

CDKN2A (p14-ARF) SUMOylates WRN 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

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- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
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- 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: 73

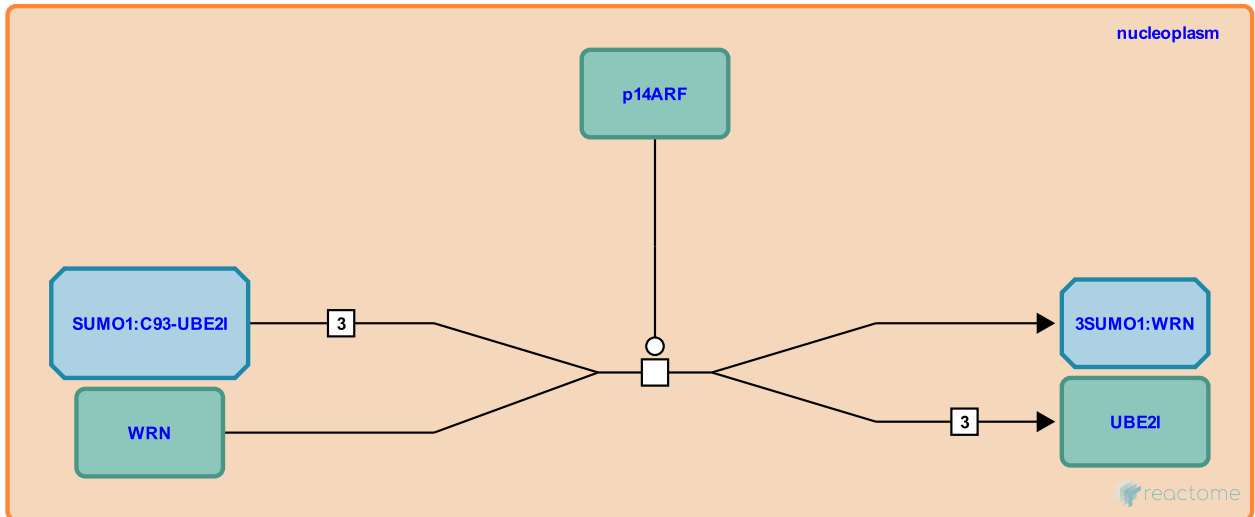
This document contains 1 reaction ([see Table of Contents](#))

CDKN2A (p14-ARF) SUMOylates WRN with SUMO1 [↗](#)

Stable identifier: R-HSA-4568846

Type: transition

Compartments: nucleoplasm



CDKN2A (p14-ARF) SUMOylates WRN at lysine-356, lysine-496, and lysine-898 with SUMO1 (Woods et al. 2004). SUMOylation of WRN causes it to be released from the nucleolus.

Literature references

Woods, YL., Xirodimas, DP., Prescott, AR., Sparks, A., Lane, DP., Saville, MK. (2004). p14 Arf promotes small ubiquitin-like modifier conjugation of Werners helicase. *J. Biol. Chem.*, 279, 50157-66. [↗](#)

Editions

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