

YWHAZ binds p-CBY:CTNNB1

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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

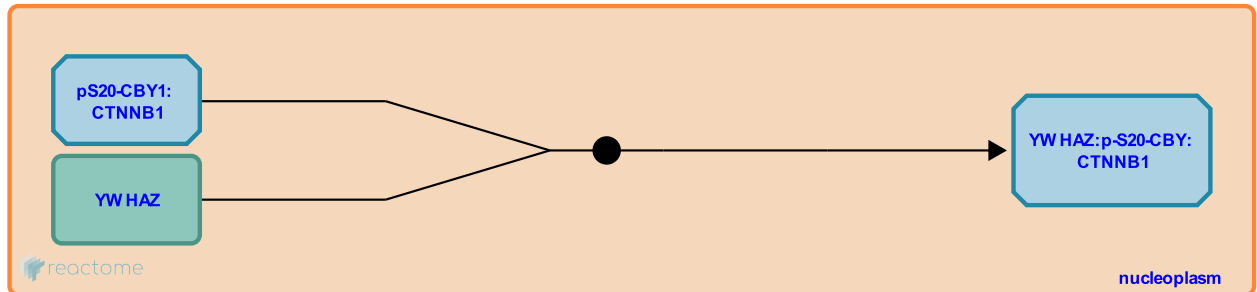
This document contains 1 reaction ([see Table of Contents](#))

YWHAZ binds p-CBY:CTNNB1 [↗](#)

Stable identifier: R-HSA-3769393

Type: binding

Compartments: nucleoplasm



14-3-3 proteins, represented here as YWHAZ, bind directly to CBY1 after AKT-dependent phosphorylation of CBY1 serine 20. Tagged versions of beta-catenin, CBY1 and 14-3-3/YWHAZ expressed in HEK293 cells co-immunoprecipitate in a CBY1-phosphorylation dependent manner. 14-3-3/YWHAZ binding promotes sequestration of CBY1 and beta-catenin in the cytoplasm, thus antagonizing beta-catenin-dependent transcription (Li et al, 2008).

Literature references

Mofunanya, A., Harris, K., Takemaru, K., Li, FQ. (2008). Chibby cooperates with 14-3-3 to regulate beta-catenin sub-cellular distribution and signaling activity. *J. Cell Biol.*, 181, 1141-54. [↗](#)

Editions

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