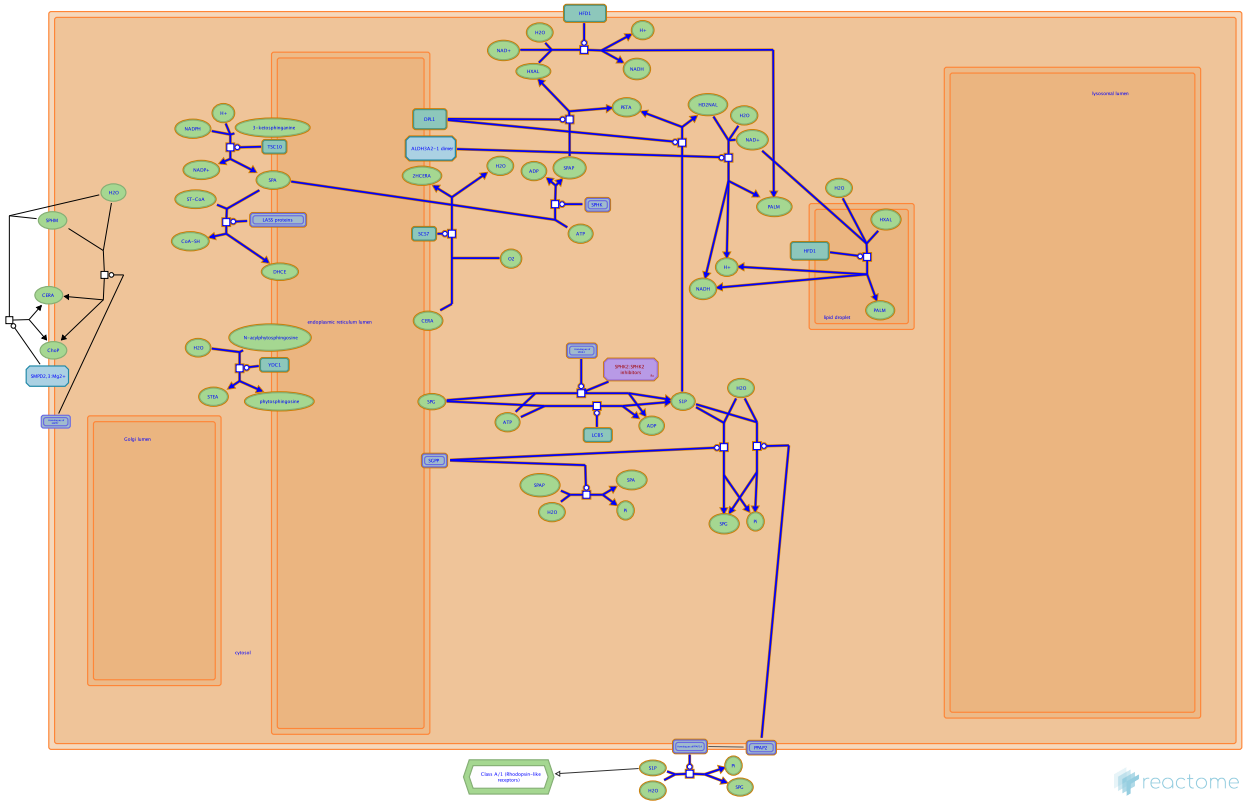
Sphingolipid de novo biosynthesis



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

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29/08/2021

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. ↗

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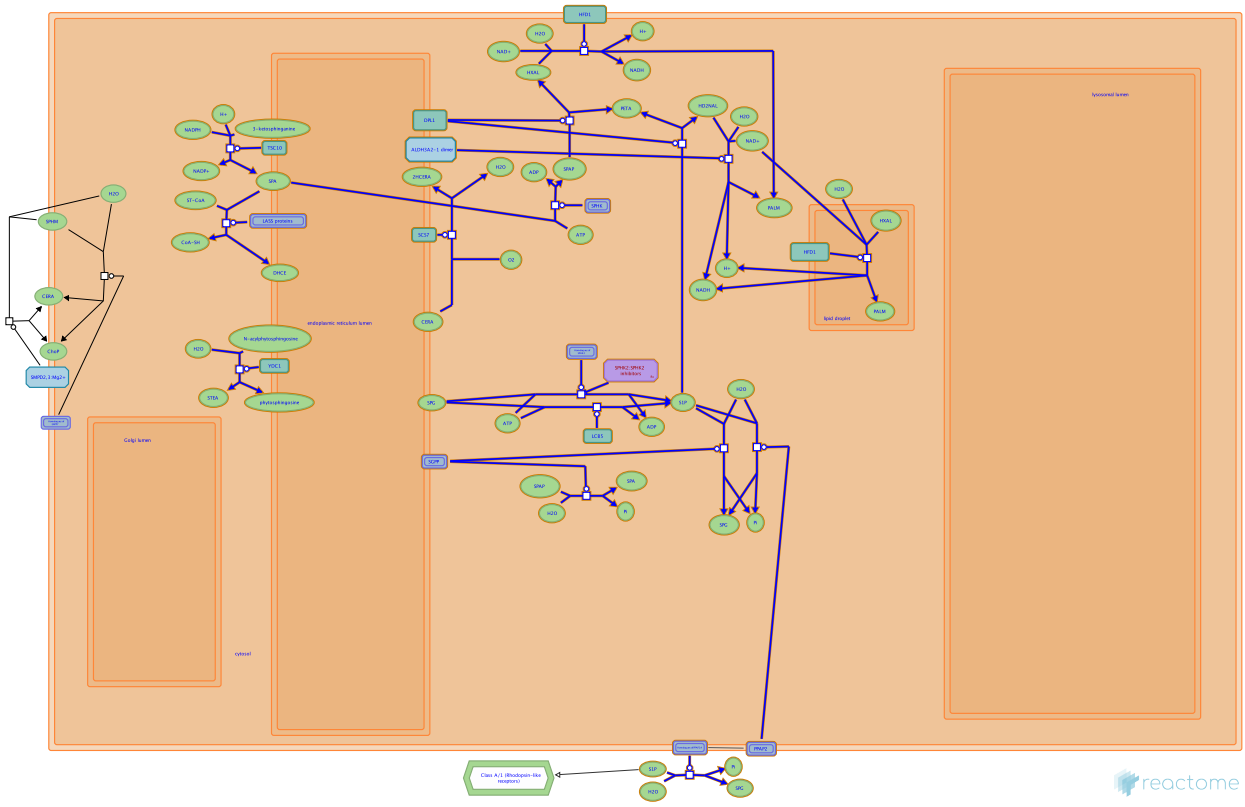
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

Sphingolipid de novo biosynthesis ↗

Stable identifier: R-SCE-1660661

Inferred from: Sphingolipid de novo biosynthesis (Homo sapiens)



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

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3-ketosphinganine + NADPH + H+ => sphinganine + NADP+ ↗

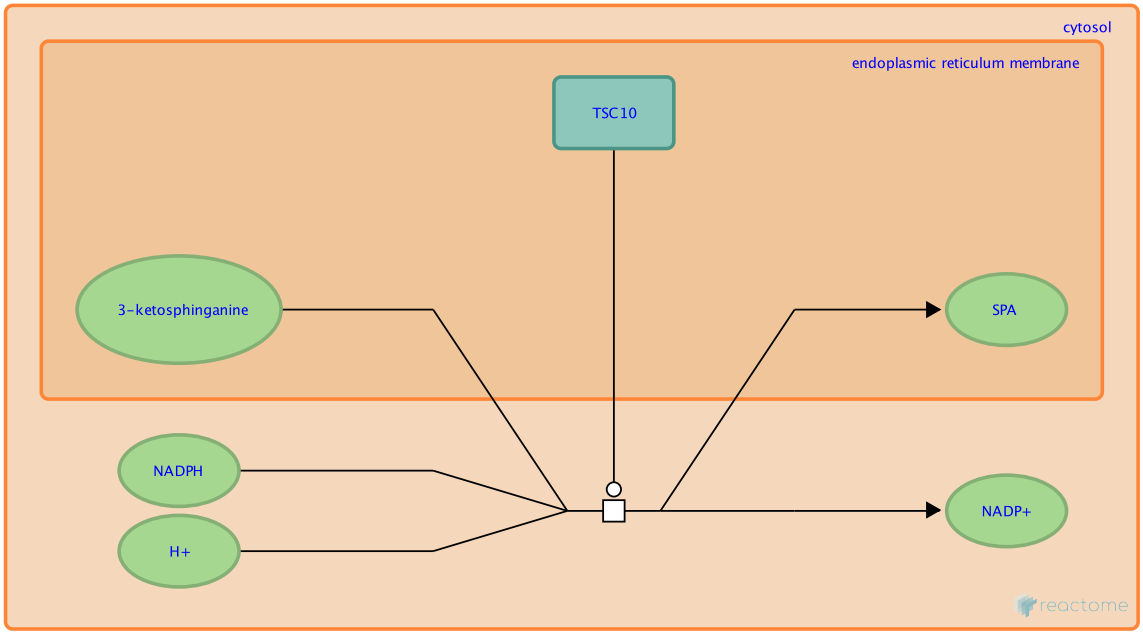
Location: Sphingolipid de novo biosynthesis

Stable identifier: R-SCE-428123

Type: transition

Compartments: cytosol, endoplasmic reticulum membrane

Inferred from: 3-ketosphinganine + NADPH + H+ => sphinganine + NADP+ (Homo sapiens)



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FA2H hydroxylates CERA ↗

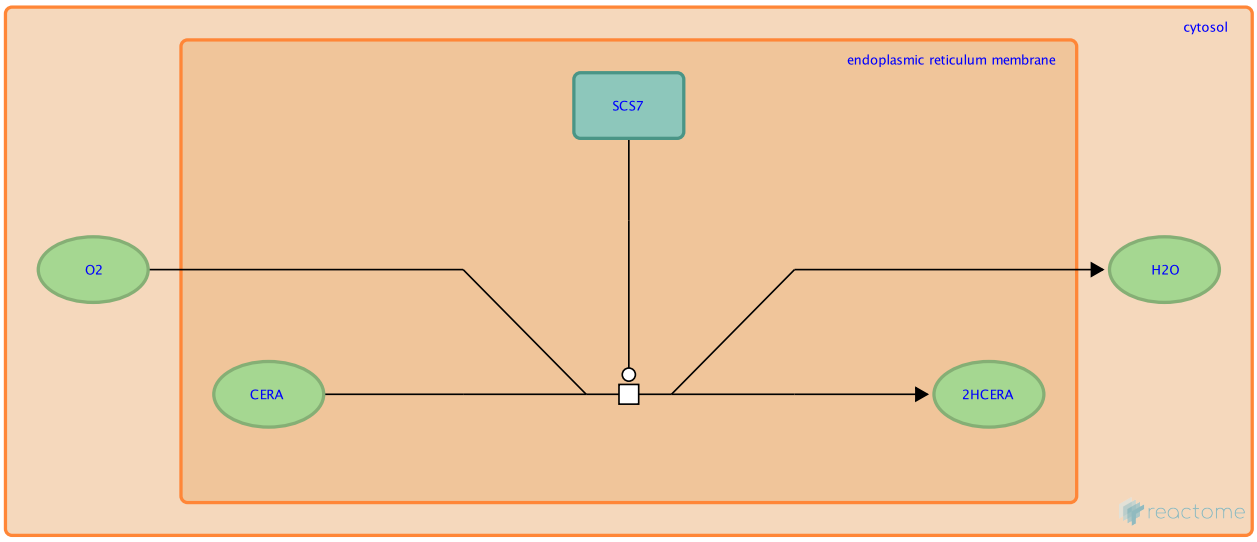
Location: Sphingolipid de novo biosynthesis

Stable identifier: R-SCE-5693761

Type: transition

Compartments: endoplasmic reticulum membrane, cytosol

Inferred from: FA2H hydroxylates CERA (Homo sapiens)



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phytoceramide + H2O => stearate + phytosphingosine ↗

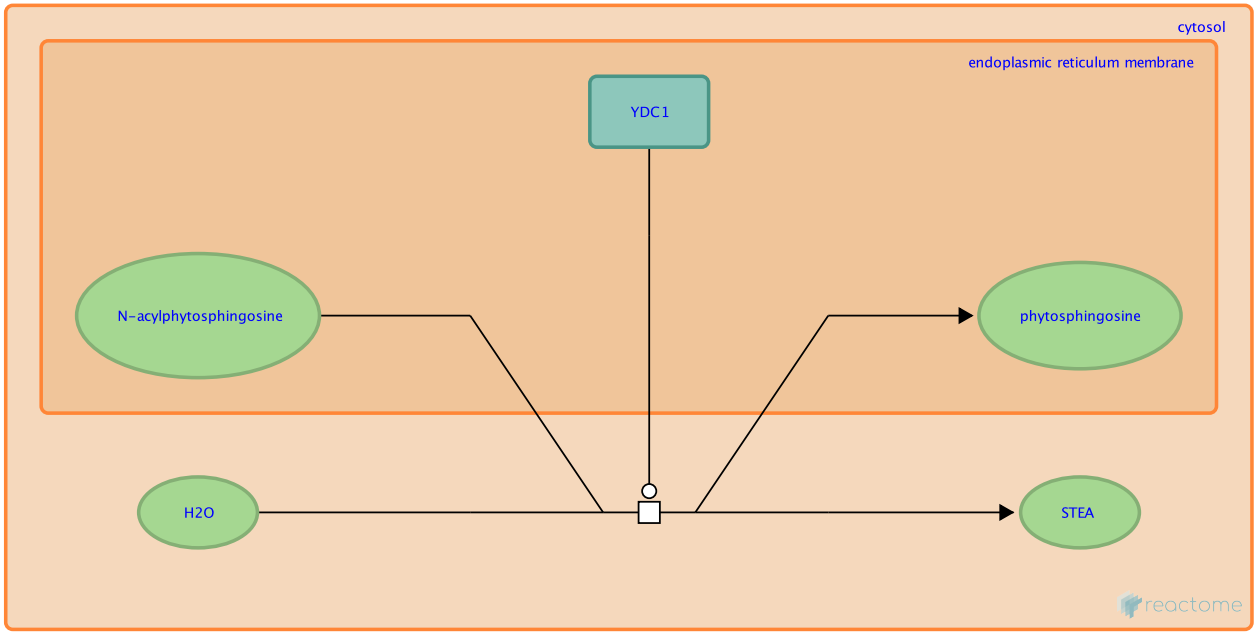
Location: Sphingolipid de novo biosynthesis

Stable identifier: R-SCE-428262

Type: transition

Compartments: cytosol, endoplasmic reticulum membrane

Inferred from: phytoceramide + H2O => stearate + phytosphingosine (Homo sapiens)



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sphinganine (dihydrosphingosine) +ATP => sphinganine 1-phosphate + ADP ↗

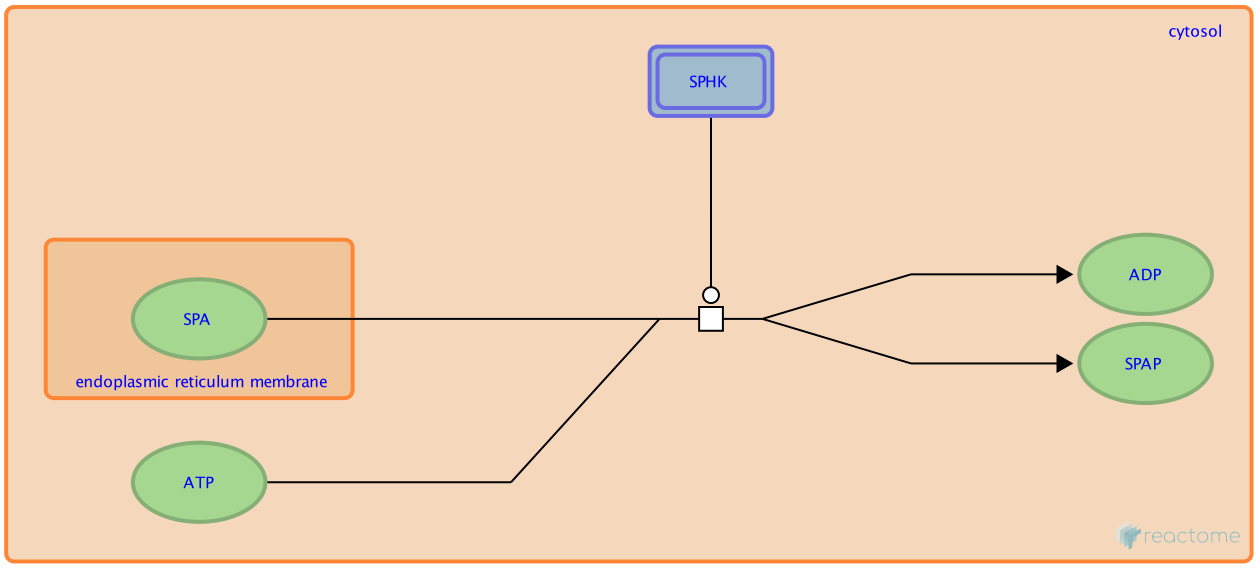
Location: Sphingolipid de novo biosynthesis

Stable identifier: R-SCE-428214

Type: transition

Compartments: cytosol, endoplasmic reticulum membrane

Inferred from: sphinganine (dihydrosphingosine) +ATP => sphinganine 1-phosphate + ADP (Homo sapiens)



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Preceded by: sphinganine 1-phosphate + H2O => sphinganine + orthophosphate

sphinganine + stearyl-CoA => dihydroceramide + CoASH ↗

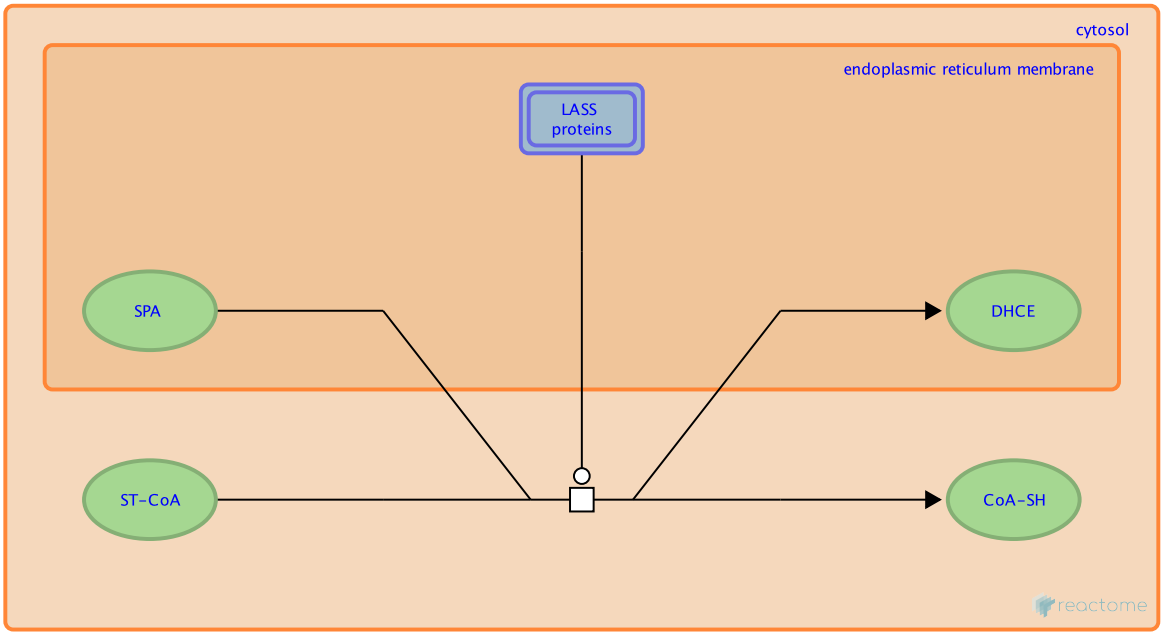
Location: Sphingolipid de novo biosynthesis

Stable identifier: R-SCE-428185

Type: transition

Compartments: cytosol, endoplasmic reticulum membrane

Inferred from: sphinganine + stearyl-CoA => dihydroceramide + CoASH (Homo sapiens)



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sphinganine 1-phosphate + H2O => sphinganine + orthophosphate ↗

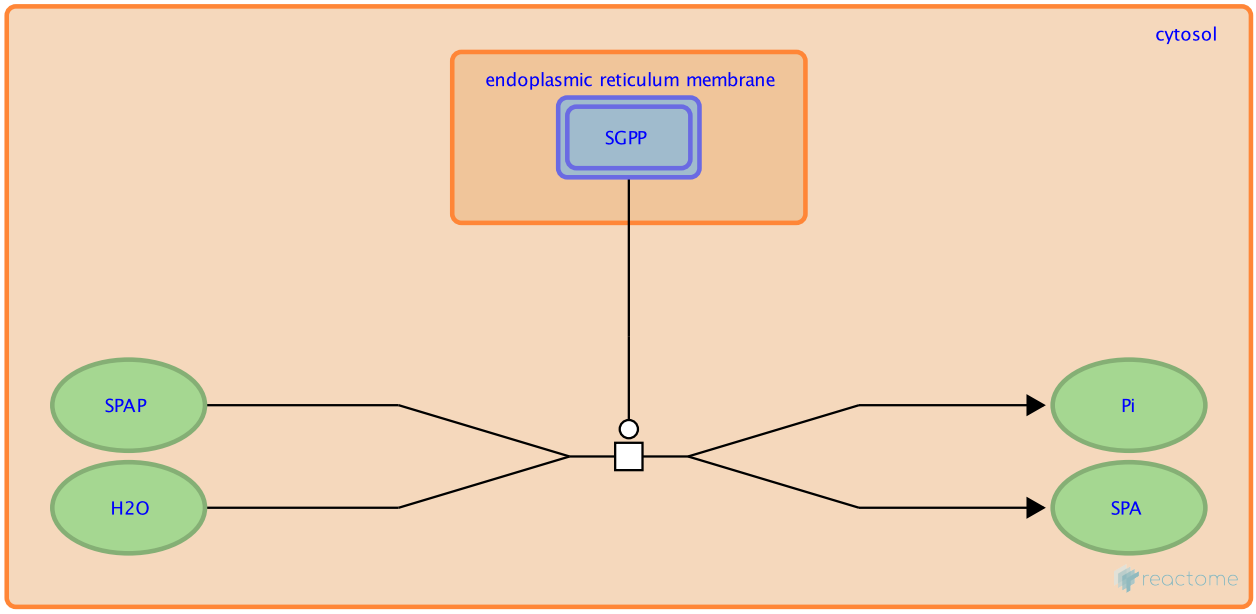
Location: Sphingolipid de novo biosynthesis

Stable identifier: R-SCE-428664

Type: transition

Compartments: cytosol, endoplasmic reticulum membrane

Inferred from: sphinganine 1-phosphate + H2O => sphinganine + orthophosphate (Homo sapiens)



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Followed by: sphinganine (dihydrosphingosine) +ATP => sphinganine 1-phosphate + ADP

sphinganine 1-phosphate => phosphoethanolamine + hexadecanal ↗

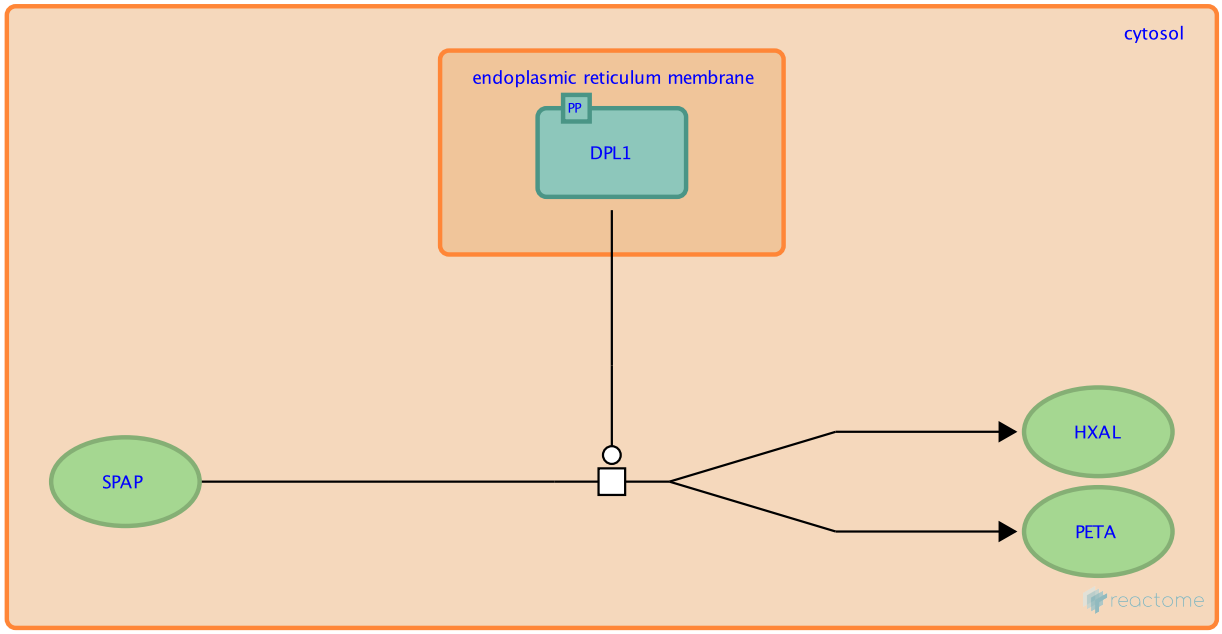
Location: Sphingolipid de novo biosynthesis

Stable identifier: R-SCE-428681

Type: transition

Compartments: cytosol, endoplasmic reticulum membrane

Inferred from: sphinganine 1-phosphate => phosphoethanolamine + hexadecanal (Homo sapiens)



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Followed by: ALDH3B1 oxidises HXAL to PALM

ALDH3B1 oxidises HXAL to PALM ↗

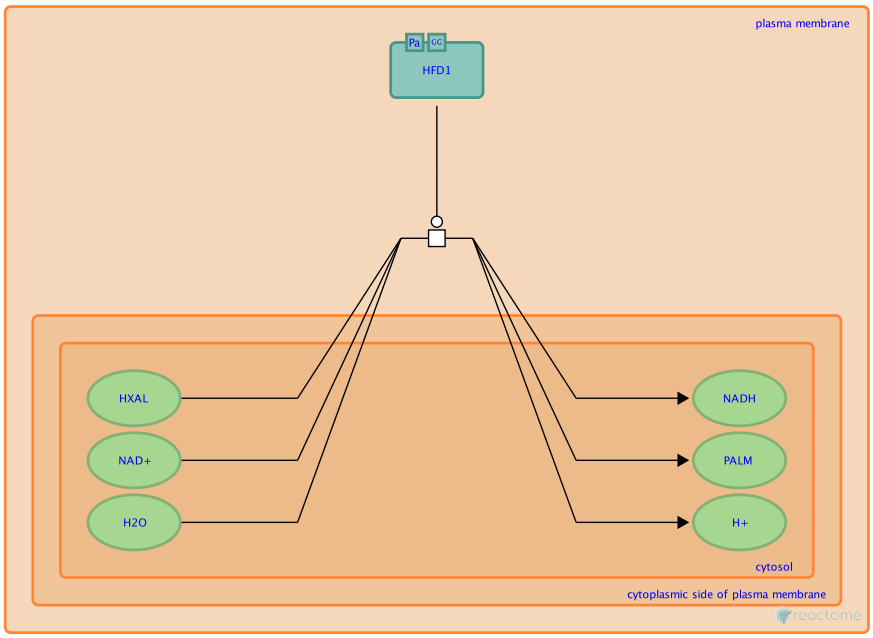
Location: Sphingolipid de novo biosynthesis

Stable identifier: R-SCE-5696080

Type: transition

Compartments: plasma membrane, cytosol

Inferred from: ALDH3B1 oxidises HXAL to PALM (Homo sapiens)



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Preceded by: sphinganine 1-phosphate => phosphoethanolamine + hexadecanal

SPHK1 phosphorylates SPG to S1P ↗

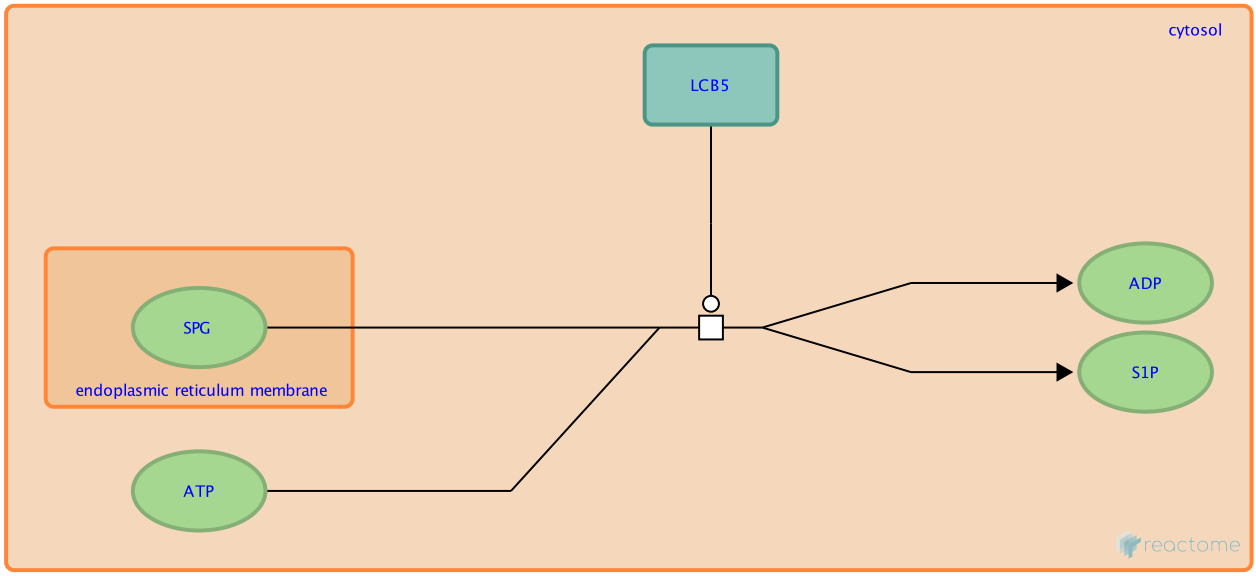
Location: Sphingolipid de novo biosynthesis

Stable identifier: R-SCE-428273

Type: transition

Compartments: cytosol, endoplasmic reticulum membrane

Inferred from: SPHK1 phosphorylates SPG to S1P (Homo sapiens)



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Preceded by: sphingosine 1-phosphate + H2O => sphingosine + orthophosphate [cytosolic - PPAP]

SPHK2 phosphorylates SPG to S1P ↗

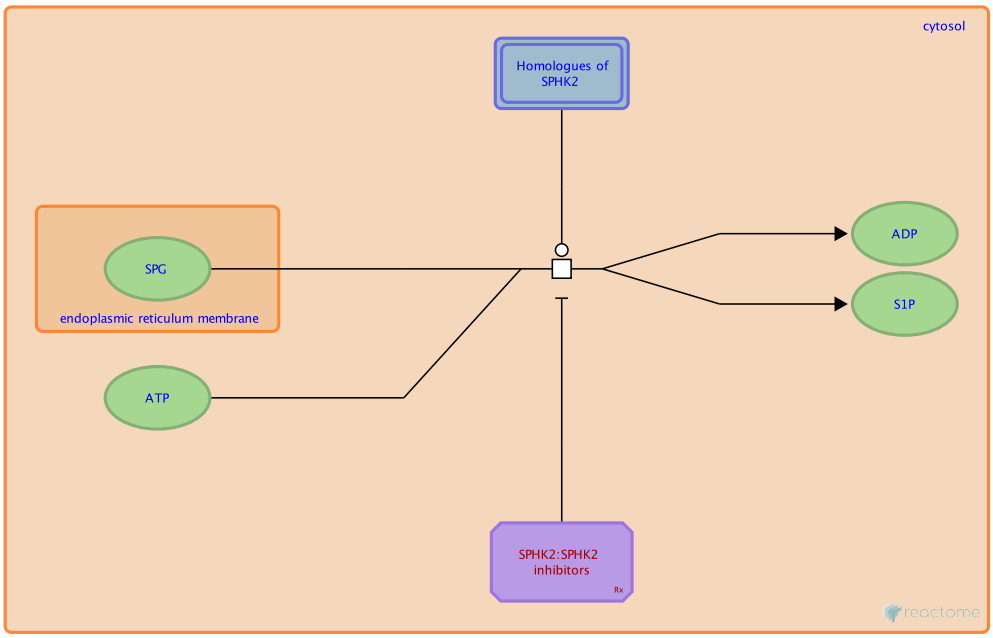
Location: Sphingolipid de novo biosynthesis

Stable identifier: R-SCE-9695949

Type: transition

Compartments: cytosol, endoplasmic reticulum membrane

Inferred from: SPHK2 phosphorylates SPG to S1P (Homo sapiens)



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Preceded by: sphingosine 1-phosphate + H2O => sphingosine + orthophosphate [cytosolic - PPAP]

sphingosine 1-phosphate + H2O => sphingosine + orthophosphate [cytosolic - PPAP]

↗

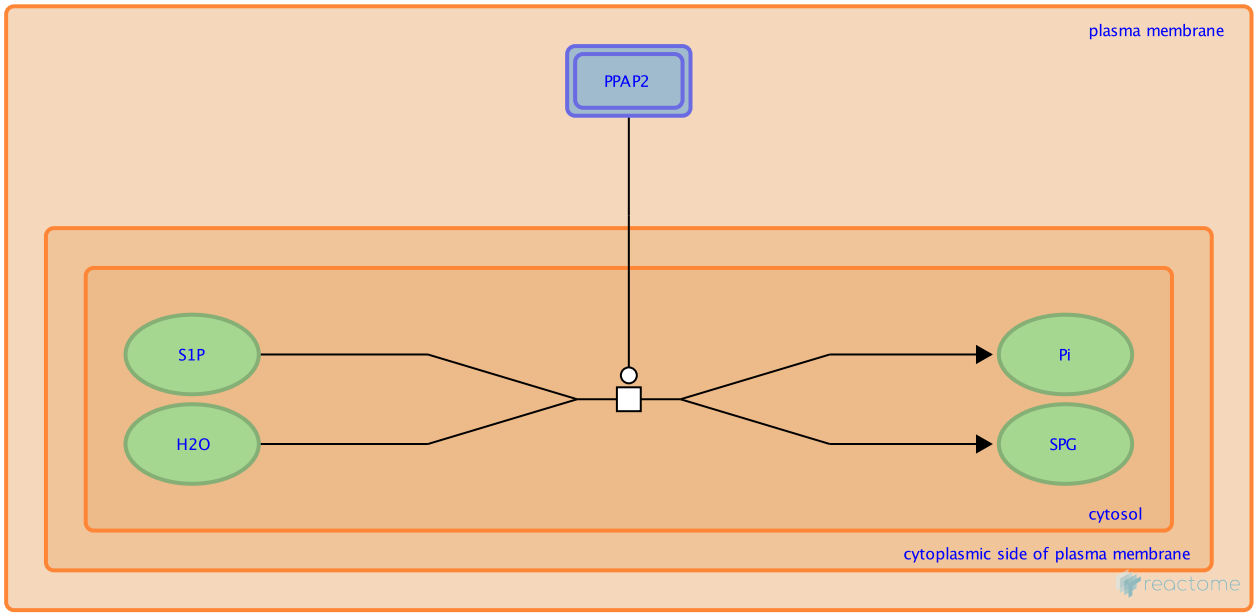
Location: Sphingolipid de novo biosynthesis

Stable identifier: R-SCE-428696

Type: transition

Compartments: cytosol, plasma membrane

Inferred from: sphingosine 1-phosphate + H2O => sphingosine + orthophosphate [cytosolic - PPAP] (Homo sapiens)



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Followed by: SPHK2 phosphorylates SPG to S1P, SPHK1 phosphorylates SPG to S1P

sphingosine 1-phosphate + H2O => sphingosine + orthophosphate [cytosolic - SGPP]

↗

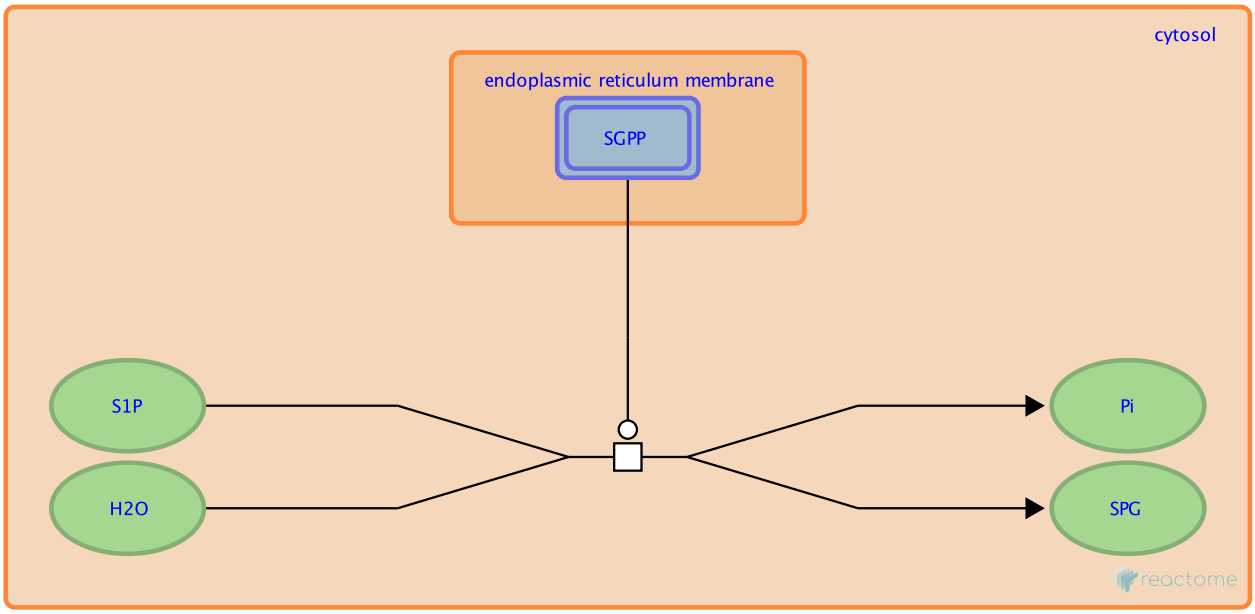
Location: Sphingolipid de novo biosynthesis

Stable identifier: R-SCE-428701

Type: transition

Compartments: cytosol, endoplasmic reticulum membrane

Inferred from: sphingosine 1-phosphate + H2O => sphingosine + orthophosphate [cytosolic - SGPP] (Homo sapiens)



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sphingosine 1-phosphate + H2O => sphingosine + orthophosphate [extracellular] ↗

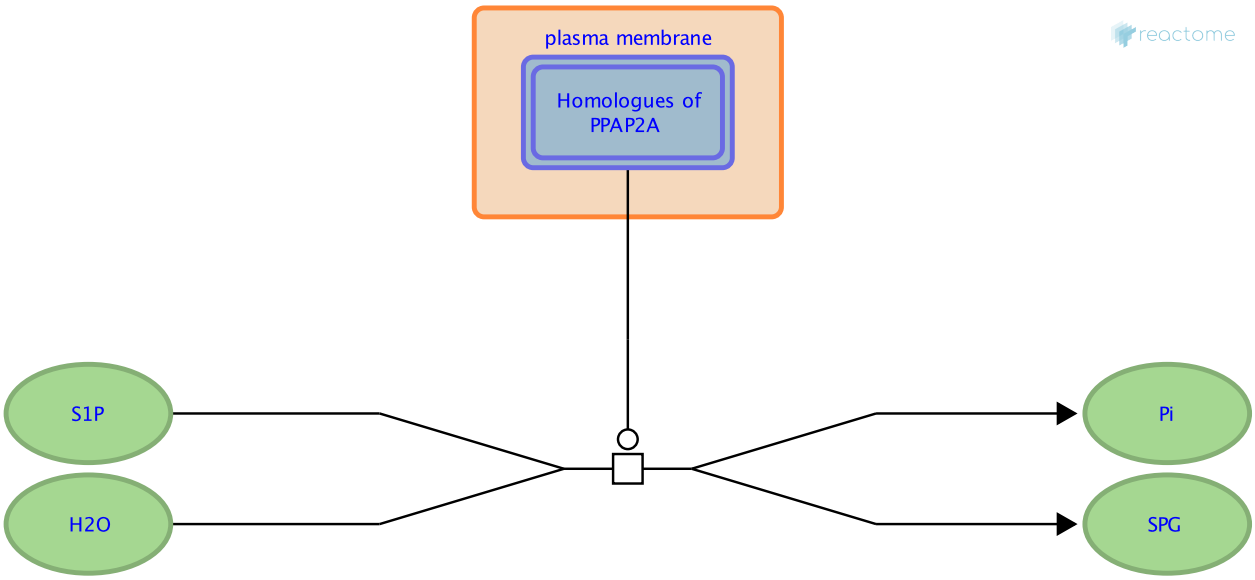
Location: Sphingolipid de novo biosynthesis

Stable identifier: R-SCE-428690

Type: transition

Compartments: extracellular region, plasma membrane

Inferred from: sphingosine 1-phosphate + H2O => sphingosine + orthophosphate [extracellular] (Homo sapiens)



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sphingosine 1-phosphate => phosphoethanolamine + hexadec-2-enal ↗

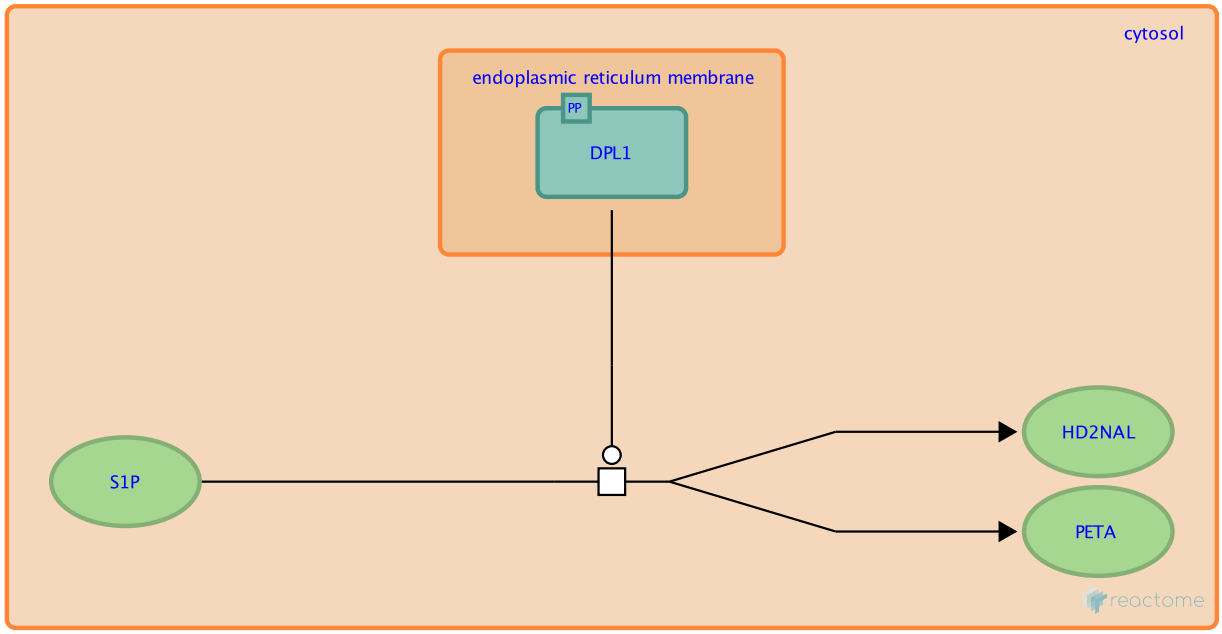
Location: Sphingolipid de novo biosynthesis

Stable identifier: R-SCE-428676

Type: transition

Compartments: cytosol, endoplasmic reticulum membrane

Inferred from: sphingosine 1-phosphate => phosphoethanolamine + hexadec-2-enal (Homo sapiens)



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ALDH3A2-1 oxidises HD2NAL to PALM ↗

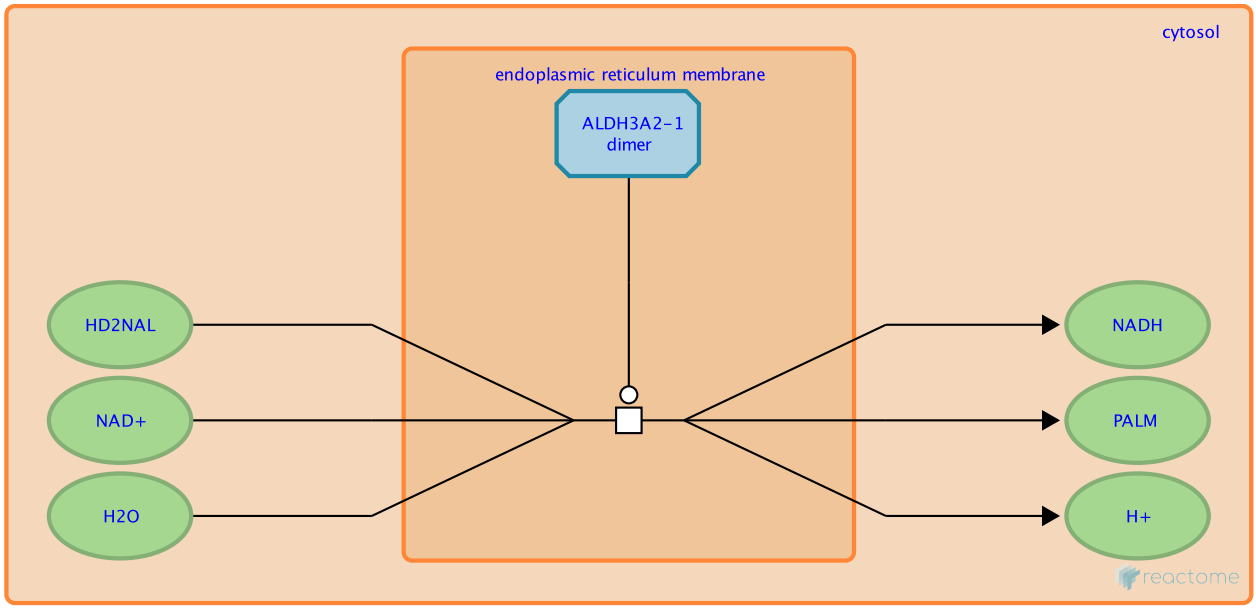
Location: Sphingolipid de novo biosynthesis

Stable identifier: R-SCE-5692261

Type: transition

Compartments: endoplasmic reticulum membrane, cytosol

Inferred from: ALDH3A2-1 oxidises HD2NAL to PALM (Homo sapiens)



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ALDH3B2 oxidises HXAL to PALM ↗

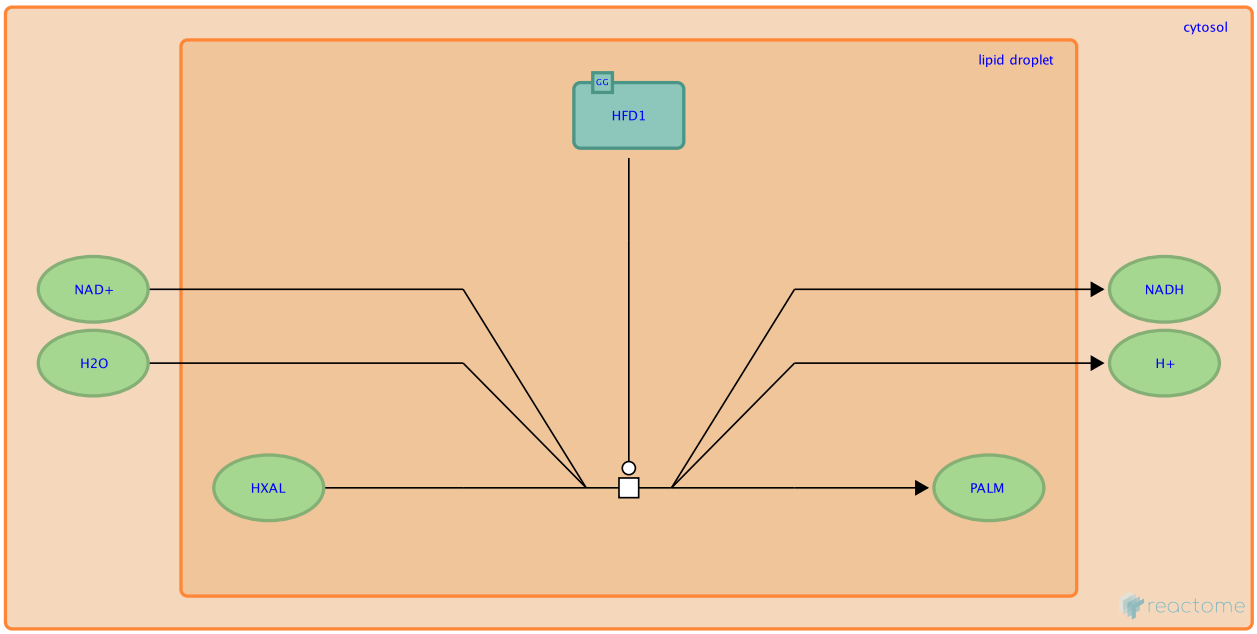
Location: Sphingolipid de novo biosynthesis

Stable identifier: R-SCE-6808464

Type: transition

Compartments: lipid droplet, cytosol

Inferred from: ALDH3B2 oxidises HXAL to PALM (Homo sapiens)



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

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