

Transphosphorylation of pLIMK1

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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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Reactome database release: 88

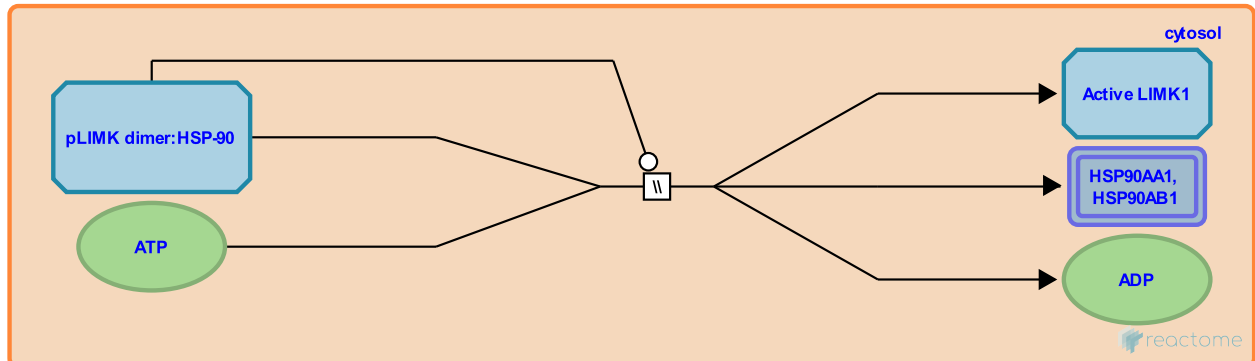
This document contains 1 reaction ([see Table of Contents](#))

Transphosphorylation of pLIMK1 [↗](#)

Stable identifier: R-HSA-419644

Type: omitted

Compartments: cytosol



Binding of Hsp90 to the LIMK proteins protects them from degradation and promotes their dimer formation and transphosphorylation. It is estimated that LIMK1 contains at least 5 phospho-amino acids primarily phospho-serines, in its kinase domain. The positions of these serine residues are not known. Transphosphorylation of these serine residues in LIMK1 increases its stability.

Literature references

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Editions

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