SUMOylation of chromatin organization proteins

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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


Reactome database release: 72

This document contains 1 pathway and 15 reactions (see Table of Contents)
SUMOylation of proteins involved in chromatin organization regulates gene expression in several ways: direct influence on catalytic activity of enzymes that modify chromatin, recruitment of proteins that form repressive (e.g. PRC1) or activating complexes on chromatin, recruitment of proteins to larger bodies (e.g. PML bodies) in the nucleus (reviewed in Cubenas-Potts and Matunis 2013).

**Literature references**


**Editions**

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PIAS1 SUMOylates L3MBTL2 with SUMO2

Location: SUMOylation of chromatin organization proteins

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