

Dnmt3a:Dnmt3l methylates cytosine in 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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Reactome database release: 88

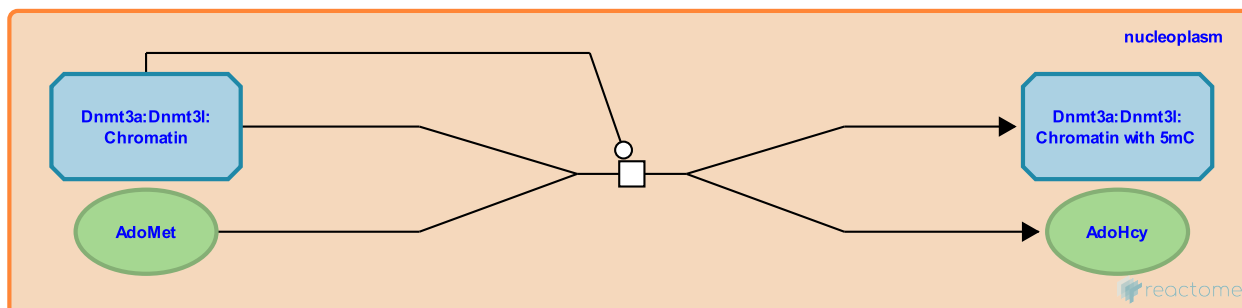
This document contains 1 reaction ([see Table of Contents](#))

Dnmt3a:Dnmt3l methylates cytosine in DNA [↗](#)

Stable identifier: R-MMU-5336316

Type: transition

Compartments: nucleoplasm



Dnmt3a methylates the 5 position of cytosine in DNA preferentially in unmethylated regions (Okano et al. 1998, Okano et al. 1999, Hsieh 1999, Yokochi and Robertson 2002, Hsieh 2005, Gowher et al. 2005). Dnmt3a generates asymmetric methylation of CG dinucleotides and non-CG cytosine residues (Lin et al. 2002, Arand et al. 2012). Dnmt3l interacts with and stimulates the catalytic activity of Dnmt3a and its homologue Dnmt3b (Gowher et al. 2005). Dnmt3a and Dnmt3a:Dnmt3l complexes preferentially methylate DNA in regions of chromatin containing unmethylated lysine-4 of histone H3 due to the interaction between Dnmt3a and Dnmt3l with unmodified histone tails (Zhang et al. 2010). In mouse oocytes and embryos, CG islands that depend on Dnmt3a for methylation tend to be located in active transcription units with low levels of methylated H3K4 (Smallwood et al. 2011)

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Editions

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