

# SH2B proteins bind JAK2

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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: 88

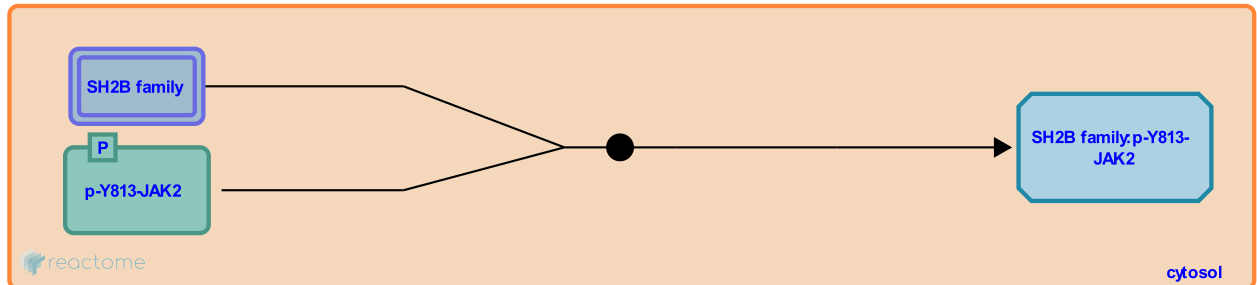
This document contains 1 reaction ([see Table of Contents](#))

## SH2B proteins bind JAK2 [↗](#)

**Stable identifier:** R-HSA-997237

**Type:** binding

**Compartments:** cytosol



The SH2B family has 3 members sharing a common domain structure, including a dimerization domain, a pleckstrin homology (PH) region, and a SH2 domain. The SH2 domain binds phosphotyrosines of various signal-transducing proteins such as c-Kit, MPL, EpoR. All are able to bind JAK2 phosphorylated at Tyr-813 (Bersenev et al. 2008, Kurzer et al. 2004, 2006), inhibiting JAK2 proliferative signaling (Gery et al. 2009).

### Literature references

Xing, H., Cao, Q., Gery, S., Koeffler, HP., Gueller, S., Tefferi, A. (2009). Lnk inhibits myeloproliferative disorder-associated JAK2 mutant, JAK2V617F. *J Leukoc Biol*, 85, 957-65. [↗](#)

### Editions

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