

# SUMOylation of TFAP2B with SUMO1

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19/05/2024

## 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

- Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*, 18, 142. [↗](#)
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
- Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res*, 46, D649-D655. [↗](#)
- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, 14, e1005968. [↗](#)

Reactome database release: 88

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

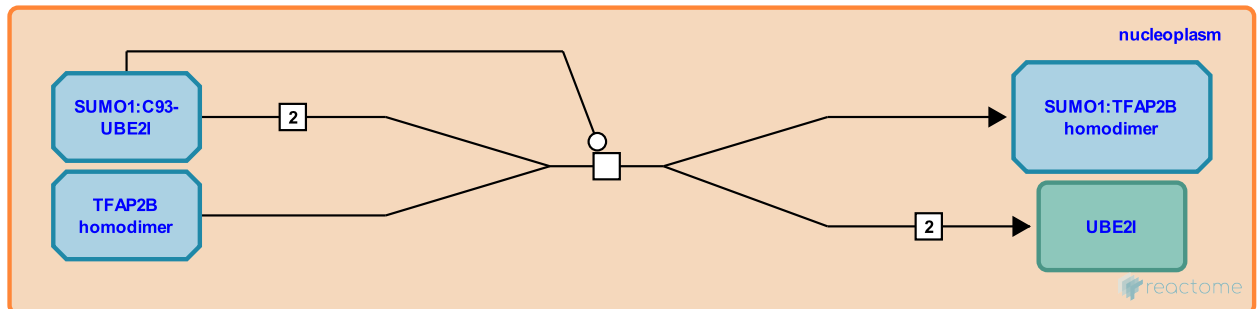
## SUMOylation of TFAP2B with SUMO1 [↗](#)

**Stable identifier:** R-HSA-3234084

**Type:** transition

**Compartments:** nucleoplasm

**Inferred from:** [SUMOylation of TFAP2C with SUMO1 \(Homo sapiens\)](#)



UBE2I (UBC9) interacts with the C terminal region of TFAP2B (Eloranta and Hurst 2002). As inferred from TFAP2C, SUMOylation of TFAP2B occurs at lysine in the VKYE motif and, therefore, UBC9 is assumed to catalyze the ligation of SUMO1 to TFAP2B.

### Literature references

Eloranta, JJ., Hurst, HC. (2002). Transcription factor AP-2 interacts with the SUMO-conjugating enzyme UBC9 and is sumolated in vivo. *J. Biol. Chem.*, 277, 30798-804. [↗](#)

### Editions

|            |                  |                            |
|------------|------------------|----------------------------|
| 2013-03-27 | Authored, Edited | May, B.                    |
| 2016-03-14 | Edited           | Orlic-Milacic, M.          |
| 2016-05-04 | Reviewed         | Dawid, IB., Zarelli, VE.   |
| 2016-05-17 | Reviewed         | Weigel, RJ., Bogachek, MV. |