Phosphorylation of ITIM motif in SIRP 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

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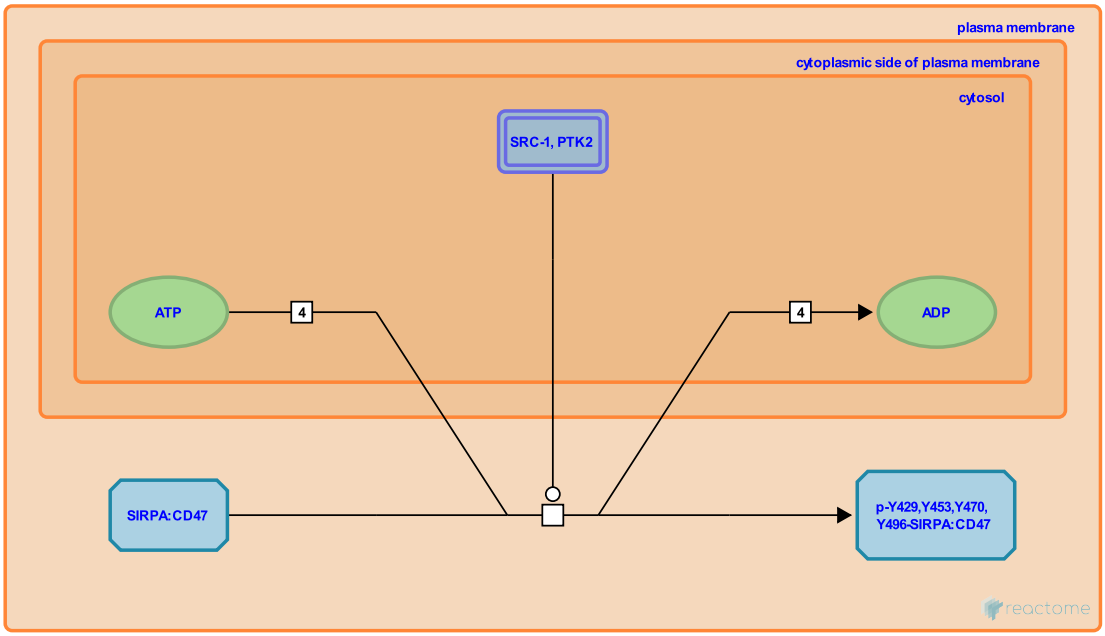
Stable identifier: R-HSA-391156

Type: transition

Compartments: cytosol, plasma membrane

Inferred from: Phosphorylation of ITIM in SIRP alpha (Mus musculus), Phosphorylation of ITIM in SIRP alpha (Rattus norvegicus)



Various growth factors and events such as integrin-mediated cell adhesion to extracellular matrix (ECM) proteins induce the tyrosine phosphorylation of SIRP alpha. The cytoplasmic tail of SIRP alpha has two ITIMs with four tyrosine residues that are potential sites for phosphorylation. Phosphorylation is not dependent on CD47 engagement but the presence of CD47 may enhance the effect. Src family kinases may be involved in the phosphorylation.

Editions

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