

MYC transcription is negatively regulated by SMAD2/3:SMAD4:RBL1:E2F4/5:DP1/2 complex

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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: 76

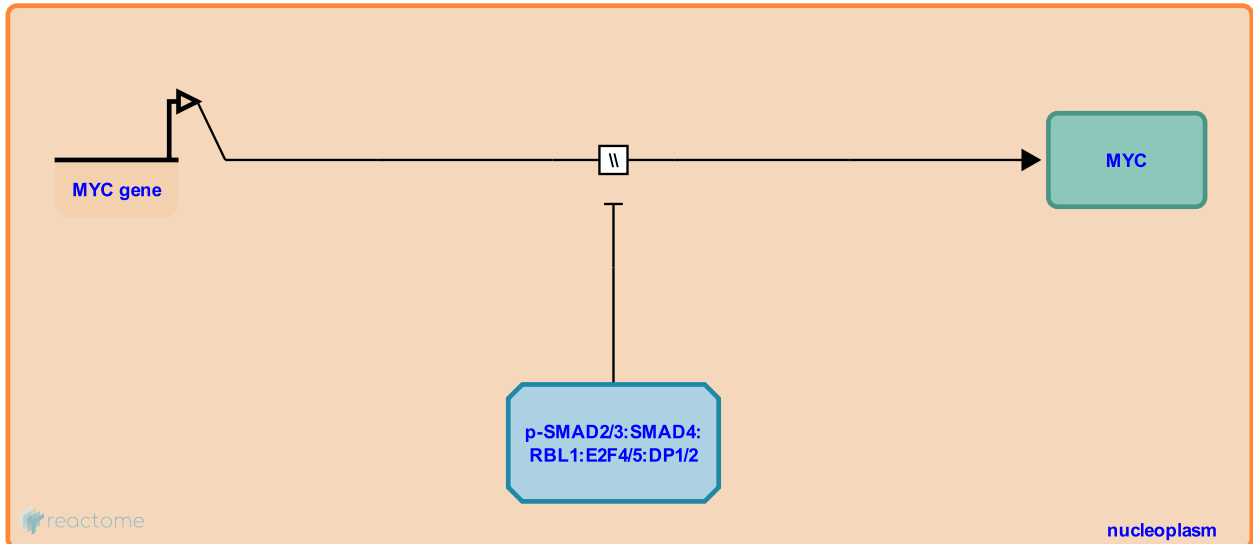
This document contains 1 reaction ([see Table of Contents](#))

MYC transcription is negatively regulated by SMAD2/3:SMAD4:RBL1:E2F4/5:DP1/2 complex [↗](#)

Stable identifier: R-HSA-1484099

Type: omitted

Compartments: nucleoplasm



Complex formed by RBL1 (p107), E2F4/5, DP1/2 and a trimer of phosphorylated R-SMADs (SMAD2/3) and SMAD4 (Co-SMAD) cooperatively binds to TIE (TGF-beta inhibitory element) and E2F sites in the MYC promoter and promotes cell-cycle independent inhibition of MYC transcription in response to TGF-beta stimulation (Chen et al. 2002).

Literature references

Chen, CR., Kang, Y., Siegel, PM., Massague, J. (2002). E2F4/5 and p107 as Smad cofactors linking the TGFbeta receptor to c-myc repression. *Cell*, 110, 19-32. [↗](#)

Editions

2012-04-05	Authored	Orlic-Milacic, M.
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