

# KAT7-containing ING4/5 complexes acetylate Me3K-histone H3

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: 70

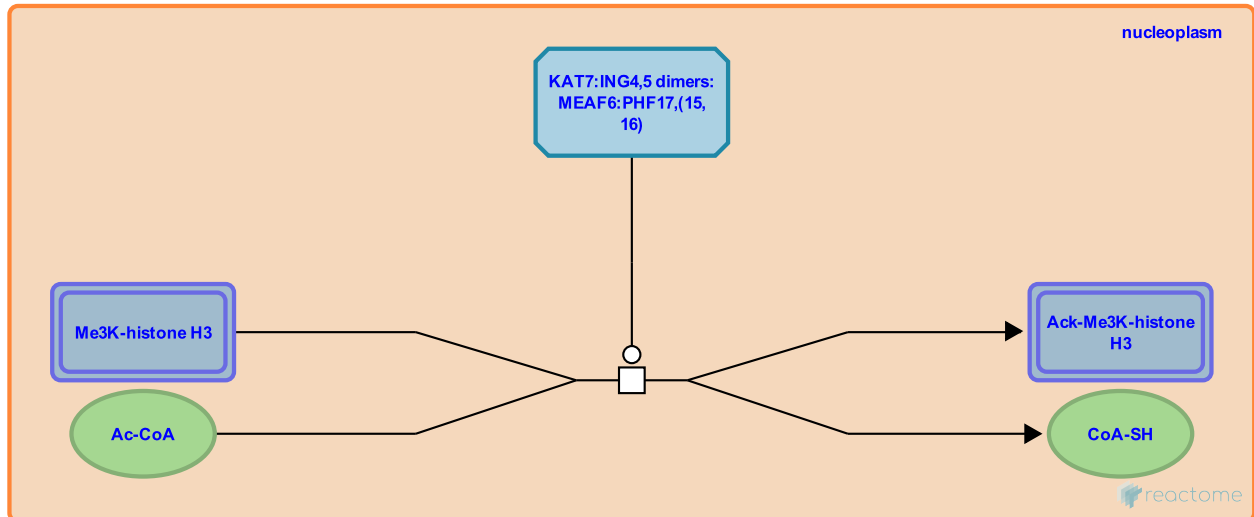
This document contains 1 reaction ([see Table of Contents](#))

## KAT7-containing ING4/5 complexes acetylate Me3K-histone H3 [↗](#)

**Stable identifier:** R-HSA-3318413

**Type:** transition

**Compartments:** nucleoplasm



The Inhibitor of Growth (ING) family are growth regulators, present in all eukaryotes, with five human proteins ING1 to ING5. ING genes are mutated or downregulated in many forms of cancer. They have roles in chromatin modification and remodeling, gene-specific transcription regulation, and DNA repair, recombination, and replication (Saksouk et al. 2008, Awakumovv et al. 2012).

Human ING proteins can be divided into three groups: ING1/2, ING3, and ING4/5, based on their association with three distinct types of protein complexes (Doyon et al. 2006). All regulate chromatin via histone acetylation and deacetylation. The catalytic histone acetyltransferase (HAT) subunits of ING complexes are members of the MYST family, KAT5 (Tip60), KAT7 (HBO1) KAT6A (MOZ), KAT6B (MORF), and KAT8 (MOF). ING4 exists in vivo as a dimer, binding two lysine-4 trimethylated histone H3 (H3K4me3) modifications (Palacios et al. 2010). Homology modeling suggests that other ING proteins are likely to be dimers (Culurgioni et al. 2012).

KAT7-ING4/5 complexes interact with lysine-4 trimethylated histone H3 (H3K4me3), acetylating surrounding histone tails to stimulate local transcription (Palacios et al. 2008, Champagne et al. 2008, Hung et al. 2009, Saksouk et al. 2009).

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### Editions

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