RANBP2 SUMOylates MDM2 with SUMO1

May, B., Niskanen, E.

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

08/05/2024

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. ↗

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. ↗

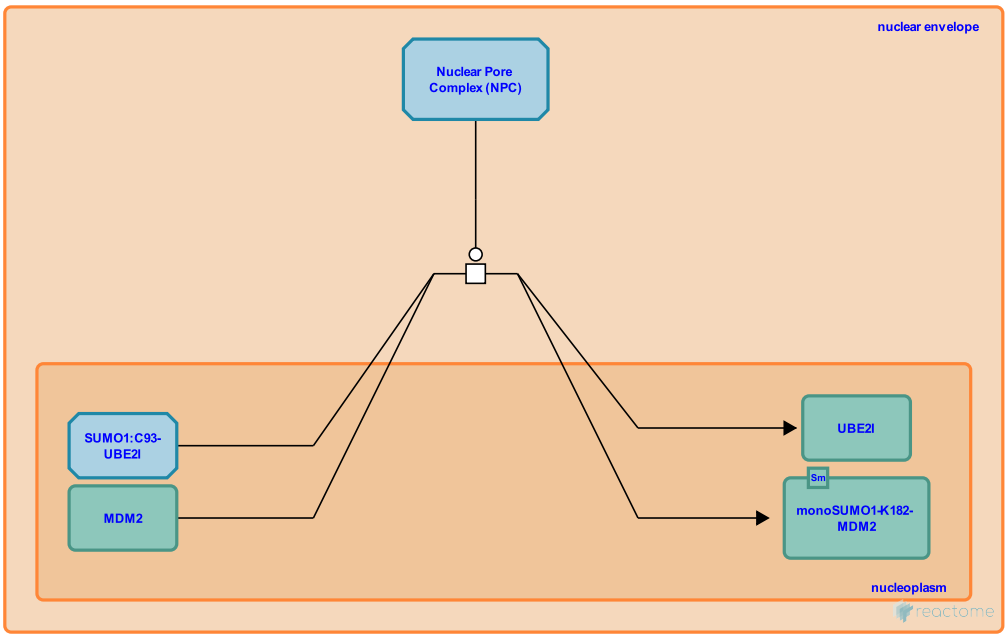
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

RANBP2 SUMOylates MDM2 with SUMO1 ↗

Stable identifier: R-HSA-5228523

Type: transition

Compartments: nucleoplasm, nuclear envelope



RANBP2 of the nuclear pore complex SUMOylates MDM2 with SUMO1 at lysine-182 (Mayauchi et al. 2002). An unSUMOylatable mutant of MDM2 accumulates in the cytosol so SUMOylation may be part of the process of nuclear import of MDM2 (Miyauchi et al. 2002).

Literature references

Honda, R., Miyauchi, Y., Nishida, T., Yogosawa, S., Yasuda, H. (2002). Sumoylation of Mdm2 by protein inhibitor of activated STAT (PIAS) and RanBP2 enzymes. *J. Biol. Chem., 277*, 50131-6. ↗

Editions

2013-01-24	Authored, Edited	May, B.
2018-05-09	Reviewed	Niskanen, E.
2018-08-08	Reviewed	Niskanen, E.