UGGT1,2 transfers glucose from DbGP to (un)folded protein:(GlcNAc)2 (Man)8b

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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

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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. ↗

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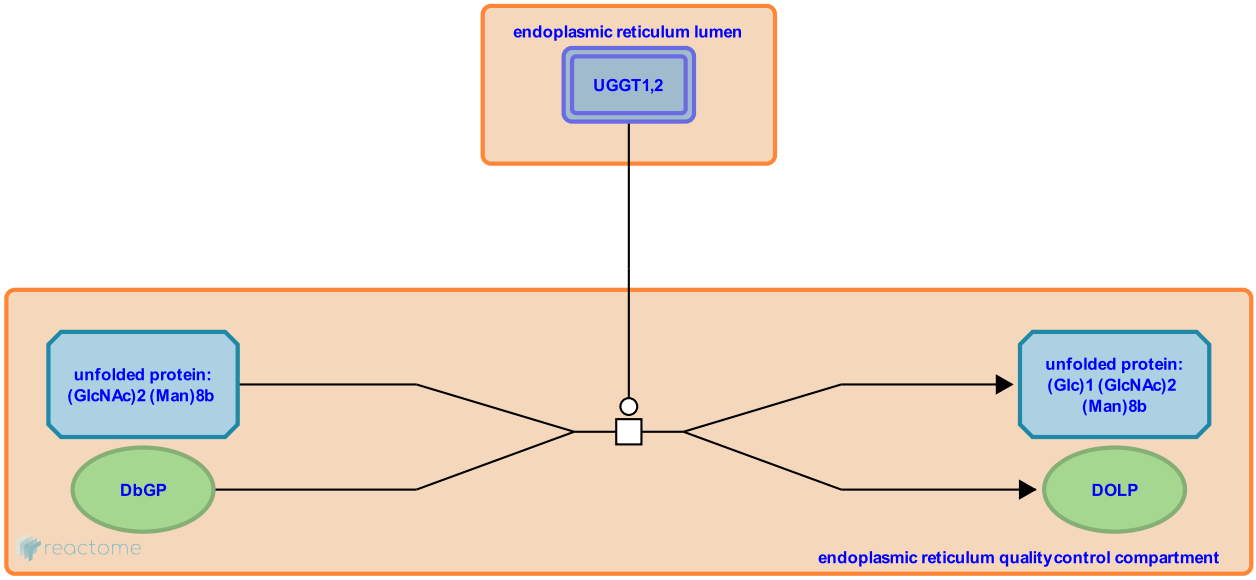
Stable identifier: R-HSA-548884

Type: transition

Compartments: endoplasmic reticulum quality control compartment



The UDP-glucose:glycoprotein glucosyltransferases 1 and 2 (UGGT1 and 2) are able to distinguish proteins with minor folding defects in the ERQC and reglucosylate them, by transferring a glucose (from dolichyl beta-D-glucosyl phosphate, DbGP) onto the alpha 1,3 mannose of the b (or c, not shown here) branch (Arnold et al. 2000, Arnold et al. 2003). The major affinity of these enzymes for proteins with minor folding defects has been demonstrated, but the exact mechanism that enable them to distinguish proteins with major and minor defects is still unknown (Pearse et al. 2008).

Literature references

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Editions

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