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

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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. ↗

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. ↗

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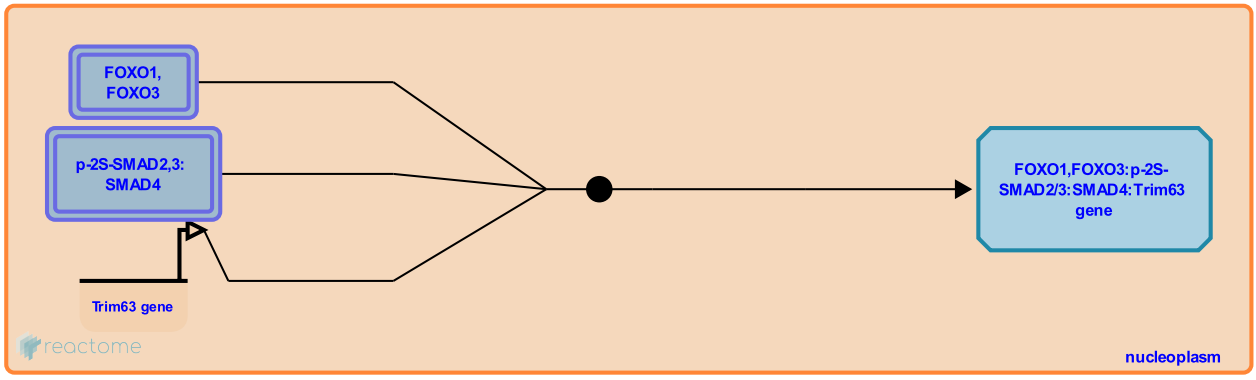
Stable identifier: R-NUL-9625758

Type: binding

Compartments: nucleoplasm



Recombinant human FOXO1 or FOXO3 bind the mouse Trim63 (Murf1) gene promoter together with recombinant human SMAD3 (Bollinger et al. 2014).

Literature references

Houmard, JA., Brault, JJ., Witczak, CA., Bollinger, LM. (2014). SMAD3 augments FoxO3-induced MuRF-1 promoter activity in a DNA-binding-dependent manner. *Am. J. Physiol., Cell Physiol., 307*, C278-87. ↗

Editions

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