PRDM9 trimethylates histone H3

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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

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. ↗

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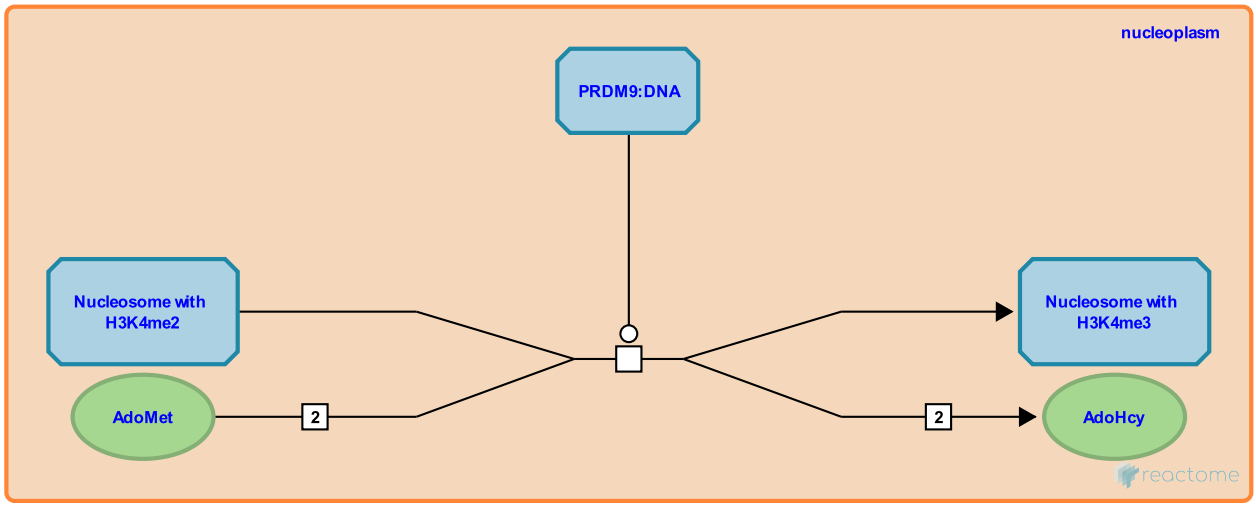
Stable identifier: R-HSA-1214188

Type: transition

Compartments: nucleoplasm

Inferred from: Prdm9 Trimethylates Histone H3 (murine, bovine) (Bos taurus), Prdm9 Trimethylates Histone H3 at Lysine-4 (Mus musculus)



As inferred from experiments in vitro with mouse Prdm9, human PRDM9 methylates histone H3 dimethylated at lysine-4 to yield histone H3 trimethylated at lysine-4.

Literature references

Matsui, Y., Yoshida, K., Hayashi, K. (2005). A histone H3 methyltransferase controls epigenetic events required for meiotic prophase. *Nature, 438*, 374-8. ↗

Editions

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