IL15:IL15RA:IL2RB:JAK1:IL2RG:p-JAK3:p-Y-SHC1:GRB2 binds GAB2

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17/05/2024

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. ↗

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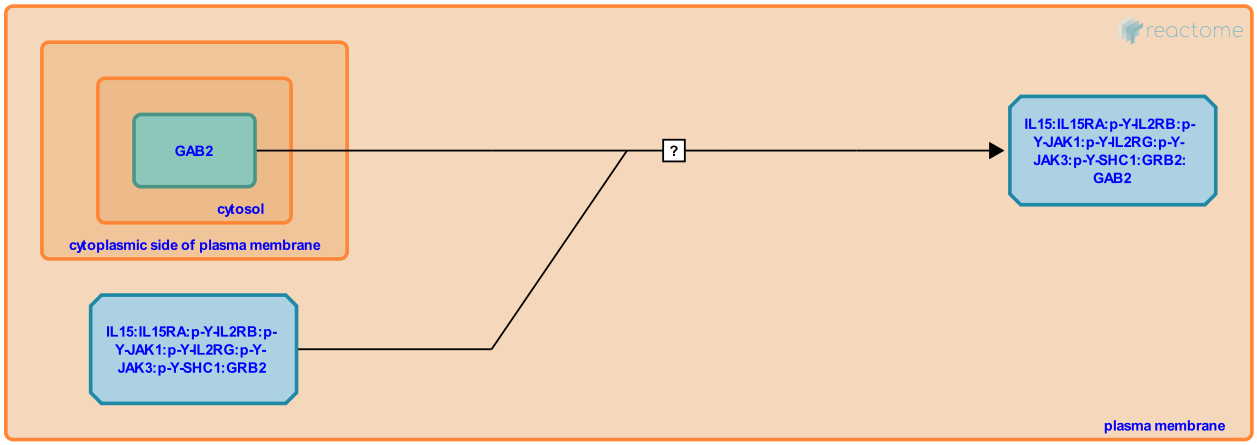
Stable identifier: R-HSA-8983425

Type: uncertain

Compartments: cytosol, extracellular region, plasma membrane

Inferred from: Il15:Il15ra:p-Y-Il2rb:p-Y-Jak1:p-Y-Il2rg:p-Y-Jak3:p-Y-Shc1:Grb2 binds Gab2 (Mus musculus)



Inferred from mouse: GRB2 associated binding protein 2 (GAB2) is believed to bind and be phosphorylated in response to Interleukin-2 (IL2) and Interleukin-15 (IL15) stimulation. Its phosphorylation is greatly diminished by mutation of the site in the Interleukin-2 Receptor beta chain (Y338F) (IL2RB, IL2Rβ) that recruits SHC transforming protein 1 (SHC1) (Gadina et al.2000, Wöhrle et al.2009, Gesbert et al. 1998, Brockdorff et al. 2001). GAB2 is a phosphoprotein that is suggested to associates with PI3kinase, Growth factor receptor-bound protein 2 (GRB2) and Tyrosine protein phosphatase non-receptor type 11 (PTPN11 or SHP2) in T and Natural Killer (NK) cells (Gu et al. 2000).This is a black box event because GAB2 binding is inferred from IL15 stimulation of GAB2 phosphorylation (Brockdorff et al. 2001). More in detail, human and mouse IL15 have 70.2% amino acid sequence similarity and exhibit similar trans-presentation mechanism, signal transduction machinery and biological activities. Similarly, human IL15 shows cross-reactivity with mouse cells and it was demonstrated that human and mouse IL15 showed similar responses in mouse models (Stoklasek et al. 2006) (Patidar et al. data not published).

Editions

2017-08-07	Authored	Duenas, C.
2017-08-07	Reviewed	Patidar, M.
2017-08-09	Edited	Duenas, C.