

SYK autophosphorylates

Akkerman, JW., Jupe, S., Kunapuli, SP.

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 <u>Creative Commons Attribution 4.0 International (CC BY 4.0)</u>
<u>License</u>. For more information see our <u>license</u>.

13/05/2024

https://reactome.org

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)

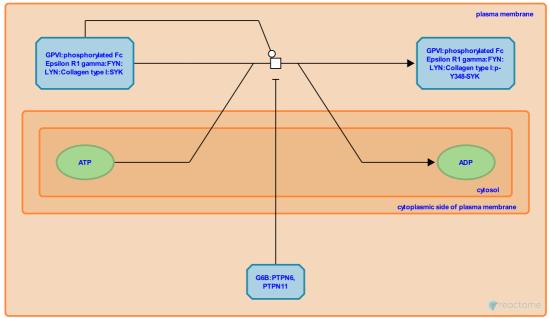
https://reactome.org Page 2

SYK autophosphorylates 7

Stable identifier: R-HSA-453200

Type: transition

Compartments: cytosol, plasma membrane



Binding of Syk causes conformational changes that lead to Syk activation by autophosphorylation. Syk can be activated by a number of phosphorylation events, and it has been proposed that Syk may function as a switch whereby any of several possible stimuli trigger the acquisition of similar activated conformations. (Tsang et al. 2008). These phosphorylations both modulate Syk's catalytic activity (Keshvara et al. 1997) and generate docking sites for SH2 domain-containing proteins, such as c-Cbl, PLC, and Vav1. Syk tyrosine phosphorylation is reduced in the presence of the ITIM-containing immunoglobulin superfamily transmembrane protein G6B (Mori et al. 2008).

Literature references

Nagai, K., Suzuki, J., Kobayashi, T., Taniguchi, T., Yamada, T., Nakamura, H. et al. (1991). Molecular cloning of a porcine gene syk that encodes a 72-kDa protein-tyrosine kinase showing high susceptibility to proteolysis. *J Biol Chem*, 266, 15790-6.

¬

Yamamura, H., Sada, K., Yanagi, S., Takano, T. (2001). Structure and function of Syk protein-tyrosine kinase. *J Bio- chem, 130*, 177-86. *¬*

Recuero-Checa, MA., Llorca, O., Bustelo, XR., Arias-Palomo, E. (2009). Conformational rearrangements upon Syk auto-phosphorylation. *Biochim Biophys Acta, 1794*, 1211-7.

Editions

2009-09-04	Authored	Akkerman, JW.
2010-06-07	Edited	Jupe, S.
2010-06-07	Reviewed	Kunapuli, SP.