

Assembly of the destruction complex

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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

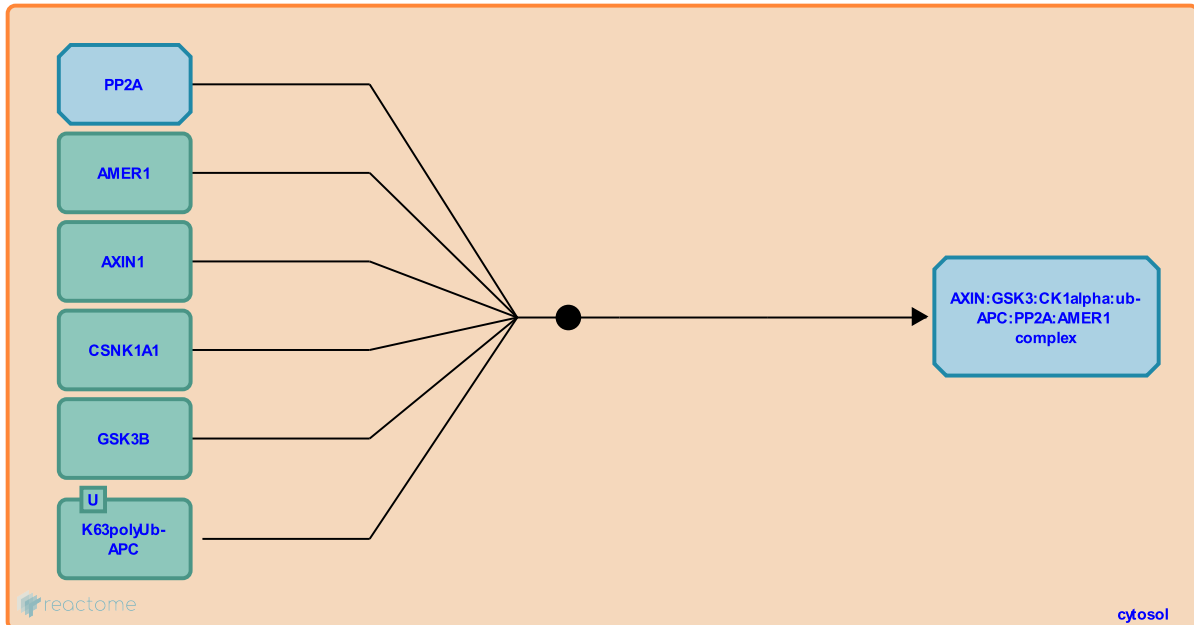
This document contains 1 reaction ([see Table of Contents](#))

Assembly of the destruction complex [↗](#)

Stable identifier: R-HSA-195251

Type: binding

Compartments: cytosol



The exact composition of the destruction complex is not known. A number of components appear to form a core complex, while others may associate with the complex transiently when a Wnt signal is present (reviewed in Kimelman and Xu, 2006). The core components include Axin, glycogen synthase kinase 3 (GSK-3), Casein kinase 1 (CKI) alpha, beta-catenin, Protein phosphatase 2A (PP2A) and Adenomatous Polyposis Coli (APC). CK1 epsilon, Diversin and PP1 may also be components of the complex.

Literature references

Roe, SM., Pearl, LH., Yeo, M., Fraser, E., Dajani, R., Dale, TC. et al. (2003). Structural basis for recruitment of glycogen synthase kinase 3beta to the axin-APC scaffold complex. *EMBO J*, 22, 494-501. [↗](#)

Gil, R., Virshup, DM., Miller, JR., White, R., Seeling, JM., Moon, RT. (1999). Regulation of beta-catenin signaling by the B56 subunit of protein phosphatase 2A. *Science*, 283, 2089-91. [↗](#)

Berndt, JD., Major, MB., Maccoss, MJ., Yi, X., Camp, ND., Biechele, TL. et al. (2007). Wilms tumor suppressor WTX negatively regulates WNT/beta-catenin signaling. *Science*, 316, 1043-6. [↗](#)

Editions

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