Core MLL complex methylates H3K4Me2-Nucleosome at the ITGA2B gene promoter

Chuang, LS., Ito, Y., Orlic-Milacic, M.

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

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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. ↗

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. ↗

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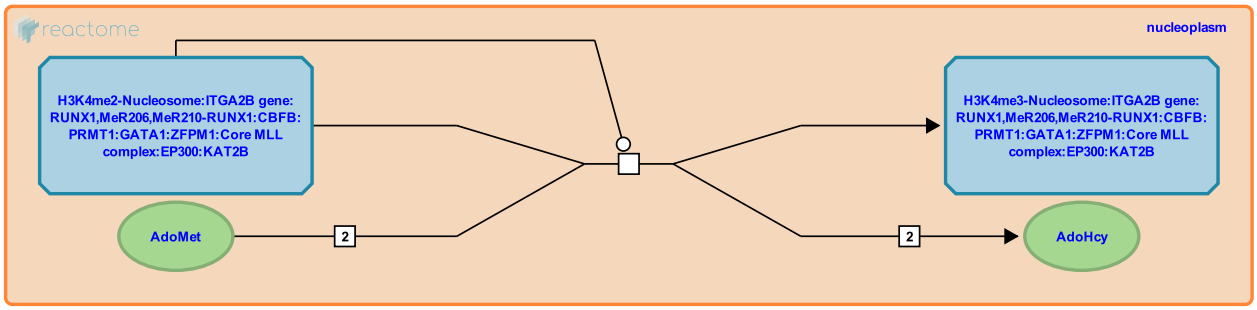
Stable identifier: R-HSA-8936481

Type: transition

Compartments: nucleoplasm



The WDR5-containing histone methyltransferase MLL complex, recruited to the ITGA2B promoter via RUNX1 (and possibly GATA1), methylates histone H3 on dimethylated lysine residue K4 (K5 when taking into account the initiator methionine), producing the H3K4me3 mark. The H3K4me3 mark is characteristic of nucleosomes associated with transcriptionally active promoters of megakaryocyte-specific genes (Herglotz et al. 2013).

Literature references

Herglotz, J., Kuvardina, ON., Kolodziej, S., Kumar, A., Hussong, H., Grez, M. et al. (2013). Histone arginine methylation keeps RUNX1 target genes in an intermediate state. *Oncogene, 32*, 2565-75. ↗

Editions

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