

UHRF1:Chromatin binds DNMT1

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02/05/2024

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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

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. [↗](#)
- 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: 88

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

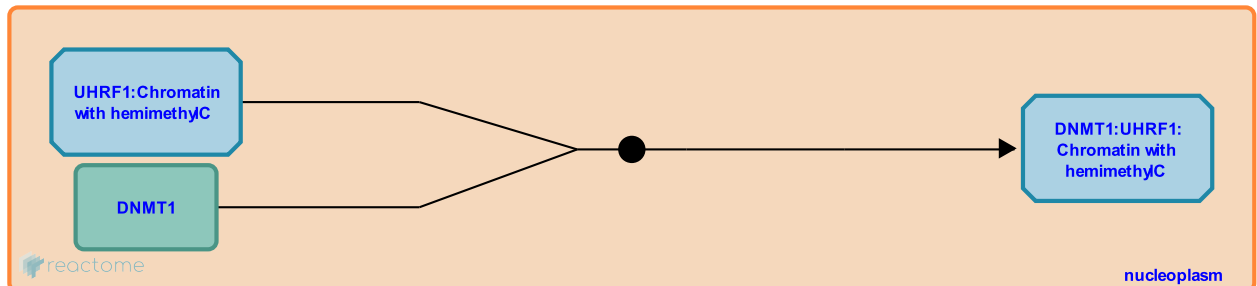
UHRF1:Chromatin binds DNMT1 [↗](#)

Stable identifier: R-HSA-5334160

Type: binding

Compartments: nucleoplasm

Inferred from: [Uhrf1:Chromatin binds Dnmt1 \(Mus musculus\)](#)



As inferred from the mouse homolog, UHRF1 associates with hemimethylated DNA and histone H3 tails methylated at lysine-9. UHRF1 recruits and tethers DNMT1 (Bostick et al. 2007). The association of UHRF1 with DNMT1 occurs preferentially during S-phase when DNA is hemimethylated as the newly replicated strand remains transiently unmethylated (Zhang et al. 2011, Hervouet et al. 2012). DNMT1 also forms complexes with transcription factors such as TP53 (p53) and YY1 at other times during the cell cycle (Hervouet et al. 2012).

Literature references

- Li, J., Koseki, H., Wu, W., Li, P., Zhang, J., Dong, S. et al. (2011). S phase-dependent interaction with DNMT1 dictates the role of UHRF1 but not UHRF2 in DNA methylation maintenance. *Cell Res.*, 21, 1723-39. [↗](#)
- Vallette, FM., Hervouet, E., Cartron, PF., Nadaradjane, A., Gueguen, M. (2012). Kinetics of DNA methylation inheritance by the Dnmt1-including complexes during the cell cycle. *Cell Div*, 7, 5. [↗](#)
- Pradhan, S., Clark, A., Jacobsen, SE., Bostick, M., Kim, JK., Estève, PO. (2007). UHRF1 plays a role in maintaining DNA methylation in mammalian cells. *Science*, 317, 1760-4. [↗](#)

Editions

2014-02-21	Authored, Edited	May, B.
2014-07-24	Reviewed	Beekman, R., Martín-Subero, JI.