

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: 88

This document contains 1 pathway and 6 reactions ([see Table of Contents](#))

CDK1 phosphorylates CDCA5 (Sororin) at chromosomal arms ↗

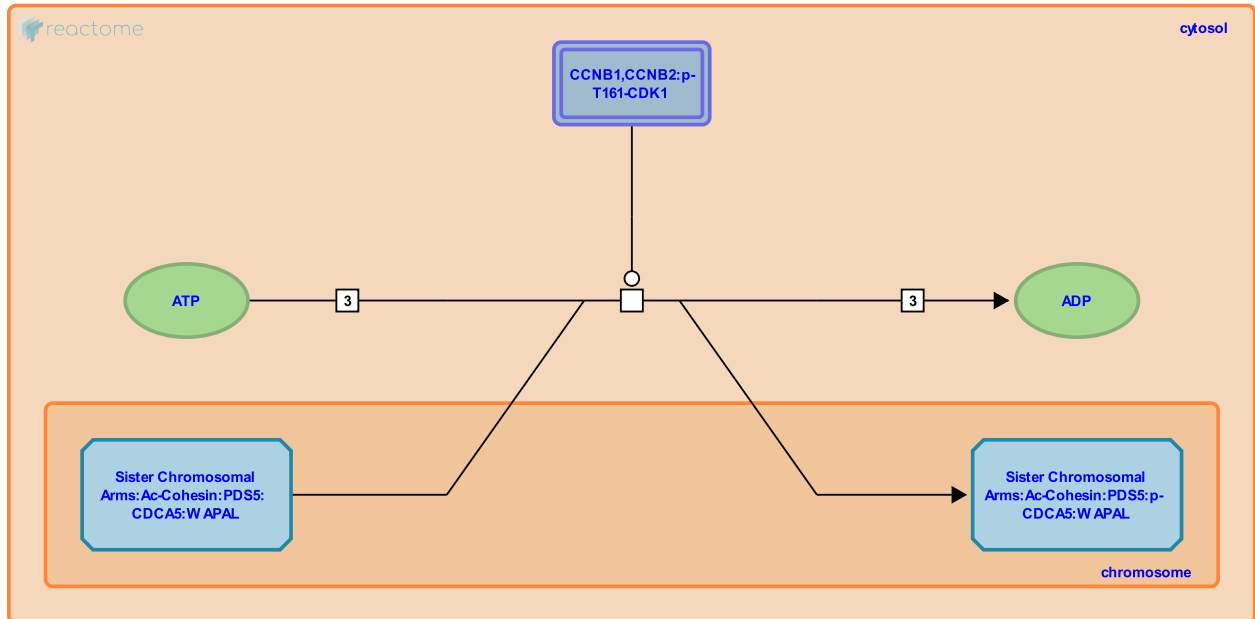
Location: [Resolution of Sister Chromatid Cohesion](#)

Stable identifier: R-DRE-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 ↗

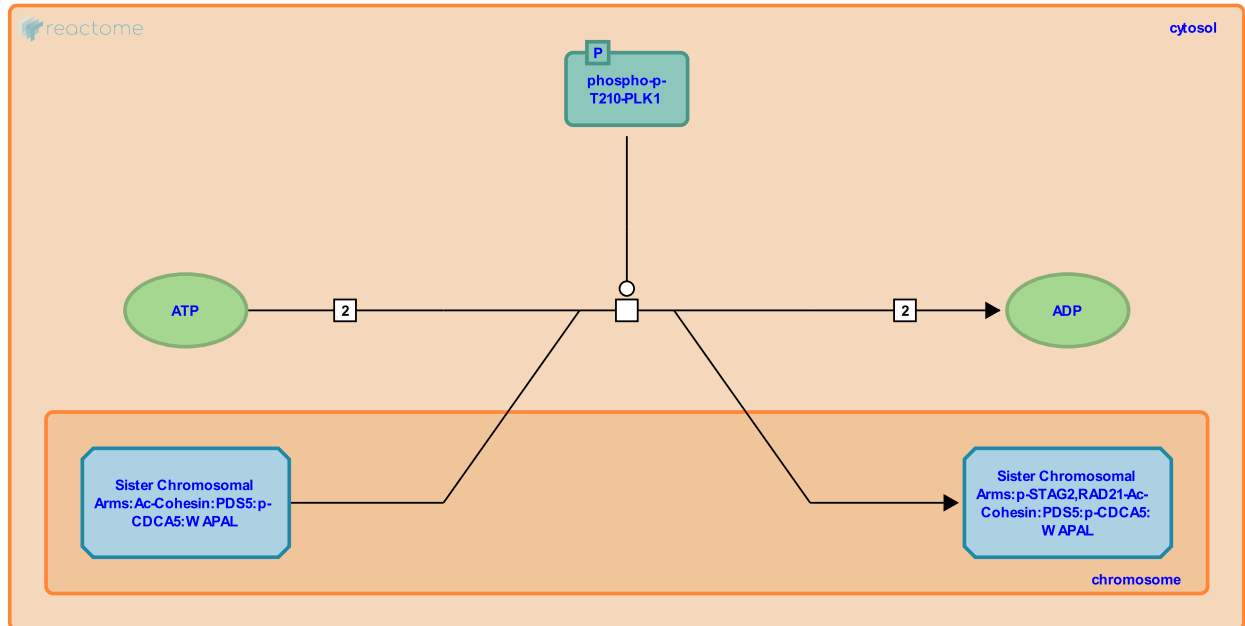
Location: [Resolution of Sister Chromatid Cohesion](#)

Stable identifier: R-DRE-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.

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

Deacetylation of cohesin ↗

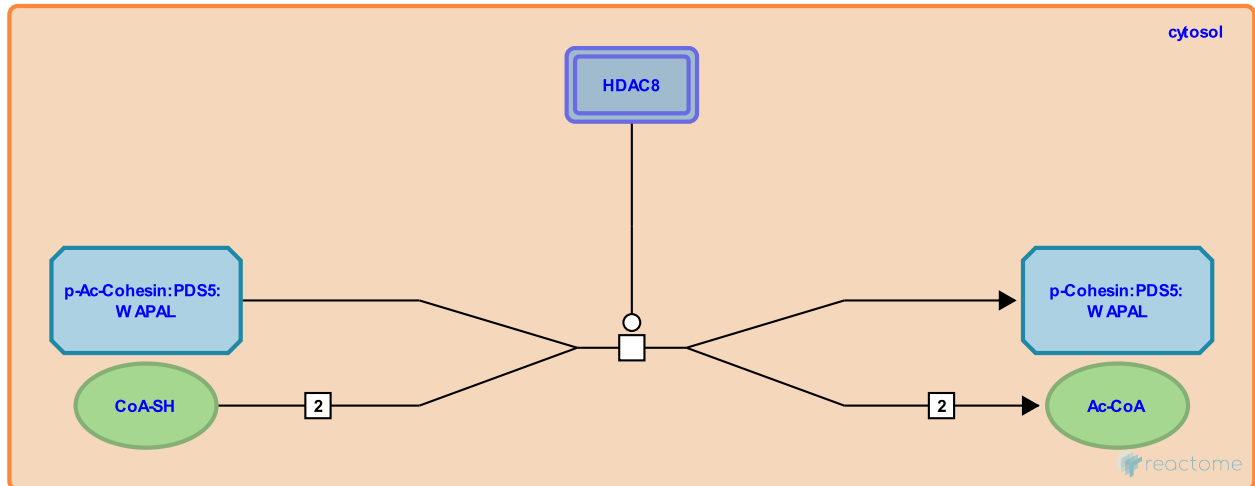
Location: [Resolution of Sister Chromatid Cohesion](#)

Stable identifier: R-DRE-2545253

Type: transition

Compartments: cytosol

Inferred from: [Deacetylation of cohesin \(Homo sapiens\)](#)



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

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FIRRM binds PLK1 ↗

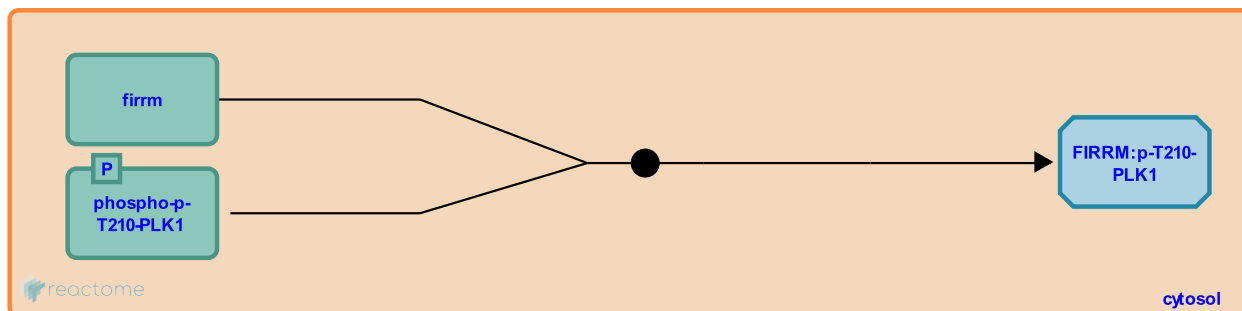
Location: [Resolution of Sister Chromatid Cohesion](#)

Stable identifier: R-DRE-9851946

Type: binding

Compartments: cytosol

Inferred from: [FIRRM binds PLK1 \(Homo sapiens\)](#)



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

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[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 phosphorylates FIRRM at S43](#)

PLK1 phosphorylates FIRRM at S43 ↗

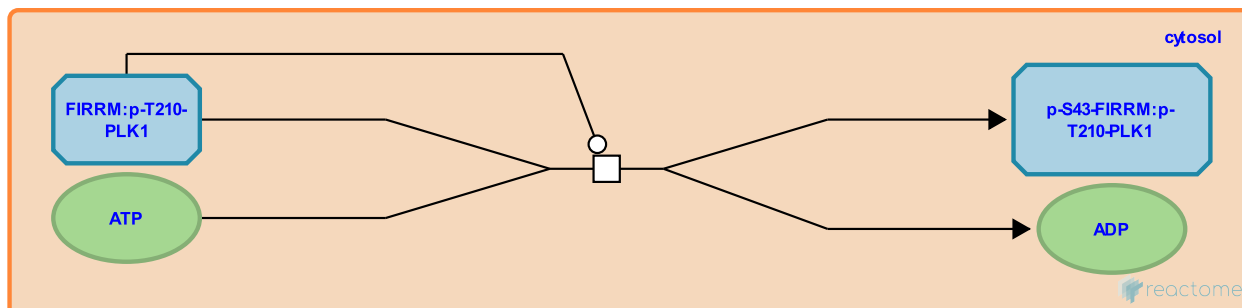
Location: [Resolution of Sister Chromatid Cohesion](#)

Stable identifier: R-DRE-9851972

Type: transition

Compartments: cytosol

Inferred from: [PLK1 phosphorylates FIRRM at S43 \(Homo sapiens\)](#)



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: [FIRRM binds PLK1](#)

PLK1 phosphorylates FIRMM at S744 ↗

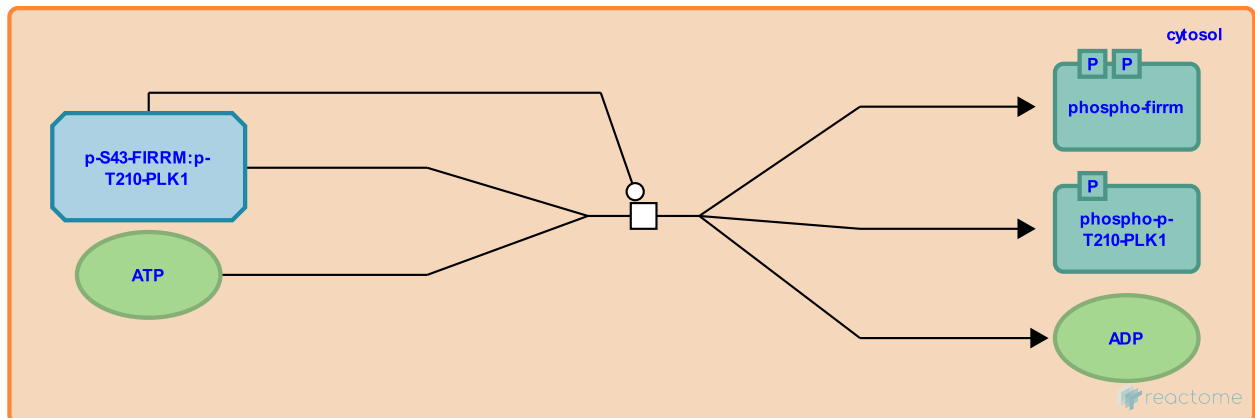
Location: [Resolution of Sister Chromatid Cohesion](#)

Stable identifier: R-DRE-9853369

Type: transition

Compartments: cytosol

Inferred from: [PLK1 phosphorylates FIRMM at S744 \(Homo sapiens\)](#)



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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