Tyrosine phosphorylation of STAT1, STAT3 by IL6 receptor

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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. ↗

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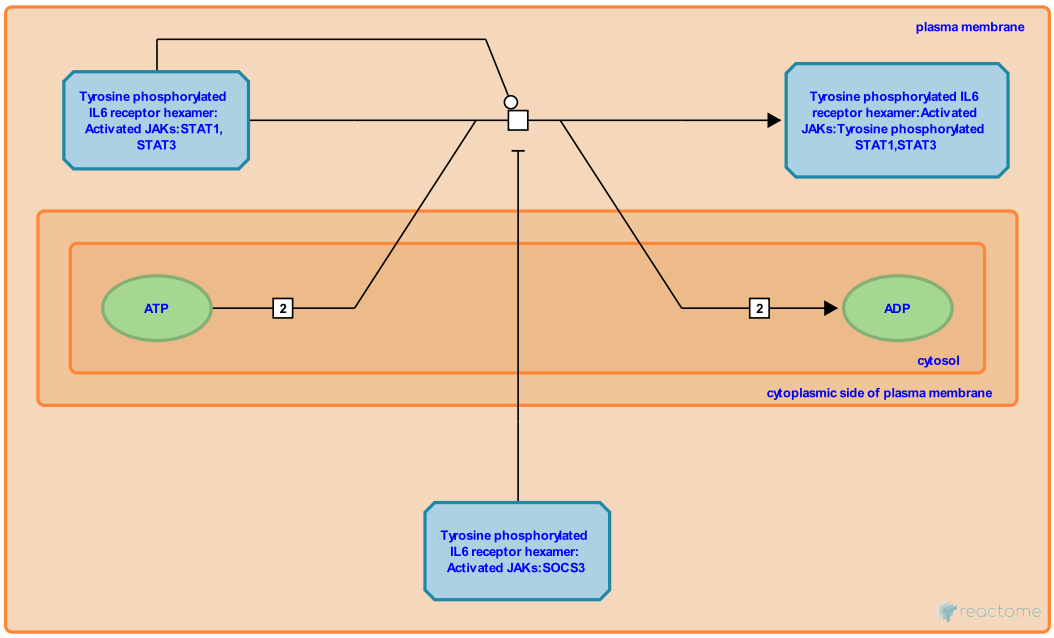
Stable identifier: R-HSA-1112602

Type: transition

Compartments: plasma membrane, cytosol



Interleukin-6 (IL6) activates the tyrosine phosphorylation of STATs (Akira et al. 1994, Zhong et al. 1994) by receptor-associated JAKs (Hemmann et al. 1996) at a site that is essential for dimerization. For STAT1 this is tyrosine-701, for STAT3 tyrosine-705 (Kaptein et al. 1996, Shuai et al. 1994). Tyrosine phosphorylation leads to homo- or heterodimerization and translocation to the nucleus (Zhong et al. 1994), where the dimers bind to enhancers of IL6- inducible genes e.g. acute phase protein genes, resulting in transcriptional activation.

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. ↗

Editions

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