

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

Jupe, S., Motamedi, M.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](#). For more information see our [license](#).

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

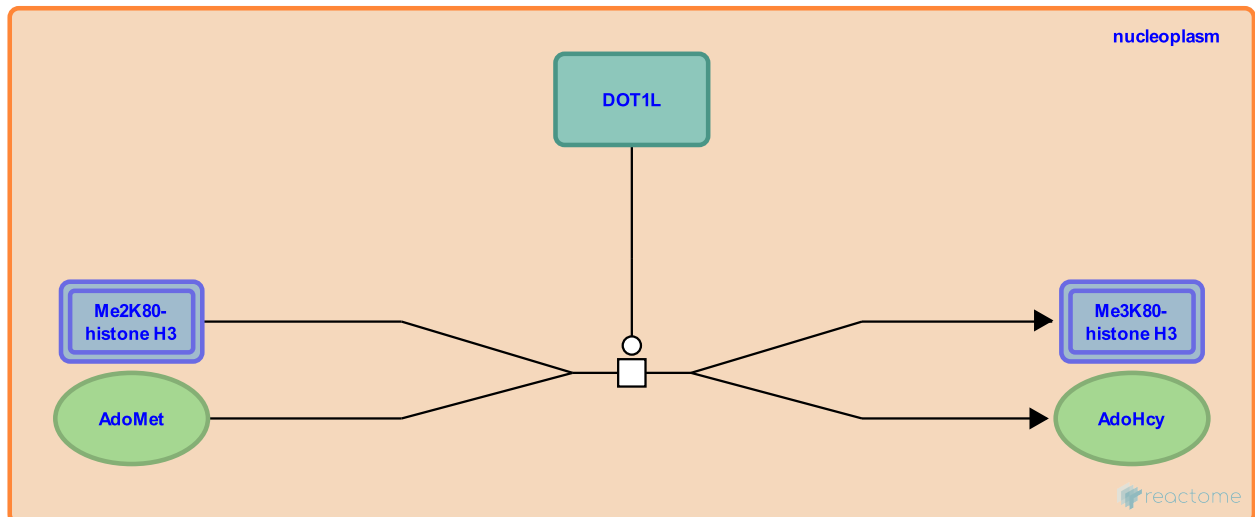
This document contains 1 reaction ([see Table of Contents](#))

DOT1L (KMT4) methylates dimethyl-lysine-80 of histone H3 (H3K79) [↗](#)

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

2014-11-13	Authored	Jupe, S.
2014-11-17	Reviewed	Motamedi, M.
2015-02-13	Edited	Jupe, S.