SMAD7 binds to SMURF1

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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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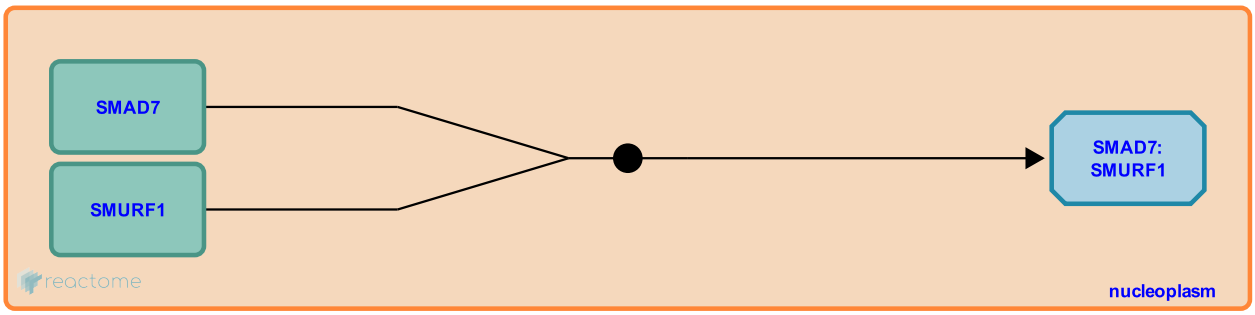
Stable identifier: R-HSA-2167917

Type: binding

Compartments: nucleoplasm

Inferred from: Smad7 binds SMURF1 (Homo sapiens)



SMAD7 binds to SMURF1 in the nucleus (Ebisawa et al. 2001, Tajima et al. 2003). SMURF1 domains WW1 and WW2, highly similar to WW2 and WW3 domains of SMURF2, are involved in SMAD7 binding. SMURF1 has two splicing isoforms. The shorter splicing isoform of SMURF1 has an inter-WW domain linker of the same length as the WW2-WW3 domain linker of SMURF2. The longer isoform of SMURF1 has a longer WW1-WW2 domain linker, resulting in decreased affinity of the longer SMURF1 isoform for SMAD7 (Chong et al. 2010). This is based on experiments with recombinant mouse Smad7 and recombinant human SMURF1.

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Editions

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