

# IL2RG binds JAK3

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17/05/2024

## 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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

## 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: 88

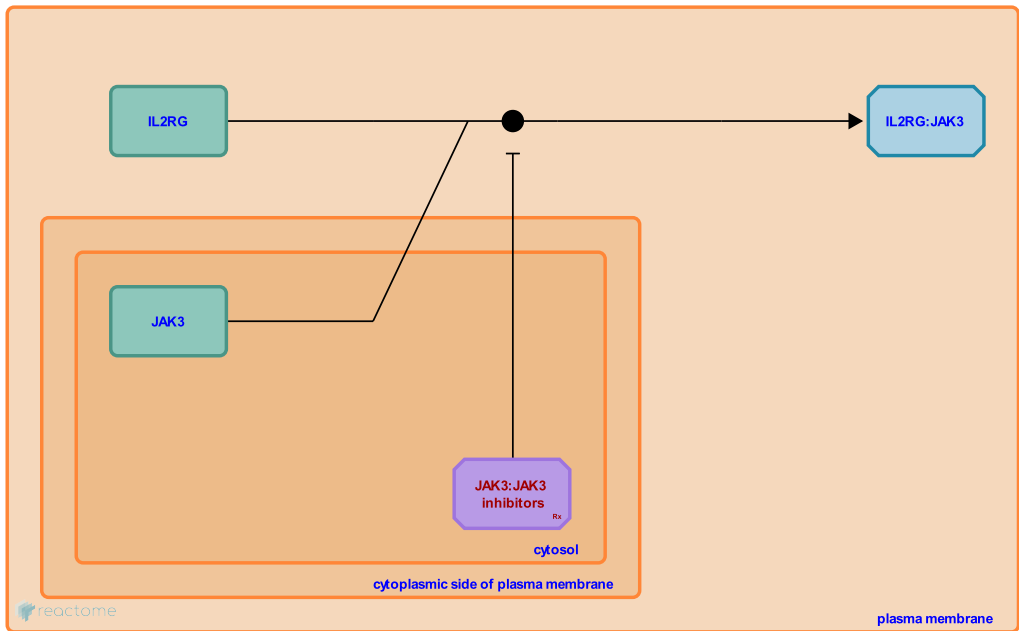
This document contains 1 reaction ([see Table of Contents](#))

IL2RG binds JAK3 ↗

Stable identifier: R-HSA-451895

Type: binding

Compartments: cytosol, plasma membrane



Cytokine receptor common gamma subunit (IL2RG, IL-2 receptor gamma chain, Gc) associates with Tyrosine-protein kinase JAK3 (JAK3). The carboxyl-terminal region of IL2RG is important for this association (Miyazaki et al. 1994, Zhu et al. 1998, Russel et al. 2004, Chen et al.1997, Nelson et al.1994) as well as the FERM domain in JAK3 (Zhou et al. 2001).

Literature references

Berry, JA., Zhu, MH., Russell, SM., Leonard, WJ. (1998). Delineation of the regions of interleukin-2 (IL-2) receptor beta chain important for association of Jak1 and Jak3. Jak1-independent functional recruitment of Jak3 to IL-2Rbeta. *J Biol Chem*, 273, 10719-25. ↗

Lord, JD., Nelson, BH., Greenberg, PD. (1994). Cytoplasmic domains of the interleukin-2 receptor beta and gamma chains mediate the signal for T-cell proliferation. *Nature*, 369, 333-6. ↗

Editions

2010-05-17	Authored	Ray, KP.
2010-08-06	Edited	Jupe, S.
2016-01-28	Reviewed	Meldal, BH.
2018-04-27	Edited	Jassal, B.
2018-04-27	Reviewed	Limon, PL.