

Glycosylation and Folding of HA

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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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Reactome database release: 88

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

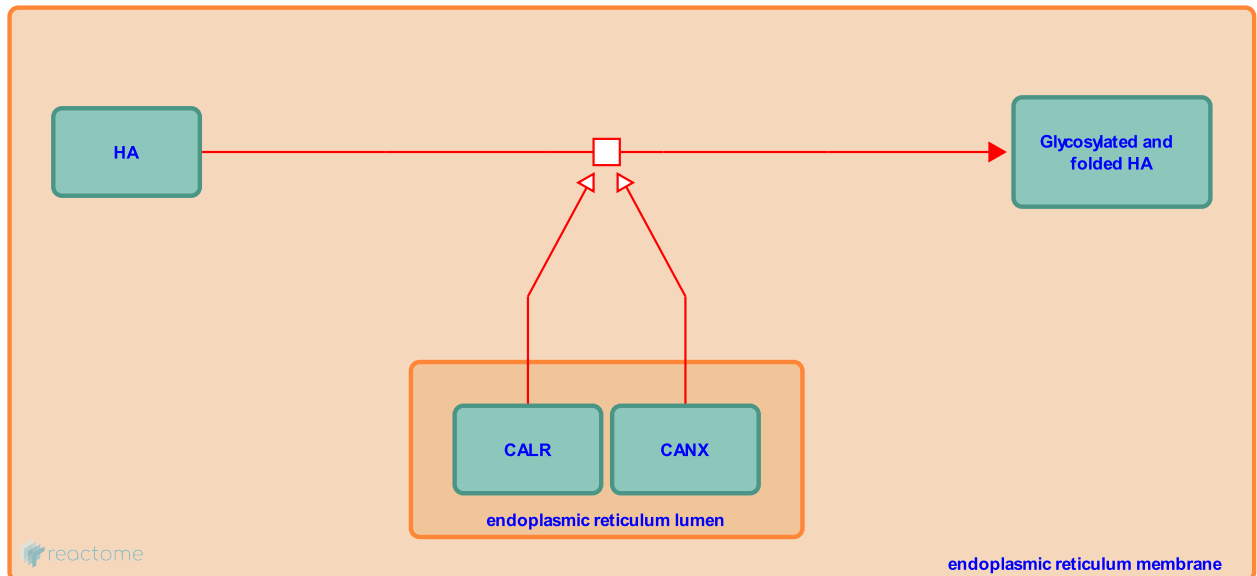
Glycosylation and Folding of HA [↗](#)

Stable identifier: R-HSA-169921

Type: transition

Compartments: endoplasmic reticulum lumen, endoplasmic reticulum membrane

Diseases: influenza



The ectodomain of HA is translocated into the ER lumen, where it undergoes a series of folding events mediated by the formation of disulfide bonds and glycosylation reactions. The formation of a discrete intermediate species of highly folded monomeric protein precedes trimerisation. The folding process is efficient and rapid, with greater than 90% of the protein trafficked to the golgi apparatus; and mature HA0 subunits appearing in a matter of a few minutes. Calnexin and calreticulin have been identified as cellular lectins which interact transiently with newly synthesized HA by attaching to partially trimmed N-linked oligosaccharides (Herbert et al., 1997), facilitating correct folding of the HA molecule.

Literature references

Helenius, A., Molinari, M. (2000). Chaperone selection during glycoprotein translocation into the endoplasmic reticulum. *Science*, 288, 331-3. [↗](#)

Kurowski, B., Daniels, R., Johnson, AE., Hebert, DN. (2003). N-linked glycans direct the cotranslational folding pathway of influenza hemagglutinin. *Mol Cell*, 11, 79-90. [↗](#)

Editions

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