

Recruitment of Shp-2 to pSirp alpha

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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

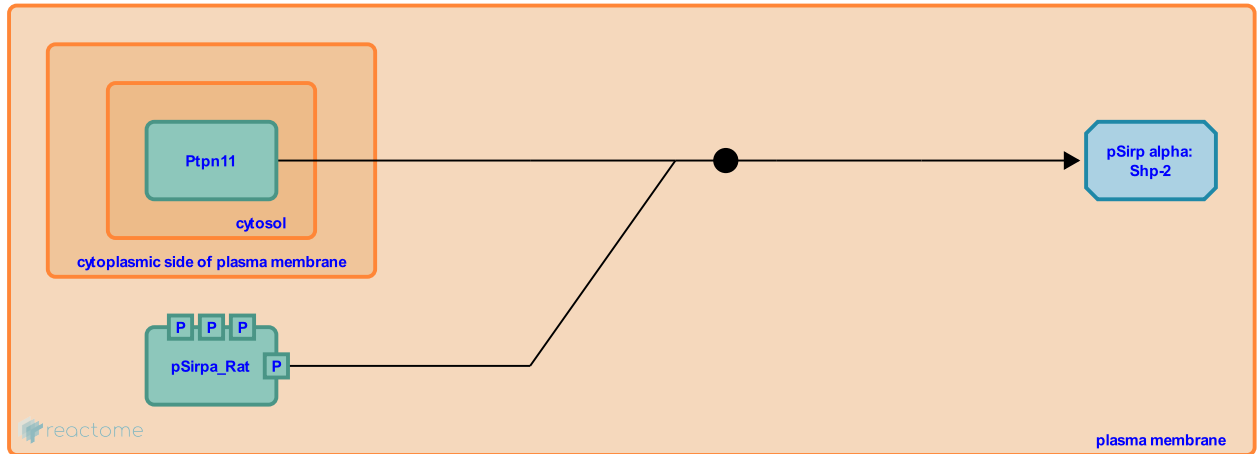
This document contains 1 reaction ([see Table of Contents](#))

Recruitment of Shp-2 to pSirp alpha [↗](#)

Stable identifier: R-RNO-548968

Type: binding

Compartments: cytosol, plasma membrane



SIRP alpha functions as a docking protein. The tyrosine-phosphorylated residues of SIRP alpha trigger the binding and activation of tyrosine phosphatases SHP-1 and SHP-2. All four phosphotyrosines of SIRP alpha may serve as substrates for SHP-1 and SHP-2. SIRP alpha binds mostly to SHP-1 in hematopoietic cells and with SHP-2 in non-hematopoietic cells. These phosphatases mediate the specific functions of SIRP alpha.

Literature references

Noguchi, T., Fujioka, Y., Takada, T., Imamoto, A., Yamamoto, T., Ochi, F. et al. (1998). Integrin-mediated tyrosine phosphorylation of SHPS-1 and its association with SHP-2. Roles of Fak and Src family kinases. *J Biol Chem*, 273, 13223-9. [↗](#)

Carter-Su, C., Stofega, MR., Ullrich, A., Wang, H. (1998). Growth hormone regulation of SIRP and SHP-2 tyrosyl phosphorylation and association. *J Biol Chem*, 273, 7112-7. [↗](#)

Editions

2009-02-12	Authored, Edited	Garapati, P V.
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