YKI is phosphorylated by and then dissociates from phosphorylated WTS

Irvine, KD., Williams, MG.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

05/05/2024

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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

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. ↗

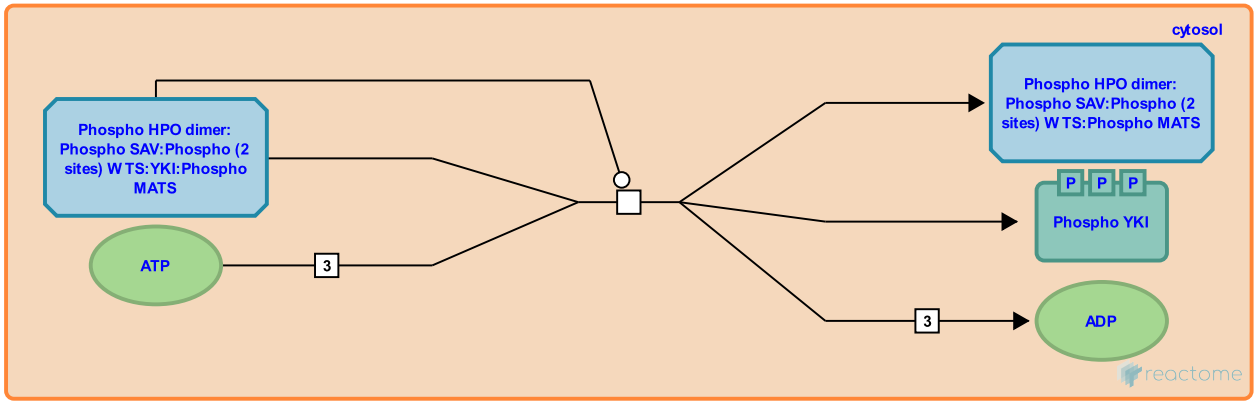
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

YKI is phosphorylated by and then dissociates from phosphorylated WTS ↗

Stable identifier: R-DME-390044

Type: transition

Compartments: cytosol



The transcription factor Yorkie (YKI) is phosphorylated at Ser111, Ser168 and Ser250 by the activated serine/threonine kinase Warts (WTS).

Literature references

Oh, H., Irvine, KD. (2008). In vivo regulation of Yorkie phosphorylation and localization. *Development, 135*, 1081-8. ↗

Wu, S., Comerford, SA., Pan, D., Maitra, A., Anders, RA., Gayyed, MF. et al. (2007). Elucidation of a universal size-control mechanism in Drosophila and mammals. *Cell, 130*, 1120-33. ↗

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. ↗

Oh, H., Irvine, KD. (2009). In vivo analysis of Yorkie phosphorylation sites. *Oncogene, 28*, 1916-27. ↗

Editions

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