

# NSL acetylates histone H4

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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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- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
- Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res*, 46, D649-D655. [↗](#)
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Reactome database release: 75

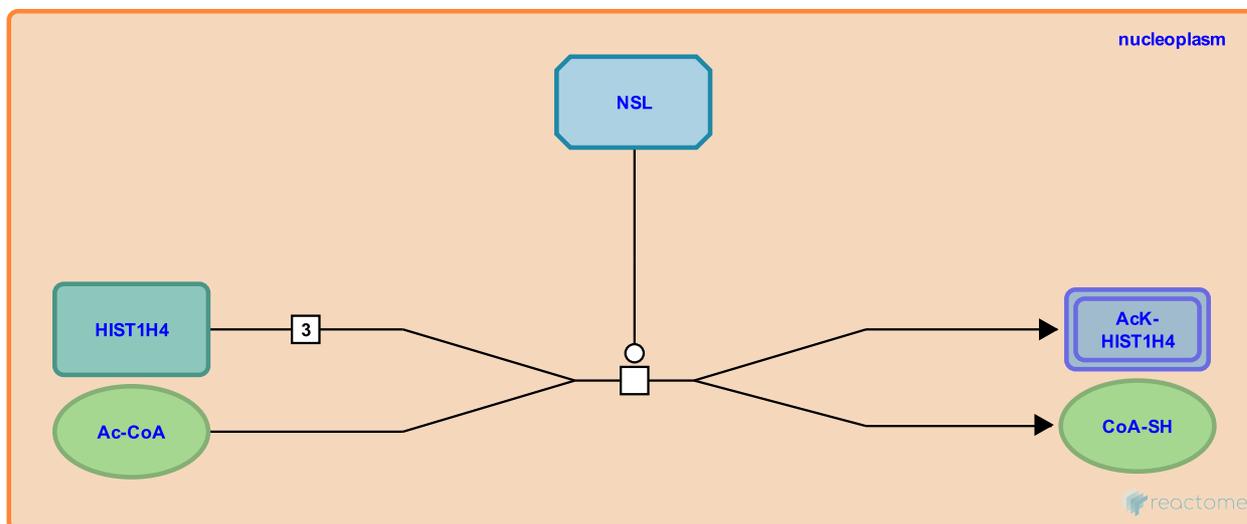
This document contains 1 reaction ([see Table of Contents](#))

## NSL acetylates histone H4 [↗](#)

**Stable identifier:** R-HSA-3321805

**Type:** transition

**Compartments:** nucleoplasm



KAT8 (MOF, MYST1) is a member of the MYST (Moz-Ybf2/Sas3-Sas2-Tip60) family of histone acetyltransferases (HATs). KAT8 is the catalytic component of the nine-subunit non-specific lethal (NSL) complex (Mendjan et al. 2006, Cai et al. 2010).

NSL acetylates histone H4 on lysines 17 (H4K16), 6 (H4K5) and 9 (H4K8) (Cai et al. 2010).

KAT8 is also the catalytic subunit of the male-specific lethal (MSL) complex, which acetylates almost exclusively H4K16 and is responsible for a large fraction of H4K16 acetylation in human cells (Smith et al. 2005).

N.B. Coordinates of post-translational modifications described here follow UniProt standard practice whereby coordinates refer to the translated protein before any further processing. Histone literature typically refers to coordinates of the protein after the initiating methionine has been removed. Therefore the coordinates of post-translated residues in the Reactome database and described here are frequently +1 when compared with the literature.

### Literature references

Cai, Y., Jin, J., Swanson, SK., Cole, MD., Choi, SH., Florens, LA. et al. (2010). Subunit composition and substrate specificity of a MOF-containing histone acetyltransferase distinct from the male-specific lethal (MSL) complex. *J. Biol. Chem.*, 285, 4268-72. [↗](#)

### Editions

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