DNMT3A:DNMT3L binds chromatin

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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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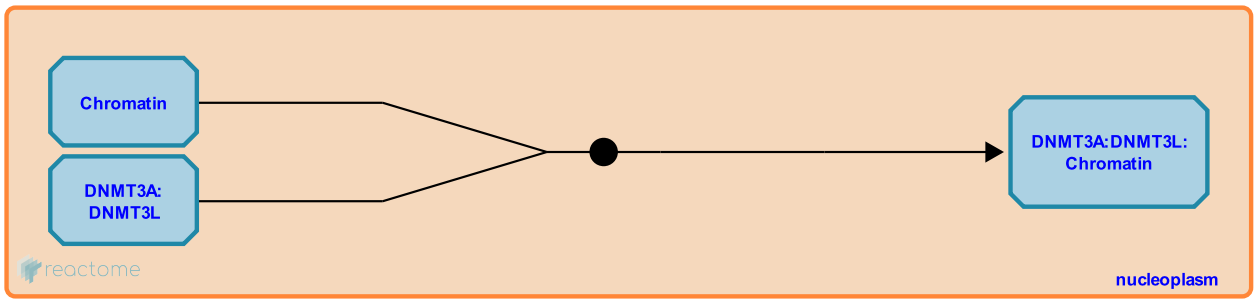
Stable identifier: R-HSA-5334179

Type: binding

Compartments: nucleoplasm

Inferred from: Dnmt3a:Dnmt3l binds chromatin (Mus musculus)



DNMT3L is a non-catalytic homologue of DNMT3A and DNMT3B which binds unmethylated lysine-4 of histone H3 (H3K4, Ooi et al. 2007) and recruits DNMT3A-isoform2 (germ cell specific) (Chen et al. 2005, Kareta et al. 2006, Ooi et al. 2007) and, to a lesser extent, other isoforms of DNMT3A via an interaction between the C-terminal regions of DNMT3L and DNMT3A (Chen et al. 2005). Furthermore, DNMT3A binds unmodified tails of histone H3 (Otani et al. 2009). DNMT3L and DNMT3A form tetramers (DNMT3L:DNMT3A:DNMT3A:DNMT3L) that bind DNA located in euchromatic regions (Holz-Schietinger et al. 2011, also inferred from mouse). DNMT3A without DNMT3L forms oligomers that are located in heterochromatin.

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Editions

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