TP53BP1 associates with H4K20Me2 at DNA DSBs

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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. ↗

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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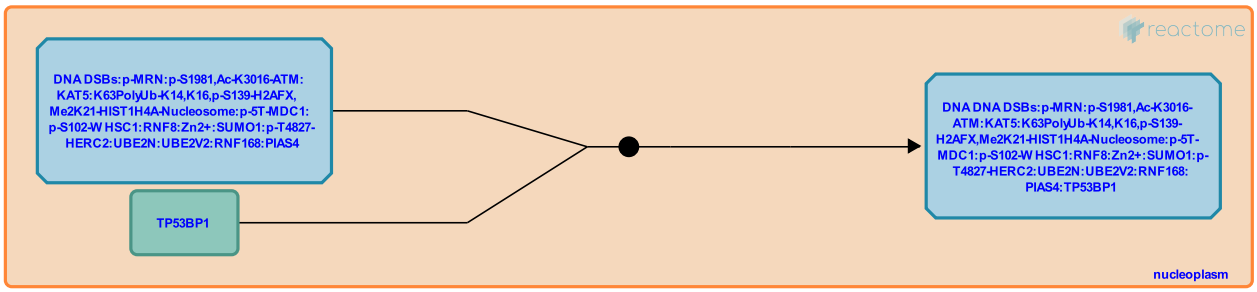
Stable identifier: R-HSA-5693566

Type: binding

Compartments: nucleoplasm



RNF8- and RNF168-mediated removal of KDM4A and KDM4B from H4K20Me2 (Me2-K21-HIST1H4A) enables TP53BP1 (53BP1) recruitment to WHSC1-methylated histone H4K20Me2 at DNA double-strand breaks (DSBs) (Pei et al. 2011, Mallette et al. 2012)

Literature references

Sixma, TK., Cui, G., Mer, G., Richard, S., Young, LC., Mallette, FA. et al. (2012). RNF8- and RNF168-dependent degradation of KDM4A/JMJD2A triggers 53BP1 recruitment to DNA damage sites. *EMBO J., 31*, 1865-78. ↗

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Editions

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