

# Interaction of IRF9 with p-STAT2:p-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. [↗](#)

Reactome database release: 75

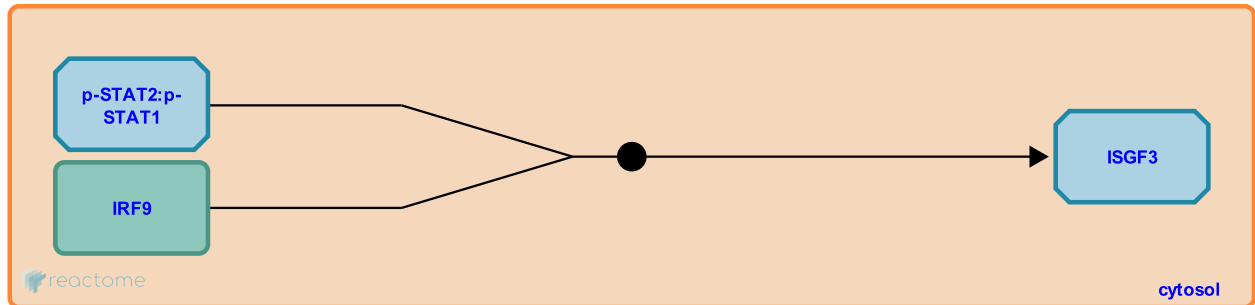
This document contains 1 reaction ([see Table of Contents](#))

## Interaction of IRF9 with p-STAT2:p-STAT1 [↗](#)

**Stable identifier:** R-HSA-909725

**Type:** binding

**Compartments:** cytosol



The phosphorylated STAT2:STAT1 heterodimer associates with interferon-regulating factor 9 (IRF9) to form the interferon-stimulated gene factor 3 (ISGF3) complex.

### Literature references

Martinez-Moczygemba, M., Gutch, MJ., French, DL., Reich, NC. (1997). Distinct STAT structure promotes interaction of STAT2 with the p48 subunit of the interferon-alpha-stimulated transcription factor ISGF3. *J Biol Chem*, 272, 20070-6. [↗](#)

Qureshi, SA., Salditt-Georgieff, M., Darnell JE, Jr. (1995). Tyrosine-phosphorylated Stat1 and Stat2 plus a 48-kDa protein all contact DNA in forming interferon-stimulated-gene factor 3. *Proc Natl Acad Sci U S A*, 92, 3829-33. [↗](#)

Li, X., Leung, S., Qureshi, S., Darnell JE, Jr., Stark, GR. (1996). Formation of STAT1-STAT2 heterodimers and their role in the activation of IRF-1 gene transcription by interferon-alpha. *J Biol Chem*, 271, 5790-4. [↗](#)

### Editions

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