

CBX4 (Pc2) SUMOylates HNRNPK with SUMO2

Bachi, A., Filosa, G., May, B.

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 [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://reactome.org/licenses/).

16/05/2024

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. [↗](#)

Reactome database release: 88

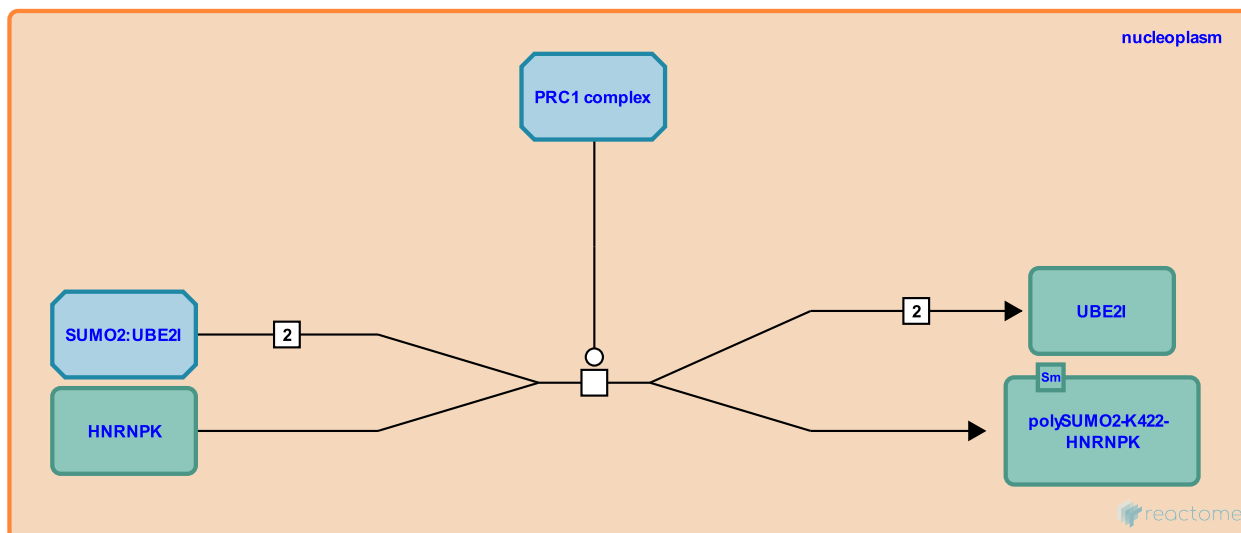
This document contains 1 reaction ([see Table of Contents](#))

CBX4 (Pc2) SUMOylates HNRNPK with SUMO2 [↗](#)

Stable identifier: R-HSA-4570499

Type: transition

Compartments: nucleoplasm



CBX4 (Pc2) SUMOylates HNRNPK at lysine-422 with SUMO2 (Li et al. 2004, Lee et al. 2012, Pelisch et al. 2012, Hendriks et al. 2014, Impens et al. 2014, Tammsalu et al. 2014). (Two molecules of SUMO2 are shown in the reaction in order to represent the oligomeric chains of SUMO2 that are attached to a target protein.) PIAS3 also SUMOylates HNRNPK predominantly with SUMO1 (Lee et al. 2012). HNRNPK is SUMOylated in response to DNA damage and SUMOylation is regulated by HIPK2 and CBX4. SUMOylation of HNRNPK is required for coactivation of TP53 (p53) activated transcription. SUMOylation increases the stability of HNRNPK, the nonSUMOylated form of which is normally ubiquitinated by HDM2 (Lee et al. 2012).

Literature references

- Srebrow, A., Pelisch, F., Risso, G., Muñoz, MJ., Pozzi, B. (2012). DNA damage-induced heterogeneous nuclear ribonucleoprotein K sumoylation regulates p53 transcriptional activation. *J. Biol. Chem.*, 287, 30789-99. [↗](#)
- Tatham, MH., Hay, RT., Tammsalu, T., Ibrahim, AF., Jaffray, EG., Matic, I. (2014). Proteome-wide identification of SUMO2 modification sites. *Sci Signal*, 7, rs2. [↗](#)
- Chao, CC., Li, T., Chock, PB., Shen, RF., Evdokimov, E., Tekle, E. et al. (2004). Sumoylation of heterogeneous nuclear ribonucleoproteins, zinc finger proteins, and nuclear pore complex proteins: a proteomic analysis. *Proc. Natl. Acad. Sci. U.S.A.*, 101, 8551-6. [↗](#)
- 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. [↗](#)
- Yoo, HM., Lee, MH., Kang, SH., Lee, SW., Ka, SH., Jeon, YJ. et al. (2012). SUMOylation of hnRNP-K is required for p53-mediated cell-cycle arrest in response to DNA damage. *EMBO J.*, 31, 4441-52. [↗](#)

Editions

2013-09-19	Authored, Edited	May, B.
2015-10-17	Reviewed	Filosa, G., Bachi, A.