reactome

Condensation of Prophase Chromosomes

27/09/2020

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 database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

Reactome database release: 73

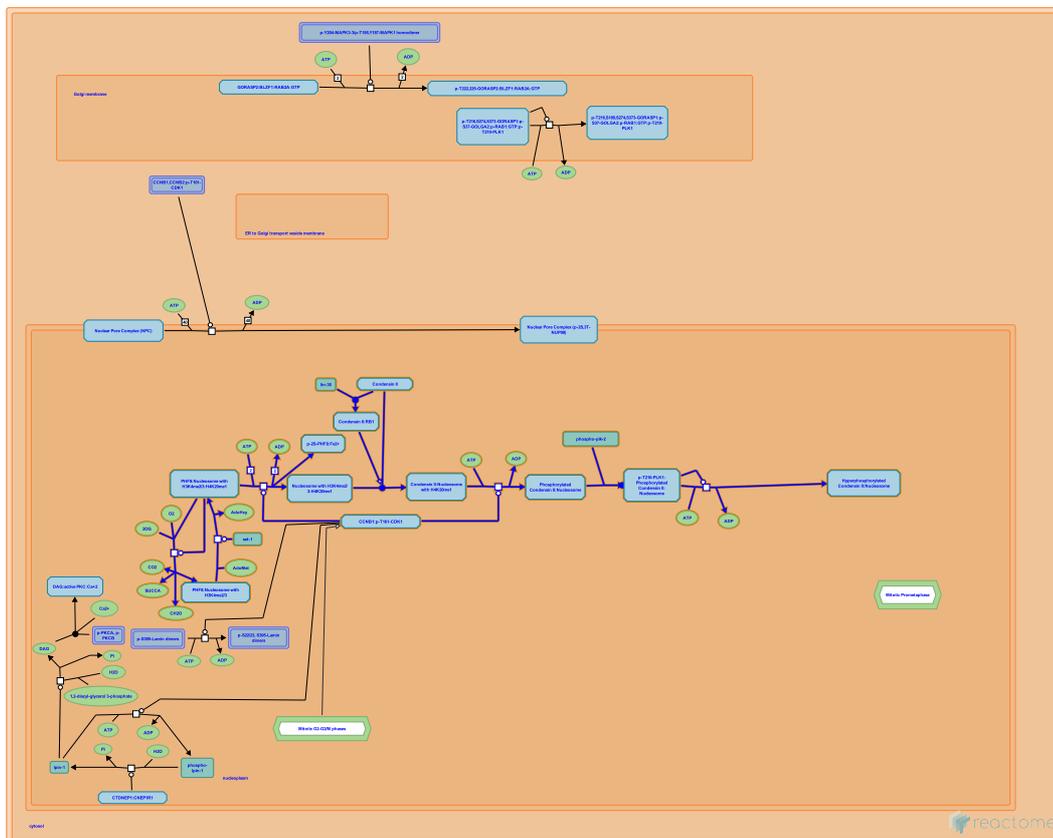This document contains 1 pathway and 8 reactions (see Table of Contents)

Condensation of Prophase Chromosomes ↗

Stable identifier: R-CEL-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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp
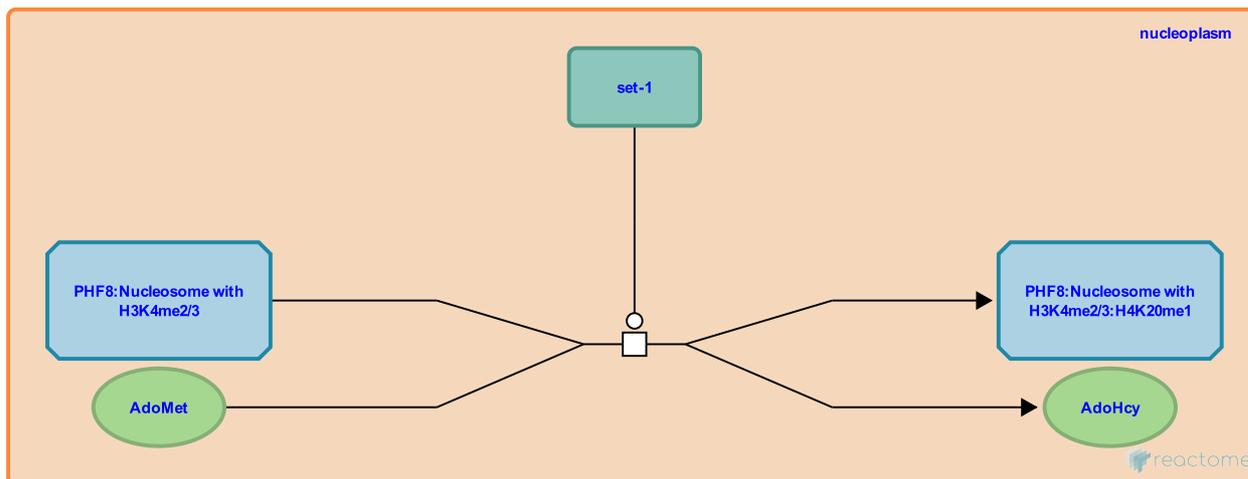
SETD8 monomethylates histone H4 ↗

Location: Condensation of Prophase Chromosomes

Stable identifier: R-CEL-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, CDK1 phosphorylates PHF8
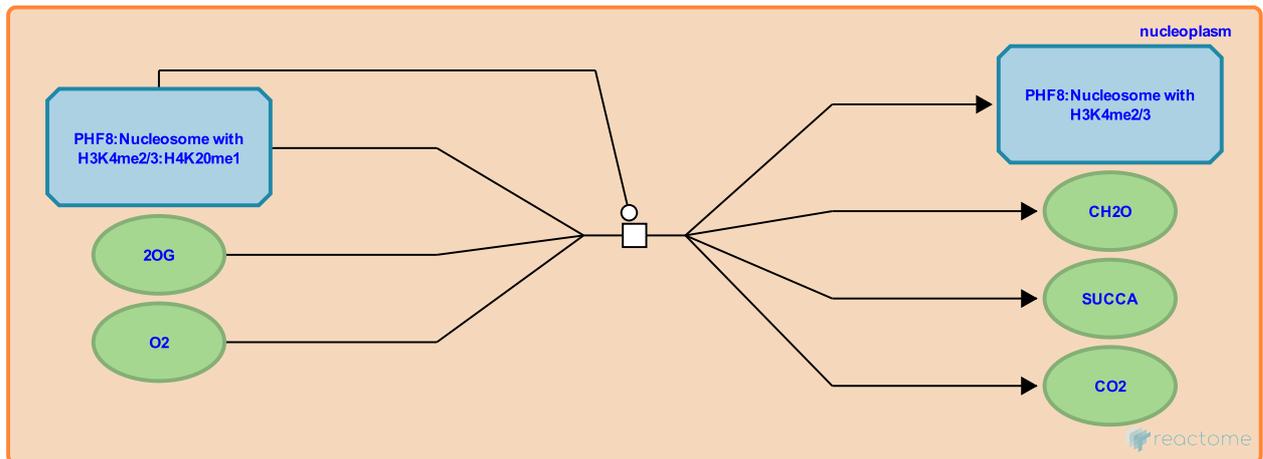
PHF8 demethylates histone H4K20me1 ↗

Location: Condensation of Prophase Chromosomes

Stable identifier: R-CEL-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
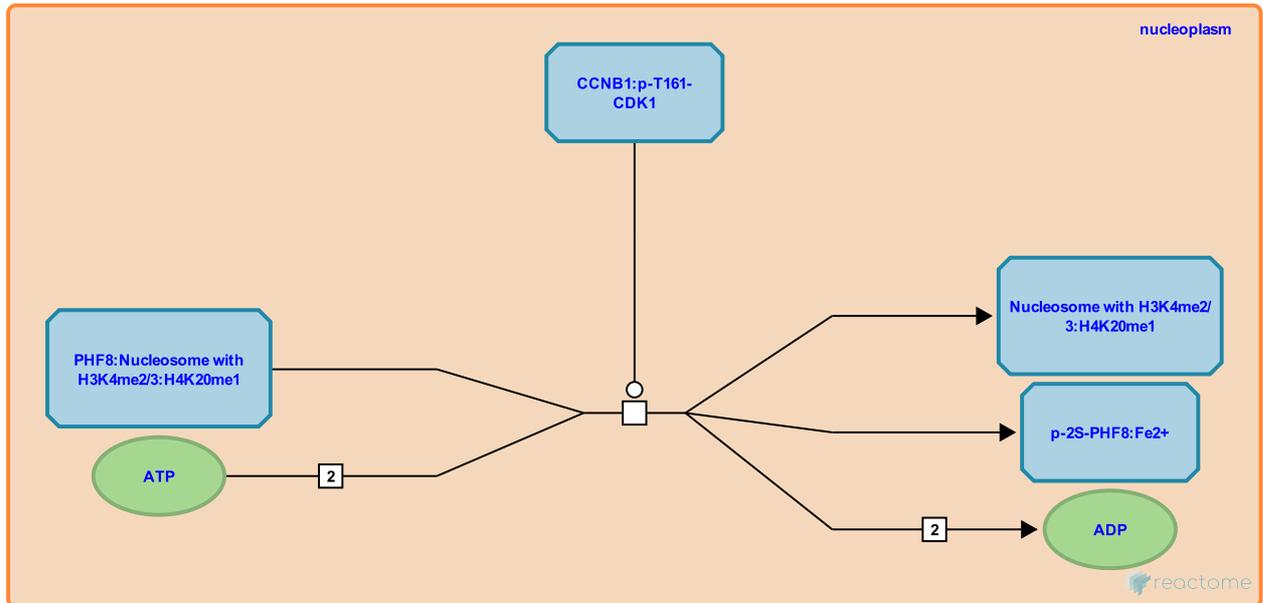
CDK1 phosphorylates PHF8 ↗

Location: Condensation of Prophase Chromosomes

Stable identifier: R-CEL-2245218

Type: transition

Compartments: nucleoplasm

Inferred from: CDK1 phosphorylates PHF8 (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

Followed by: Condensin II complex binds H4K20me1-containing nucleosomes
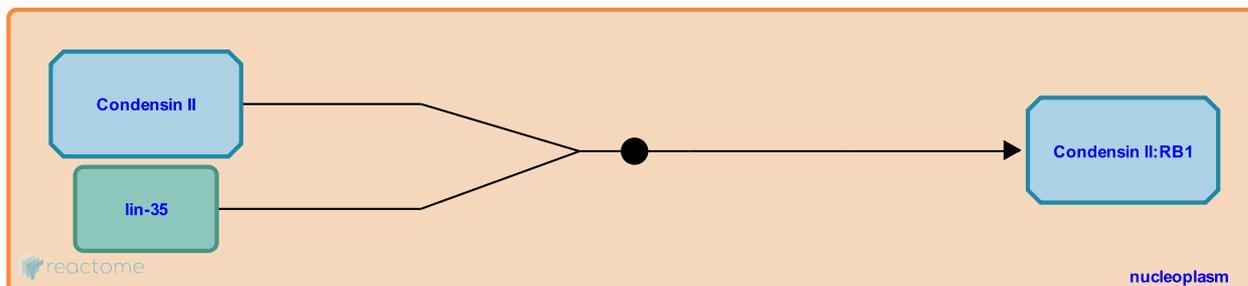
RB1 binds condensin II ↗

Location: Condensation of Prophase Chromosomes

Stable identifier: R-CEL-2172666

Type: binding

Compartments: nucleoplasm

Inferred from: RB1 binds condensin II (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: Condensin II complex binds H4K20me1-containing nucleosomes

Condensin II complex binds H4K20me1-containing nucleosomes ↗

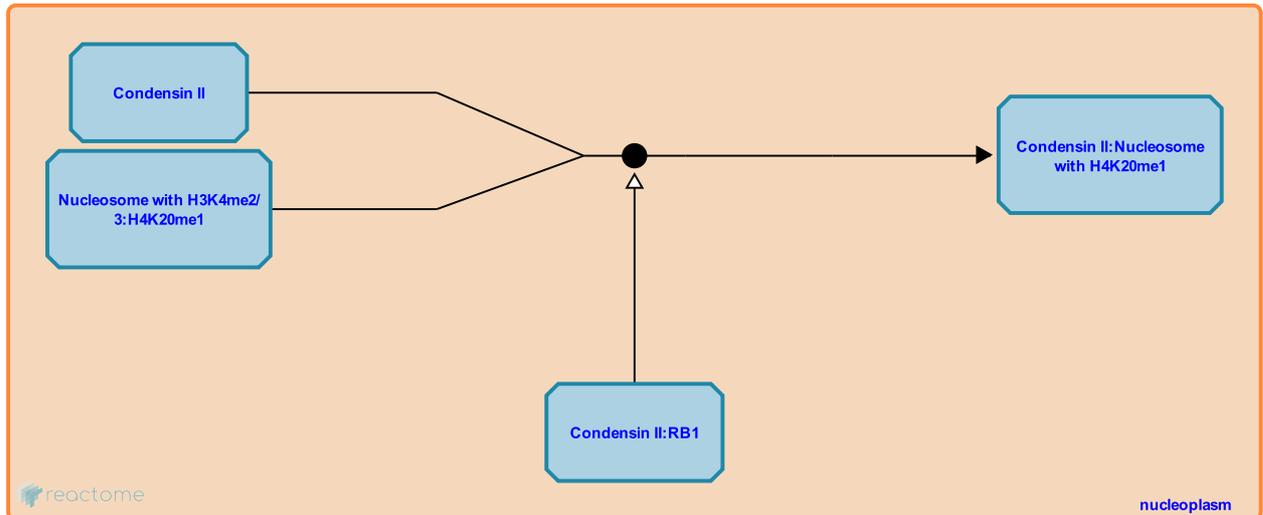**Location:** Condensation of Prophase Chromosomes

Stable identifier: R-CEL-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.

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Preceded by: RB1 binds condensin II, CDK1 phosphorylates PHF8

Followed by: CDK1 phosphorylates condensin II subunit NCAPD3

CDK1 phosphorylates condensin II subunit NCAPD3 ↗

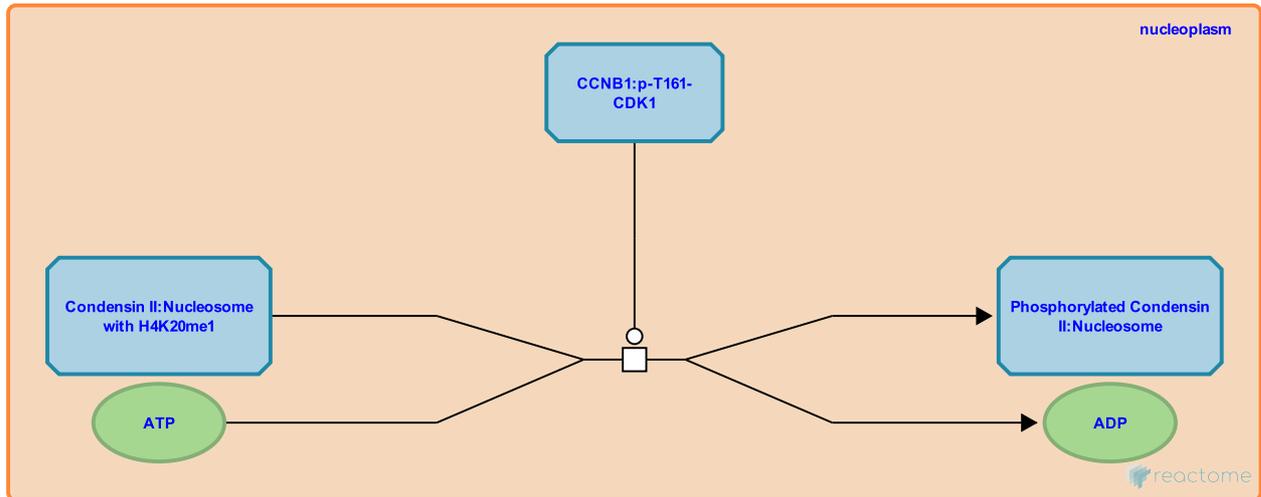**Location:** Condensation of Prophase Chromosomes

Stable identifier: R-CEL-2294600

Type: transition

Compartments: nucleoplasm

Inferred from: CDK1 phosphorylates condensin II subunit NCAPD3 (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: Condensin II complex binds H4K20me1-containing nucleosomes

Followed by: PLK1 binds phosphorylated condensin II complex
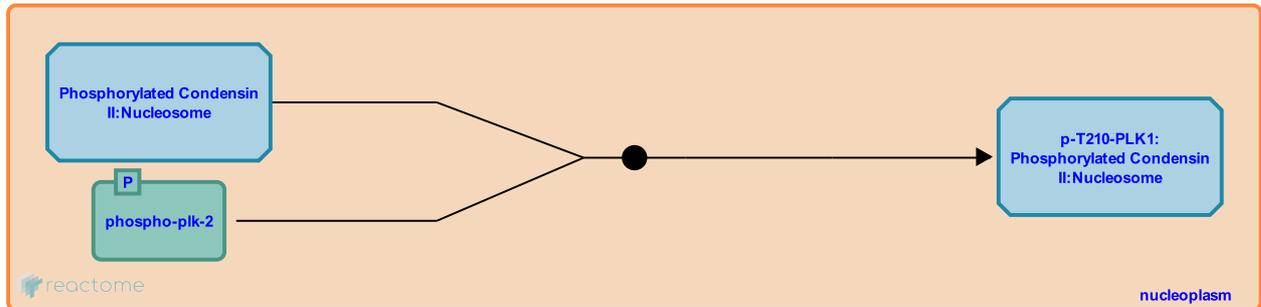
PLK1 binds phosphorylated condensin II complex ↗

Location: Condensation of Prophase Chromosomes

Stable identifier: R-CEL-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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Preceded by: CDK1 phosphorylates condensin II subunit NCAPD3

Followed by: PLK1 hyperphosphorylates Condensin II complex
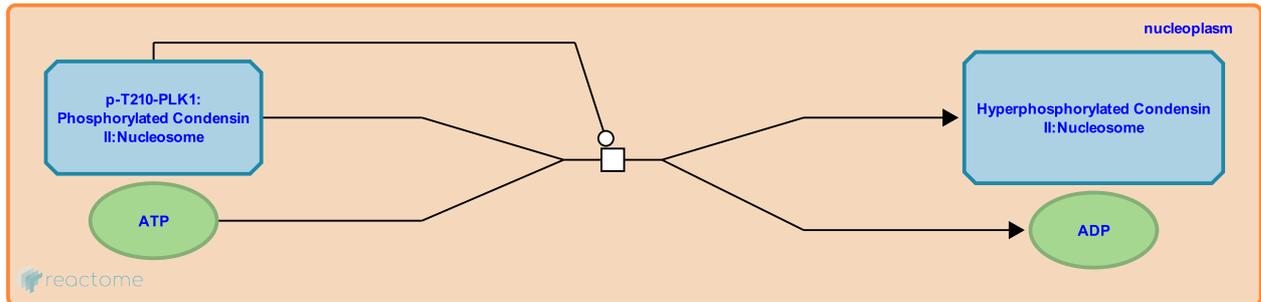
PLK1 hyperphosphorylates Condensin II complex ↗

Location: Condensation of Prophase Chromosomes

Stable identifier: R-CEL-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.

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Preceded by: PLK1 binds phosphorylated condensin II complex

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