

# JMJD6 demethylates Me<sup>2</sup>R<sup>3</sup>-histone H3

Hopkinson, J., Jupe, S., Schofield, C.J., Walport, L.J.

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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://reactome.org/licenses/).

17/05/2024

## 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: 88

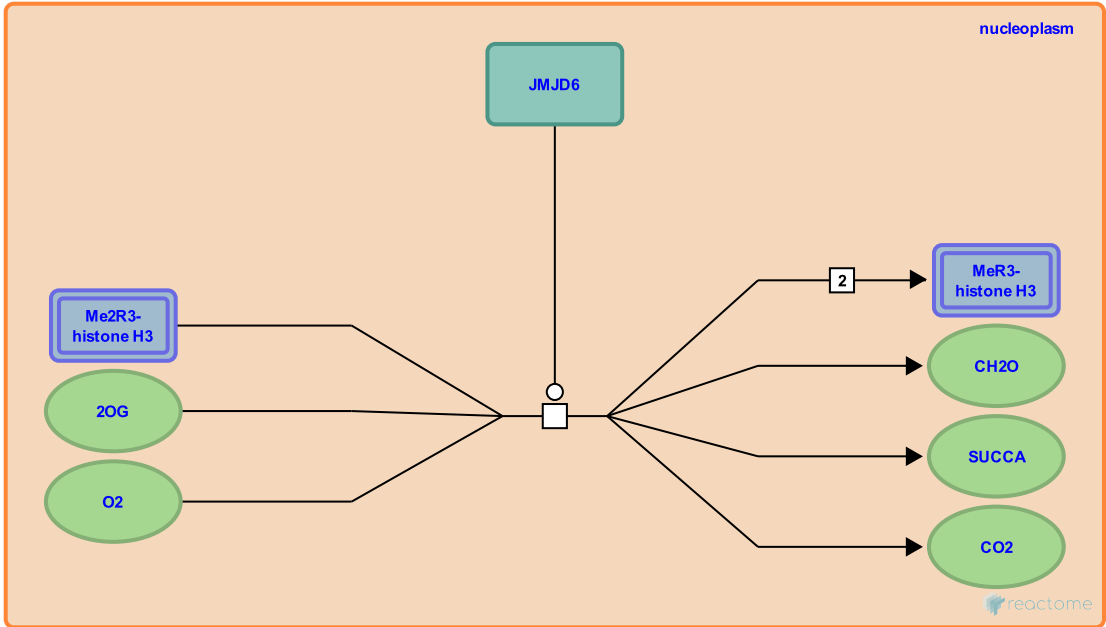
This document contains 1 reaction ([see Table of Contents](#))

**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.
2014-02-05	Edited	Jupe, S.
2014-05-08	Reviewed	Schofield, CJ., Hopkinson, J., Walport, LJ.