Phosphorylation of PF2K-Pase by PKA catalytic subunit

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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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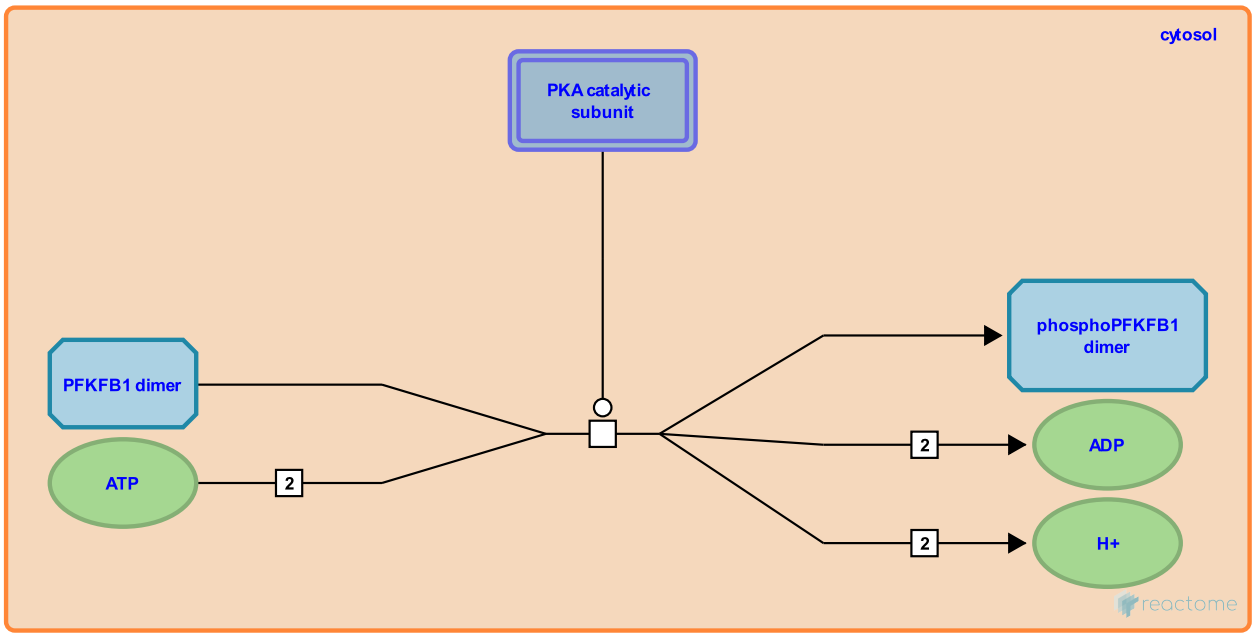
Stable identifier: R-HSA-163773

Type: transition

Compartments: cytosol

Inferred from: Phosphorylation of rPF2K-Pase by rPKA (Rattus norvegicus)



Activated PKA (protein kinase A) phosphorylates serine 36 of the bifunctional 6-Phosphofructo-2-kinase /Fructose-2,6-bisphosphatase (PFKFB1) enzyme. This phosphorylation inhibits the enzyme's phosphofructokinase (PFK-2) activity while activating its phosphatase activity. As a result, cytosolic levels of Fructose-2,6-bisphosphate (F-2,6-P2) are reduced. F-2,6-P2 in turn is a key positive regulator of the committed step of glycolysis, so the net effect of this phosphorylation event is a reduced rate of glycolysis.

Editions

2005-05-11	Authored	Gopinathrao, G.
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