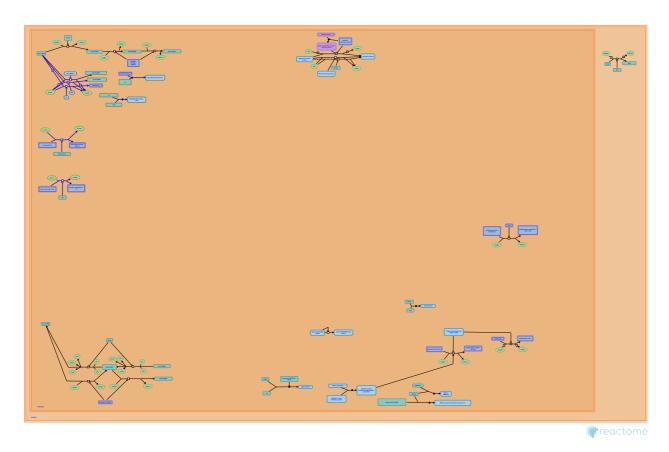


HATs acetylate histones



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

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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.

19/05/2024

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

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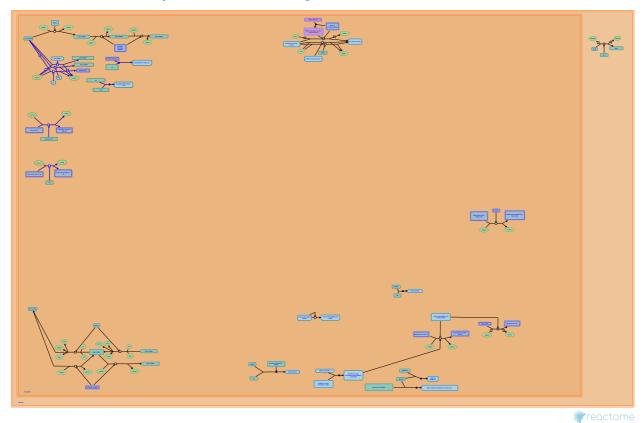
Reactome database release: 88

This document contains 1 pathway and 7 reactions (see Table of Contents)

HATs acetylate histones ↗

Stable identifier: R-DME-3214847

Inferred from: HATs acetylate 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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Type B histone acetlytransferase complex acetylates histone H4 7

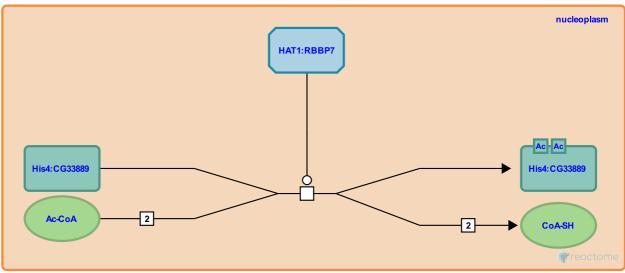
Location: HATs acetylate histones

Stable identifier: R-DME-3662318

Type: transition

Compartments: nucleoplasm

Inferred from: Type B histone acetlytransferase complex acetylates histone H4 (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.

 $\underline{More\ details\ and\ cave ats\ of\ the\ event\ inference\ in\ Reactome.}\ For\ details\ on\ PANTHER\ see\ also: \\ \underline{http://www.pantherdb.org/about.jsp}$

EP300 acetylates histone H2A, H2B, H3, H4 7

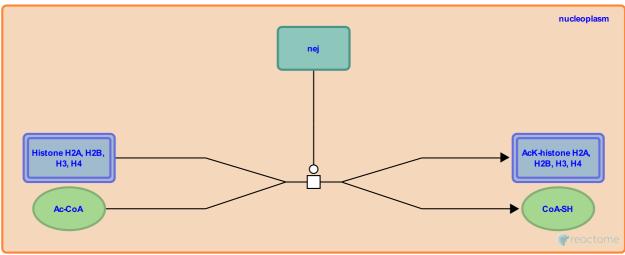
Location: HATs acetylate histones

Stable identifier: R-DME-3662335

Type: transition

Compartments: nucleoplasm

Inferred from: EP300 acetylates histone H2A, H2B, H3, H4 (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.

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ATF2 acetylates histone H2B, H4 对

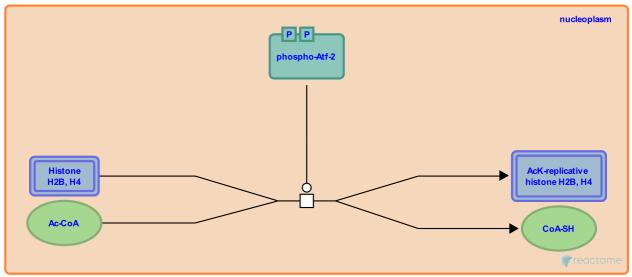
Location: HATs acetylate histones

Stable identifier: R-DME-3318415

Type: transition

Compartments: nucleoplasm

Inferred from: ATF2 acetylates histone H2B, H4 (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

MSL acetylates histone H4 **才**

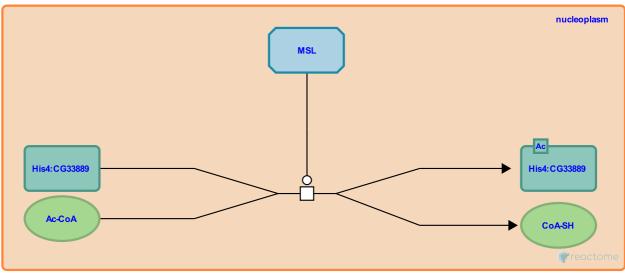
Location: HATs acetylate histones

Stable identifier: R-DME-3321883

Type: transition

Compartments: nucleoplasm

Inferred from: MSL acetylates histone H4 (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.

 $\underline{More\ details\ and\ cave ats\ of\ the\ event\ inference\ in\ Reactome.}\ For\ details\ on\ PANTHER\ see\ also: \\ \underline{http://www.pantherdb.org/about.jsp}$

NSL acetylates histone H4 **才**

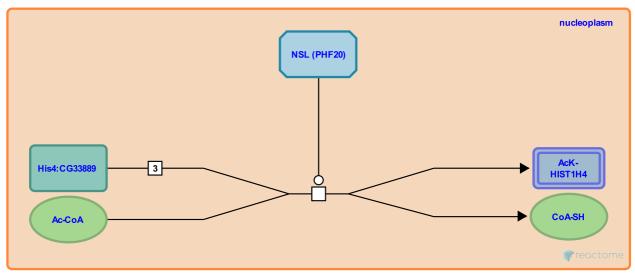
Location: HATs acetylate histones

Stable identifier: R-DME-3321805

Type: transition

Compartments: nucleoplasm

Inferred from: NSL acetylates histone H4 (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

NCOA1(868-1441) binds PAX3(1-319) 7

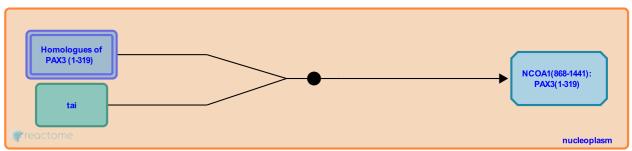
Location: HATs acetylate histones

Stable identifier: R-DME-5579018

Type: binding

Compartments: nucleoplasm

Inferred from: NCOA1(868-1441) binds PAX3(1-319) (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

NCOA2(869-1464) binds KAT6A(1-1118) **对**

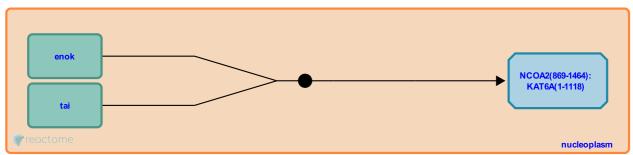
Location: HATs acetylate histones

Stable identifier: R-DME-5579023

Type: binding

Compartments: nucleoplasm

Inferred from: NCOA2(869-1464) binds KAT6A(1-1118) (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

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