Phosphorylation of ITIM in SIRP alpha

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03/05/2024

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

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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. ↗

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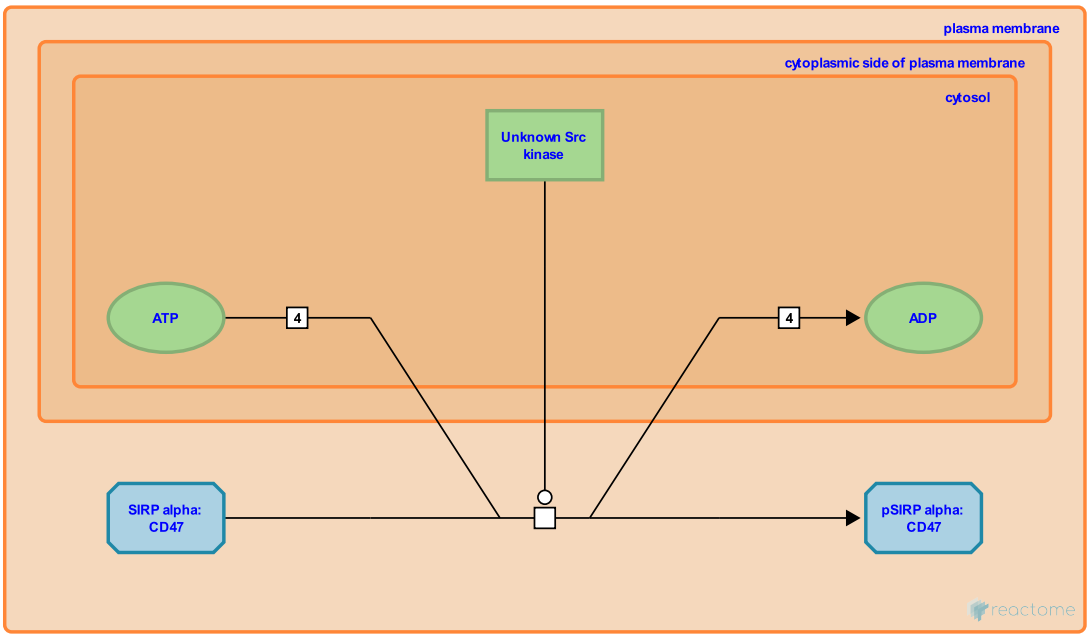
Stable identifier: R-MMU-548973

Type: transition

Compartments: cytosol, plasma membrane



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.

Literature references

Brown, EJ., Johansen, ML. (2007). Dual regulation of SIRPalpha phosphorylation by integrins and CD47. *J Biol Chem, 282*, 24219-30. ↗

Editions

2009-02-12	Authored, Edited	Garapati, P V.
2010-05-20	Reviewed	Barclay, AN.