

PHF8 demethylates histone H4K20me1

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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: 75

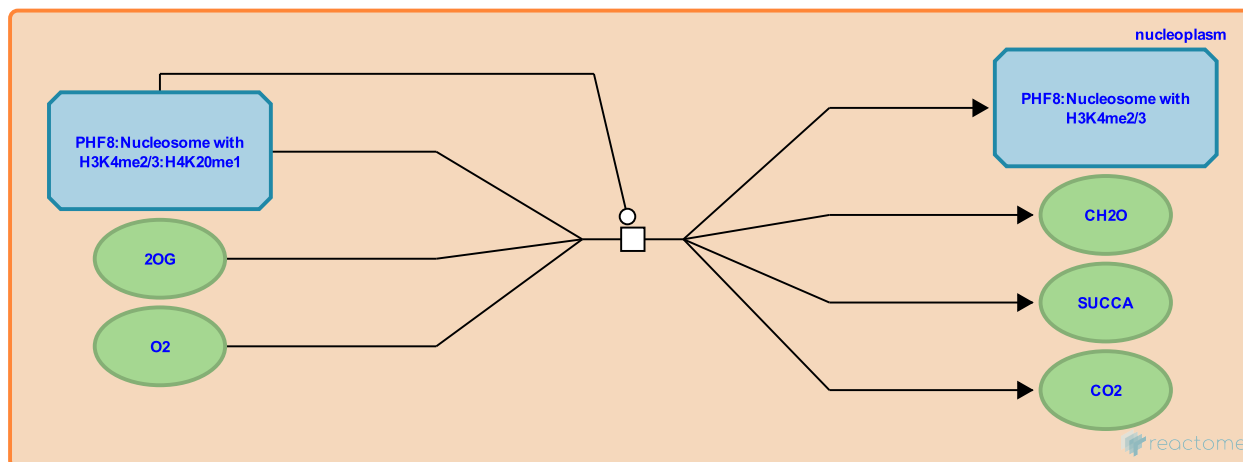
This document contains 1 reaction ([see Table of Contents](#))

PHF8 demethylates histone H4K20me1 [↗](#)

Stable identifier: R-HSA-2172678

Type: transition

Compartments: nucleoplasm



PHF8, a PHD and Jumonji C domain-containing protein, is recruited to chromatin by binding to dimethylated or trimethylated histone H3 - H3K4me2 and/or H3K4me3. PHF8 demethylates monomethylated histone H4, H4K20me1, a docking site for the condensin II complex (Liu et al. 2010).

Literature references

Liu, W., Tanasa, B., Tyurina, OV., Zhou, TY., Gassmann, R., Liu, WT. et al. (2010). PHF8 mediates histone H4 lysine 20 demethylation events involved in cell cycle progression. *Nature*, 466, 508-12. [↗](#)

Editions

2013-04-23	Edited	Matthews, L.
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