KDM3A, KDM3B, KDM7A, PHF2:ARID5B, PHF8 demethylate MeK10-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

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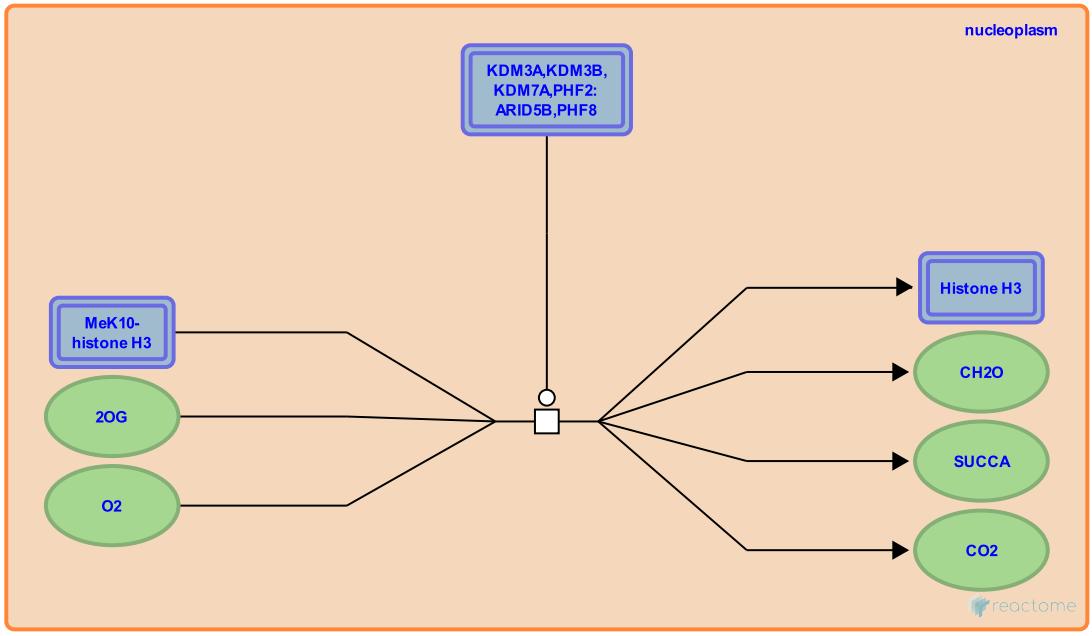
Stable identifier: R-HSA-4724284

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 catalyse demethylateion of tri , di and monomethylated lysines. KDM3A (JHDM2A), KDM3B (JHDM2B), KDM7A (JHDM1D), PHF8 (JHDM1E) and PHF2 when complexed with ARID5B (Wen et al. 2010, Baba et al. 2011) are specific for mono or di-methylated lysine-10 on histone H3 (H3K9Me1/2) (Yamane et al. 2006, Kim et al. 2012, Horton et al. 2010, Huang et al. 2010, Loenarz et al. 2008, Feng et al. 2010, Fortschegger et al. 2010, Qi et al. 2010).

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Editions

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