The SMAD2/3:SMAD4 complex transfers to the nucleus

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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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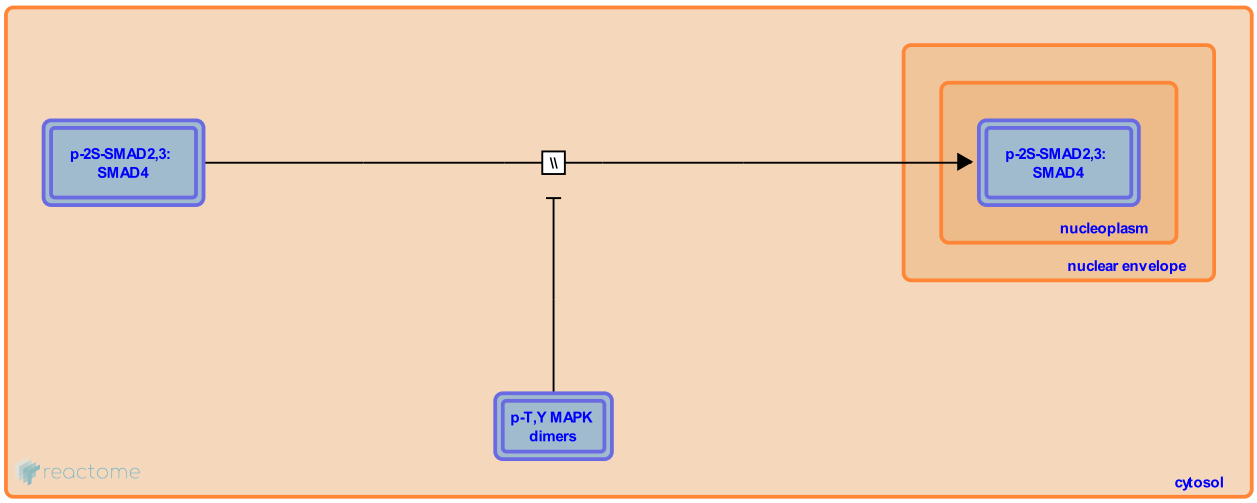
Stable identifier: R-HSA-173488

Type: omitted

Compartments: cytosol, nucleoplasm



The phosphorylated R-SMAD:CO-SMAD complex rapidly translocates to the nucleus (Xu et al. 2000, Kurisaki et al. 2001, Xiao et al. 2003) where it binds directly to DNA and interacts with a plethora of transcription co-factors. Translocation of SMAD2 and SMAD3 to the nucleus is negatively regulated by ERK-mediated phosphorylation (Kretzschmar et al. 1999). Regulation of target gene expression can be either positive or negative. A classic example of a target gene of the pathway are the genes encoding for I-SMADs. Thus, TGF-beta/SMAD signaling induces the expression of the negative regulators of the pathway (negative feedback loop).

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