

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 11 reactions ([see Table of Contents](#))

PGM1:Mg2+ isomerises G6P to G1P ↗

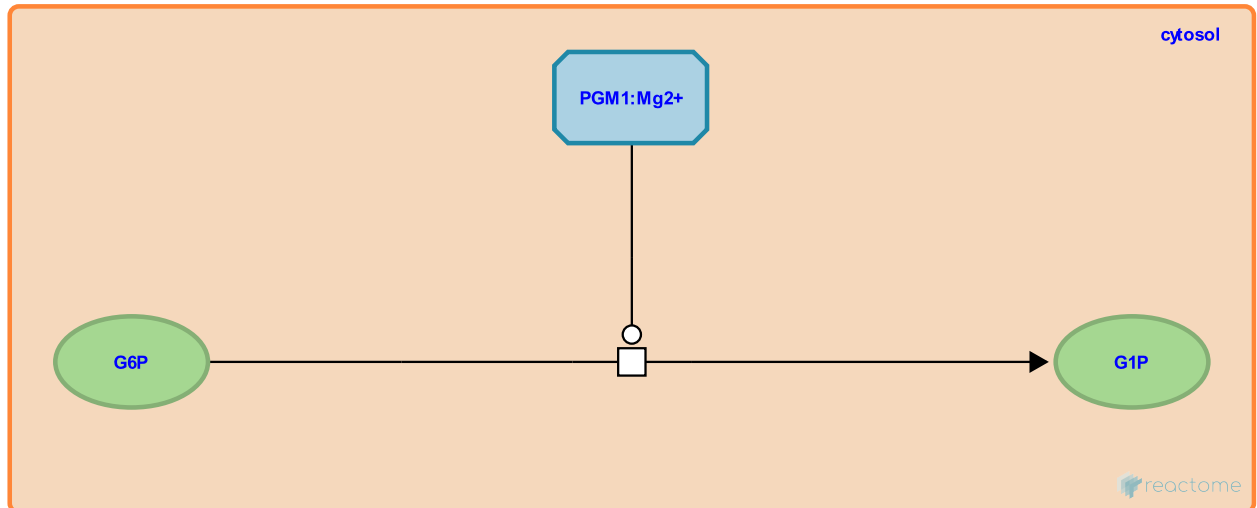
Location: [Glycogen synthesis](#)

Stable identifier: R-MMU-9638127

Type: transition

Compartments: cytosol

Inferred from: [PGM1:Mg2+ isomerises G6P to G1P \(Homo sapiens\)](#)



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: [UTP + D-glucose 1-phosphate <=> pyrophosphate + UDP-glucose](#)

UTP + D-glucose 1-phosphate <=> pyrophosphate + UDP-glucose ↗

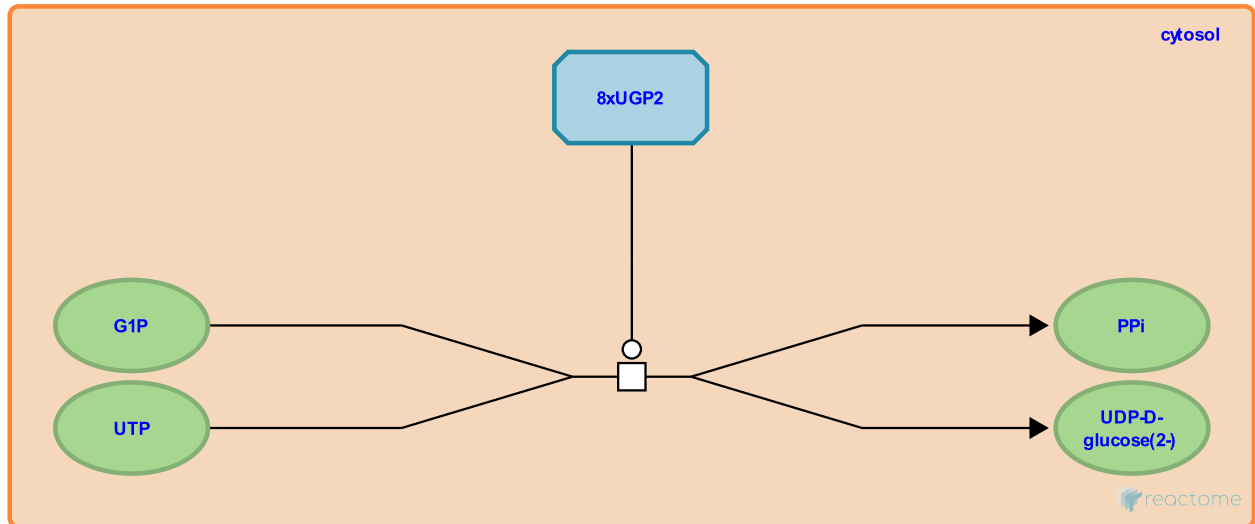
Location: [Glycogen synthesis](#)

Stable identifier: R-MMU-70286

Type: transition

Compartments: cytosol

Inferred from: [UTP + D-glucose 1-phosphate <=> pyrophosphate + UDP-glucose \(Homo sapiens\)](#)



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: [PGM1:Mg2+ isomerises G6P to G1P](#)

Followed by: [Autoglucoxylation of GYG1 complexed with GYS1-a](#), [Autoglucoxylation of GYG1 complexed with GYS1-b](#)

Autoglucoxylation of GYG1 complexed with GYS1-a ↗

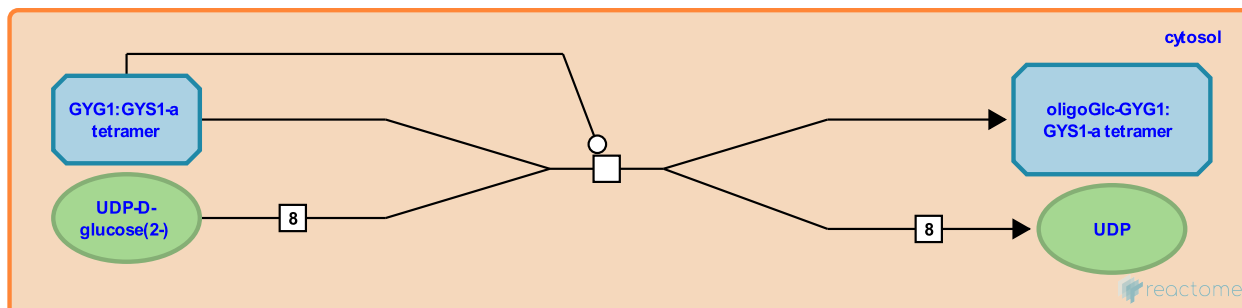
Location: Glycogen synthesis

Stable identifier: R-MMU-3322025

Type: transition

Compartments: cytosol

Inferred from: Autoglucoxylation of GYG1 complexed with GYS1-a (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: UTP + D-glucose 1-phosphate \rightleftharpoons pyrophosphate + UDP-glucose

Followed by: GYS1 catalyzes the polyglucosylation of oligoGlc-GYG1

Autogluosylation of GYG1 complexed with GYS1-b ↗

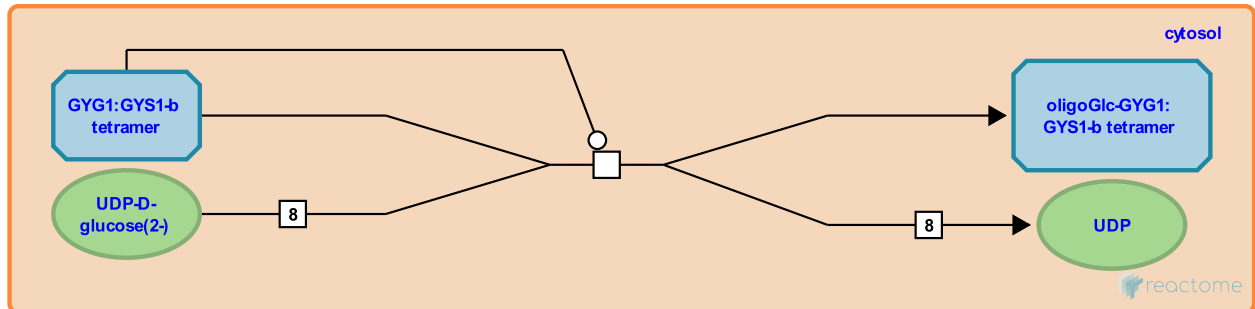
Location: Glycogen synthesis

Stable identifier: R-MMU-3322003

Type: transition

Compartments: cytosol

Inferred from: Autogluosylation of GYG1 complexed with GYS1-b (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [UTP + D-glucose 1-phosphate <=> pyrophosphate + UDP-glucose](#)

Followed by: [Phosphorylated GYS1 catalyzes the polyglucosylation of oligoGlc-GYG1](#)

GYS1 catalyzes the polyglucosylation of oligoGlc-GYG1 ↗

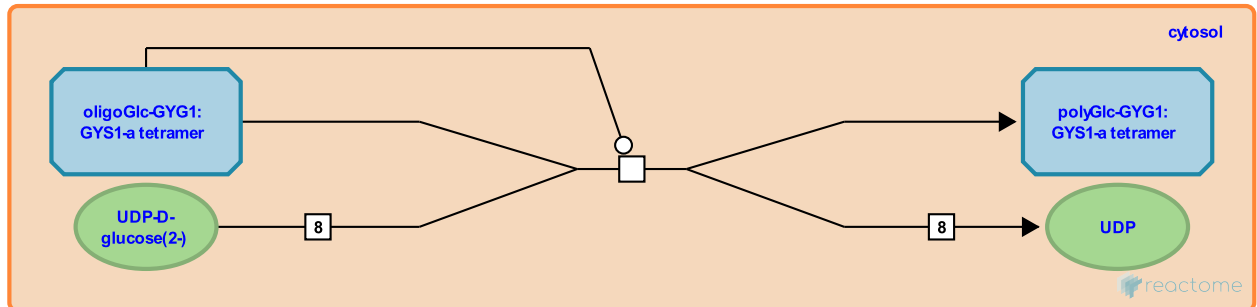
Location: [Glycogen synthesis](#)

Stable identifier: R-MMU-3322001

Type: transition

Compartments: cytosol

Inferred from: [GYS1 catalyzes the polyglucosylation of oligoGlc-GYG1 \(Homo sapiens\)](#)



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: [Autoglucoxylation of GYG1 complexed with GYS1-a](#)

Followed by: [GBE1 catalyzes branch formation in polyGlc-GYG1 complexed with GYS1-a](#)

Phosphorylated GYS1 catalyzes the polyglucosylation of oligoGlc-GYG1 ↗

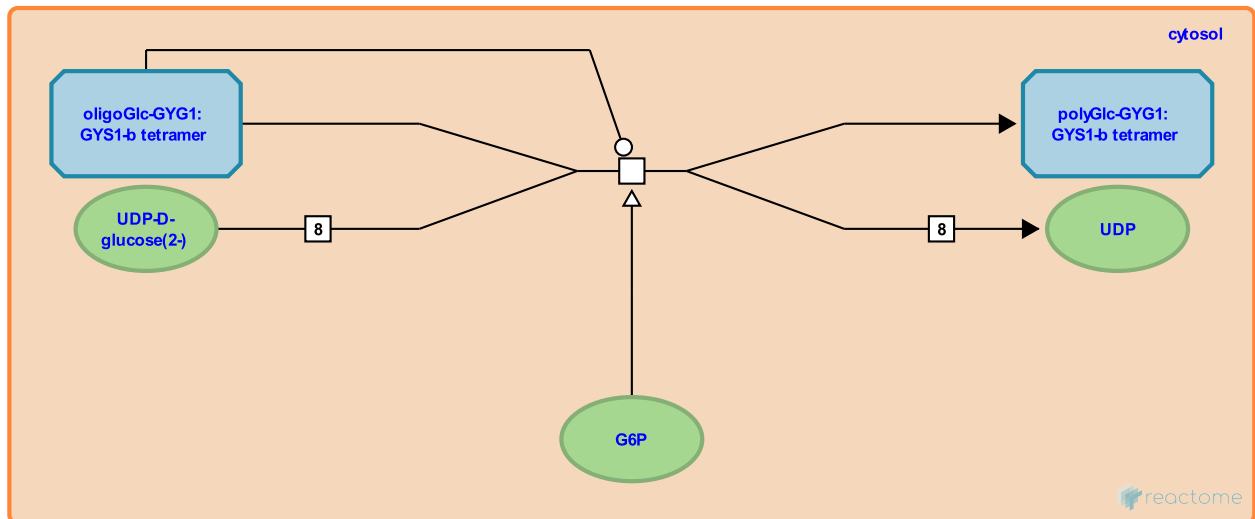
Location: [Glycogen synthesis](#)

Stable identifier: R-MMU-3322041

Type: transition

Compartments: cytosol

Inferred from: [Phosphorylated GYS1 catalyzes the polyglucosylation of oligoGlc-GYG1 \(Homo sapiens\)](#)



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: [Autoglucosylation of GYG1 complexed with GYS1-b](#)

Followed by: [GBE1 catalyzes branch formation in polyGlc-GYG1 complexed with GYS1-b](#)

GBE1 catalyzes branch formation in polyGlc-GYG1 complexed with GYS1-a [↗](#)

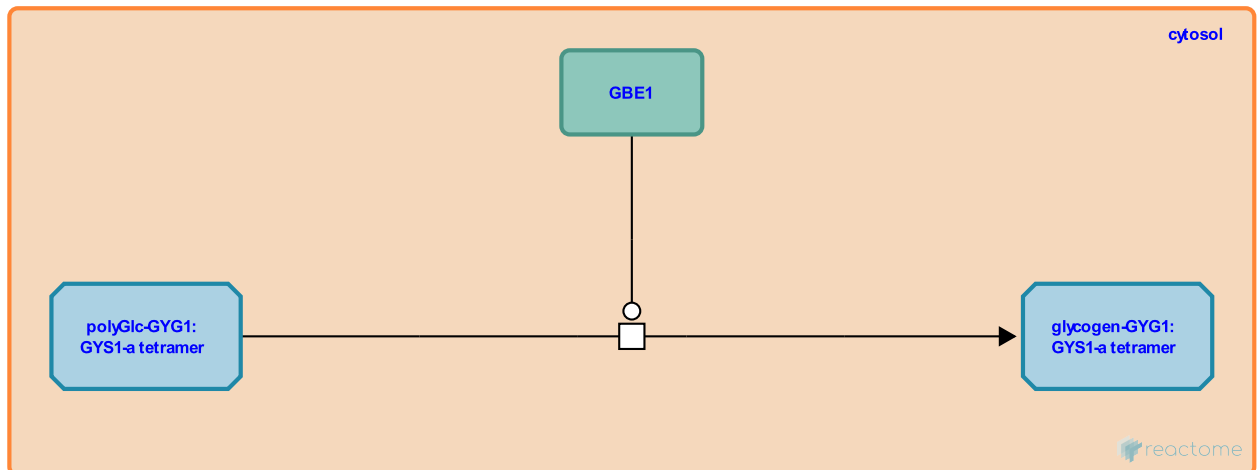
Location: [Glycogen synthesis](#)

Stable identifier: R-MMU-3322005

Type: transition

Compartments: cytosol

Inferred from: [GBE1 catalyzes branch formation in polyGlc-GYG1 complexed with GYS1-a \(Homo sapiens\)](#)



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: [GYS1 catalyzes the polyglucosylation of oligoGlc-GYG1](#)

Followed by: [PPP1R3C binds to glycogen:GYG1:GYS1](#)

GBE1 catalyzes branch formation in polyGlc-GYG1 complexed with GYS1-b ↗

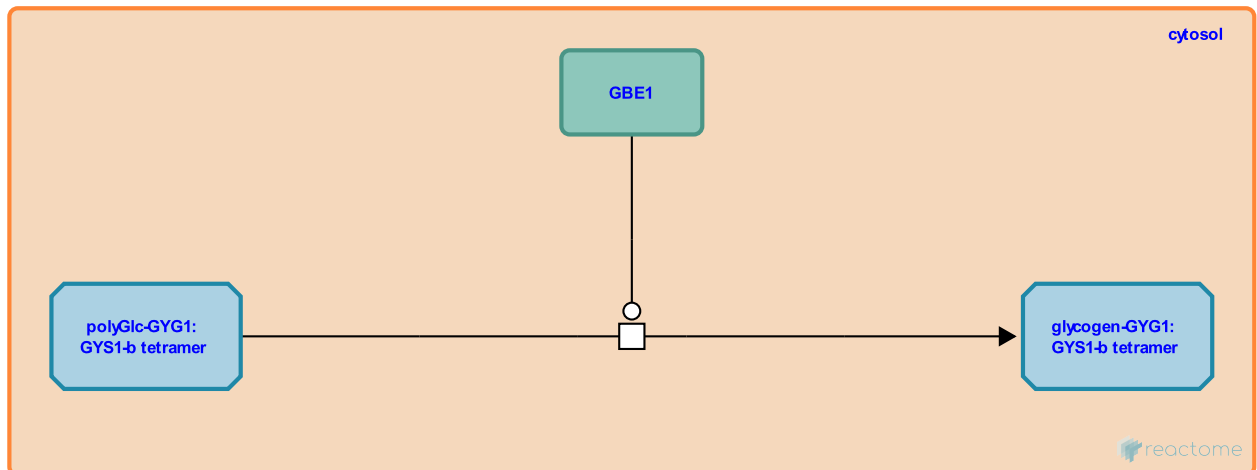
Location: [Glycogen synthesis](#)

Stable identifier: R-MMU-3322057

Type: transition

Compartments: cytosol

Inferred from: [GBE1 catalyzes branch formation in polyGlc-GYG1 complexed with GYS1-b \(Homo sapiens\)](#)



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: [Phosphorylated GYS1 catalyzes the polyglucosylation of oligoGlc-GYG1](#)

PPP1R3C binds to glycogen:GYG1:GYS1 ↗

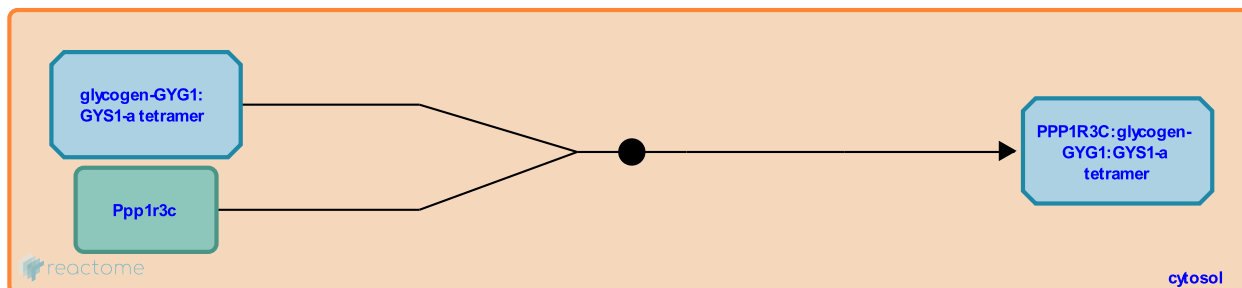
Location: [Glycogen synthesis](#)

Stable identifier: R-MMU-3781023

Type: binding

Compartments: cytosol

Inferred from: [PPP1R3C binds to glycogen:GYG1:GYS1 \(Homo sapiens\)](#)



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: [GBE1 catalyzes branch formation in polyGlc-GYG1 complexed with GYS1-a](#)

Followed by: [GYS1 catalyzes the incorporation of phosphoglucose into glycogen-GYG1](#)

GYS1 catalyzes the incorporation of phosphoglucose into glycogen-GYG1 ↗

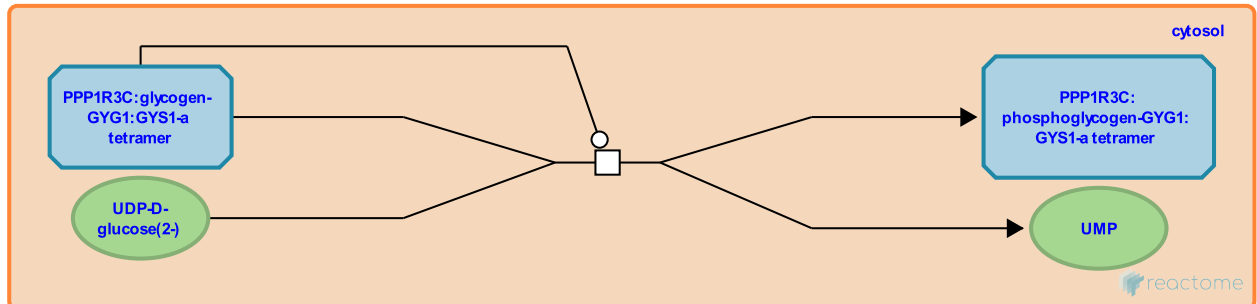
Location: [Glycogen synthesis](#)

Stable identifier: R-MMU-3781024

Type: transition

Compartments: cytosol

Inferred from: [GYS1 catalyzes the incorporation of phosphoglucose into glycogen-GYG1 \(Homo sapiens\)](#)



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: [PPP1R3C binds to glycogen:GYG1:GYS1](#)

EPM2A dimer dephosphorylates phosphoglycogen-GYG1 ↗

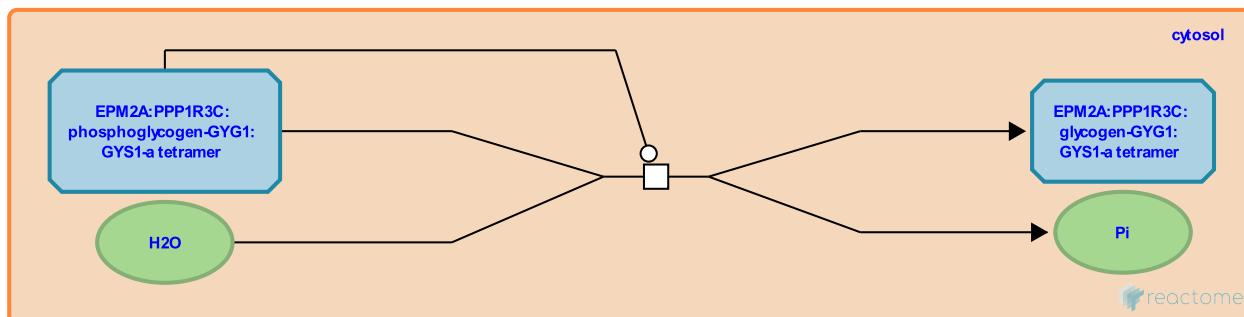
Location: [Glycogen synthesis](#)

Stable identifier: R-MMU-3781018

Type: transition

Compartments: cytosol

Inferred from: [EPM2A dimer dephosphorylates phosphoglycogen-GYG1 \(Homo sapiens\)](#)



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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