

IRF2 binds the promoters of Interferon al- pha and beta

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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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- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
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Reactome database release: 88

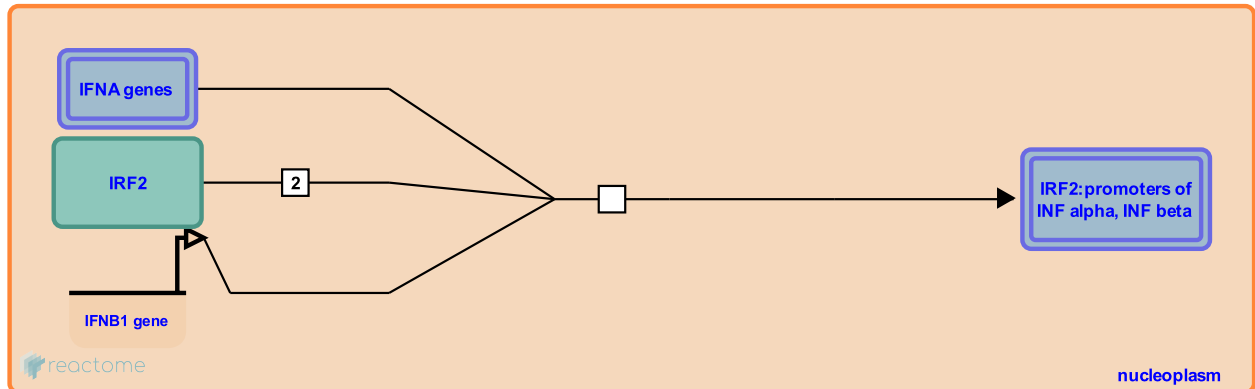
This document contains 1 reaction ([see Table of Contents](#))

IRF2 binds the promoters of Interferon alpha and beta ↗

Stable identifier: R-HSA-994038

Type: transition

Compartments: nucleoplasm



Interferon regulatory factor 2 (IRF-2) represses the action of IRF-1 on type I interferon genes (Harada et al, 1989, 1990; Palombella & Maniatis, 1992) by competing with IRF-1 for binding at the PRDI site.

Literature references

Palombella, VJ., Maniatis, T. (1992). Inducible processing of interferon regulatory factor-2. *Mol Cell Biol*, 12, 3325-36.

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Editions

2010-10-29	Authored	Akkerman, JW.
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