

# SETD8 (KMT5A) methylates lysine-21 of histone H4 (H4K20)

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01/05/2024

https://reactome.org

## 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

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Reactome database release: 88

This document contains 1 reaction (see Table of Contents)

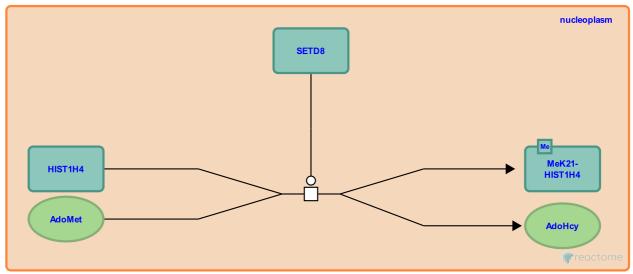
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Stable identifier: R-HSA-5423038

Type: transition

Compartments: nucleoplasm



Monomethylation of lysine-21 of histone H4 (H4K20) is performed by SETD8 (KMT5A) (Yin et al. 2005). Trimethylation, performed by SUV420H1 and SUV420H2 and possibly SMYD3 (Foreman et al. 2011), is associated with heterochromatin formation and gene repression (Schotta et al. 2004).

### Literature references

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Liu, C., Yin, Y., Zhou, B., Ngai, SM., Zhu, G., Tsai, SN. (2005). SET8 recognizes the sequence RHRK20VLRDN within the N terminus of histone H4 and mono-methylates lysine 20. *J. Biol. Chem.*, 280, 30025-31.

# **Editions**

2014-11-13	Authored	Jupe, S.
2014-11-17	Reviewed	Motamedi, M.
2015-02-13	Edited	Jupe, S.