YAP1- and WWTR1 (TAZ)-stimulated gene expression

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21/03/2022
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


Reactome database release: 79

This document contains 1 pathway and 9 reactions (see Table of Contents)
YAP1- and WWTR1 (TAZ)-stimulated gene expression

Stable identifier: R-HSA-2032785

Compartments: cytosol, nucleoplasm

YAP1 and WWTR1 (TAZ) are transcriptional co-activators, both homologues of the Drosophila Yorkie protein. They both interact with members of the TEAD family of transcription factors, and WWTR1 interacts as well with TBX5 and RUNX2, to promote gene expression. Their transcriptional targets include genes critical to regulation of cell proliferation and apoptosis. Their subcellular location is regulated by the Hippo signaling cascade: phosphorylation mediated by this cascade leads to the cytosolic sequestration of both proteins (Murakami et al. 2005; Oh and Irvine 2010).

Literature references


Editions

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**WWTR1 (TAZ) binds TEAD**

**Location:** YAP1- and WWTR1 (TAZ)-stimulated gene expression

**Stable identifier:** R-HSA-2032781