

# **B4GAT1:GYLTL1B transfers GlcA from UDP-GlcA to Xyl-GlcA**

Hansen, L., Jassal, B., Joshi, HJ.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://reactome.org/licenses/).

19/05/2024

## 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. [↗](#)

Reactome database release: 88

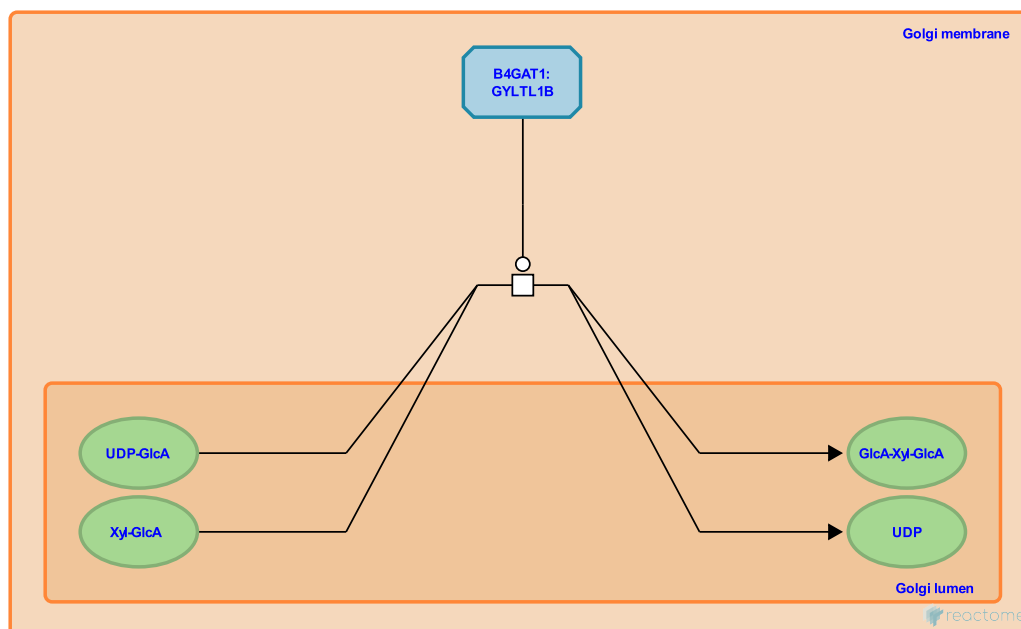
This document contains 1 reaction ([see Table of Contents](#))

## B4GAT1:GYLTL1B transfers GlcA from UDP-GlcA to Xyl-GlcA ↗

**Stable identifier:** R-HSA-5617143

**Type:** transition

**Compartments:** Golgi lumen, Golgi membrane



Glycosyltransferase-like protein LARGE2 (GYLTL1B) is a bifunctional glycosyltransferases with both xylosyltransferase and beta-1,3-glucuronyltransferase activities which can form polymeric Xyl-GlcA repeats. GYLTL1B is involved in the physiological function of alpha-dystroglycan (DAG1) which plays a key role in skeletal muscle function and regeneration (Inamori et al. 2013, Wells 2013, Inamori et al. 2014).

### Literature references

Inamori, K., Yoshida-Moriguchi, T., Zhu, Z., Willer, T., Anderson, ME., Hara, Y. et al. (2013). Xylosyl- and glucuronyltransferase functions of LARGE in  $\alpha$ -dystroglycan modification are conserved in LARGE2. *Glycobiology*, 23, 295-302. ↗

Inamori, K., Moore, SA., Bönnemann, CG., Clarke, NF., Willer, T., Guicheney, P. et al. (2014). Endogenous glucuronyltransferase activity of LARGE or LARGE2 required for functional modification of  $\alpha$ -dystroglycan in cells and tissues. *J. Biol. Chem.*, 289, 28138-48. ↗

Wells, L. (2013). The o-mannosylation pathway: glycosyltransferases and proteins implicated in congenital muscular dystrophy. *J. Biol. Chem.*, 288, 6930-5. ↗

### Editions

2014-07-31	Authored, Edited	Jassal, B.
2015-12-18	Reviewed	Joshi, HJ., Hansen, L.