# Phosphorylation of STAT1

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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. ↗

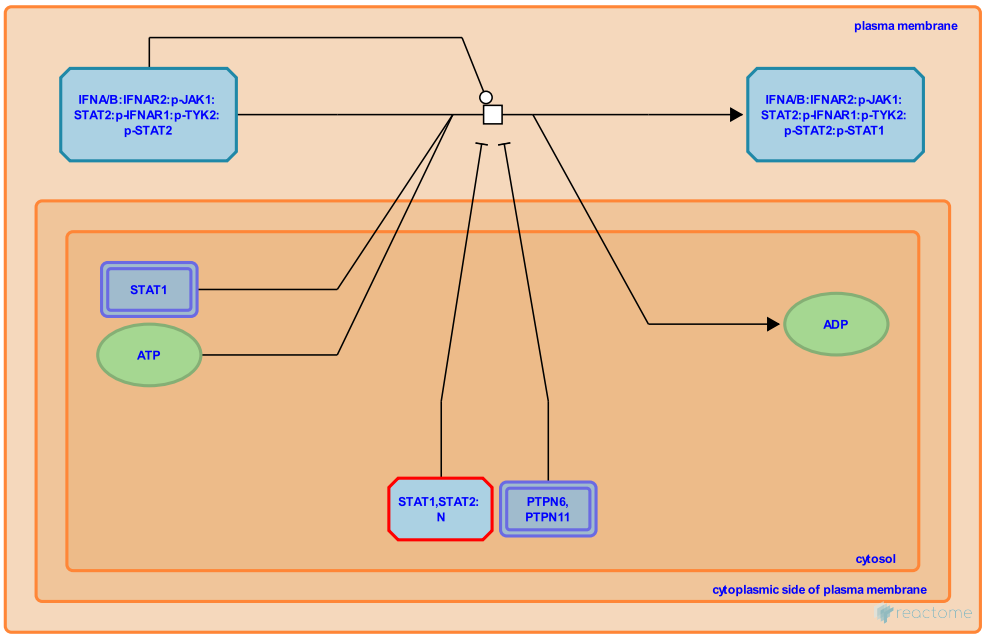
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

## Phosphorylation of STAT1 ↗

**Stable identifier:** R-HSA-909726

**Type:** transition

**Compartments:** cytosol, plasma membrane




Phosphotyrosine on STAT2 acts as docking site for STAT1 molecules. STAT1 binds to phosphorylated STAT2 and this is followed by STAT1 phosphorylation on tyrosine residue 701 (Y701). These STATs recruited to the phosporylated IFNAR1 form two distinct transcriptional activator complexes, namely, IFN-alpha-activated factor (AAF) and IFN-stimulated gene factor 3 (ISGF3). AAF is a homodimer of STAT1, whereas ISGF3 is a heterotrimeric complex of STAT1, STAT2 and IRF9 (also known as p48 or ISGF3gamma) (Honda et al. 2005).
SARS-CoV-2 nucleoprotein (N) binds to both STAT1 and STAT2, prevents their phosphorylation, and suppresses their nuclear translocation induced by IFN (Mu J et al. 2020).
Protein tyrosine phosphatases SHP-1 and SHP-2 dephosphorylate JAK1 and STAT1 and suppress their signaling.

## Literature references

David, M., Mowen, K. (2000). Regulation of STAT1 nuclear export by Jak1. *Mol Cell Biol, 20*, 7273-81. ↗

Witthuhn, BA., Barbieri, G., Ziemiecki, A., Briscoe, J., Harpur, AG., Laxton, C. et al. (1993). The protein tyrosine kinase JAK1 complements defects in interferon-alpha/beta and -gamma signal transduction. *Nature, 366*, 129-35. ↗

## Editions

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|---|---|---|
| 2010-07-07 | Authored, Edited | Garapati, P V. |
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