Phosphorylation of STAT2

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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

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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. ↗

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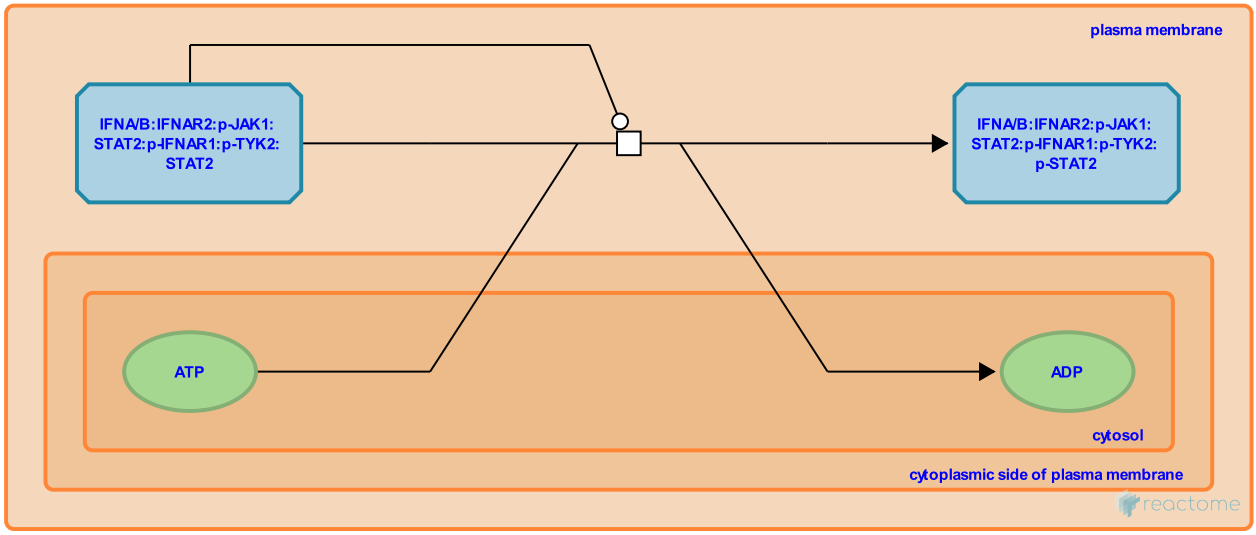
Stable identifier: R-HSA-909732

Type: transition

Compartments: cytosol, plasma membrane



STAT2 recruited to the IFNAR1 subunit then becomes tyrosine phosphorylated on residue 690 by TYK2 kinase. This phosphotyrosine provides a docking site for recruitment of STAT1 to IFNAR1, which is then tyrosine phosphorylated and activated.

Literature references

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Editions

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