

KDM5A-D demethylate Me2K5-histone H3

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03/05/2024

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

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Reactome database release: 88

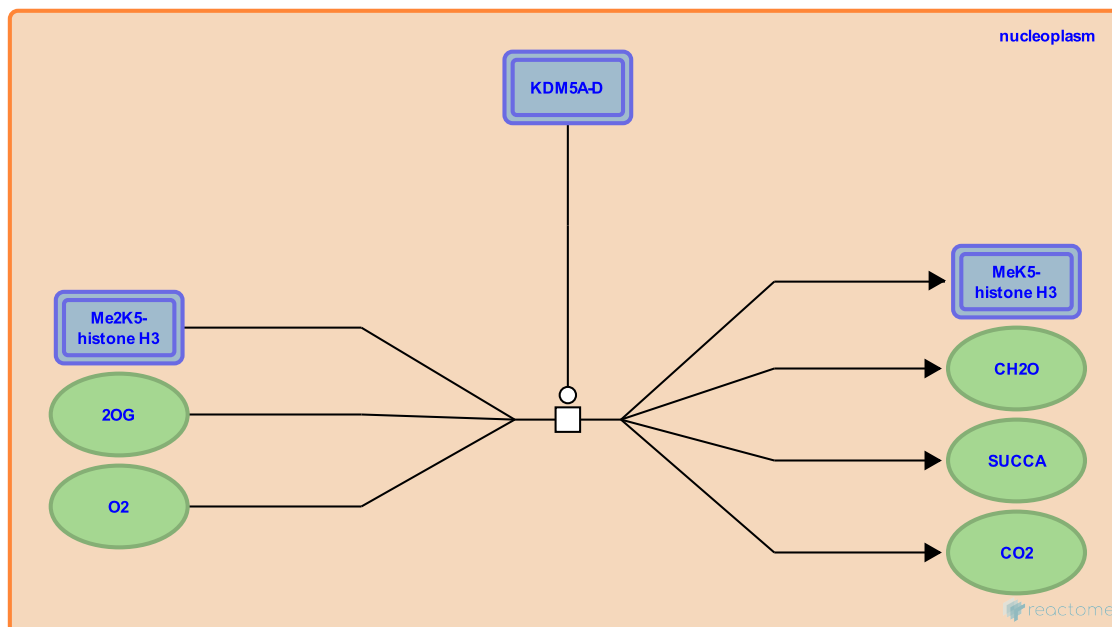
This document contains 1 reaction ([see Table of Contents](#))

KDM5A-D demethylate Me2K5-histone H3 [↗](#)

Stable identifier: R-HSA-4754181

Type: transition

Compartments: nucleoplasm



All characterized lysine demethylases other than KDM1A belong to the jumonjiC domain (JmjC) containing family. The JmjC KDMs are members of the Cupin superfamily of mononuclear Fe (II) dependent oxygenases, which are characterized by the presence of a double-stranded beta-helix core fold. The JmjC KDMs require 2 oxoglutarate (2 OG) and molecular oxygen as co substrates, producing, along with formaldehyde, succinate and carbon dioxide. This hydroxylation based mechanism does not require a protonatable lysine epsilon-amine group and consequently JmjC containing demethylases are able to demethylate tri-, di- and monomethylated lysines. KDM5A-D (JARID1A-D) catalyse the demethylation of di- or tri-methylated lysine-5 of histone H3 (H3K4Me_{2/3}) (Christensen et al. 2007, Klose et al. 2007, Lee et al. 2007, Secombe et al. 2007, Seward et al. 2007, Iwase et al. 2007).

Literature references

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Editions

2013-03-12	Authored	Jupe, S.
2014-02-05	Edited	Jupe, S.
2014-05-08	Reviewed	Schofield, CJ., Hopkinson, J., Walport, LJ.