

JAK1/JAK2/TYK2 bound to IL6ST:IL6ST are phosphorylated

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https://reactome.org

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 data-base: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968.

Reactome database release: 88

This document contains 1 reaction (see Table of Contents)

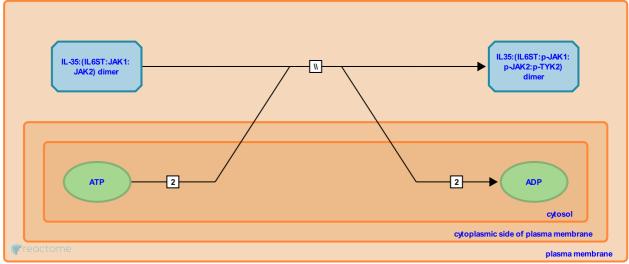
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Stable identifier: R-HSA-8983834

Type: omitted

Compartments: plasma membrane, cytosol, extracellular region



Interleukin 35 (IL35) may presumably signal via a complex that includes Tyrosine protein kinase JAK1 (JAK1) and JAK2 associated with Interleukin 6 receptor beta subunit (IL6ST) dimers (Collison et al. 2012). These JAKs are believed to phosphorylate Signal transducer and activator of transcription 1 (STAT) (Stark GR and Darnell JE, 2012). As the series of events that induces JAK/STAT phosphorylation events in response to IL35 are not clear, this event is represented as a black box.

Literature references

Delgoffe, GM., Murray, PJ., Drake, CG., Satoskar, AR., Fairweather, D., Guy, CS. et al. (2012). The composition and signaling of the IL-35 receptor are unconventional. *Nat. Immunol.*, 13, 290-9.

Editions

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