

PRC2 (EZH2) Core:AEBP2 methylates lysine-28 of histone H3 (H3K27)

Jupe, S., Motamedi, 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. [↗](#)

Reactome database release: 88

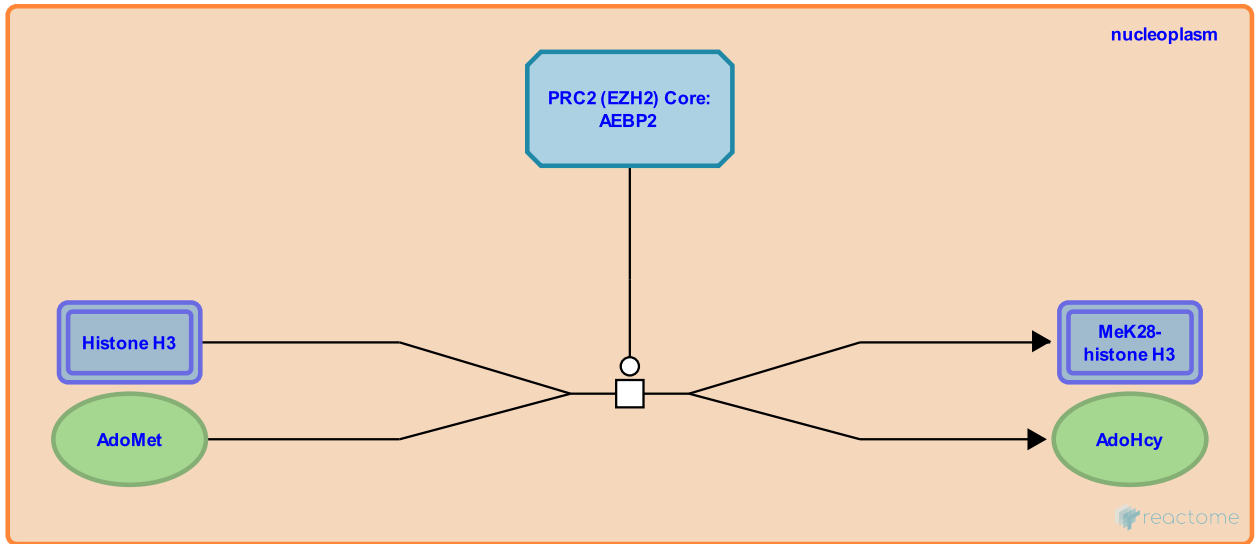
This document contains 1 reaction ([see Table of Contents](#))

PRC2 (EZH2) Core:AEBP2 methylates lysine-28 of histone H3 (H3K27) ↗

Stable identifier: R-HSA-5638332

Type: transition

Compartments: nucleoplasm



EZH2 (KMT6, PRC2) is the catalytic subunit of the PRC2 (EZH2) Core complex, which additionally contains EED, SUZ12, AEBP2 and one of RBBP4 or RBBP7. It methylates lysine-28 (H3K27) of histone H3 (Cao et al. 2002, Czermin et al. 2002, Kuzmichev et al. 2002, Muller et al. 2002) leading to transcriptional repression of the affected target gene. It is able to mono-, di- and trimethylate lysine-28 (Cao & Zhang 2004).

Editions

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