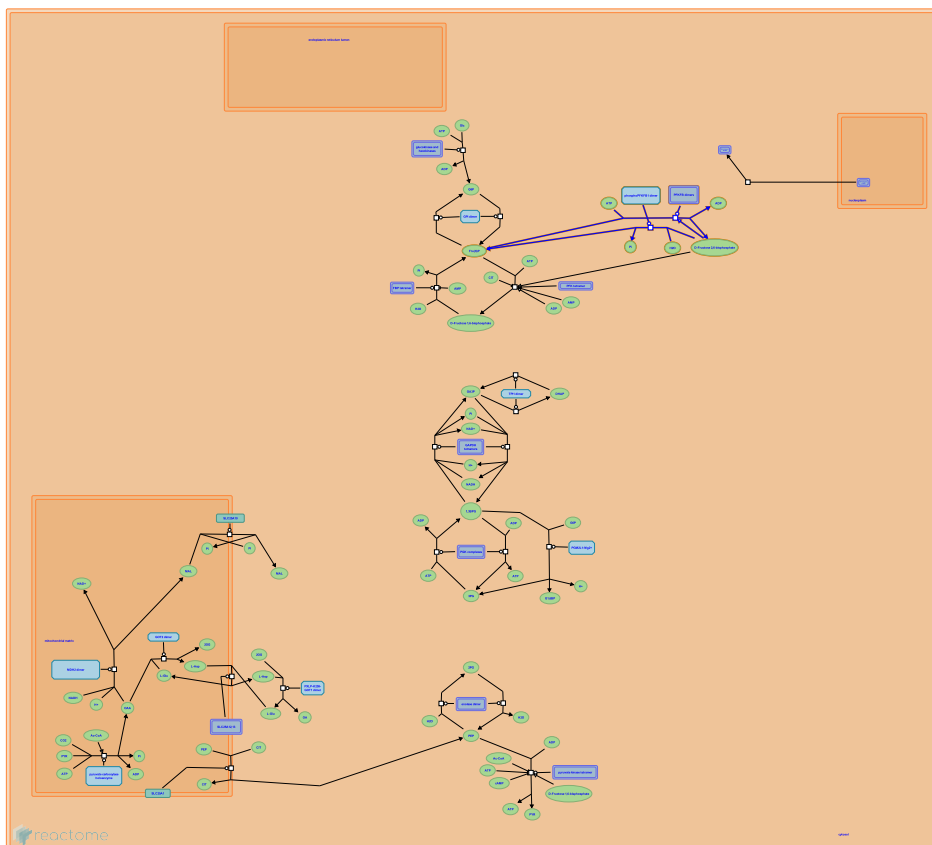


Regulation of glycolysis by fructose 2,6-bisphosphate metabolism



European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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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: 70

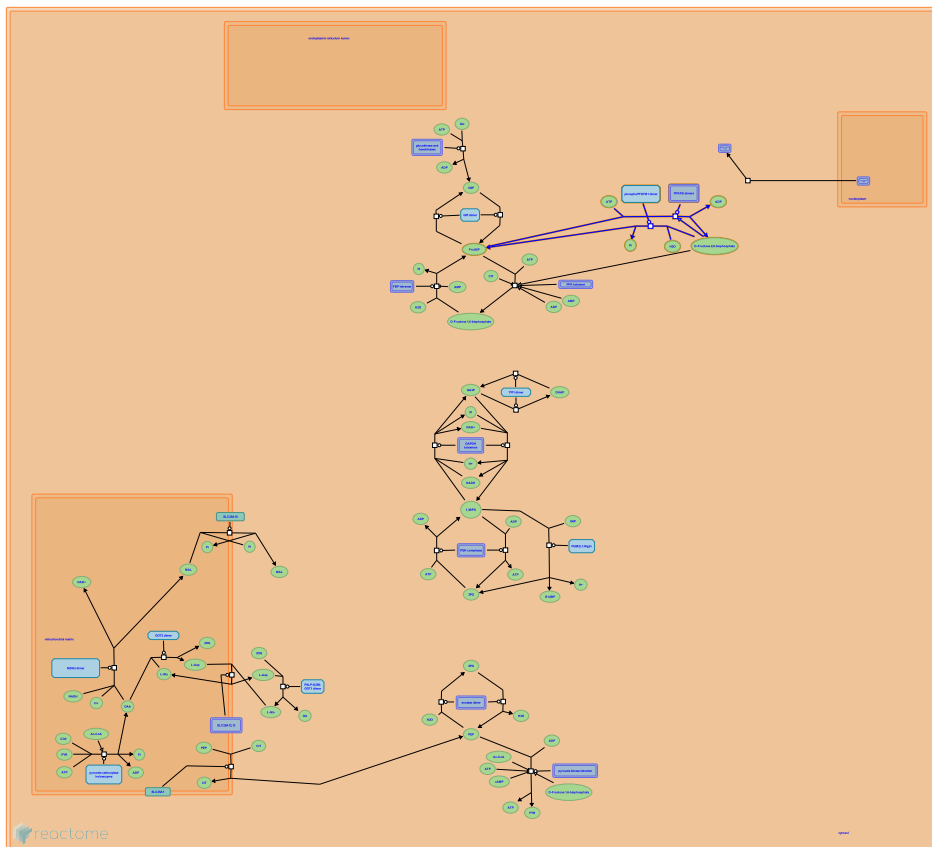
This document contains 1 pathway and 2 reactions ([see Table of Contents](#))

Regulation of glycolysis by fructose 2,6-bisphosphate metabolism ↗

Stable identifier: R-SCE-9634600

Compartments: cytosol

Inferred from: [Regulation of glycolysis by fructose 2,6-bisphosphate metabolism \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

D-fructose 6-phosphate + ATP => D-fructose 2,6-bisphosphate + ADP ↗

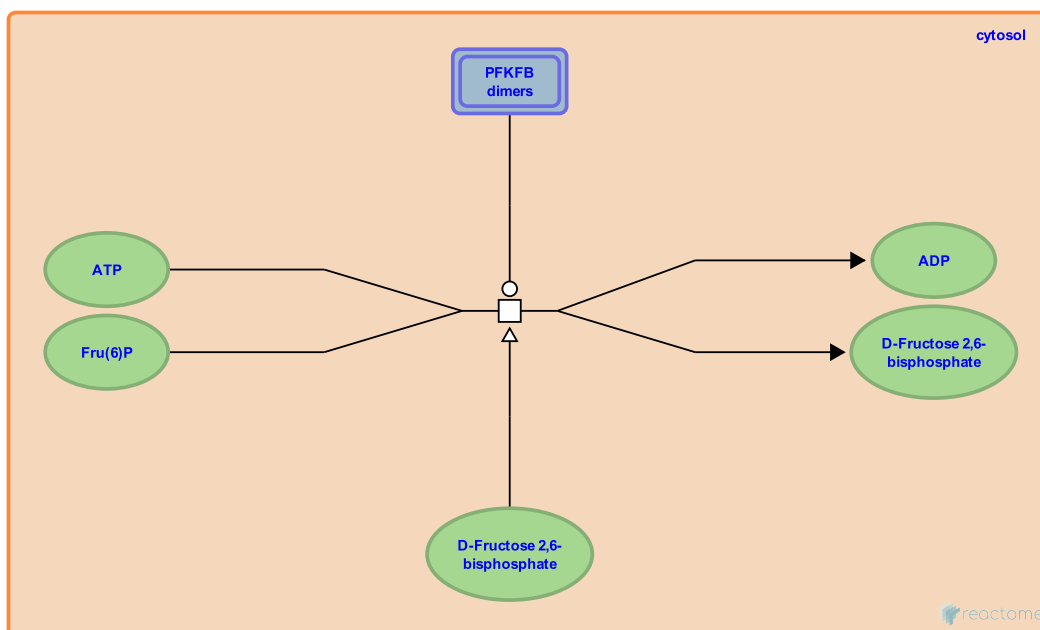
Location: Regulation of glycolysis by fructose 2,6-bisphosphate metabolism

Stable identifier: R-SCE-71802

Type: transition

Compartments: cytosol

Inferred from: D-fructose 6-phosphate + ATP => D-fructose 2,6-bisphosphate + ADP (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Fructose 2,6-bisphosphate is hydrolyzed to form fructose-6-phosphate and orthophosphate ↗

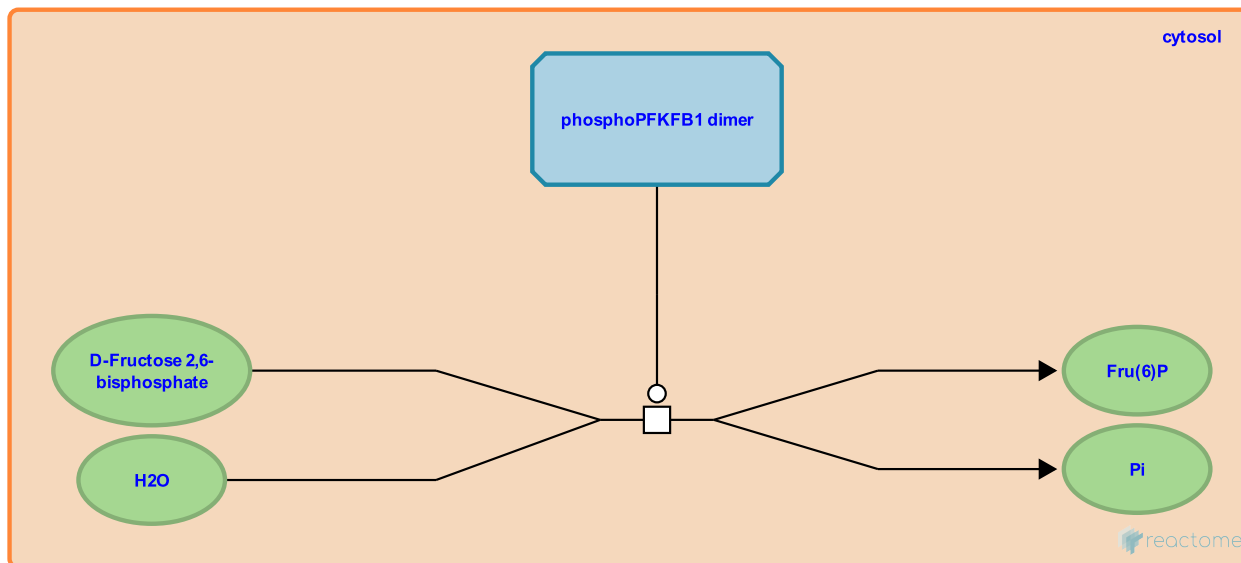
Location: [Regulation of glycolysis by fructose 2,6-bisphosphate metabolism](#)

Stable identifier: R-SCE-70262

Type: transition

Compartments: cytosol

Inferred from: [Fructose 2,6-bisphosphate is hydrolyzed to form fructose-6-phosphate and orthophosphate \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

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