Il2rb and Il2rg are phosphorylated

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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

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Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

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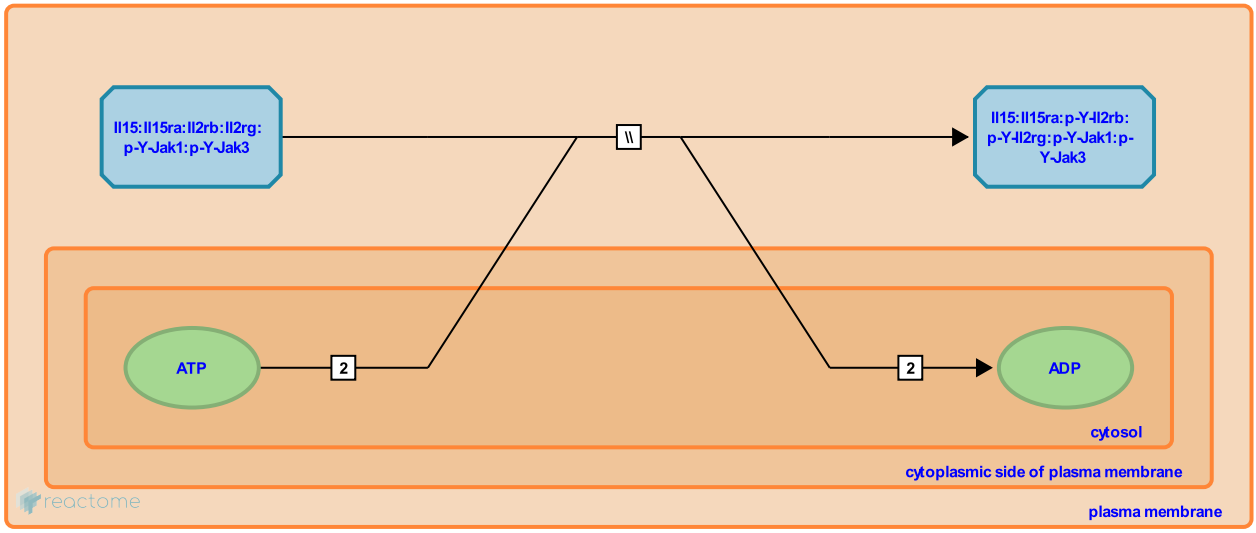
Stable identifier: R-MMU-9009867

Type: omitted

Compartments: cytosol, plasma membrane, extracellular region



Interleukin-2 receptor subunit beta (IL2RB, IL2Rβ) and Cytokine receptor common subunit gamma (IL2RG, IL2Rγ) is tyrosine phosphorylated after Interleukin-15 (IL15) / IL15 receptor complex interaction (Adunyah et al. 1997, Zambricki et al. 2005). 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). This is a black box event because more evidence to support this reaction is needed.

Literature references

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Editions

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