

SETD8 monomethylates histone H4

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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.

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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 data-base: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968.

Reactome database release: 88

This document contains 1 reaction (see Table of Contents)

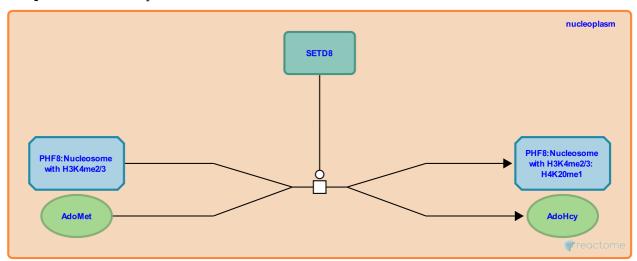
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Stable identifier: R-HSA-2301205

Type: transition

Compartments: nucleoplasm



SETD8 is a protein-lysine N-methyltransferase that monomethylates H4 histone to produce H4K20me1 (Nishioka et al. 2002, Wu et al. 2010). SETD8 levels peak at G2/M transition, and regulated SETD8 activity is required for normal cell cycle progression (Rice et al. 2002, Wu et al. 2010).

Literature references

Rice, JC., Nishioka, K., Lis, JT., Tempst, P., Werner, J., Allis, CD. et al. (2002). PR-Set7 is a nucleosome-specific methyltransferase that modifies lysine 20 of histone H4 and is associated with silent chromatin. *Mol. Cell*, 9, 1201-13.

Rice, JC., Yokomori, K., Wu, S., Wang, W., Kirschner, MW., Congdon, LM. et al. (2010). Dynamic regulation of the PR-Set7 histone methyltransferase is required for normal cell cycle progression. *Genes Dev.*, 24, 2531-42.

Rice, JC., Nishioka, K., Reinberg, D., Steward, R., Sarma, K., Allis, CD. (2002). Mitotic-specific methylation of histone H4 Lys 20 follows increased PR-Set7 expression and its localization to mitotic chromosomes. *Genes Dev., 16*, 2225-30.

Editions

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