

MSL acetylates histone H4

Jupe, S., Karagiannis, T.

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

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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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Reactome database release: 75

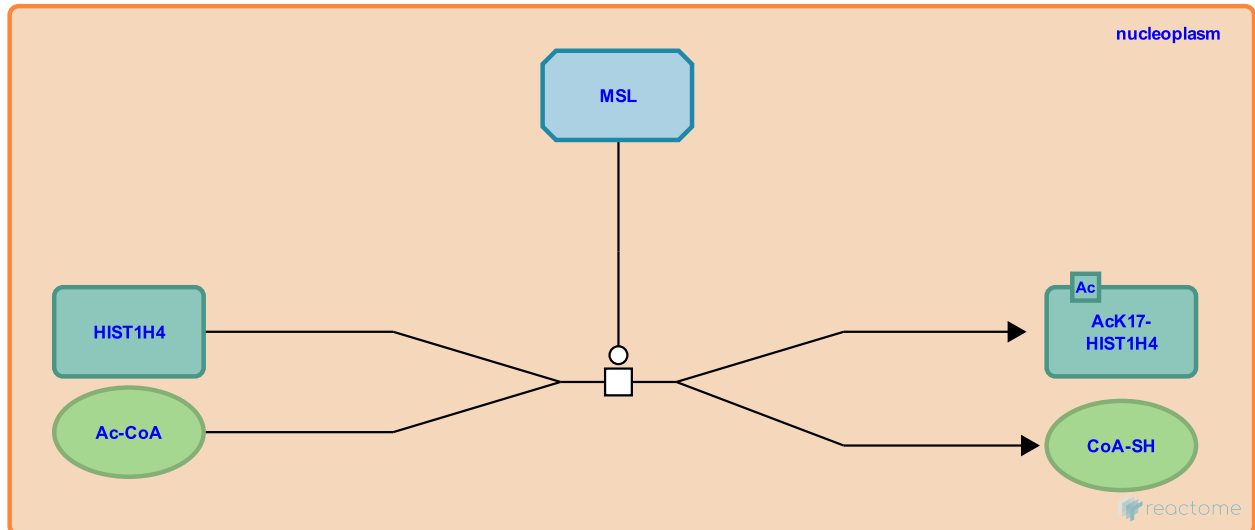
This document contains 1 reaction ([see Table of Contents](#))

MSL acetylates histone H4 [↗](#)

Stable identifier: R-HSA-3321883

Type: transition

Compartments: nucleoplasm



The MSL complex has histone acetyltransferase (HAT) activity with a high specificity for histone H4 lysine-17 (H4K16) (Smith et al. 2000, 2005, Conrad et al. 2012). The subunit responsible for this activity is KAT8 (Males Absent on the First, MOF) a member of the MYST (named for yeast and human members MOZ, YBF2, SAS2, and Tip60) HAT family. In *Drosophilla*, the MSL complex associates at hundreds of sites along the X chromosome in somatic cells, resulting in the hyperacetylation of H4K16 (Lavender et al. 1994, Smith et al. 2000). In humans MSL is responsible for the majority of H4 acetylation at lysine-17 in the cell. KAT8 is a component of other complexes (Smith et al. 2005, Mendjan et al. 2006, Cai et al. 2010).

Literature references

Neal, KC., Pannuti, A., Smith, ER., Lucchesi, JC. (2000). A new human member of the MYST family of histone acetyltransferases with high sequence similarity to *Drosophila* MOF. *Biochim. Biophys. Acta*, 1490, 170-4. [↗](#)

Editions

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