

YKI binds to phosphorylated 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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- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph data-base: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968.

Reactome database release: 88

This document contains 1 reaction (see Table of Contents)

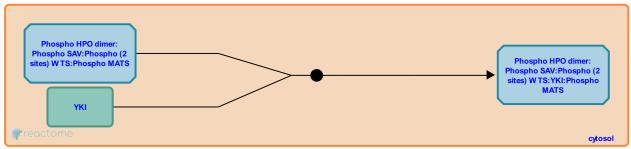
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YKI binds to phosphorylated WTS **→**

Stable identifier: R-DME-390061

Type: binding

Compartments: cytosol



The transcriptional factor Yorkie (YKI) via it's two WW domains binds to activated Warts (WTS) kinase. However, it appears that this particular binding has no detectable influence on YKI phosphorylation.

Literature references

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Wu, S., Pan, D., Matthews, K., Barrera, J., Huang, J. (2005). The Hippo signaling pathway coordinately regulates cell proliferation and apoptosis by inactivating Yorkie, the Drosophila Homolog of YAP. *Cell*, 122, 421-34.

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Editions

2009-01-23	Authored, Edited	Williams, MG.
2009-11-25	Reviewed	Irvine, KD.