

# **RANBP2 SUMOylates RANBP2 with SUM01**

May, B., Niskanen, E.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of <u>Creative Commons Attribution 4.0 International (CC BY 4.0)</u> <u>License</u>. For more information see our <u>license</u>.

18/05/2024

# 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. 7
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. A
- 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. *オ*

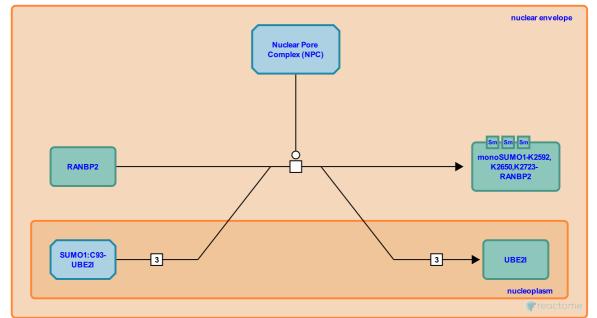
This document contains 1 reaction (see Table of Contents)

## RANBP2 SUMOylates RANBP2 with SUMO1 7

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 HECTnor RING-type. *Nat. Struct. Mol. Biol.*, 11, 984-91. 7

#### Editions

2013-09-13	Authored, Edited	May, B.
2018-05-09	Reviewed	Niskanen, E.
2018-08-08	Reviewed	Niskanen, E.