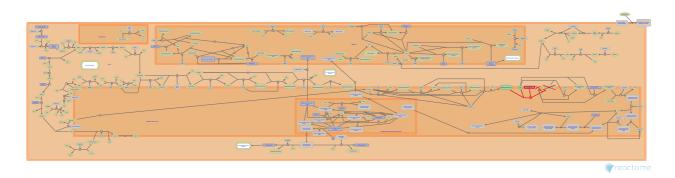


Defective ALG6 causes CDG-1c



Belaya, K., Jassal, B.

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 CC BY 4.0
License. For more information see our License.

This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the Reactome-Textbook.

30/04/2024

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 data-base: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968.

Reactome database release: 88

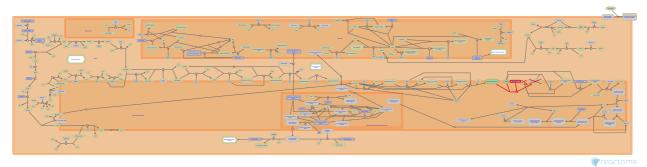
This document contains 1 pathway and 1 reaction (see Table of Contents)

https://reactome.org Page 2

Defective ALG6 causes CDG-1c

Stable identifier: R-HSA-4724289

Diseases: congenital disorder of glycosylation type I



Dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase (ALG6) normally adds the first glucose moiety to the lipid-linked oligosaccharide precursor (LLO aka N-glycan precursor) which is required for subsequent N-glycosylation of proteins (Imbach et al. 1999). Defects in ALG6 can cause congenital disorder of glycosylation 1c (ALG6-CDG, CDG-1c; MIM:603147), a multisystem disorder characterised by under-glycosylated serum glycoproteins (Imbach et al. 1999, Imbach et al. 2000, Westphal et al. 2000, Sun et al. 2005). ALG6 deficiency is accompanied by an accumulation of the N-glycan precursor (GlcNAc)2 (Man)9 (PP-Dol)1 and is the second most common CDG disease subtype after PMM2-CDG (CDG-1a) (Imbach et al. 1999). CDG type 1 diseases result in a wide variety of clinical features, such as defects in the nervous system development, psychomotor retardation, dysmorphic features, hypotonia, coagulation disorders, and immunodeficiency.

Literature references

Hennet, T., Wevers, RA., Burda, P., Berger, EG., Imbach, T., Aebi, M. et al. (1999). A mutation in the human ortholog of the Saccharomyces cerevisiae ALG6 gene causes carbohydrate-deficient glycoprotein syndrome type-Ic. *Proc Natl Acad Sci U S A*, 96, 6982-7.

7

Thomas, JA., Freeze, HH., Eklund, EA., Sun, L., Van Hove, JL. (2005). Clinical and molecular characterization of the first adult congenital disorder of glycosylation (CDG) type Ic patient. *Am J Med Genet A*, 137, 22-6. *¬*

Schenk, B., Berger, EG., Schollen, E., Grünewald, S., Hennet, T., Imbach, T. et al. (2000). Multi-allelic origin of congenital disorder of glycosylation (CDG)-Ic. *Hum. Genet.*, 106, 538-45.

Editions

2013-10-23	Authored, Edited	Jassal, B.
2014-10-31	Reviewed	Belaya, K.

Defective ALG6 does not add glucose to the N-glycan precursor

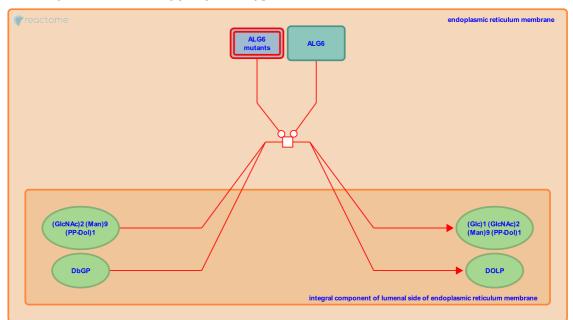
Location: Defective ALG6 causes CDG-1c

Stable identifier: R-HSA-4724291

Type: transition

Compartments: endoplasmic reticulum membrane, integral component of lumenal side of endoplasmic reticulum membrane

Diseases: congenital disorder of glycosylation type I



Dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase (ALG6) normally adds the first glucose moiety to the lipid-linked oligosaccharide precursor (LLO aka N-glycan precursor) which is required for subsequent N-glycosylation of proteins (Imbach et al. 1999). Defects in ALG6 can cause congenital disorder of glycosylation 1c (ALG6-CDG, CDG-1c; MIM:603147), a multisystem disorder characterised by under-glycosylated serum glycoproteins (Imbach et al. 1999, Imbach et al. 2000, Westphal et al. 2000, Sun et al. 2005). ALG6 deficiency is accompanied by an accumulation of the N-glycan precursor (GlcNAc)2 (Man)9 (PP-Dol)1 (Imbach et al. 1999). CDG type 1 diseases result in a wide variety of clinical features, such as defects in the nervous system development, psychomotor retardation, dysmorphic features, hypotonia, coagulation disorders, and immunodeficiency. Mutations that can cause ALG6-CDG are A333V and S478P. The A333V mutation is the most common mutation seen in ALG6-CDG patients. These mutations result in altered activity of ALG6 but don't completely abolish its activity (Imbach et al. 1999, Imbach et al. 2000, Dercksen et al. 2013). A c.257+5G>A splice site mutation (not shown here) that causes exon 3 skipping leads to a nonfunctional protein (Imbach et al. 2000, Westphal et al. 2000). Two more mutations can cause the build up of the N-glycan precursor (GlcNAc)2 (Man)9 (PP-Dol)1; a three bp deletion (897-899delAAT) in exon 9 and an intronic

mutation (680+2T>G) in intron 7 (neither shown here). Transduction of patient fibroblasts with a lentivirus carrying wildtype hALG6 improved the biochemical phenotype of the cells, confirming that these two mutations are disease-causing (Sun et al. 2005).

Literature references

Hennet, T., Wevers, RA., Burda, P., Berger, EG., Imbach, T., Aebi, M. et al. (1999). A mutation in the human ortholog of the Saccharomyces cerevisiae ALG6 gene causes carbohydrate-deficient glycoprotein syndrome type-Ic. *Proc Natl Acad Sci U S A*, 96, 6982-7.

Schuman, HC., Matthijs, G., Vorster, BC., Mienie, LJ., Lippert, MM., Dercksen, M. et al. (2013). ALG6-CDG in South Africa: Genotype-Phenotype Description of Five Novel Patients. *JIMD Rep, 8*, 17-23.

Thomas, JA., Freeze, HH., Eklund, EA., Sun, L., Van Hove, JL. (2005). Clinical and molecular characterization of the first adult congenital disorder of glycosylation (CDG) type Ic patient. *Am J Med Genet A*, 137, 22-6.

Schenk, B., Berger, EG., Schollen, E., Grünewald, S., Hennet, T., Imbach, T. et al. (2000). Multi-allelic origin of congenital disorder of glycosylation (CDG)-Ic. *Hum. Genet.*, 106, 538-45.

Westphal, V., Schottstädt, C., Freeze, HH., Marquardt, T. (2000). Analysis of multiple mutations in the hALG6 gene in a patient with congenital disorder of glycosylation Ic. *Mol. Genet. Metab.*, 70, 219-23.

Editions

2013-10-23	Authored, Edited	Jassal, B.
2014-10-31	Reviewed	Belaya, K.

Table of Contents

Introduction	1
Defective ALG6 causes CDG-1c	2
$oldsymbol{\mathcal{H}}$ Defective ALG6 does not add glucose to the N-glycan precursor	3
Table of Contents	5