NoRC:HDAC:DNMT methylates cytosine of the rRNA genes

May, B., Shiao, YH.

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

09/05/2024

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. ↗

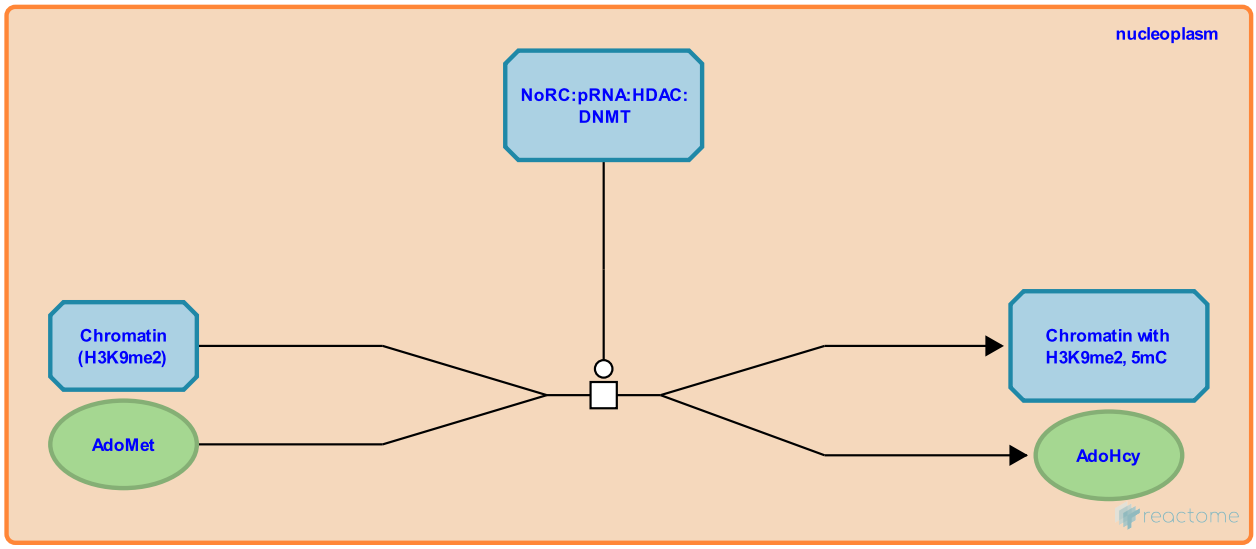
NoRC:HDAC:DNMT methylates cytosine of the rRNA genes ↗

Stable identifier: R-HSA-5227490

Type: transition

Compartments: nucleoplasm

Inferred from: NoRC:intergenic spacer:Hdac:Dnmt complex methylates cytosine in the rRNA genes (Mus musculus)



From research with human cells (Espada et al. 2007) and inferences from mouse cell models, cytosine residues in the main promoter of silenced rRNA gene copiess are methylated by DNMT1 and DNMT3B. DNMT3B directly binds a triple helix formed by pRNA and the main promoter of rDNA. The methylated cytosines prevent binding of the UBF transcription factor, thus preventing transcription of silenced rRNA gene copies. Histone deacetylation is required for DNA methylation.

Literature references

Längst, G., Fraga, MF., Villar-Garea, A., Esteller, M., Santoro, R., Ballestar, E. et al. (2007). Epigenetic disruption of ribosomal RNA genes and nucleolar architecture in DNA methyltransferase 1 (Dnmt1) deficient cells. *Nucleic Acids Res, 35*, 2191-8. ↗

Editions

2014-01-09	Authored, Edited	May, B.
2014-02-18	Reviewed	Shiao, YH.