USP10 deubiquitinates

monoUb:K164,ISG:K164,ISG:K168-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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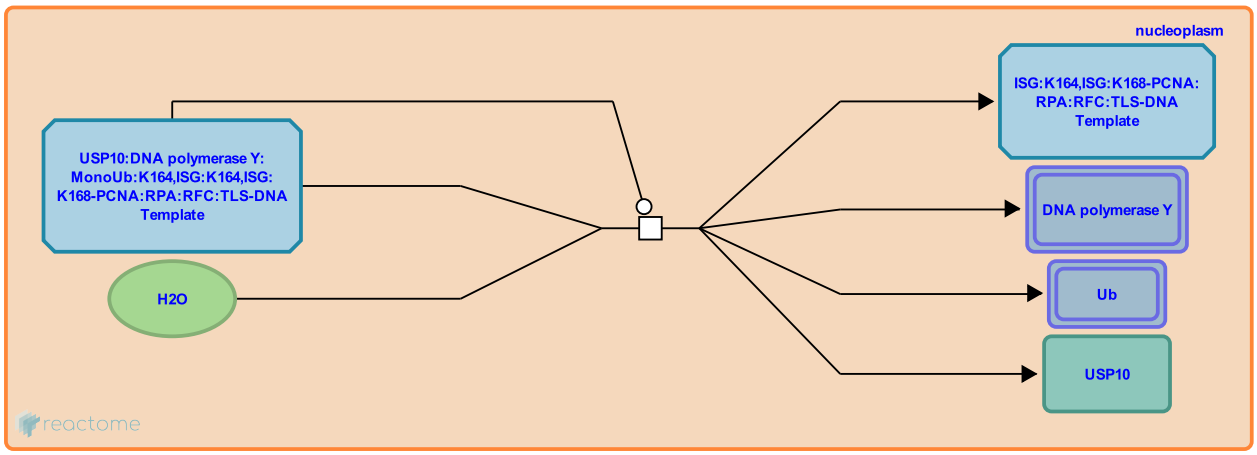
Stable identifier: R-HSA-5653770

Type: transition

Compartments: nucleoplasm



USP10 acts as a ubiquitin protease to remove ubiquitin from lysine K164 residue of doubly ISGylated PCNA. Deubiquitination of PCNA by USP10 causes dissociation of Y family DNA damage bypass polymerases, thus ending translesion DNA synthesis (TLS) and limiting TLS-induced mutagenesis (Park et al. 2014).

Literature references

Park, JM., Yang, SW., Yu, KR., Ka, SH., Lee, SW., Seol, JH. et al. (2014). Modification of PCNA by ISG15 plays a crucial role in termination of error-prone translesion DNA synthesis. *Mol. Cell, 54*, 626-38.

Editions

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