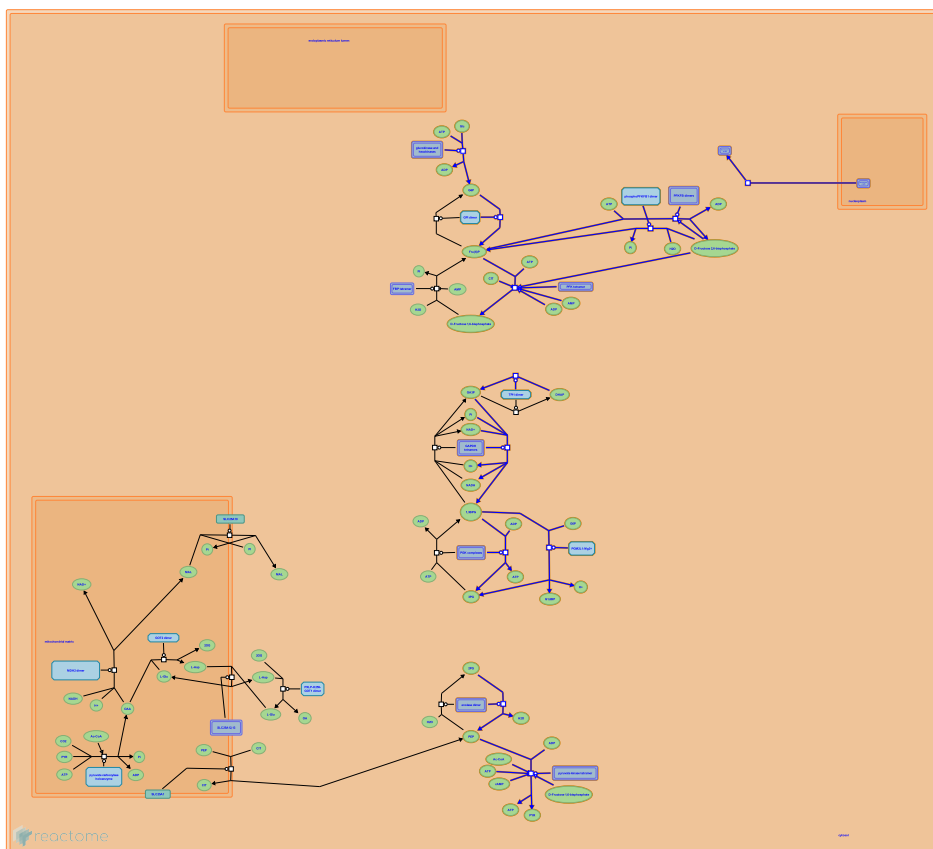


# Glycolysis



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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

## Literature references

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- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, 14, e1005968. [↗](#)

Reactome database release: 70

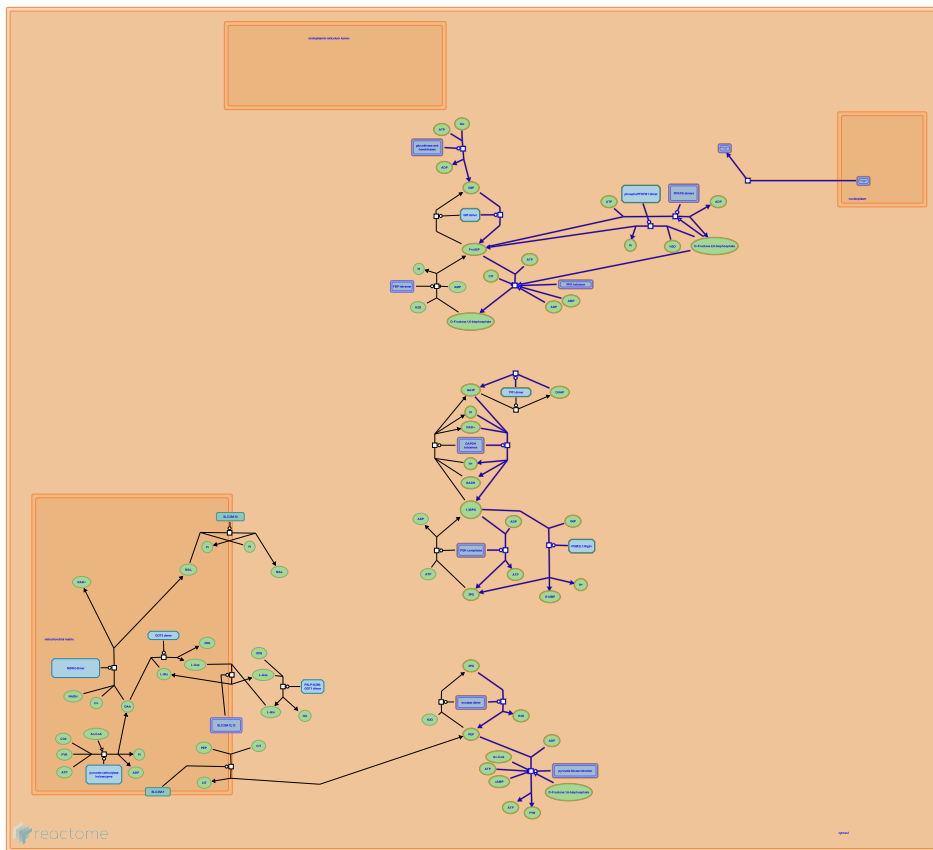
This document contains 3 pathways and 9 reactions ([see Table of Contents](#))

## Glycolysis ↗

**Stable identifier:** R-SCE-70171

**Compartments:** cytosol

**Inferred from:** Glycolysis (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.

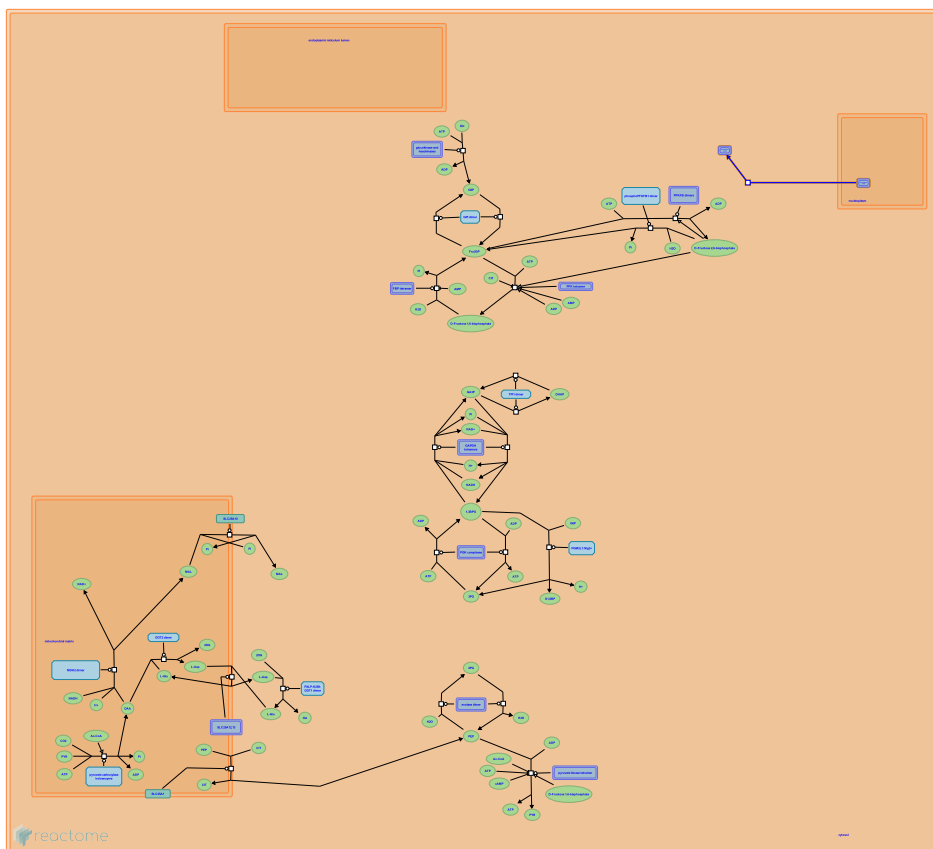
[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## Regulation of Glucokinase by Glucokinase Regulatory Protein ↗

**Location:** Glycolysis

**Stable identifier:** R-SCE-170822

**Inferred from:** Regulation of Glucokinase by Glucokinase Regulatory Protein (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>

## HK1,2,3,GCK phosphorylate Glc to form G6P ↗

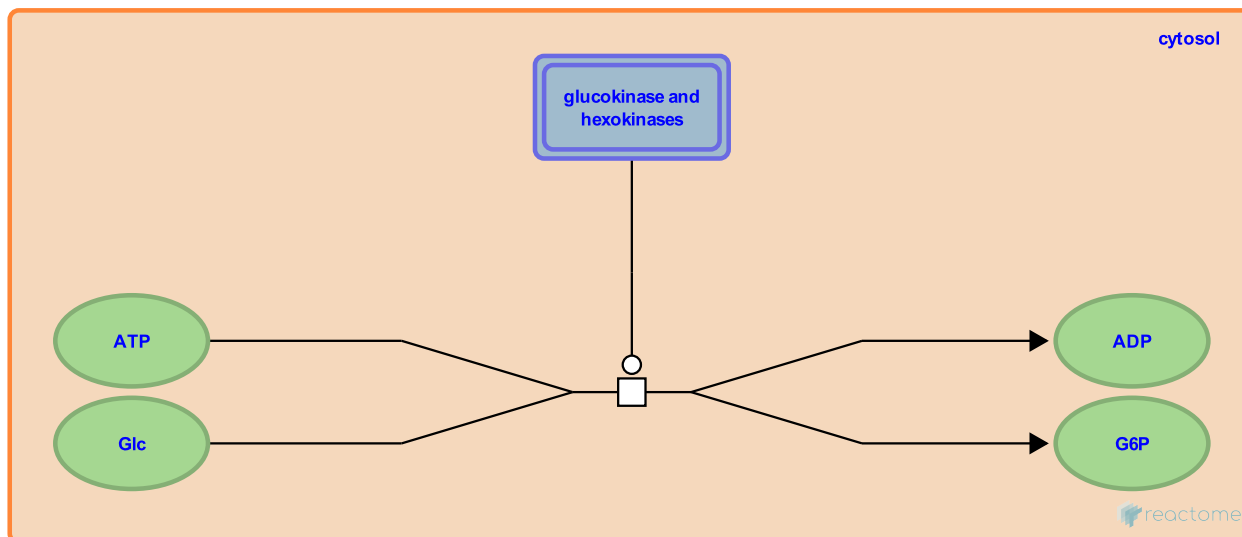
**Location:** [Glycolysis](#)

**Stable identifier:** R-SCE-70420

**Type:** transition

**Compartments:** cytosol

**Inferred from:** [HK1,2,3,GCK phosphorylate Glc to form G6P \(Homo sapiens\)](#)



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>

**Followed by:** [PGM2L1:Mg<sup>2+</sup> phosphorylates G6P to G1,6BP](#), [alpha-D-glucose 6-phosphate <=> D-fructose 6-phosphate](#)

## alpha-D-glucose 6-phosphate <=> D-fructose 6-phosphate ↗

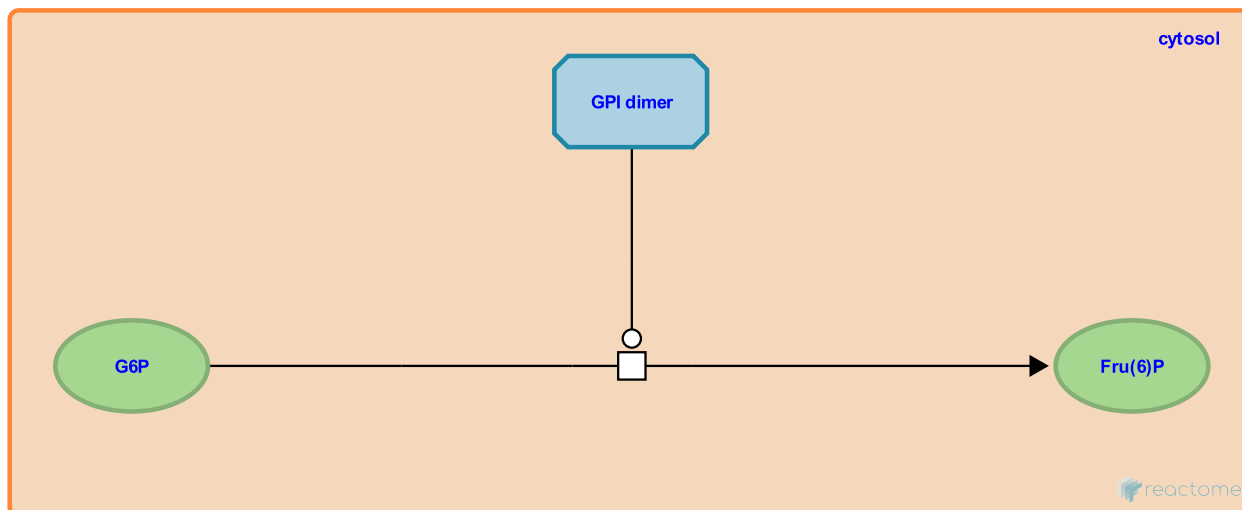
**Location:** [Glycolysis](#)

**Stable identifier:** R-SCE-70471

**Type:** transition

**Compartments:** cytosol

**Inferred from:** [alpha-D-glucose 6-phosphate <=> D-fructose 6-phosphate \(Homo sapiens\)](#)



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>

**Preceded by:** [HK1,2,3,GCK phosphorylate Glc to form G6P](#)

**Followed by:** [D-fructose 6-phosphate + ATP => D-fructose 1,6-bisphosphate + ADP](#)

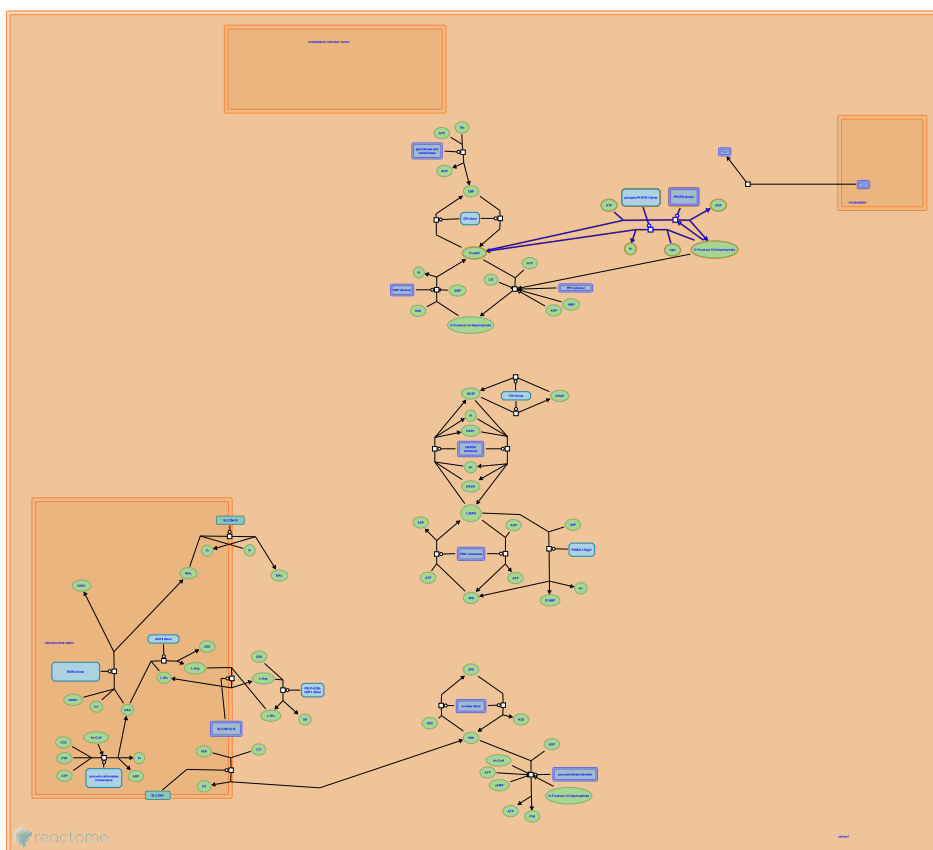
## Regulation of glycolysis by fructose 2,6-bisphosphate metabolism ↗

**Location:** Glycolysis

**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 1,6-bisphosphate + ADP ↗

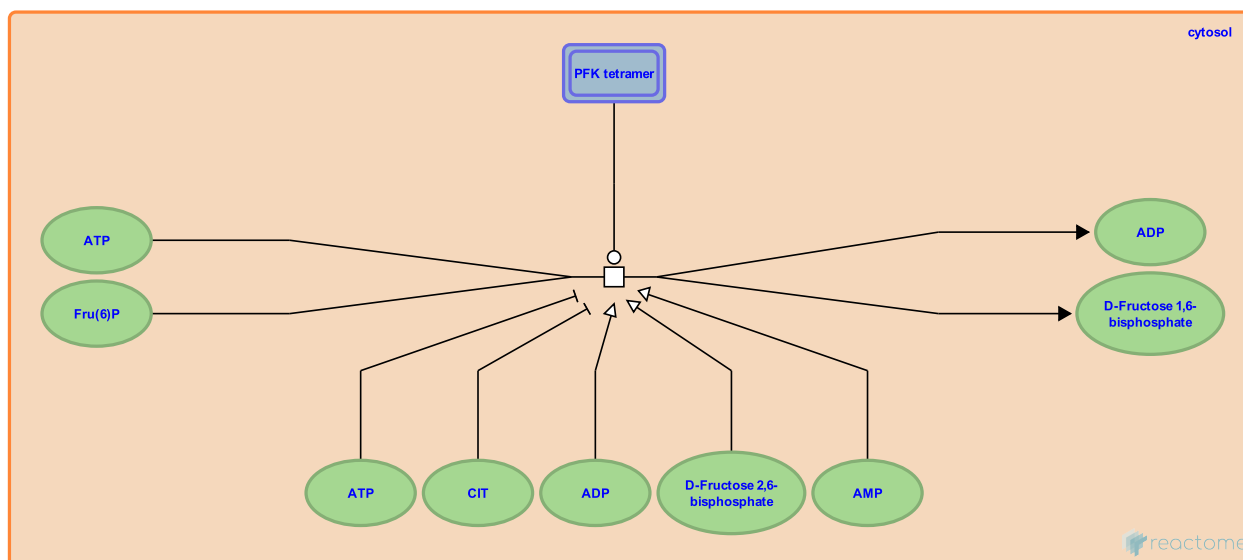
**Location:** Glycolysis

**Stable identifier:** R-SCE-70467

**Type:** transition

**Compartments:** cytosol

**Inferred from:** D-fructose 6-phosphate + ATP => D-fructose 1,6-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>

**Preceded by:** [alpha-D-glucose 6-phosphate <=> D-fructose 6-phosphate](#)



## dihydroxyacetone phosphate $\rightleftharpoons$ D-glyceraldehyde 3-phosphate ↗

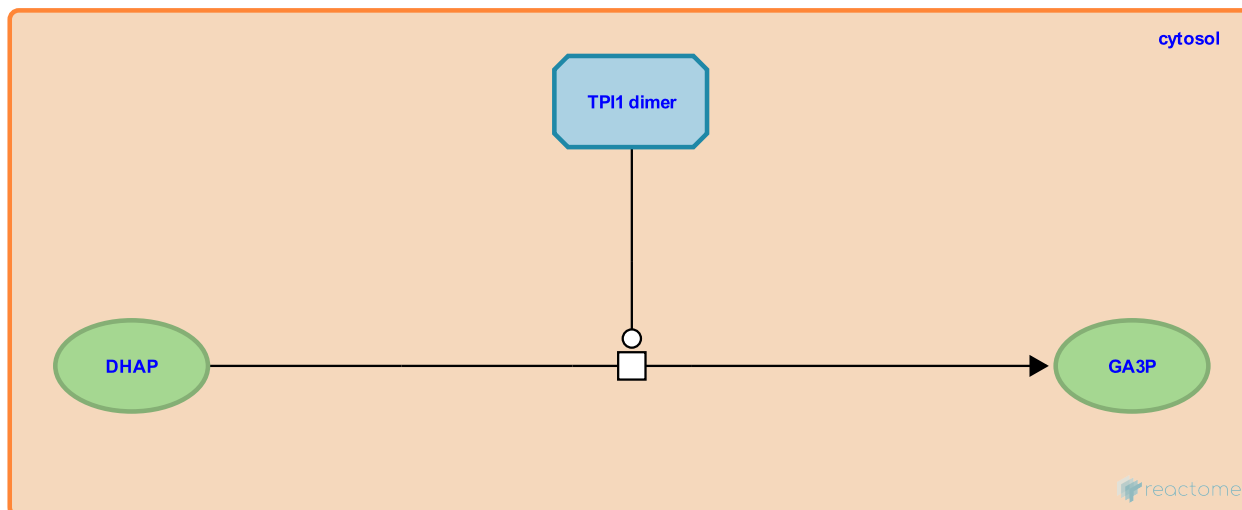
**Location:** [Glycolysis](#)

**Stable identifier:** R-SCE-70454

**Type:** transition

**Compartments:** cytosol

**Inferred from:** [dihydroxyacetone phosphate  \$\rightleftharpoons\$  D-glyceraldehyde 3-phosphate \(Homo sapiens\)](#)



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>

**Followed by:** [D-glyceraldehyde 3-phosphate + orthophosphate + NAD<sup>+</sup>  \$\rightleftharpoons\$  1,3-bisphospho-D-glycerate + NADH + H<sup>+</sup>](#)

**D-glyceraldehyde 3-phosphate + orthophosphate + NAD+  $\rightleftharpoons$  1,3-bisphospho-D-glycerate + NADH + H+ ↗**

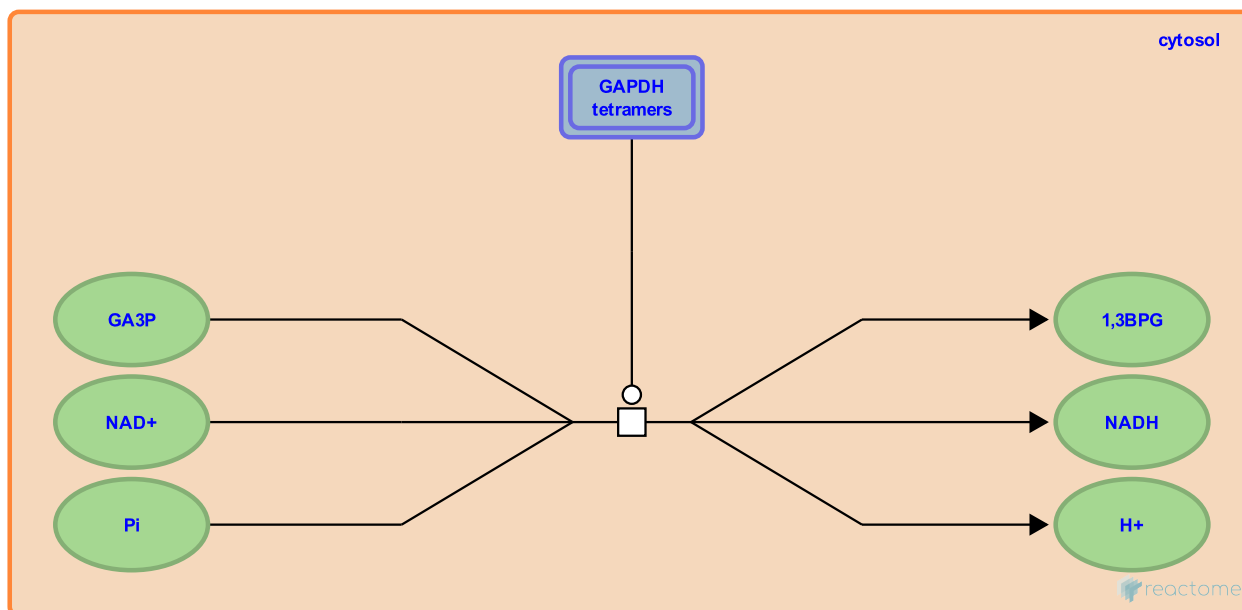
**Location:** [Glycolysis](#)

**Stable identifier:** R-SCE-70449

**Type:** transition

**Compartments:** cytosol

**Inferred from:** [D-glyceraldehyde 3-phosphate + orthophosphate + NAD+  \$\rightleftharpoons\$  1,3-bisphospho-D-glycerate + NADH + H+ \(Homo sapiens\)](#)



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>

**Preceded by:** [dihydroxyacetone phosphate  \$\rightleftharpoons\$  D-glyceraldehyde 3-phosphate](#)

**Followed by:** [1,3-bisphospho-D-glycerate + ADP  \$\rightleftharpoons\$  3-phospho-D-glycerate + ATP](#)

## PGM2L1:Mg<sup>2+</sup> phosphorylates G6P to G1,6BP ↗

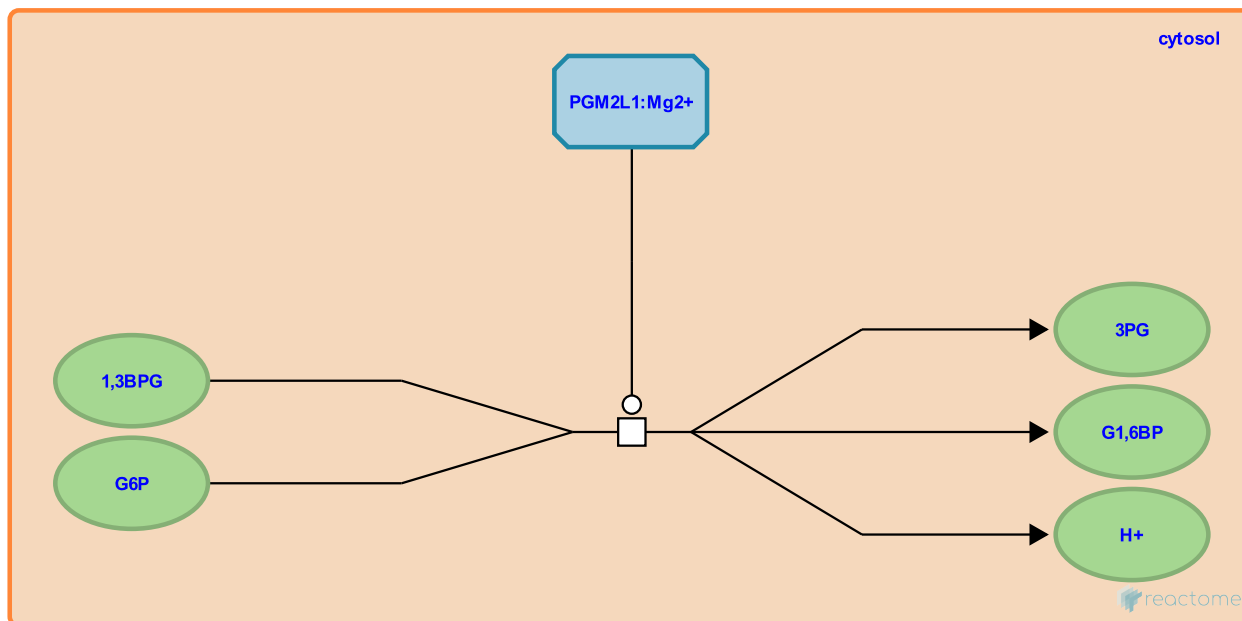
**Location:** [Glycolysis](#)

**Stable identifier:** R-SCE-8955760

**Type:** transition

**Compartments:** cytosol

**Inferred from:** [PGM2L1:Mg<sup>2+</sup> phosphorylates G6P to G1,6BP \(Homo sapiens\)](#)



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>

**Preceded by:** [HK1,2,3,GCK phosphorylate Glc to form G6P](#)

## 1,3-bisphospho-D-glycerate + ADP <=> 3-phospho-D-glycerate + ATP ↗

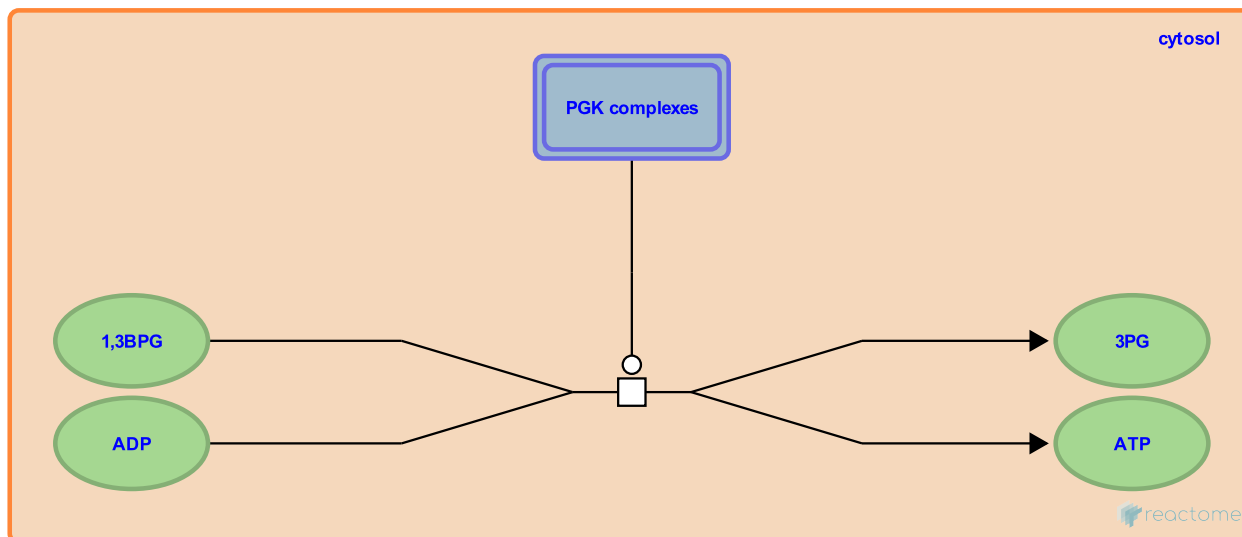
**Location:** [Glycolysis](#)

**Stable identifier:** R-SCE-71850

**Type:** transition

**Compartments:** cytosol

**Inferred from:** [1,3-bisphospho-D-glycerate + ADP <=> 3-phospho-D-glycerate + ATP \(Homo sapiens\)](#)



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>

**Preceded by:** [D-glyceraldehyde 3-phosphate + orthophosphate + NAD+ <=> 1,3-bisphospho-D-glycerate + NADH + H+](#)

## 2-Phospho-D-glycerate <=> Phosphoenolpyruvate + H2O ↗

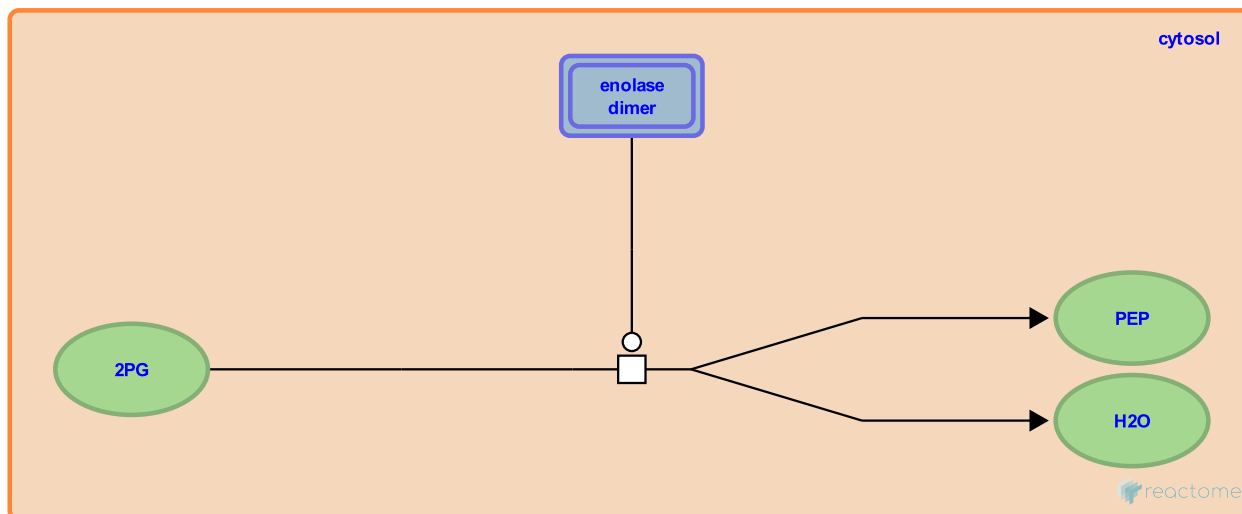
**Location:** [Glycolysis](#)

**Stable identifier:** R-SCE-71660

**Type:** transition

**Compartments:** cytosol

**Inferred from:** [2-Phospho-D-glycerate <=> Phosphoenolpyruvate + H2O \(Homo sapiens\)](#)



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>

**Followed by:** [phosphoenolpyruvate + ADP => pyruvate + ATP](#)

## phosphoenolpyruvate + ADP => pyruvate + ATP ↗

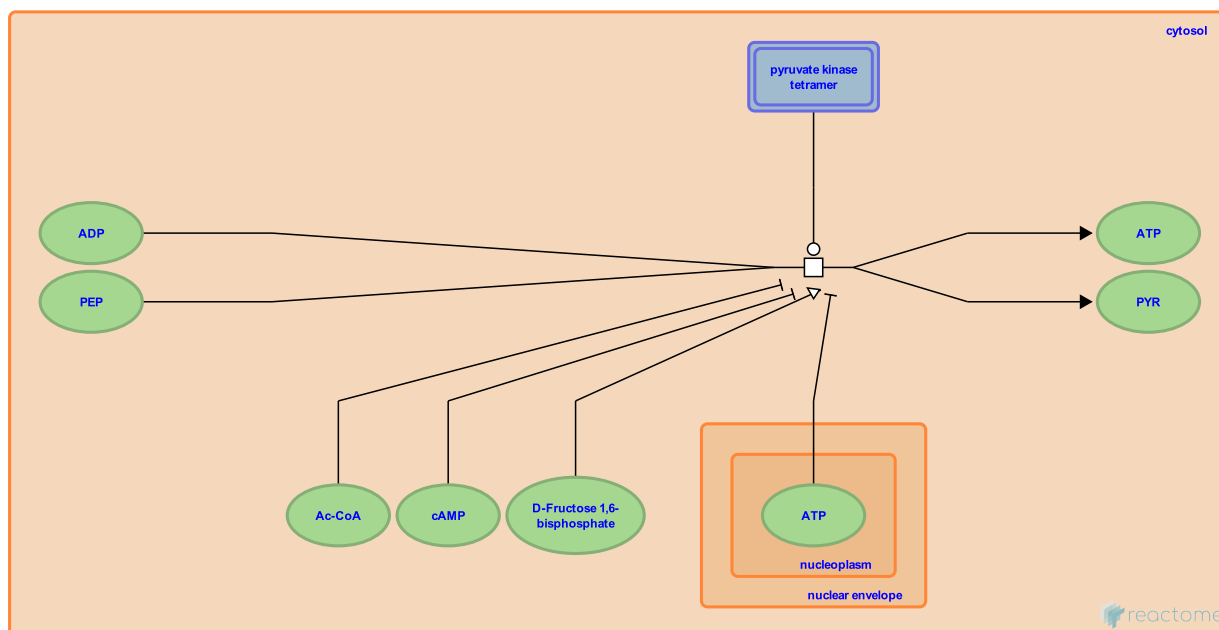
**Location:** Glycolysis

**Stable identifier:** R-SCE-71670

**Type:** transition

**Compartments:** cytosol

**Inferred from:** [phosphoenolpyruvate + ADP => pyruvate + ATP \(Homo sapiens\)](#)





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>

**Preceded by:** [2-Phospho-D-glycerate <=> Phosphoenolpyruvate + H2O](#)

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