JAK2, TYK2 in IL12A:IL12RB1:TYK2:IL12B:IL12RB2:JAK2 are phosphorylated

Duenas, C., van de Vosse, E.

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 Creative Commons Attribution 4.0 International (CC BY 4.0) License. For more information see our license.

16/05/2024

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. ↗

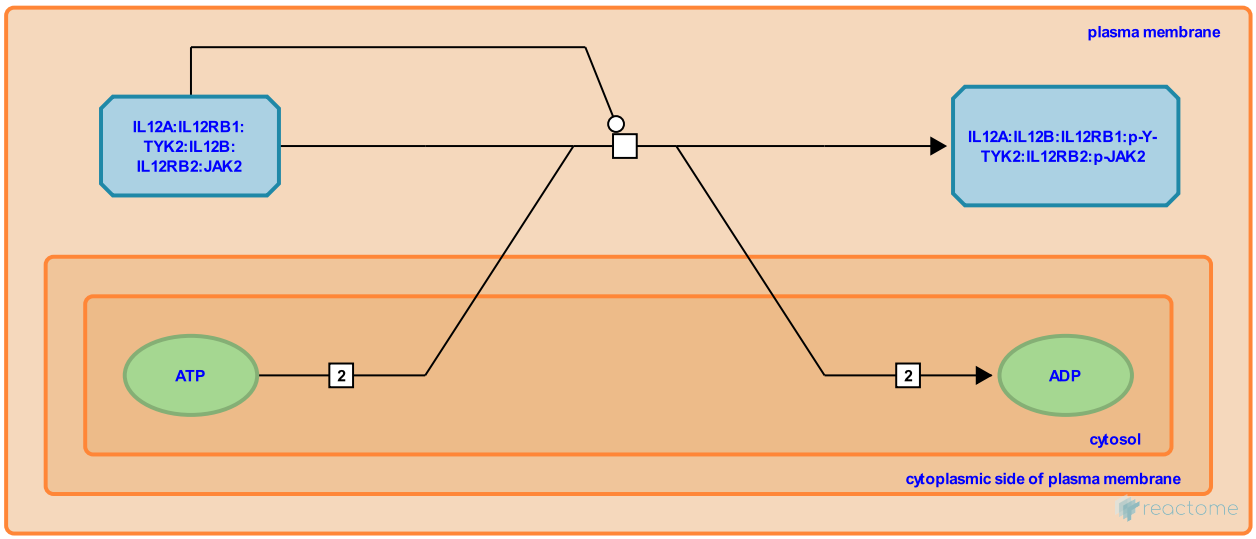
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

JAK2, TYK2 in IL12A:IL12RB1:TYK2:IL12B:IL12RB2:JAK2 are phosphorylated ↗

Stable identifier: R-HSA-8950423

Type: transition

Compartments: cytosol, plasma membrane, extracellular region



Interleukin-12 phosphorylates and thereby activates Tyrosine-protein kinase JAK2 (JAK2) and non-receptor tyrosine-protein kinase TYK2 (TYK2) (Bacon et al.1995, Kanda & Watanabe 2008).

Literature references

Kanda, N., Watanabe, S. (2008). IL-12, IL-23, and IL-27 enhance human beta-defensin-2 production in human keratinocytes. *Eur. J. Immunol., 38*, 1287-96. ↗

Ortaldo, JR., Johnston, JA., Petricoin, EF., Rees, RC., Bacon, CM., O'Shea, JJ. et al. (1995). Interleukin 12 induces tyrosine phosphorylation and activation of STAT4 in human lymphocytes. *Proc. Natl. Acad. Sci. U.S.A., 92*, 7307-11. ↗

Editions

2016-12-02	Authored	Duenas, C.
2017-05-11	Edited	Duenas, C.
2017-05-12	Reviewed	van de Vosse, E.