

Phosphorylated STAT1, STAT3 form di- mers

Jupe, S., Ray, KP., Rose-John, S.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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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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- 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. [↗](#)
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Reactome database release: 88

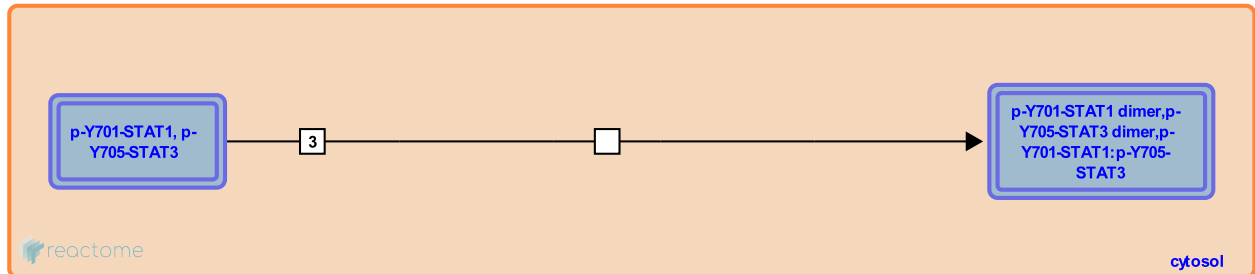
This document contains 1 reaction ([see Table of Contents](#))

Phosphorylated STAT1, STAT3 form dimers [↗](#)

Stable identifier: R-HSA-1112538

Type: transition

Compartments: cytosol



STATs can form dimers in the unphosphorylated state but only phosphorylated dimers are in the correct conformation to bind consensus DNA sequences of target genes in the nucleus (Riech & Liu 2006).

Literature references

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Darnell JE, Jr., Zhong, Z., Wen, Z. (1994). Stat3: a STAT family member activated by tyrosine phosphorylation in response to epidermal growth factor and interleukin-6. *Science*, 264, 95-8. [↗](#)

Editions

2010-12-10	Edited	Jupe, S.
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