

IL21 receptor JAK phosphorylation

Jupe, S., Meldal, BH.

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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of <u>Creative Commons Attribution 4.0 International (CC BY 4.0)</u> <u>License</u>. For more information see our <u>license</u>.

11/05/2024

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. 7
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. A
- 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. *オ*

This document contains 1 reaction (see Table of Contents)

IL21 receptor JAK phosphorylation 7

Stable identifier: R-HSA-9006850

Type: omitted

Compartments: cytosol, extracellular region, plasma membrane



The IL21 heteromeric receptor complex can activate JAK1 and JAK3 in response to Interleukin-21 (IL21), leading to JAK tyrosine phosphorylation (Asao et al. 2001, Habib et al. 2002).

This is a black box event because the mechanism leading to JAK phosphorylation is not established for this receptor complex.

Literature references

- Weinberg, K., Senadheera, S., Kaushansky, K., Habib, T. (2002). The common gamma chain (gamma c) is a required signaling component of the IL-21 receptor and supports IL-21-induced cell proliferation via JAK3. *Biochemistry*, *41*, 8725-31. *¬*
- Ishii, N., Okuyama, C., Foster, D., Asao, H., Kumaki, S., Sugamura, K. et al. (2001). Cutting edge: the common gamma-chain is an indispensable subunit of the IL-21 receptor complex. J. Immunol., 167, 1-5. *¬*

Editions

2017-05-11	Authored	Jupe, S.
2017-11-03	Edited	Jupe, S.
2017-11-03	Reviewed	Meldal, BH.