

# **RUNX1:CBFB, SIN3A(SIN3B), PRMT6 and HDAC1 bind the ITGA2B 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

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Reactome database release: 70

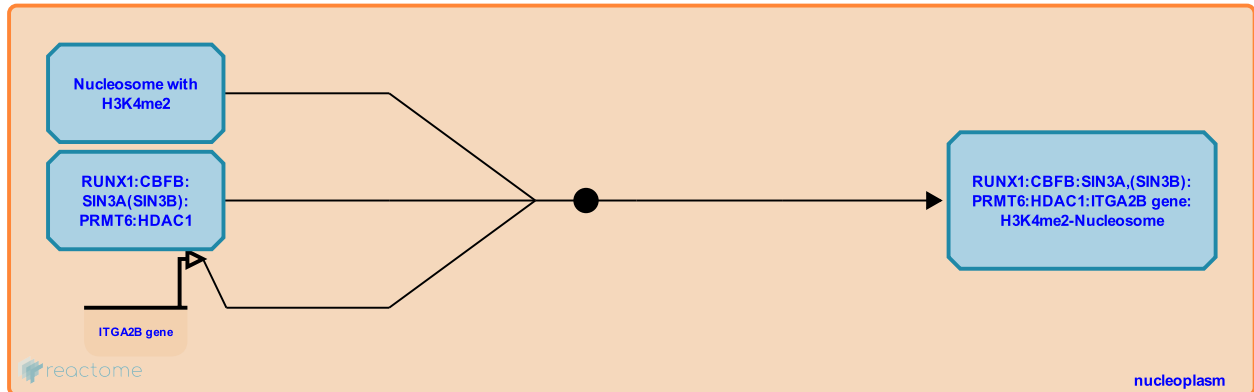
This document contains 1 reaction ([see Table of Contents](#))

## RUNX1:CBFB, SIN3A(SIN3B), PRMT6 and HDAC1 bind the ITGA2B promoter ↗

**Stable identifier:** R-HSA-8935730

**Type:** binding

**Compartments:** nucleoplasm



The transcriptional co-repressor SIN3A (and possibly SIN3B) can bind to the RUNX1:CBFB complex at the promoter of the ITGA2B (CD41) gene, encoding Integrin alpha IIb. Binding of SIN3A (and probably SIN3B) to RUNX1 is inhibited by PRMT1-mediated arginine methylation of RUNX1 arginine residues R206 and R210 (Zhao et al. 2008). In addition to SIN3A, the RUNX1-containing transcriptional repressor complex at the ITGA2B promoter also includes histone arginine methyltransferase PRMT6 and histone deacetylase HDAC1 (Herglotz et al. 2013). Dimethylation of histone H3 on lysine residue K4 (K5 when taking into account the initiator methionine), known as the H3K4me2 mark, is characteristic of nucleosomes associated with megakaryocyte specific promoters, including the ITGA2B gene, prior to the onset of differentiation (Herglotz et al. 2013).

### Literature references

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### Editions

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