

# SUMOylation of Histone H4 with SUMO3

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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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Reactome database release: 88

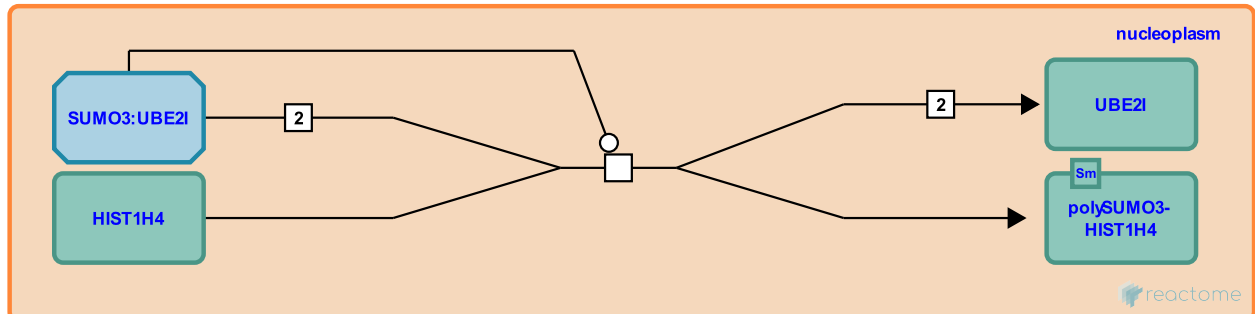
This document contains 1 reaction ([see Table of Contents](#))

## SUMOylation of Histone H4 with SUMO3 [↗](#)

**Stable identifier:** R-HSA-4570485

**Type:** transition

**Compartments:** nucleoplasm



Histone H4 (HIST1H4) is SUMOylated at an unknown residue with SUMO3 (Shiio and Eisenman 2003). SUMOylation of histone H4 is associated with repression of transcription.

### Literature references

Eisenman, RN., Shiio, Y. (2003). Histone sumoylation is associated with transcriptional repression. *Proc. Natl. Acad. Sci. U.S.A.*, 100, 13225-30. [↗](#)

### Editions

2013-09-19	Authored, Edited	May, B.
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