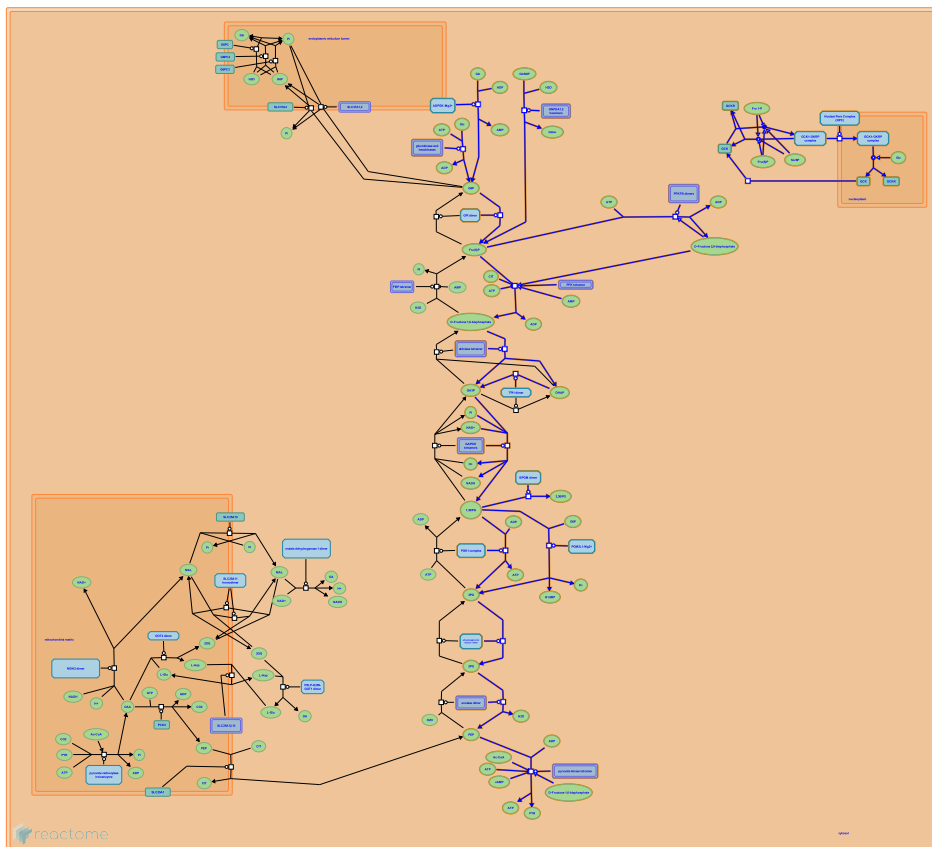


Glycolysis



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

- Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*, 18, 142. [↗](#)
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
- 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. [↗](#)
- 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

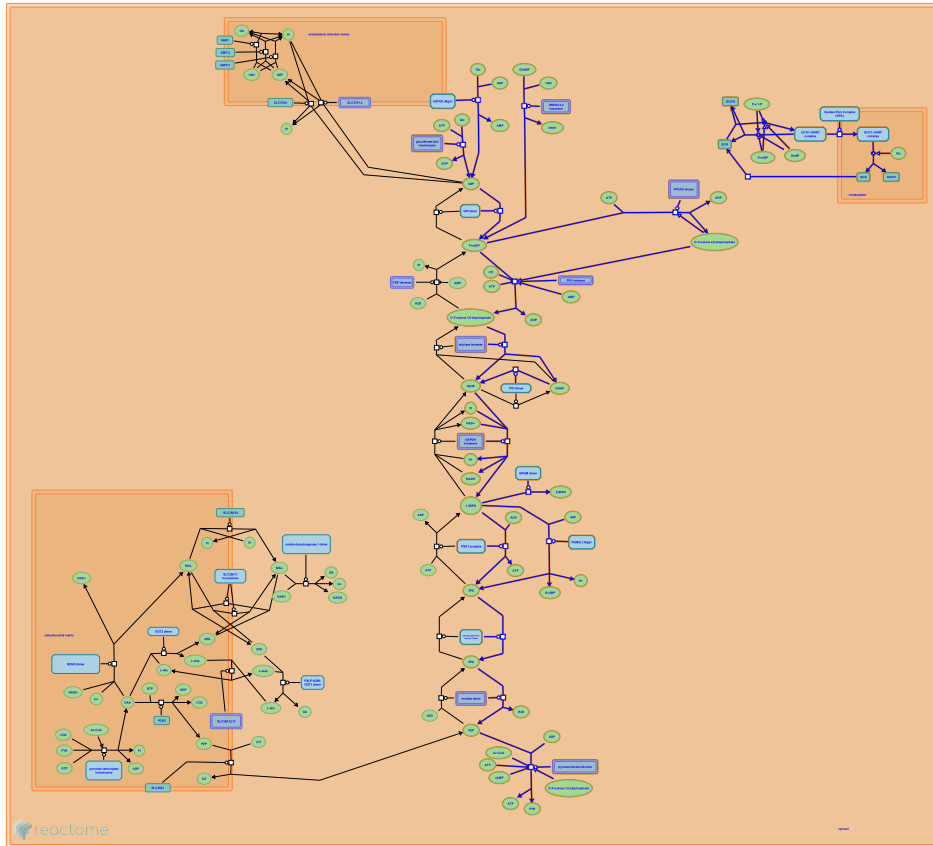
This document contains 3 pathways and 14 reactions ([see Table of Contents](#))

Glycolysis ↗

Stable identifier: R-BTA-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.

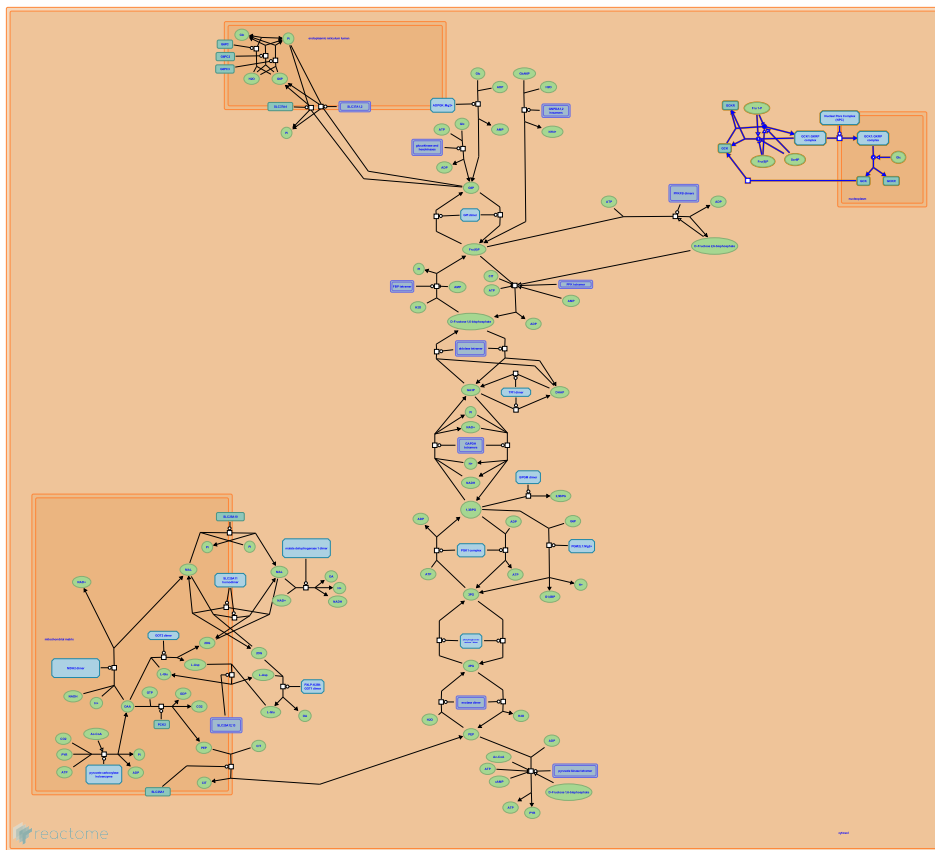
[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Regulation of Glucokinase by Glucokinase Regulatory Protein ↗

Location: Glycolysis

Stable identifier: R-BTA-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 ↗

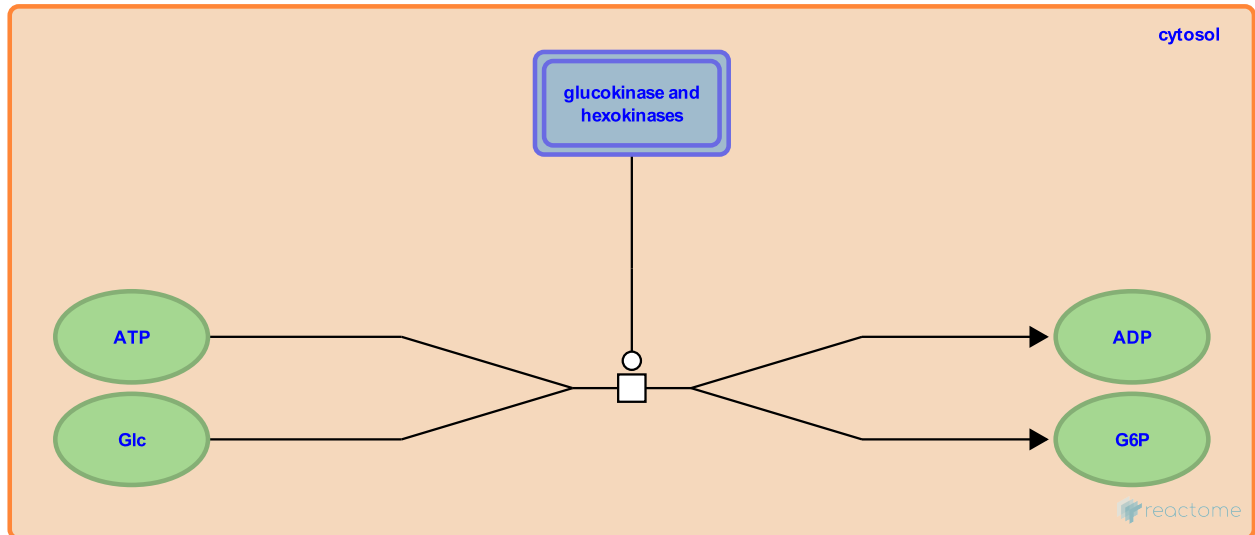
Location: Glycolysis

Stable identifier: R-BTA-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:Mg²⁺ phosphorylates G6P to G1,6BP](#), [alpha-D-glucose 6-phosphate <=> D-fructose 6-phosphate](#)

ADPGK:Mg²⁺ phosphorylates Glc to G6P ↗

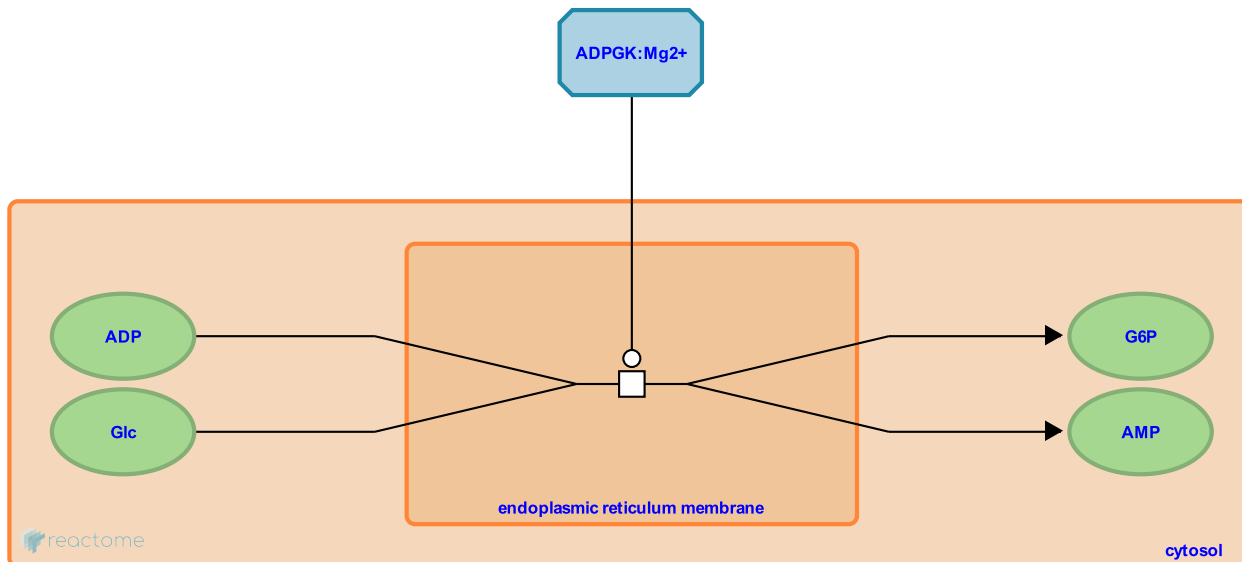
Location: [Glycolysis](#)

Stable identifier: R-BTA-5696021

Type: transition

Compartments: endoplasmic reticulum membrane, cytosol

Inferred from: [ADPGK:Mg²⁺ phosphorylates Glc to 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>

alpha-D-glucose 6-phosphate \rightleftharpoons D-fructose 6-phosphate ↗

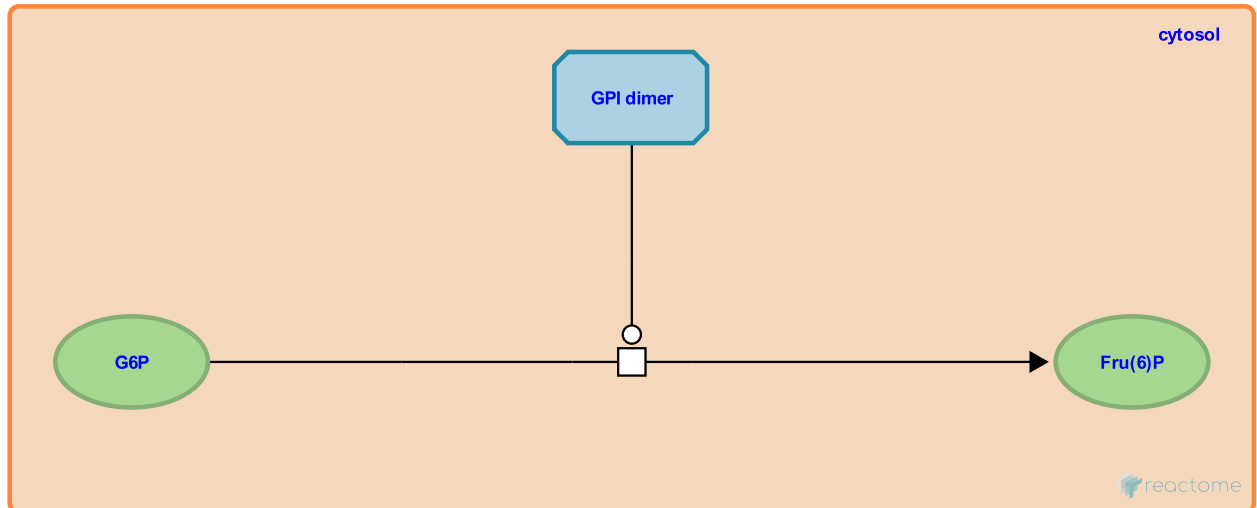
Location: [Glycolysis](#)

Stable identifier: R-BTA-70471

Type: transition

Compartments: cytosol

Inferred from: [alpha-D-glucose 6-phosphate \$\rightleftharpoons\$ 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](#)

GNPDA1,2 hexamers deaminate GlcN6P to Fru(6)P ↗

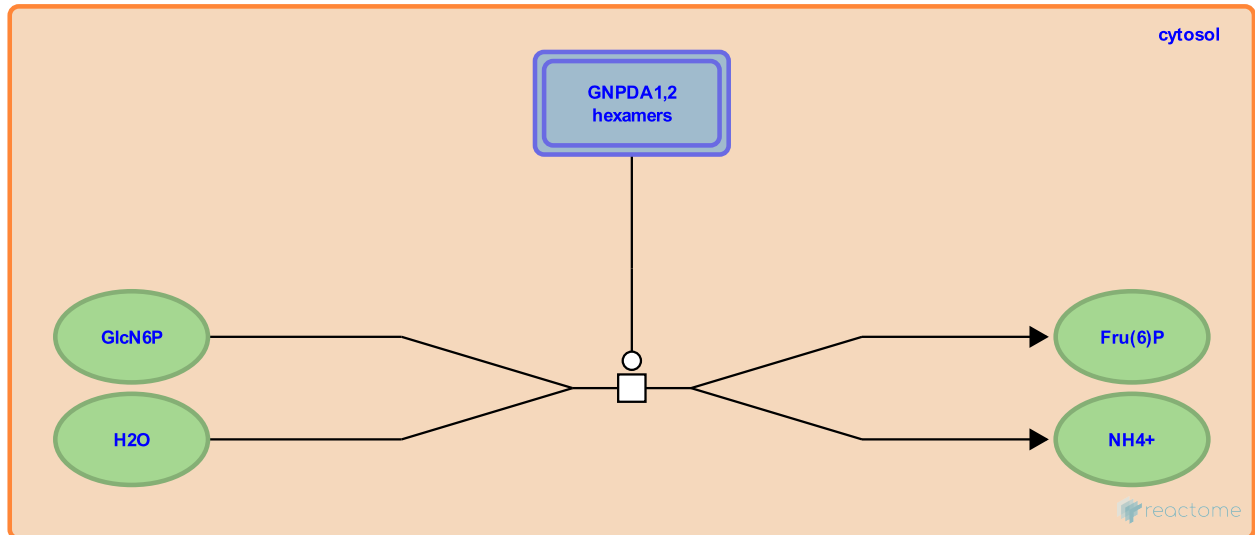
Location: [Glycolysis](#)

Stable identifier: R-BTA-6799604

Type: transition

Compartments: cytosol

Inferred from: [GNPDA1,2 hexamers deaminate GlcN6P to Fru\(6\)P \(Homo sapiens\)](#)



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-fructose 6-phosphate + ATP => D-fructose 1,6-bisphosphate + ADP](#)

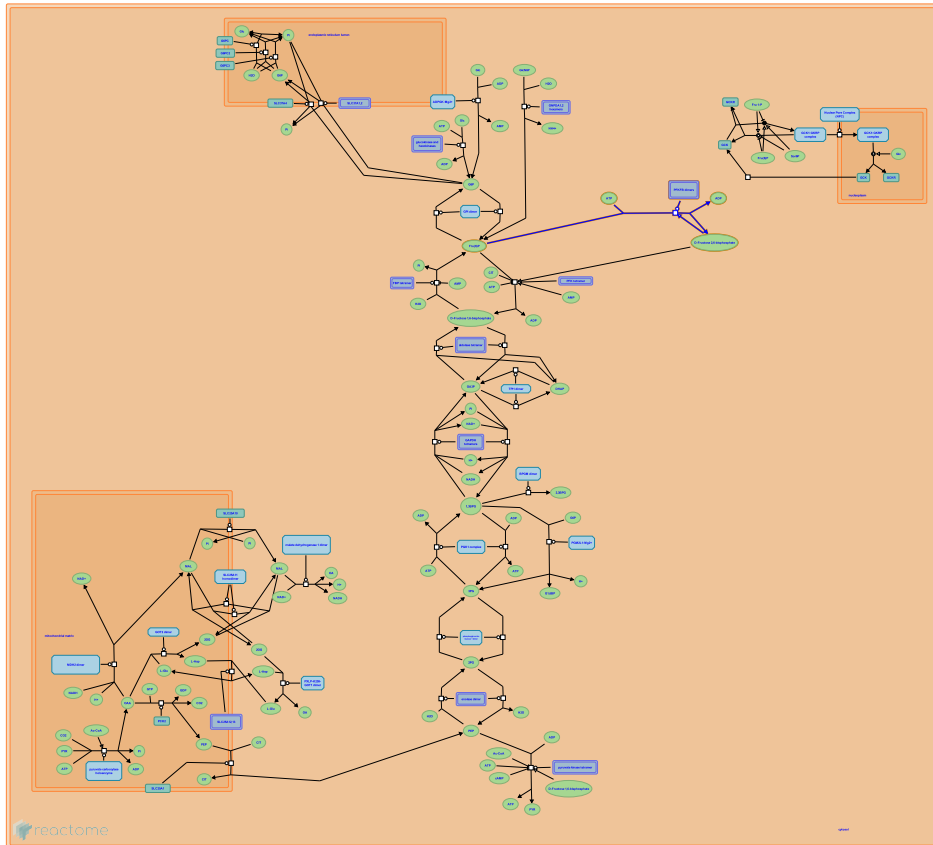
Regulation of glycolysis by fructose 2,6-bisphosphate metabolism ↗

Location: Glycolysis

Stable identifier: R-BTA-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 ↗

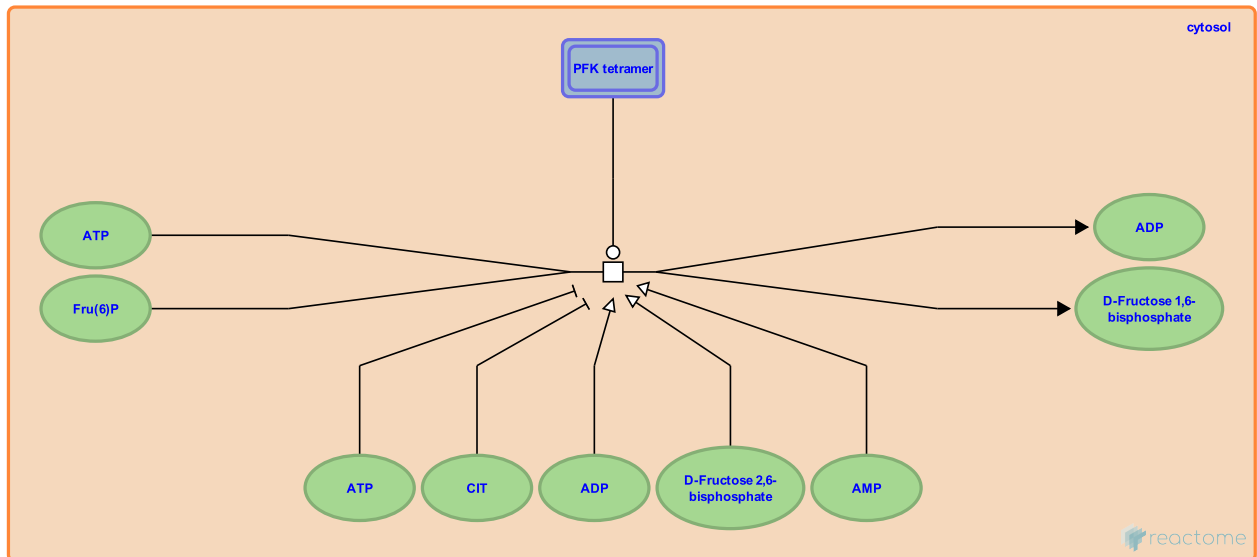
Location: Glycolysis

Stable identifier: R-BTA-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](#), [GNPDA1,2 hexamers deaminate GlcN6P to Fru\(6P\)](#)

Followed by: [D-fructose 1,6-bisphosphate <=> dihydroxyacetone phosphate + D-glyceraldehyde 3-phosphate](#)

D-fructose 1,6-bisphosphate \rightleftharpoons dihydroxyacetone phosphate + D-glyceraldehyde 3-phosphate ↗

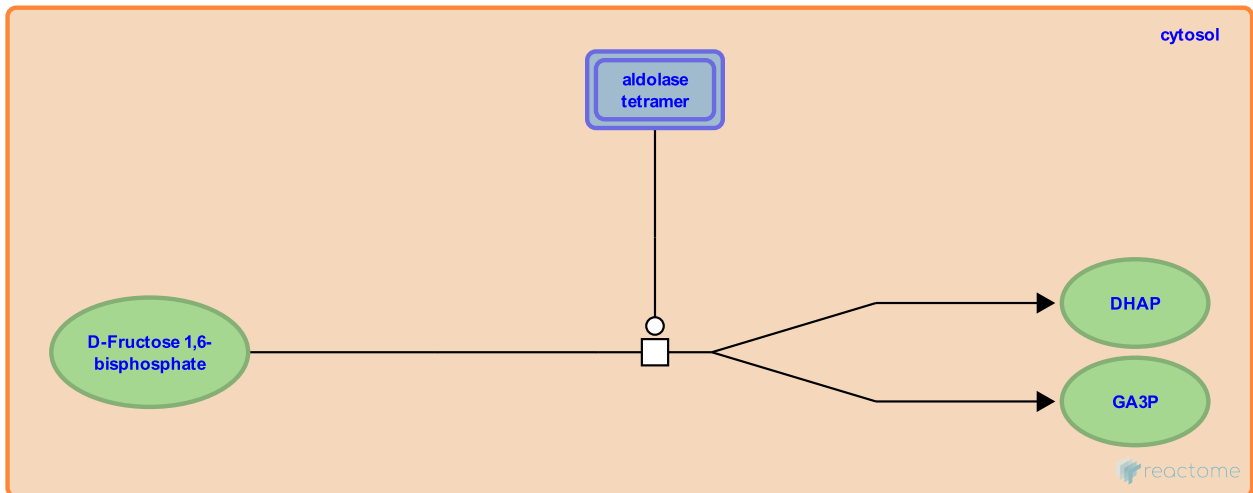
Location: [Glycolysis](#)

Stable identifier: R-BTA-71496

Type: transition

Compartments: cytosol

Inferred from: [D-fructose 1,6-bisphosphate \$\rightleftharpoons\$ dihydroxyacetone phosphate + 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>

Preceded by: [D-fructose 6-phosphate + ATP \$\Rightarrow\$ D-fructose 1,6-bisphosphate + ADP](#)

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

dihydroxyacetone phosphate \rightleftharpoons D-glyceraldehyde 3-phosphate ↗

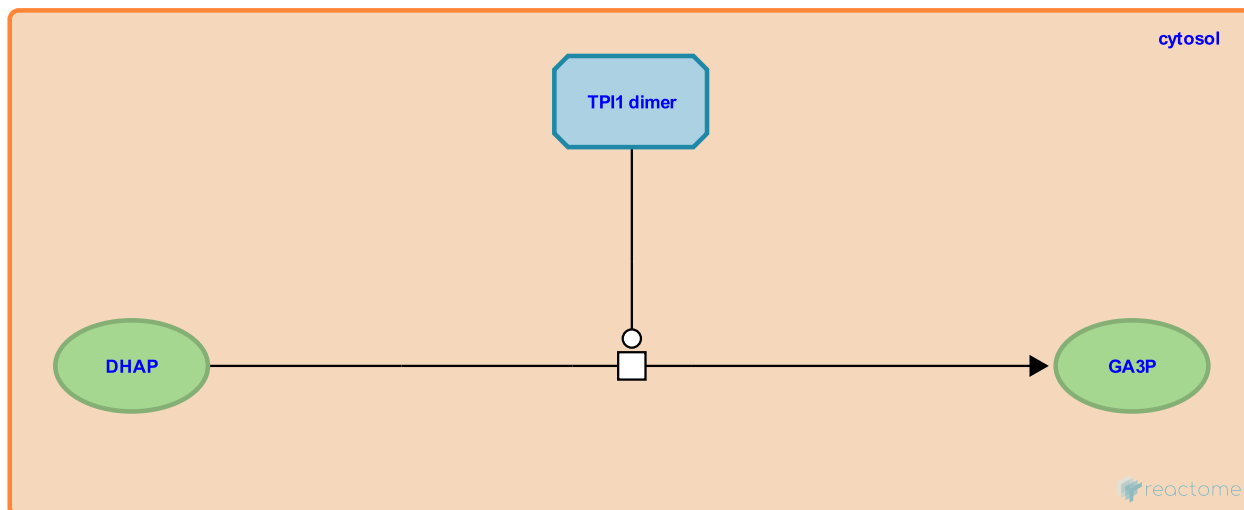
Location: Glycolysis

Stable identifier: R-BTA-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>

Preceded by: D-fructose 1,6-bisphosphate \rightleftharpoons dihydroxyacetone phosphate + D-glyceraldehyde 3-phosphate

Followed by: D-glyceraldehyde 3-phosphate + orthophosphate + NAD⁺ \rightleftharpoons 1,3-bisphospho-D-glycerate + NADH + H⁺

D-glyceraldehyde 3-phosphate + orthophosphate + NAD+ <=> 1,3-bisphospho-D-glycerate + NADH + H+ ↗

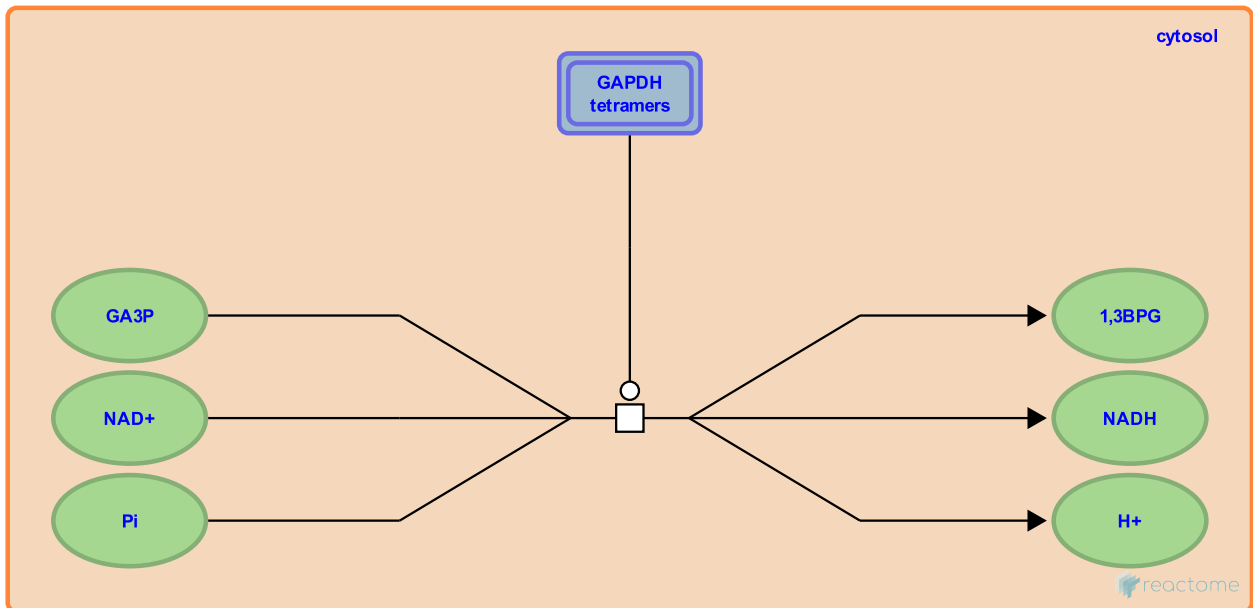
Location: [Glycolysis](#)

Stable identifier: R-BTA-70449

Type: transition

Compartments: cytosol

Inferred from: [D-glyceraldehyde 3-phosphate + orthophosphate + NAD+ <=> 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 <=> D-glyceraldehyde 3-phosphate](#)

Followed by: [BPGM dimer isomerises 1,3BPG to 2,3BPG](#), [1,3-bisphospho-D-glycerate + ADP <=> 3-phospho-D-glycerate + ATP](#)

BPGM dimer isomerises 1,3BPG to 2,3BPG ↗

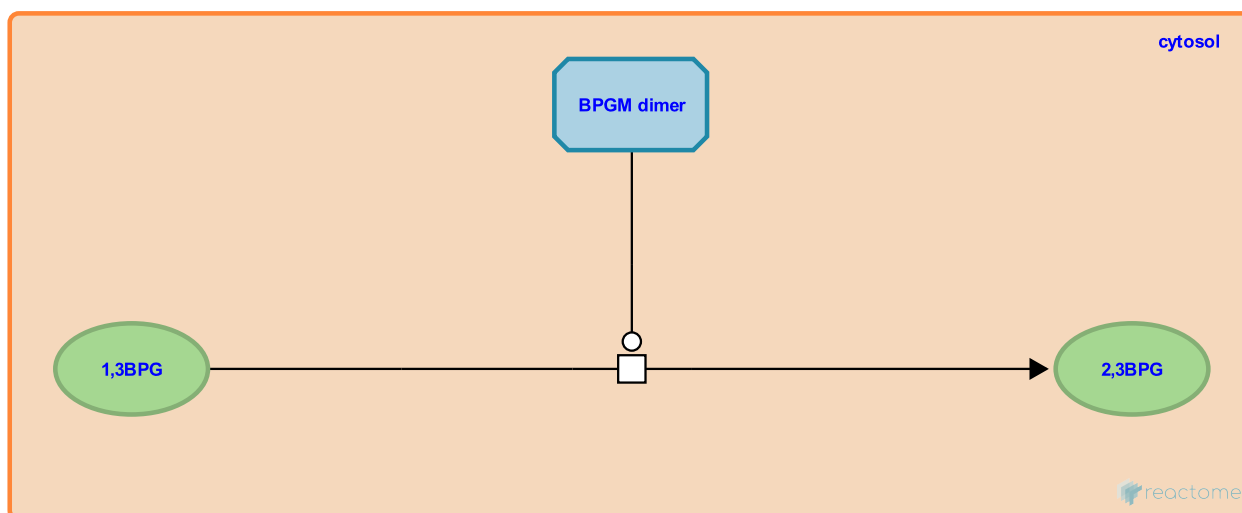
Location: [Glycolysis](#)

Stable identifier: R-BTA-6798335

Type: transition

Compartments: cytosol

Inferred from: [BPGM dimer isomerises 1,3BPG to 2,3BPG \(Homo sapiens\)](#)



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+](#)

PGM2L1:Mg²⁺ phosphorylates G6P to G1,6BP ↗

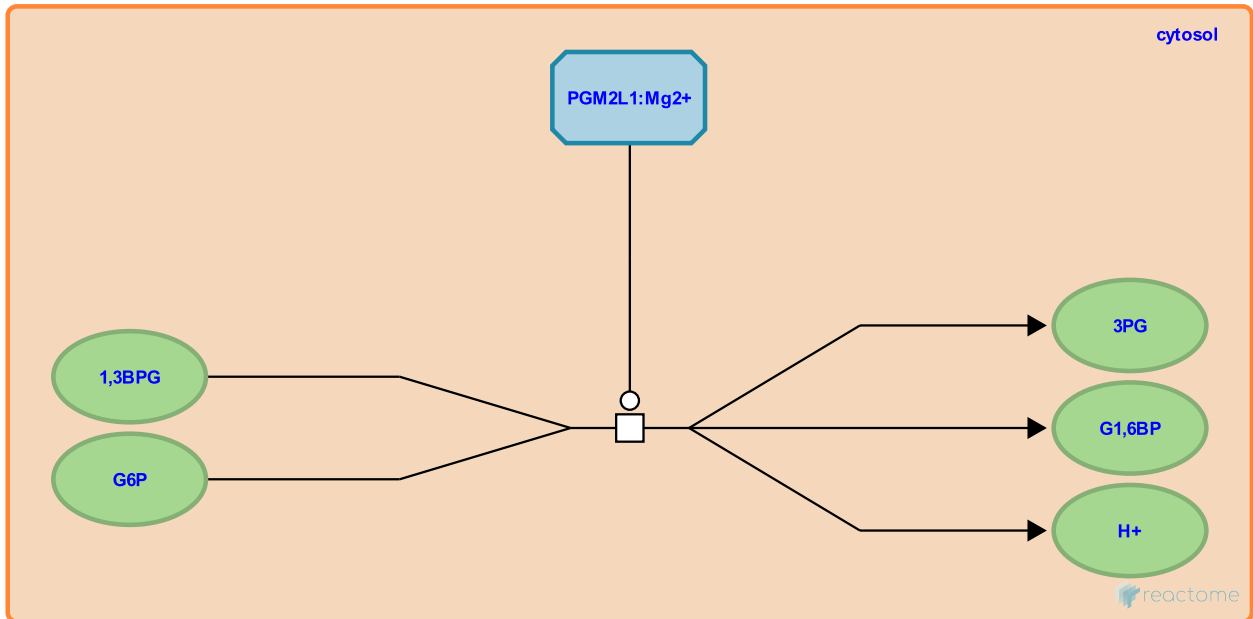
Location: Glycolysis

Stable identifier: R-BTA-8955760

Type: transition

Compartments: cytosol

Inferred from: PGM2L1:Mg²⁺ 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 \rightleftharpoons 3-phospho-D-glycerate + ATP ↗

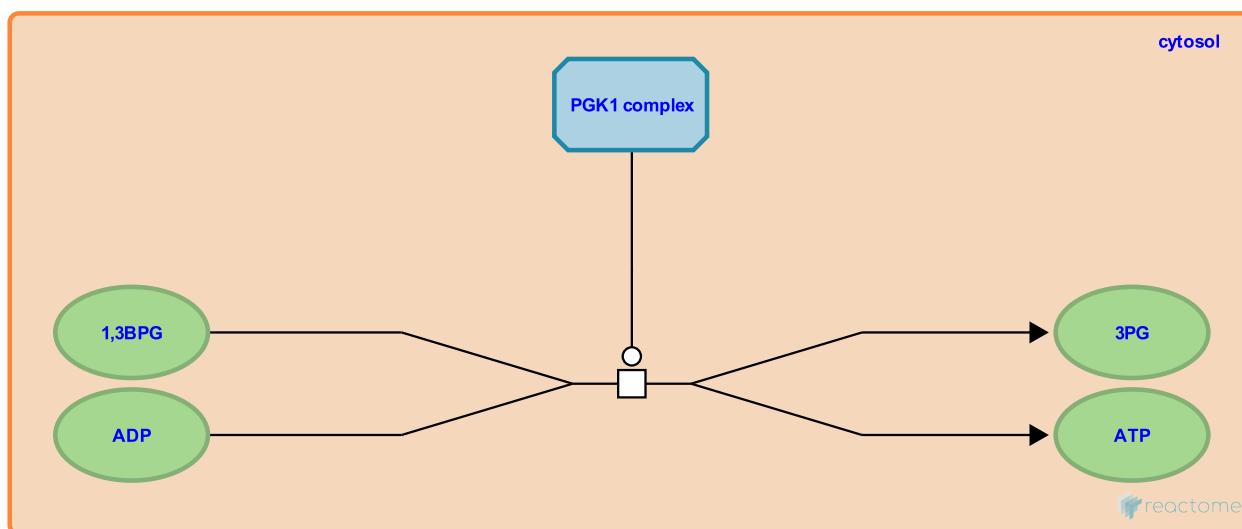
Location: Glycolysis

Stable identifier: R-BTA-71850

Type: transition

Compartments: cytosol

Inferred from: 1,3-bisphospho-D-glycerate + ADP \rightleftharpoons 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⁺ \rightleftharpoons 1,3-bisphospho-D-glycerate + NADH + H⁺

Followed by: 3-Phospho-D-glycerate \rightleftharpoons 2-Phospho-D-glycerate

3-Phospho-D-glycerate <=> 2-Phospho-D-glycerate ↗

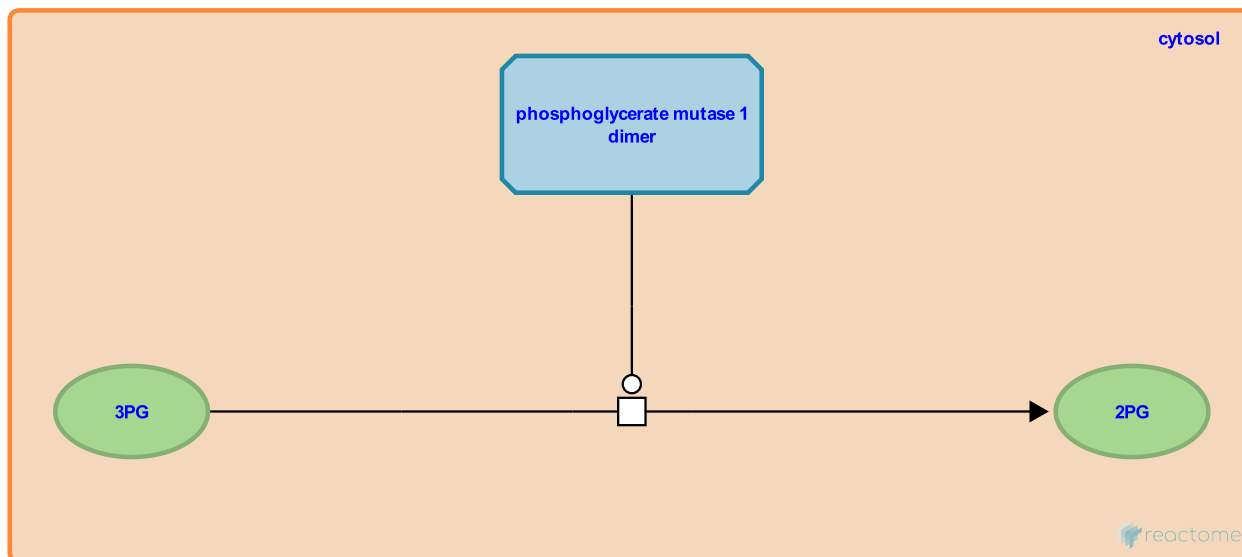
Location: [Glycolysis](#)

Stable identifier: R-BTA-71654

Type: transition

Compartments: cytosol

Inferred from: [3-Phospho-D-glycerate <=> 2-Phospho-D-glycerate \(Homo sapiens\)](#)



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.

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Preceded by: [1,3-bisphospho-D-glycerate + ADP <=> 3-phospho-D-glycerate + ATP](#)

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

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

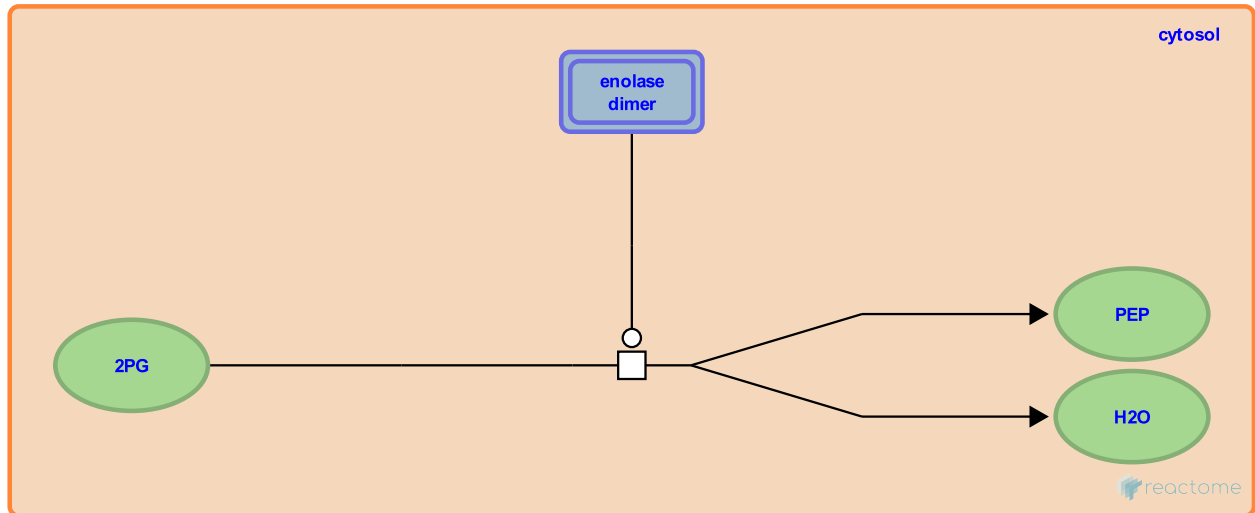
Location: [Glycolysis](#)

Stable identifier: R-BTA-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>

Preceded by: [3-Phospho-D-glycerate <=> 2-Phospho-D-glycerate](#)

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

phosphoenolpyruvate + ADP => pyruvate + ATP ↗

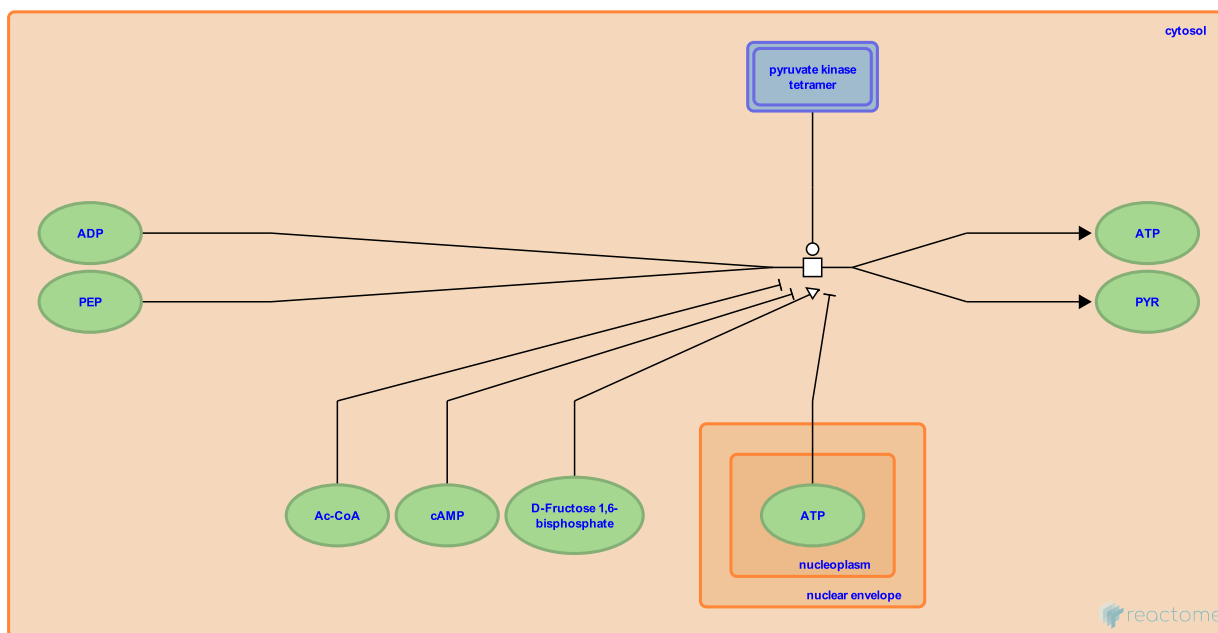
Location: Glycolysis

Stable identifier: R-BTA-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](#)

Table of Contents

Introduction	1
☒ Glycolysis	2
☒ Regulation of Glucokinase by Glucokinase Regulatory Protein	3
↗ HK1,2,3,GCK phosphorylate Glc to form G6P	4
↗ ADPGK:Mg ²⁺ phosphorylates Glc to G6P	5
↗ alpha-D-glucose 6-phosphate <=> D-fructose 6-phosphate	6
↗ GNPDA1,2 hexamers deaminate GlcN6P to Fru(6)P	7
☒ Regulation of glycolysis by fructose 2,6-bisphosphate metabolism	8
↗ D-fructose 6-phosphate + ATP => D-fructose 1,6-bisphosphate + ADP	9
↗ D-fructose 1,6-bisphosphate <=> dihydroxyacetone phosphate + D-glyceraldehyde 3-phosphate	10
↗ dihydroxyacetone phosphate <=> D-glyceraldehyde 3-phosphate	11
↗ D-glyceraldehyde 3-phosphate + orthophosphate + NAD ⁺ <=> 1,3-bisphospho-D-glycerate + NADH + H ⁺	12
↗ BPGM dimer isomerises 1,3BPG to 2,3BPG	13
↗ PGM2L1:Mg ²⁺ phosphorylates G6P to G1,6BP	14
↗ 1,3-bisphospho-D-glycerate + ADP <=> 3-phospho-D-glycerate + ATP	15
↗ 3-Phospho-D-glycerate <=> 2-Phospho-D-glycerate	16
↗ 2-Phospho-D-glycerate <=> Phosphoenolpyruvate + H ₂ O	17
↗ phosphoenolpyruvate + ADP => pyruvate + ATP	18
Table of Contents	19