SMAD2/3 Phosphorylation Motif Mutants in Cancer

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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


Reactome database release: 72

This document contains 1 pathway and 1 reaction (see Table of Contents)
SMAD2/3 Phosphorylation Motif Mutants in Cancer

Stable identifier: R-HSA-3304356

Diseases: cancer

The conserved phosphorylation motif Ser-Ser-X-Ser at the C-terminus of SMAD2 and SMAD3 is subject to disruptive mutations in cancer. The last two serine residues in this conserved motif, namely Ser465 and Ser467 in SMAD2 and Ser423 and Ser425 in SMAD3, are phosphorylated by the activated TGF beta receptor complex (Macias Silva et al. 1996, Nakao et al. 1997). Once phosphorylated, SMAD2 and SMAD3 form transcriptionally active heterotrimers with SMAD4 (Chacko et al. 2001, Chacko et al. 2004). Phosphorylation motif mutants of SMAD2 and SMAD3 cannot be activated by the TGF-beta receptor complex either because serine residues are substituted with amino acid residues that cannot be phosphorylated or because the phosphorylation motif is deleted from the protein sequence or truncated (Fleming et al. 2013).

Literature references


Editions

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Activated TGFBR1 cannot phosphorylate SMAD2 and SMAD3 Phosphorylation Motif Mutants

Location: SMAD2/3 Phosphorylation Motif Mutants in Cancer

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