PIAS4 SUMOylates HERC2 with SUMO1 at DNA DSBs

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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

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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. ↗

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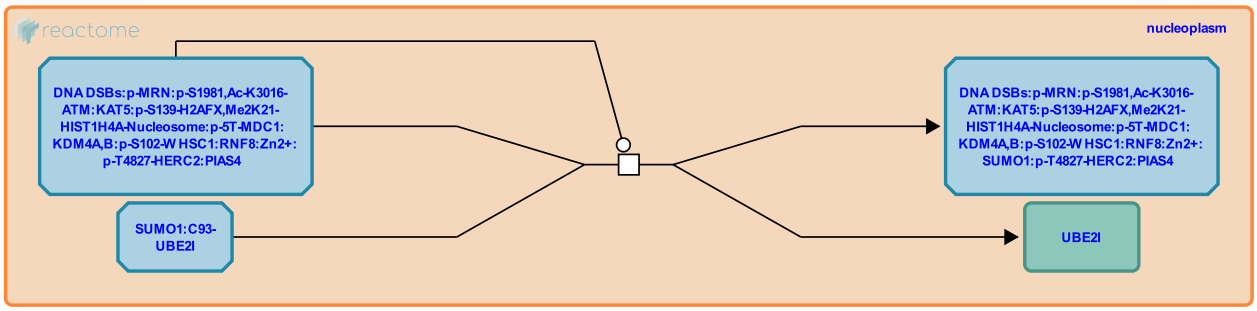
Stable identifier: R-HSA-5682607

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

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Editions

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