

FOXO1,FOXO3 and SMAD3 bind TRIM63 gene promoter

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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: 77

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

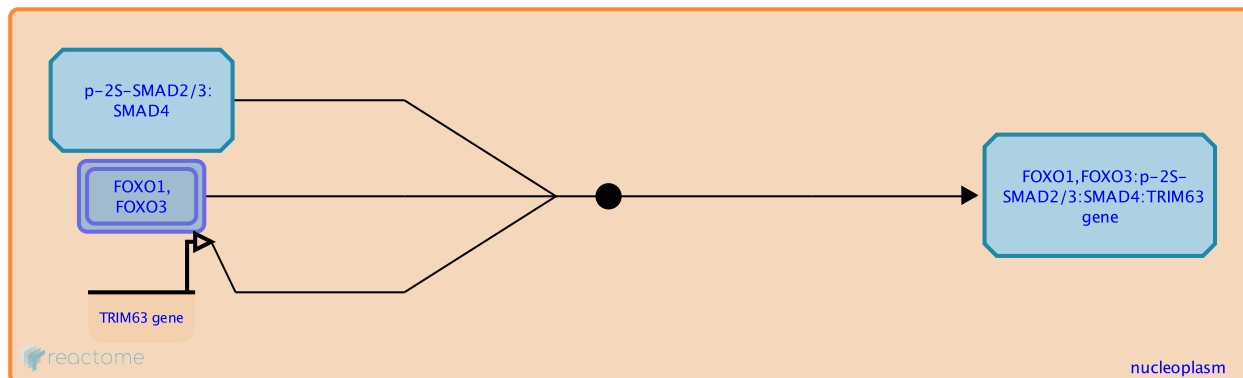
FOXO1,FOXO3 and SMAD3 bind TRIM63 gene promoter ↗

Stable identifier: R-HSA-9625749

Type: binding

Compartments: nucleoplasm

Inferred from: FOXO1,FOXO3 and SMAD3 bind Trim63 gene promoter (Homo sapiens)



FOXO1 and FOXO3 can bind to the promoter of the TRIM63 gene, encoding an E3 ubiquitin ligase MURF1, together with SMAD3 (Bollinger et al. 2014, Wang et al. 2017). SMAD3 in the nucleus exist as a heterotrimer composed of two molecules of SMAD2 or SMAD3 and one molecule of SMAD4.

Editions

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