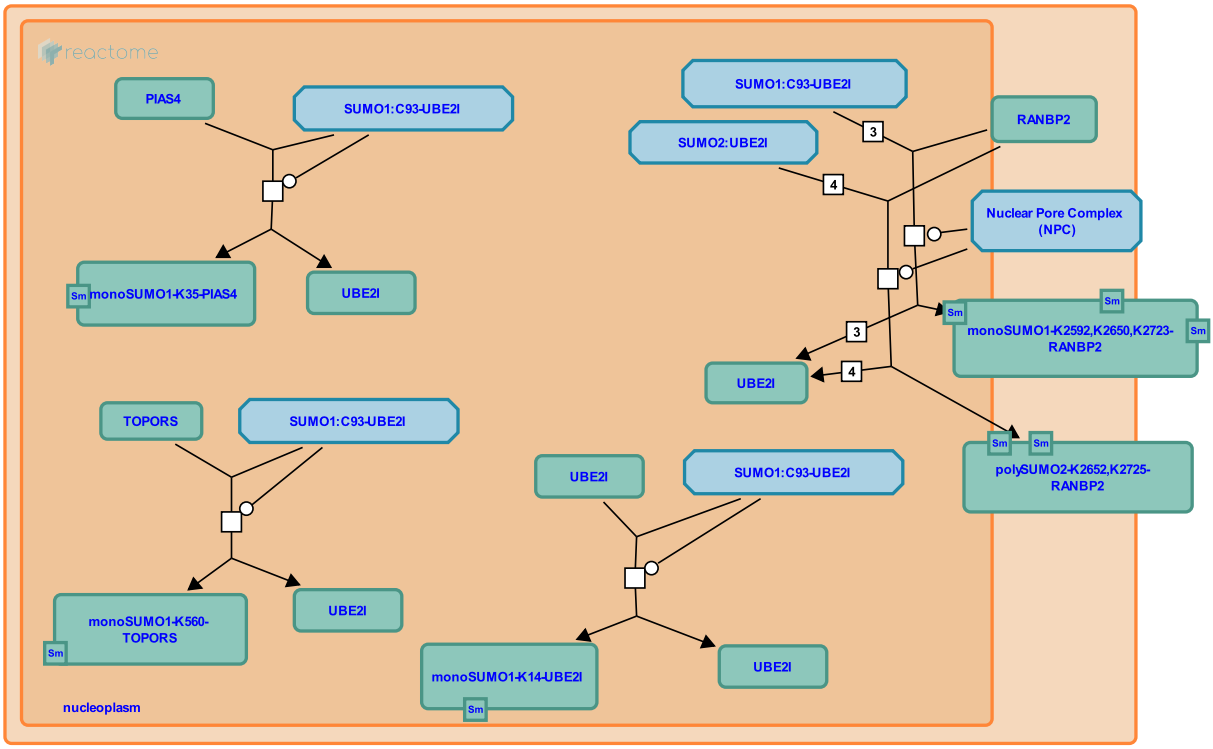
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

## SUMOylation of SUMOylation proteins ↗

**Stable identifier:** R-HSA-4085377

**Compartments:** nucleoplasm, nuclear envelope




SUMOylation processes themselves can be controlled by SUMOylation (reviewed in Wilkinson and Henley 2010). The SUMO E3 ligases PIAS4, RANBP2, and TOPORS are SUMOylated, as is the single SUMO E2 enzyme, UBE2I (UBC9). SUMOylation affects the subcellular location of PIAS4 and TOPORS and affects the activity of PIAS4 and UBE2I.

## Literature references


Henley, JM., Wilkinson, KA. (2010). Mechanisms, regulation and consequences of protein SUMOylation. *Biochem. J., 428*, 133-45. ↗


## Editions

| | | |
|---|---|---|
| 2013-08-03 | Authored, Edited | May, B. |
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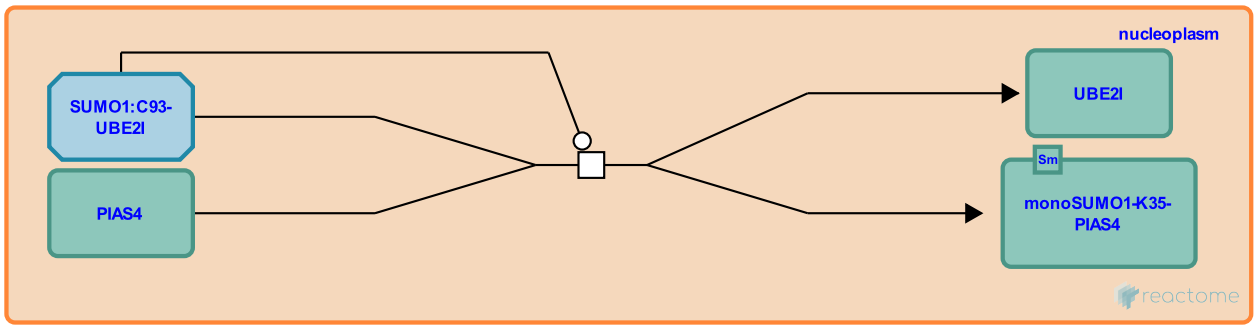
## SUMOylation of PIAS4 with SUMO1 ↗

**Location:** SUMOylation of SUMOylation proteins

**Stable identifier:** R-HSA-3968362

**Type:** transition

**Compartments:** nucleoplasm




PIAS4 is SUMOylated at lysine-35 with SUMO1 (Ihara et al. 2005). SUMOylation of PIAS4 at lysine-35 decreases its localization with PML. SUMOylated PIAS4 is able to increase SUMOylation and transcriptional activity of TCF4.

## Literature references

Kikuchi, A., Ihara, M., Yamamoto, H. (2005). SUMO-1 modification of PIASy, an E3 ligase, is necessary for PIASy-dependent activation of Tcf-4. *Mol. Cell. Biol., 25*, 3506-18. ↗

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| 2013-07-21 | Authored, Edited | May, B. |
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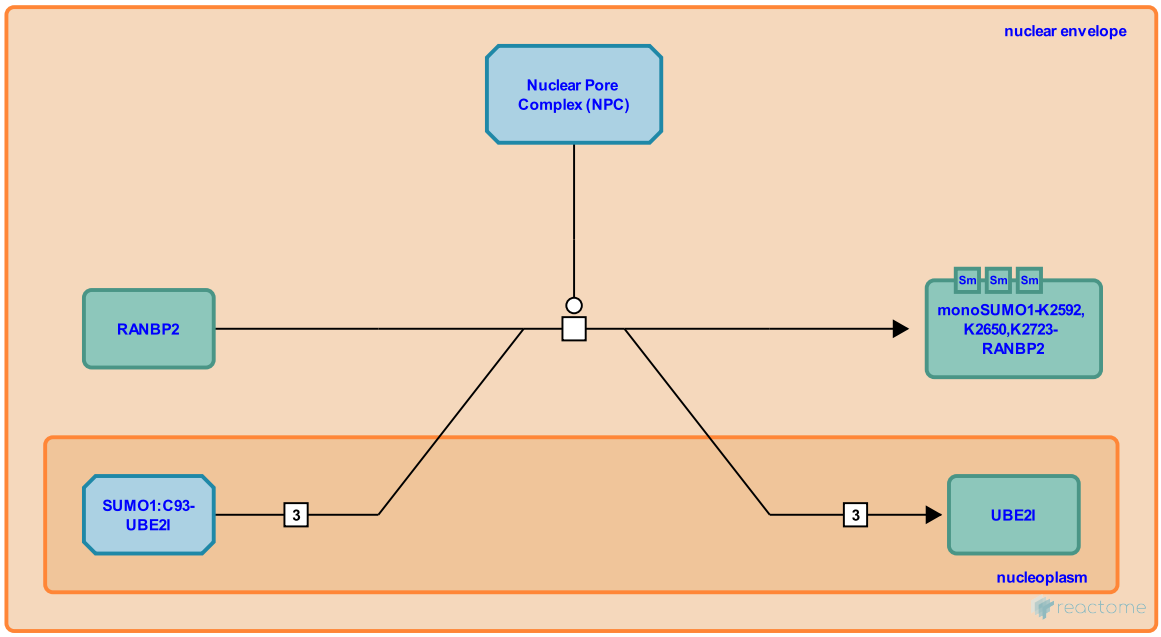
## RANBP2 SUMOylates RANBP2 with SUMO1 ↗

**Location:** SUMOylation of SUMOylation proteins

**Stable identifier:** R-HSA-4551649

**Type:** transition

**Compartments:** nuclear envelope, nucleoplasm




RANBP2 SUMOylates RANBP2 at lysine-2592, lysine-2650, and lysine-2723 with SUMO1 (Pichler et al. 2002, Pichler et al. 2004, Cooper et al. 2005). RANBP2 does not resemble HECT or RING type SUMO E3 ligases and instead uses hydrophobic interactions with UBE2I (UBC9) to catalyze SUMOylation.

## Literature references


Lam, TT., Tatham, MH., Hay, RT., Heath, JK., Jaffray, E., Cooper, HJ. et al. (2005). Fourier transform ion cyclotron resonance mass spectrometry for the analysis of small ubiquitin-like modifier (SUMO) modification: identification of lysines in RanBP2 and SUMO targeted for modification during the E3 autoSUMOylation reaction. *Anal. Chem., 77*, 6310-9. ↗

Dejean, A., Seeler, JS., Gast, A., Melchior, F., Pichler, A. (2002). The nucleoporin RanBP2 has SUMO1 E3 ligase activity. *Cell, 108*, 109-20. ↗

Sixma, TK., Melchior, F., Pichler, A., Saitoh, H., Knipscheer, P. (2004). The RanBP2 SUMO E3 ligase is neither HECT- nor RING-type. *Nat. Struct. Mol. Biol., 11*, 984-91. ↗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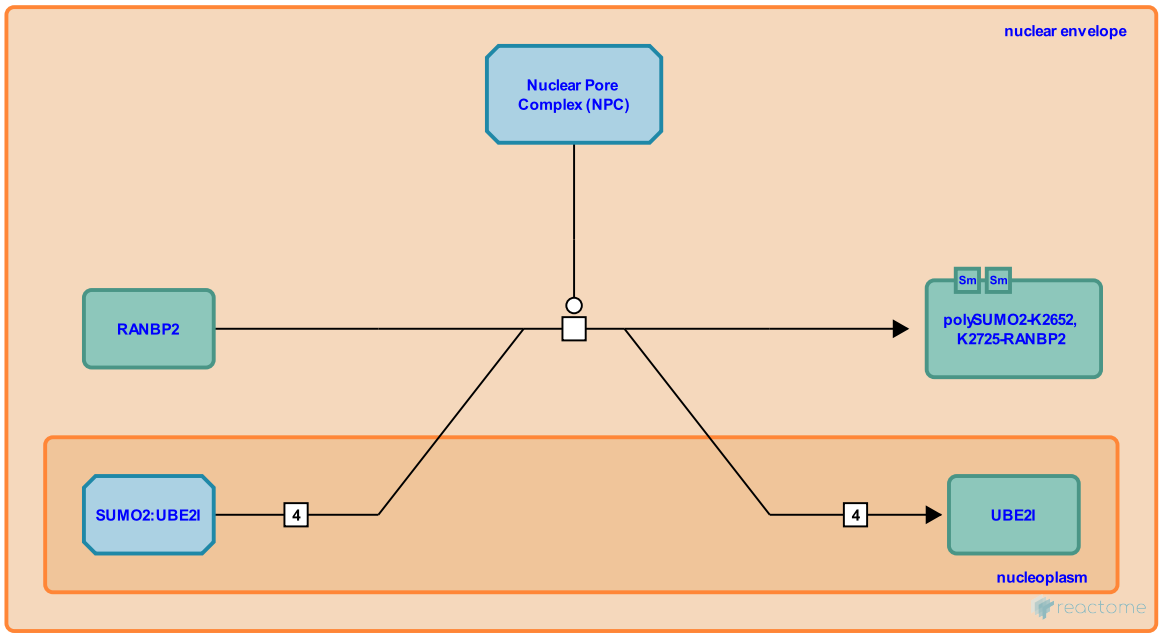
## RANBP2 SUMOylates RANBP2 with SUMO2 ↗

**Location:** SUMOylation of SUMOylation proteins

**Stable identifier:** R-HSA-4551679

**Type:** transition

**Compartments:** nuclear envelope, nucleoplasm




RANBP2 SUMOylates RANBP2 at lysine-2652 and lysine-2725 with SUMO2 (Cooper et al. 2005, Hendriks et al. 2014).

## Literature references


Lam, TT., Tatham, MH., Hay, RT., Heath, JK., Jaffray, E., Cooper, HJ. et al. (2005). Fourier transform ion cyclotron resonance mass spectrometry for the analysis of small ubiquitin-like modifier (SUMO) modification: identification of lysines in RanBP2 and SUMO targeted for modification during the E3 autoSUMOylation reaction. *Anal. Chem., 77*, 6310-9. ↗

Yang, B., Hendriks, IA., Verlaan-de Vries, M., Vertegaal, AC., D'Souza, RC., Mann, M. (2014). Uncovering global SUMOylation signaling networks in a site-specific manner. *Nat. Struct. Mol. Biol., 21*, 927-36. ↗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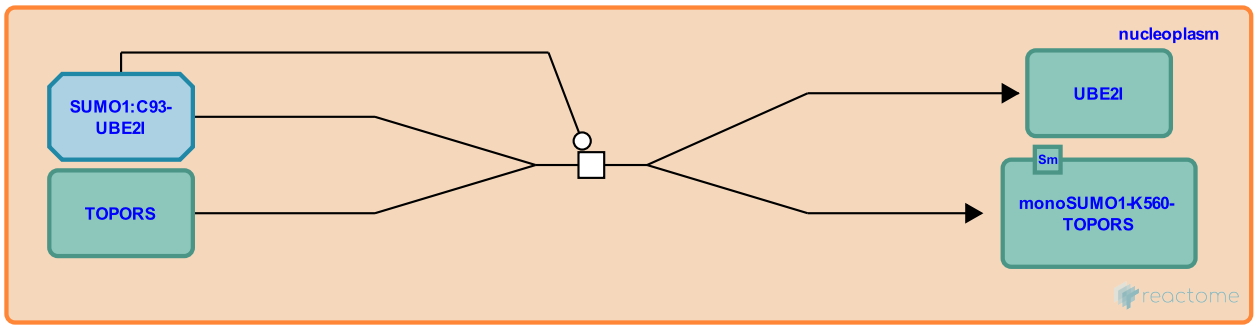
## SUMOylation of TOPORS with SUMO1 ↗

**Location:** SUMOylation of SUMOylation proteins

**Stable identifier:** R-HSA-4551683

**Type:** transition

**Compartments:** nucleoplasm




TOPORS is SUMOylated at lysine-560 with SUMO1 (Weger et al. 2003).

## Literature references

Engstler, M., Weger, S., Hammer, E. (2003). The DNA topoisomerase I binding protein topors as a novel cellular target for SUMO-1 modification: characterization of domains necessary for subcellular localization and sumolation. *Exp. Cell Res., 290*, 13-27. ↗

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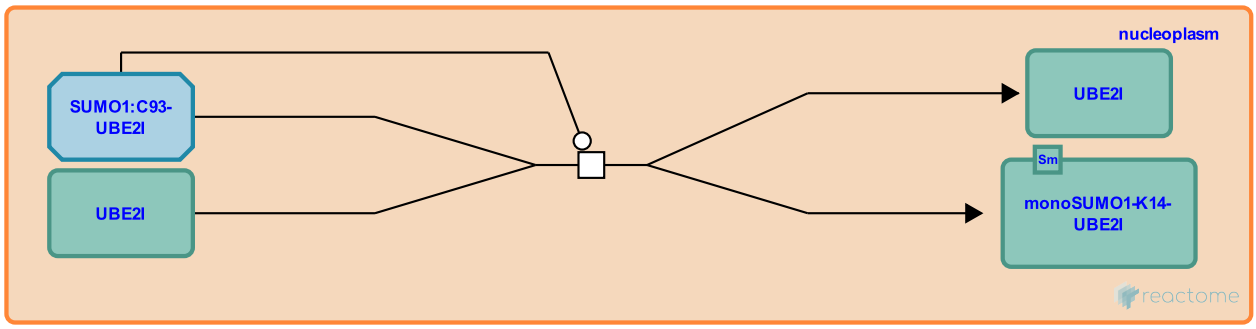
## SUMOylation of UBE2I with SUMO1 ↗

**Location:** SUMOylation of SUMOylation proteins

**Stable identifier:** R-HSA-4085350

**Type:** transition

**Compartments:** nucleoplasm




UBE2I (UBC9) is SUMOylated at lysine-14 with SUMO1 (Knipscheer et al. 2008). SUMOylation alters the target specificity of UBE2I, decreasing its SUMOylation activity towards RanGAP1 and increasing it towards SP100.

## Literature references

Sixma, TK., Fish, A., Olsen, JV., Klug, H., Pichler, A., Flotho, A. et al. (2008). Ubc9 sumoylation regulates SUMO target discrimination. *Mol. Cell, 31*, 371-82. ↗

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