

# KAT6A, KAT6B-containing ING5 complexes acetylate replicative histone H3

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05/05/2024

## 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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

## Literature references

- Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*, 18, 142. [↗](#)
- 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. [↗](#)
- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, 14, e1005968. [↗](#)

Reactome database release: 88

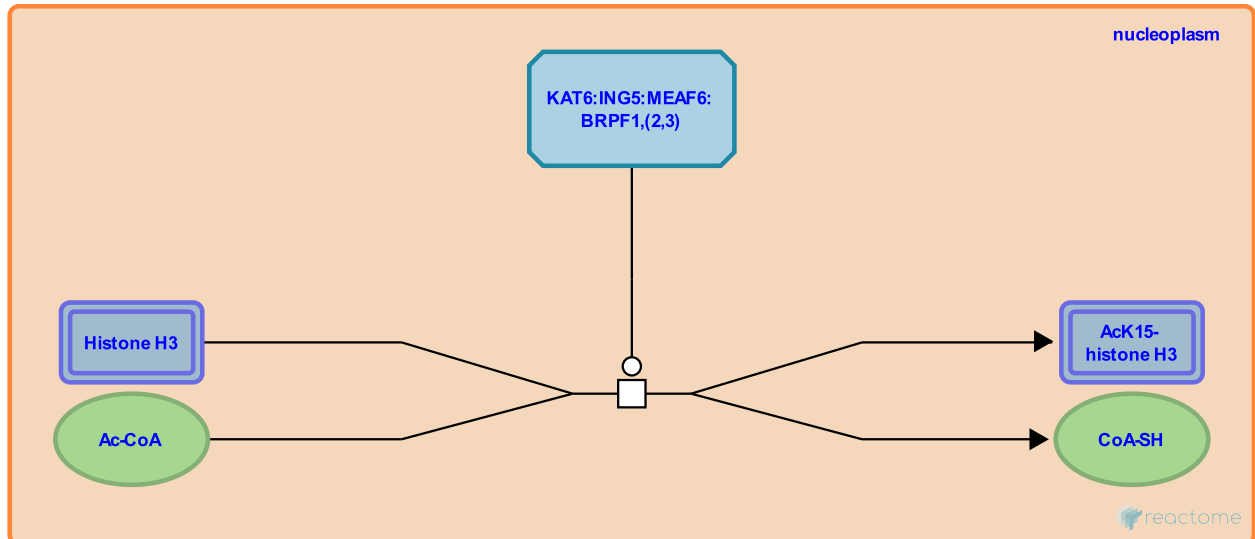
This document contains 1 reaction ([see Table of Contents](#))

## KAT6A, KAT6B-containing ING5 complexes acetylate replicative histone H3 [↗](#)

**Stable identifier:** R-HSA-3318486

**Type:** transition

**Compartments:** nucleoplasm



KAT6A (Monocytic leukemia zinc finger protein, MOZ) and KAT6B (Monocytic leukemia zinc finger protein-related factor, MORF) are member of the MYST family of histone acetyltransferases, named after the founding members MOZ, Ybf2/Sas3, Sas2 and TIP60 (Borrow et al. 1996, Reifsnnyder et al. 1996). The presence of a MYST domain is the only common structural motif in this family. MOZ and MORF are highly homologous (overall amino-acid sequence identity, 60%; similarity, 66%) but distinct from other family members (Yang & Ullah 2007).

KAT6A and KAT6B have intrinsic histone acetyltransferase activity (Champagne et al. 1999, 2001). Both can form tetrameric 'ING5' complexes with BRPF1 (possibly BRPF2 and 3), EAF6 and ING5. BRPF1 and EAF6 drastically stimulate the acetyltransferase activities of KAT6A/B against nucleosomal histone H3 (Doyon et al. 2006, Ullah et al. 2008). ING5-MOZ/MORF complexes acetylate only histone H3 at lysine-14.

KAT6A homozygous mice die at birth, with reduced hematopoiesis and profound defects in the stem cell compartment. These mice have no long-term repopulating stem cells and display substantial reduction in the number of multipotent cells able to form spleen colonies (Thomas et al. 2006). Chromosomal rearrangements of the KAT6A gene are associated with acute myeloid leukemia (AML), uterine leiomyomata and therapy-related myelodysplastic syndromes (Yang & Ullah, 2007).

Mutations in KAT6B are the cause of the Say-Barber-Biesecker variant of Ohdo syndrome and Genitopatellar syndrome (Campeau et al. 2012, Szakszon et al. 2013).

### Literature references

Lane, WS., Yang, XJ., Côté, J., Landry, AJ., Cayrou, C., Tan, S. et al. (2006). ING tumor suppressor proteins are critical regulators of chromatin acetylation required for genome expression and perpetuation. *Mol. Cell*, 21, 51-64. [↗](#)

### Editions

2013-03-12	Authored	Jupe, S.
2013-11-18	Edited	Jupe, S.
2013-11-18	Reviewed	Karagiannis, T.