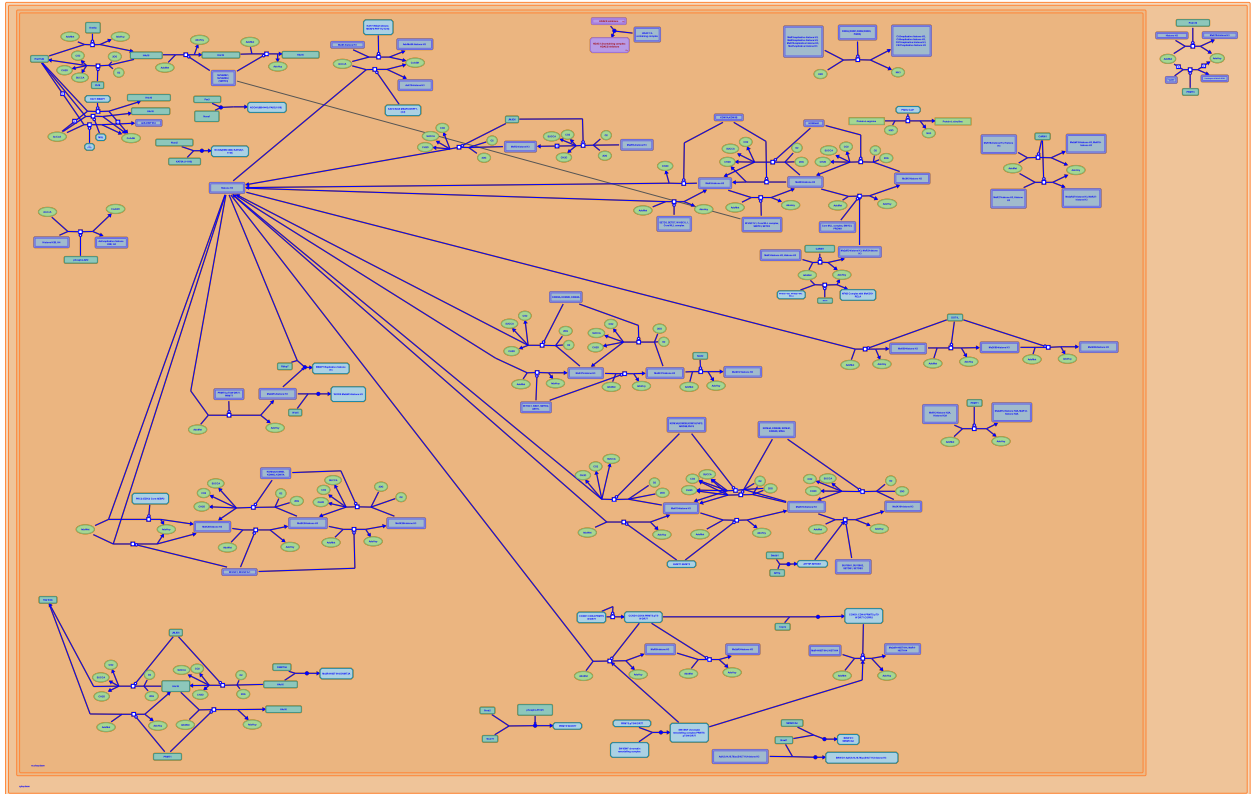


# Chromatin modifying enzymes



European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://reactome.org/licenses).

This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the [Reactome Textbook](https://reactome.org/textbook).

06/05/2024

## 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. [↗](#)

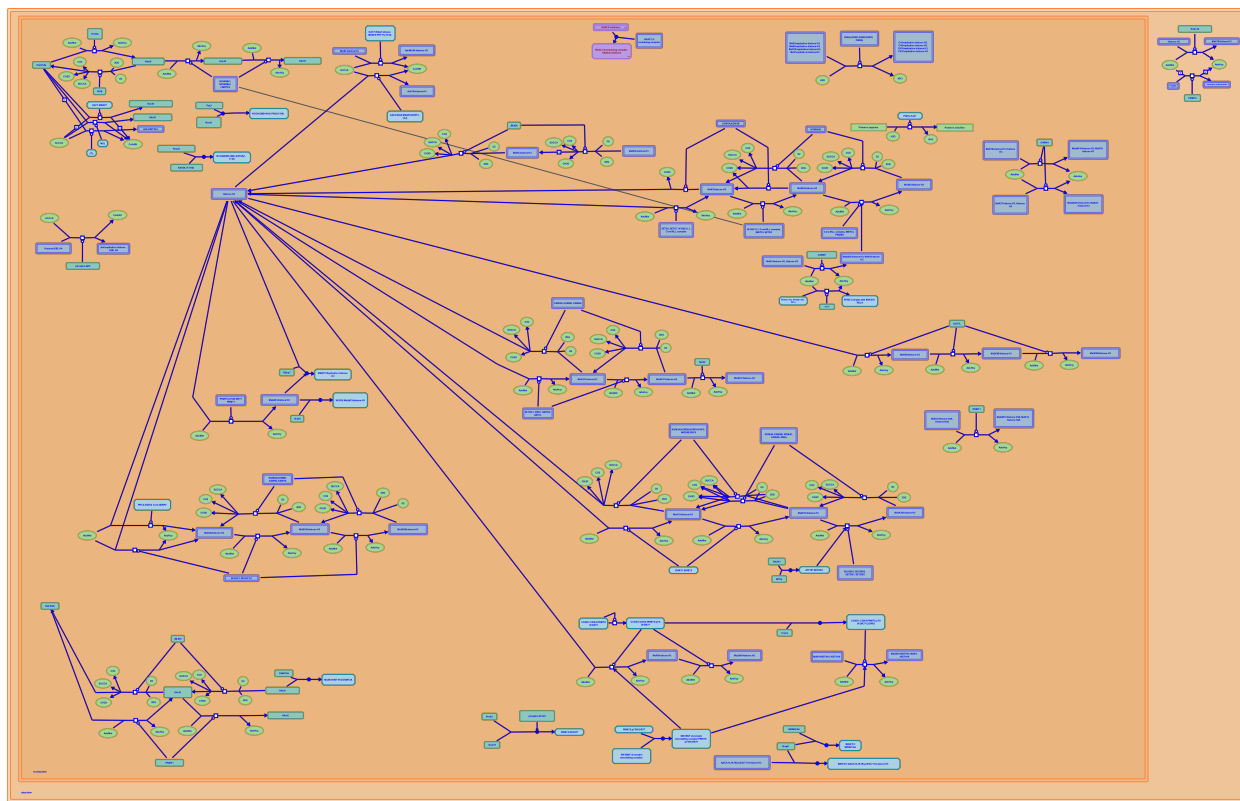
Reactome database release: 88

This document contains 6 pathways and 4 reactions ([see Table of Contents](#))

## Chromatin modifying enzymes ↗

**Stable identifier:** R-RNO-3247509

**Inferred from:** Chromatin modifying enzymes (Homo sapiens)



 reactome

This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

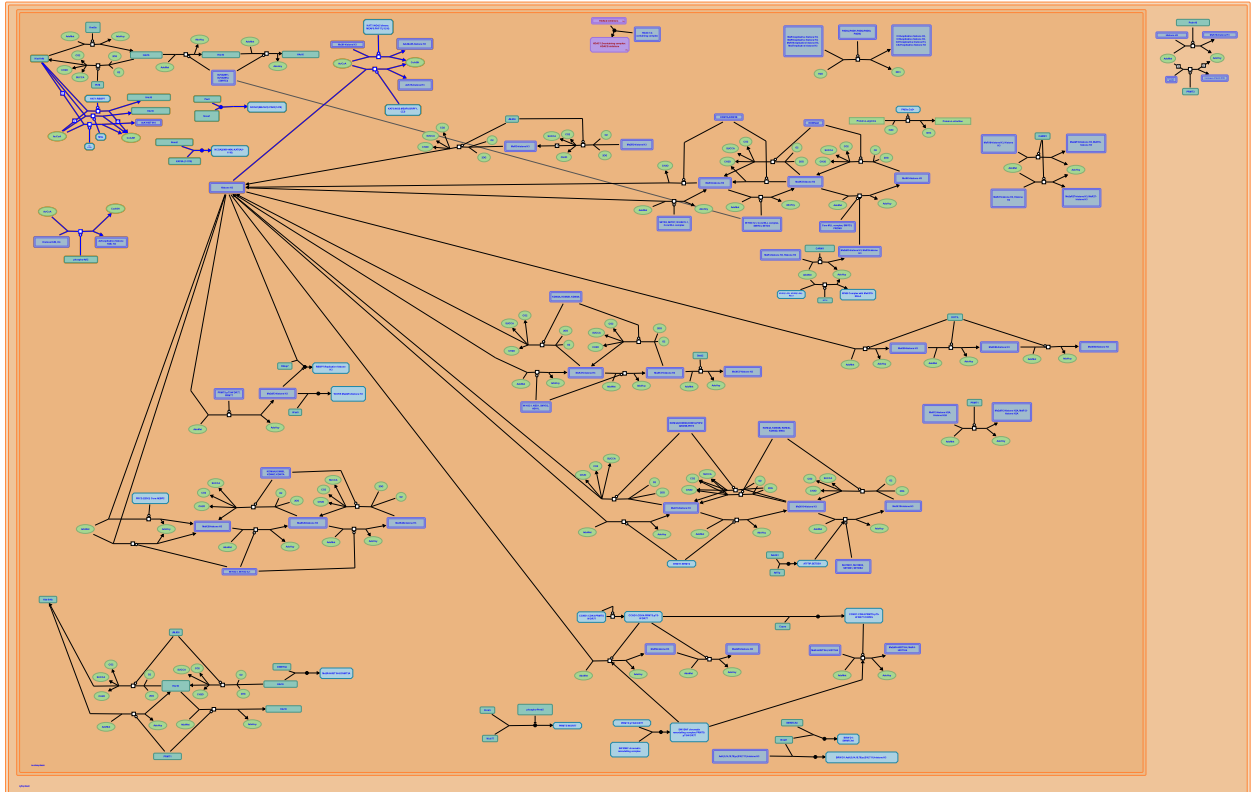
[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## HATs acetylate histones ↗

**Location:** Chromatin modifying enzymes

**Stable identifier:** R-RNO-3214847

**Inferred from:** HATs acetylate histones (Homo sapiens)



reactome

This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

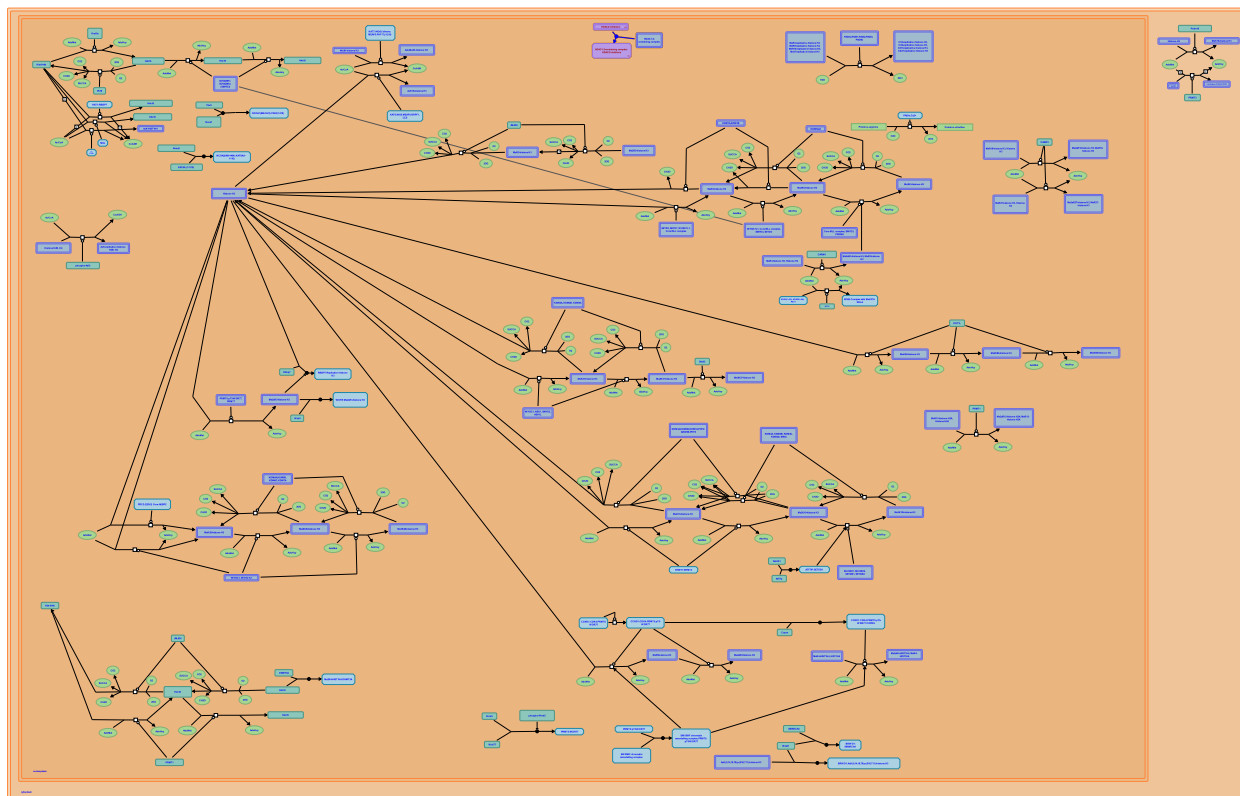
[More details and caveats of the event inference in Reactome.](https://www.reactome.org) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## HDACs deacetylate histones ↗

**Location:** Chromatin modifying enzymes

**Stable identifier:** R-RNO-3214815

**Inferred from:** HDACs deacetylate histones (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

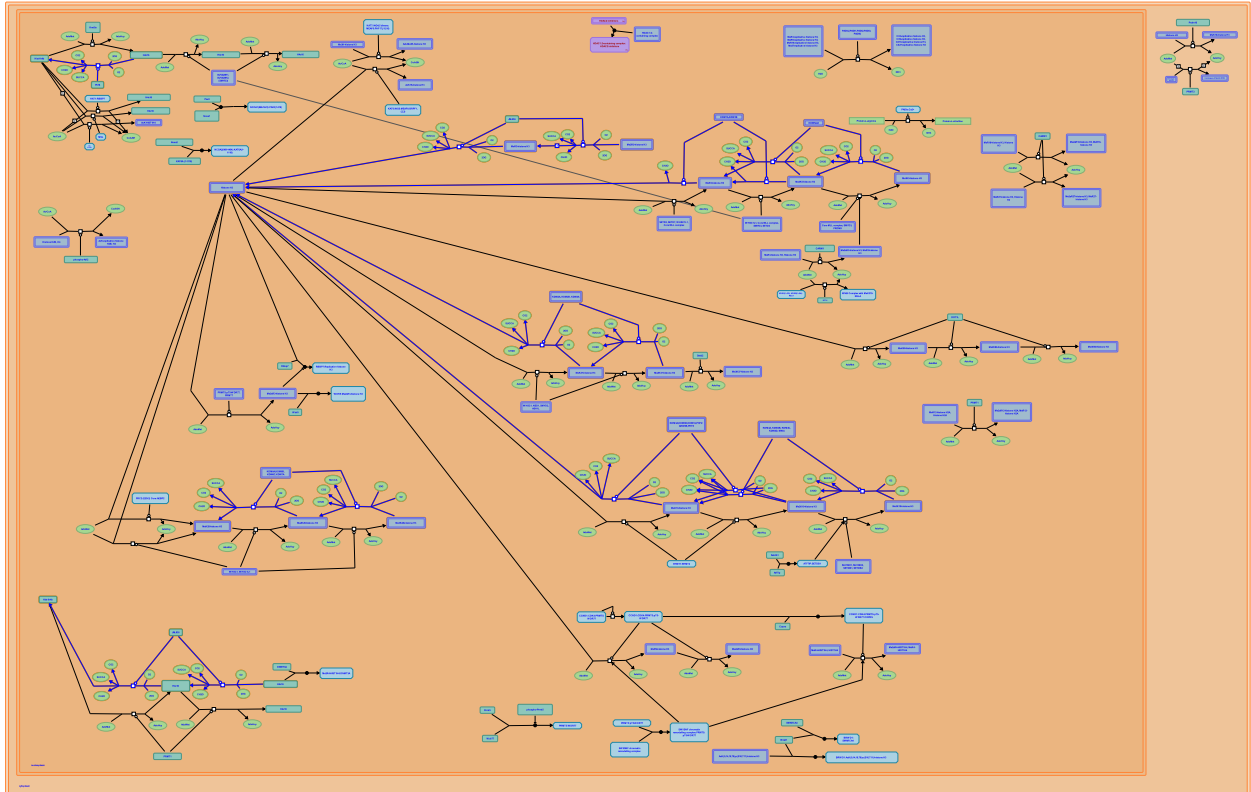
[More details and caveats of the event inference in Reactome.](https://www.reactome.org) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## HDMs demethylate histones ↗

**Location:** Chromatin modifying enzymes

**Stable identifier:** R-RNO-3214842

**Inferred from:** HDMs demethylate histones (Homo sapiens)



reactome

This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

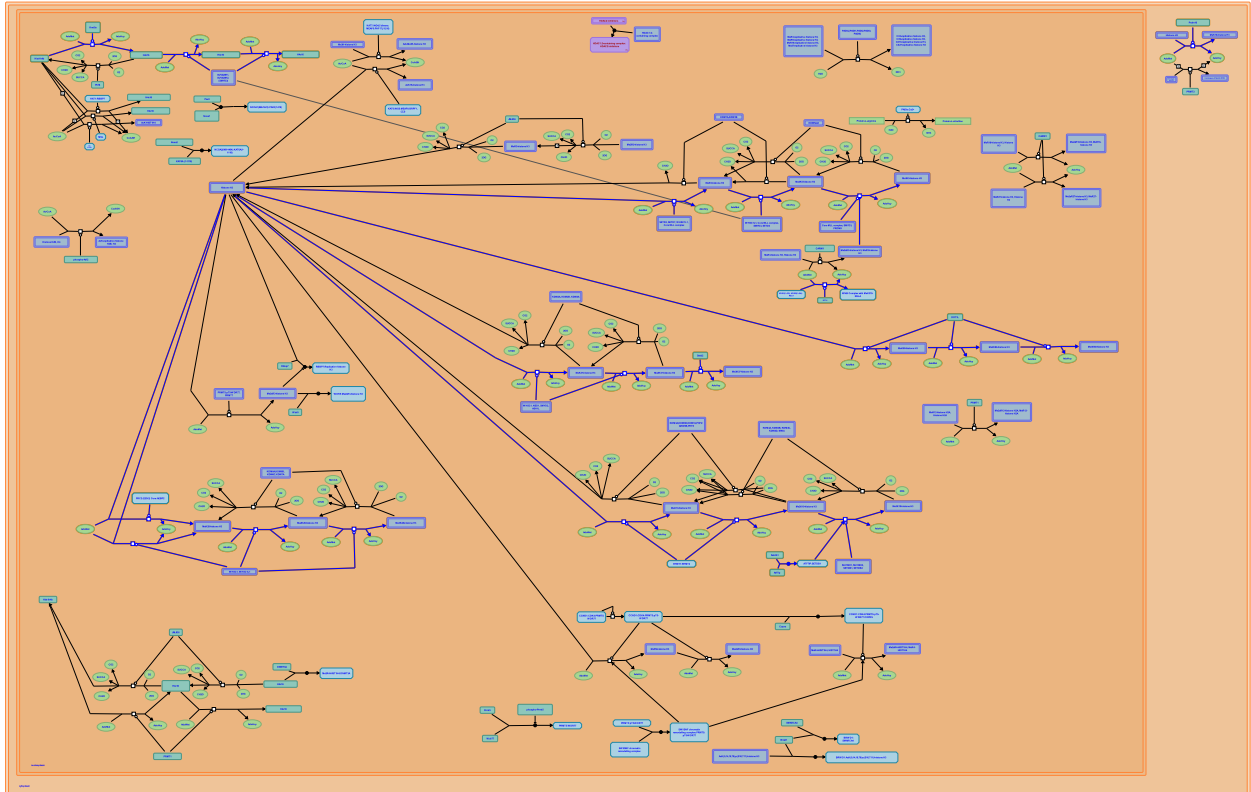
[More details and caveats of the event inference in Reactome.](https://www.reactome.org) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## PKMTs methylate histone lysines ↗

**Location:** Chromatin modifying enzymes

**Stable identifier:** R-RNO-3214841

**Inferred from:** PKMTs methylate histone lysines (Homo sapiens)



reactome

This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

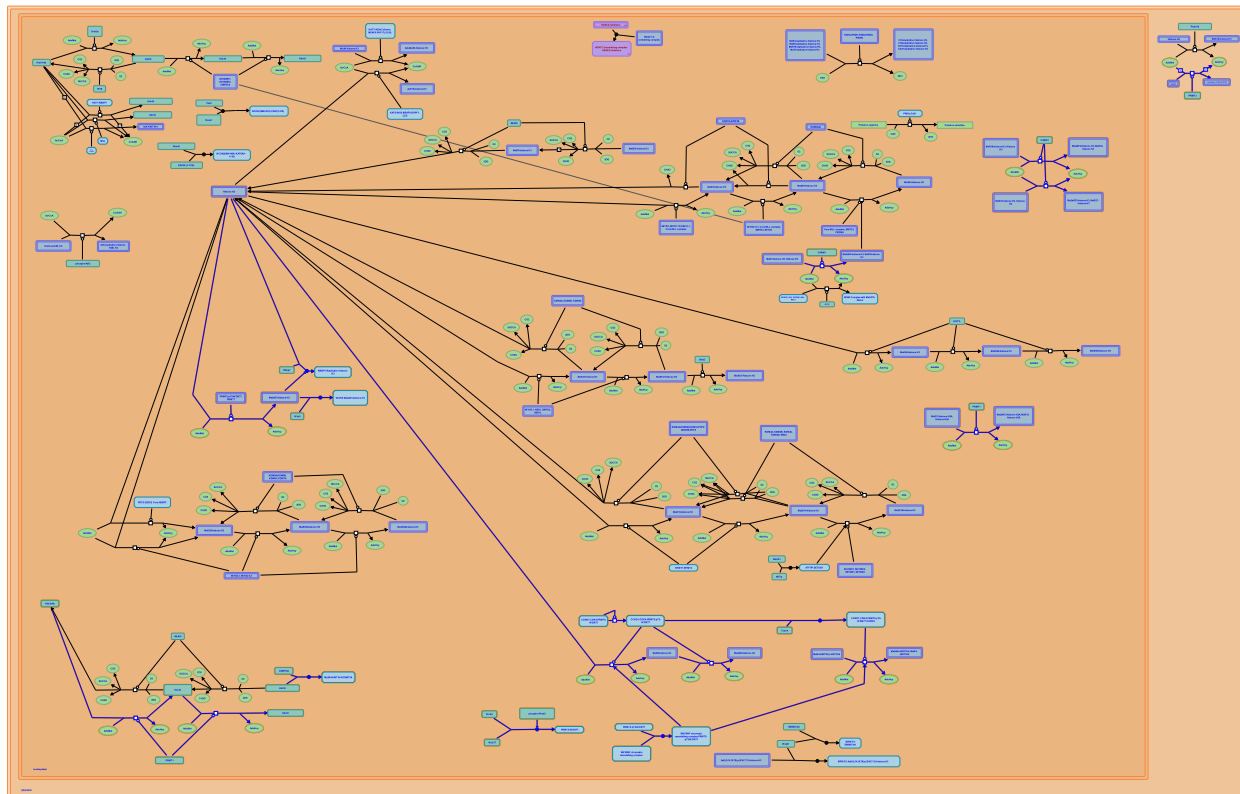
[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## RMTs methylate histone arginines ↗

**Location:** Chromatin modifying enzymes

**Stable identifier:** R-RNO-3214858

**Inferred from:** RMTs methylate histone arginines (Homo sapiens)



reactome

This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](https://www.reactome.org/docs/inferring_reactions.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>



## PADI4 deiminates Histones ↗

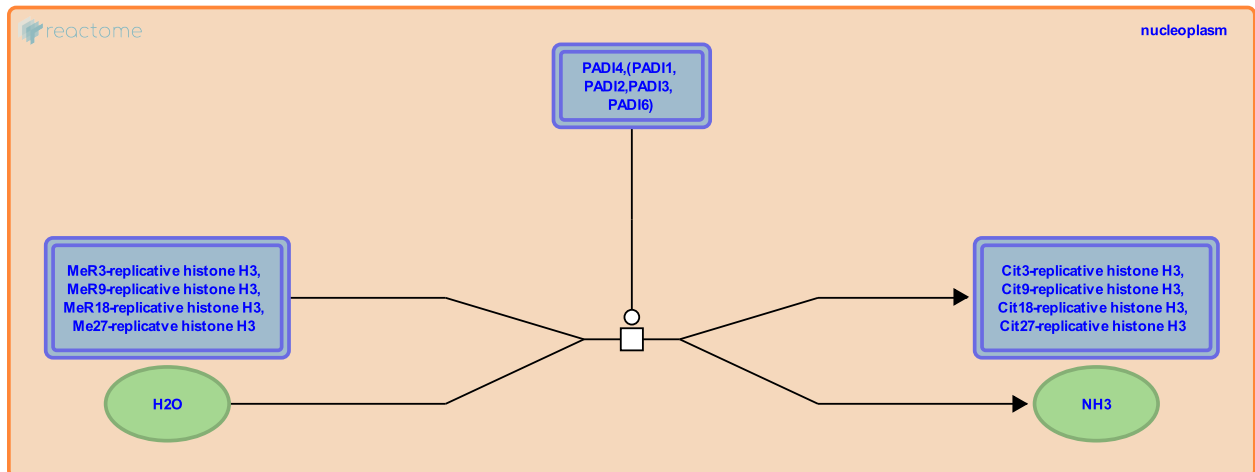
**Location:** Chromatin modifying enzymes

**Stable identifier:** R-RNO-3247569

**Type:** transition

**Compartments:** nucleoplasm

**Inferred from:** PADI4 deiminates Histones (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## PADIs:Ca<sup>2+</sup> deiminate L-Arg to L-Cit in proteins ↗

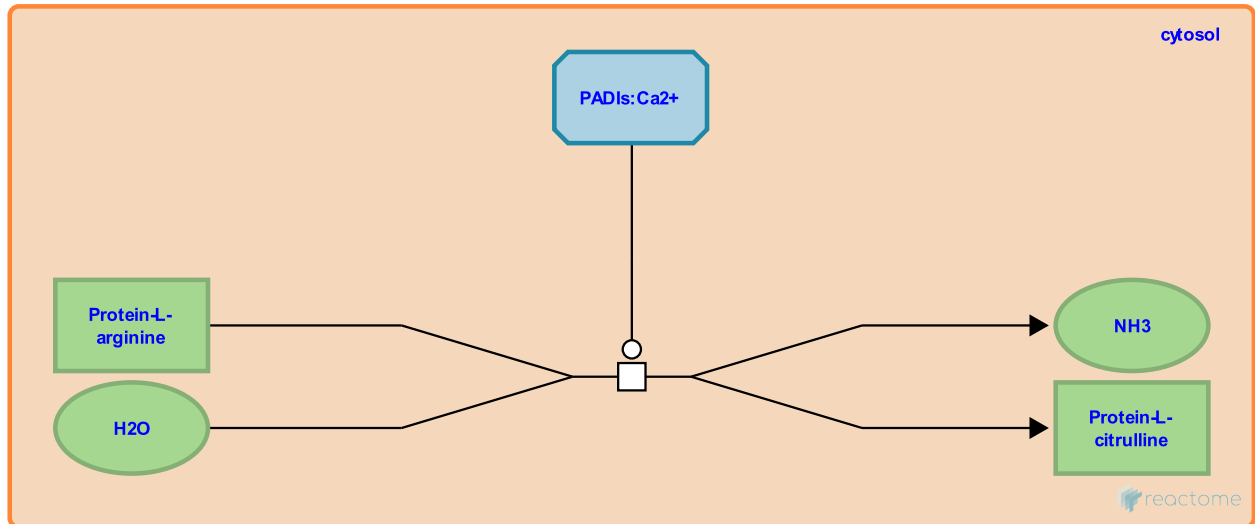
**Location:** [Chromatin modifying enzymes](#)

**Stable identifier:** R-RNO-1183128

**Type:** transition

**Compartments:** cytosol

**Inferred from:** [PADIs:Ca<sup>2+</sup> deiminate L-Arg to L-Cit in proteins \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## BRWD1 binds SMARCA4 ↗

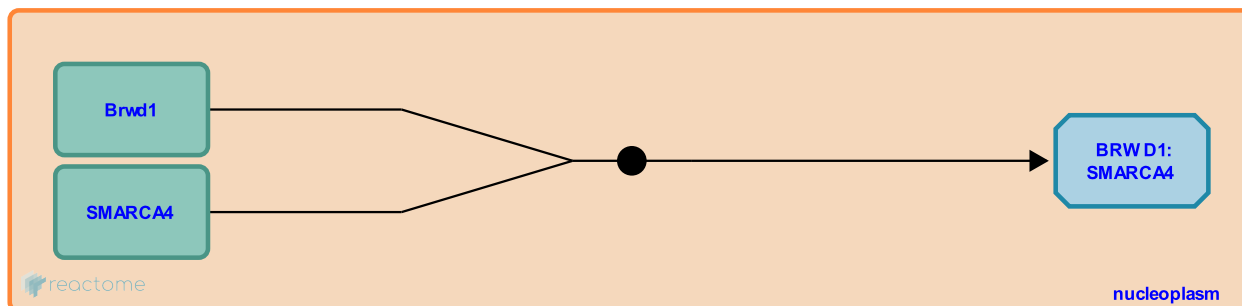
**Location:** [Chromatin modifying enzymes](#)

**Stable identifier:** R-RNO-8865605

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** [BRWD1 binds SMARCA4 \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## BRWD1 binds AcK(9,14,18,79)-p(S10,T11)-histone H3 ↗

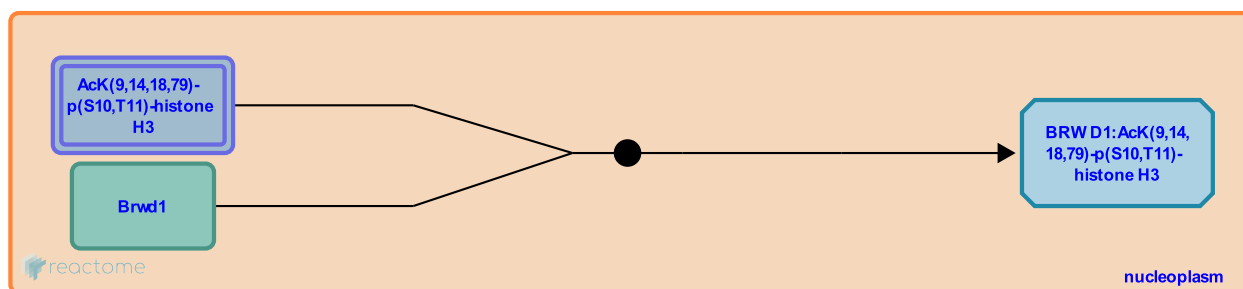
**Location:** [Chromatin modifying enzymes](#)

**Stable identifier:** R-RNO-8865613

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** [BRWD1 binds AcK\(9,14,18,79\)-p\(S10,T11\)-histone H3 \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

# Table of Contents

Introduction	1
❖ Chromatin modifying enzymes	2
❖ HATs acetylate histones	3
❖ HDACs deacetylate histones	4
❖ HDMs demethylate histones	5
❖ PKMTs methylate histone lysines	6
❖ RMTs methylate histone arginines	7
⤵ PADI4 deiminates Histones	8
⤵ PADIs:Ca <sup>2+</sup> deiminate L-Arg to L-Cit in proteins	9
⤵ BRWD1 binds SMARCA4	10
⤵ BRWD1 binds AcK(9,14,18,79)-p(S10,T11)-histone H3	11
Table of Contents	12