

RUNX1 binds the SOCS4 gene

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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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

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: 70

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

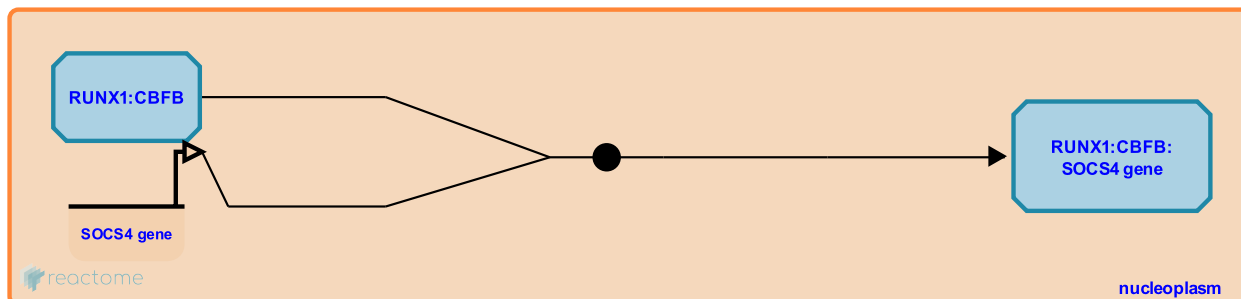
RUNX1 binds the SOCS4 gene [↗](#)

Stable identifier: R-HSA-8955822

Type: binding

Compartments: nucleoplasm

Inferred from: [Runx1 binds the Socs4 gene \(Mus musculus\)](#)



Based on studies in mouse keratinocytes, RUNX1, presumably in complex with CBFβ, binds the SOCS4 gene (Scheitz et al. 2012). Runx binding elements are found in the promoter region and enhancer elements downstream of the mouse *Socs4* gen. In the human SOCS4 gene, Runx binding elements can be found in the first intron and downstream of the SOCS4 gene.

Literature references

Scheitz, CJ., Lee, TS., McDermit, DJ., Tumber, T. (2012). Defining a tissue stem cell-driven Runx1/Stat3 signalling axis in epithelial cancer. *EMBO J.*, 31, 4124-39. [↗](#)

Editions

2016-09-14	Authored	Orlic-Milacic, M.
2016-12-20	Reviewed	Ito, Y., Chuang, LS.
2017-05-09	Edited	Orlic-Milacic, M.