Phosphorylation of pPTK2 by SRC

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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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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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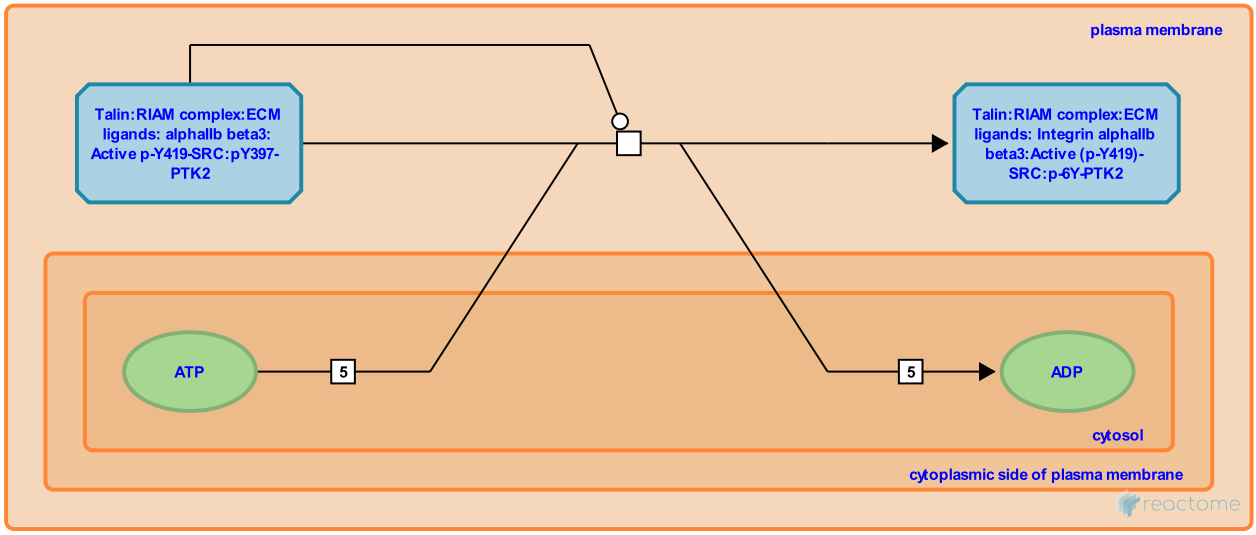
Stable identifier: R-HSA-354124

Type: transition

Compartments: cytosol, plasma membrane



The recruitment of FADK1 to active SRC leads to the efficient tyrosine phosphorylation of multiple additional sites on FADK1. SRC trans-phosphorylates FADK1 within the kinase doman activation loop (Y576 and Y577) and within the FADK1 C-terminal domain (Y861 and Y925).

Literature references

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Editions

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