RORC gene expression is stimulated by RUNX3: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

Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics, 18*, 142. ↗

Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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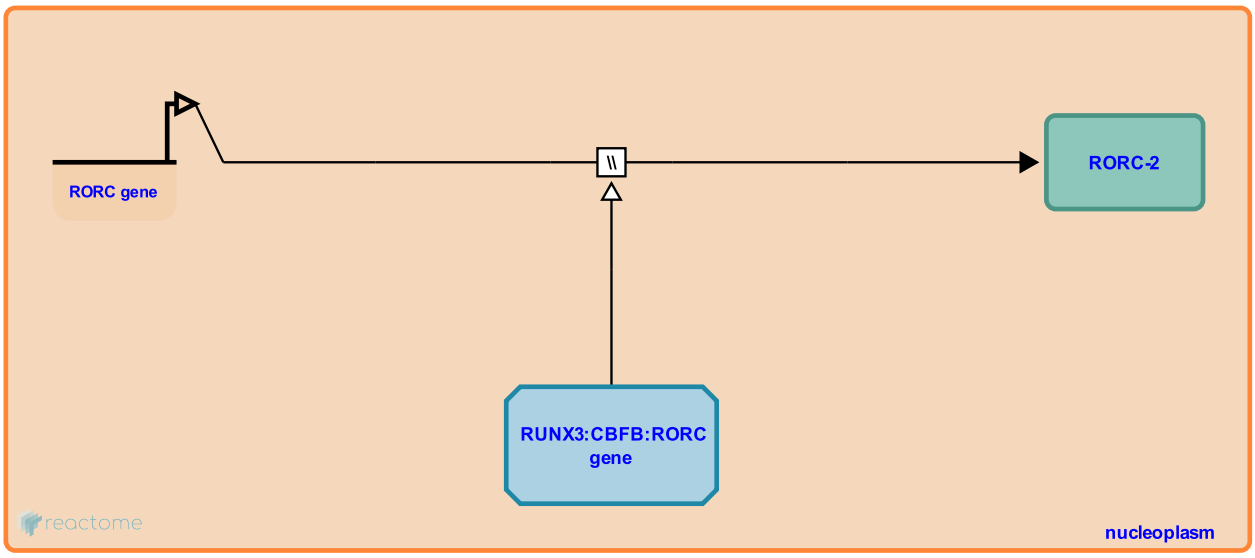
Stable identifier: R-HSA-8949301

Type: omitted

Compartments: nucleoplasm

Inferred from: Rorc gene expression is stimulated by Runx3:Cbfb (Mus musculus)



Based on mouse studies, binding of the RUNX3:CBFB heterodimer to the RUNX binding motif TGTGGT conserved between the mouse and human promoters of the RORC (RORgamma) gene, stimulates transcription of the RORC transcript variant 2 (RORC-2), also known as RORgT (RORgamma-t). In the ILC3 lineage of innate lymphoid cells in mice, expression of the Ahr transcription factor is positively indirectly regulated by Runx3, most likely through RORgT (Ebihara et al. 2015).

Literature references

Stappenbeck, TS., Yang, L., Egawa, T., Yokoyama, WM., Ebihara, T., Groner, Y. et al. (2015). Runx3 specifies lineage commitment of innate lymphoid cells. *Nat. Immunol., 16*, 1124-33. ↗

Editions

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