

Glycoproteins with lesser folding defects get transported back to the ER and the CNX/CRT complex

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06/05/2024

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

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

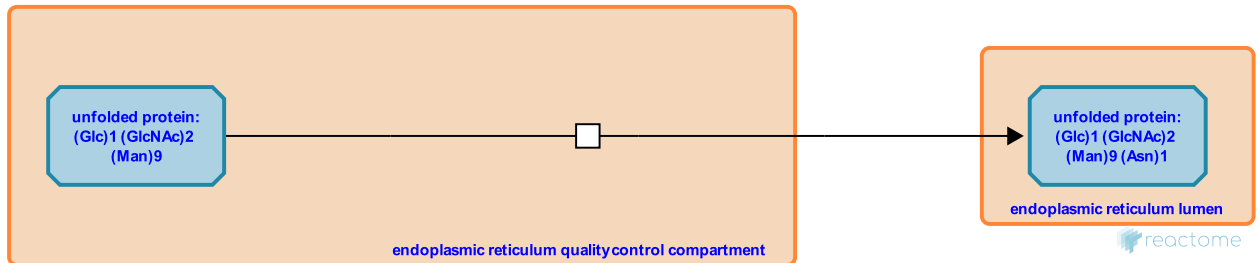
This document contains 1 reaction ([see Table of Contents](#))

Glycoproteins with lesser folding defects get transported back to the ER and the CNX/CRT complex [↗](#)

Stable identifier: R-HSA-1017228

Type: transition

Compartments: endoplasmic reticulum lumen, endoplasmic reticulum quality control compartment



Glycoproteins with lesser folding defects get transported back to the ER and the CNX/CRT complex (Lederkremer, 2009).

Literature references

Lederkremer, GZ. (2009). Glycoprotein folding, quality control and ER-associated degradation. *Curr Opin Struct Biol*, 19, 515-23. [↗](#)

Editions

2010-11-16	Edited	Jassal, B.
2010-11-18	Authored	Dall'Olio, GM.
2010-11-18	Reviewed	Gagneux, P.
2015-06-03	Revised	Jassal, B.