

# The complex of RUNX3, SMAD3 and SMAD4 binds the CDKN1A 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: 75

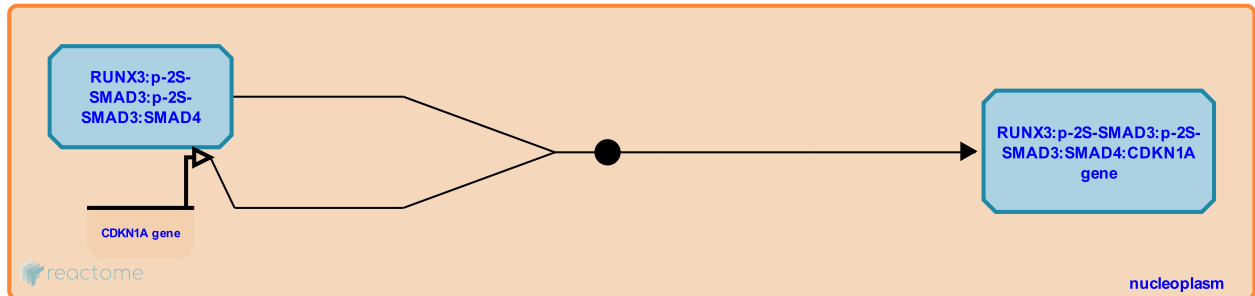
This document contains 1 reaction ([see Table of Contents](#))

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**Stable identifier:** R-HSA-8878178

**Type:** binding

**Compartments:** nucleoplasm



The CDKN1A (p21) gene promoter contains five putative RUNX3 binding sites. RUNX3 binds the CDKN1A promoter. The complex of SMAD4 and activated SMAD3, a known CDKN1A transcriptional activator, can bind to RUNX3 to cooperatively activate the CDKN1A gene transcription (Chi et al. 2005).

### Literature references

Chi, XZ., Yang, JO., Lee, KY., Ito, K., Sakakura, C., Li, QL. et al. (2005). RUNX3 suppresses gastric epithelial cell growth by inducing p21(WAF1/Cip1) expression in cooperation with transforming growth factor {beta}-activated SMAD. *Mol. Cell. Biol.*, 25, 8097-107. ↗

### Editions

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