UBE2I (UBC9), PIAS1 SUMOylate FOXL2 with SUMO1

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06/05/2024

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

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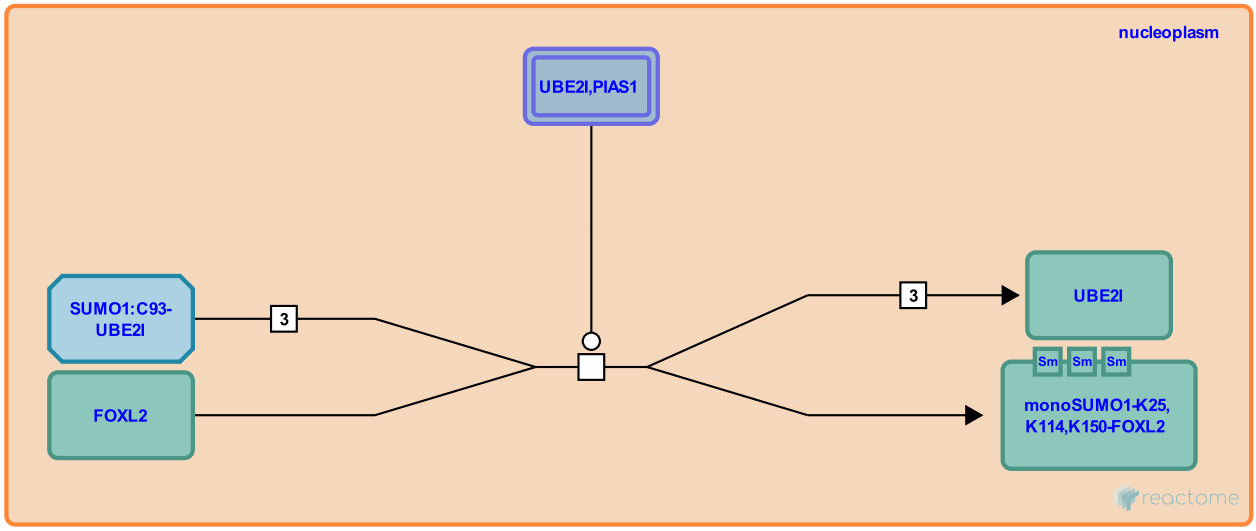
Stable identifier: R-HSA-3968414

Type: transition

Compartments: nucleoplasm



UBC9 and PIAS1 SUMOylate FOXL2 with SUMO1 (Kuo et al. 2009, Marongiu et al 2010, Georges et al. 2011). This modification changes its cellular localization, stability and transcriptional activity (Marongiu et al, 2010). SUMOylation localizes FOXL2 to PML bodies in the nucleus. SUMOylation is required for repression of transcription by FOXL2 at the StAR promoter and reduces transactivation by FOXL2 at the PER2 promoter. Hypophosphorylation of serine-33 correlates with SUMOylation and stablization of FOXL2, leading to enhanced transcriptional activation of TNF-R1, FAS, caspase 8, p21, and aromatase (Kim et al. 2014).

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Editions

2013-07-21	Authored, Edited	May, B.
2017-01-12	Edited, Reviewed	Bae, J.
2017-01-12	Edited, Reviewed	Crisponi, L.