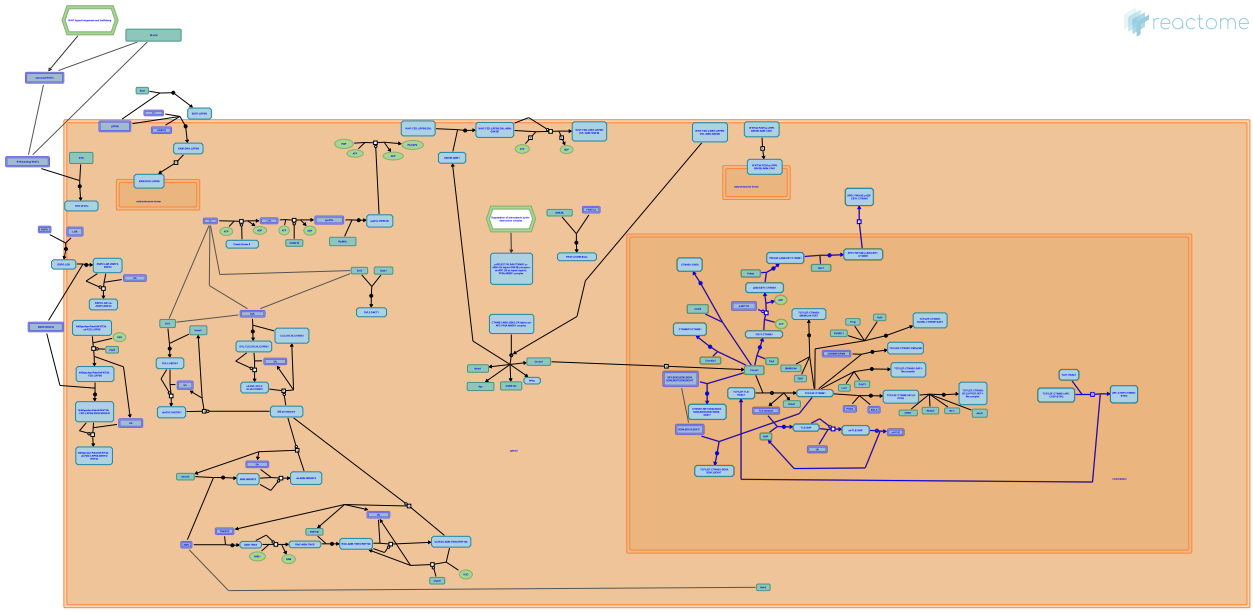
Deactivation of the beta-catenin trans-activating complex



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

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.

06/05/2024

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).

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Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

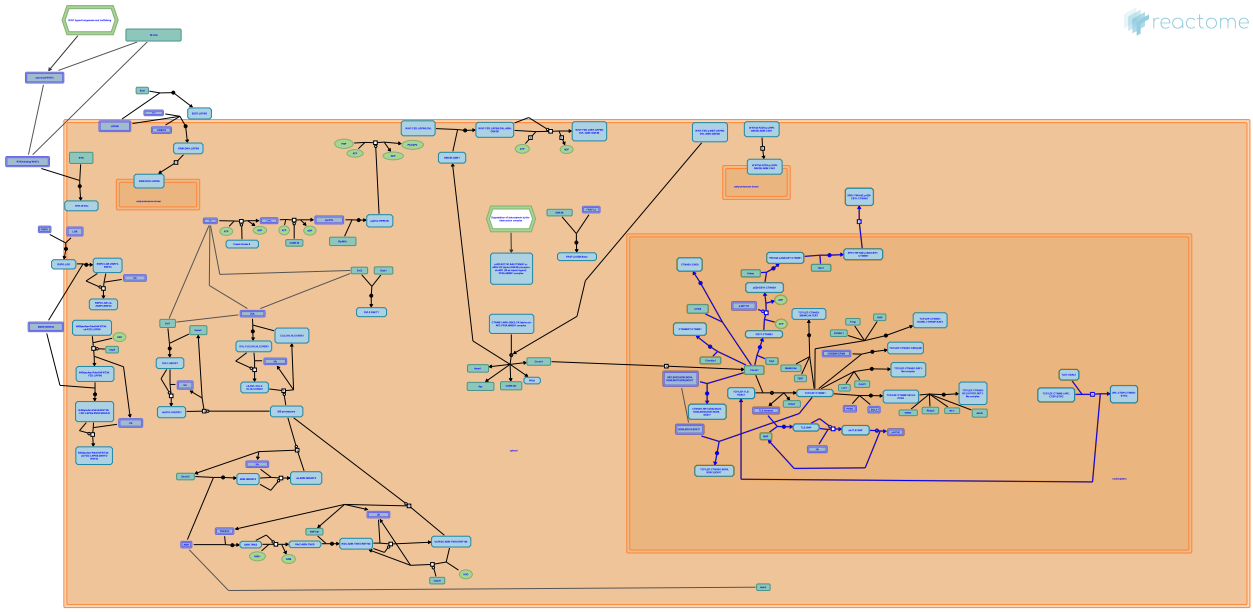
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

Deactivation of the beta-catenin transactivating complex ↗

Stable identifier: R-MMU-3769402

Inferred from: Deactivation of the beta-catenin transactivating 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

XIAP binds TLE ↗

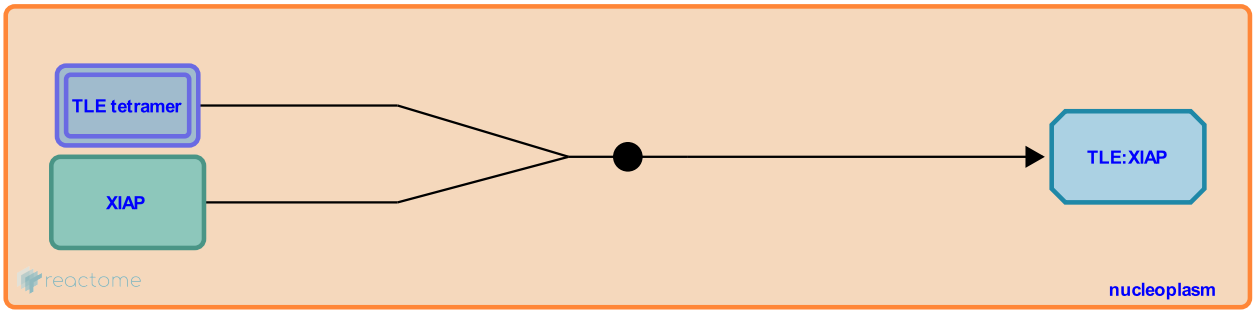
Location: Deactivation of the beta-catenin transactivating complex

Stable identifier: R-MMU-3322431

Type: binding

Compartments: nucleoplasm

Inferred from: XIAP binds TLE (Homo sapiens)



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Followed by: XIAP monoubiquinates TLE

XIAP monoubiquinates TLE ↗

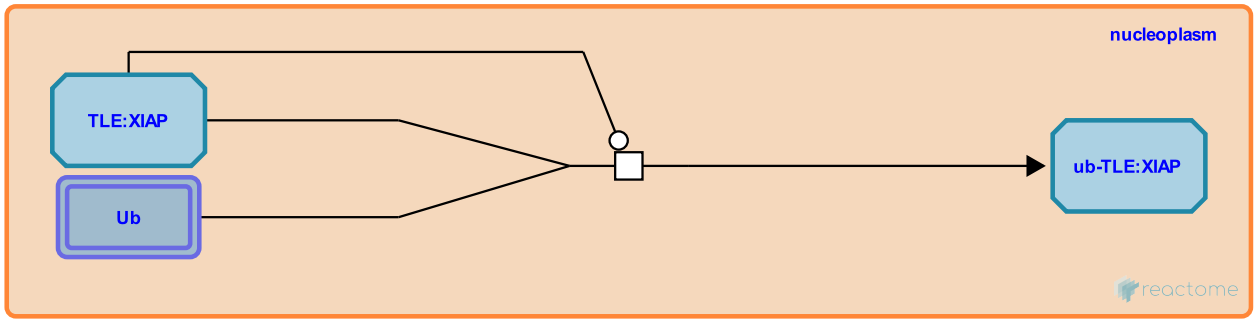
Location: Deactivation of the beta-catenin transactivating complex

Stable identifier: R-MMU-3322429

Type: transition

Compartments: nucleoplasm

Inferred from: XIAP monoubiquinates TLE (Homo sapiens)



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Preceded by: XIAP binds TLE

Followed by: XIAP dissociates from ub-TLE

XIAP dissociates from ub-TLE ↗

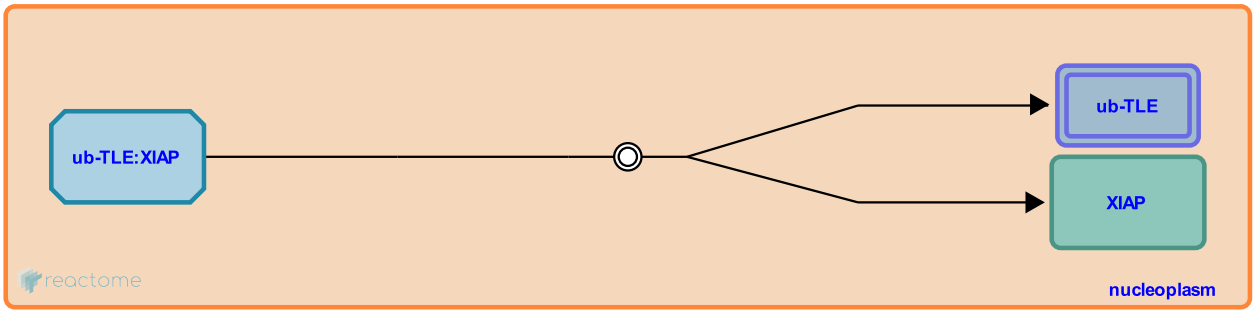
Location: Deactivation of the beta-catenin transactivating complex

Stable identifier: R-MMU-3322434

Type: dissociation

Compartments: nucleoplasm

Inferred from: XIAP dissociates from ub-TLE (Homo sapiens)



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Preceded by: XIAP monoubiquinates TLE

beta-catenin is replaced by repression complexes at the promoter ↗

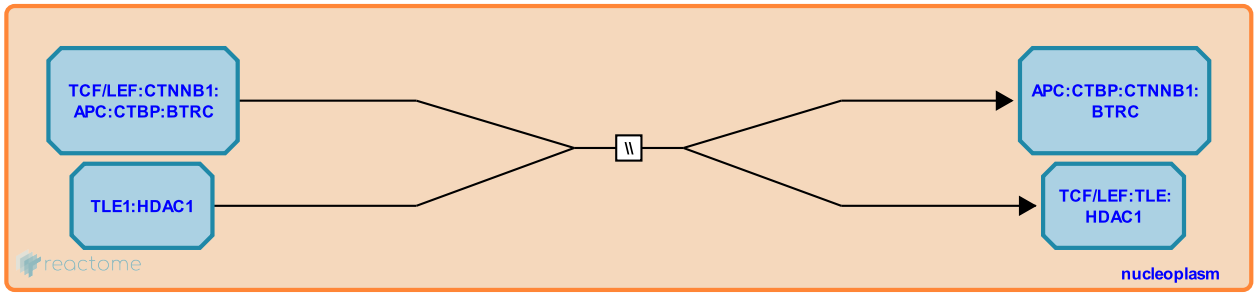
Location: Deactivation of the beta-catenin transactivating complex

Stable identifier: R-MMU-3361751

Type: omitted

Compartments: nucleoplasm

Inferred from: beta-catenin is replaced by repression complexes at the promoter (Homo sapiens)



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CBY1 binds beta-catenin ↗

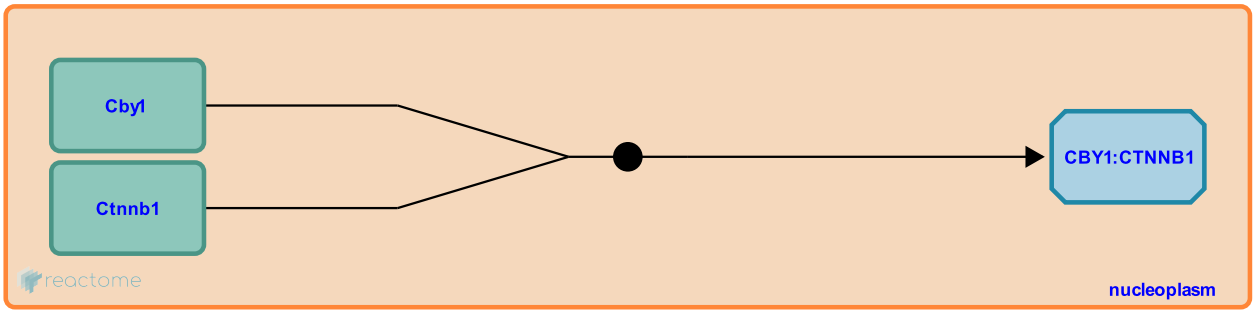
Location: Deactivation of the beta-catenin transactivating complex

Stable identifier: R-MMU-3769383

Type: binding

Compartments: nucleoplasm

Inferred from: CBY1 binds beta-catenin (Homo sapiens)



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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: AKT phosphorylates CBY1

AKT phosphorylates CBY1 ↗

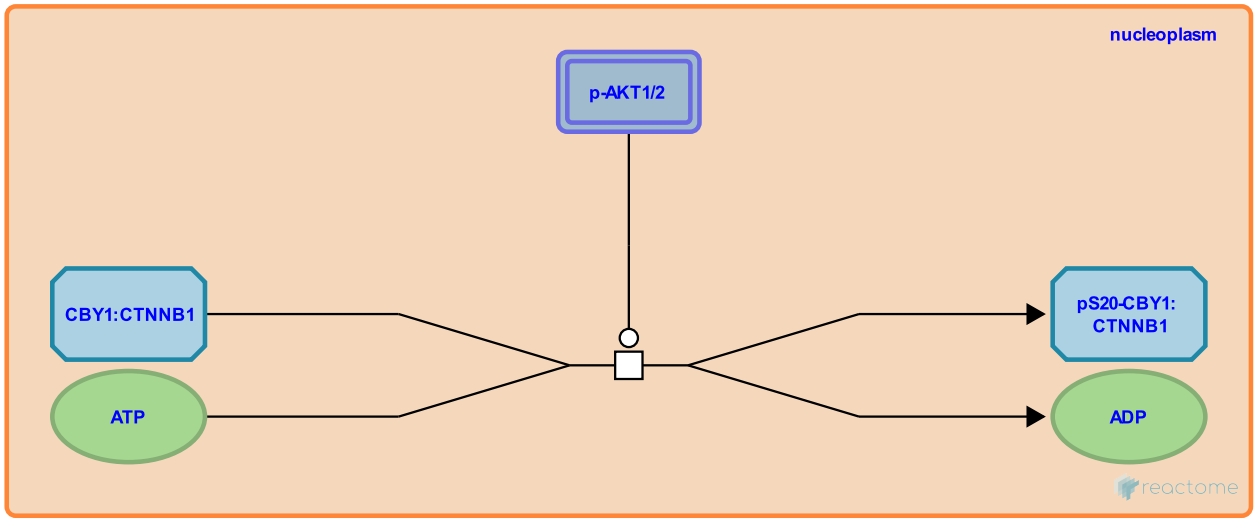
Location: Deactivation of the beta-catenin transactivating complex

Stable identifier: R-MMU-3769394

Type: transition

Compartments: nucleoplasm

Inferred from: AKT phosphorylates CBY1 (Homo sapiens)



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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

Preceded by: CBY1 binds beta-catenin

Followed by: YWHAZ binds p-CBY:CTNNB1

YWHAZ binds p-CBY:CTNNB1 ↗

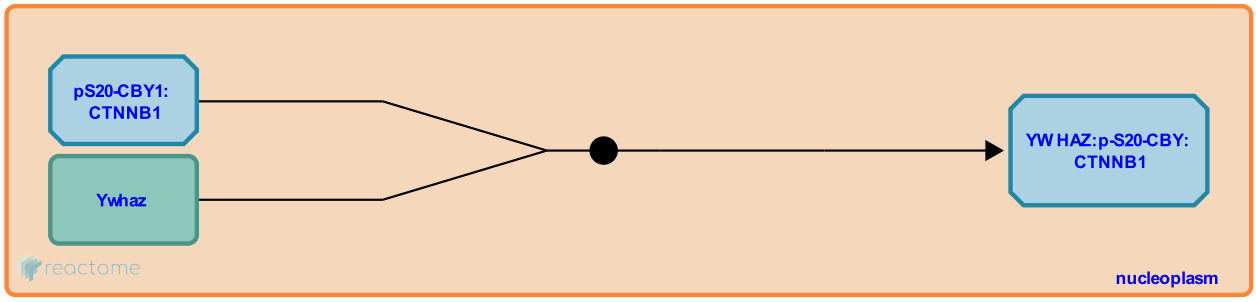
Location: Deactivation of the beta-catenin transactivating complex

Stable identifier: R-MMU-3769393

Type: binding

Compartments: nucleoplasm

Inferred from: YWHAZ binds p-CBY:CTNNB1 (Homo sapiens)



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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

Preceded by: AKT phosphorylates CBY1

Followed by: XPO1 binds the beta-catenin:CBY complex

XPO1 binds the beta-catenin:CBY complex ↗

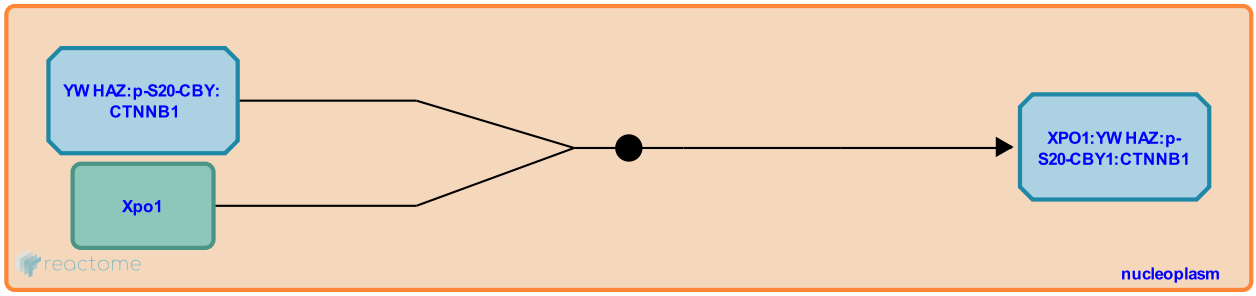
Location: Deactivation of the beta-catenin transactivating complex

Stable identifier: R-MMU-3769391

Type: binding

Compartments: nucleoplasm

Inferred from: XPO1 binds the beta-catenin:CBY complex (Homo sapiens)



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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

Preceded by: YWHAZ binds p-CBY:CTNNB1

Followed by: YWHAZ and XPO1 mediate the nuclear export of beta-catenin

YWHAZ and XPO1 mediate the nuclear export of beta-catenin ↗

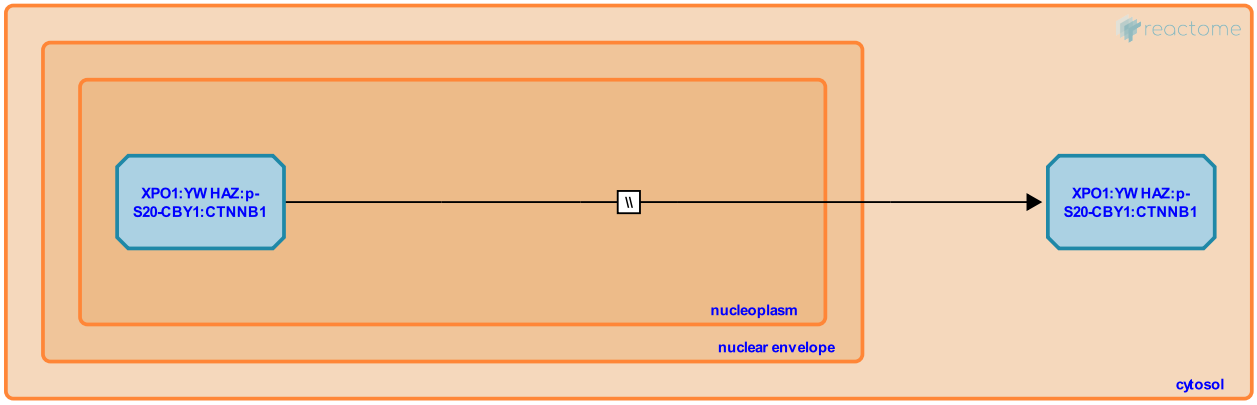
Location: Deactivation of the beta-catenin transactivating complex

Stable identifier: R-MMU-3769392

Type: omitted

Compartments: nucleoplasm, cytosol

Inferred from: YWHAZ and XPO1 mediate the nuclear export of beta-catenin (Homo sapiens)



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Preceded by: XPO1 binds the beta-catenin:CBY complex

CTNNBIP1 binds beta-catenin ↗

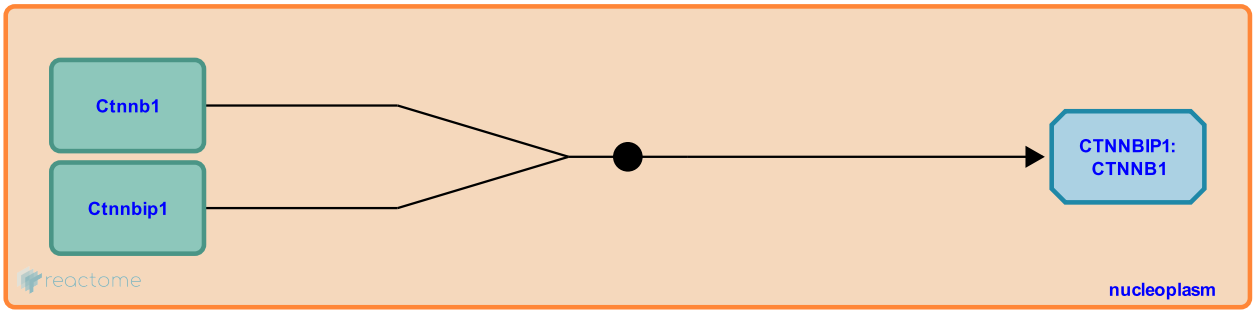
Location: Deactivation of the beta-catenin transactivating complex

Stable identifier: R-MMU-3772430

Type: binding

Compartments: nucleoplasm

Inferred from: CTNNBIP1 binds beta-catenin (Homo sapiens)



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CHD8 binds beta-catenin to negatively regulate WNT-dependent gene expression ↗

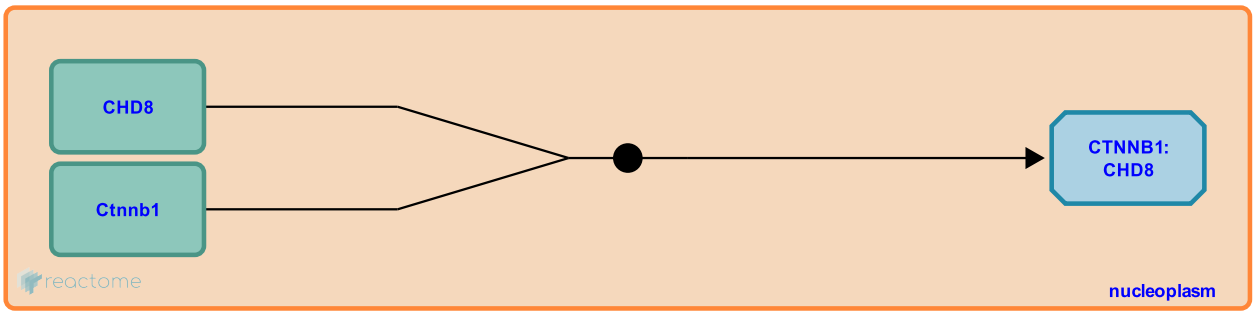
Location: Deactivation of the beta-catenin transactivating complex

Stable identifier: R-MMU-5368580

Type: binding

Compartments: nucleoplasm

Inferred from: CHD8 binds beta-catenin to negatively regulate WNT-dependent gene expression (Homo sapiens)



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Beta-catenin binds SOX proteins ↗

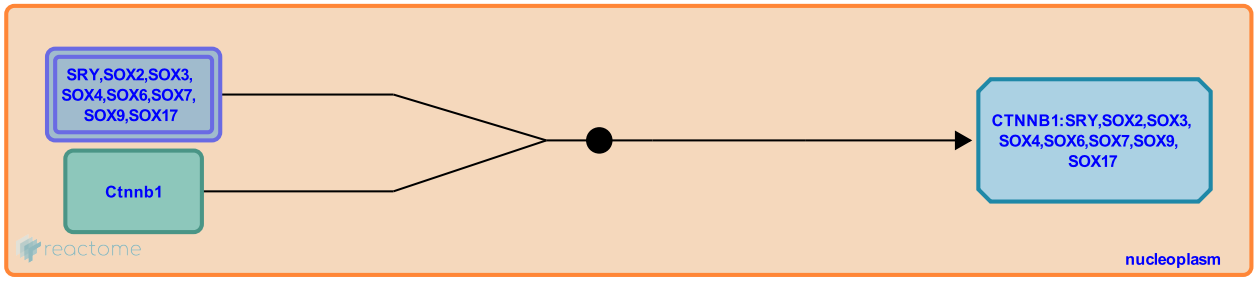
Location: Deactivation of the beta-catenin transactivating complex

Stable identifier: R-MMU-5626938

Type: binding

Compartments: nucleoplasm

Inferred from: Beta-catenin binds SOX proteins (Homo sapiens)



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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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TCF:Beta-catenin binds SOX proteins ↗

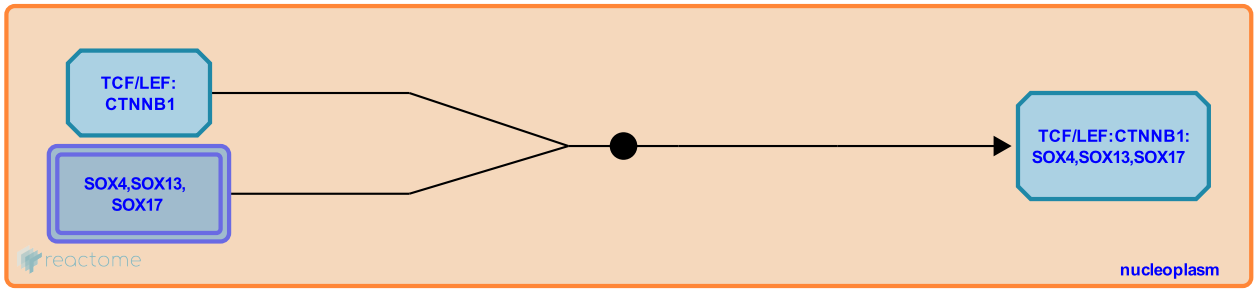
Location: Deactivation of the beta-catenin transactivating complex

Stable identifier: R-MMU-5665608

Type: binding

Compartments: nucleoplasm

Inferred from: TCF:Beta-catenin binds SOX proteins (Homo sapiens)



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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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