B4GALNT2 transfers GalNAc to Type 2 MSGG to form Sda

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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.

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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. ↗

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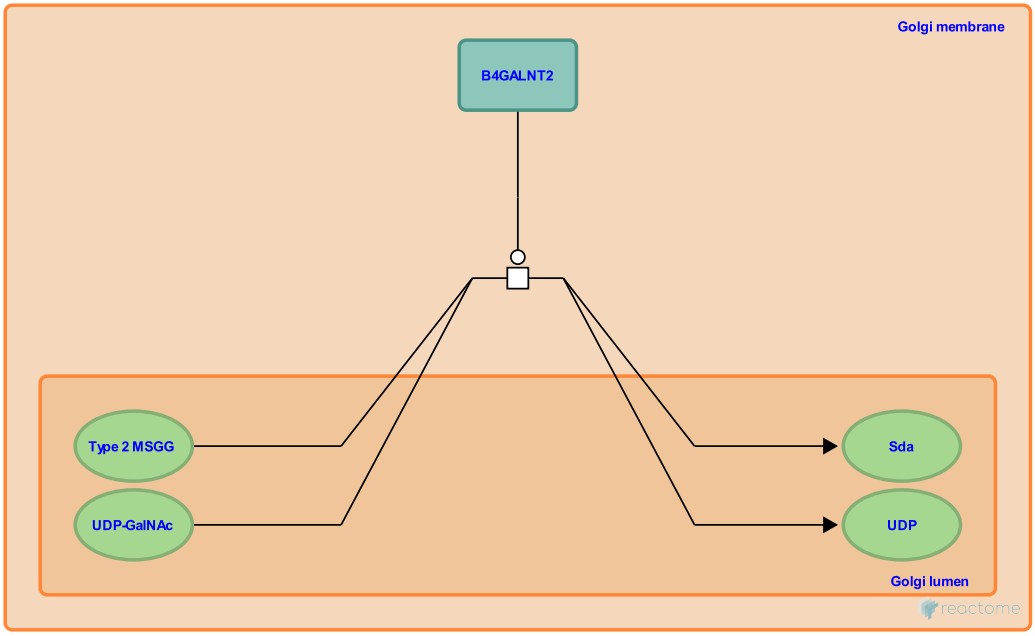
Stable identifier: R-HSA-9605700

Type: transition

Compartments: Golgi lumen, Golgi membrane



Beta-1,4 N-acetylgalactosaminyltransferase 2 (B4GALNT2), resident on the Golgi membrane, mediates the formation of the Sda antigen through the addition of an N-acetylgalactosamine (GalNAc) residue via a β1,4-linkage to the sub-terminal galactose residue substituted with an α2,3-linked sialic acid residue (Montiel et al. 2003, Lo Presti et al. 2003). The Sda antigen is a carbohydrate determinant expressed on erythrocytes and secretions of the vast majority of Caucasians and ethnic groups and its expression has an impact on the physiology and the pathology of several biological systems (Dall'Olio et al. 2014). In normal colon, B4GALNT2 levels are high and control the biosynthesis of Sda while at the same time inhibiting the formation of sialyl-Lewis X antigen (sLeX), involved in metastasis (Groux-Degroote et al. 2014).

Literature references

Cabuy, E., Dall'Olio, F., Chiricolo, M., Lo Presti, L. (2003). Molecular cloning of the human beta1,4 N-acetylgalactosaminyltransferase responsible for the biosynthesis of the Sd(a) histo-blood group antigen: the sequence predicts a very long cytoplasmic domain. *J. Biochem., 134*, 675-82. ↗

Delannoy, P., Krzewinski-Recchi, MA., Montiel, MD., Harduin-Lepers, A. (2003). Molecular cloning, gene organization and expression of the human UDP-GalNAc:Neu5Acalpha2-3Galbeta-R beta1,4-N-acetylgalactosaminyltransferase responsible for the biosynthesis of the blood group Sda/Cad antigen: evidence for an unusual extended cytoplasmic domain. *Biochem. J., 373*, 369-79. ↗

Dall'Olio, F., Chiricolo, M., Delannoy, P., Wavelet, C., Malagolini, N., Krzewinski-Recchi, MA. et al. (2014). B4GALNT2 gene expression controls the biosynthesis of Sda and sialyl Lewis X antigens in healthy and cancer human gastrointestinal tract. *Int. J. Biochem. Cell Biol., 53*, 442-9. ↗

Editions

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