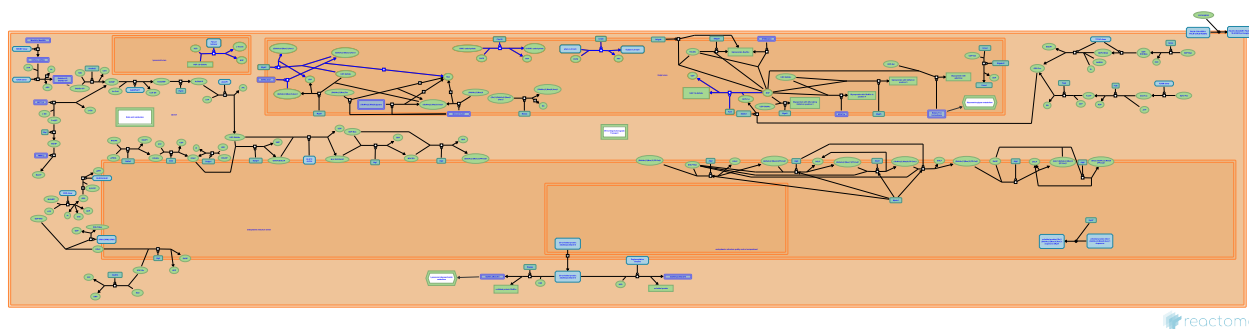


# Reactions specific to the complex N-glycan synthesis pathway



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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. [↗](#)

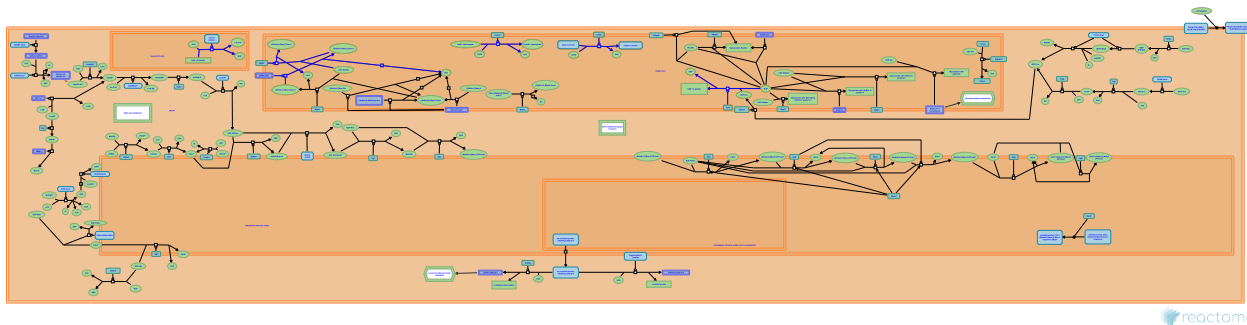
Reactome database release: 73

This document contains 1 pathway and 6 reactions ([see Table of Contents](#))

## Reactions specific to the complex N-glycan synthesis pathway ↗

**Stable identifier:** R-MMU-975578

**Inferred from:** [Reactions specific to the complex N-glycan synthesis pathway \(Homo sapiens\)](#)



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>

## Trimming of mannoses on the alpha1,6 arm by MAN2A1 ↗

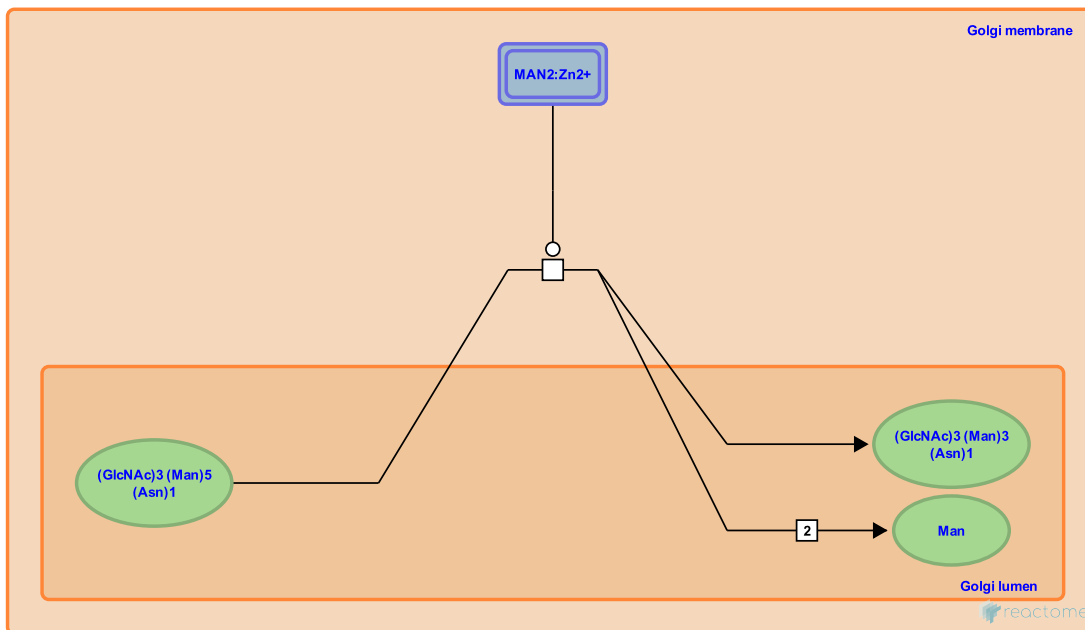
**Location:** Reactions specific to the complex N-glycan synthesis pathway

**Stable identifier:** R-MMU-975814

**Type:** transition

**Compartments:** Golgi membrane, Golgi lumen

**Inferred from:** [Trimming of mannoses on the alpha1,6 arm by MAN2A1 \(Homo sapiens\)](#)



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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**Followed by:** [Addition of a GlcNAc on the alpha 1,4 branch by MGAT2](#)

## Addition of a GlcNAc on the alpha 1,4 branch by MGAT2 ↗

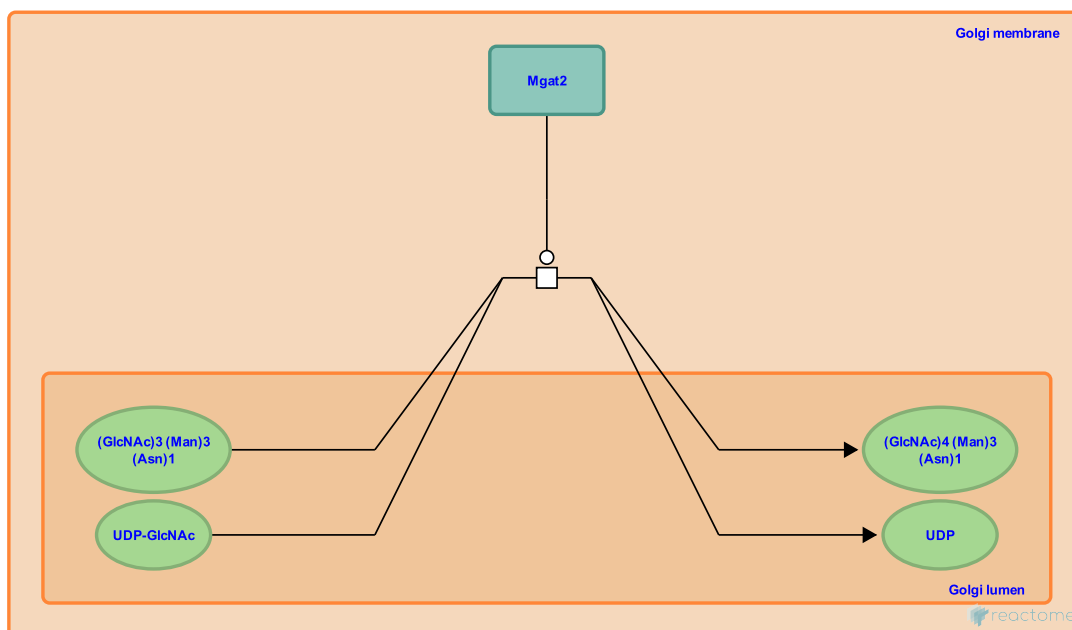
**Location:** Reactions specific to the complex N-glycan synthesis pathway

**Stable identifier:** R-MMU-975829

**Type:** transition

**Compartments:** Golgi membrane, Golgi lumen

**Inferred from:** Addition of a GlcNAc on the alpha 1,4 branch by MGAT2 (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:** [Trimming of mannoses on the alpha1,6 arm by MAN2A1](#)

## FUT8 transfers fucosyl group from GDP-Fuc to GlcNAc of NGP ↗

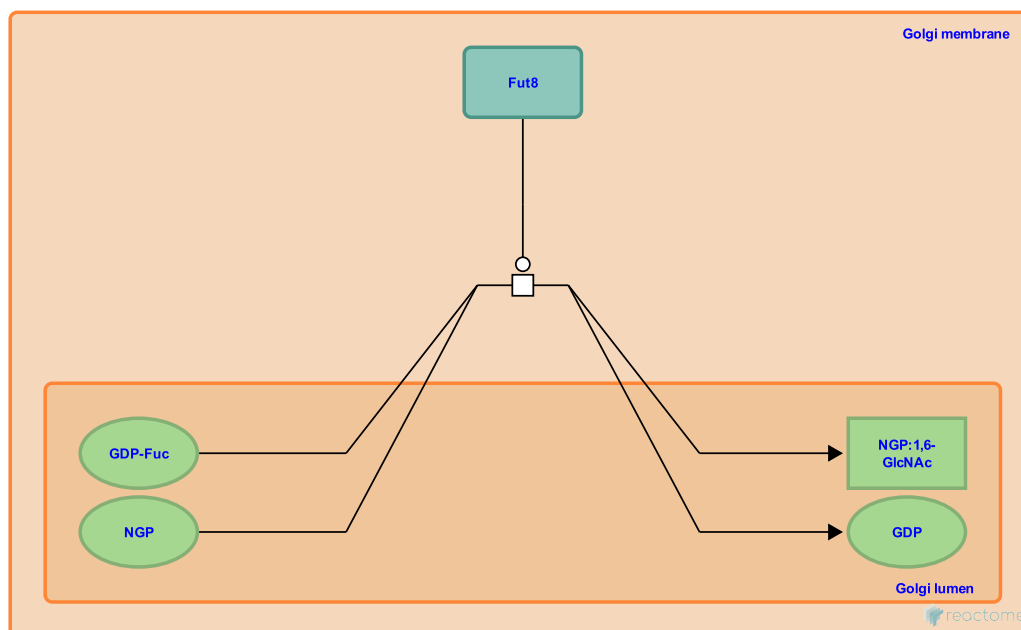
**Location:** Reactions specific to the complex N-glycan synthesis pathway

**Stable identifier:** R-MMU-1028788

**Type:** transition

**Compartments:** Golgi membrane, Golgi lumen

**Inferred from:** FUT8 transfers fucosyl group from GDP-Fuc to GlcNAc of NGP (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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**Followed by:** [FUCA1 hydrolyses NGP:1,6-GlcNAc](#)

## FUCA1 hydrolyses NGP:1,6-GlcNAc ↗

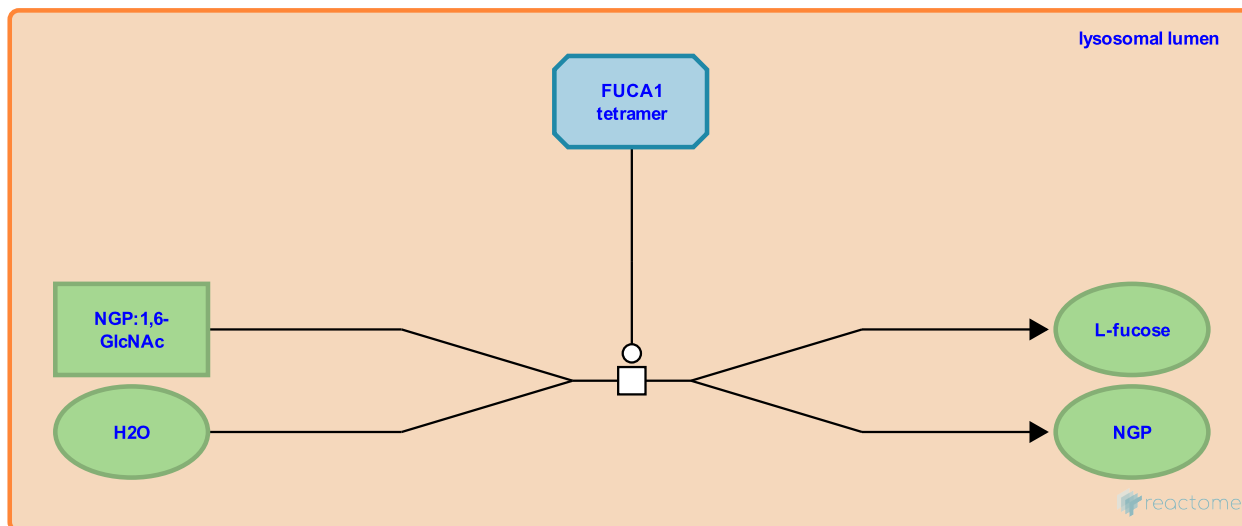
**Location:** Reactions specific to the complex N-glycan synthesis pathway

**Stable identifier:** R-MMU-5693807

**Type:** transition

**Compartments:** lysosomal lumen

**Inferred from:** [FUCA1 hydrolyses NGP:1,6-GlcNAc \(Homo sapiens\)](#)



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:** [FUT8 transfers fucosyl group from GDP-Fuc to GlcNAc of NGP](#)

## CHST8 transfers SO4(2-) from PAPS to glyco-Lutropin ↗

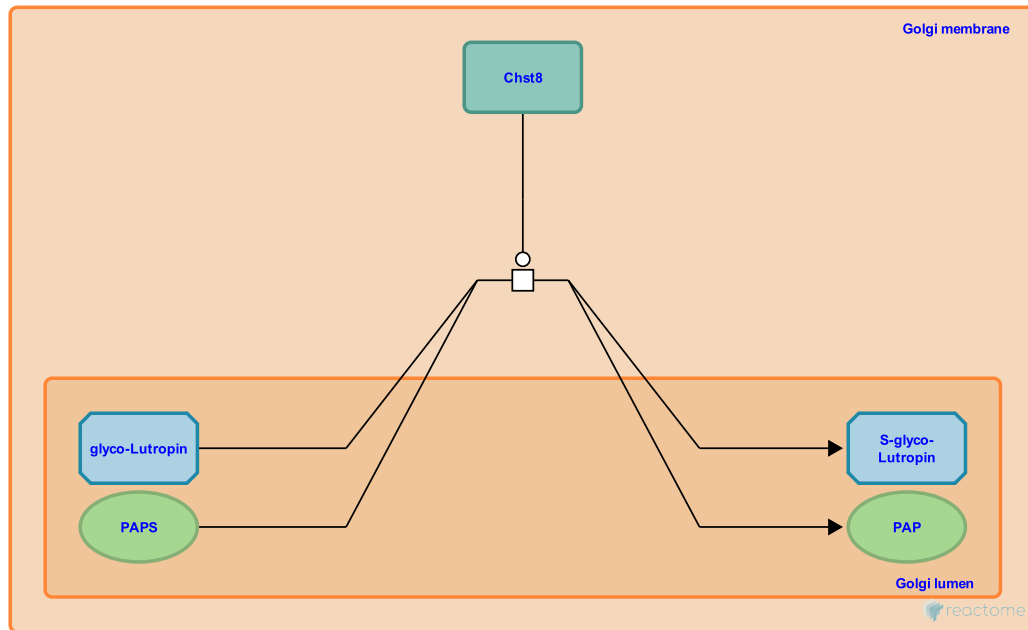
**Location:** Reactions specific to the complex N-glycan synthesis pathway

**Stable identifier:** R-MMU-6786034

**Type:** transition

**Compartments:** Golgi membrane, Golgi lumen

**Inferred from:** CHST8 transfers SO4(2-) from PAPS to glyco-Lutropin (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>



## CHST10 transfers SO4(2-) from PAPS to GlcA-LacN on NCAM1 ↗

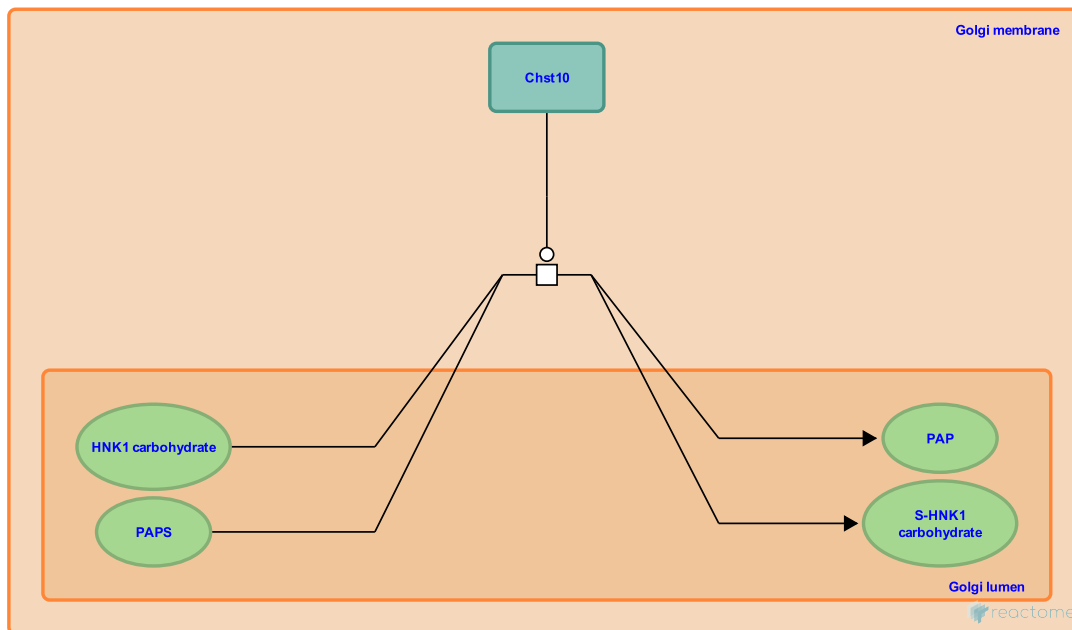
**Location:** Reactions specific to the complex N-glycan synthesis pathway

**Stable identifier:** R-MMU-6786048

**Type:** transition

**Compartments:** Golgi membrane, Golgi lumen

**Inferred from:** CHST10 transfers SO4(2-) from PAPS to GlcA-LacN on NCAM1 (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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