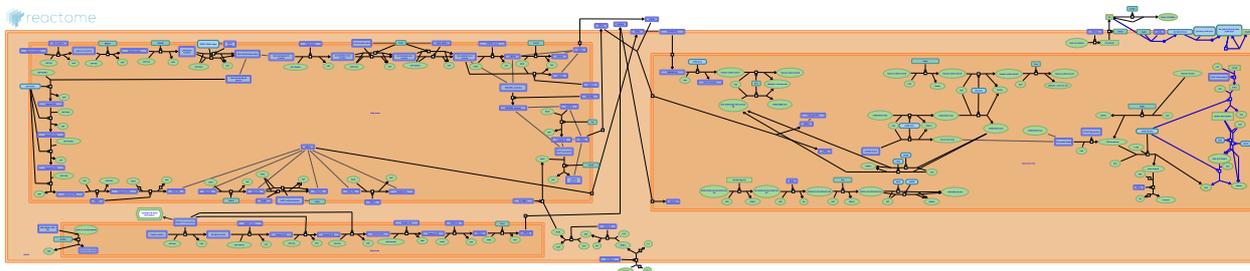


Hyaluronan uptake and degradation



European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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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.

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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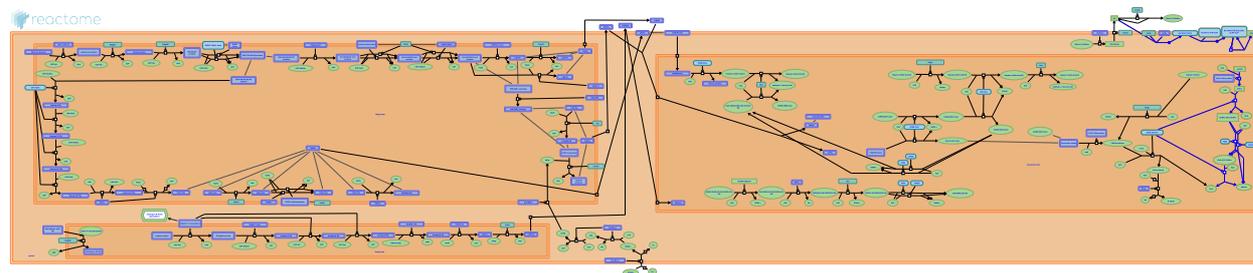
Reactome database release: 74

This document contains 1 pathway and 8 reactions ([see Table of Contents](#))

Hyaluronan uptake and degradation ↗

Stable identifier: R-RNO-2160916

Inferred from: [Hyaluronan uptake and degradation \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Receptor-mediated uptake of HA ↗

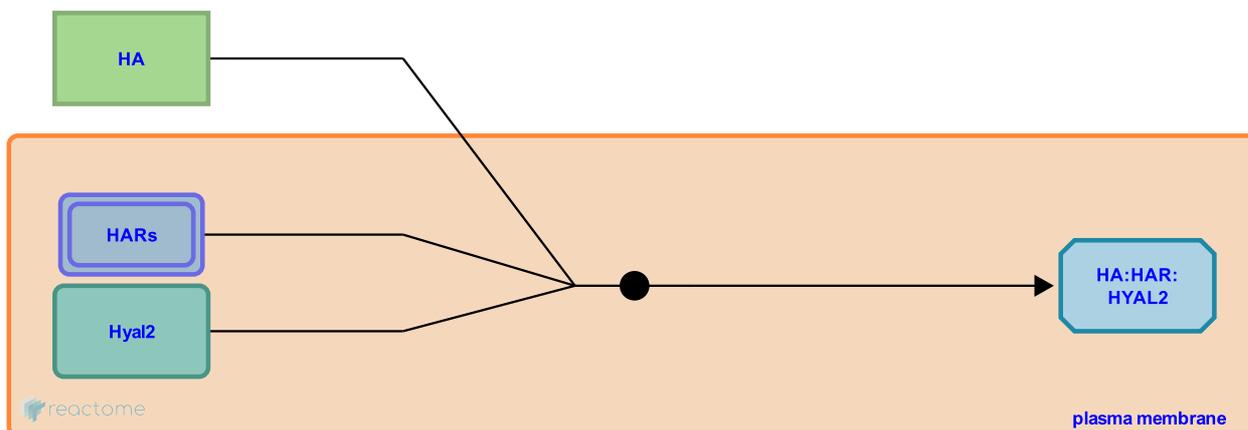
Location: [Hyaluronan uptake and degradation](#)

Stable identifier: R-RNO-2160915

Type: binding

Compartments: plasma membrane, extracellular region

Inferred from: [Receptor-mediated uptake of HA \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

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Followed by: [HA:HAR:HYAL2 binds to SLC9A1;p-CHP:Ca2+](#)

HA:HAR:HYAL2 binds to SLC9A1:p-CHP:Ca2+ ↗

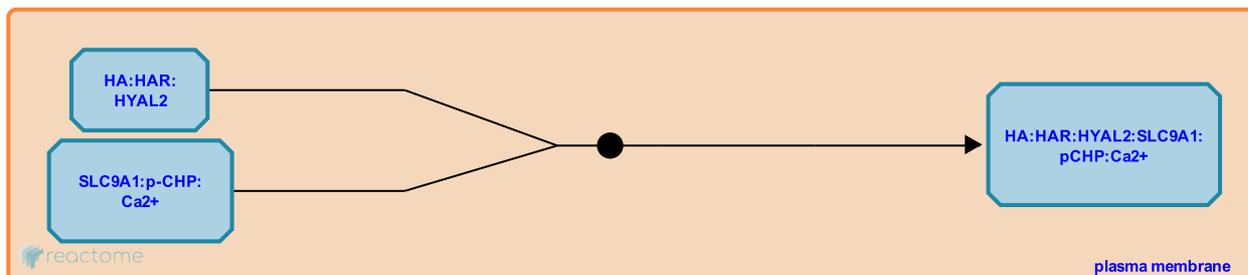
Location: [Hyaluronan uptake and degradation](#)

Stable identifier: R-RNO-2160884

Type: binding

Compartments: plasma membrane

Inferred from: [HA:HAR:HYAL2 binds to SLC9A1:p-CHP:Ca2+ \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [Receptor-mediated uptake of HA](#)

Followed by: [Hyaluronidase 2 \(HYAL2\) hydrolyses HA into 20kDa fragments](#)

Hyaluronidase 2 (HYAL2) hydrolyses HA into 20kDa fragments ↗

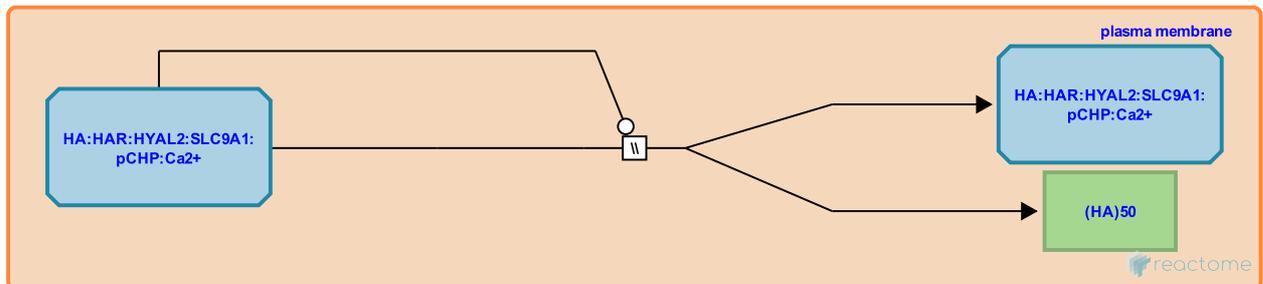
Location: [Hyaluronan uptake and degradation](#)

Stable identifier: R-RNO-2160892

Type: omitted

Compartments: plasma membrane

Inferred from: [Hyaluronidase 2 \(HYAL2\) hydrolyses HA into 20kDa fragments \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [HA:HAR:HYAL2 binds to SLC9A1:p-CHP:Ca2+](#)

HYAL1 hydrolyses (HA)50 ↗

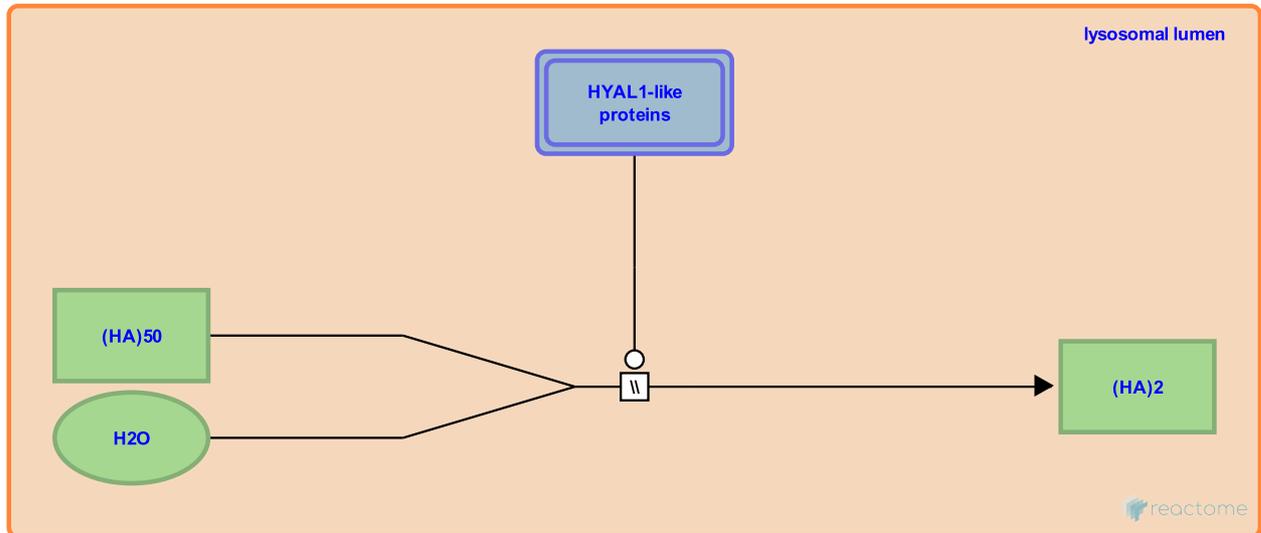
Location: [Hyaluronan uptake and degradation](#)

Stable identifier: R-RNO-2160874

Type: omitted

Compartments: lysosomal lumen

Inferred from: [HYAL1 hydrolyses \(HA\)50 \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Followed by: [GUSB tetramer hydrolyses \(HA\)2](#)

GUSB tetramer hydrolyses (HA)2 ↗

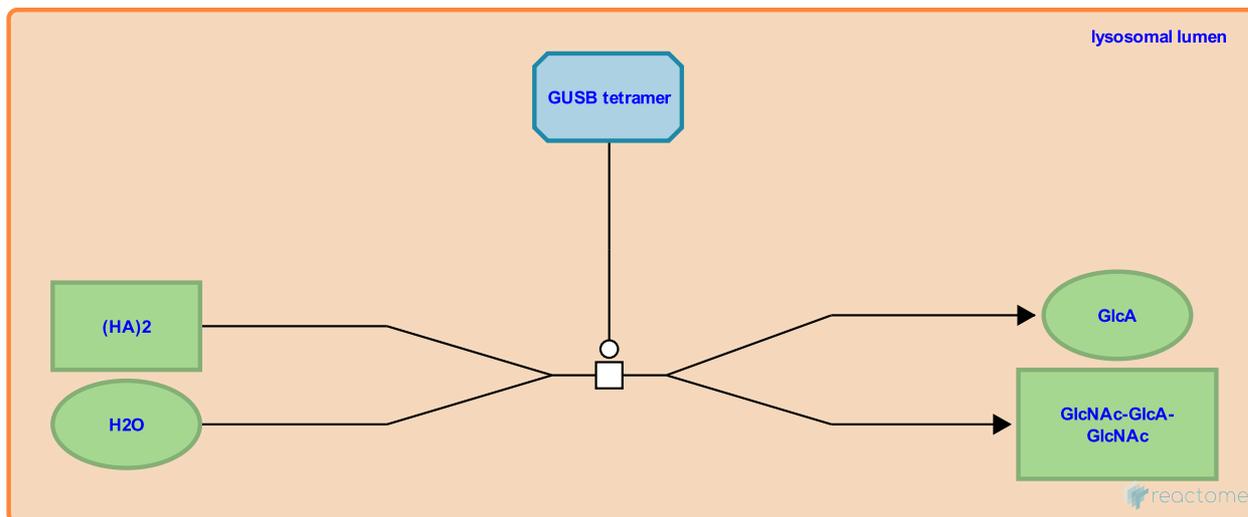
Location: [Hyaluronan uptake and degradation](#)

Stable identifier: R-RNO-2162227

Type: transition

Compartments: lysosomal lumen

Inferred from: [GUSB tetramer hydrolyses \(HA\)2 \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [HYAL1 hydrolyses \(HA\)50](#)

Followed by: [HEXB cleaves the terminal GalNAc from small HA fragments](#), [HEXA cleaves the terminal GalNAc from small HA fragments](#)

HEXA cleaves the terminal GalNAc from small HA fragments ↗

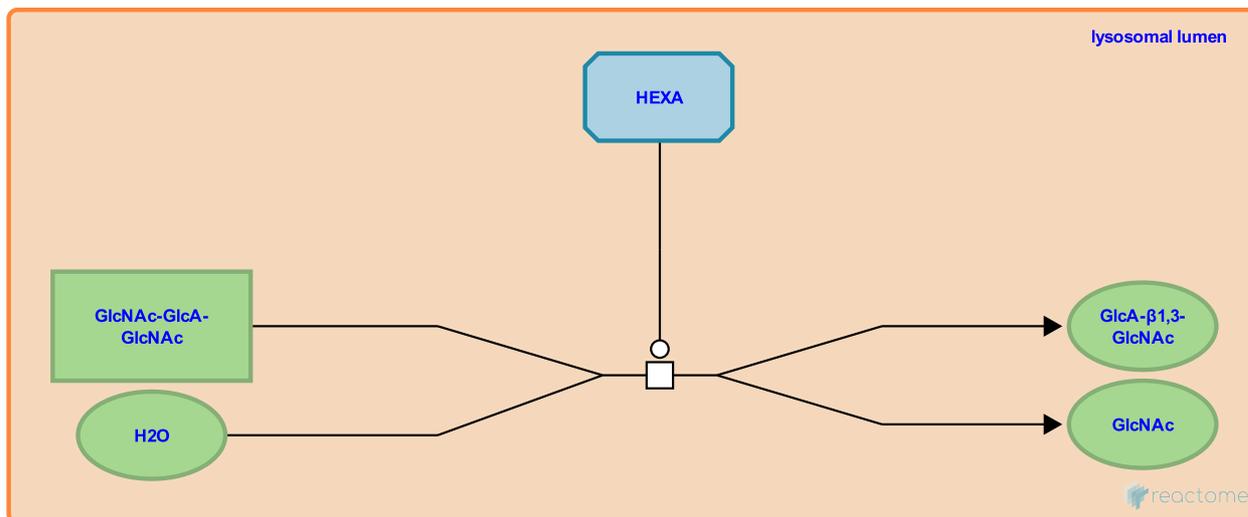
Location: [Hyaluronan uptake and degradation](#)

Stable identifier: R-RNO-2162225

Type: transition

Compartments: lysosomal lumen

Inferred from: [HEXA cleaves the terminal GalNAc from small HA fragments \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [GUSB tetramer hydrolyses \(HA\)²](#)

Followed by: [GUSB tetramer hydrolyses GlcA-β1,3-GlcNAc](#)

HEXB cleaves the terminal GalNAc from small HA fragments ↗

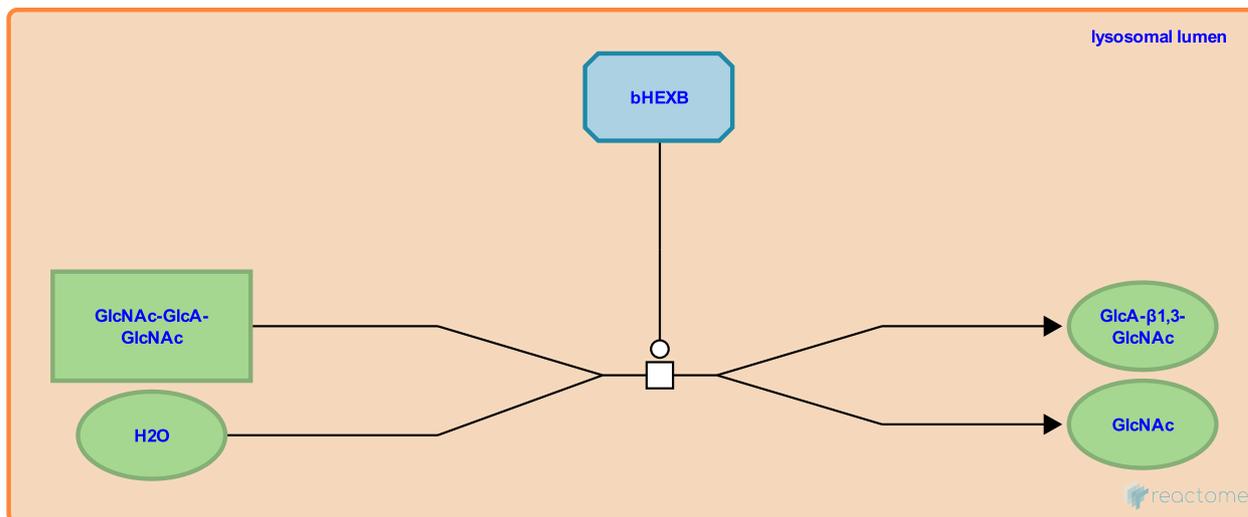
Location: [Hyaluronan uptake and degradation](#)

Stable identifier: R-RNO-9638076

Type: transition

Compartments: lysosomal lumen

Inferred from: [HEXB cleaves the terminal GalNAc from small HA fragments \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [GUSB tetramer hydrolyses \(HA\)2](#)

GUSB tetramer hydrolyses GlcA- β 1,3-GlcNAc [↗](#)

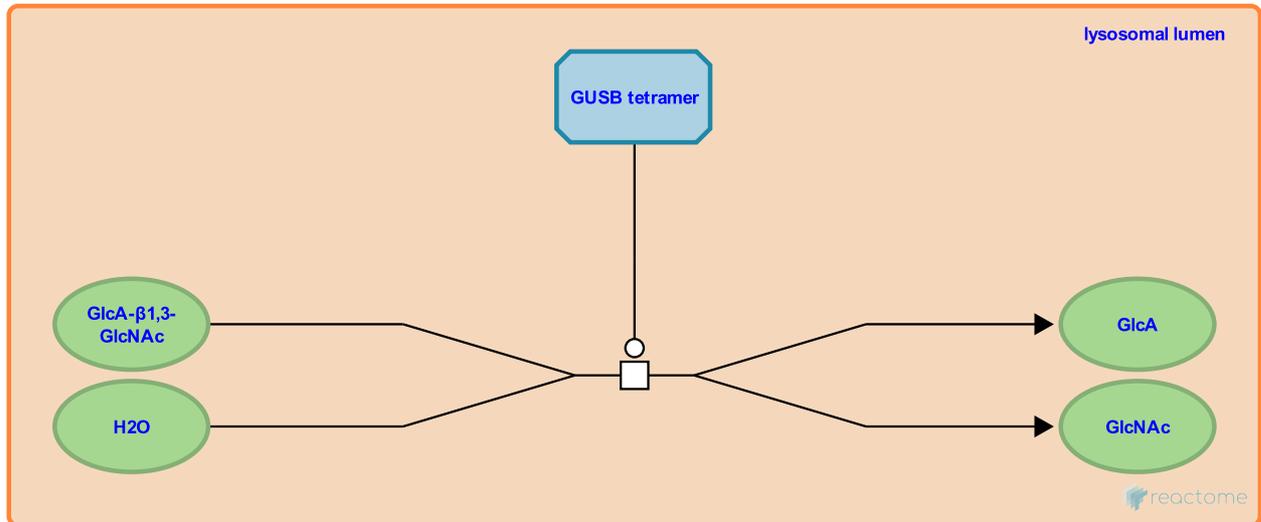
Location: [Hyaluronan uptake and degradation](#)

Stable identifier: R-RNO-2162226

Type: transition

Compartments: lysosomal lumen

Inferred from: [GUSB tetramer hydrolyses GlcA- \$\beta\$ 1,3-GlcNAc \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [HEXA cleaves the terminal GalNAc from small HA fragments](#)

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