SUMOylation of transcription factors


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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: 79

This document contains 1 pathway and 11 reactions (see Table of Contents)
Proteins classified as transcription factors constitute a disproportionate number of SUMOylation targets. In most cases SUMOylation inhibits transcriptional activation, however in some cases such as TP53 (p53) SUMOylation can enhance activation. Inhibition of transcription by SUMOylation may be due to interference with DNA binding, re-localization to inactive nuclear bodies, or recruitment of repressive cofactors such as histone deacetylases (reviewed in Girdwood et al. 2004, Gill 2005).

**Literature references**


**Editions**

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PIAS3 SUMOylates MITF with SUMO1

Location: SUMOylation of transcription factors

Stable identifier: R-HSA-3232162