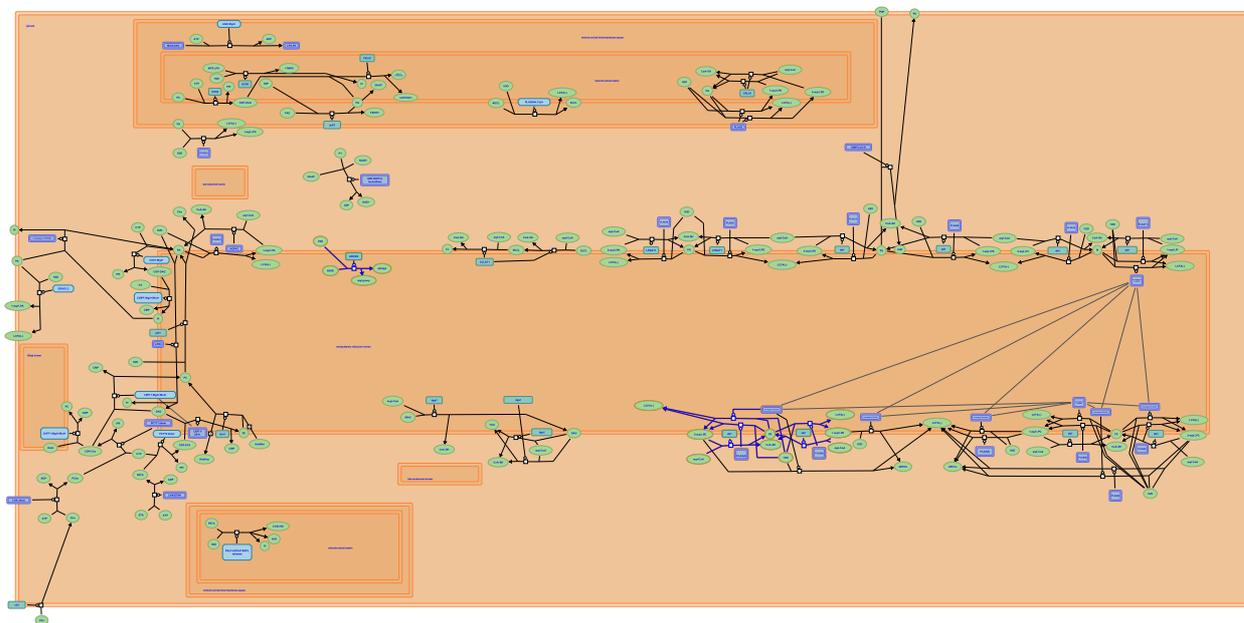


Acyl chain remodelling of PE



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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](#). For more information see our [license](#).

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. [↗](#)

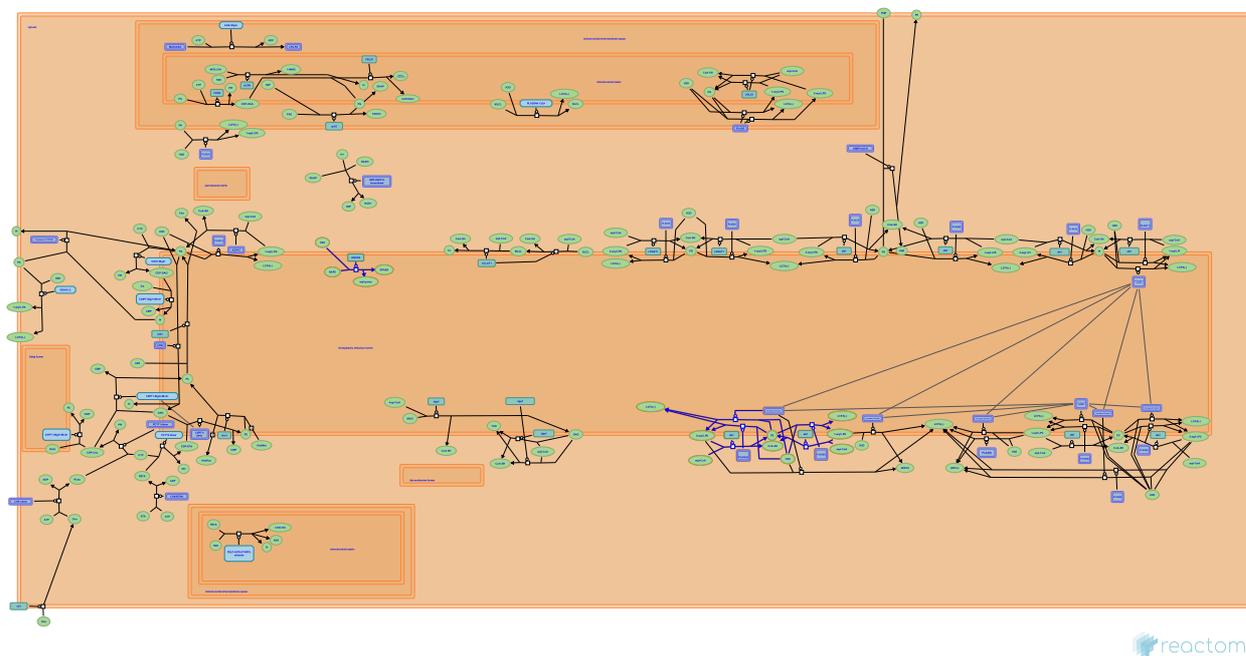
Reactome database release: 73

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

Acyl chain remodelling of PE ↗

Stable identifier: R-SPO-1482839

Inferred from: [Acyl chain remodelling of PE \(Homo sapiens\)](#)



 reactome

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>

PE is hydrolyzed to 1-acyl LPE by PLA2[2] ↗

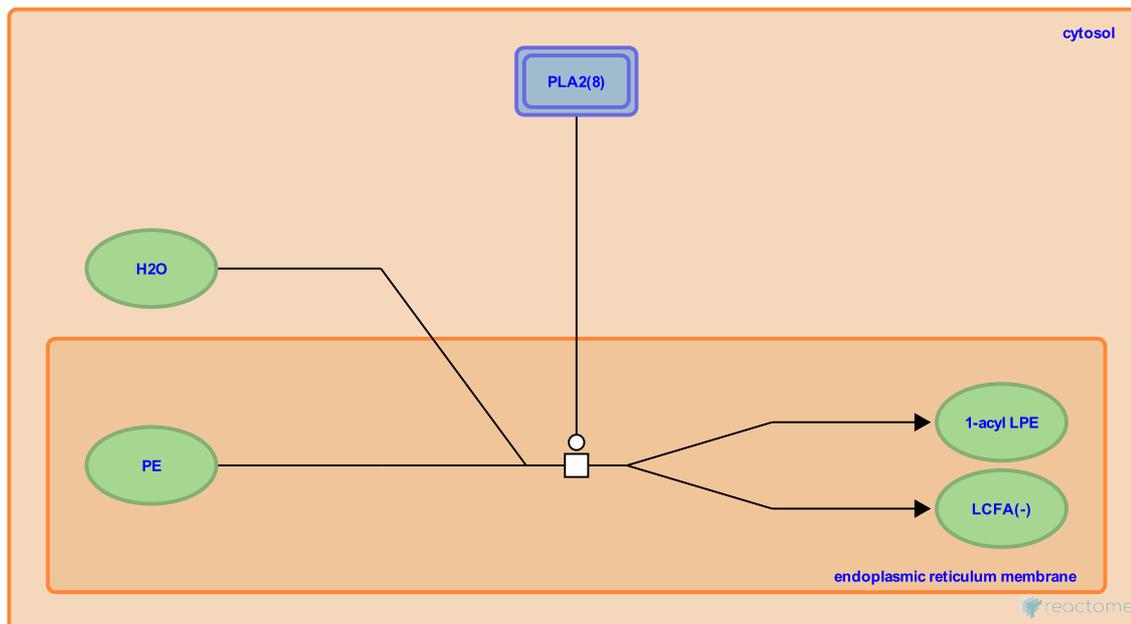
Location: [Acyl chain remodelling of PE](#)

Stable identifier: R-SPO-1482884

Type: transition

Compartments: endoplasmic reticulum membrane, cytosol

Inferred from: [PE is hydrolyzed to 1-acyl LPE by PLA2\[2\] \(Homo sapiens\)](#)



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: [1-acyl LPE is acylated to PE by LPEAT](#), [2-acyl LPE is acylated to PE by LPEAT](#)

Followed by: [1-acyl LPE is acylated to PE by LPEAT](#)

1-acyl LPE is acylated to PE by LPEAT ↗

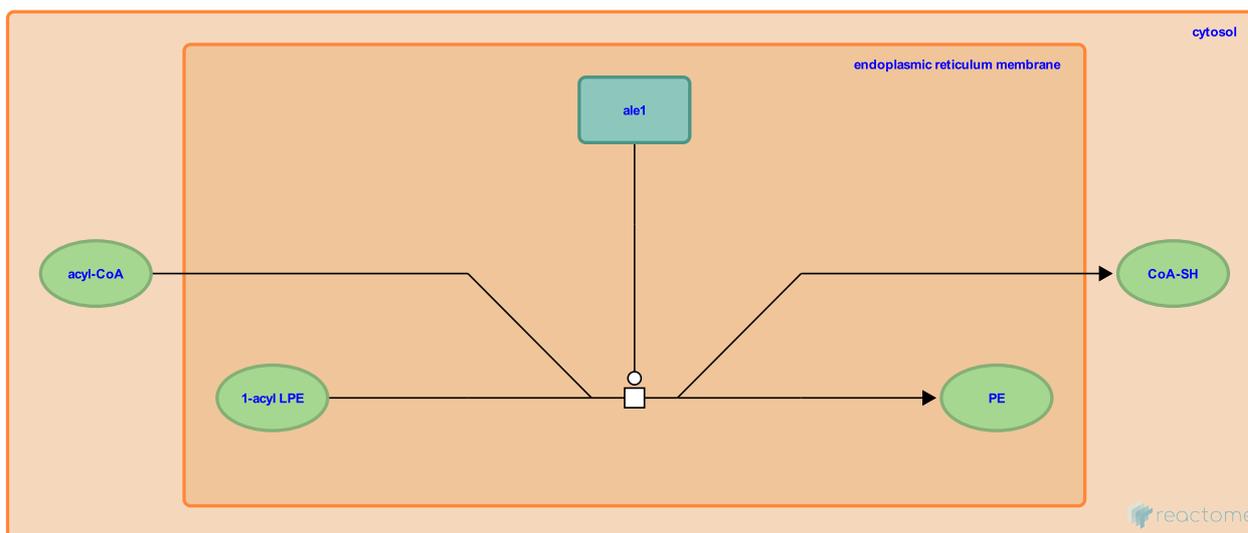
Location: [Acyl chain remodelling of PE](#)

Stable identifier: R-SPO-1482667

Type: transition

Compartments: endoplasmic reticulum membrane, cytosol

Inferred from: [1-acyl LPE is acylated to PE by LPEAT \(Homo sapiens\)](#)



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: [PE is hydrolyzed to 1-acyl LPE by PLA2\[2\]](#)

Followed by: [PE is hydrolyzed to 2-acyl LPE by PLA2\[4\]](#), [PE is hydrolyzed to 2-acyl LPE by PLA2G4C](#), [PE is hydrolyzed to 1-acyl LPE by PLA2\[2\]](#)

PE is hydrolyzed to 2-acyl LPE by PLA2[4] ↗

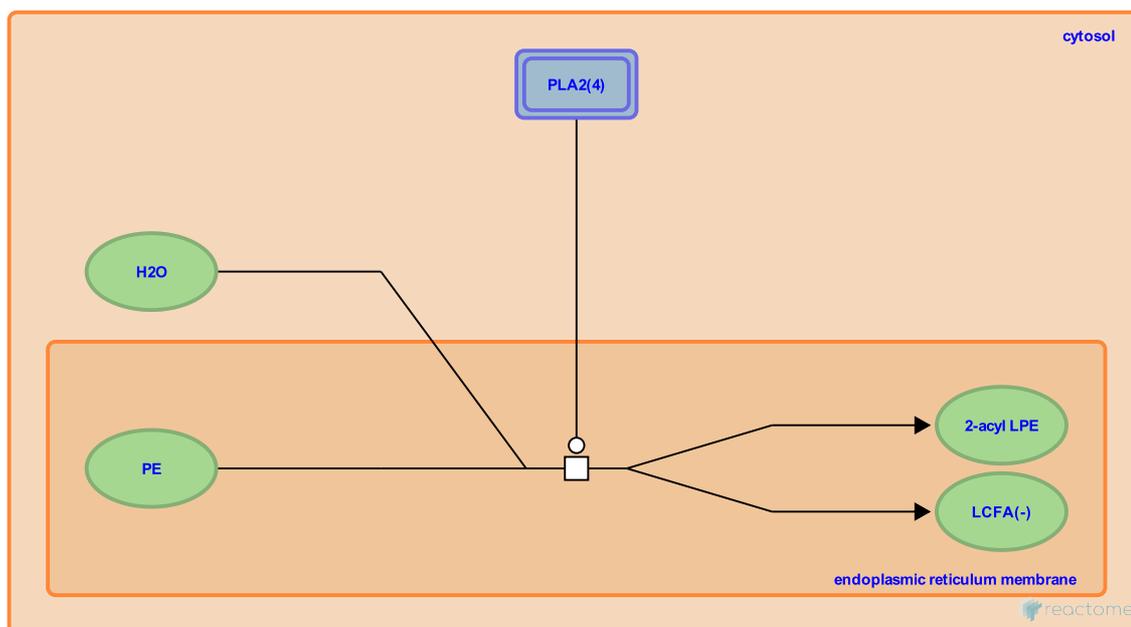
Location: [Acyl chain remodelling of PE](#)

Stable identifier: R-SPO-1482828

Type: transition

Compartments: endoplasmic reticulum membrane, cytosol

Inferred from: [PE is hydrolyzed to 2-acyl LPE by PLA2\[4\] \(Homo sapiens\)](#)



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: [1-acyl LPE is acylated to PE by LPEAT](#), [2-acyl LPE is acylated to PE by LPEAT](#)

Followed by: [2-acyl LPE is acylated to PE by LPEAT](#)

PE is hydrolyzed to 2-acyl LPE by PLA2G4C ↗

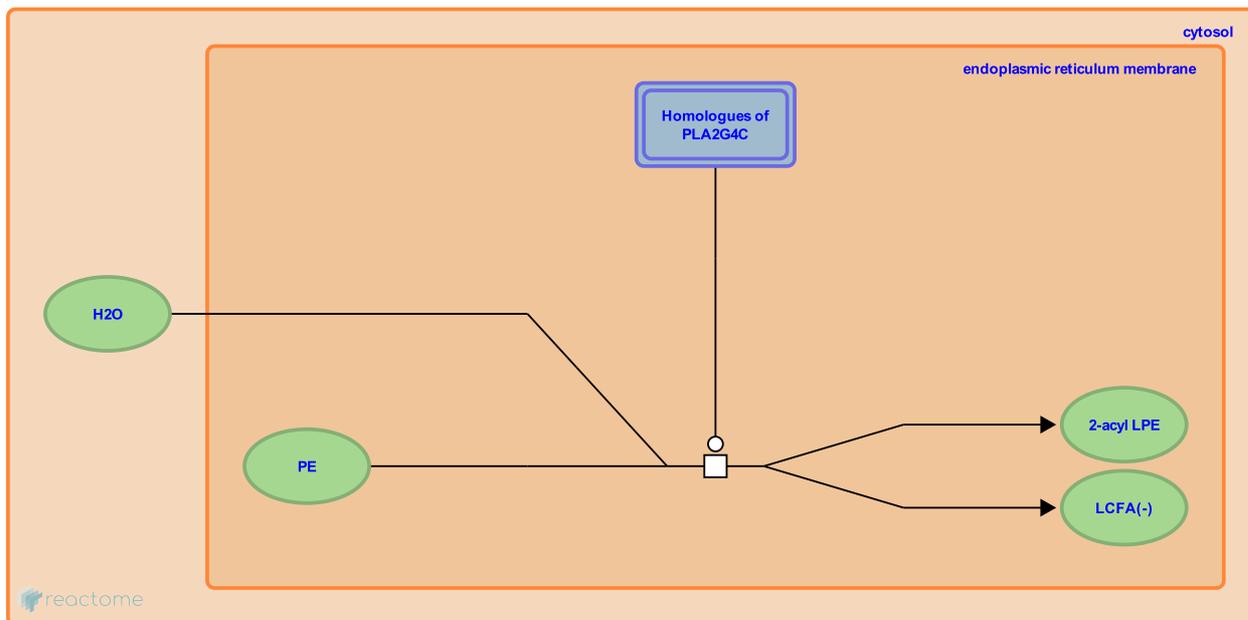
Location: [Acyl chain remodelling of PE](#)

Stable identifier: R-SPO-1482892

Type: transition

Compartments: endoplasmic reticulum membrane, cytosol

Inferred from: [PE is hydrolyzed to 2-acyl LPE by PLA2G4C \(Homo sapiens\)](#)



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: [1-acyl LPE is acylated to PE by LPEAT](#), [2-acyl LPE is acylated to PE by LPEAT](#)

Followed by: [2-acyl LPE is acylated to PE by LPEAT](#)

2-acyl LPE is acylated to PE by LPEAT ↗

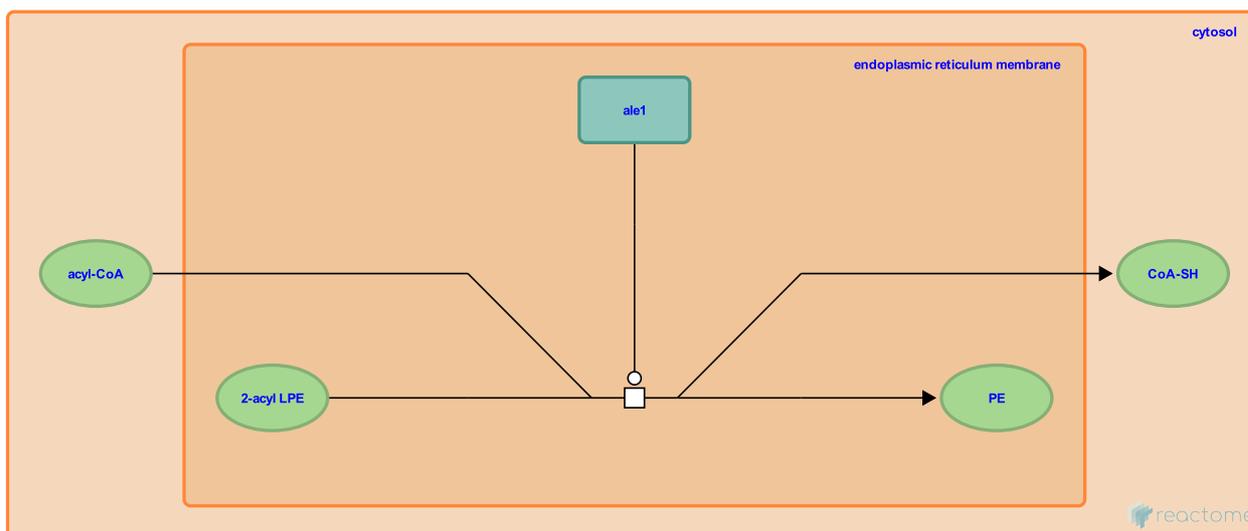
Location: [Acyl chain remodelling of PE](#)

Stable identifier: R-SPO-1482646

Type: transition

Compartments: endoplasmic reticulum membrane, cytosol

Inferred from: [2-acyl LPE is acylated to PE by LPEAT \(Homo sapiens\)](#)



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: [PE is hydrolyzed to 2-acyl LPE by PLA2\[4\]](#), [PE is hydrolyzed to 2-acyl LPE by PLA2G4C](#)

Followed by: [PE is hydrolyzed to 2-acyl LPE by PLA2\[4\]](#), [PE is hydrolyzed to 1-acyl LPE by PLA2\[2\]](#), [PE is hydrolyzed to 2-acyl LPE by PLA2G4C](#)

ABHD4 hydrolyses NAPE ↗

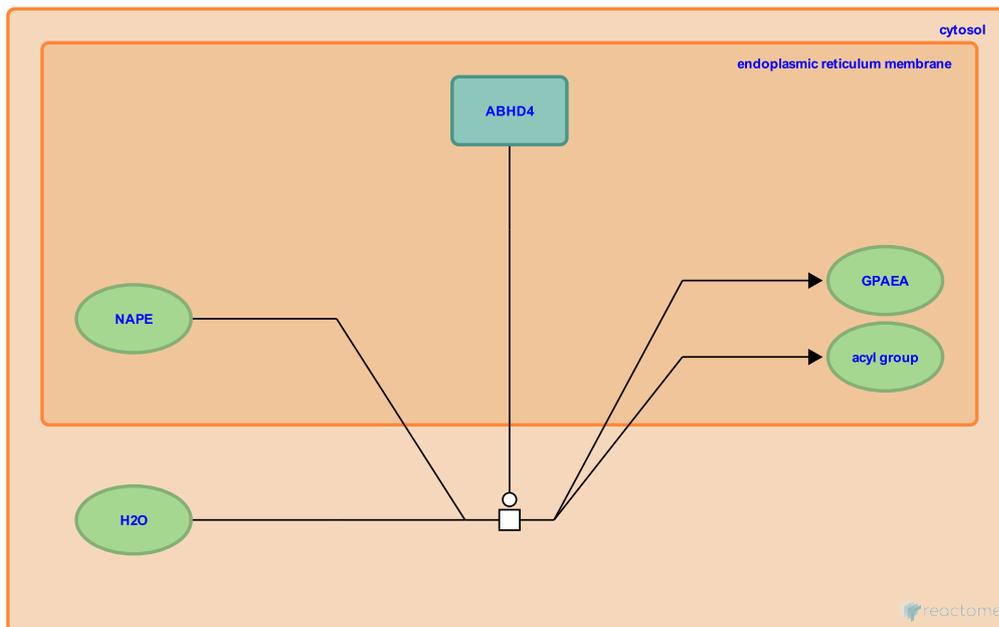
Location: [Acyl chain remodelling of PE](#)

Stable identifier: R-SPO-5694583

Type: transition

Compartments: cytosol, endoplasmic reticulum membrane

Inferred from: [ABHD4 hydrolyses NAPE \(Homo sapiens\)](#)



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>

Table of Contents

Introduction	1
☒ Acyl chain remodelling of PE	2
↳ PE is hydrolyzed to 1-acyl LPE by PLA2[2]	3
↳ 1-acyl LPE is acylated to PE by LPEAT	4
↳ PE is hydrolyzed to 2-acyl LPE by PLA2[4]	5
↳ PE is hydrolyzed to 2-acyl LPE by PLA2G4C	6
↳ 2-acyl LPE is acylated to PE by LPEAT	7
↳ ABHD4 hydrolyses NAPE	8
Table of Contents	9