

p-Smad2,3:Smad4:Foxh1 binds Activin Response Element

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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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Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)

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Reactome database release: 88

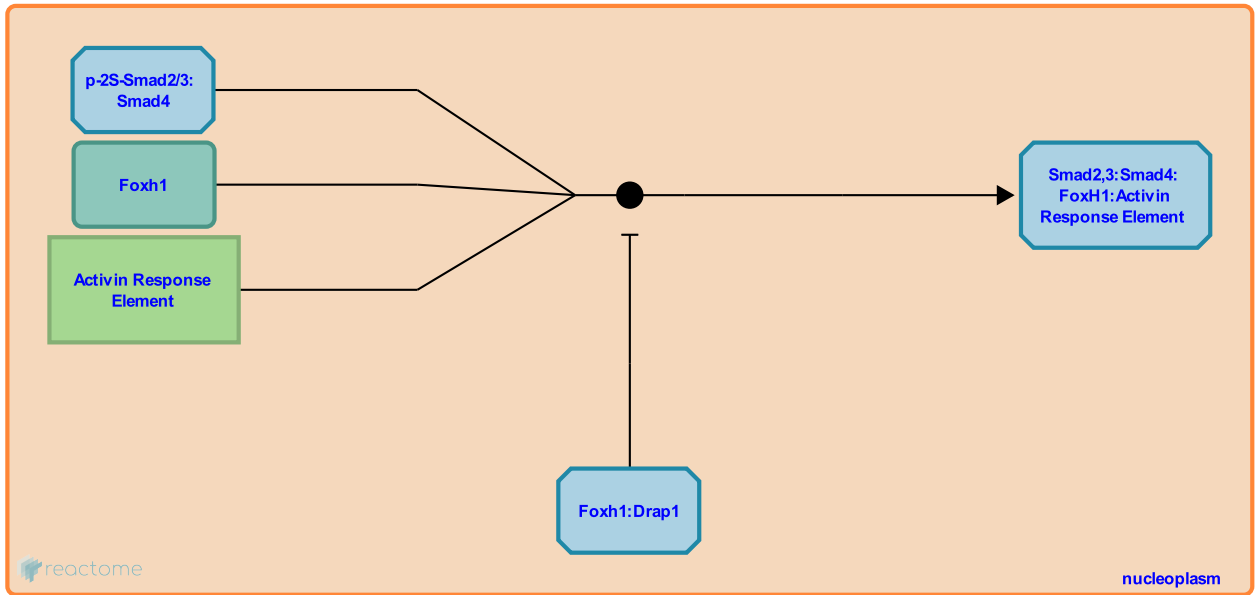
This document contains 1 reaction ([see Table of Contents](#))

p-Smad2,3:Smad4:Foxh1 binds Activin Response Element ↗

Stable identifier: R-MMU-9717136

Type: binding

Compartments: nucleoplasm



Smad2 and Smad3 do not bind DNA efficiently. They must interact with DNA-binding proteins to activate transcription. Foxh1 interacts with phospho-Smad2 and phospho-Smad3 complexed with Smad4 at promoters containing the Activin Response Element (Labbe et al. 1998, Weisberg et al. 1998, Liu et al. 1999, Izzi et al. 2007).

Literature references

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Editions

2011-08-25	Reviewed	Peng, C.
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