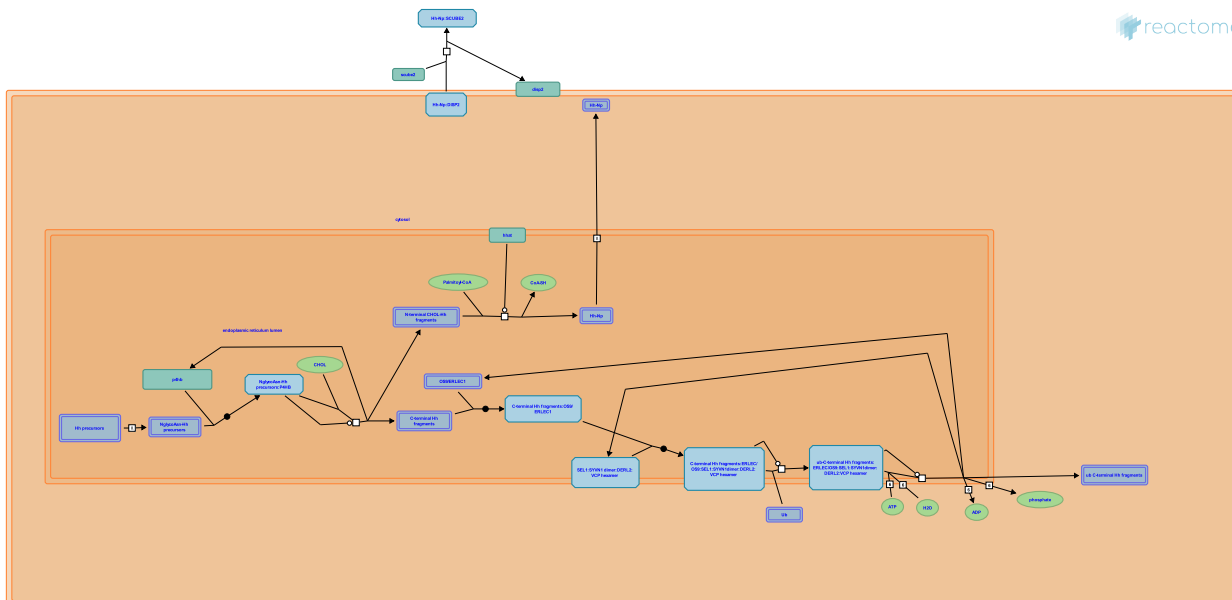


Hedgehog ligand biogenesis



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

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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](#).

17/05/2024

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

- Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*, 18, 142. [↗](#)
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
- 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. [↗](#)
- 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 2 pathways and 9 reactions ([see Table of Contents](#))

Glycosylation of Hh ↗

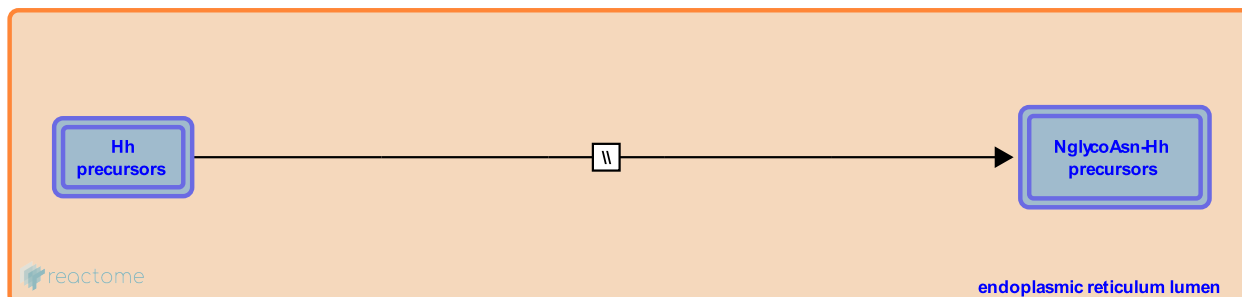
Location: [Hedgehog ligand biogenesis](#)

Stable identifier: R-XTR-5362386

Type: omitted

Compartments: endoplasmic reticulum lumen

Inferred from: [Glycosylation of Hh \(Homo sapiens\)](#)



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.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Followed by: [P4HB forms mixed disulphides with Hh precursors](#)

P4HB forms mixed disulphides with Hh precursors ↗

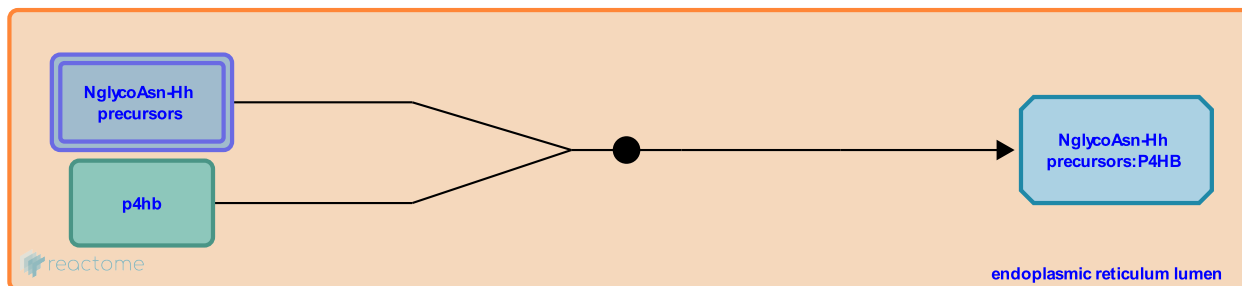
Location: [Hedgehog ligand biogenesis](#)

Stable identifier: R-XTR-5358336

Type: binding

Compartments: endoplasmic reticulum lumen

Inferred from: [P4HB forms mixed disulphides with Hh precursors \(Homo sapiens\)](#)



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.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [Glycosylation of Hh](#)

Followed by: [Autoproteolytic cleavage of Hh precursors](#)

Autoproteolytic cleavage of Hh precursors ↗

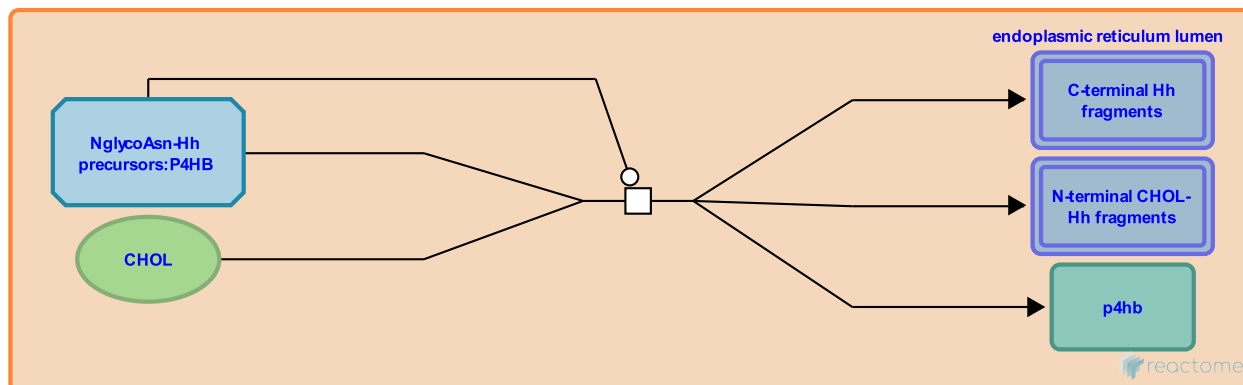
Location: [Hedgehog ligand biogenesis](#)

Stable identifier: R-XTR-5358340

Type: transition

Compartments: endoplasmic reticulum lumen

Inferred from: [Autoproteolytic cleavage of Hh precursors \(Homo sapiens\)](#)



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.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [P4HB forms mixed disulphides with Hh precursors](#)

Followed by: [HHAT palmitoylates Hh N-terminal fragment, C-terminal Hh fragments are bound by lectins](#)

HHAT palmitoylates Hh N-terminal fragment ↗

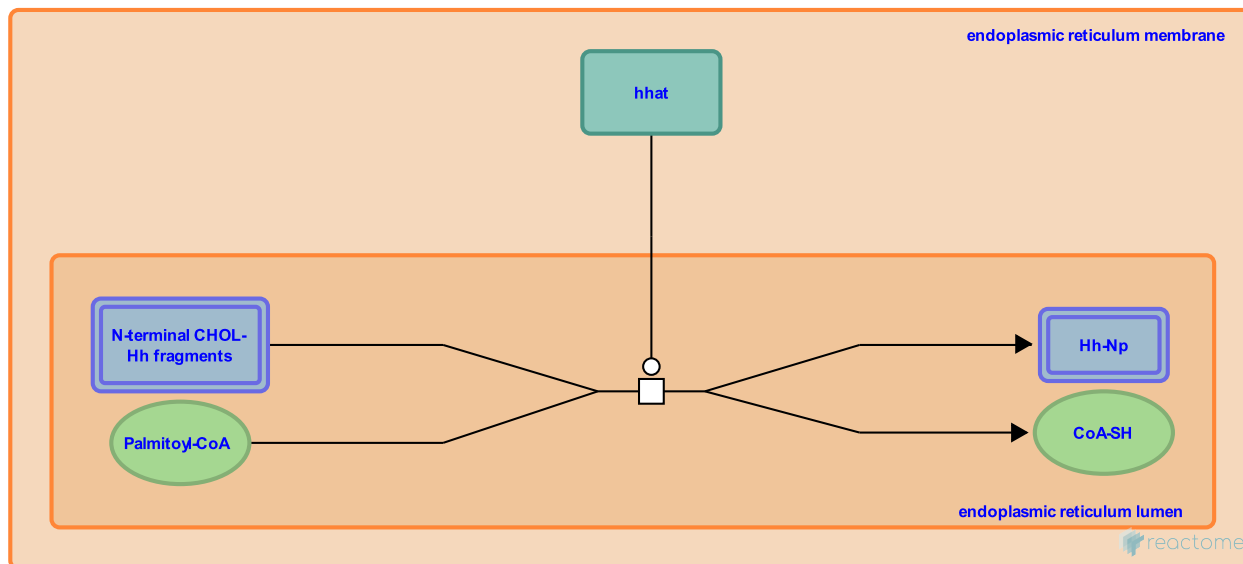
Location: [Hedgehog ligand biogenesis](#)

Stable identifier: R-XTR-5358343

Type: transition

Compartments: endoplasmic reticulum lumen

Inferred from: [HHAT palmitoylates Hh N-terminal fragment \(Homo sapiens\)](#)



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.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [Autoproteolytic cleavage of Hh precursors](#)

Followed by: [Hh-Np traffics to the plasma membrane](#)

Hh-Np traffics to the plasma membrane ↗

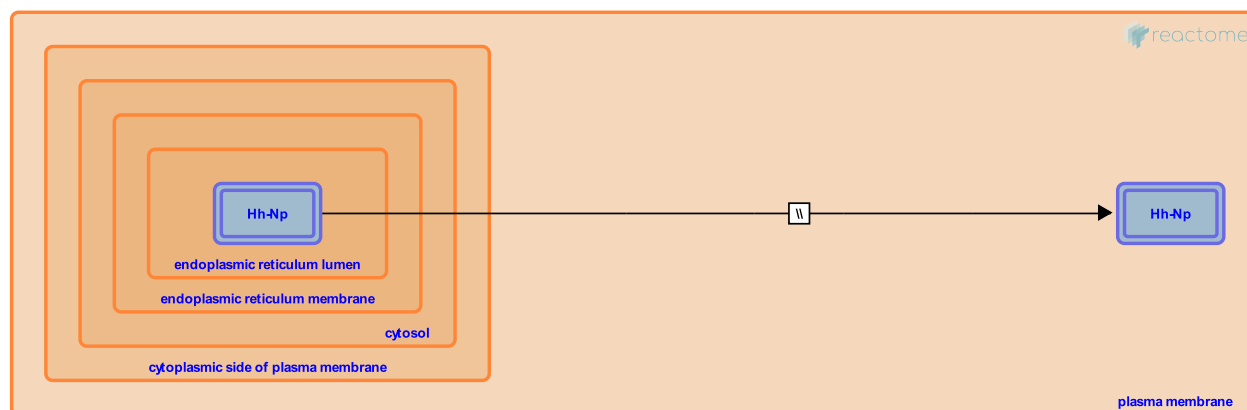
Location: [Hedgehog ligand biogenesis](#)

Stable identifier: R-XTR-5362549

Type: omitted

Compartments: plasma membrane

Inferred from: [Hh-Np traffics to the plasma membrane \(Homo sapiens\)](#)



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.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

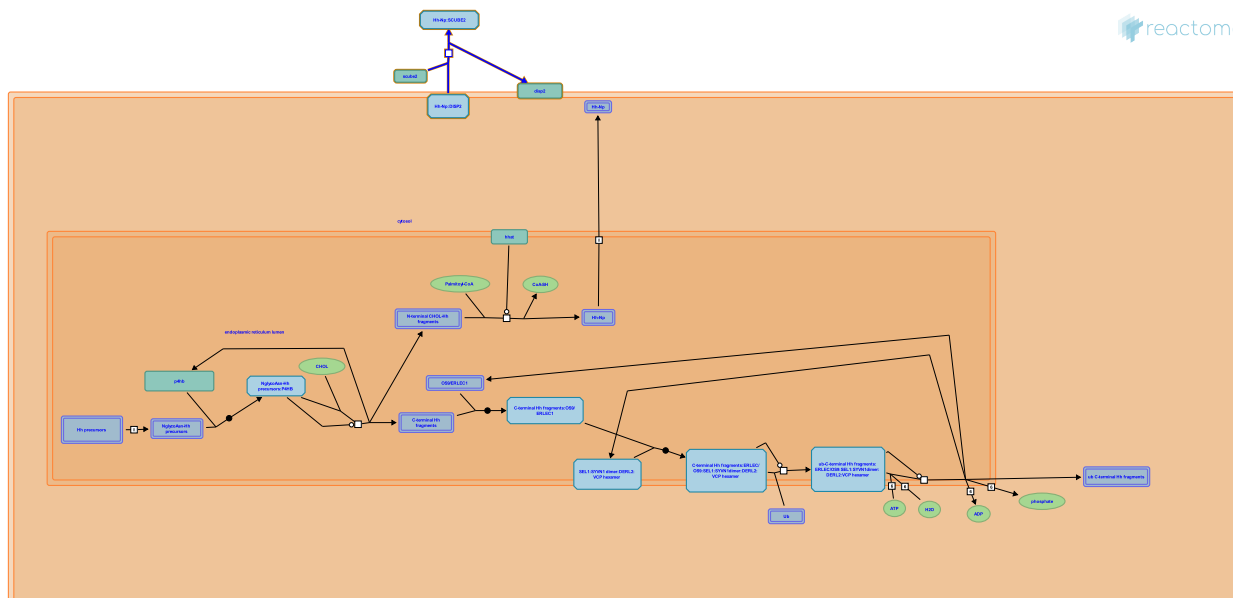
Preceded by: [HHAT palmitoylates Hh N-terminal fragment](#)

Release of Hh-Np from the secreting cell ↗

Location: [Hedgehog ligand biogenesis](#)

Stable identifier: R-XTR-5362798

Inferred from: [Release of Hh-Np from the secreting cell \(Homo sapiens\)](#)



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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C-terminal Hh fragments are bound by lectins ↗

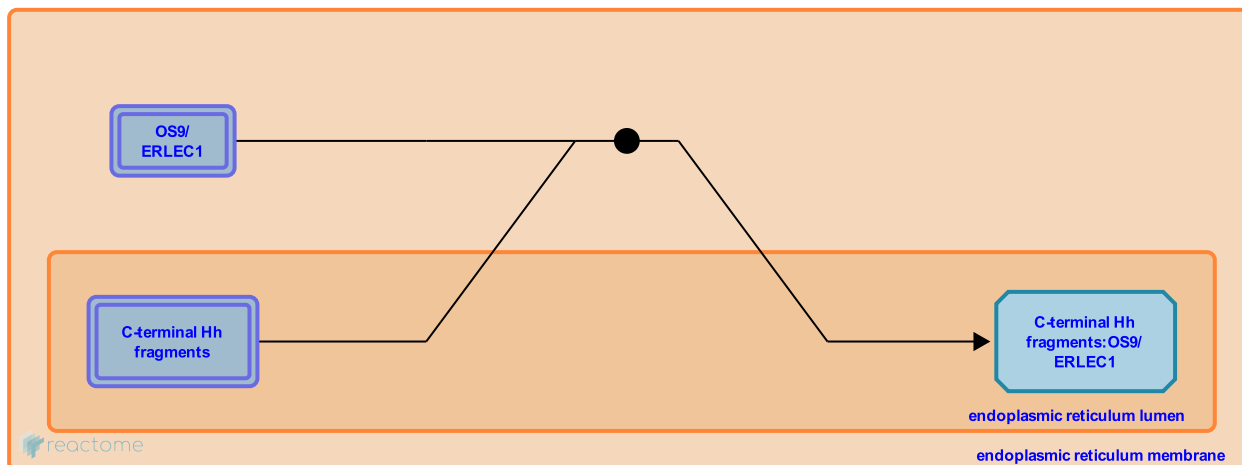
Location: [Hedgehog ligand biogenesis](#)

Stable identifier: R-XTR-5362437

Type: binding

Compartments: endoplasmic reticulum membrane

Inferred from: [C-terminal Hh fragments are bound by lectins \(Homo sapiens\)](#)



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.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [Autoproteolytic cleavage of Hh precursors](#)

Followed by: [C-terminal Hh fragments are recruited to SEL1:SYVN1 at the ER membrane](#)

C-terminal Hh fragments are recruited to SEL1:SYVN1 at the ER membrane [↗](#)

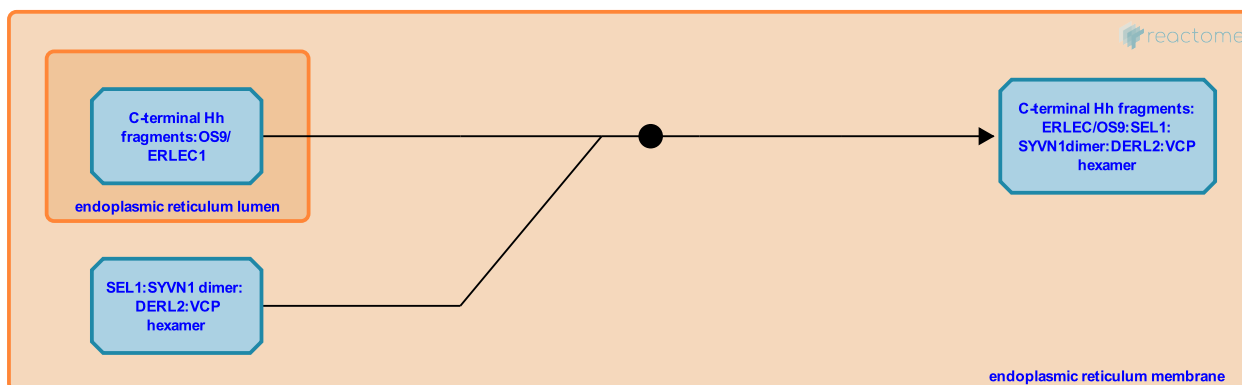
Location: [Hedgehog ligand biogenesis](#)

Stable identifier: R-XTR-5362441

Type: binding

Compartments: endoplasmic reticulum membrane

Inferred from: [C-terminal Hh fragments are recruited to SEL1:SYVN1 at the ER membrane \(Homo sapiens\)](#)



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.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [C-terminal Hh fragments are bound by lectins](#)

Followed by: [SYVN1 ubiquitinates Hh C-terminal fragments](#)

SYVN1 ubiquitinates Hh C-terminal fragments ↗

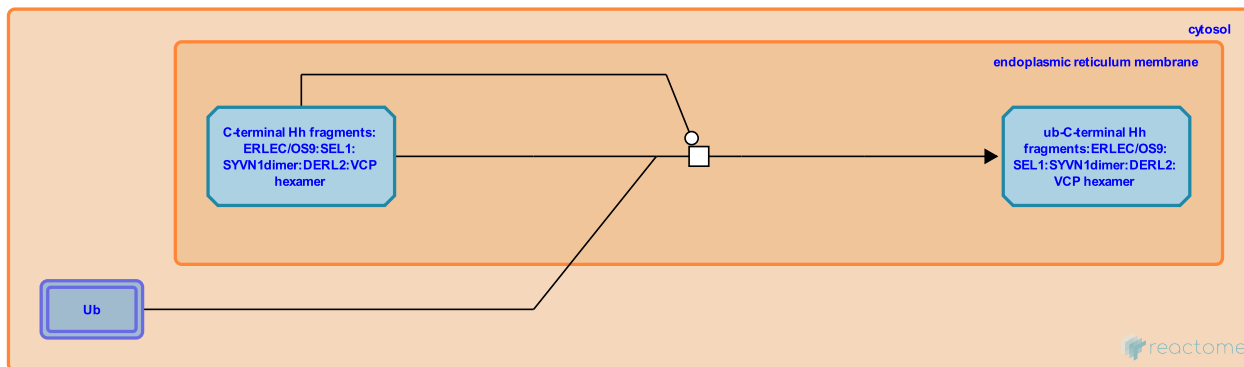
Location: [Hedgehog ligand biogenesis](#)

Stable identifier: R-XTR-5362412

Type: transition

Compartments: endoplasmic reticulum membrane

Inferred from: [SYVN1 ubiquitinates Hh C-terminal 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.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [C-terminal Hh fragments are recruited to SEL1:SYVN1 at the ER membrane](#)

Followed by: [VCP-catalyzed ATP hydrolysis promotes the translocation of Hh-C into the cytosol](#)

VCP-catalyzed ATP hydrolysis promotes the translocation of Hh-C into the cytosol ↗

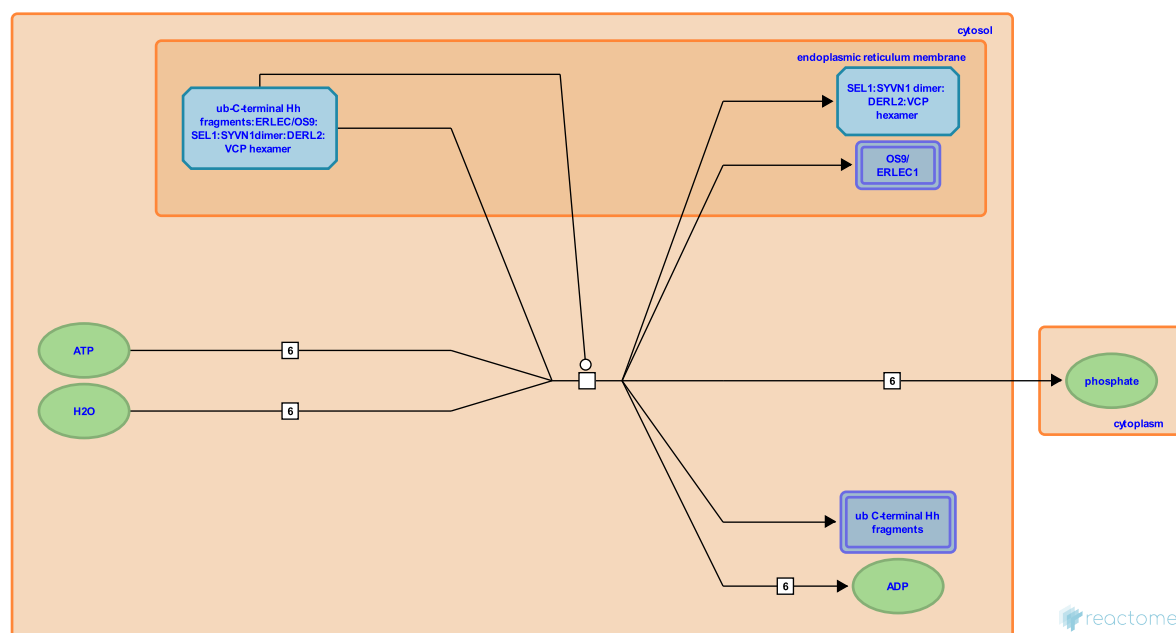
Location: [Hedgehog ligand biogenesis](#)

Stable identifier: R-XTR-5362459

Type: transition

Compartments: cytosol

Inferred from: [VCP-catalyzed ATP hydrolysis promotes the translocation of Hh-C into the cytosol \(Homo sapiens\)](#)














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

Preceded by: [SYVN1 ubiquitinates Hh C-terminal fragments](#)

Table of Contents

Introduction	1
 Hedgehog ligand biogenesis	2
 Glycosylation of Hh	3
 P4HB forms mixed disulphides with Hh precursors	4
 Autoproteolytic cleavage of Hh precursors	5
 HHAT palmitoylates Hh N-terminal fragment	6
 Hh-Np traffics to the plasma membrane	7
 Release of Hh-Np from the secreting cell	8
 C-terminal Hh fragments are bound by lectins	9
 C-terminal Hh fragments are recruited to SEL1:SYVN1 at the ER membrane	10
 SYVN1 ubiquitinates Hh C-terminal fragments	11
 VCP-catalyzed ATP hydrolysis promotes the translocation of Hh-C into the cytosol	12
Table of Contents	13