

JMJD6 demethylates Me₂R₃-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. [↗](#)
- 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

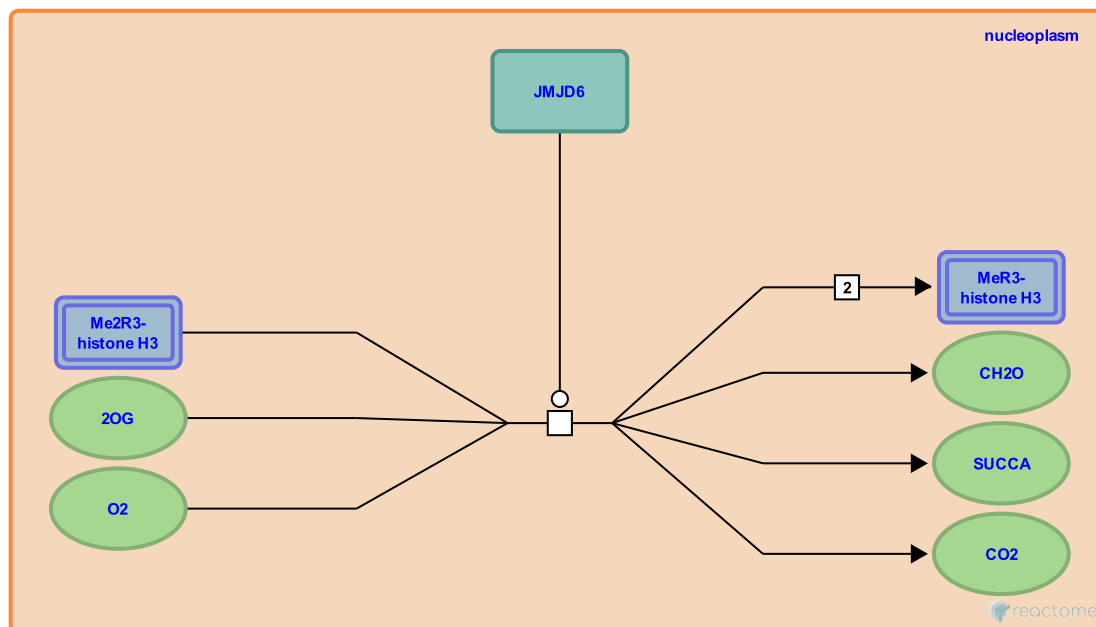
This document contains 1 reaction ([see Table of Contents](#))

JMJD6 demethylates Me2R3-histone H3 [↗](#)

Stable identifier: R-HSA-5661122

Type: transition

Compartments: nucleoplasm



JMJD6 catalyses demethylation of mono- or di-methylated arginine-3 of histone H3 (H3R2Me1/2) and arginine-4 of histone H4 (H4R3Me1/2) (Chang et al. 2007). Non-histone substrates of JMJD6 arginine demethylation have also been reported (Poulard et al. 2014, Lawrence et al. 2014). Subsequent to its characterization as an arginine demethylase, JMJD6 was reported to be a lysine hydroxylase (Webby et al 2009).

Literature references

Zhao, Y., Chen, Y., Bruick, RK., Chang, B. (2007). JMJD6 is a histone arginine demethylase. *Science*, 318, 444-7. [↗](#)

Editions

2013-03-12	Authored	Jupe, S.
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