

# RUNX1 binds the SOCS3 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.

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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. [↗](#)
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Reactome database release: 73

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

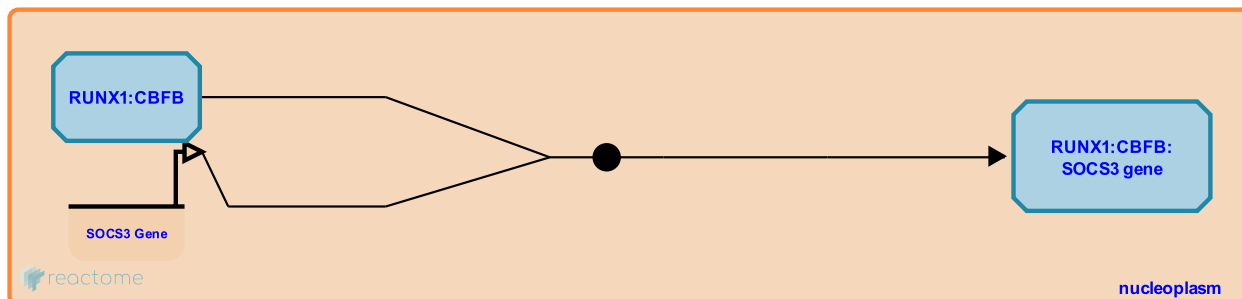
## RUNX1 binds the SOCS3 gene [↗](#)

**Stable identifier:** R-HSA-8955748

**Type:** binding

**Compartments:** nucleoplasm

**Inferred from:** [Runx1 binds the Socs3 gene \(Mus musculus\)](#)



Based on studies in mouse keratinocytes, RUNX1, presumably in complex with CBFB, binds the SOCS3 gene (Scheitz et al. 2012). By sequence similarity, at least one Runx binding element is conserved between human and mouse SOCS3 gene loci.

### Literature references

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

### Editions

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