

p-Y-Stat1,3,5 dimerize

May, B., Touw, IP.

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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](#). For more information see our [license](#).

03/05/2024

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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

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: 88

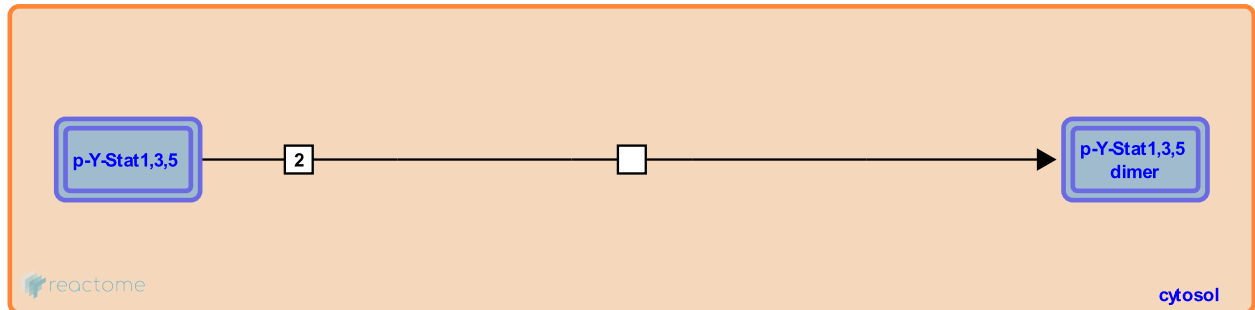
This document contains 1 reaction ([see Table of Contents](#))

p-Y-Stat1,3,5 dimerize [↗](#)

Stable identifier: R-MMU-9676912

Type: transition

Compartments: cytosol



After being phosphorylated, Stat1, Stat3, and Stat5 (Stat5a and Stat5b) form homodimers (de Koning et al. 1996, Gits et al. 2006). Phospho-Stat1 and phospho-Stat3 can also form heterodimers (de Koning et al. 1996, Gits et al. 2006).

Literature references

van der Plas, DC., Schelen, AM., Barge, RM., Smith, L., Touw, IP., Löwenberg, B. et al. (1996). The membrane-distal cytoplasmic region of human granulocyte colony-stimulating factor receptor is required for STAT3 but not STAT1 homodimer formation. *Blood*, 87, 1335-42. [↗](#)

Ward, AC., Touw, IP., Carroll, HP., van Leeuwen, D., Gits, J. (2006). Multiple pathways contribute to the hyperproliferative responses from truncated granulocyte colony-stimulating factor receptors. *Leukemia*, 20, 2111-8. [↗](#)

Editions

2020-02-23	Authored, Edited	May, B.
2020-12-12	Reviewed	Touw, IP.