

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.

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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: 75

This document contains 1 pathway and 8 reactions ([see Table of Contents](#))

B3GALTs transfer Gal to GlcNAc- β 1,3-Gal-R to form Type 1 chain ↗

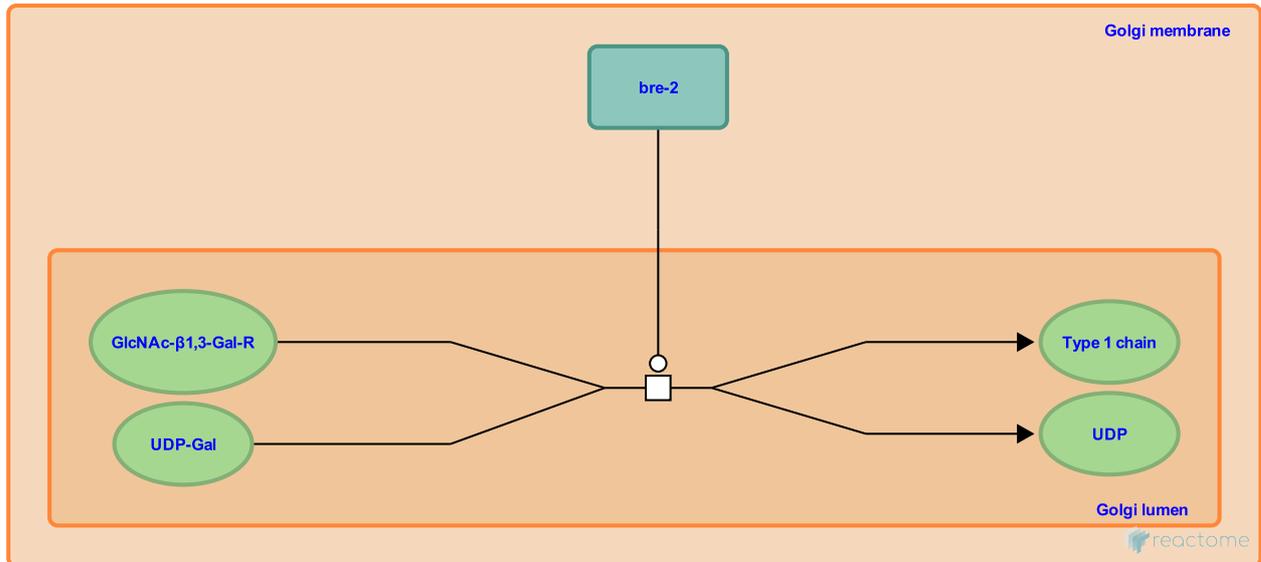
Location: [Lewis blood group biosynthesis](#)

Stable identifier: R-CEL-9603989

Type: transition

Compartments: Golgi lumen, Golgi membrane

Inferred from: [B3GALTs transfer Gal to GlcNAc- \$\beta\$ 1,3-Gal-R to form Type 1 chain \(Homo sapiens\)](#)



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: [FUT3 transfers Fuc to Type 1 chains to form LeA](#)

FUT3 transfers Fuc to Type 1 chains to form LeA ↗

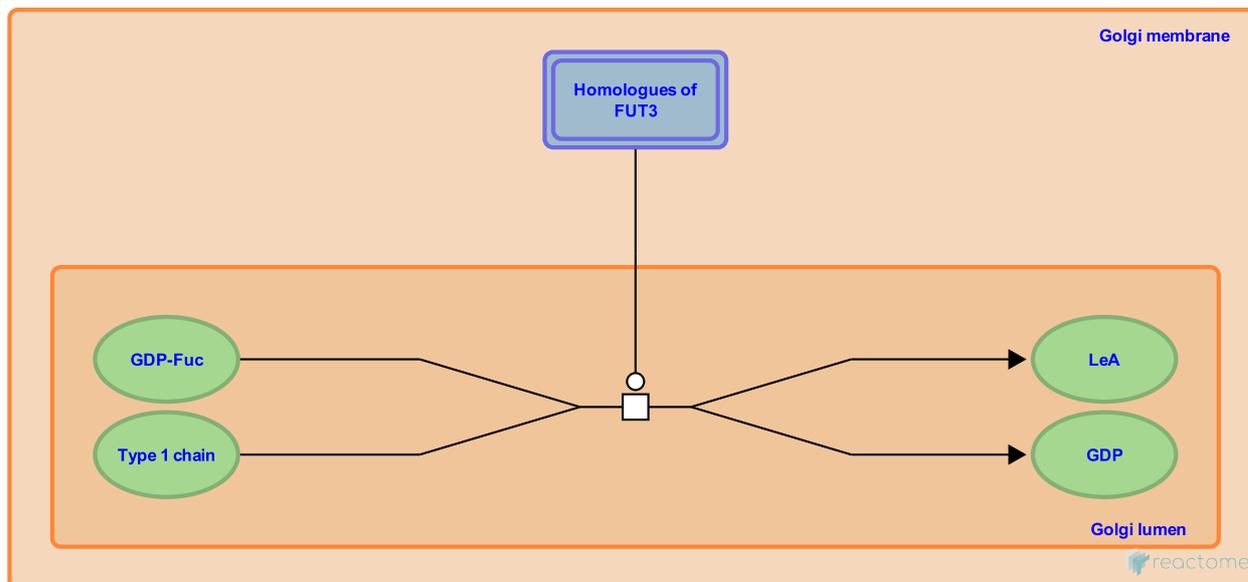
Location: [Lewis blood group biosynthesis](#)

Stable identifier: R-CEL-9603986

Type: transition

Compartments: Golgi lumen, Golgi membrane

Inferred from: [FUT3 transfers Fuc to Type 1 chains to form LeA \(Homo sapiens\)](#)



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Preceded by: [B3GALTs transfer Gal to GlcNAc- \$\beta\$ 1,3-Gal-R to form Type 1 chain](#)

FUT2 transfers Fuc to LeA to form LeB ↗

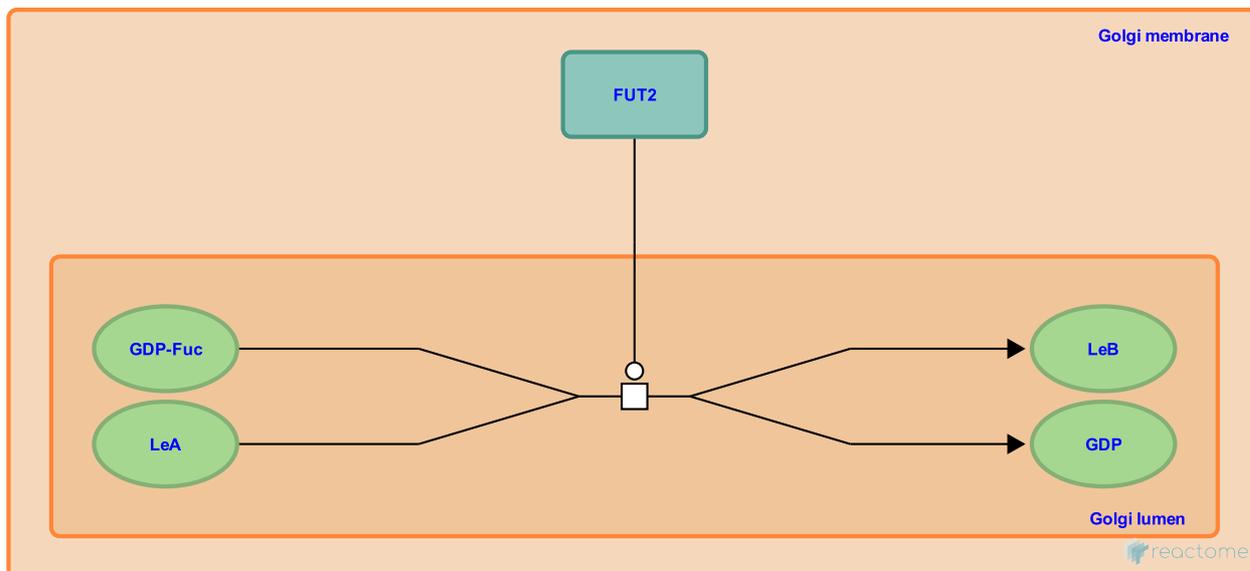
Location: [Lewis blood group biosynthesis](#)

Stable identifier: R-CEL-9603982

Type: transition

Compartments: Golgi lumen, Golgi membrane

Inferred from: [FUT2 transfers Fuc to LeA to form LeB \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

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FUT4,5,9,(10,11) transfer Fuc to Type 2 chains to form LeX ↗

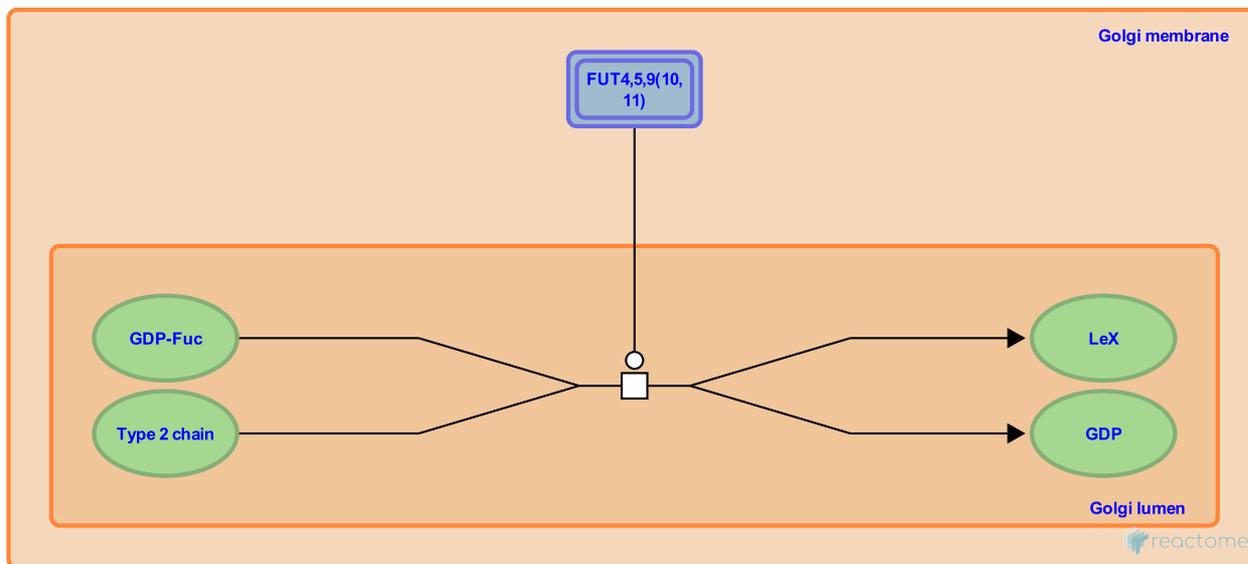
Location: Lewis blood group biosynthesis

Stable identifier: R-CEL-9603984

Type: transition

Compartments: Golgi lumen, Golgi membrane

Inferred from: FUT4,5,9,(10,11) transfer Fuc to Type 2 chains to form LeX (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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FUT2 transfers Fuc to LeX to form LeY ↗

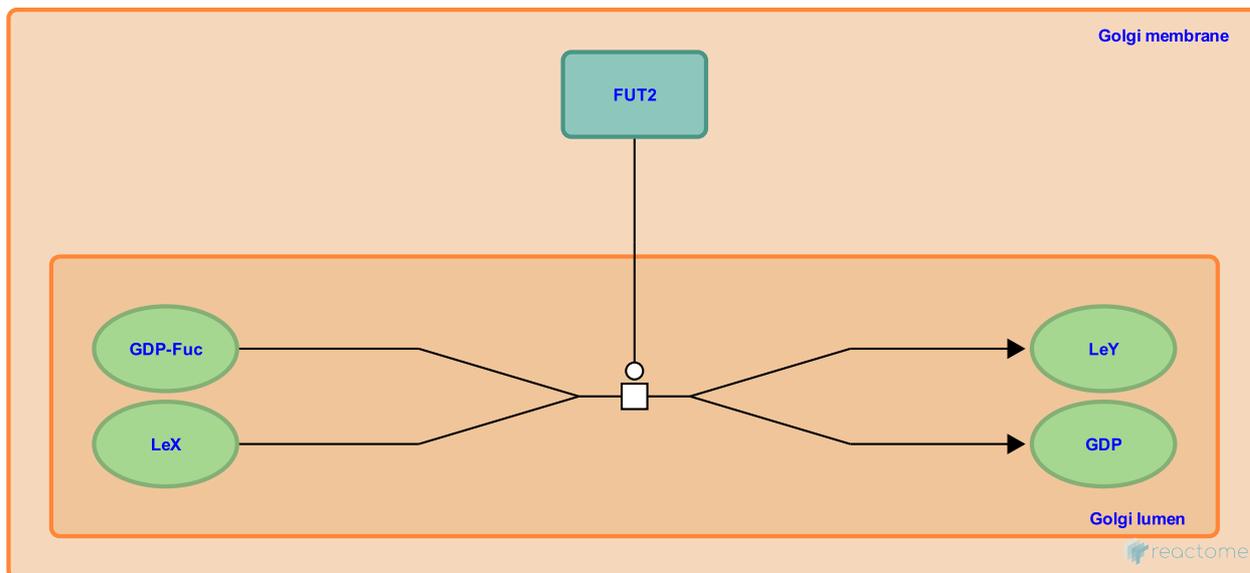
Location: [Lewis blood group biosynthesis](#)

Stable identifier: R-CEL-9603983

Type: transition

Compartments: Golgi lumen, Golgi membrane

Inferred from: [FUT2 transfers Fuc to LeX to form LeY \(Homo sapiens\)](#)



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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FUT3 transfers Fuc to Type 1 MSGG to form sLeA ↗

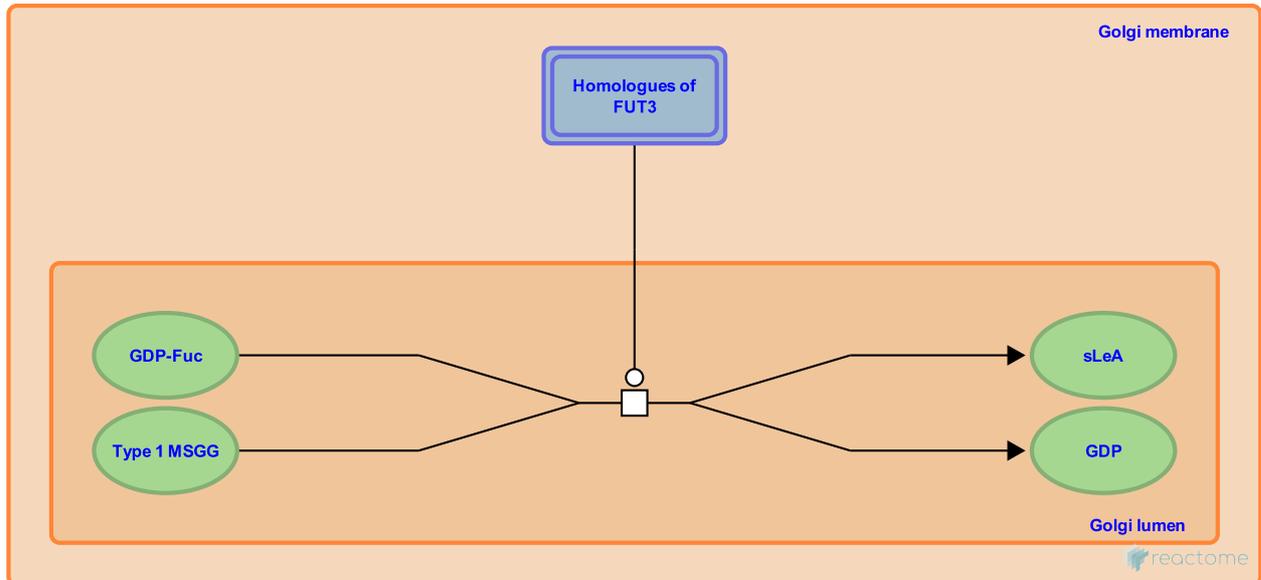
Location: [Lewis blood group biosynthesis](#)

Stable identifier: R-CEL-9605609

Type: transition

Compartments: Golgi lumen, Golgi membrane

Inferred from: [FUT3 transfers Fuc to Type 1 MSGG to form sLeA \(Homo sapiens\)](#)



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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FUT3 transfers Fuc to Type 1 DSGG to form dsLeA ↗

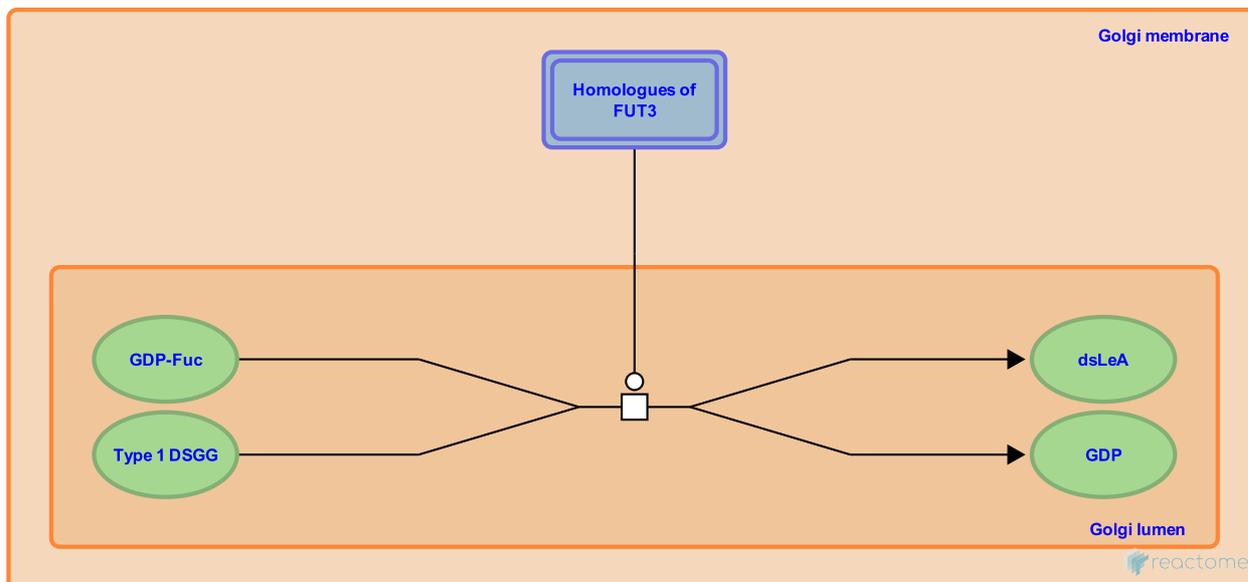
Location: [Lewis blood group biosynthesis](#)

Stable identifier: R-CEL-9605644

Type: transition

Compartments: Golgi lumen, Golgi membrane

Inferred from: [FUT3 transfers Fuc to Type 1 DSGG to form dsLeA \(Homo sapiens\)](#)



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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FUT3,5,6,7 transfers Fuc to Type 2 MSGG to form sLeX ↗

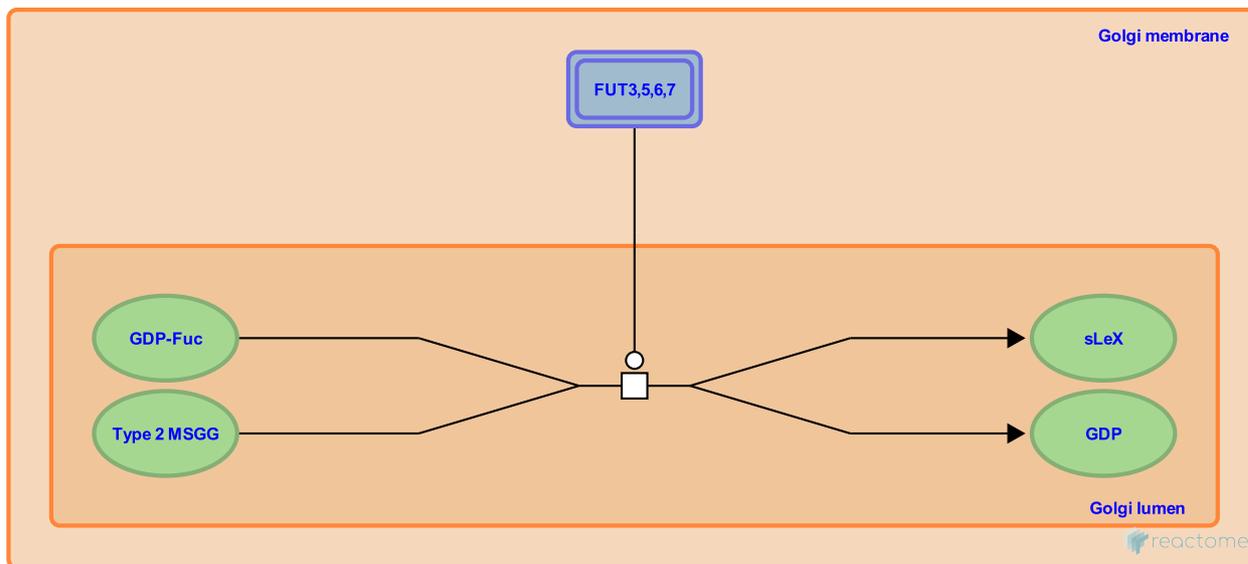
Location: Lewis blood group biosynthesis

Stable identifier: R-CEL-9605682

Type: transition

Compartments: Golgi lumen, Golgi membrane

Inferred from: FUT3,5,6,7 transfers Fuc to Type 2 MSGG to form sLeX (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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