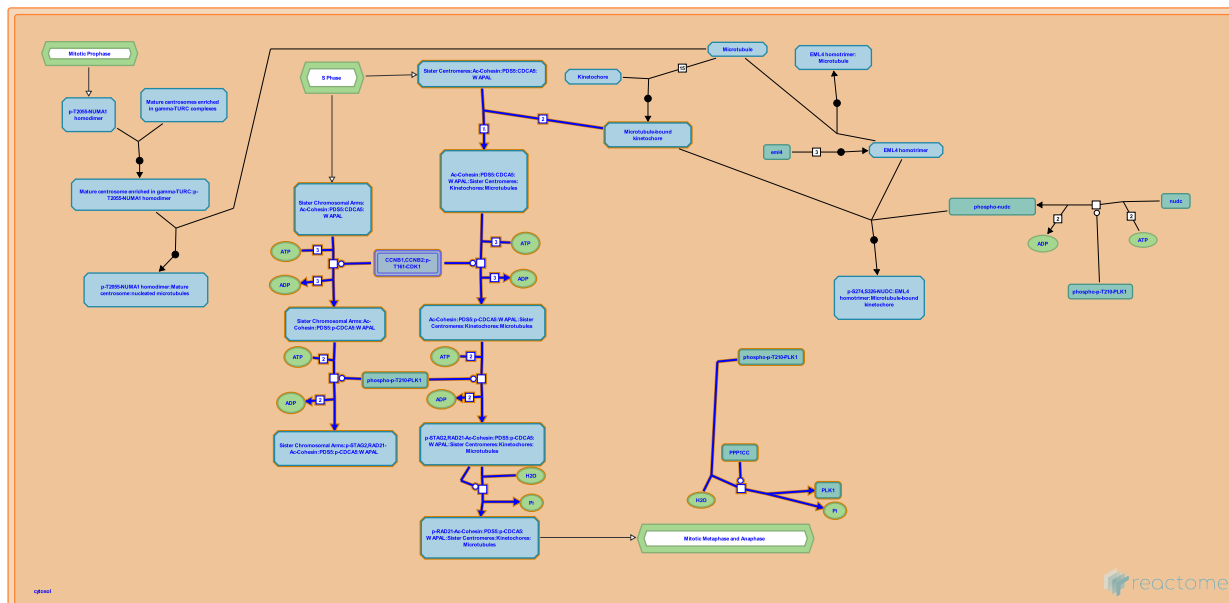


Resolution of Sister Chromatid Cohesion



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).

18/05/2024

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

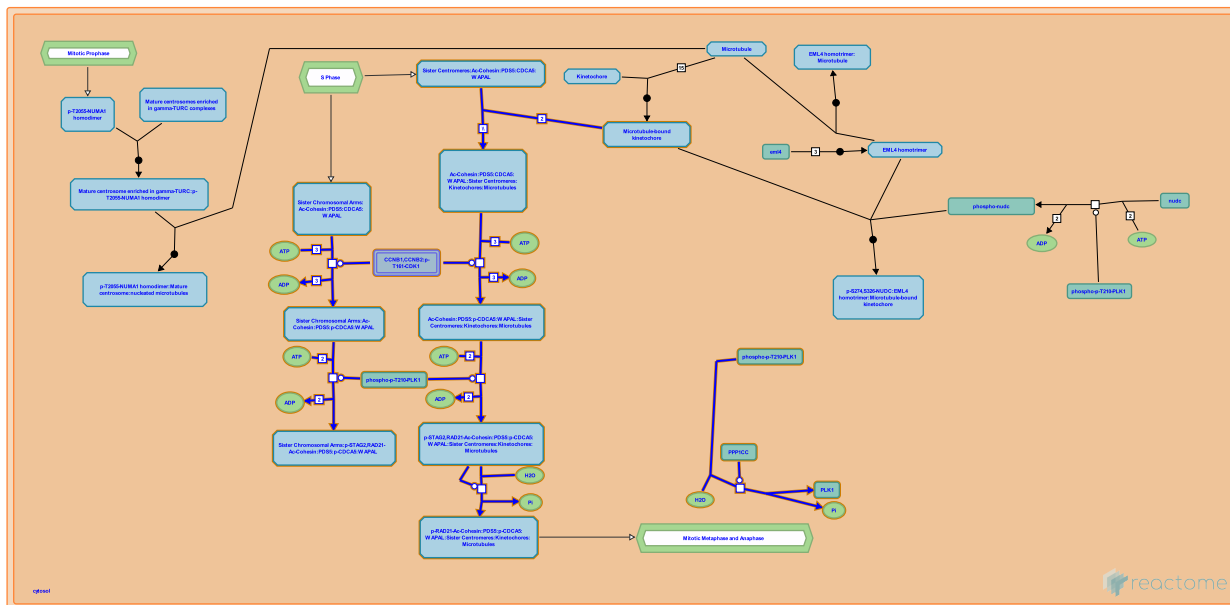
This document contains 1 pathway and 7 reactions ([see Table of Contents](#))

Resolution of Sister Chromatid Cohesion [↗](#)

Stable identifier: R-XTR-2500257

Compartments: cytosol, chromosome, chromosome, centromeric region

Inferred from: Resolution of Sister Chromatid Cohesion (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/parologue (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>

CDK1 phosphorylates CDCA5 (Sororin) at chromosomal arms [↗](#)

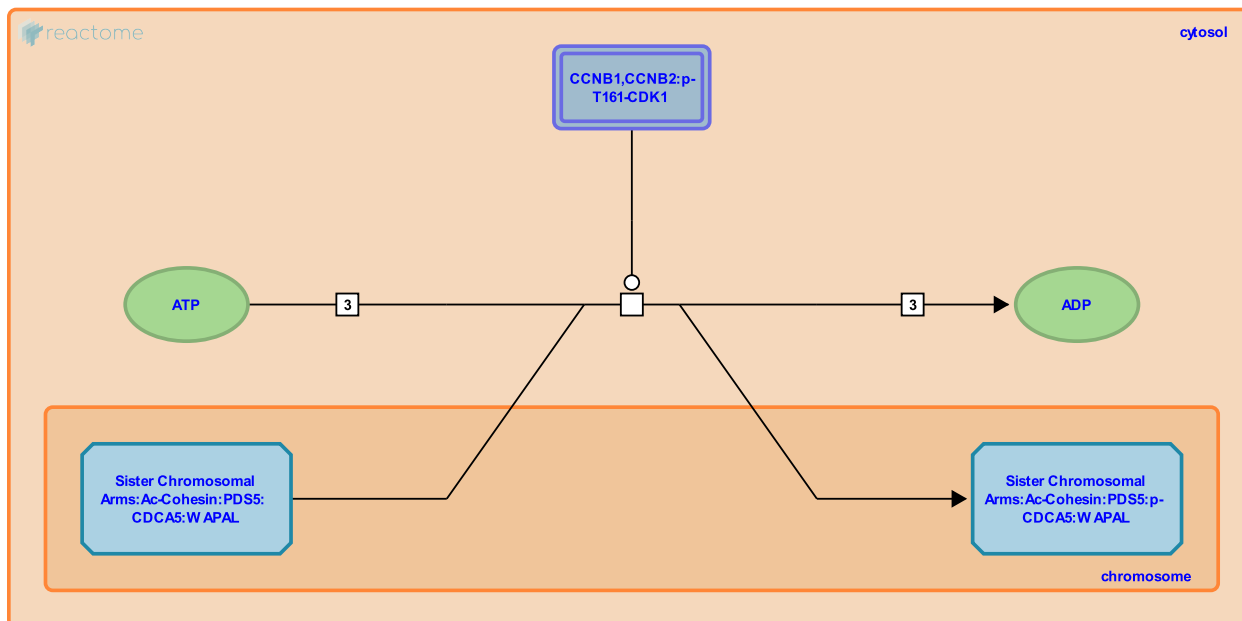
Location: [Resolution of Sister Chromatid Cohesion](#)

Stable identifier: R-XTR-2468293

Type: transition

Compartments: cytosol, chromosome

Inferred from: [CDK1 phosphorylates CDCA5 \(Sororin\) at chromosomal arms \(Homo sapiens\)](#)



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: [Phosphorylation of cohesin by PLK1 at chromosomal arms](#)

Phosphorylation of cohesin by PLK1 at chromosomal arms ↗

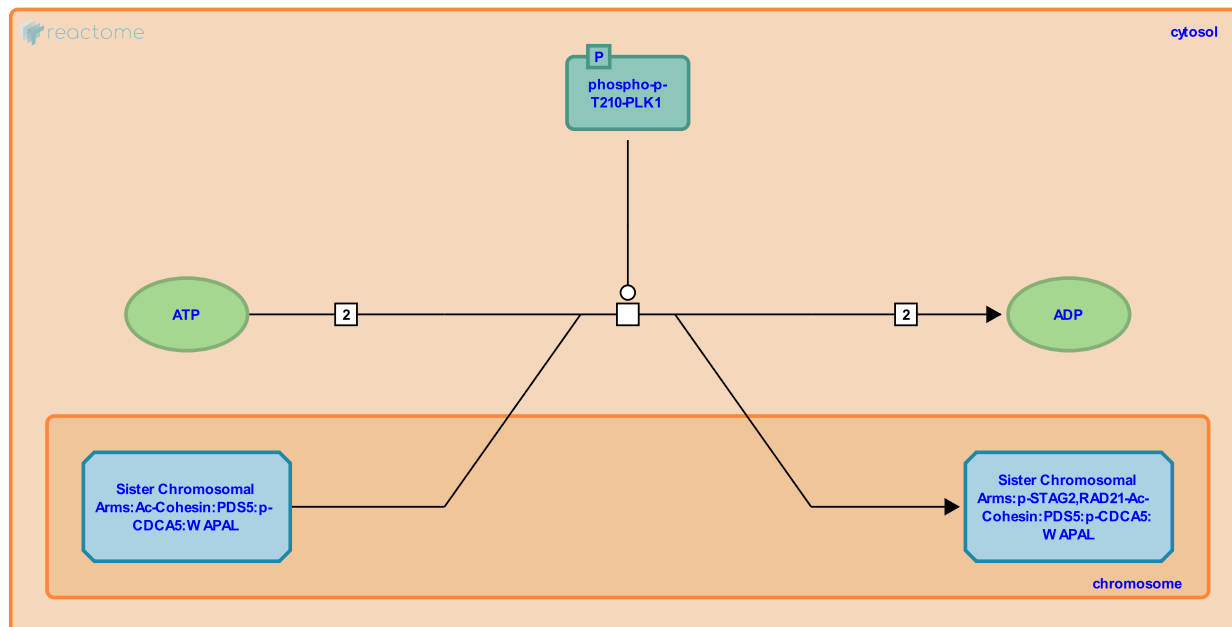
Location: [Resolution of Sister Chromatid Cohesion](#)

Stable identifier: R-XTR-2466068

Type: transition

Compartments: cytosol, chromosome

Inferred from: [Phosphorylation of cohesin by PLK1 at chromosomal arms \(Homo sapiens\)](#)



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: [CDK1 phosphorylates CDCA5 \(Sororin\) at chromosomal arms](#)

Kinetochores assembly ↗

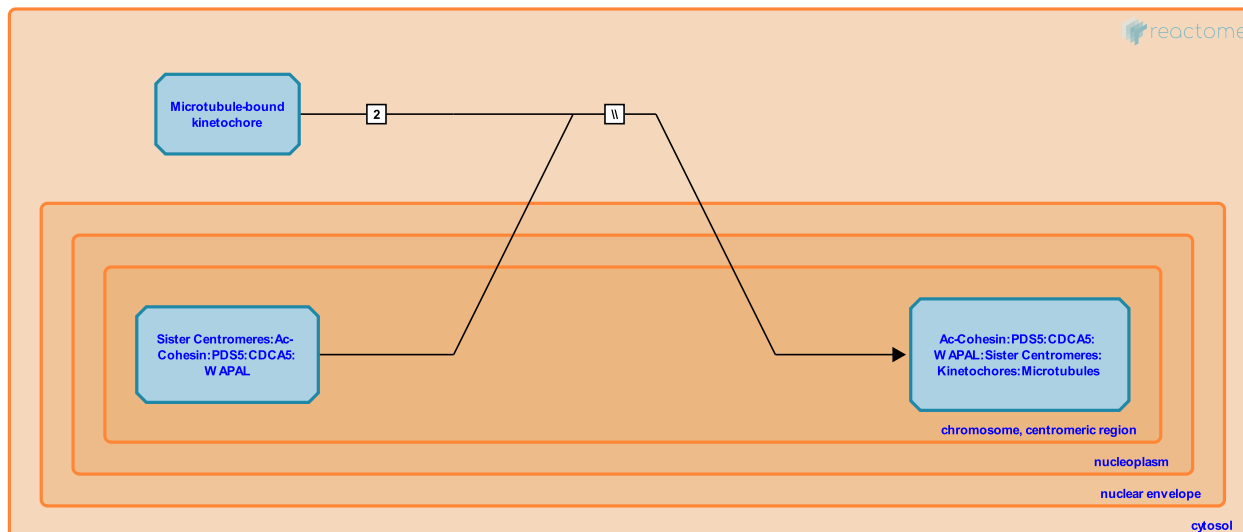
Location: [Resolution of Sister Chromatid Cohesion](#)

Stable identifier: R-XTR-2484822

Type: omitted

Compartments: cytosol, chromosome, centromeric region

Inferred from: [Kinetochores assembly \(Homo sapiens\)](#)



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: [CDK1 phosphorylates CDCA5 \(Sororin\) at centromeres](#)

CDK1 phosphorylates CDCA5 (Sororin) at centromeres ↗

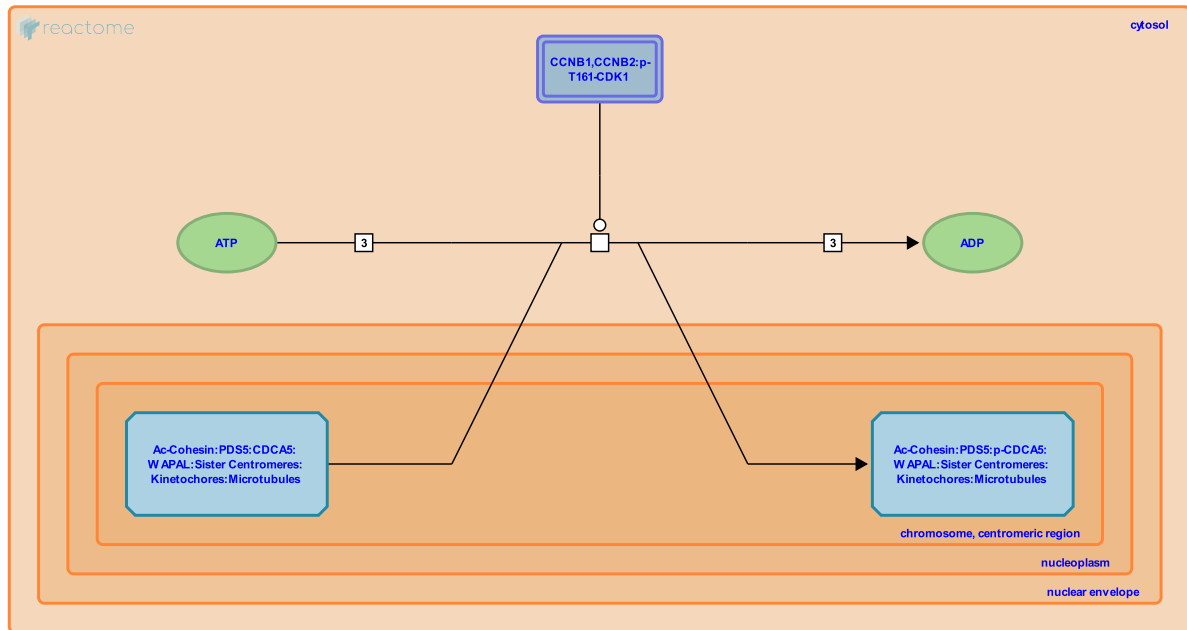
Location: [Resolution of Sister Chromatid Cohesion](#)

Stable identifier: R-XTR-2468287

Type: transition

Compartments: cytosol, chromosome, centromeric region

Inferred from: [CDK1 phosphorylates CDCA5 \(Sororin\) at centromeres \(Homo sapiens\)](#)



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: [Kinetochore assembly](#)

Followed by: [Phosphorylation of cohesin by PLK1 at centromeres](#)

Phosphorylation of cohesin by PLK1 at centromeres ↗

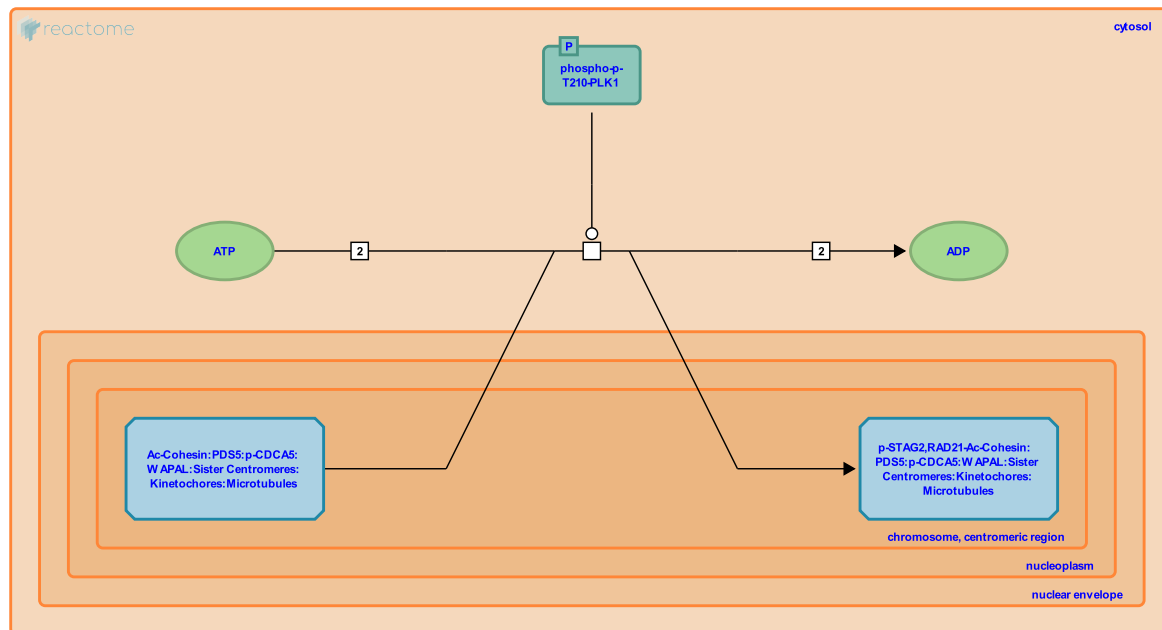
Location: [Resolution of Sister Chromatid Cohesion](#)

Stable identifier: R-XTR-1638803

Type: transition

Compartments: cytosol, chromosome, centromeric region

Inferred from: [Phosphorylation of cohesin by PLK1 at centromeres \(Homo sapiens\)](#)



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: [CDK1 phosphorylates CDCA5 \(Sororin\) at centromeres](#)

Followed by: [PP2A-B56 dephosphorylates centromeric cohesin](#)

PP2A-B56 dephosphorylates centromeric cohesin ↗

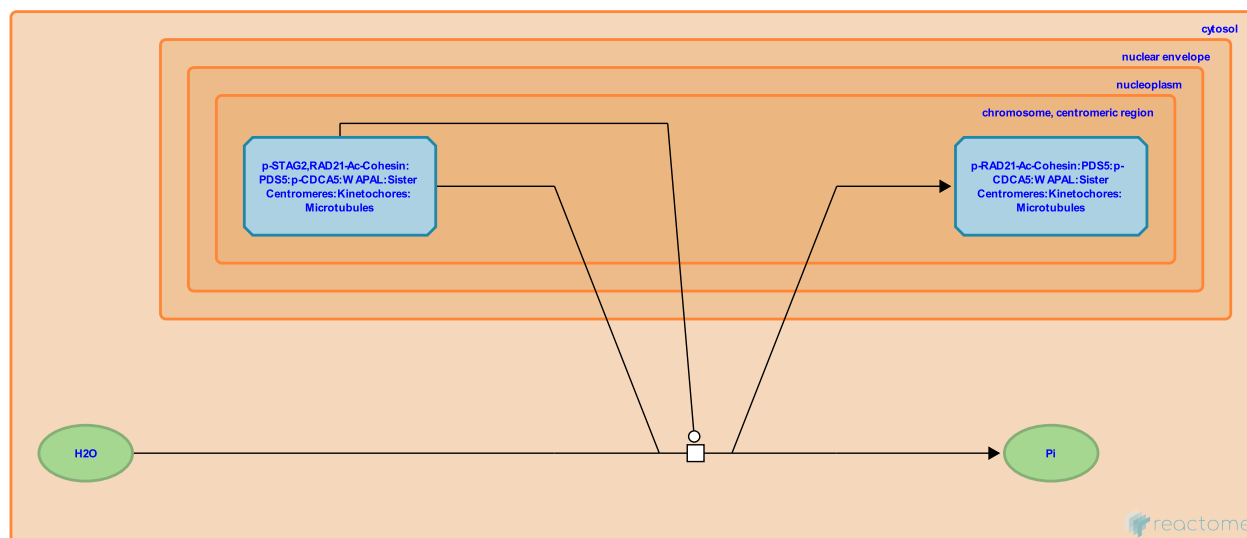
Location: [Resolution of Sister Chromatid Cohesion](#)

Stable identifier: R-XTR-1638821

Type: transition

Compartments: cytosol, chromosome

Inferred from: [PP2A-B56 dephosphorylates centromeric cohesin \(Homo sapiens\)](#)



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: [Phosphorylation of cohesin by PLK1 at centromeres](#)

PPP1CC dephosphorylates PLK1 ↗

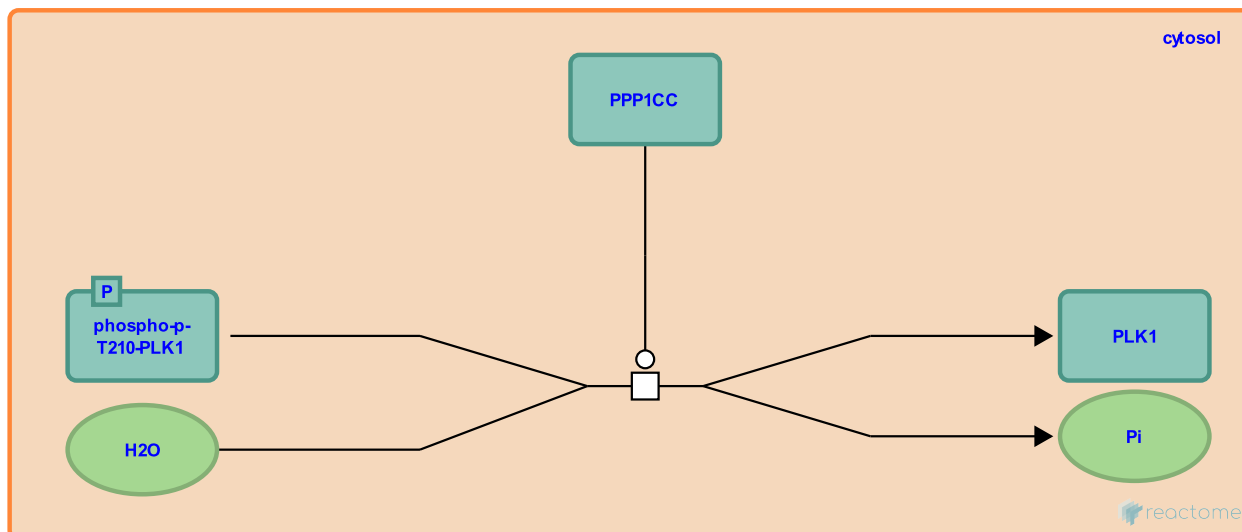
Location: [Resolution of Sister Chromatid Cohesion](#)

Stable identifier: R-XTR-9853385

Type: transition

Compartments: cytosol

Inferred from: [PPP1CC dephosphorylates PLK1 \(Homo sapiens\)](#)



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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