DNMT1 methylates cytosine in hemi-methylated DNA

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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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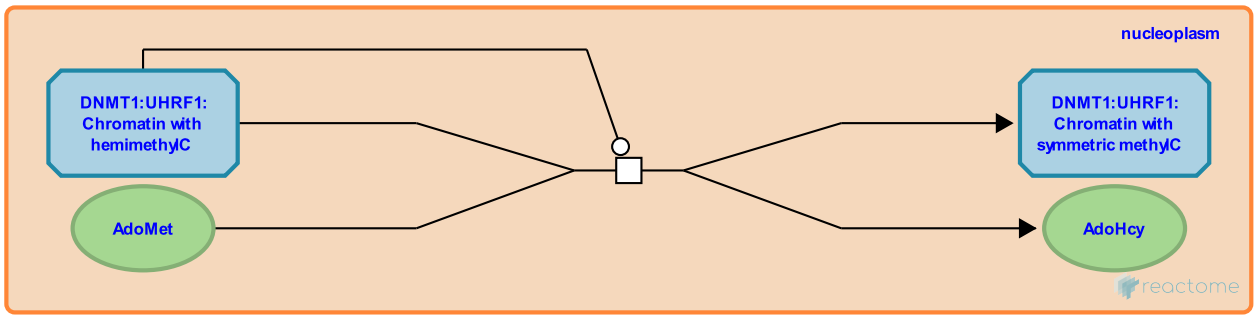
DNMT1 methylates cytosine in hemimethylated DNA ↗

Stable identifier: R-HSA-5334151

Type: transition

Compartments: nucleoplasm

Inferred from: Dnmt1 methylates cytosine in hemimethylated DNA (Mus musculus)



DNMT1 transfers a methyl group from S-adenosylmethionine to the 5-position of the cytosine ring of cytosine residues in DNA. Purified human DNMT1 shows a 7 to 21-fold preference for hemimethylated CG motifs in DNA compared to unmethylated CG motifs (Pradhan et al. 1999) thus DNMT1 tends to maintain existing methylation through DNA replication. The binding of the CXXC motif of DNMT1 to cytosine in symmetrically unmethylated CG dinucleotides prevents access of cytosine to the active site and thereby prevents de novo methylation (Song et al. 2011). UHRF1 binds hemimethylated DNA and histone H3 tails methylated at lysine-9 and recruits DNMT1 to methylate hemimethylated DNA (Bostick et al. 2007, reviewed in Ooi and Bestor 2008). Interaction of UHRF1 with DNMT1 increases the methylation activity of DNMT1 about 5-fold (Bashtrykov et al. 2014).

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Editions

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