CSF3R gene expression is enhanced by SPI1 (PU.1), CEBPA, and DEK

May, B., Skokowa, J.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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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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Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

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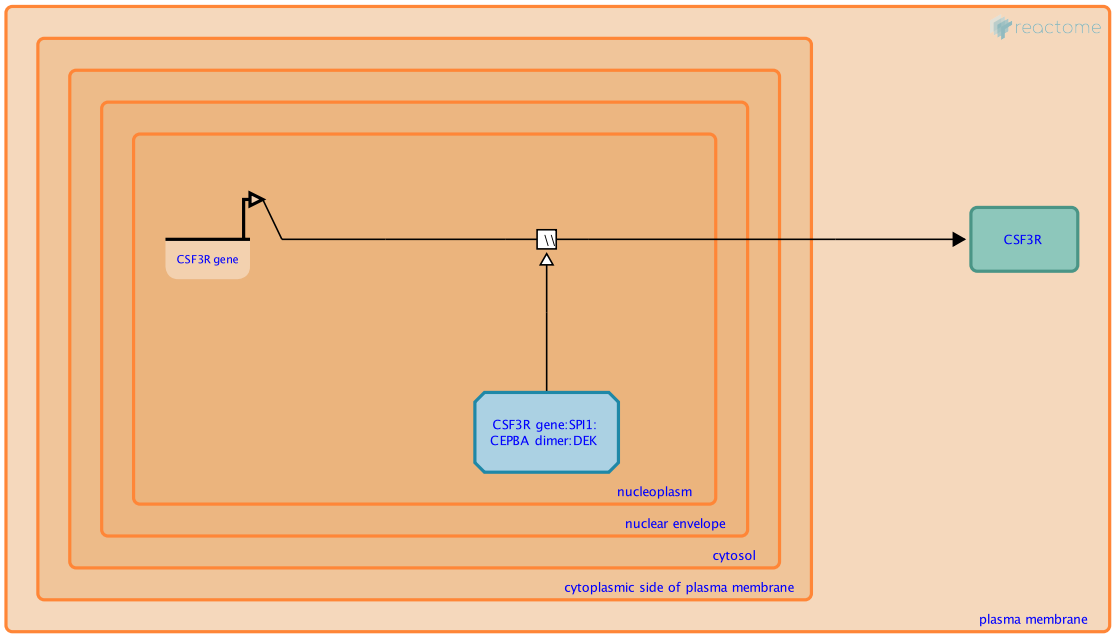
Stable identifier: R-HSA-9634429

Type: omitted

Compartments: nucleoplasm, cytosol

Inferred from: Csf3r gene expression is enhanced by Cebpa (Mus musculus)



SPI1 (PU.1) and CEBPA bind the promoter of the CSF3R (G-CSFR) gene and synergistically activate transcription of CSF3R (Smith et al. 1996, Tavor et al. 2003). Absence of CEBPA binding reduces transcription by about 60% and absence of SPI1 binding reduces transcription by about 75% (Smith et al. 1996). DEK interacts with CEBPA at the CSF3R promoter and enhances transcription (Koleva et al. 2012). DEK is required for CSF3 (G-CSF) mediated granulocyte differentiation (Koleva et al. 2012).

Literature references

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Editions

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