NR4A3 gene expression is stimulated by RUNX1:CBFB

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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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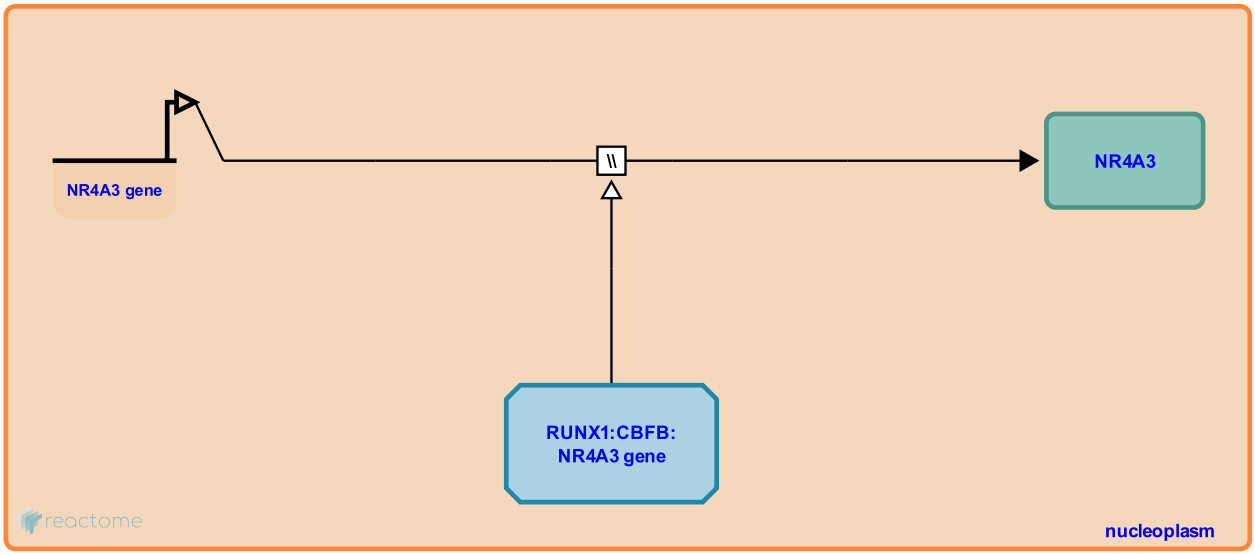
Stable identifier: R-HSA-8938034

Type: omitted

Compartments: nucleoplasm



Binding of the RUNX1:CBFB complex to the NR4A3 gene promoter stimulates NR4A3 gene transcription, leading to reduction in the clonogenic potential of hematopoietic progenitors. RUNX1 mutants associated with familial platelet disorders (FPD) and acute myeloid leukemia (AML) are unable to transactivate the NR4A3 gene (Bluteau et al. 2011).

Literature references

Bluteau, D., Gilles, L., Hilpert, M., Antony-Debré, I., James, C., Debili, N. et al. (2011). Down-regulation of the RUNX1-target gene NR4A3 contributes to hematopoiesis deregulation in familial platelet disorder/acute myelogenous leukemia. *Blood, 118*, 6310-20. ↗

Editions

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