Phosphorylation of WWTR1 (TAZ) by LATS1

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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. ↗

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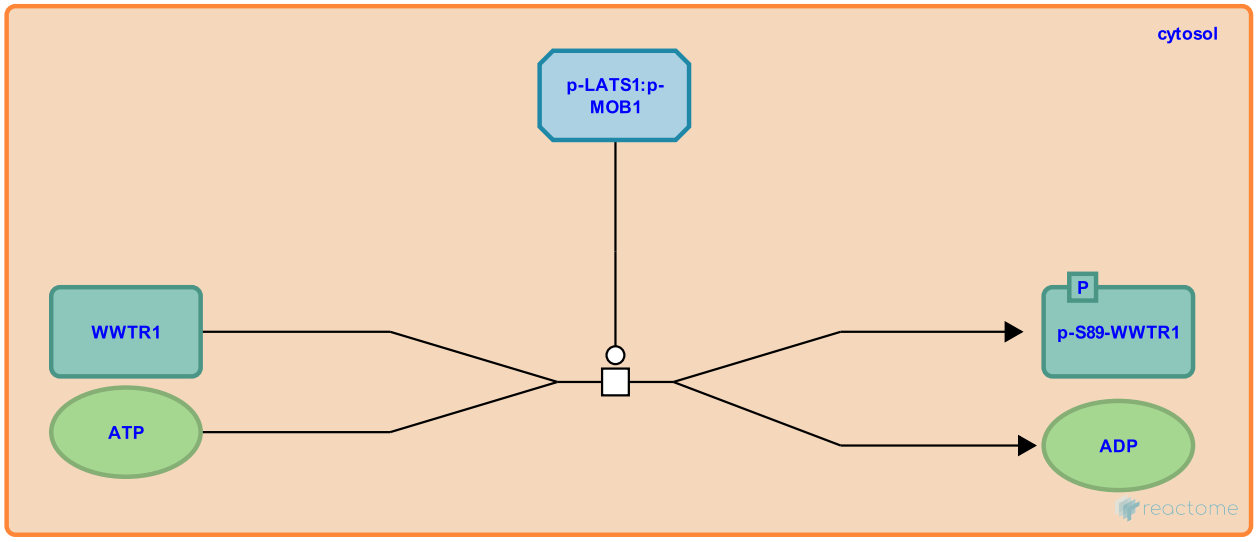
Stable identifier: R-HSA-2060328

Type: transition

Compartments: cytosol



Cytosolic phospho-LATS1, complexed with MOB1, catalyzes the phosphorylation of WWTR1 (TAZ) on serine residue 89. This activity of human LATS1 protein has not been demonstrated experimentally but is inferred from the activity of human paralogue LATS2 and of mouse homologue LATS1 (Varelas et al. 2010).

Literature references

Varelas, X., Miller, BW., Sopko, R., Song, S., Gregorieff, A., Fellouse, FA. et al. (2010). The Hippo pathway regulates Wnt/beta-catenin signaling. *Dev Cell, 18*, 579-91.

Editions

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