KDM1A, KDM1B demethylate Me2K5-histone H3

Hopkinson, J., Jupe, S., Schofield, C.J., Walport, I.J.
**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**


Reactome database release: 78

This document contains 1 reaction (see Table of Contents)
KDM1A, KDM1B demethylate Me2K5-histone H3

Stable identifier: R-HSA-5661123

Type: transition

Compartments: nucleoplasm

Histone demethylases (HDMs) belong to two groups with distinct catalytic mechanisms. KDM1A and KDM1B (formerly known as Lysine Specific Demethylases 1 and 2), belong to the flavin adenine dinucleotide (FAD)-dependent amino oxidase family, releasing formaldehyde. The reaction mechanism requires a protonatable lysine epsilon-amino group, not available in trimethylated lysines (Shi et al. 2004). KDM1A and subsequently KDM1B were shown to catalyse demethylation of monomethyl and dimethyl, but not trimethyl, histone H3 at lysine 5 (H3K4) in vitro (Shi et al. 2004, Ciccone et al. 2009).

Subsequently KDM1A was found to be much more proficient at catalysing demethylation of H3K4 when part of a multiprotein complex (Lee et al. 2005) and shown to catalyse demethylation of histone H3 at lysine 10 (H3K9) in vivo when associated with the androgen receptor (Metzger et al. 2007), suggesting that its substrate specificity is modulated by interacting proteins. KDM1A is a subunit of several complexes, including CtBP, Co-REST, NRD and BRAF35 (Lan et al. 2008). It is also able to catalyse demethylation of a number of non-histone proteins (Nicholson & Chen 2009).

Literature references


Editions

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<th>Reviewer</th>
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