WHSC1 (KMT3G), NSD1 (KMT3B), SMYD2 (KMT3C), ASH1L methylate methyl-lysine-37 of histone H3 (H3K36)

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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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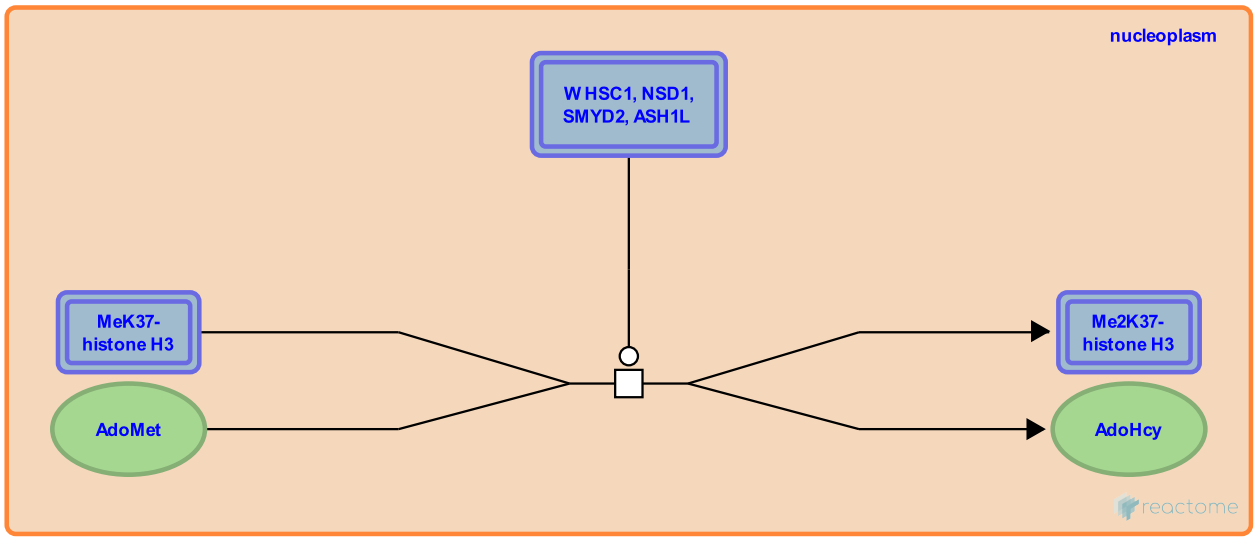
WHSC1 (KMT3G), NSD1 (KMT3B), SMYD2 (KMT3C), ASH1L methylate methyl-lysine-37 of histone H3 (H3K36)

Stable identifier: R-HSA-5638157

Type: transition

Compartments: nucleoplasm



Methylation of histone H3 lysine-37 (H3K36) is tightly associated with actively transcribed genes and appears to correspond primarily with coding regions (Wagner & Carpenter 2011). WHSC1 (KMT3G, NSD2, MMSET), a member of the SET2 family, dimethylates H3K36 when provided with nucleosome substrates (Li et al 2009; Qiao et al. 2011). Dimethylation of histone H3 at lysine-37 (H3K36me2) is thought to be the principal chromatin-regulatory activity of WHSC1 (Kuo et al. 2011), SMYD2 (KMT3C) (Brown et al 2006) and NSD1 (KMT3B) (Li et al. 2009, Qiao et al. 2011). ASH1L can perform histone H3 lysine-37 di-methylation (Tanaka et al. 2007, An et al. 2011, Miyazaki et al. 2013, Zhu et al. 2016).

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Editions

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