TTF1:rRNA promoter:ERCC6:EHMT2 complex dimethylates histone H3 at lysine-9.

Iben, S., May, B.

01/12/2020

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: 74

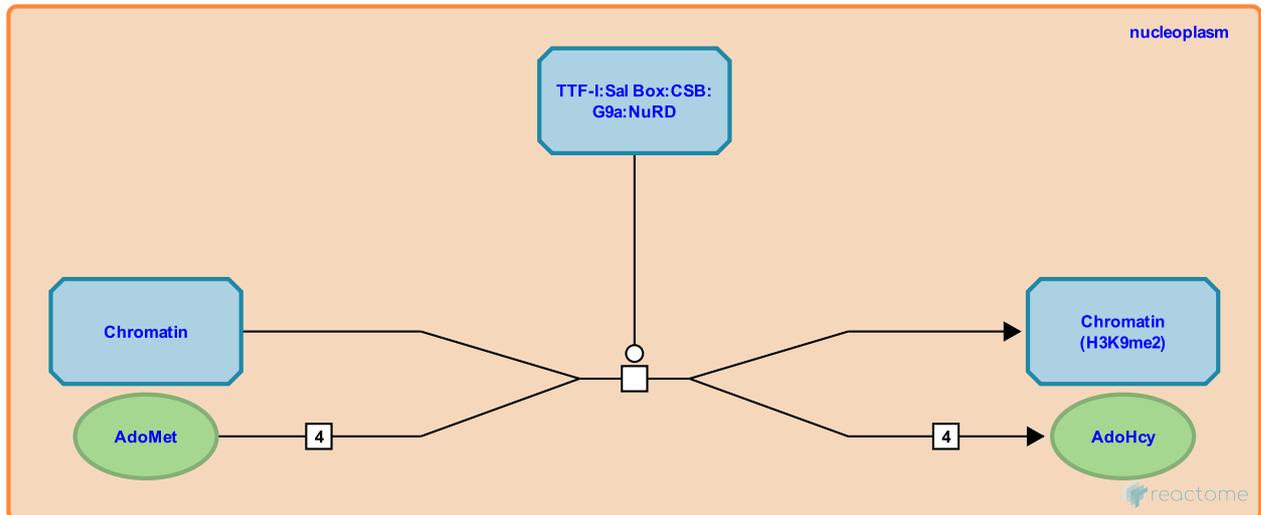This document contains 1 reaction (see Table of Contents)

TTF1:rRNA promoter:ERCC6:EHMT2 complex dimethylates histone H3 at lysine-9. ↗

Stable identifier: R-HSA-427336

Type: transition

Compartments: nucleoplasm

Inferred from: Ttf-I:rRNA Promoter:Ercc6:Ehmt2 complex dimethylates histone H3 at lysine-9 (Homo sapiens)

As inferred from mouse, EHMT2 (histone methyltransferase G9a) dimethylates histone H3 at lysine-9 (H3K9me2) in the transcribed region of the rRNA gene. Dimethylation of histone H3 in the transcribed region causes increased rRNA expression, which contrasts with the repressive effect of H3K9me2 in other regions of the genome. The histone binding activity and ATPase activity of CHD4 in the NuRD complex are also needed for activation.

Editions

2009-06-19	Edited	May, B.
2009-06-21	Authored	May, B.
2016-02-12	Reviewed	Iben, S.