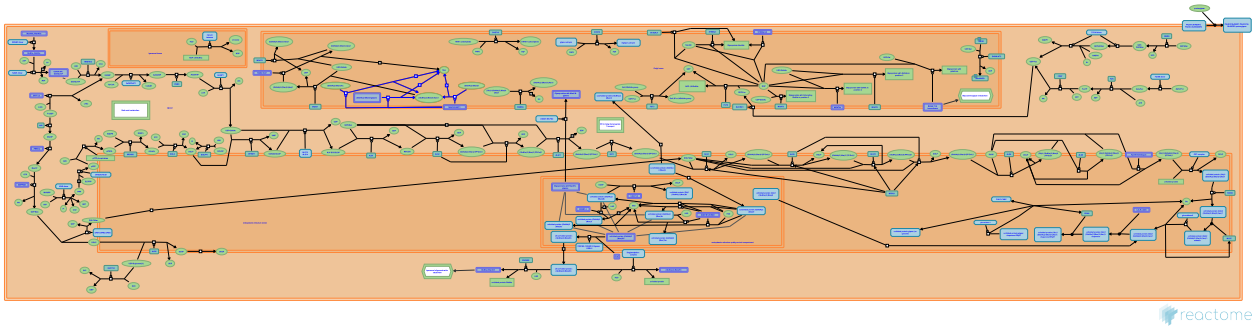
Progressive trimming of alpha-1,2-linked mannose residues from Man9/8/7GlcNAc2 to produce Man5GlcNAc2



Dall'Olio, GM., Gagneux, P., Jassal, B.

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07/05/2024

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. ↗

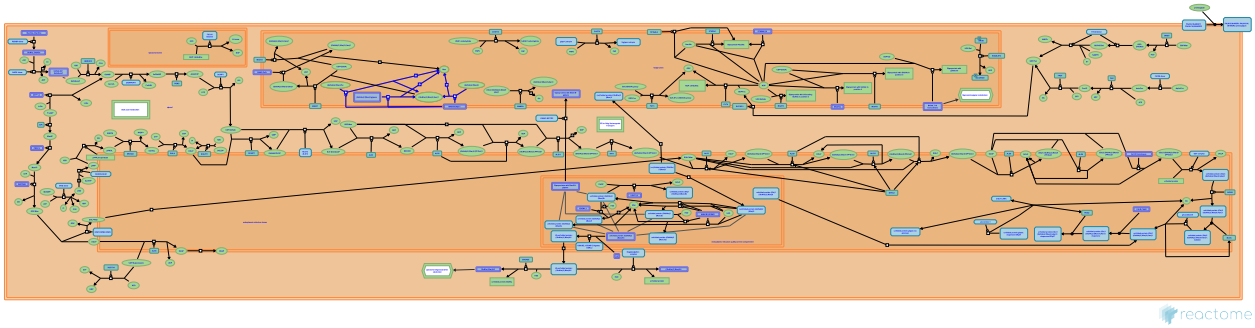
Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

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. ↗

Progressive trimming of alpha-1,2-linked mannose residues from Man9/8/7GlcNAc2 to produce Man5GlcNAc2 ↗

Stable identifier: R-HSA-964827



In the cis-Golgi, Man7, Man8 or Man9 N-glycans are progressively trimmed to Man5 N-glycans. The reaction can be catalyzed by one of three known mannosidases, expressed in different tissues and with slightly different affinity. These enzymes trim the mannoses in a different order (Tremblay and Herscovics, 2000), but produce the same output with 5 mannoses.
A small confusion on the nomenclature of these genes coding for these enzymes is present in the literature: the standard HGNC symbols are MAN1A1, MAN1A2, MAN1C1, but MAN1A2 is also referred to as MAN1B in certain publications, while MAN1B1 is the enzyme acting in the ERQC compartment on unfolded glycoproteins. Moreover, the names do not correspond to a preference of these enzymes for which of the three mannose branches these trim first.

Literature references

Herscovics, A., Tremblay, LO. (2000). Characterization of a cDNA encoding a novel human Golgi alpha 1, 2-mannosidase (IC) involved in N-glycan biosynthesis. *J Biol Chem, 275*, 31655-60. ↗

Editions

2009-11-10	Authored	Dall'Olio, GM.
2010-09-17	Edited	Jassal, B.
2010-11-18	Reviewed	Gagneux, P.

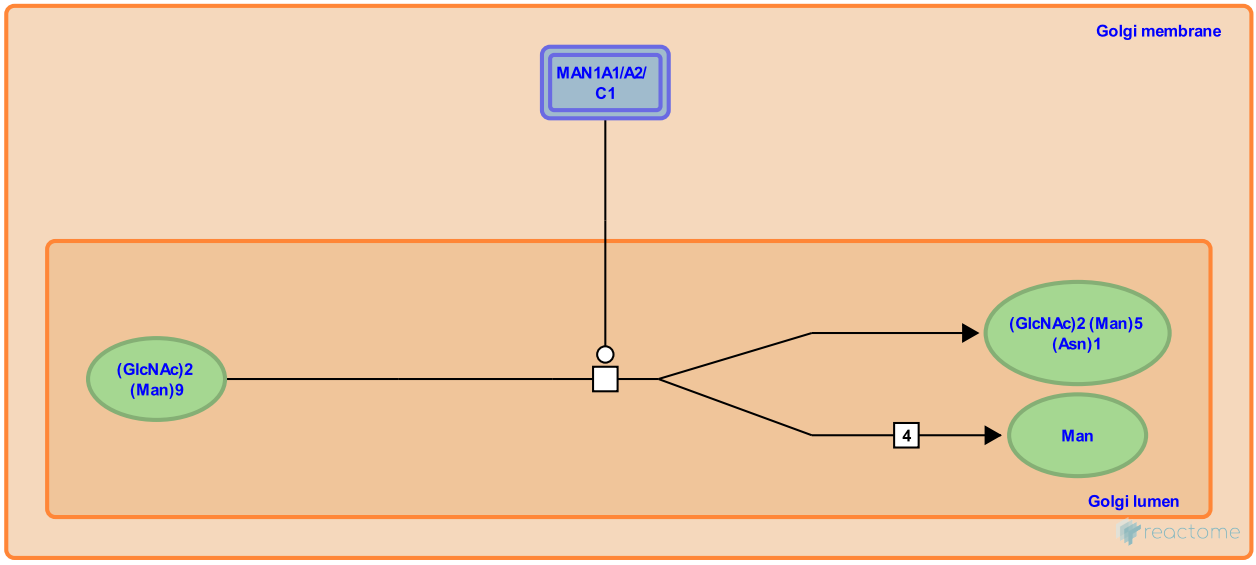
Progressive trimming of alpha-1,2-linked mannose residues from Man9GlcNAc2 to produce Man5GlcNAc2 ↗

Location: Progressive trimming of alpha-1,2-linked mannose residues from Man9/8/7GlcNAc2 to produce Man5GlcNAc2

Stable identifier: R-HSA-964737

Type: transition

Compartments: Golgi lumen, Golgi membrane



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Editions

2009-11-10	Authored	Dall'Olio, GM.
2010-09-17	Edited	Jassal, B.
2010-11-18	Reviewed	Gagneux, P.

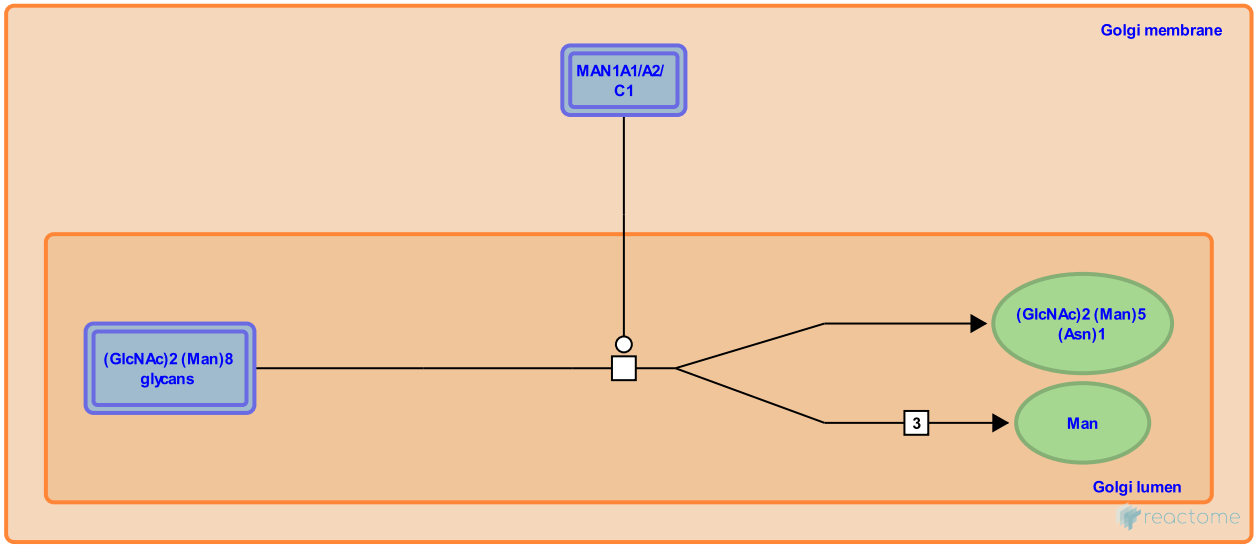
Progressive trimming of alpha-1,2-linked mannose residues from Man8GlcNAc2 to produce Man5GlcNAc2 ↗

Location: Progressive trimming of alpha-1,2-linked mannose residues from Man9/8/7GlcNAc2 to produce Man5GlcNAc2

Stable identifier: R-HSA-964825

Type: transition

Compartments: Golgi lumen, Golgi membrane



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Editions

2009-11-10	Authored	Dall'Olio, GM.
2010-09-17	Edited	Jassal, B.
2010-11-18	Reviewed	Gagneux, P.

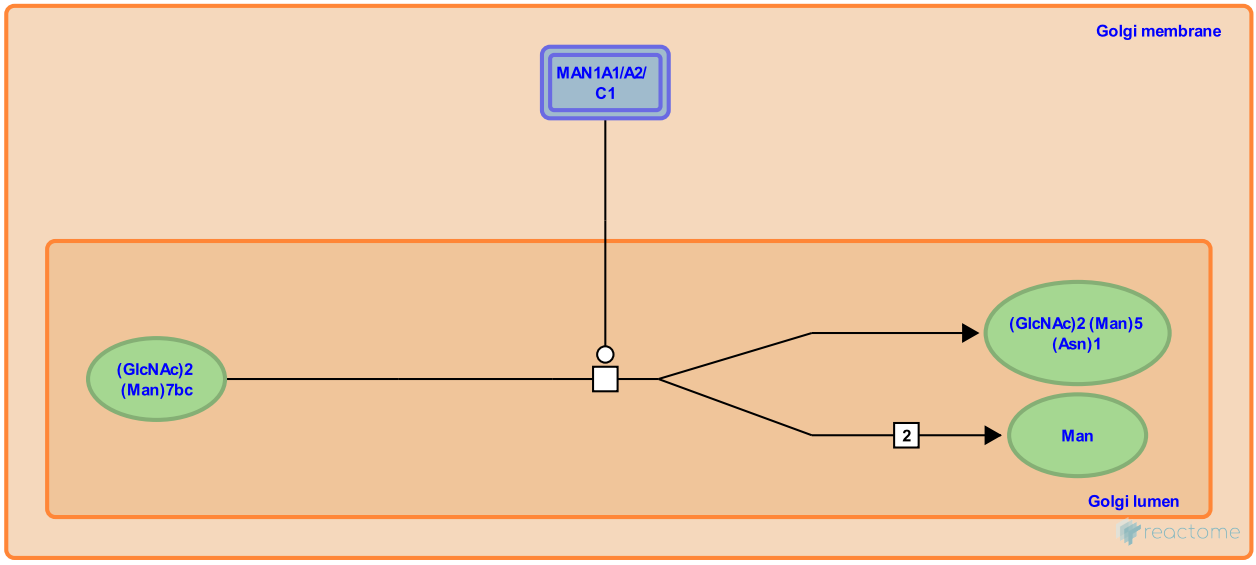
Progressive trimming of alpha-1,2-linked mannose residues from Man7GlcNAc2 to produce Man5GlcNAc2 ↗

Location: Progressive trimming of alpha-1,2-linked mannose residues from Man9/8/7GlcNAc2 to produce Man5GlcNAc2

Stable identifier: R-HSA-964830

Type: transition

Compartments: Golgi lumen, Golgi membrane



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