

# Beta-catenin recruits TRRAP/KAT5 HAT components

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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

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Reactome database release: 88

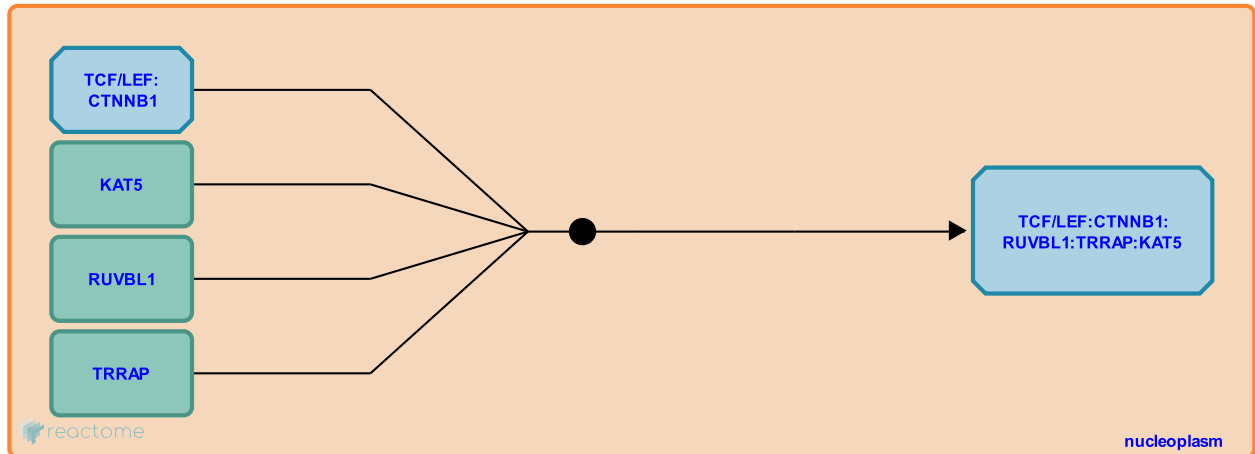
This document contains 1 reaction ([see Table of Contents](#))

## Beta-catenin recruits TRRAP/KAT5 HAT components [↗](#)

**Stable identifier:** R-HSA-3451153

**Type:** binding

**Compartments:** nucleoplasm



Pulldown experiments in colorectal cancer cells show an interaction between the C-terminal region of beta-catenin (ARM domains 11 and 12 through the C terminal) with a number of TRRAP-KAT5 HAT complex members including TRRAP, TIP49, p400 and KAT5 (TIP60), among others (Sierra et al, 2006; Bauer et al, 1998; Bauer et al, 2000; Feng et al, 2003). KAT5 and TIP49 have been shown to directly regulate WNT target genes in vivo and are associated with increased H4 acetylation (Bauer et al, 2000; Feng et al, 2003; Kim et al, 2005).

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### Editions

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