RUNX1 binds the SWI/SNF complex

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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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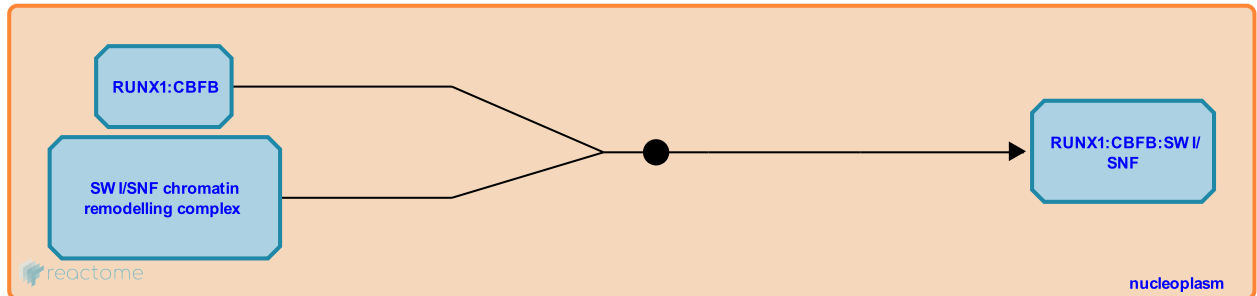
Reactome database release: 89

This document contains 1 reaction (see Table of Contents)

RUNX1 binds the SWI/SNF complex ↗

Stable identifier: R-HSA-8938217

Type: binding

Compartments: nucleoplasm

The RUNX1:CBFB complex can bind the SWI/SNF chromatin remodeling complex by directly interacting with at least three subunits of the SWI/SNF: BRG1 (SMARCA4), BAF155 (SMARCC1) and INI1 (SMARCB1). RUNX1 recruits the SWI/SNF complex to many of its target promoters, which is associated with changes in histone modifications at these promoters, but precise changes and their effect on gene expression have not been fully elucidated (Bakshi et al. 2010).

Literature references

van Wijnen, AJ., Lian, JB., Stein, JL., Montecino, MA., Stein, GS., Hassan, MQ. et al. (2010). The human SWI/SNF complex associates with RUNX1 to control transcription of hematopoietic target genes. *J. Cell. Physiol., 225*, 569-76. ↗

Editions

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