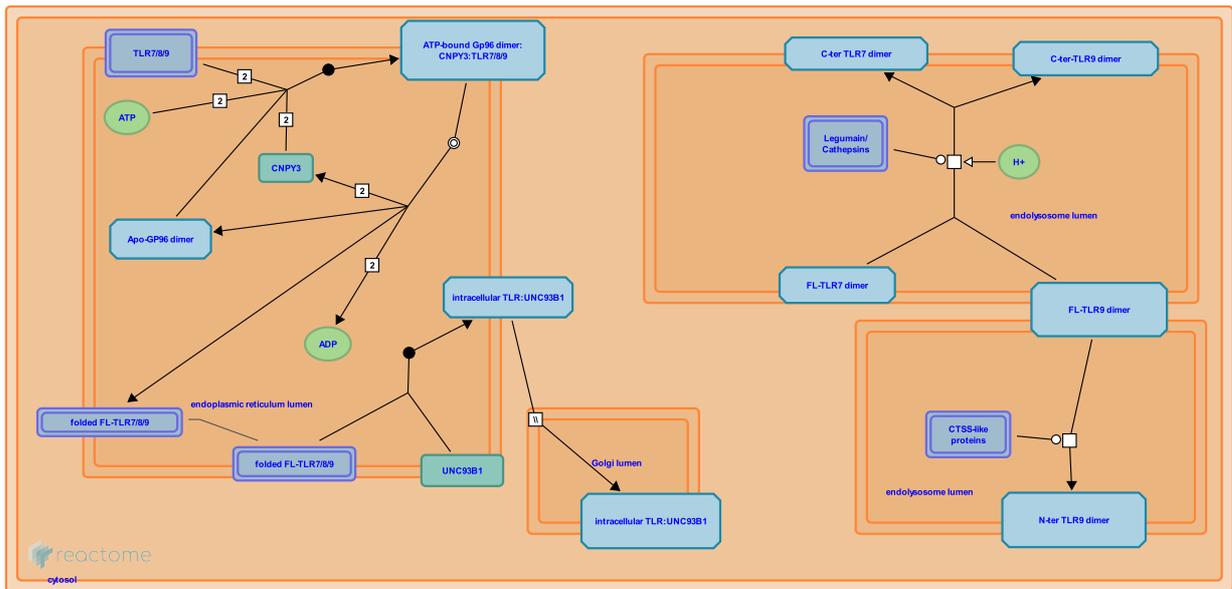


Trafficking and processing of endosomal TLR



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](#).

06/12/2022

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. [↗](#)

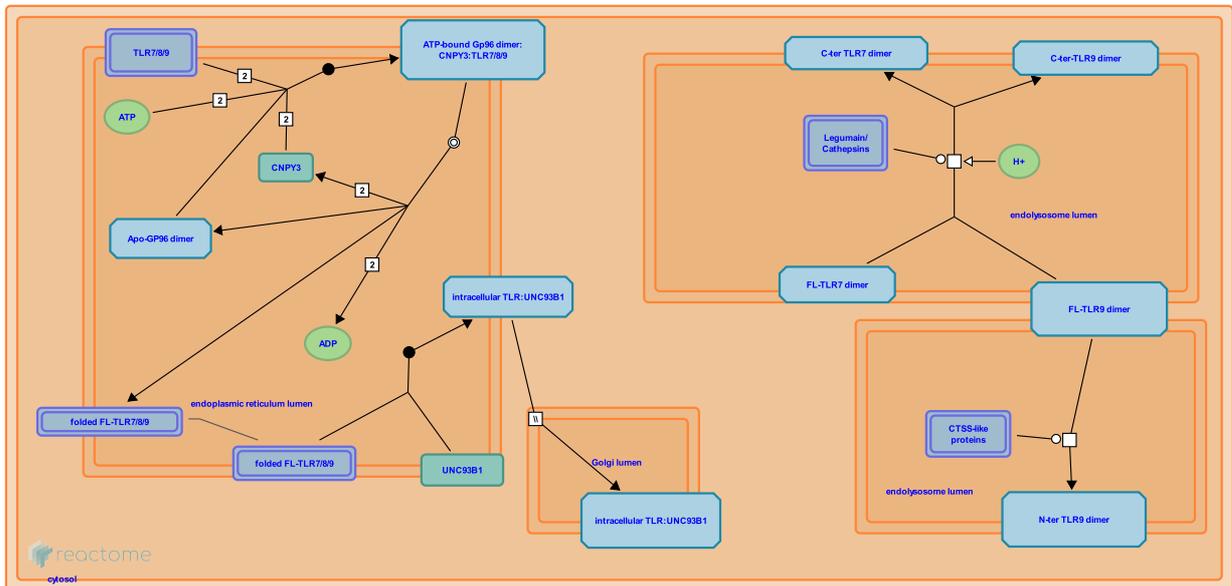
Reactome database release: 82

This document contains 1 pathway and 6 reactions ([see Table of Contents](#))

Trafficking and processing of endosomal TLR [↗](#)

Stable identifier: R-SSC-1679131

Inferred from: [Trafficking and processing of endosomal TLR \(Homo sapiens\)](#)



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>

TLR folding by chaperones GP96 and CNPY3 ↗

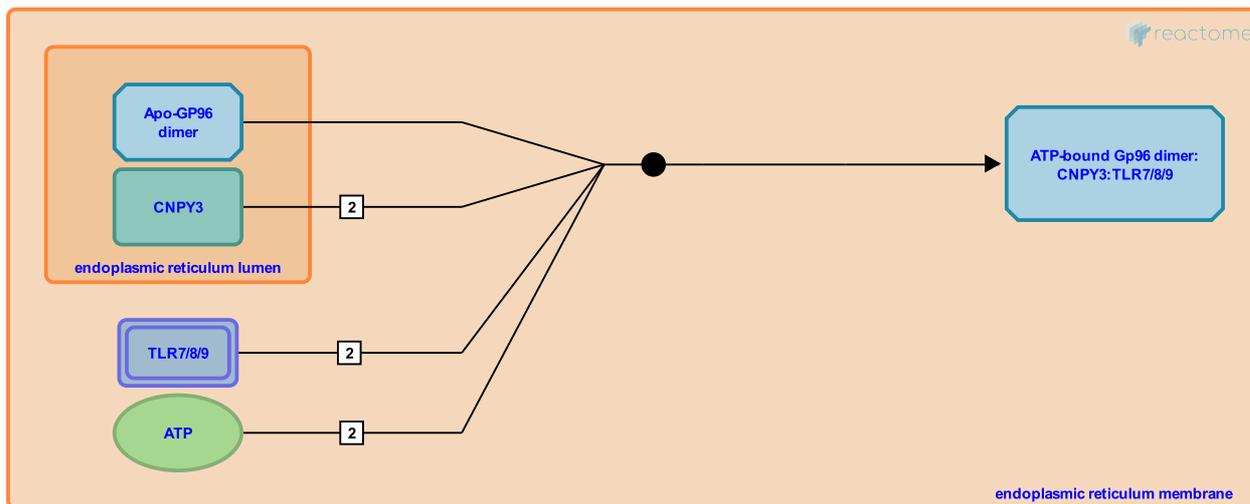
Location: [Trafficking and processing of endosomal TLR](#)

Stable identifier: R-SSC-1678923

Type: binding

Compartments: endoplasmic reticulum membrane, endoplasmic reticulum lumen

Inferred from: [TLR folding by chaperones GP96 and CNPY3 \(Homo sapiens\)](#)



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: [Folded full-length TLR7/8/9 dissociates from the GP96:CNPY3 complex](#)

Folded full-length TLR7/8/9 dissociates from the GP96:CNPY3 complex ↗

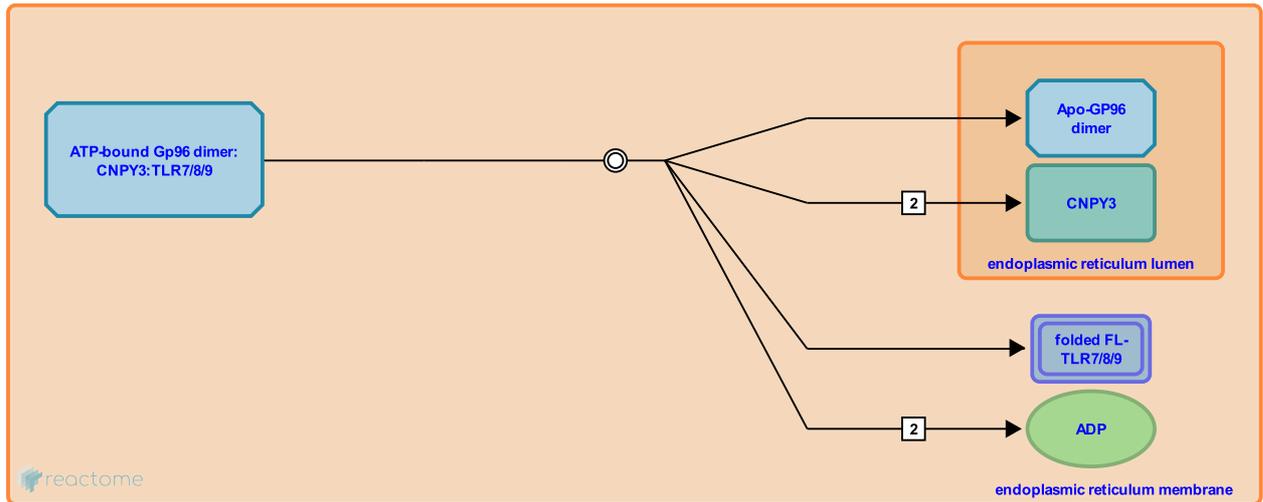
Location: [Trafficking and processing of endosomal TLR](#)

Stable identifier: R-SSC-1678944

Type: dissociation

Compartments: endoplasmic reticulum membrane, endoplasmic reticulum lumen

Inferred from: [Folded full-length TLR7/8/9 dissociates from the GP96:CNPY3 complex \(Homo sapiens\)](#)



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: [TLR folding by chaperones GP96 and CNPY3](#)

Followed by: [Full-length TLR3/7/8/9 binds to UNC93B1](#)

Full-length TLR3/7/8/9 binds to UNC93B1 ↗

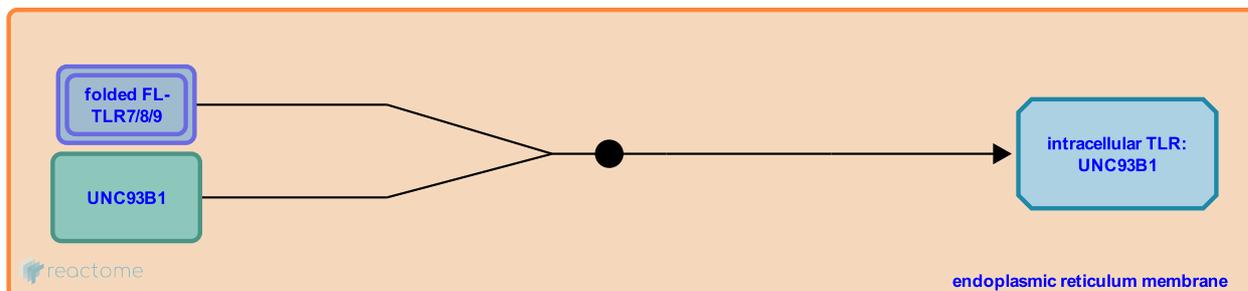
Location: [Trafficking and processing of endosomal TLR](#)

Stable identifier: R-SSC-1678921

Type: binding

Compartments: endoplasmic reticulum membrane

Inferred from: [Full-length TLR3/7/8/9 binds to UNC93B1 \(Homo sapiens\)](#)



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: [Folded full-length TLR7/8/9 dissociates from the GP96:CNPY3 complex](#)

Followed by: [Endosomal TLRs pass through the Golgi](#)

Endosomal TLRs pass through the Golgi ↗

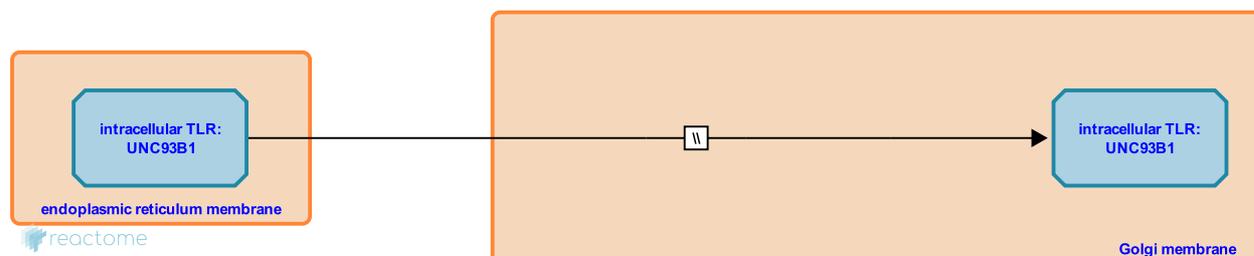
Location: [Trafficking and processing of endosomal TLR](#)

Stable identifier: R-SSC-1678998

Type: omitted

Compartments: Golgi membrane, endoplasmic reticulum lumen

Inferred from: [Endosomal TLRs pass through the Golgi \(Homo sapiens\)](#)



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: [Full-length TLR3/7/8/9 binds to UNC93B1](#)

TLR processing at low pH ↗

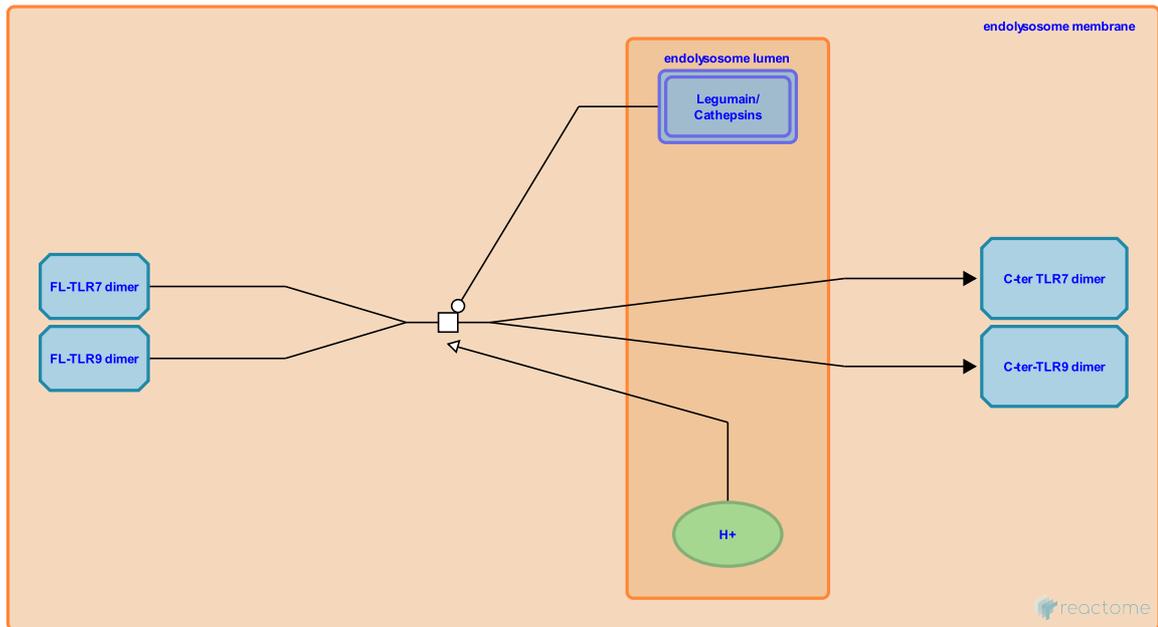
Location: [Trafficking and processing of endosomal TLR](#)

Stable identifier: R-SSC-1678920

Type: transition

Compartments: endolysosome membrane

Inferred from: [TLR processing at low pH \(Homo sapiens\)](#)



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>

TLR9 processing at neutral pH ↗

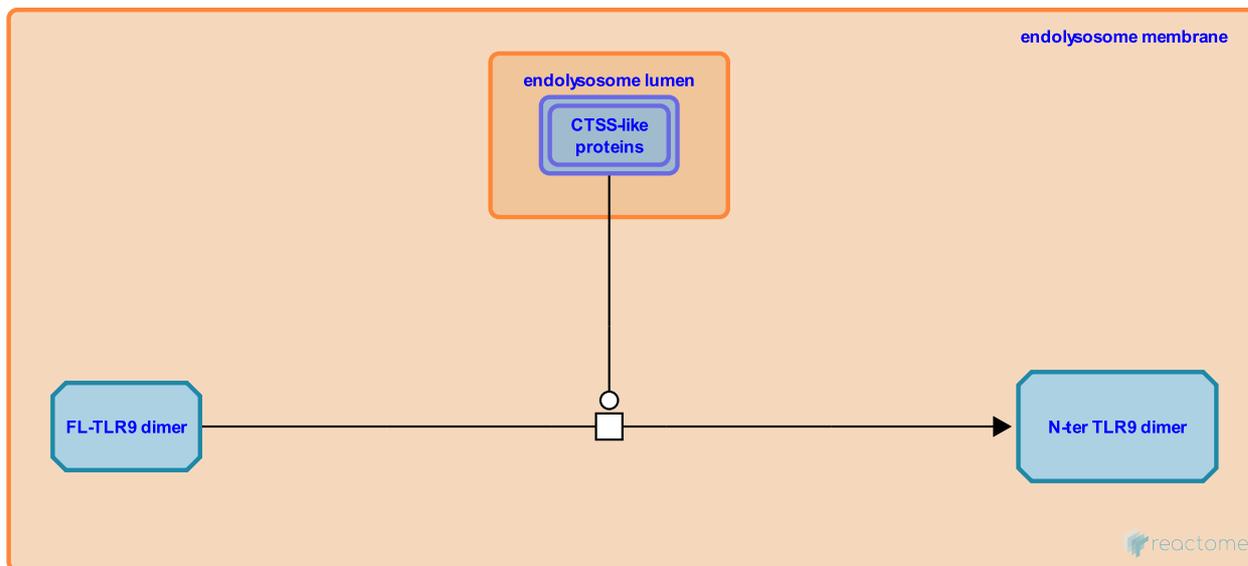
Location: [Trafficking and processing of endosomal TLR](#)

Stable identifier: R-SSC-1678981

Type: transition

Compartments: endolysosome membrane

Inferred from: [TLR9 processing at neutral pH \(Homo sapiens\)](#)



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>

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