

Tyrosine phosphorylated IL6ST binds STAT1,STAT3

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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: 88

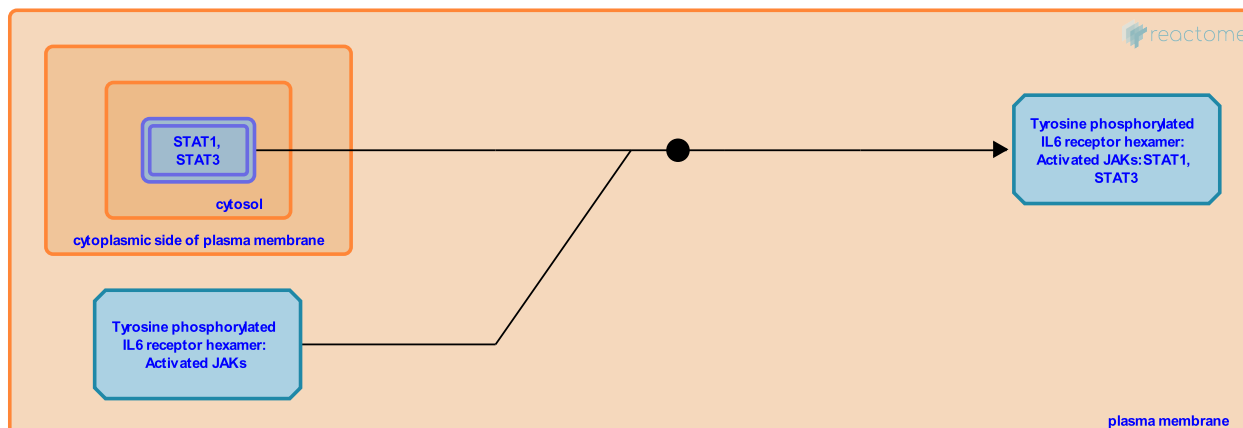
This document contains 1 reaction ([see Table of Contents](#))

Tyrosine phosphorylated IL6ST binds STAT1,STAT3 ↗

Stable identifier: R-HSA-1112565

Type: binding

Compartments: plasma membrane, cytosol



STAT1 binds to IL6ST (gp130) via phosphotyrosine residues 905 and 915 within two YXPD recognition motifs. STAT3 can be recruited to these sites and to two additional sites around Y767 and Y814 that have less restricted sequence recognition requirements (YXXQ) (Gerhartz et al. 1996). After receptor binding, STATs are phosphorylated on a single tyrosine residue by JAKs (Hemmann et al. 1996).

Literature references

- Heinrich, PC., Sasse, J., Horn, F., Darnell JE, Jr., Zhong, Z., Graeve, L. et al. (1996). Differential activation of acute phase response factor/Stat3 and Stat1 via the cytoplasmic domain of the interleukin 6 signal transducer gp130. II. Src homology SH2 domains define the specificity of stat factor activation. *J Biol Chem*, 271, 12999-3007. ↗
- Heinrich, PC., Landgraf, C., Sasse, J., Horn, F., Schneider-Mergener, J., Graeve, L. et al. (1996). Differential activation of acute phase response factor/STAT3 and STAT1 via the cytoplasmic domain of the interleukin 6 signal transducer gp130. I. Definition of a novel phosphotyrosine motif mediating STAT1 activation. *J Biol Chem*, 271, 12991-8. ↗

Editions

2010-12-10	Edited	Jupe, S.
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