Dephosphorylation of inactive SRC by PT-PB1

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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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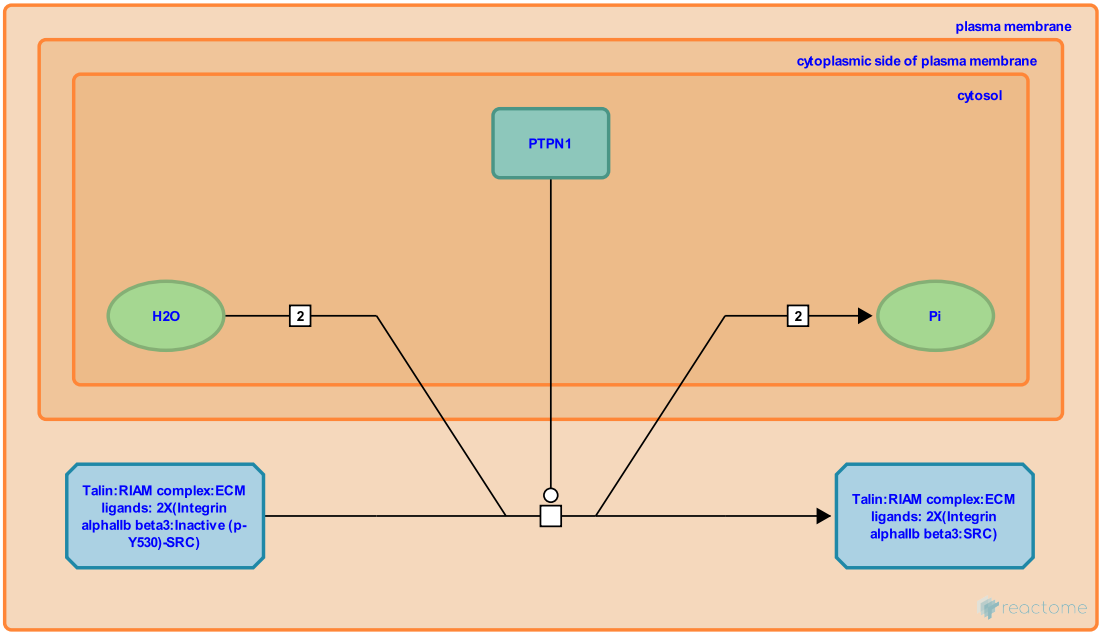
Stable identifier: R-HSA-377643

Type: transition

Compartments: cytosol, plasma membrane



The integrin alphaIIb beta3:Inactive SRC complex recruits PTP1B protein tyrosine phosphatase resulting in the dephosphorylation of SRC tyrosine 530. The phosphorylated tail of SRC tail interacts with the SH2 domain thereby repressing kinase activity; removal of phosphorylation activates SRC kinase activity.

Literature references

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Editions

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