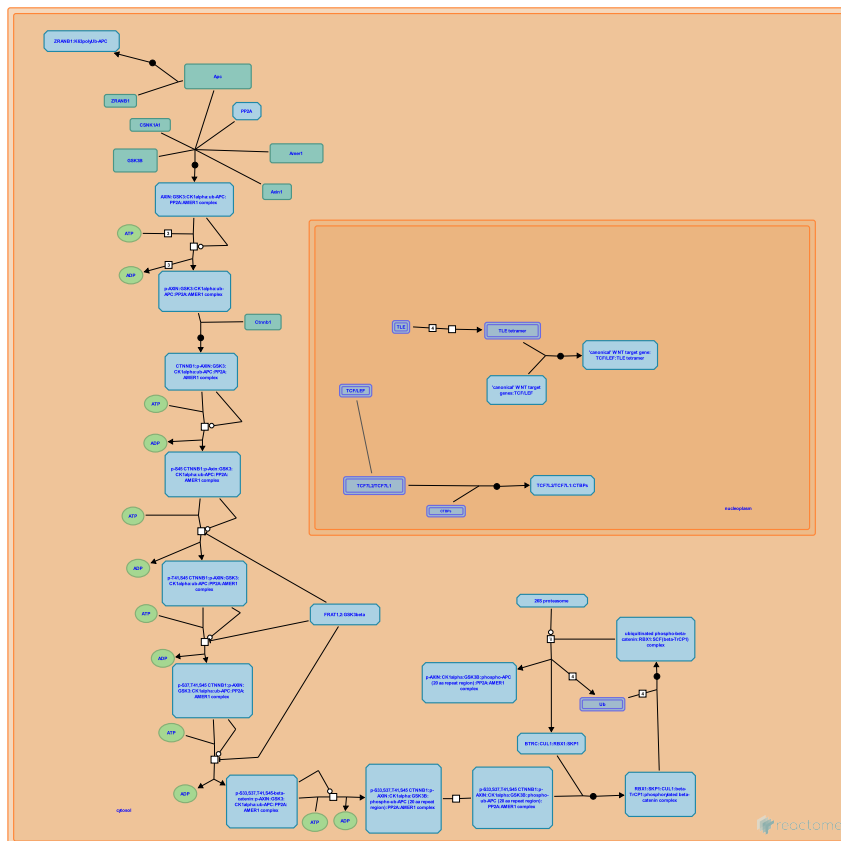


# Degradation of beta-catenin by the destruction complex



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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/).

05/05/2024

## 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. [↗](#)

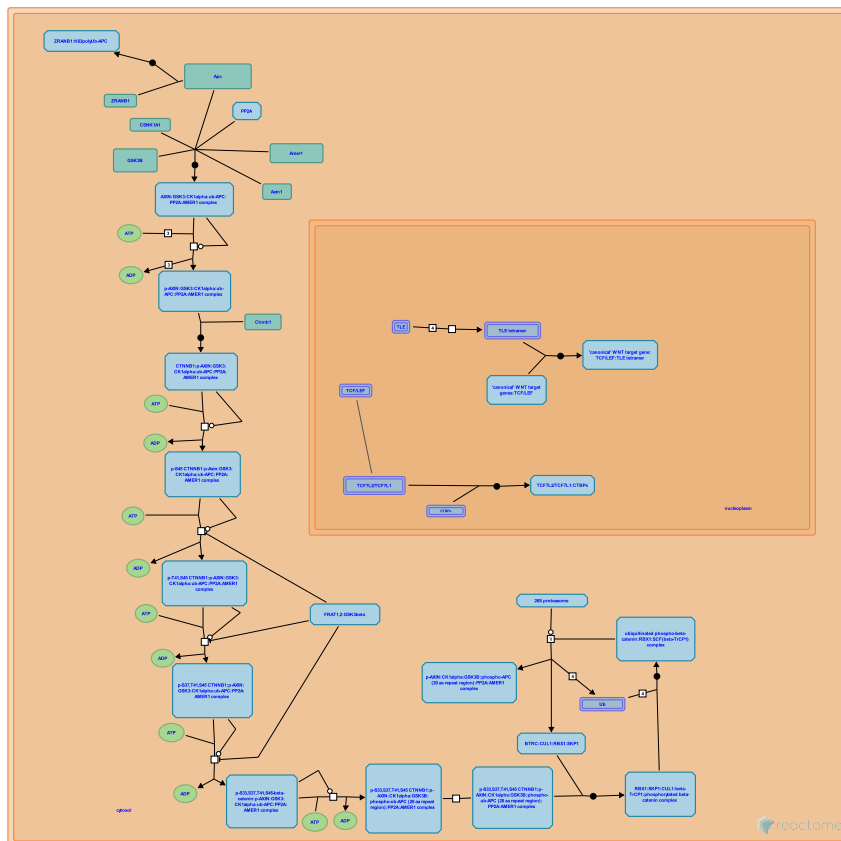
Reactome database release: 88

This document contains 3 pathways and 9 reactions ([see Table of Contents](#))

## Degradation of beta-catenin by the destruction complex ↗

**Stable identifier:** R-MMU-195253

**Inferred from:** [Degradation of beta-catenin by the destruction 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>

## ZRANB1 binds APC ↗

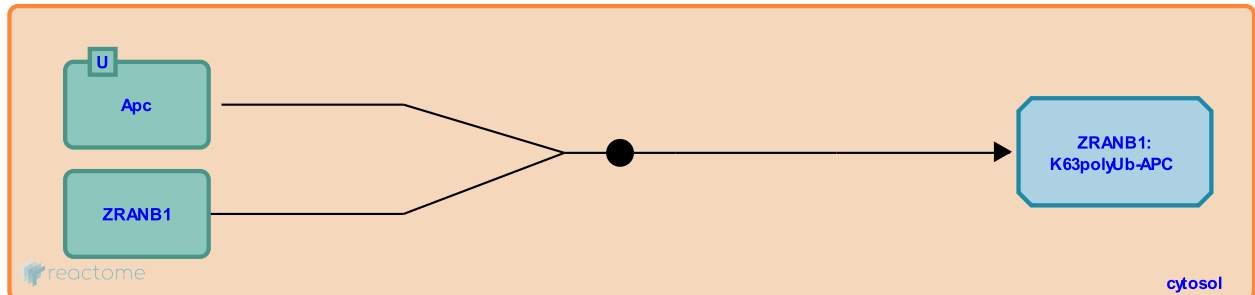
**Location:** [Degradation of beta-catenin by the destruction complex](#)

**Stable identifier:** R-MMU-6781905

**Type:** binding

**Compartments:** cytosol

**Inferred from:** [ZRANB1 binds APC \(Homo sapiens\)](#)



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>

## Assembly of the destruction complex ↗

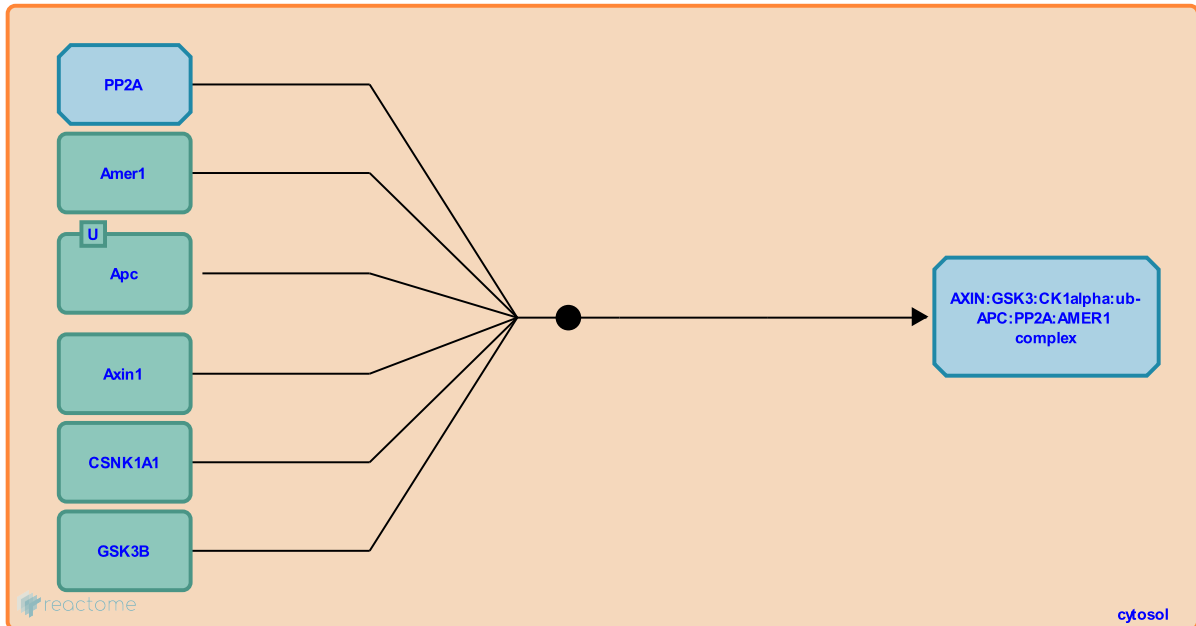
**Location:** [Degradation of beta-catenin by the destruction complex](#)

**Stable identifier:** R-MMU-195251

**Type:** binding

**Compartments:** cytosol

**Inferred from:** [Assembly of the destruction 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:** [AXIN is phosphorylated in the destruction complex](#)

## AXIN is phosphorylated in the destruction complex ↗

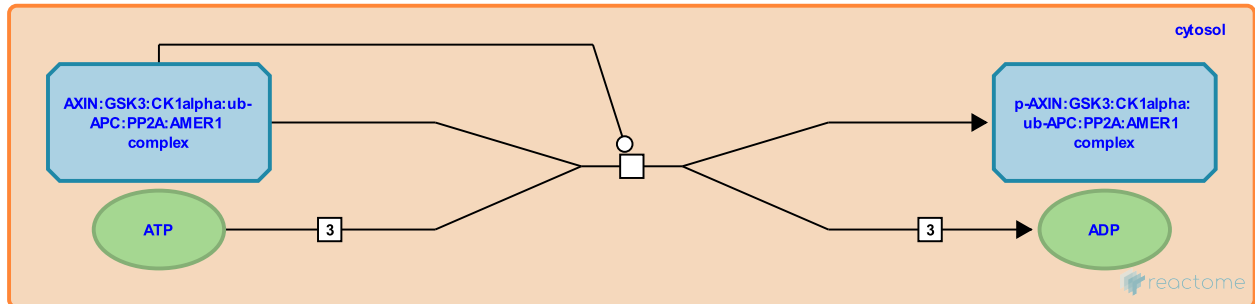
**Location:** Degradation of beta-catenin by the destruction complex

**Stable identifier:** R-MMU-5229343

**Type:** transition

**Compartments:** cytosol

**Inferred from:** AXIN is phosphorylated in the destruction 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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** Assembly of the destruction complex

**Followed by:** Association of beta-catenin with the destruction complex

## Association of beta-catenin with the destruction complex ↗

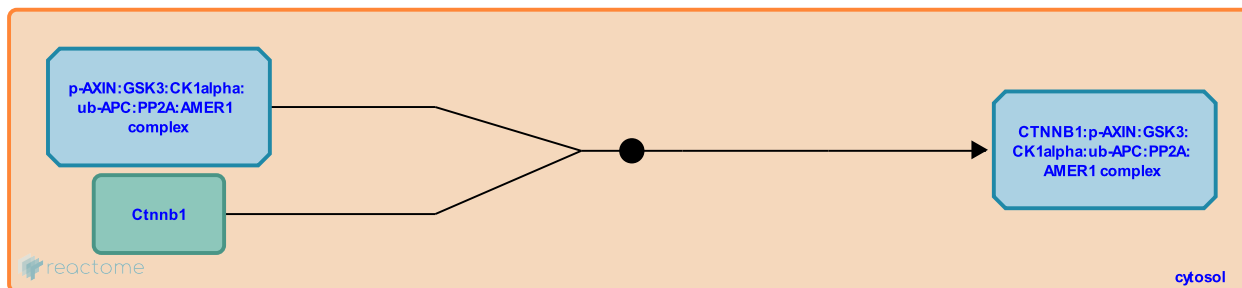
**Location:** [Degradation of beta-catenin by the destruction complex](#)

**Stable identifier:** R-MMU-195304

**Type:** binding

**Compartments:** cytosol

**Inferred from:** [Association of beta-catenin with the destruction 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:** [AXIN is phosphorylated in the destruction complex](#)

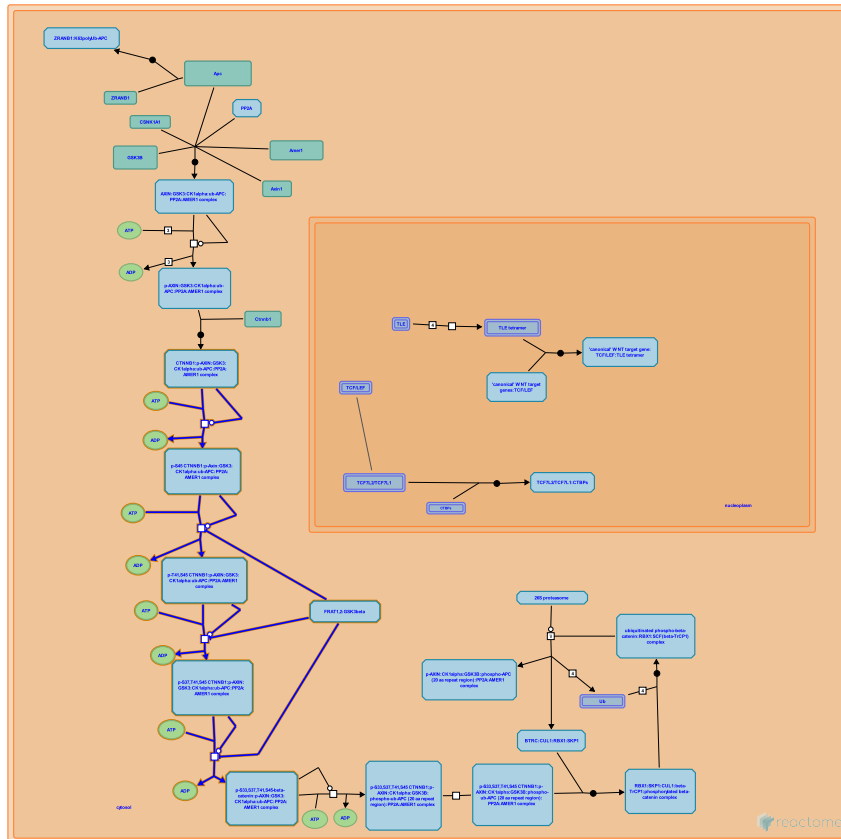
## Beta-catenin phosphorylation cascade ↗

**Location:** Degradation of beta-catenin by the destruction complex

**Stable identifier:** R-MMU-196299

**Compartments:** cytosol

**Inferred from:** Beta-catenin phosphorylation cascade (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>



## Phosphorylation of APC component of the destruction complex ↗

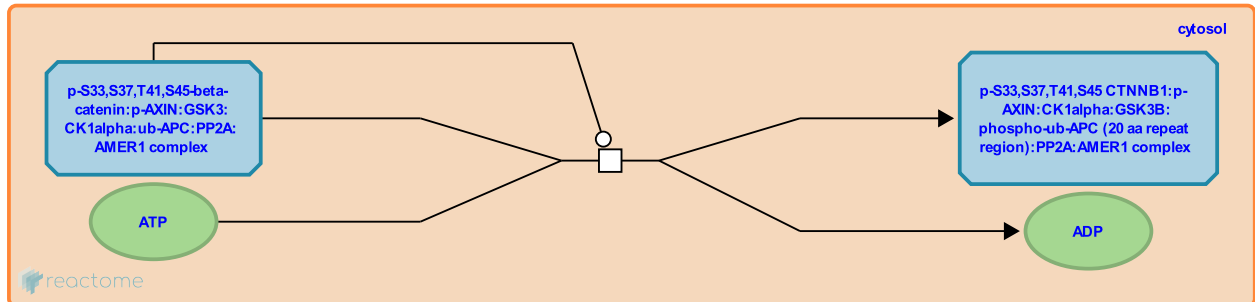
**Location:** Degradation of beta-catenin by the destruction complex

**Stable identifier:** R-MMU-195275

**Type:** transition

**Compartments:** cytosol

**Inferred from:** Phosphorylation of APC component of the destruction 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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Followed by:** Dissociation of beta-catenin from Axin and association of beta catenin with phospho-(20 aa) APC in the destruction complex

## Dissociation of beta-catenin from Axin and association of beta catenin with phospho-(20 aa) APC in the destruction complex ↗

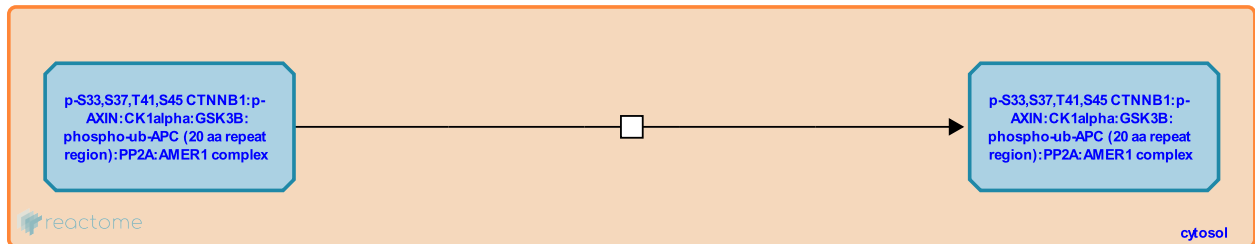
**Location:** Degradation of beta-catenin by the destruction complex

**Stable identifier:** R-MMU-195280

**Type:** transition

**Compartments:** cytosol

**Inferred from:** Dissociation of beta-catenin from Axin and association of beta catenin with phospho-(20 aa) APC in the destruction 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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** Phosphorylation of APC component of the destruction complex

**Followed by:** Association of beta-catenin with the RBX1:SCF(beta-TrCP1) ubiquitin ligase complex

## Association of beta-catenin with the RBX1:SCF(beta-TrCP1) ubiquitin ligase complex



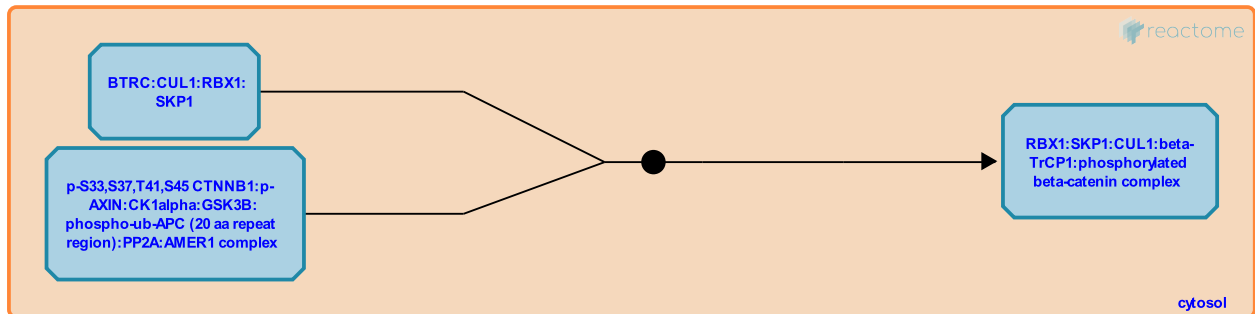
**Location:** Degradation of beta-catenin by the destruction complex

**Stable identifier:** R-MMU-2130279

**Type:** binding

**Compartments:** cytosol

**Inferred from:** Association of beta-catenin with the RBX1:SCF(beta-TrCP1) ubiquitin ligase 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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** Dissociation of beta-catenin from Axin and association of beta catenin with phospho-(20 aa) APC in the destruction complex

**Followed by:** Multi-ubiquitination of phospho-beta-catenin by RBX1:SCF(beta-TrCP1)

## Multi-ubiquitination of phospho-beta-catenin by RBX1:SCF(beta-TrCP1) ↗

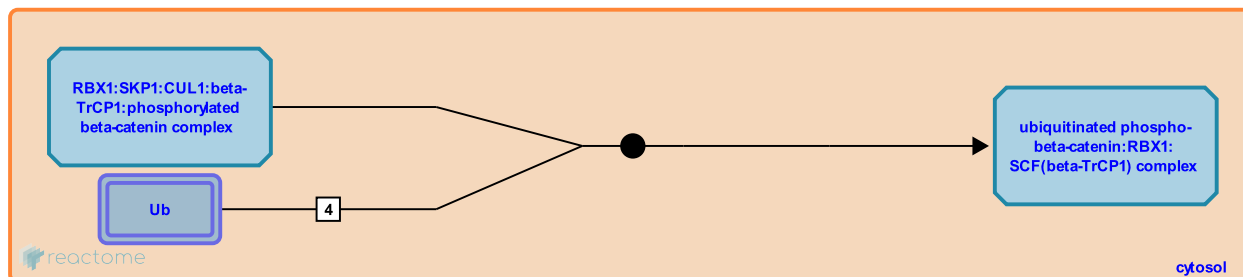
**Location:** [Degradation of beta-catenin by the destruction complex](#)

**Stable identifier:** R-MMU-2130286

**Type:** binding

**Compartments:** cytosol

**Inferred from:** [Multi-ubiquitination of phospho-beta-catenin by RBX1:SCF\(beta-TrCP1\) \(Homo sapiens\)](#)



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:** [Association of beta-catenin with the RBX1:SCF\(beta-TrCP1\) ubiquitin ligase complex](#)

**Followed by:** [Degradation of ubiquitinated beta catenin by the proteasome](#)

## Degradation of ubiquitinated beta catenin by the proteasome ↗

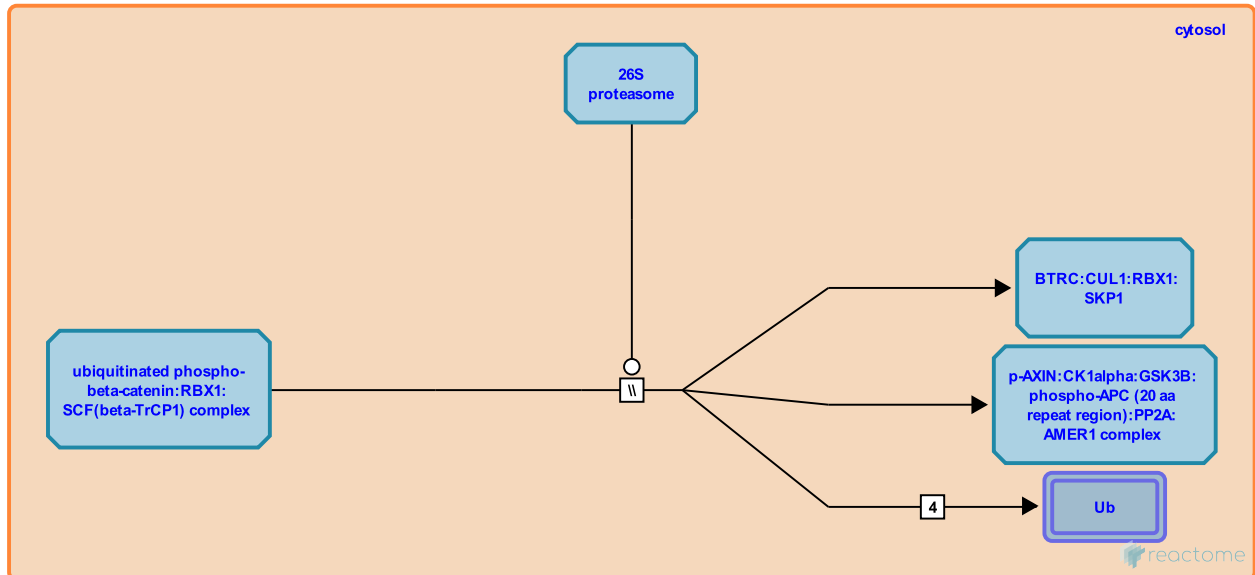
**Location:** [Degradation of beta-catenin by the destruction complex](#)

**Stable identifier:** R-MMU-2130282

**Type:** omitted

**Compartments:** cytosol

**Inferred from:** [Degradation of ubiquitinated beta catenin by the proteasome \(Homo sapiens\)](#)



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:** [Multi-ubiquitination of phospho-beta-catenin by RBX1:SCF\(beta-TrCP1\)](#)

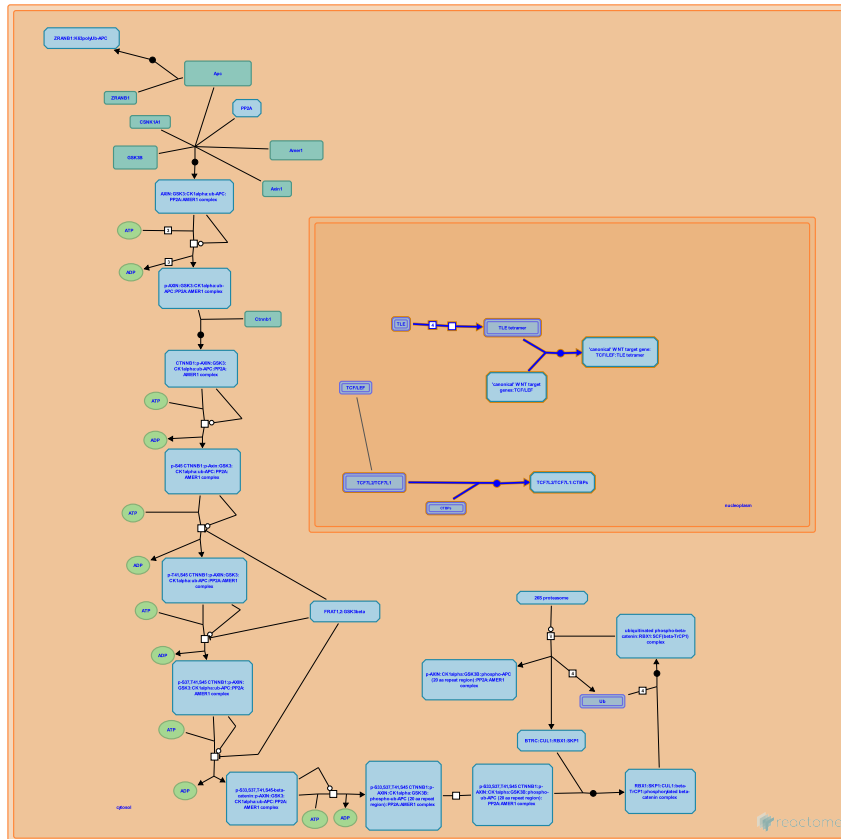
## Repression of WNT target genes ↗

**Location:** Degradation of beta-catenin by the destruction complex

**Stable identifier:** R-MMU-4641265

**Compartments:** nucleoplasm

**Inferred from:** Repression of WNT target genes (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

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