USP1:WDR48 deubiquitinates monoUb:K164-PCNA

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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

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. ↗

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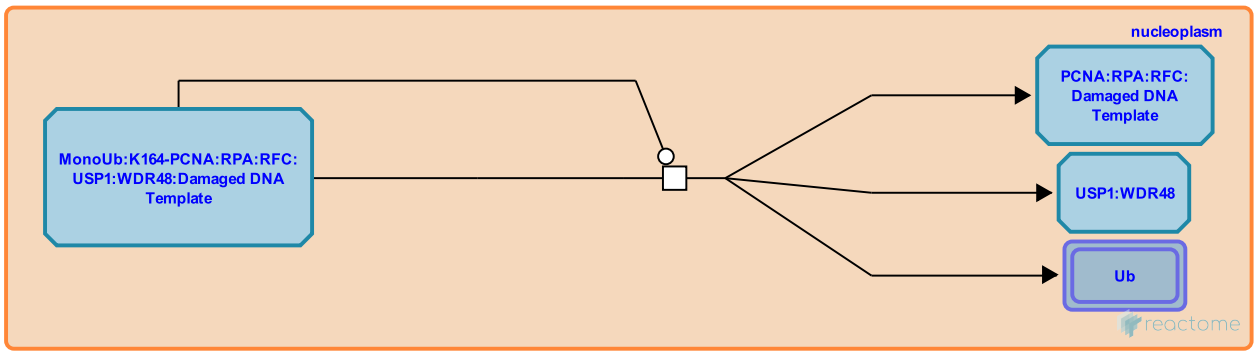
Stable identifier: R-HSA-5655466

Type: transition

Compartments: nucleoplasm



Deubiquitinating enzyme USP1, bound to its accessory protein WDR48 (UAF1), deubiquitinates PCNA (MonoUb:K164-PCNA), thus preventing excessive activation of DNA translesion synthesis (TLS) (Huang et al. 2006).

Literature references

Huang, TT., Nijman, SM., Mirchandani, KD., Galardy, PJ., Cohn, MA., Haas, W. et al. (2006). Regulation of monoubiquitinated PCNA by DUB autocleavage. *Nat. Cell Biol.*, *8*, 339-47. ↗

Editions

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