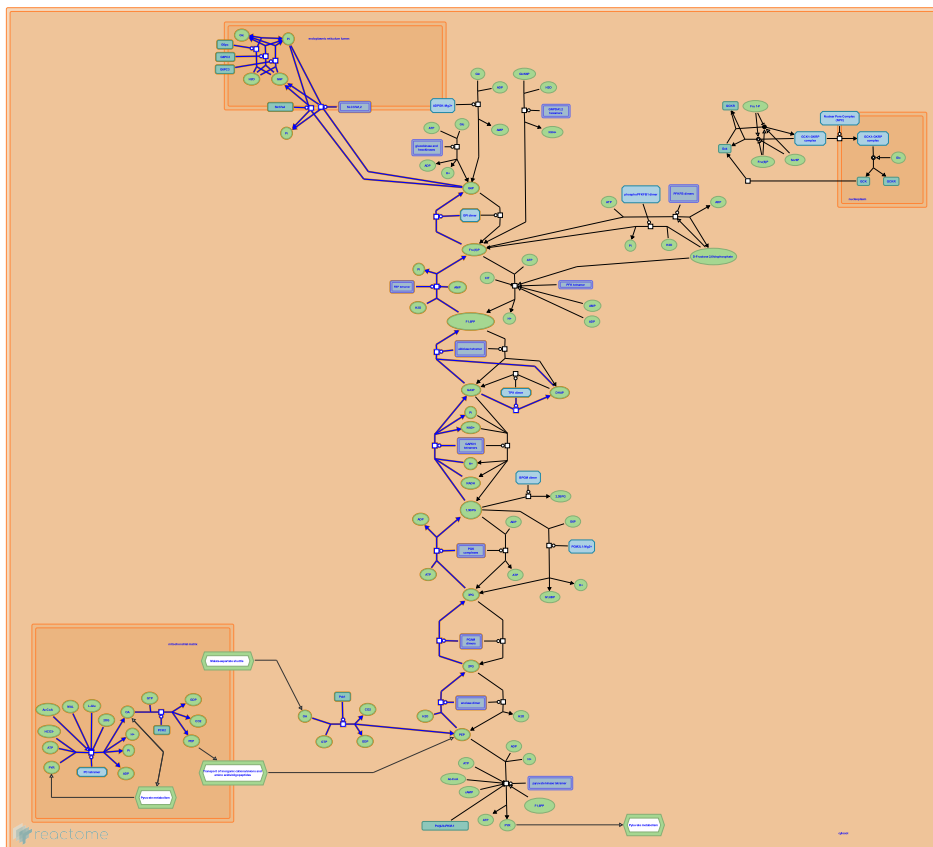# Gluconeogenesis

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

This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the Reactome Textbook.

15/05/2024

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. ↗
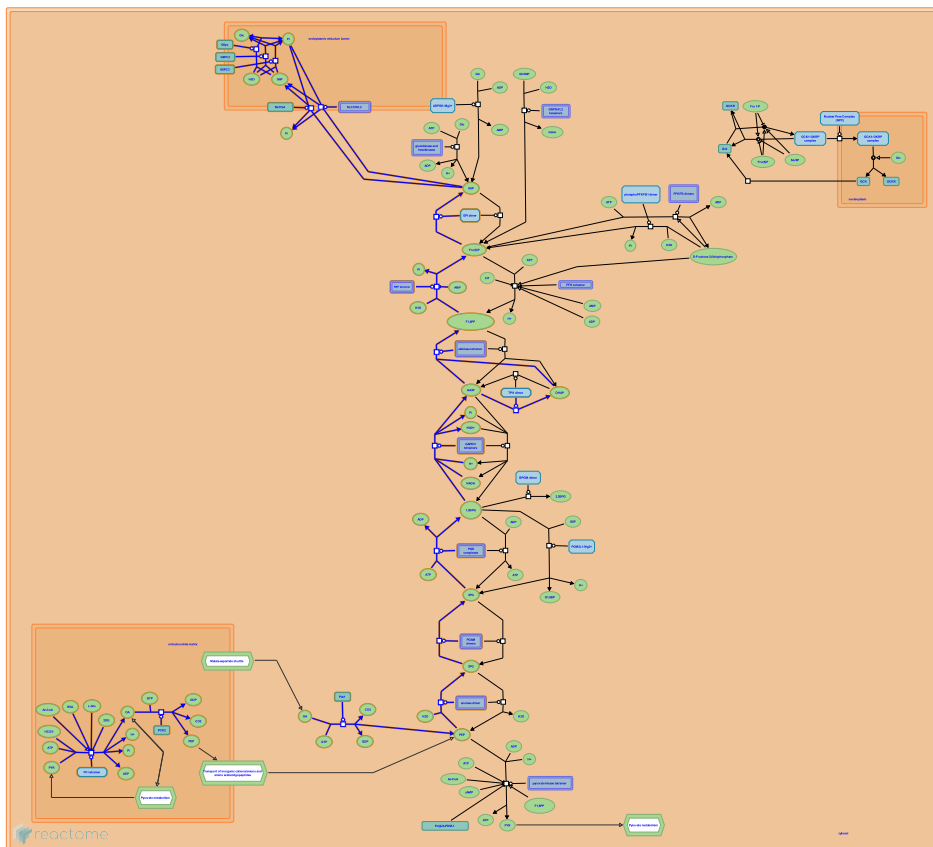
Reactome database release: 88

This document contains 1 pathway and 16 reactions (see Table of Contents)

Gluconeogenesis ↗

Stable identifier: R-MMU-70263

Inferred from: Gluconeogenesis (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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp
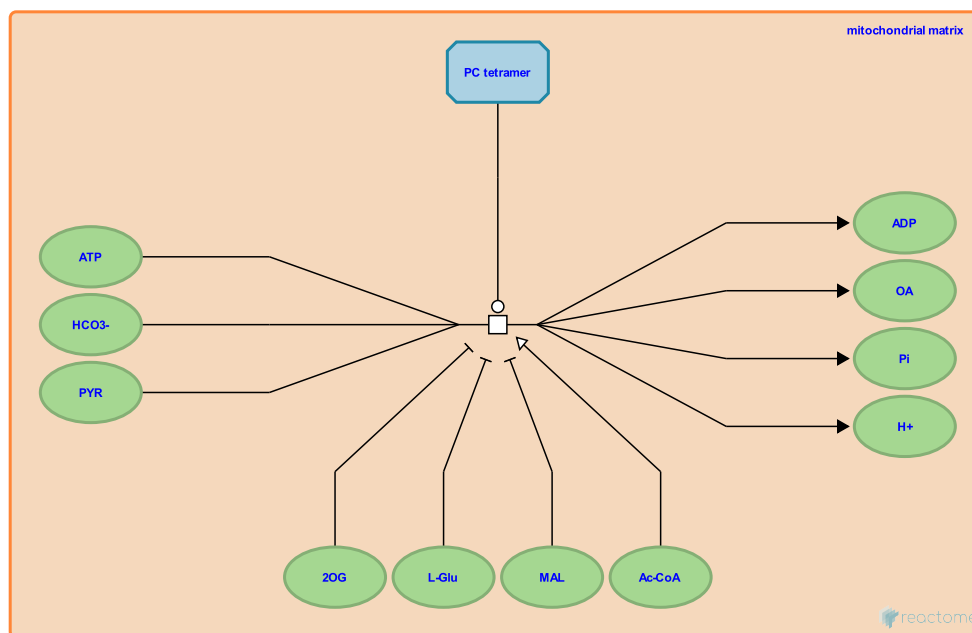
PC carboxylates PYR to OA ↗

Location: Gluconeogenesis

Stable identifier: R-MMU-70501

Type: transition

Compartments: mitochondrial matrix

Inferred from: PC carboxylates PYR to OA (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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Followed by: PCK2 phosphorylates OA to yield PEP

PCK1 phosphorylates OA to yield PEP ↗
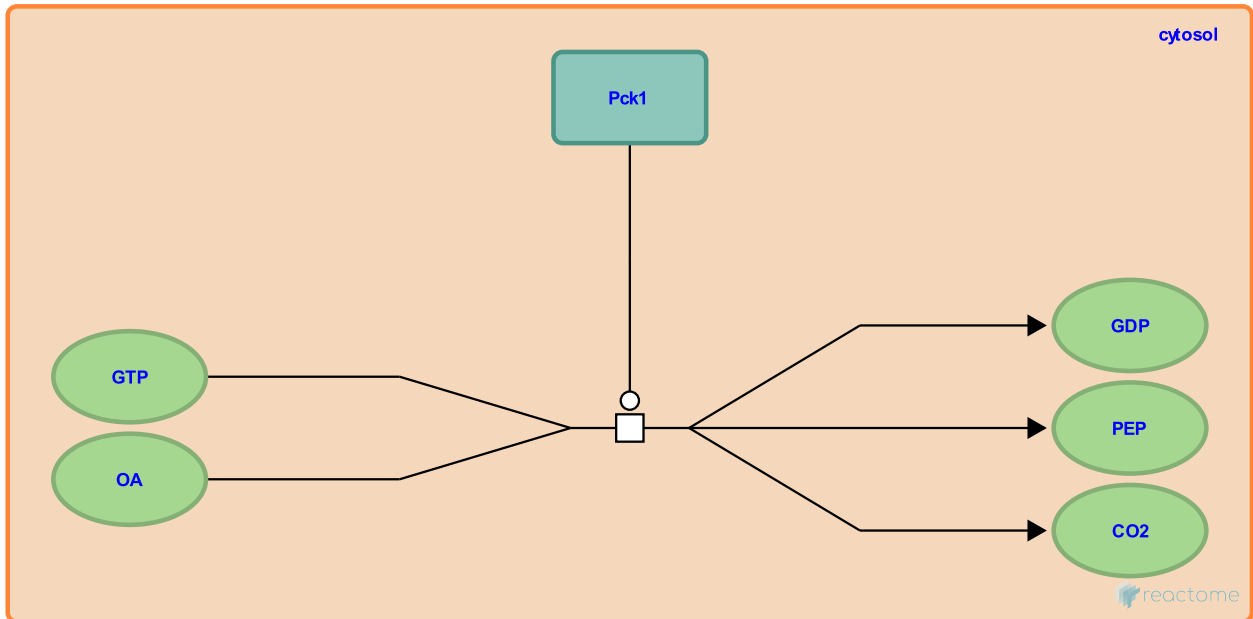
Location: Gluconeogenesis

Stable identifier: R-MMU-70241

Type: transition

Compartments: cytosol

Inferred from: PCK1 phosphorylates OA to yield PEP (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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Followed by: Enolase dimers (ENO1,2,3) convert PEP to 2PG

PCK2 phosphorylates OA to yield PEP ↗
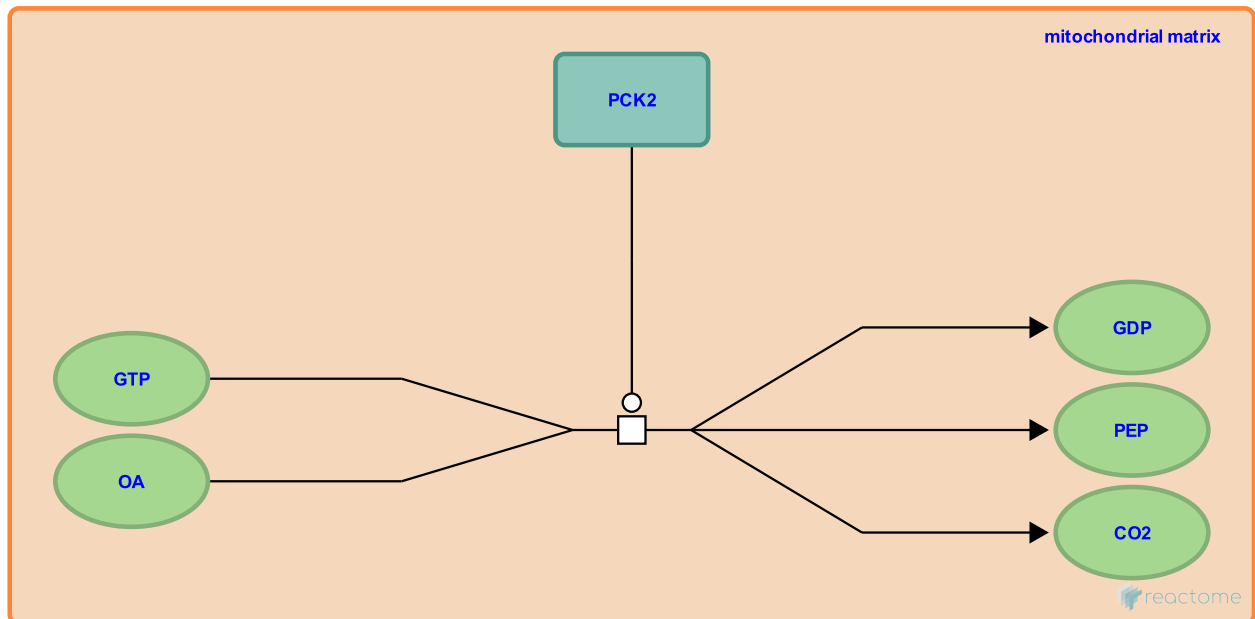
Location: Gluconeogenesis

Stable identifier: R-MMU-372819

Type: transition

Compartments: mitochondrial matrix

Inferred from: PCK2 phosphorylates OA to yield PEP (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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: PC carboxylates PYR to OA

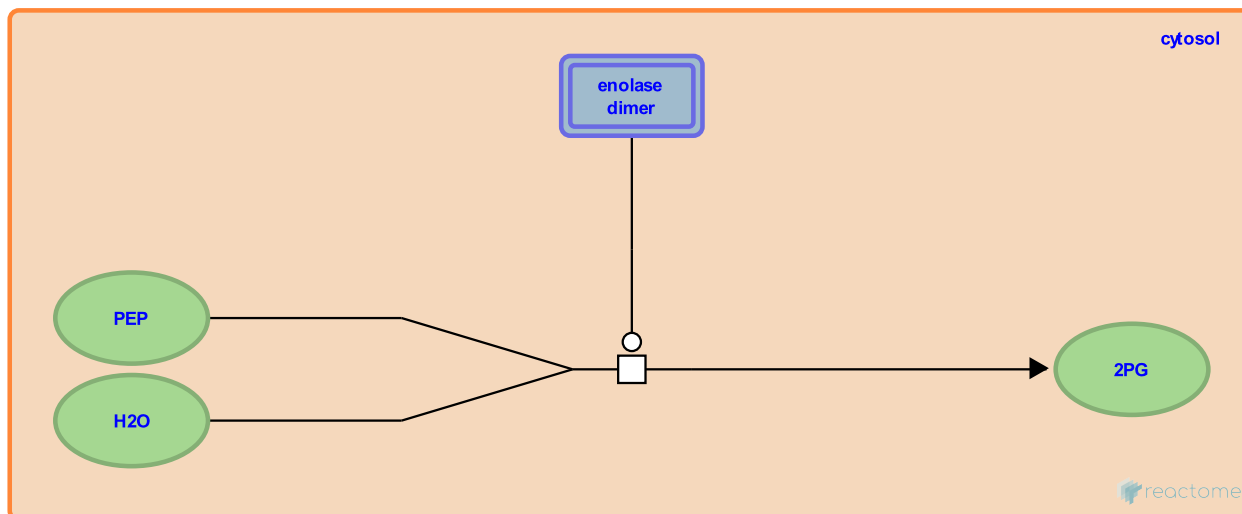## Enolase dimers (ENO1,2,3) convert PEP to 2PG ↗

Location: Gluconeogenesis

Stable identifier: R-MMU-70494

Type: transition

Compartments: cytosol

Inferred from: Enolase dimers (ENO1,2,3) convert PEP to 2PG (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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: PCK1 phosphorylates OA to yield PEP

Followed by: PGAM dimers (PGAM1,2) isomerise 2PG to 3PG
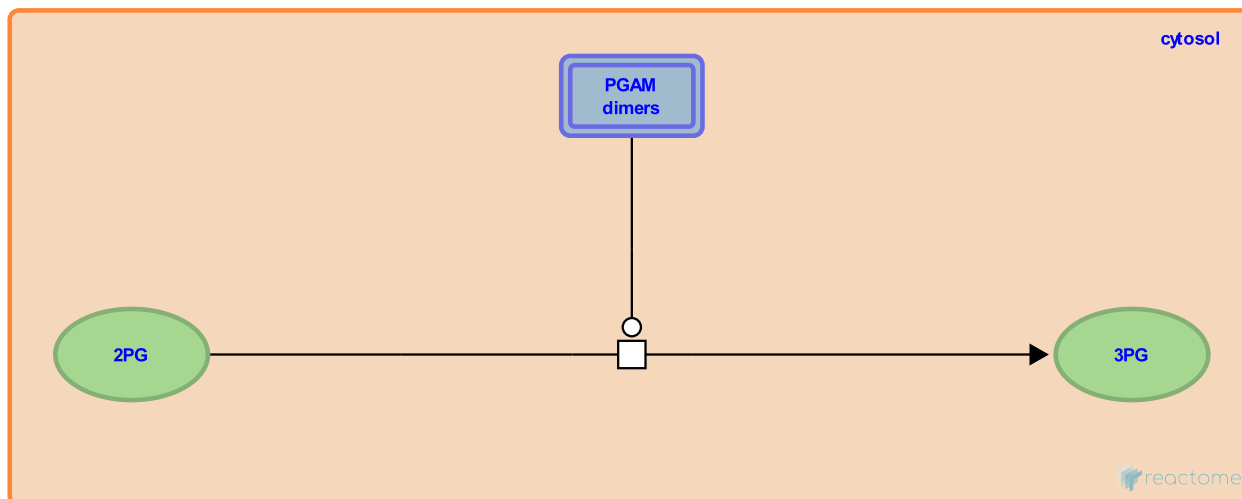
PGAM dimers (PGAM1,2) isomerise 2PG to 3PG ↗

Location: Gluconeogenesis

Stable identifier: R-MMU-71445

Type: transition

Compartments: cytosol

Inferred from: PGAM dimers (PGAM1,2) isomerise 2PG to 3PG (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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: Enolase dimers (ENO1,2,3) convert PEP to 2PG

Followed by: PGK complexes (PGK1,2) phosphorylate 3PG to form 1,3BPG

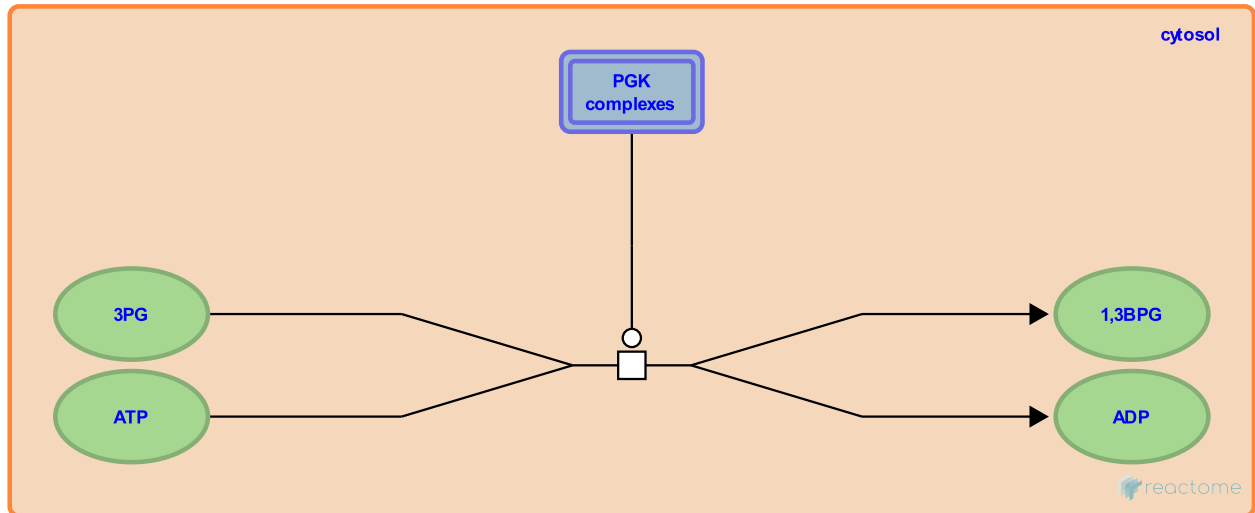**PGK complexes (PGK1,2) phosphorylate 3PG to form 1,3BPG** ↗

Location: Gluconeogenesis

Stable identifier: R-MMU-70486

Type: transition

Compartments: cytosol

Inferred from: PGK complexes (PGK1,2) phosphorylate 3PG to form 1,3BPG (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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: PGAM dimers (PGAM1,2) isomerise 2PG to 3PG

Followed by: GAPDH tetramers reduce 1,3BPG to GA3P
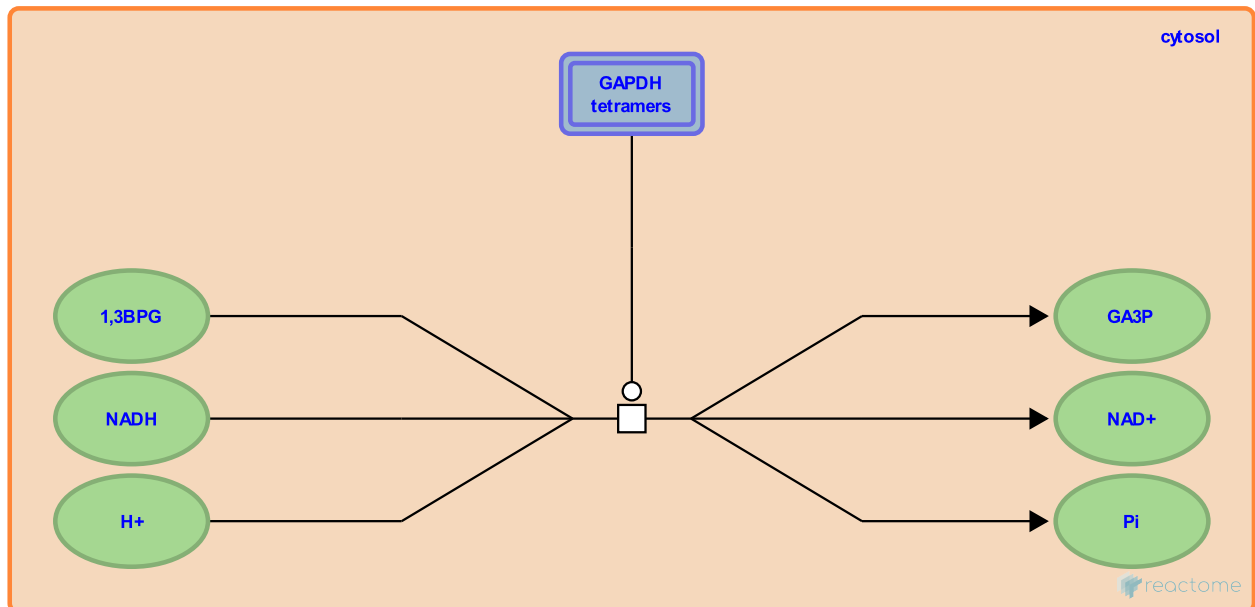
GAPDH tetramers reduce 1,3BPG to GA3P ↗

Location: Gluconeogenesis

Stable identifier: R-MMU-70482

Type: transition

Compartments: cytosol

Inferred from: GAPDH tetramers reduce 1,3BPG to GA3P (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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: PGK complexes (PGK1,2) phosphorylate 3PG to form 1,3BPG

Followed by: TPI1 isomerizes GA3P to DHAP, Aldolase tetramers convert GA3P and DHAP to F1,6PP
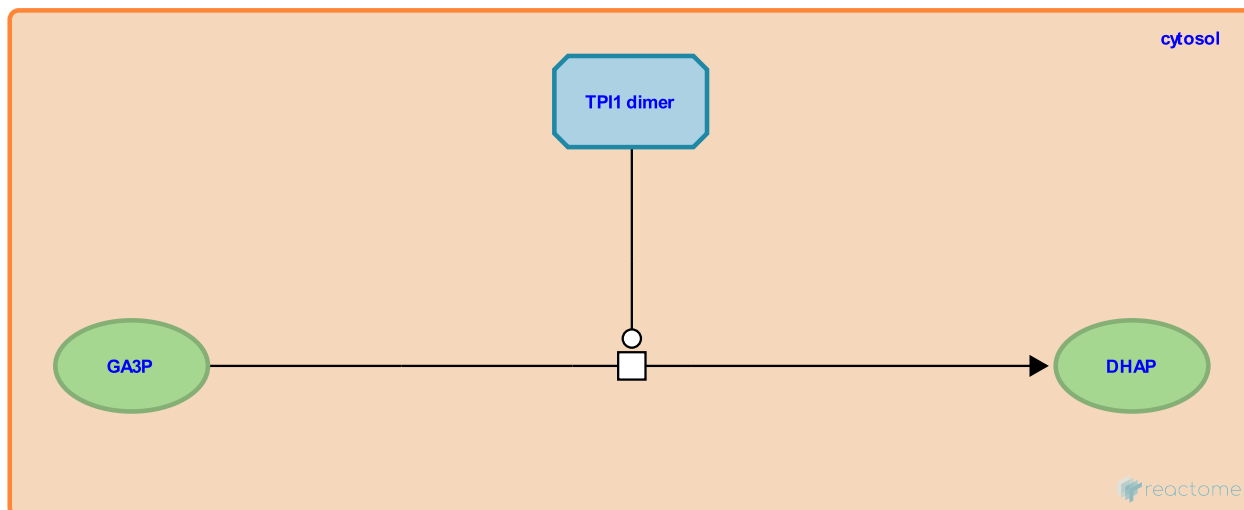
TPI1 isomerizes GA3P to DHAP ↗

Location: Gluconeogenesis

Stable identifier: R-MMU-70481

Type: transition

Compartments: cytosol

Inferred from: TPI1 isomerizes GA3P to DHAP (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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: GAPDH tetramers reduce 1,3BPG to GA3P

Followed by: Aldolase tetramers convert GA3P and DHAP to F1,6PP
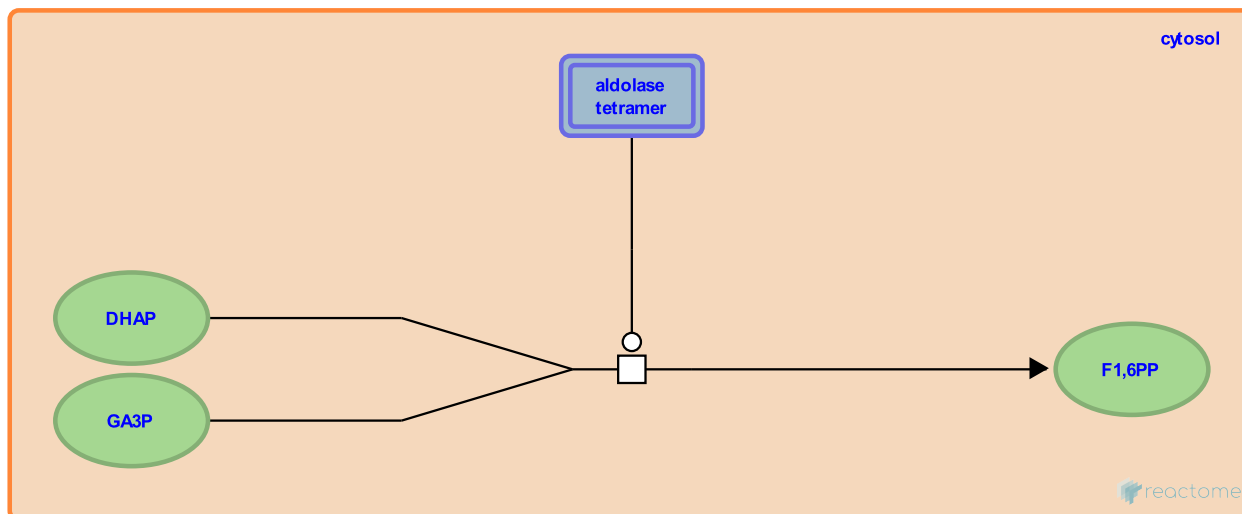
Aldolase tetramers convert GA3P and DHAP to F1,6PP ↗

Location: Gluconeogenesis

Stable identifier: R-MMU-71495

Type: transition

Compartments: cytosol

Inferred from: Aldolase tetramers convert GA3P and DHAP to F1,6PP (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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: TPI1 isomerizes GA3P to DHAP, GAPDH tetramers reduce 1,3BPG to GA3P

Followed by: FBP tetramers hydrolyze F1,6PP to Fru(6)P
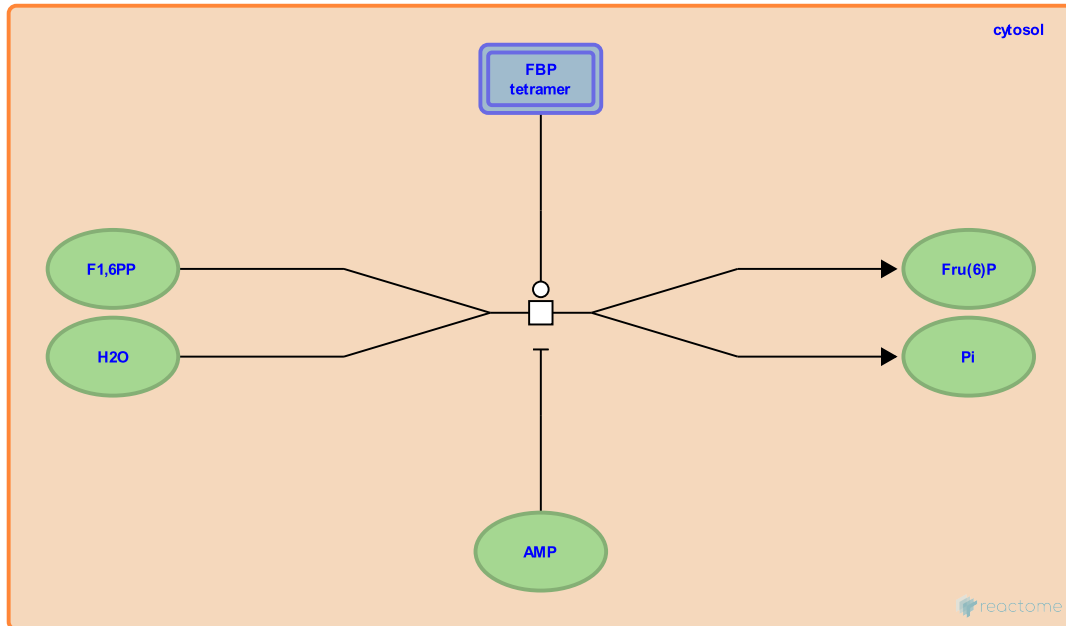
FBP tetramers hydrolyze F1,6PP to Fru(6)P ↗

Location: Gluconeogenesis

Stable identifier: R-MMU-70479

Type: transition

Compartments: cytosol

Inferred from: FBP tetramers hydrolyze F1,6PP 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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: Aldolase tetramers convert GA3P and DHAP to F1,6PP

Followed by: GPI dimer isomerizes Fru(6)P to G6P
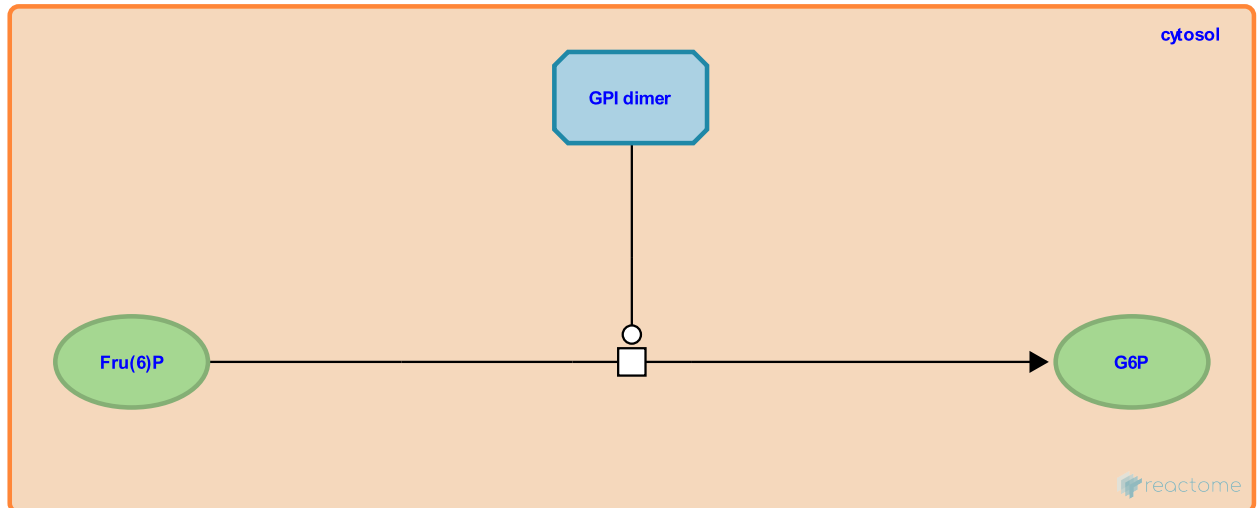
GPI dimer isomerizes Fru(6)P to G6P ↗

Location: Gluconeogenesis

Stable identifier: R-MMU-70475

Type: transition

Compartments: cytosol

Inferred from: GPI dimer isomerizes Fru(6)P 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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: FBP tetramers hydrolyze F1,6PP to Fru(6)P

Followed by: SLC7A4 exchanges G6P for Pi across the ER membrane
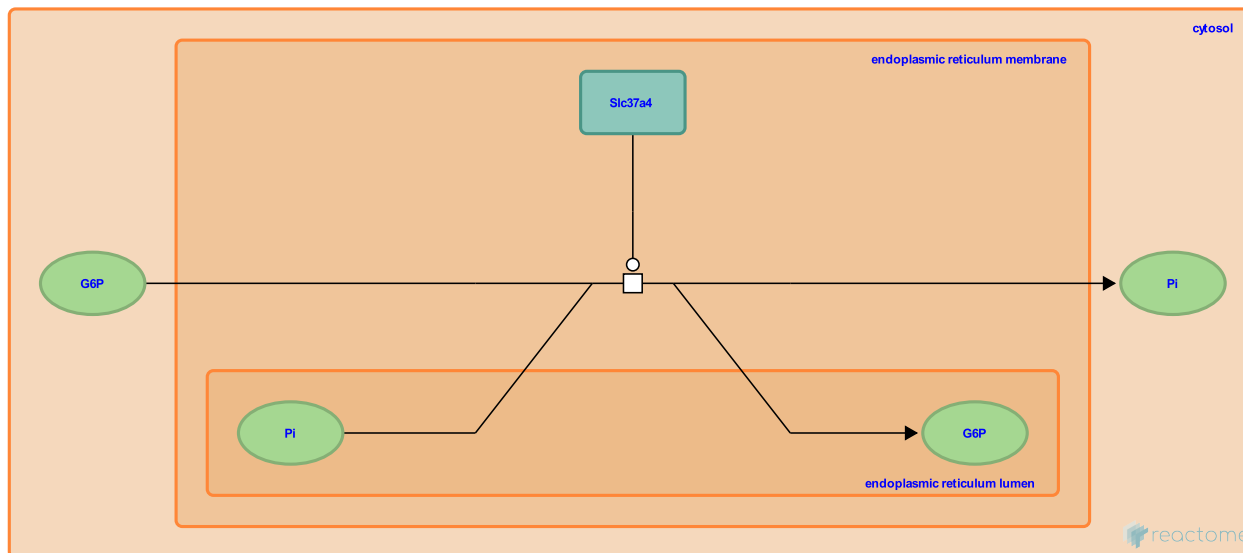
SLC7A4 exchanges G6P for Pi across the ER membrane ↗

Location: Gluconeogenesis

Stable identifier: R-MMU-198513

Type: transition

Compartments: endoplasmic reticulum membrane, endoplasmic reticulum lumen, cytosol

Inferred from: SLC7A4 exchanges G6P for Pi across the ER membrane (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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: GPI dimer isomerizes Fru(6)P to G6P

Followed by: G6PC hydrolyzes G6P to Glc and Pi (liver)

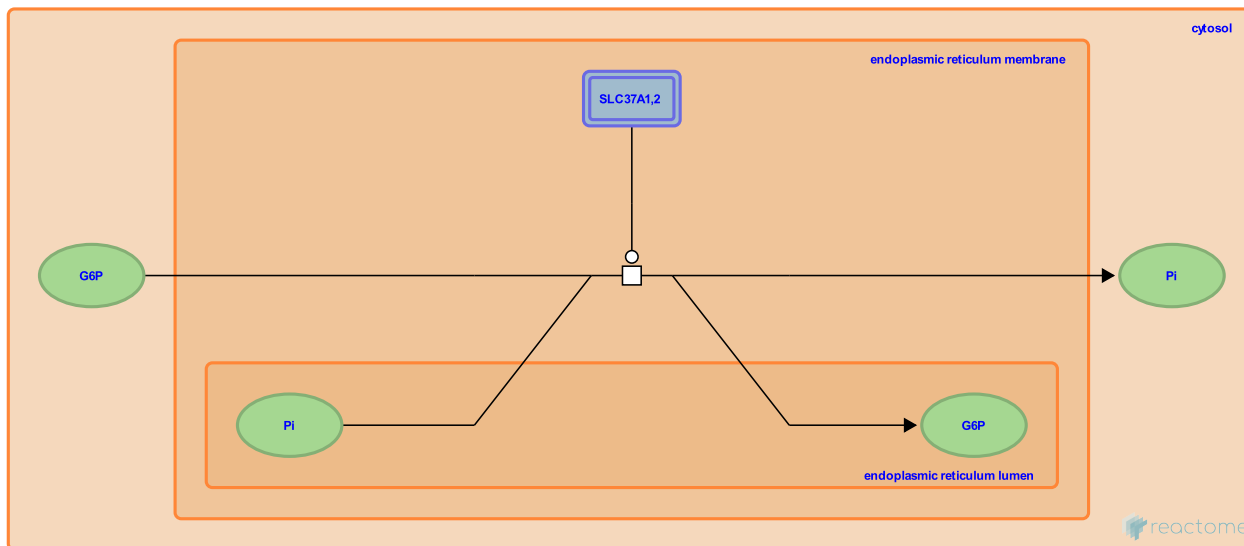# SLC37A1, SLC37A2 exchange G6P for Pi across the ER membrane ↗

Location: Gluconeogenesis

Stable identifier: R-MMU-3257122

Type: transition

Compartments: endoplasmic reticulum membrane, endoplasmic reticulum lumen, cytosol

Inferred from: SLC37A1, SLC37A2 exchange G6P for Pi across the ER membrane (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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

# G6PC hydrolyzes G6P to Glc and Pi (liver) ↗

Location: Gluconeogenesis

Stable identifier: R-MMU-71825

Type: transition

Compartments: endoplasmic reticulum membrane, endoplasmic reticulum lumen

Inferred from: G6PC hydrolyzes G6P to Glc and Pi (liver) (Homo sapiens)
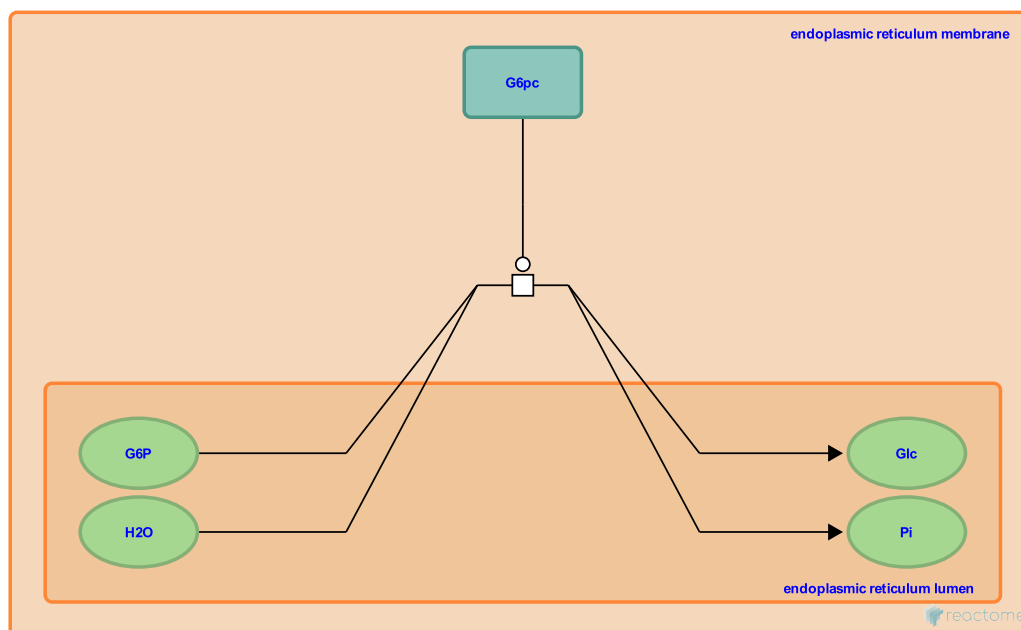
This event has been computationally inferred from an event that has been demonstrated in another species.

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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: SLC7A4 exchanges G6P for Pi across the ER membrane

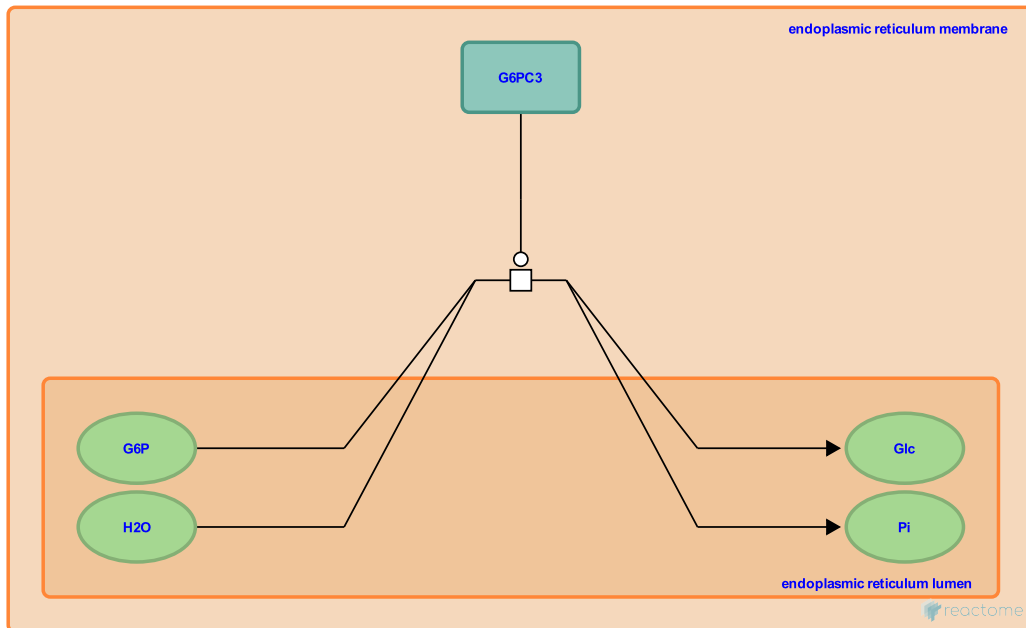## G6PC2 hydrolyzes G6P to form Glc and Pi (islet) ↗

Location: Gluconeogenesis

Stable identifier: R-MMU-3266566

Type: transition

Compartments: endoplasmic reticulum membrane, endoplasmic reticulum lumen

Inferred from: G6PC2 hydrolyzes G6P to form Glc and Pi (islet) (Homo sapiens)
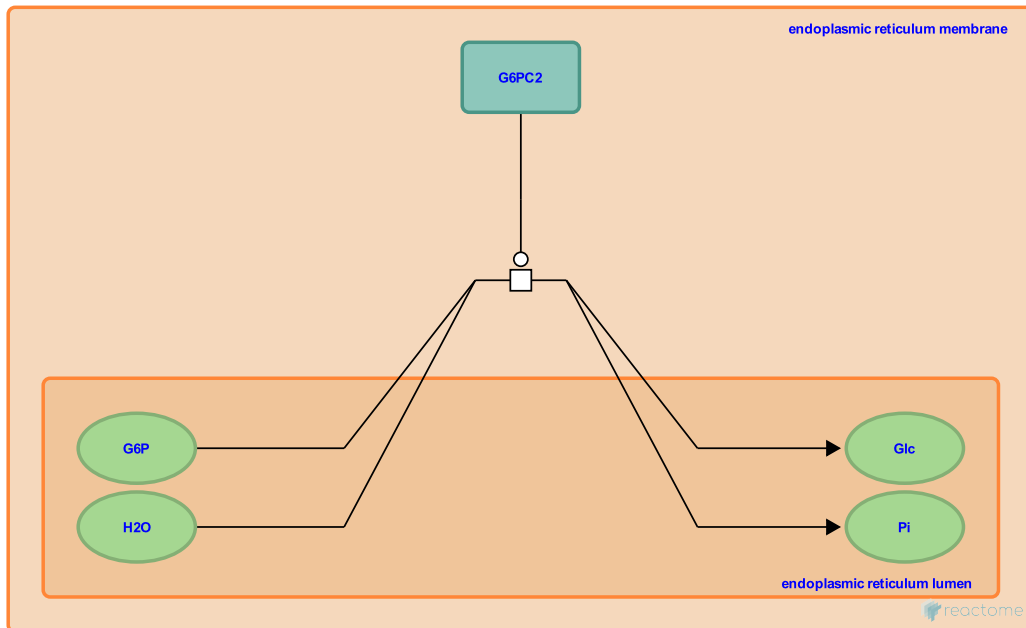
This event has been computationally inferred from an event that has been demonstrated in another species.

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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

G6PC3 hydrolyzes G6P to form Glc and Pi (ubiquitous) ↗

Location: Gluconeogenesis

Stable identifier: R-MMU-3262512

Type: transition

Compartments: endoplasmic reticulum membrane, endoplasmic reticulum lumen

Inferred from: G6PC3 hydrolyzes G6P to form Glc and Pi (ubiquitous) (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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Table of Contents