PIAS4 SUMOylates HERC2 with SUMO1 at DNA DSBs

Borowiec, JA., May, B., Orlic-Milacic, M.

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

17/05/2024

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. ↗

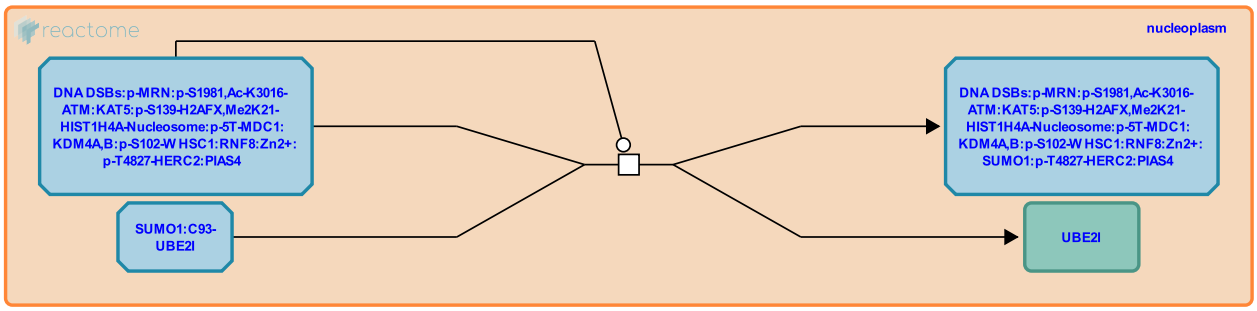
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

PIAS4 SUMOylates HERC2 with SUMO1 at DNA DSBs ↗

Stable identifier: R-HSA-5682607

Type: transition

Compartments: nucleoplasm



PIAS4 SUMOylates HERC2 at an unknown lysine residue with SUMO1. ATM activity is needed for PIAS4-mediated HERC2 SUMOylation and it is therefore plausible that the ATM-mediated phosphorylation of HERC2 precedes HERC2 SUMOylation. Once SUMOylated, the ZZ domain of HERC2 interacts with the attached SUMO1 group, probably leading to a conformational change that allows binding of phosphorylated HERC2 to RNF8 (Bekker-Jensen et al. 2010, Danielsen et al. 2012).

Literature references

Lukas, J., Gromova, I., Rendtlew Danielsen, J., Bartek, J., Nerstedt, A., Lukas, C. et al. (2010). HERC2 coordinates ubiquitin-dependent assembly of DNA repair factors on damaged chromosomes. *Nat. Cell Biol., 12*, 80-6; sup pp 1-12. ↗

Wikström, M., Nilsson, J., Povlsen, LK., Danielsen, JR., Streicher, W., Bekker-Jensen, S. et al. (2012). DNA damage-inducible SUMOylation of HERC2 promotes RNF8 binding via a novel SUMO-binding Zinc finger. *J. Cell Biol., 197*, 179-87. ↗

Editions

2013-09-13	Authored, Edited	May, B.
2015-03-09	Revised	Orlic-Milacic, M.
2015-05-12	Edited	Orlic-Milacic, M.
2015-06-12	Reviewed	Borowiec, JA.