PIAS3 SUMOylates MITF with SUMO1

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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: 83

This document contains 1 reaction (see Table of Contents)

https://reactome.org
PIAS3 SUMOylates MITF with SUMO1

**Stable identifier:** R-HSA-3232162

**Type:** transition

**Compartments:** nucleoplasm

PIAS3 SUMOylates MITF at lysine-289 and lysine-423 (lysine-182 and lysine-316 of the M2 isoform, Miller et al. 2005). SUMOylation reduces transcriptional activation by MITF at promoters containing multiple binding sites for MITF.

**Literature references**


**Editions**

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