

CTF1 binds LIFR:JAKs

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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. [↗](#)
- 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. [↗](#)

Reactome database release: 75

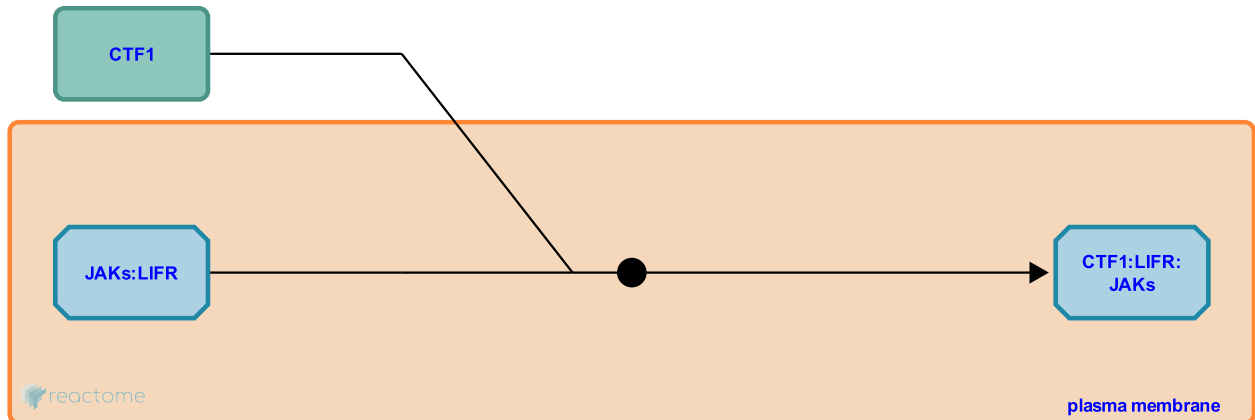
This document contains 1 reaction ([see Table of Contents](#))

CTF1 binds LIFR:JAKs ↗

Stable identifier: R-HSA-5696482

Type: binding

Compartments: plasma membrane, extracellular region



Cardiotrophin-1 (CTF1/CT-1) is a member of the IL-6 family of cytokines which was originally discovered as a factor which can induce hypertrophy of cardiac myocytes both in vitro and in vivo (Pennica et al. 1995a). Subsequently, CTF1 has been shown to have a wide variety of different effects on cardiac and non cardiac cells including the ability to stimulate the survival of both cardiac and neuronal cells (Latchman 1999). Leukemia inhibitory factor (LIF), CTF1, and oncostatin M (OSM) are four helix bundle cytokines acting through a common heterodimeric receptor composed of gp130 and LIF receptor (LIFR) (Pennica et al. 1995b).

Literature references

Tsuruda, T., Jougasaki, M., Boerrigter, G., Huntley, BK., Chen, HH., D'Assoro, AB. et al. (2002). Cardiotrophin-1 stimulation of cardiac fibroblast growth: roles for glycoprotein 130/leukemia inhibitory factor receptor and the endothelin type A receptor. *Circ. Res.*, 90, 128-34. ↗

Pennica, D., Shaw, KJ., Swanson, TA., Moore, MW., Shelton, DL., Zioncheck, KA. et al. (1995). Cardiotrophin-1. Biological activities and binding to the leukemia inhibitory factor receptor/gp130 signaling complex. *J. Biol. Chem.*, 270, 10915-22. ↗

Pennica, D., King, KL., Shaw, KJ., Luis, E., Rullamas, J., Luoh, SM. et al. (1995). Expression cloning of cardiotrophin 1, a cytokine that induces cardiac myocyte hypertrophy. *Proc. Natl. Acad. Sci. U.S.A.*, 92, 1142-6. ↗

Editions

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