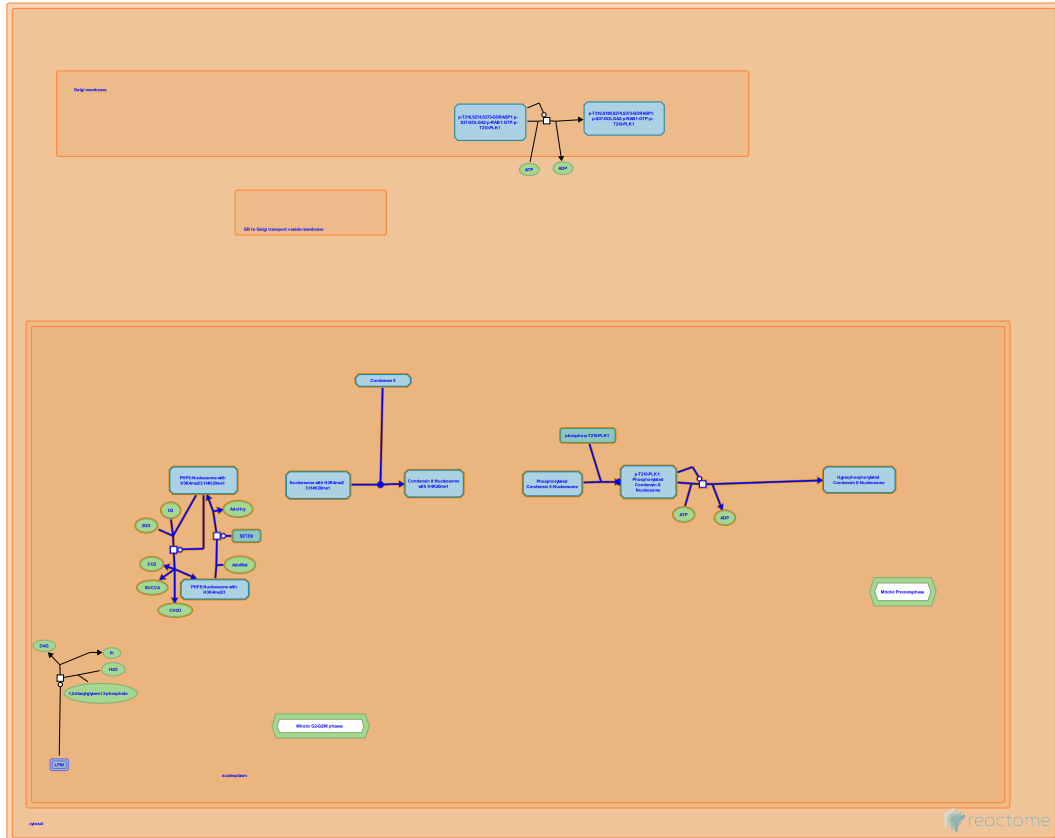


Condensation of Prophase Chromosomes



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](https://reactome.org/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

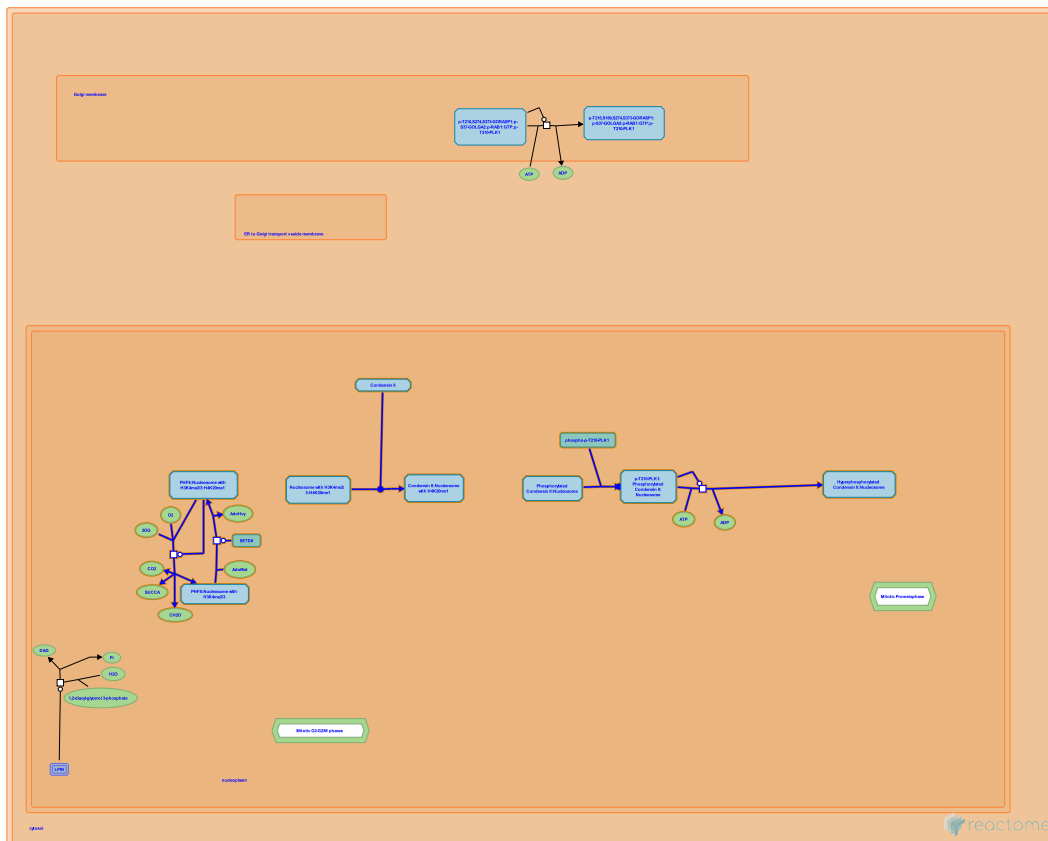
This document contains 1 pathway and 5 reactions ([see Table of Contents](#))

Condensation of Prophase Chromosomes ↗

Stable identifier: R-PFA-2299718

Compartments: nucleoplasm

Inferred from: [Condensation of Prophase Chromosomes \(Homo sapiens\)](#)



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>

SETD8 monomethylates histone H4 ↗

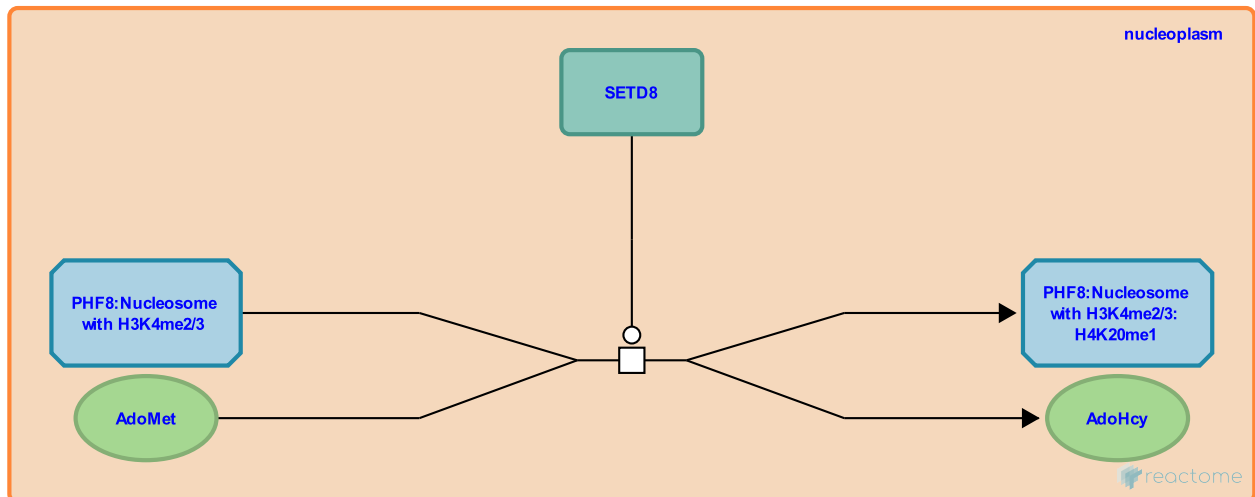
Location: [Condensation of Prophase Chromosomes](#)

Stable identifier: R-PFA-2301205

Type: transition

Compartments: nucleoplasm

Inferred from: [SETD8 monomethylates 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.

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Followed by: [PHF8 demethylates histone H4K20me1](#)

PHF8 demethylates histone H4K20me1 ↗

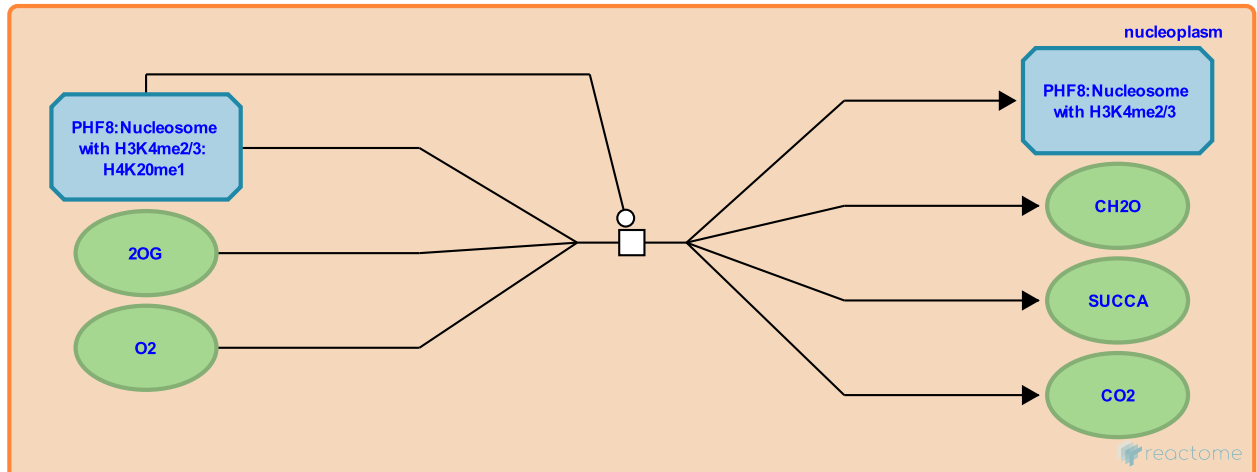
Location: [Condensation of Prophase Chromosomes](#)

Stable identifier: R-PFA-2172678

Type: transition

Compartments: nucleoplasm

Inferred from: [PHF8 demethylates histone H4K20me1 \(Homo sapiens\)](#)



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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Preceded by: [SETD8 monomethylates histone H4](#)

Condensin II complex binds H4K20me1-containing nucleosomes ↗

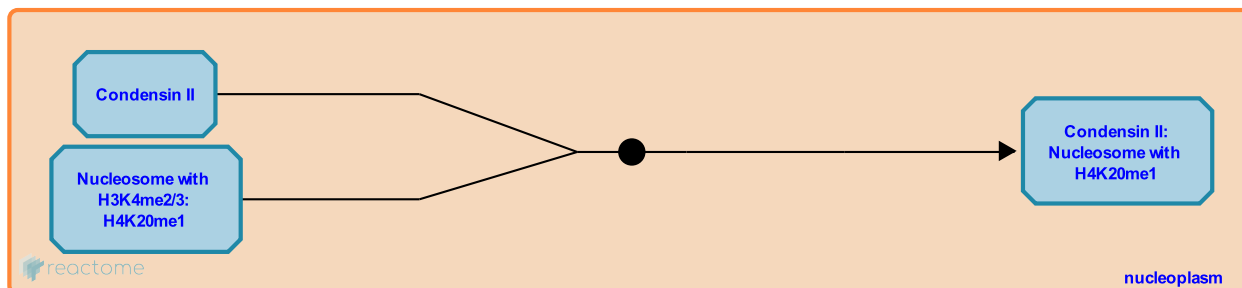
Location: [Condensation of Prophase Chromosomes](#)

Stable identifier: R-PFA-2288097

Type: binding

Compartments: nucleoplasm

Inferred from: [Condensin II complex binds H4K20me1-containing nucleosomes \(Homo sapiens\)](#)



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>

PLK1 binds phosphorylated condensin II complex ↗

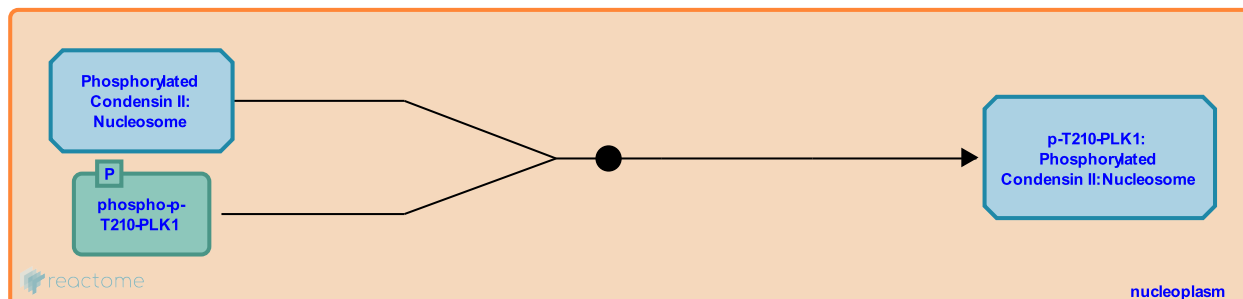
Location: [Condensation of Prophase Chromosomes](#)

Stable identifier: R-PFA-2294590

Type: binding

Compartments: nucleoplasm

Inferred from: [PLK1 binds phosphorylated condensin II complex \(Homo sapiens\)](#)



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>

Followed by: [PLK1 hyperphosphorylates Condensin II complex](#)

PLK1 hyperphosphorylates Condensin II complex ↗

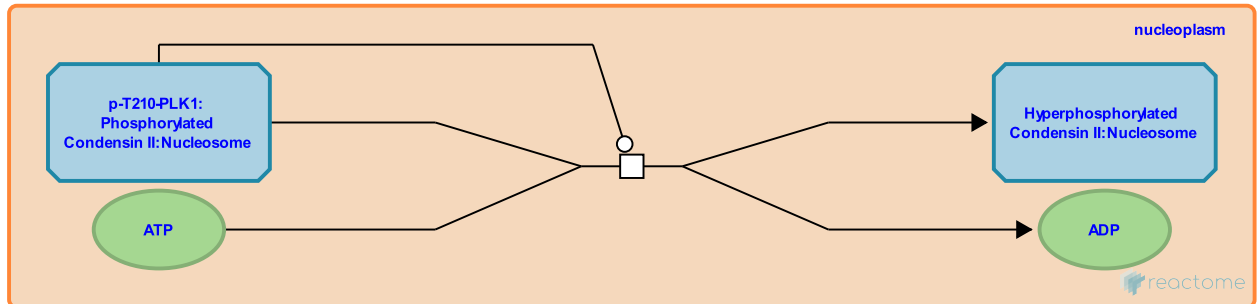
Location: [Condensation of Prophase Chromosomes](#)

Stable identifier: R-PFA-2294580

Type: transition

Compartments: nucleoplasm

Inferred from: [PLK1 hyperphosphorylates Condensin II complex \(Homo sapiens\)](#)



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>

Preceded by: [PLK1 binds phosphorylated condensin II complex](#)

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