Phosphorylation of SMAD2 and SMAD3 linker regions by CDK8 or CDK9

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14/12/2022
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: 83

This document contains 1 reaction (see Table of Contents)
Phosphorylation of SMAD2 and SMAD3 linker regions by CDK8 or CDK9

Stable identifier: R-HSA-2176475

Type: transition

Compartments: nucleoplasm

CDK8 in complex with cyclin C (CDK8:CCNC) and CDK9 in complex with cyclin T (CDK9:CCNT) are able to phosphorylate the linker region of SMAD2 and SMAD3. In SMAD3, CDK8/CDK9 preferentially targets threonine residue T179, although serine residues S208 and S213 can also be phosphorylated. In SMAD2, CDK8/9 preferentially targets threonine residue T220 (corresponds to T190 in the short isoform of SMAD2, SMAD2-2). Phosphorylation of serine residues that correspond to serines S208 and S213 of SMAD3 has not been examined. Phosphorylation of the linker region of SMAD2 and SMAD3 by CDK8/CDK9 enhances transcriptional activity of SMAD2/3:SMAD4 complex, but also primes SMAD2 and SMAD3 for ubiquitination and subsequent degradation (Alarcon et al. 2009).

Literature references


Editions

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<tr>
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<td>Huang, T.</td>
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<td>2022-05-09</td>
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