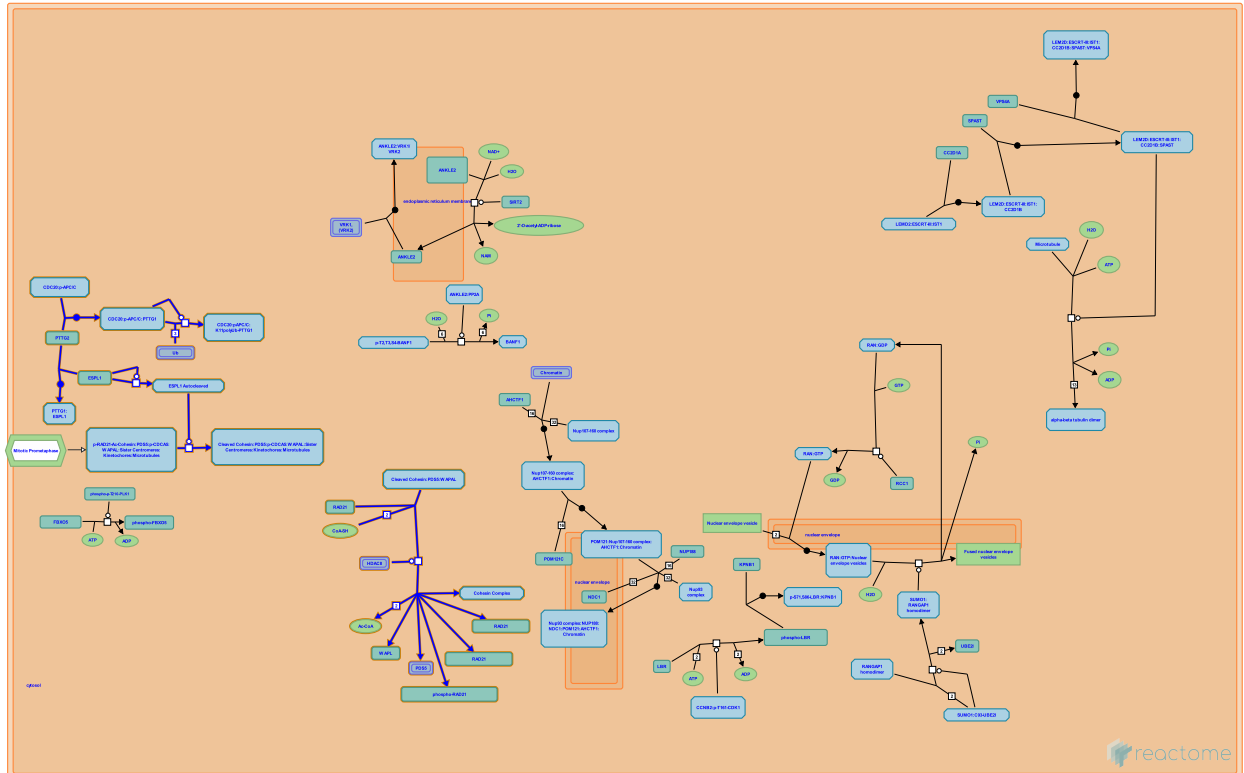


# Separation of Sister Chromatids



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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://www.reactome.org/licenses/).

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://www.reactome.org/).

31/01/2023

## 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: 83

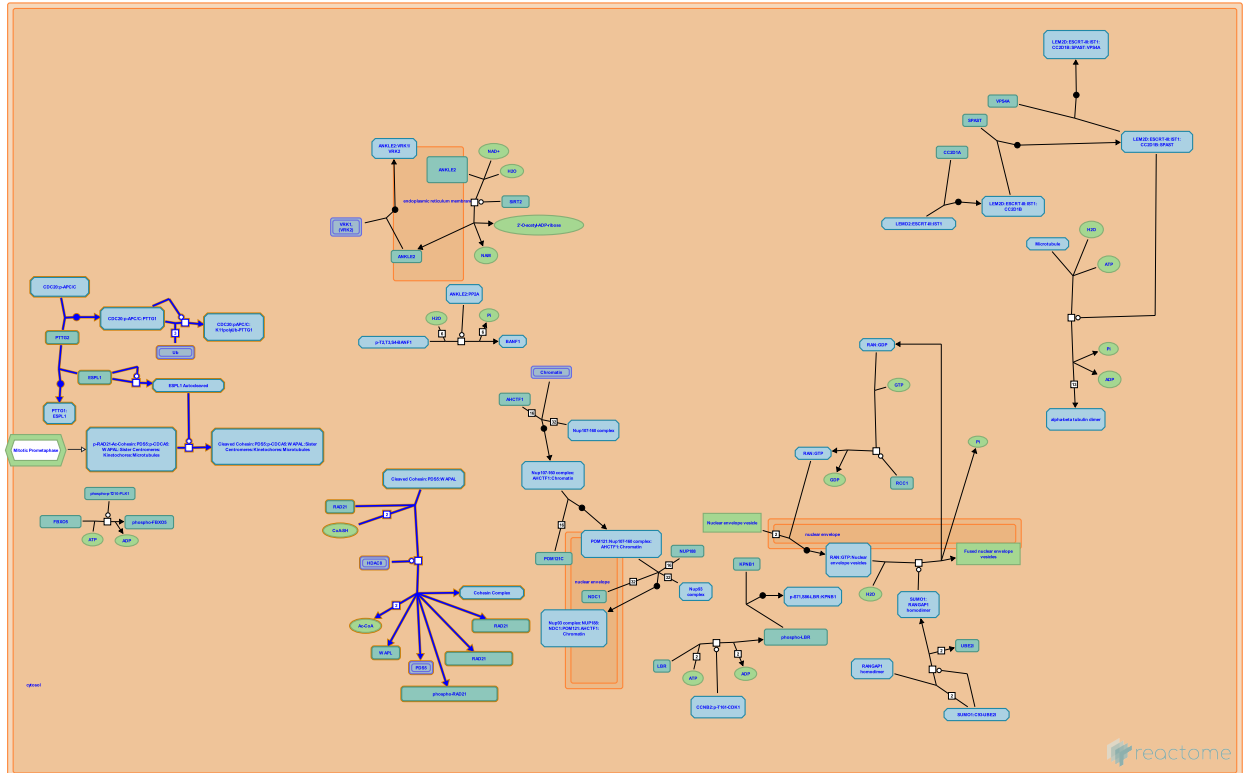
This document contains 1 pathway and 6 reactions ([see Table of Contents](#))

## Separation of Sister Chromatids ↗

**Stable identifier:** R-GGA-2467813

**Compartments:** cytosol

**Inferred from:** Separation of Sister Chromatids (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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## Association of Securin with Cdc20:APC/C complex ↗

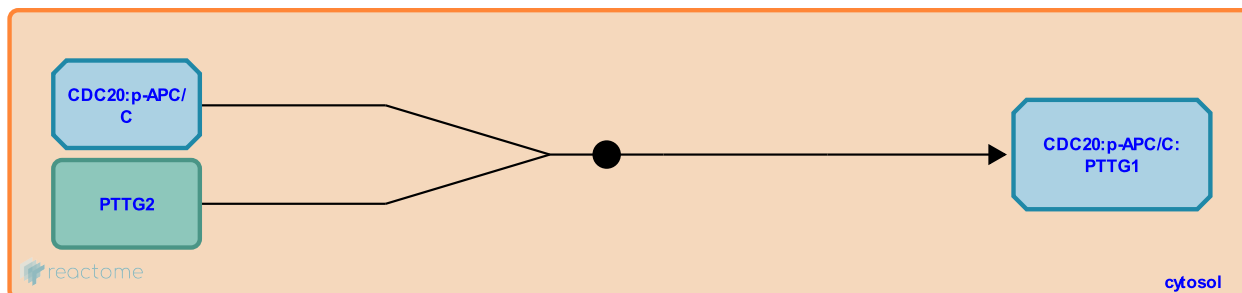
**Location:** [Separation of Sister Chromatids](#)

**Stable identifier:** R-GGA-174121

**Type:** binding

**Compartments:** cytosol

**Inferred from:** [Association of Securin with Cdc20:APC/C 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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Followed by:** [Ubiquitination of Securin by phospho-APC/C:Cdc20 complex](#)

## Ubiquitination of Securin by phospho-APC/C:Cdc20 complex ↗

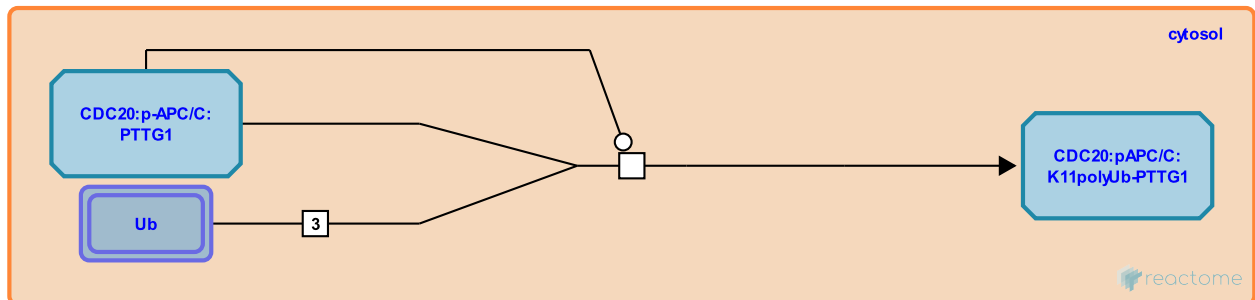
**Location:** [Separation of Sister Chromatids](#)

**Stable identifier:** R-GGA-174144

**Type:** transition

**Compartments:** cytosol

**Inferred from:** [Ubiquitination of Securin by phospho-APC/C:Cdc20 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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [Association of Securin with Cdc20:APC/C complex](#)

## PTTG1 (Securin) sequesters ESPL1 (Separase) ↗

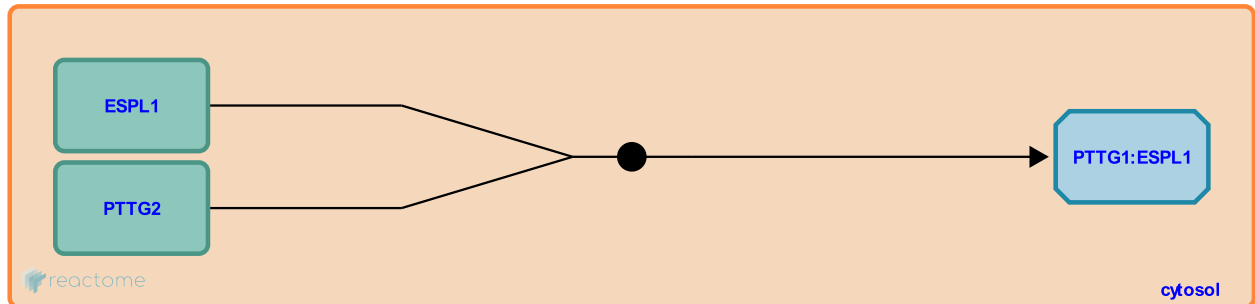
**Location:** [Separation of Sister Chromatids](#)

**Stable identifier:** R-GGA-2467798

**Type:** binding

**Compartments:** cytosol

**Inferred from:** [PTTG1 \(Securin\) sequesters ESPL1 \(Separase\) \(Homo sapiens\)](#)



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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## Autocleavage of ESPL1 (Separase) ↗

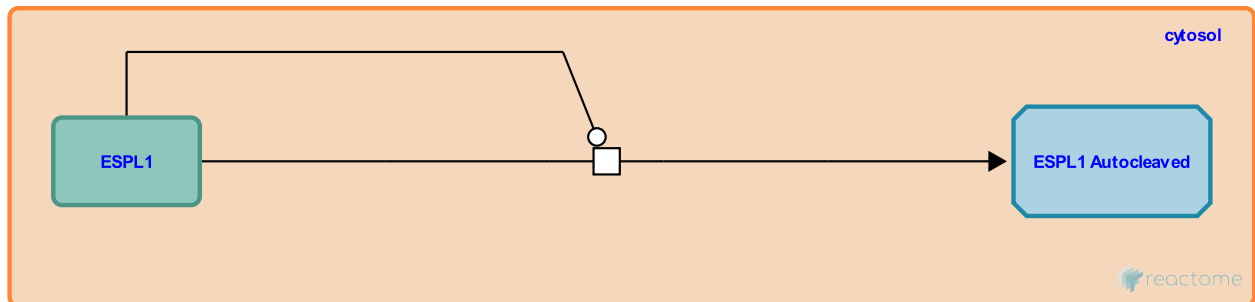
**Location:** [Separation of Sister Chromatids](#)

**Stable identifier:** R-GGA-2467775

**Type:** transition

**Compartments:** cytosol

**Inferred from:** [Autocleavage of ESPL1 \(Separase\) \(Homo sapiens\)](#)



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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Followed by:** [ESPL1 \(Separase\) cleaves centromeric cohesin](#)

## ESPL1 (Separase) cleaves centromeric cohesin [↗](#)

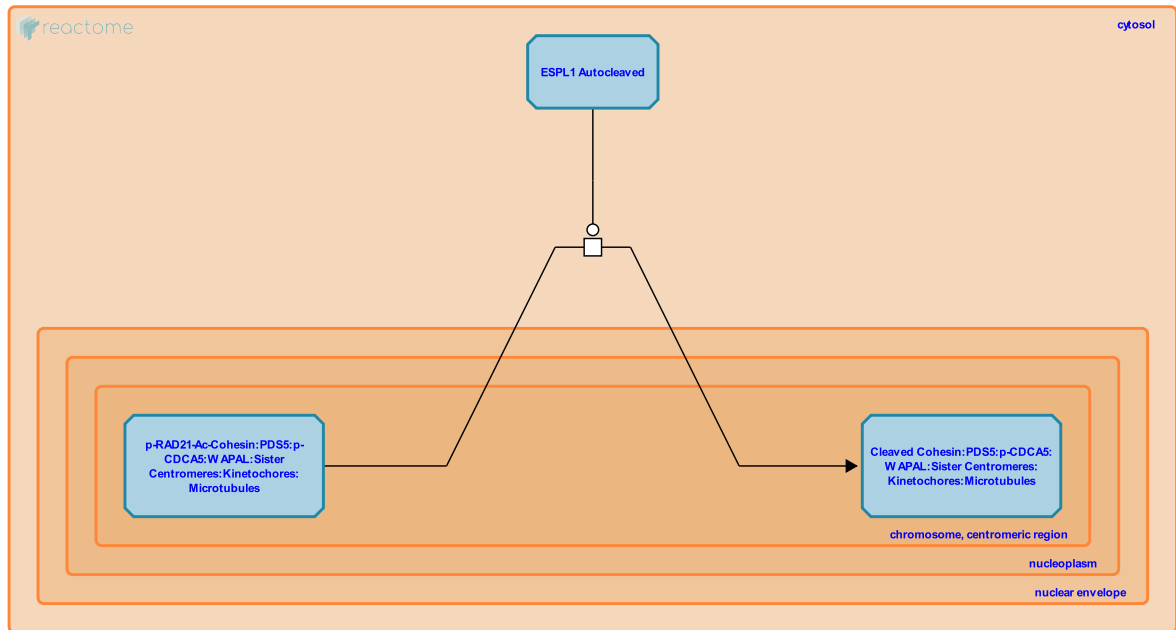
**Location:** [Separation of Sister Chromatids](#)

**Stable identifier:** R-GGA-2467809

**Type:** transition

**Compartments:** cytosol, chromosome, centromeric region

**Inferred from:** [ESPL1 \(Separase\) cleaves 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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [Autocleavage of ESPL1 \(Separase\)](#)



## Deacetylation of cleaved cohesin ↗

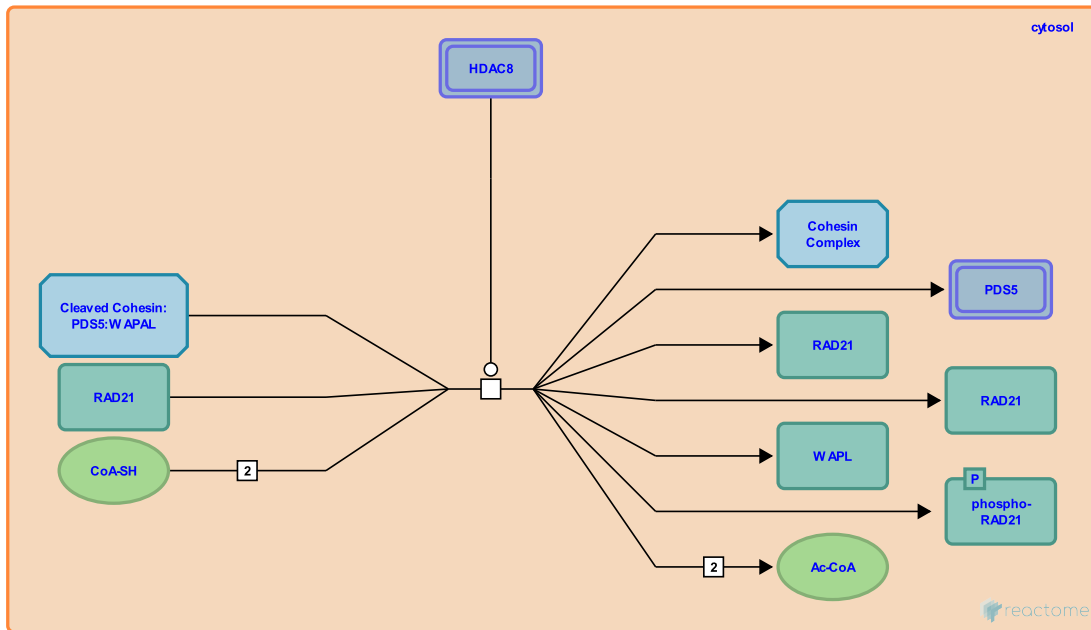
**Location:** [Separation of Sister Chromatids](#)

**Stable identifier:** R-GGA-2545203

**Type:** transition

**Compartments:** cytosol

**Inferred from:** [Deacetylation of cleaved 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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

# Table of Contents

Introduction	1
☒ Separation of Sister Chromatids	2
↳ Association of Securin with Cdc20:APC/C complex	3
↳ Ubiquitination of Securin by phospho-APC/C:Cdc20 complex	4
↳ PTTG1 (Securin) sequesters ESPL1 (Separase)	5
↳ Autocleavage of ESPL1 (Separase)	6
↳ ESPL1 (Separase) cleaves centromeric cohesin	7
↳ Deacetylation of cleaved cohesin	8
Table of Contents	9