Phosphorylation of IL2RB Y338 enables SHC recruitment

Dooms, H., Jupe, S., Ray, KP., Villarino, A.

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

17/01/2021

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. ↗

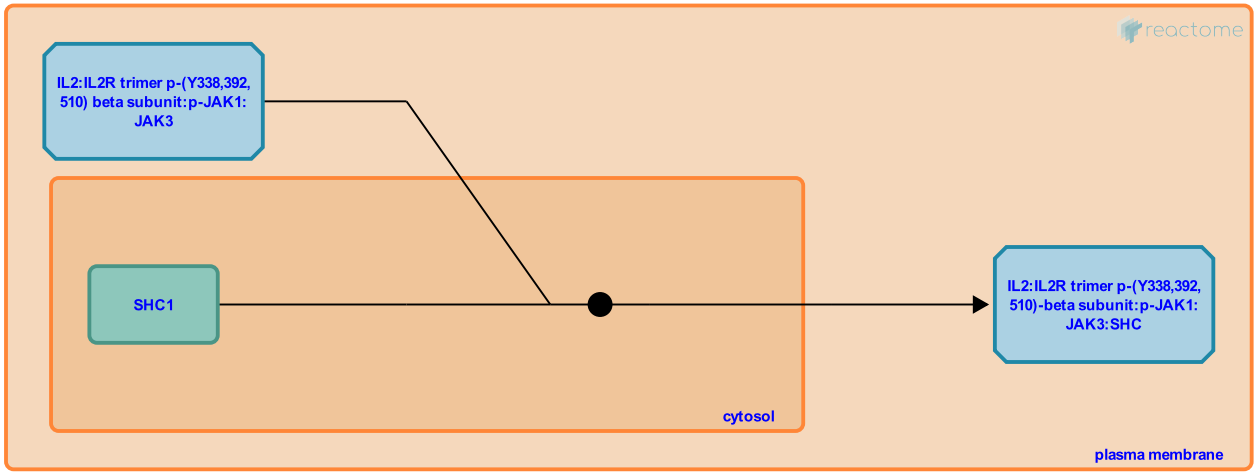
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

Phosphorylation of IL2RB Y338 enables SHC recruitment ↗

Stable identifier: R-HSA-452091

Type: binding

Compartments: cytosol, plasma membrane



Phosphorylation of IL2RB Y338 creates a binding site for the accessory protein SHC, which then becomes tyrosine phosphorylated and recruits the Grb2/Sos and Grb2:Gab2 complexes.

Literature references

Friedmann, MC., Migone, TS., Russell, SM., Leonard, WJ. (1996). Different interleukin 2 receptor beta-chain tyrosines couple to at least two signaling pathways and synergistically mediate interleukin 2-induced proliferation. *Proc Natl Acad Sci U S A, 93*, 2077-82. ↗

Evans, GA., Goldsmith, MA., Johnston, JA., Xu, W., Weiler, SR., Erwin, R. et al. (1995). Analysis of interleukin-2-dependent signal transduction through the Shc/Grb2 adapter pathway. Interleukin-2-dependent mitogenesis does not require Shc phosphorylation or receptor association. *J Biol Chem, 270*, 28858-63. ↗

Ravichandran, KS., Igras, V., Shoelson, SE., Fesik, SW., Burakoff, SJ. (1996). Evidence for a role for the phosphotyrosine-binding domain of Shc in interleukin 2 signaling. *Proc Natl Acad Sci U S A, 93*, 5275-80. ↗

Editions

2010-05-17	Authored	Ray, KP.
2010-08-06	Edited	Jupe, S.
2011-02-11	Reviewed	Villarino, A.
2011-03-17	Reviewed	Dooms, H.