

YKI binds to WTS

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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

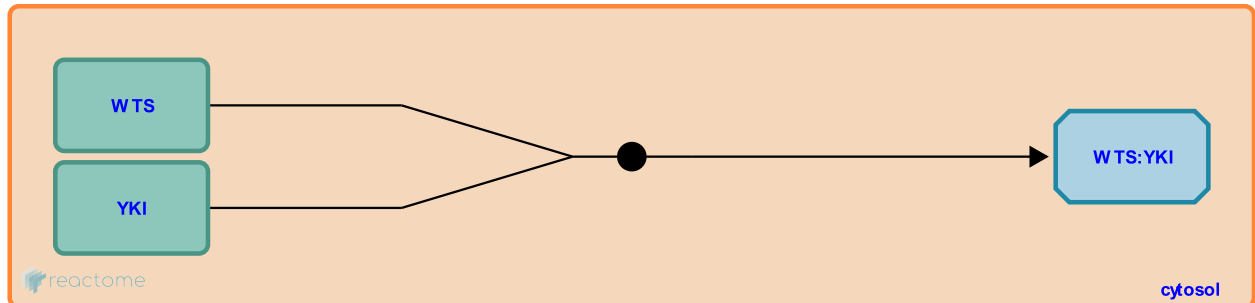
This document contains 1 reaction ([see Table of Contents](#))

YKI binds to WTS [↗](#)

Stable identifier: R-DME-451811

Type: binding

Compartments: cytosol



Yorkie (YKI), which has two WW domains, binds to Warts (WTS) PPXY sequence motif, of which WTS has five. YKI remains in the cytosol where it is unable to activate its target genes.

Literature references

Oh, H., Irvine, KD., Reddy, BV. (2009). Phosphorylation-independent repression of Yorkie in Fat-Hippo signaling. *Dev Biol*, 335, 188-97. [↗](#)

Amin, N., Gardano, L., Badouel, C., Le Bihan, T., Rosenfeld, R., McNeill, H. et al. (2009). The FERM-domain protein Expanded regulates Hippo pathway activity via direct interactions with the transcriptional activator Yorkie. *Dev Cell*, 16, 411-20. [↗](#)

Editions

2009-11-25	Reviewed	Irvine, KD.
2010-01-14	Authored, Edited	Williams, MG.