CDKN1A gene transcription is stimulated by FOXO1,FOXO3,FOXO4

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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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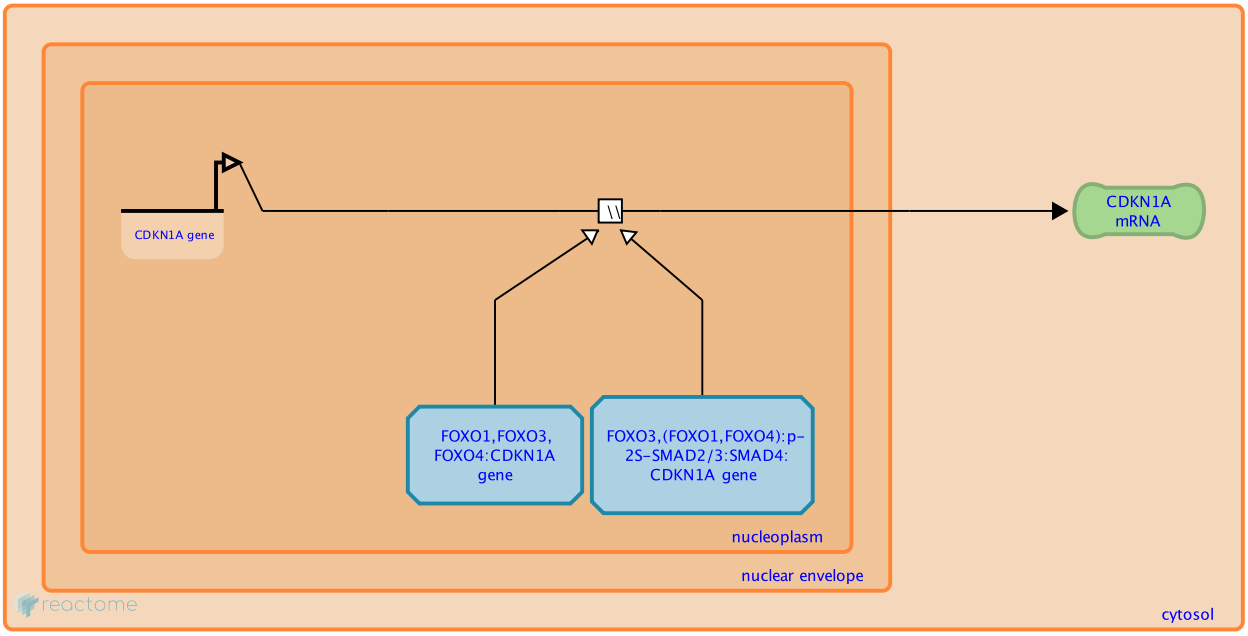
Stable identifier: R-HSA-9617838

Type: omitted

Compartments: nucleoplasm, cytosol



FOXO1, FOXO3 and FOXO4 stimulate transcription from the CDKN1A gene promoter. In response to TGF-beta signaling, FOXO transcription factors may cooperate with the active SMAD2/3:SMAD4 complexes to upregulate CDKN1A transcription (Seoane et al. 2004). FOXO1-mediated induction of CDKN1A gene transcription is implicated in CDKN1A upregulation in liver cells during fasting (Tinkum et al. 2013). Acetylation of FOXO4 by EP300 (p300) or CREBBP (CBP) in response to oxidative stress does not affect FOXO4-mediated induction of CDKN1A gene transcription (Dansen et al. 2009).

Literature references

Seoane, J., Le, HV., Shen, L., Anderson, SA., Massague, J. (2004). Integration of Smad and forkhead pathways in the control of neuroepithelial and glioblastoma cell proliferation. *Cell, 117*, 211-23.

Editions

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