DOT1L (KMT4) methylates dimethyl-lysine-80 of histone H3 (H3K79)

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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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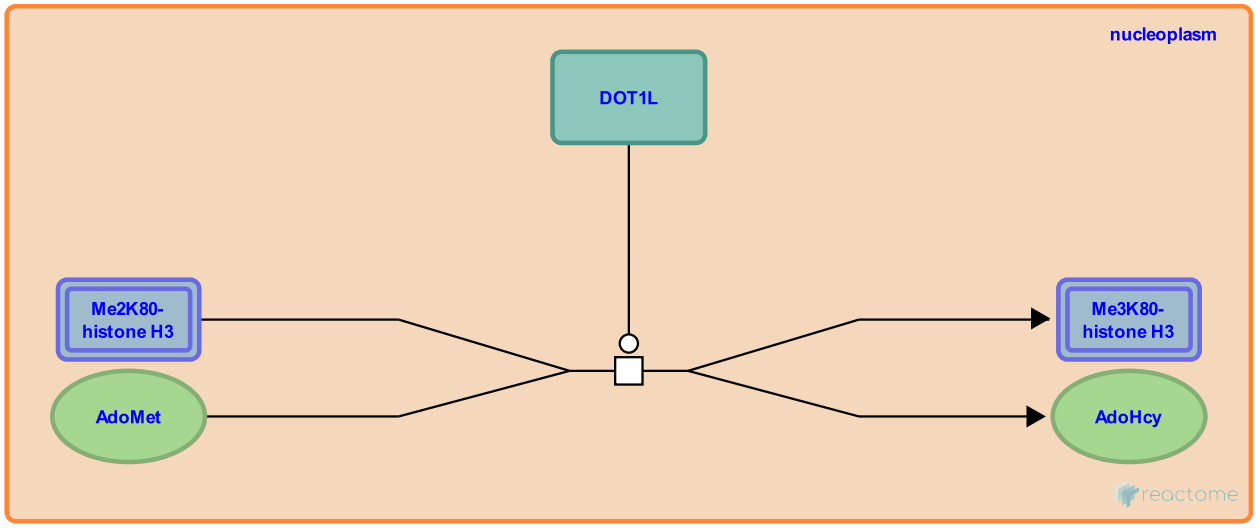
Stable identifier: R-HSA-5649799

Type: transition

Compartments: nucleoplasm



DOT1L is responsible for the mono-, di-, and trimethylation of histone H3 in a nonprocessive manner (Min et al. 2003, Frederiks et al. 2008). It appear to be solely responsible for H3K79 methylation, since knockout of Dot1 in yeast, flies and mice results in complete loss of H3K79 methylation (van Leeuwen et al. 2002, Shanower et al. 2005, Jones et al. 2008).

Literature references

Ng, HH., Zhang, Y., Wang, H., Feng, Q., Struhl, K., Tempst, P. et al. (2002). Methylation of H3-lysine 79 is mediated by a new family of HMTases without a SET domain. *Curr. Biol., 12*, 1052-8.

Editions

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