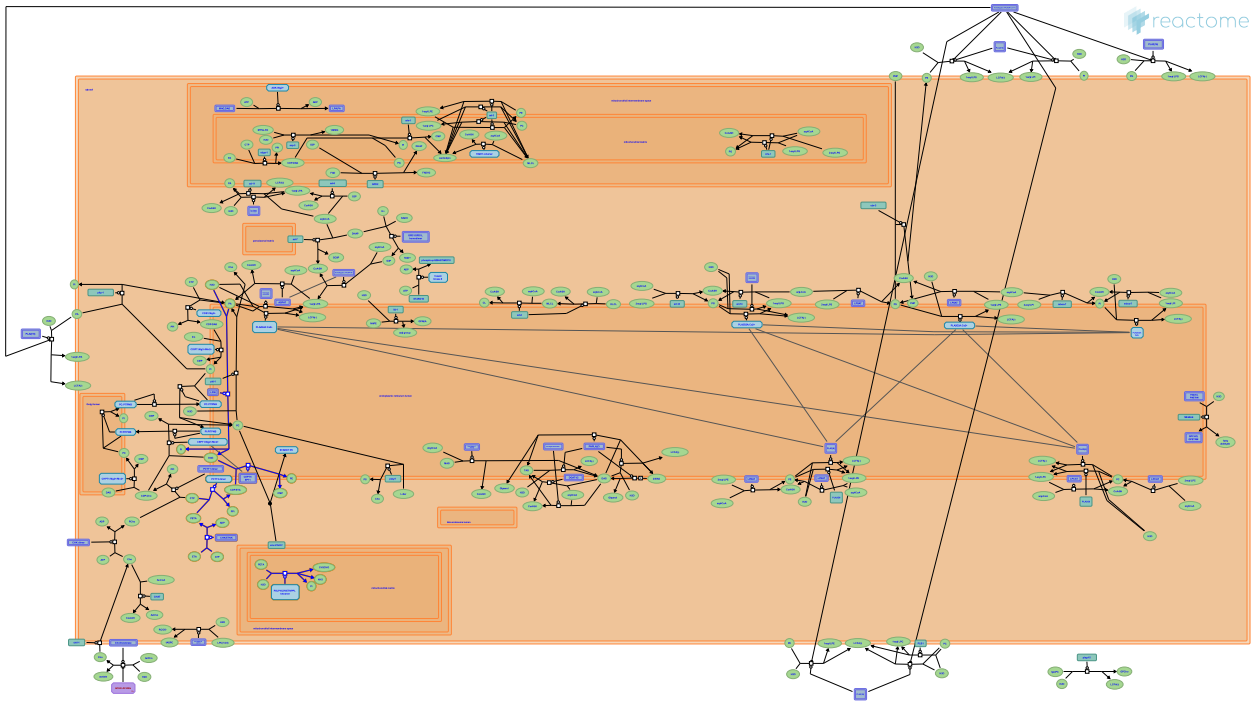
Synthesis of PE



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

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. ↗

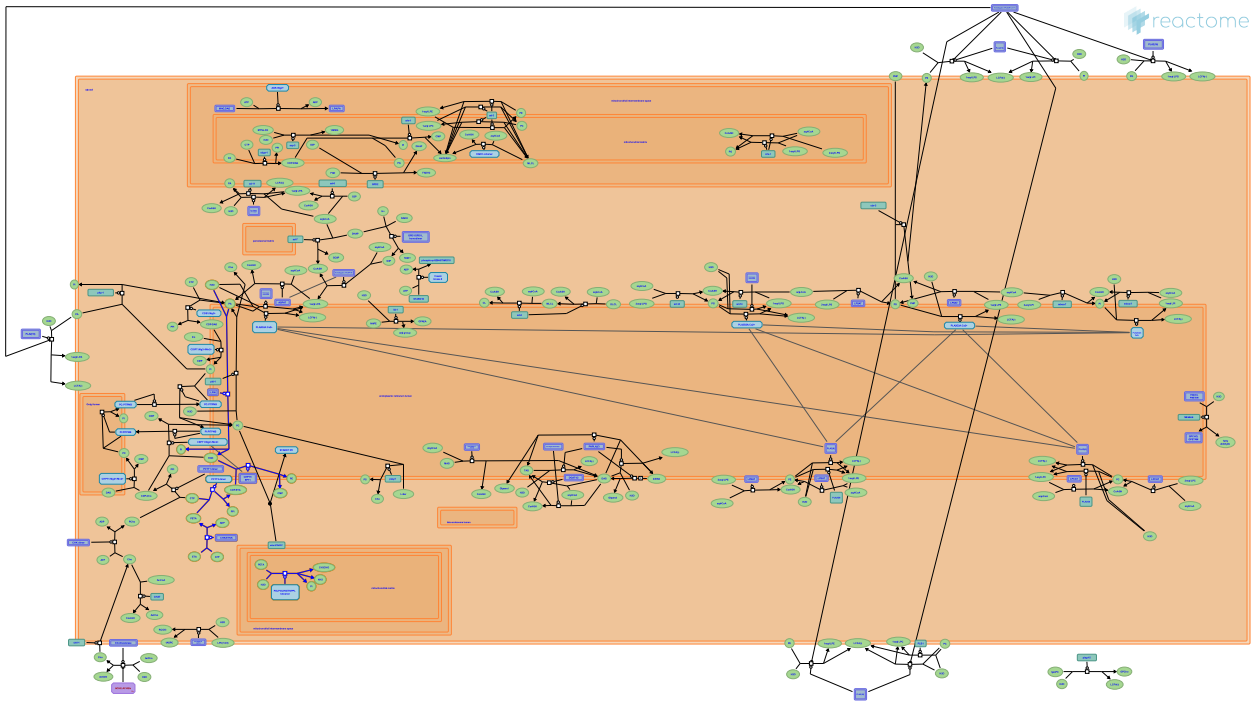
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

Synthesis of PE ↗

Stable identifier: R-CEL-1483213

Inferred from: Synthesis of PE (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

ETA is phosphorylated to PETA by CHK/ETNK ↗

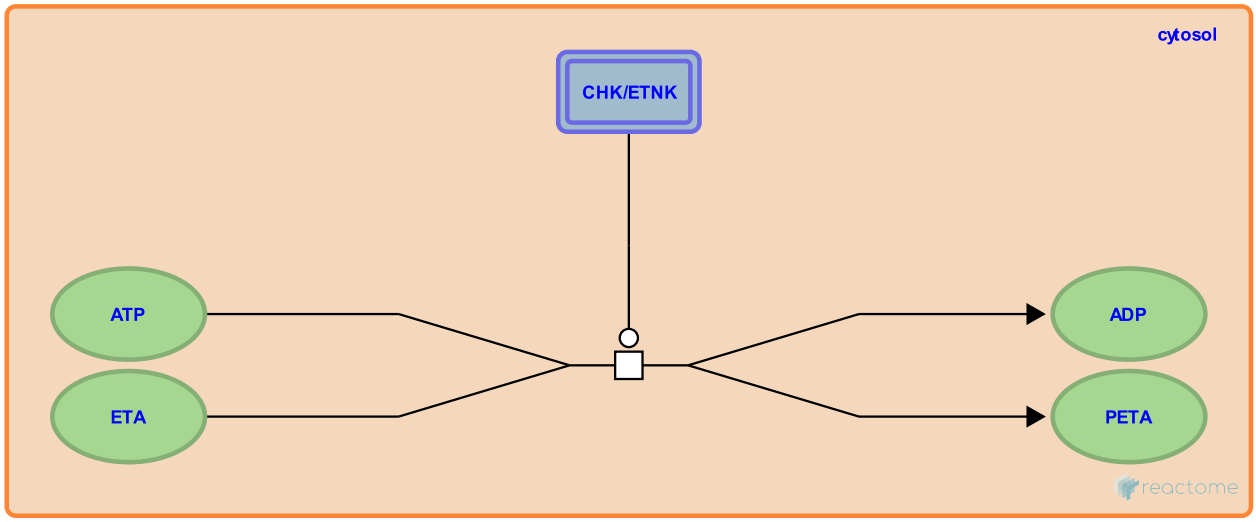
Location: Synthesis of PE

Stable identifier: R-CEL-1483222

Type: transition

Compartments: cytosol

Inferred from: ETA is phosphorylated to PETA by CHK/ETNK (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

Followed by: PXLP-K278-ETNPPL tetramer hydrolyses PETA, PETA and CTP are condensed to CDP-ETA by PCY2

PXLP-K278-ETNPPL tetramer hydrolyses PETA ↗

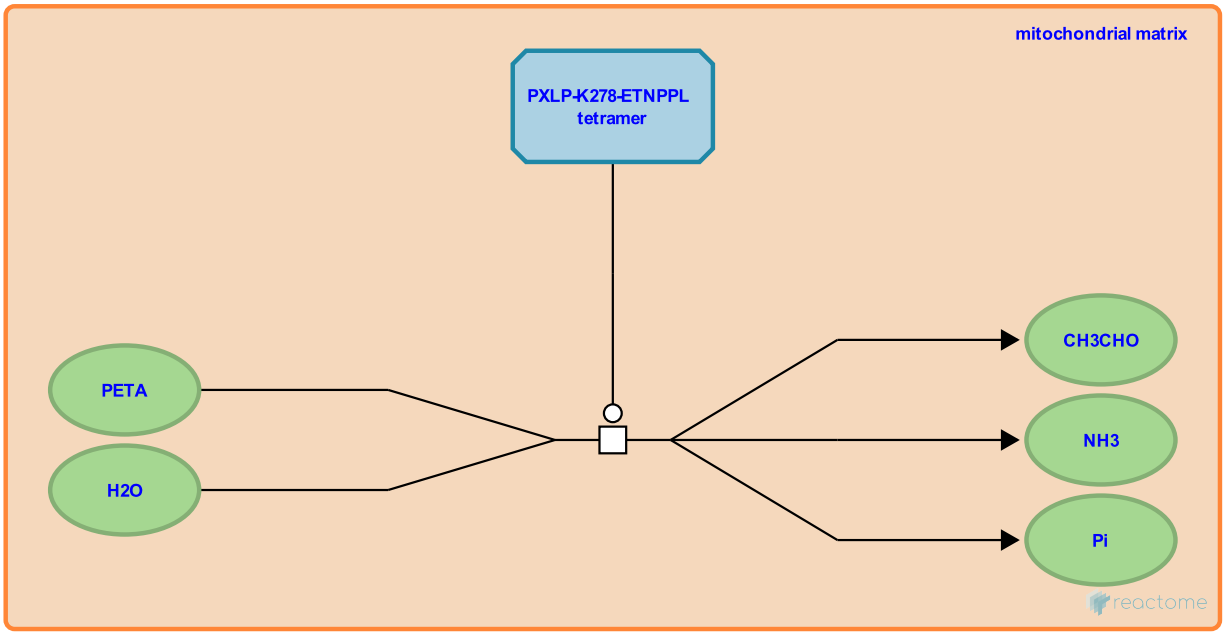
Location: Synthesis of PE

Stable identifier: R-CEL-5696415

Type: transition

Compartments: mitochondrial matrix

Inferred from: PXLP-K278-ETNPPL tetramer hydrolyses PETA (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: ETA is phosphorylated to PETA by CHK/ETNK

PETA and CTP are condensed to CDP-ETA by PCY2 ↗

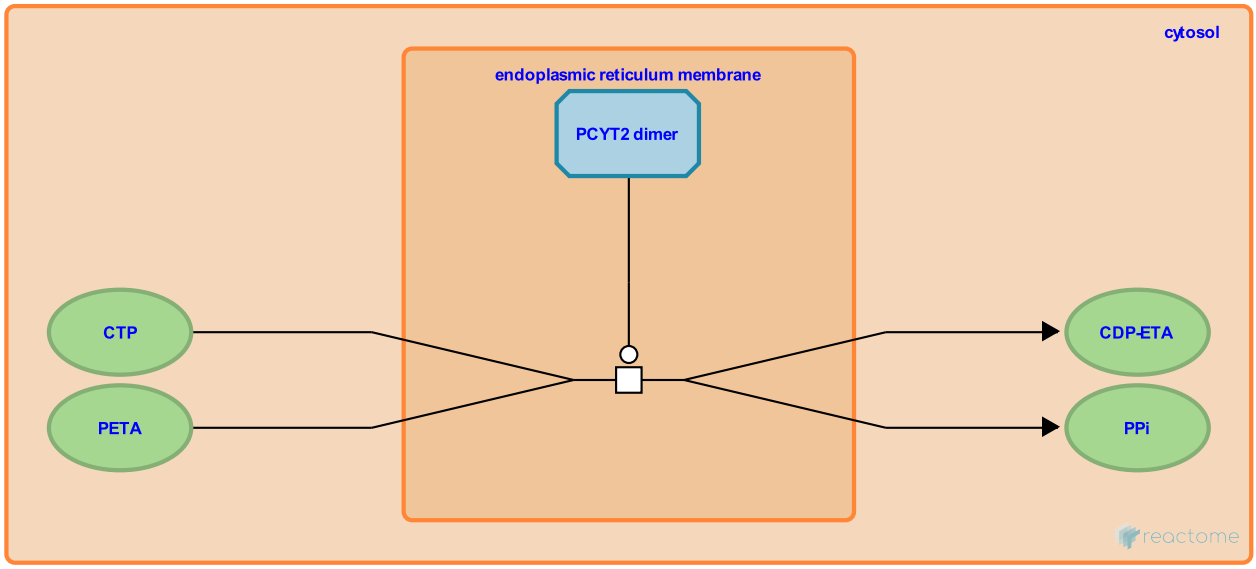
Location: Synthesis of PE

Stable identifier: R-CEL-1483190

Type: transition

Compartments: endoplasmic reticulum membrane, cytosol

Inferred from: PETA and CTP are condensed to CDP-ETA by PCY2 (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: ETA is phosphorylated to PETA by CHK/ETNK

Followed by: CDP-ETA and DAG are converted to PE by CEPT1/EPT1

PA is dephosphorylated to DAG by LPIN ↗

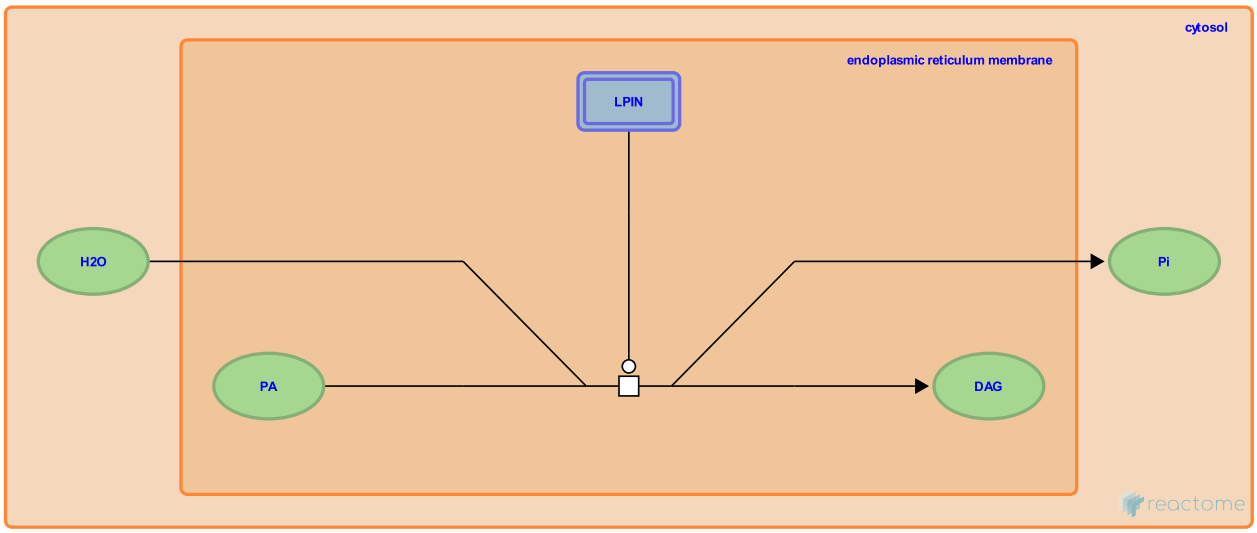
Location: Synthesis of PE

Stable identifier: R-CEL-1483203

Type: transition

Compartments: endoplasmic reticulum membrane, cytosol

Inferred from: PA is dephosphorylated to DAG by LPIN (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: CDP-ETA and DAG are converted to PE by CEPT1/EPT1

CDP-ETA and DAG are converted to PE by CEPT1/EPT1 ↗

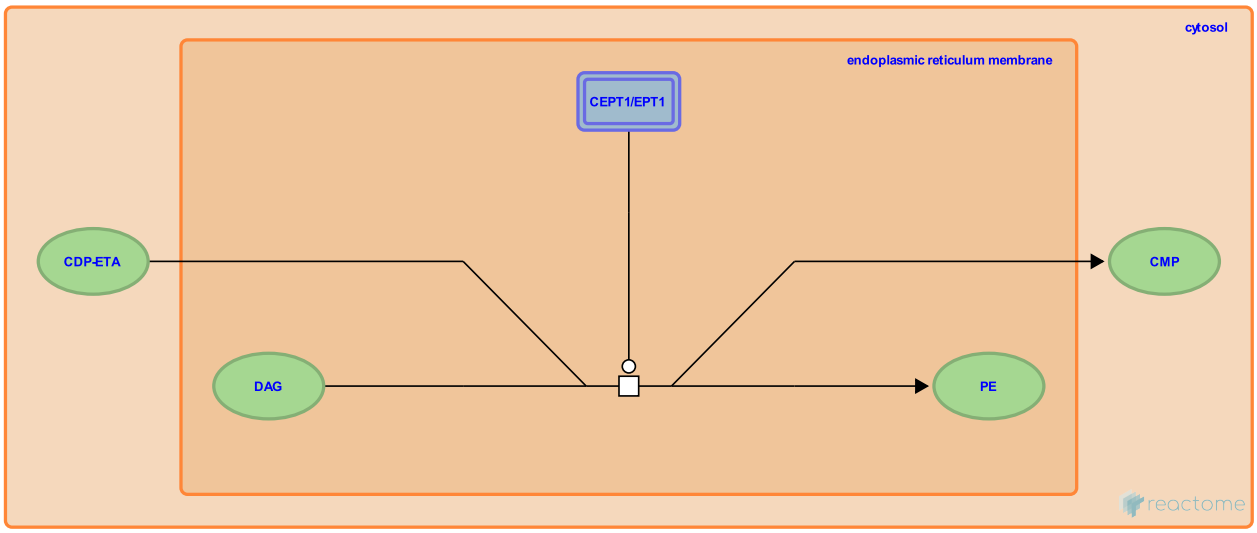
Location: Synthesis of PE

Stable identifier: R-CEL-1482962

Type: transition

Compartments: endoplasmic reticulum membrane, cytosol

Inferred from: CDP-ETA and DAG are converted to PE by CEPT1/EPT1 (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: PA is dephosphorylated to DAG by LPIN, PETA and CTP are condensed to CDP-ETA by PCY2

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