

SUMOylation of NOP58 with SUMO1

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https://reactome.org

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 data-base: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968.

Reactome database release: 88

This document contains 1 reaction (see Table of Contents)

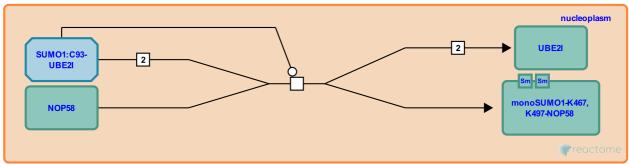
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SUMOylation of NOP58 with SUMO1 >

Stable identifier: R-HSA-4570467

Type: transition

Compartments: nucleoplasm



NOP58 (NOP5) is SUMOylated at lysine-467 and lysine-497 with SUMO1 (Matafora et al. 2009, Westman et al. 2010, Westman and Lamond 2011, Impens et al. 2014). SUMOylation is required for binding of snoRNAs by NOP58.

Literature references

Blasi, F., Mori, S., Bachi, A., Matafora, V., D'Amato, A. (2009). Proteomics analysis of nucleolar SUMO-1 target proteins upon proteasome inhibition. *Mol. Cell Proteomics*, 8, 2243-55.

Matunis, MJ., Cronshaw, JM., Chait, BT., Zhang, W., Krutchinsky, AN. (2002). Proteomic analysis of the mammalian nuclear pore complex. *J Cell Biol*, 158, 915-27. *¬*

Lam, YW., Lamond, AI., Bertrand, E., Westman, BJ., Verheggen, C., Hutten, S. (2010). A proteomic screen for nucleolar SUMO targets shows SUMOylation modulates the function of Nop5/Nop58. *Mol. Cell*, 39, 618-31.

Impens, F., Cossart, P., Radoshevich, L., Ribet, D. (2014). Mapping of SUMO sites and analysis of SUMOylation changes induced by external stimuli. *Proc. Natl. Acad. Sci. U.S.A.*, 111, 12432-7.

Lamond, AI., Westman, BJ. (2011). A role for SUMOylation in snoRNP biogenesis revealed by quantitative proteomics. *Nucleus*, 2, 30-7. *¬*

Editions

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