

# MSTN gene expression is stimulated by FOXO1 and p-2S-SMAD2/3:SMAD4

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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

Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*, 18, 142. [↗](#)

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

Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res*, 46, D649-D655. [↗](#)

Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, 14, e1005968. [↗](#)

Reactome database release: 90

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

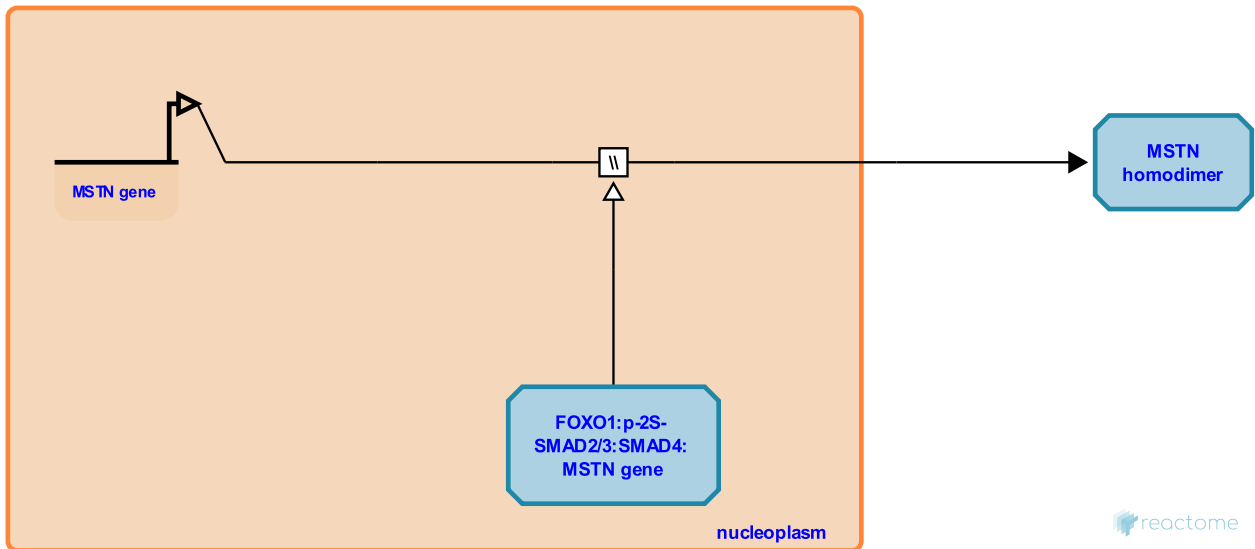
**MSTN gene expression is stimulated by FOXO1 and p-2S-SMAD2/3:SMAD4** ↗

**Stable identifier:** R-HSA-9625520

**Type:** omitted

**Compartments:** nucleoplasm, extracellular region

**Inferred from:** [Mstn gene expression is stimulated by FOXO1 and p-2S-Smad2/3:Smad4 \(Homo sapiens\)](#)



Based on studies in mice, FOXO1 and the p-2S-SMAD2/3:SMAD4 complex directly stimulate transcription of the MSTN gene, encoding myostatin. Myostatin is a TGF-beta family member that restricts muscle growth by stimulating differentiation of myoblasts (Allen and Unterman 2007).

**Editions**

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