

UHRF1 binds chromatin with hemimethylated cytosine

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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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Reactome database release: 88

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

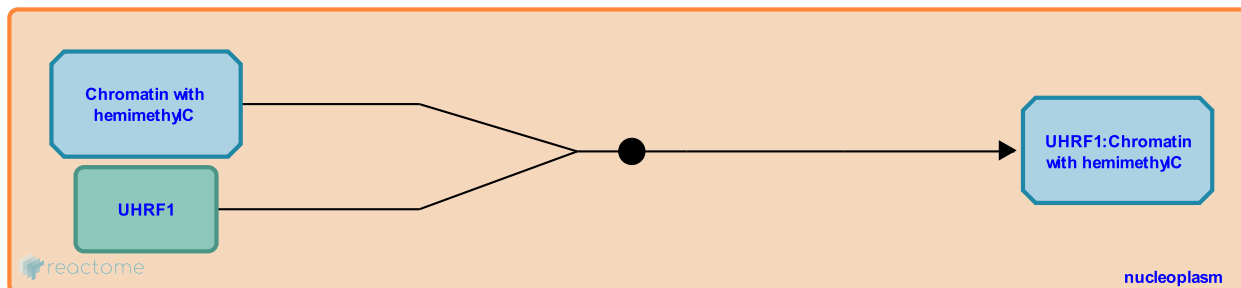
UHRF1 binds chromatin with hemimethylated cytosine ↗

Stable identifier: R-HSA-5334099

Type: binding

Compartments: nucleoplasm

Inferred from: [Uhrf1 binds chromatin with hemimethylC \(Mus musculus\)](#)



UHRF1 (also known as Np95) preferentially binds hemimethylated CG dinucleotides in DNA via its SRA domain (Avvakumov et al. 2008, Qian et al. 2008, and inferred from the mouse homolog). The UHRF1-bound unmethylated cytosine base is flipped out of the DNA helix and into a pocket of UHRF1 (Avvakumov et al. 2008). UHRF1 also binds dimethylated and trimethylated lysine-9 of histone H3 through its tandem Tudor domain (Nady et al. 2011, Rothbart et al. 2012, Rothbart et al. 2013, Cheng et al. 2013) and unmethylated histone H3 through its PHD domain (Hu et al. 2011, Wang et al. 2011, Rajakumara et al. 2011, Cheng et al. 2013).

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Editions

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