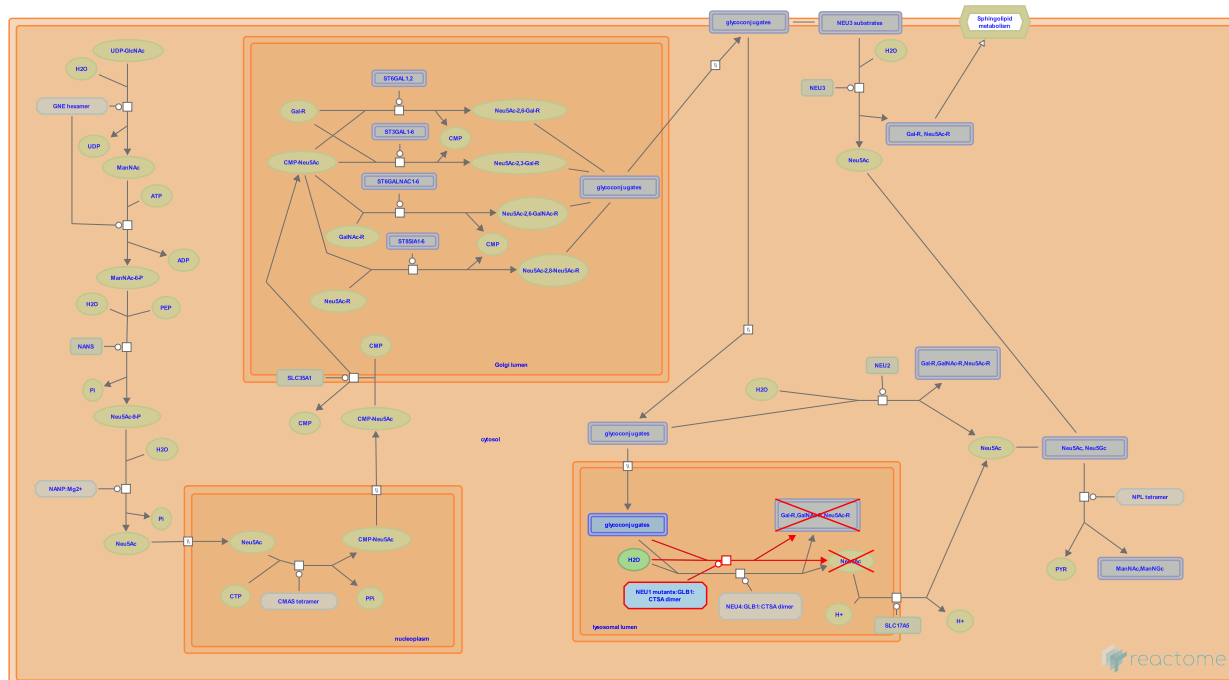


# Defective NEU1 causes sialidosis



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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](https://reactome.org).

29/09/2024

## 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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Reactome database release: 89

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



## Defective NEU1 does not hydrolyse Neu5Ac from glycoconjugates ↗

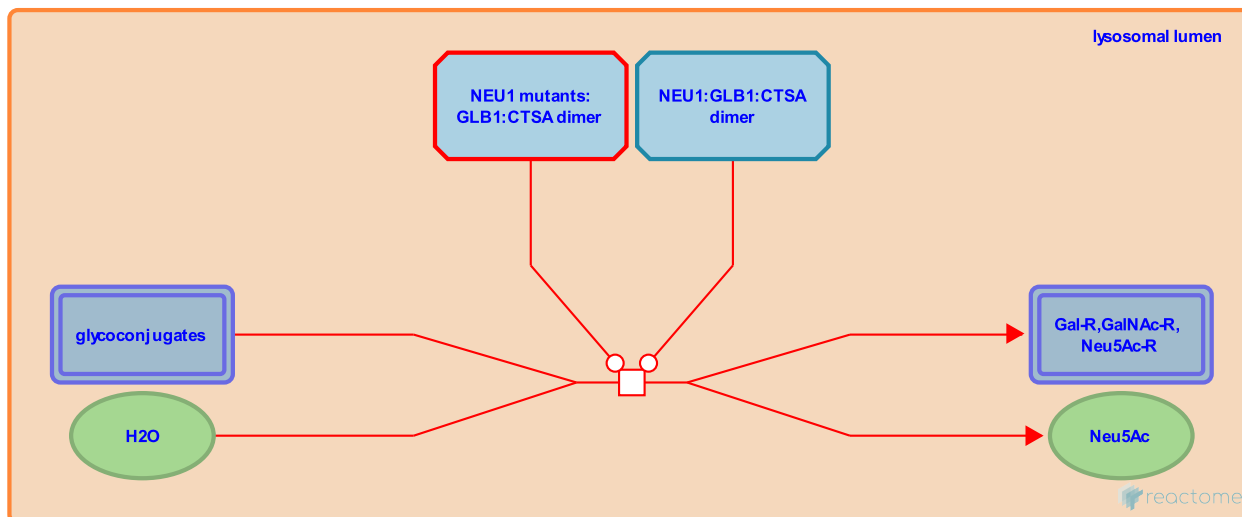
**Location:** Defective NEU1 causes sialidosis

**Stable identifier:** R-HSA-4341669

**Type:** transition

**Compartments:** lysosomal lumen

**Diseases:** lysosomal storage disease



NEU1 Sialidase 1 (NEU1, neuraminidase, receptor-destroying enzyme, RDE) normally hydrolyses N-acetylneuraminic acid (Neu5Ac) from glycoconjugates with alpha2,3-, alpha2,6- or alpha2,8-linked terminal sialated residues in the lysosomal lumen, a step in the degradation process of glycoproteins and gangliosides. NEU1 is active in a multienzyme complex comprising cathepsin A protective protein (CTSA) and beta-galactosidase (Bonten et al. 1996, Rudenko et al. 1995). Defects in NEU1 cause Sialidosis (MIM:256550), a lysosomal storage disorder manifesting as type I (late-onset) or type II (earlier-onset) (Bonten et al. 1996). Generally, patients with the more severe type II disease have catalytically inactive enzymes whereas patients with the milder type I disease have some residual activity. Mutations causing the severest type II disease include E377\*, L303P, W29\*, R225P and W23\* (Bonten et al. 1996, Pshezhetsky et al. 1997, Sergi et al. 2001, Pattison et al. 2004).

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### Editions

2013-08-21	Authored, Edited	Jassal, B.
2015-04-30	Reviewed	Spillmann, D.

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