RUNX1, SPI1 (PU.1), GATA2, TAL1 (SCL), FLI1, and MYB bind the CEBPA 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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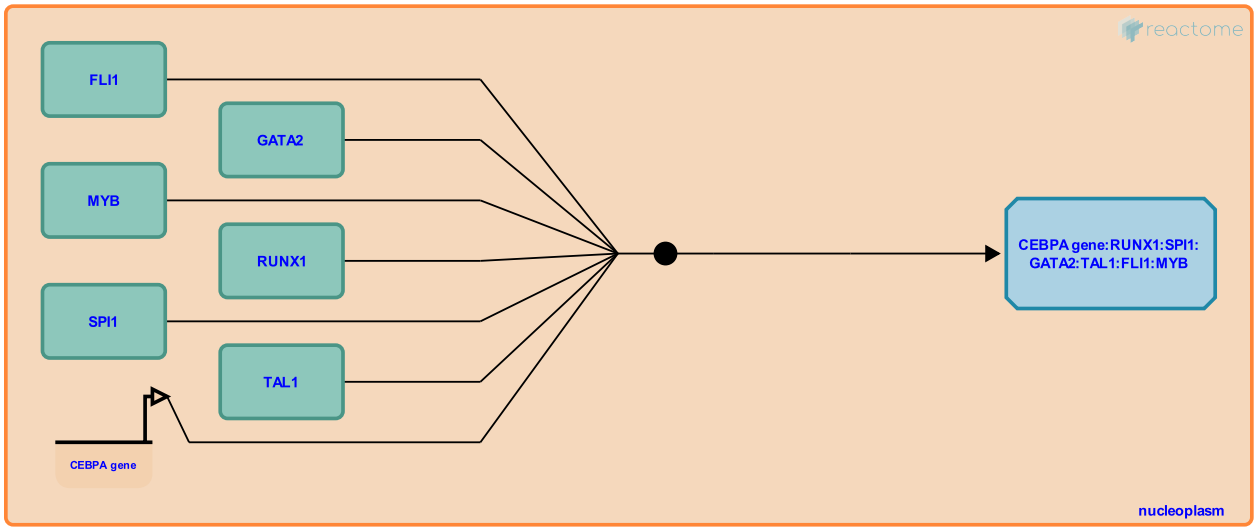
Stable identifier: R-HSA-9616214

Type: binding

Compartments: nucleoplasm

Inferred from: Runx1, Spi1, Gata2, Tal1, Fli1, Myb, and Cebpa bind the promoter of the Cebpa gene (Mus musculus)



The evolutionarily conserved upstream enhancer of the CEBPA gene binds RUNX1, SPI1 (PU.1), GATA2, TAL1 (SCL), FLI1, and MYB in hemopoietic progenitor cells and myeloid progenitor cells (inferred from mouse). Unlike the promoter of the mouse Cebpa gene, the human CEBPA promoter does not bind CEBPA and autoregulation of CEBPA occurs indirectly through CEBPA-stimulated binding of USF to the promoter of the CEBPA gene (Timchenko et al. 1995). As inferred from mouse homologs, RUNX1, GATA2, SCL, SPI1, and FLI1 bind concomitantly.

Literature references

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Editions

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