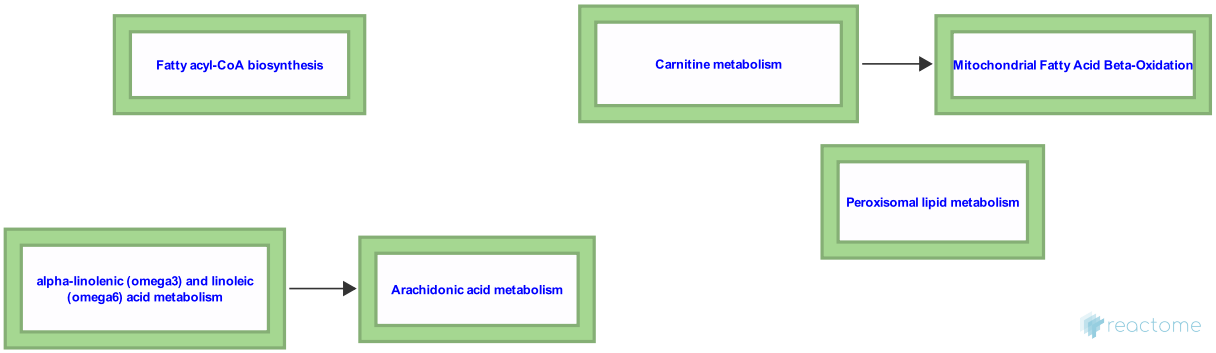
Fatty acid metabolism



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

21/10/2020

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.

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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. ↗

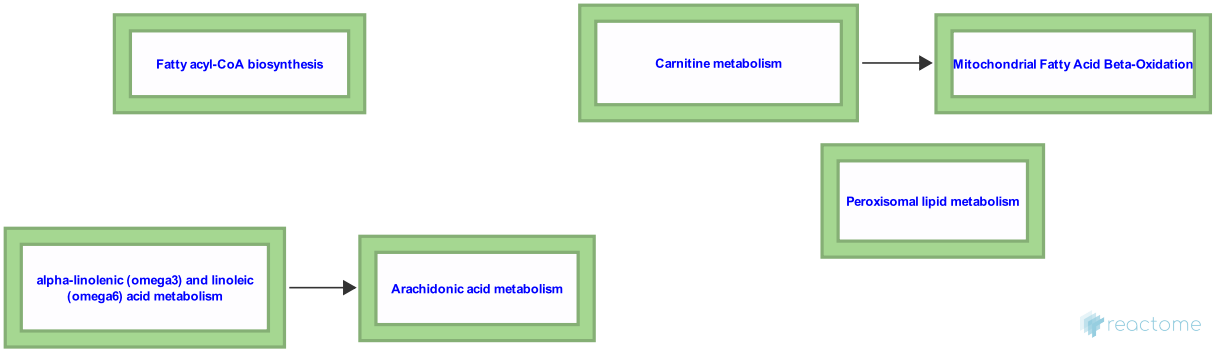
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

Fatty acid metabolism ↗

Stable identifier: R-SCE-8978868

Inferred from: Fatty acid metabolism (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

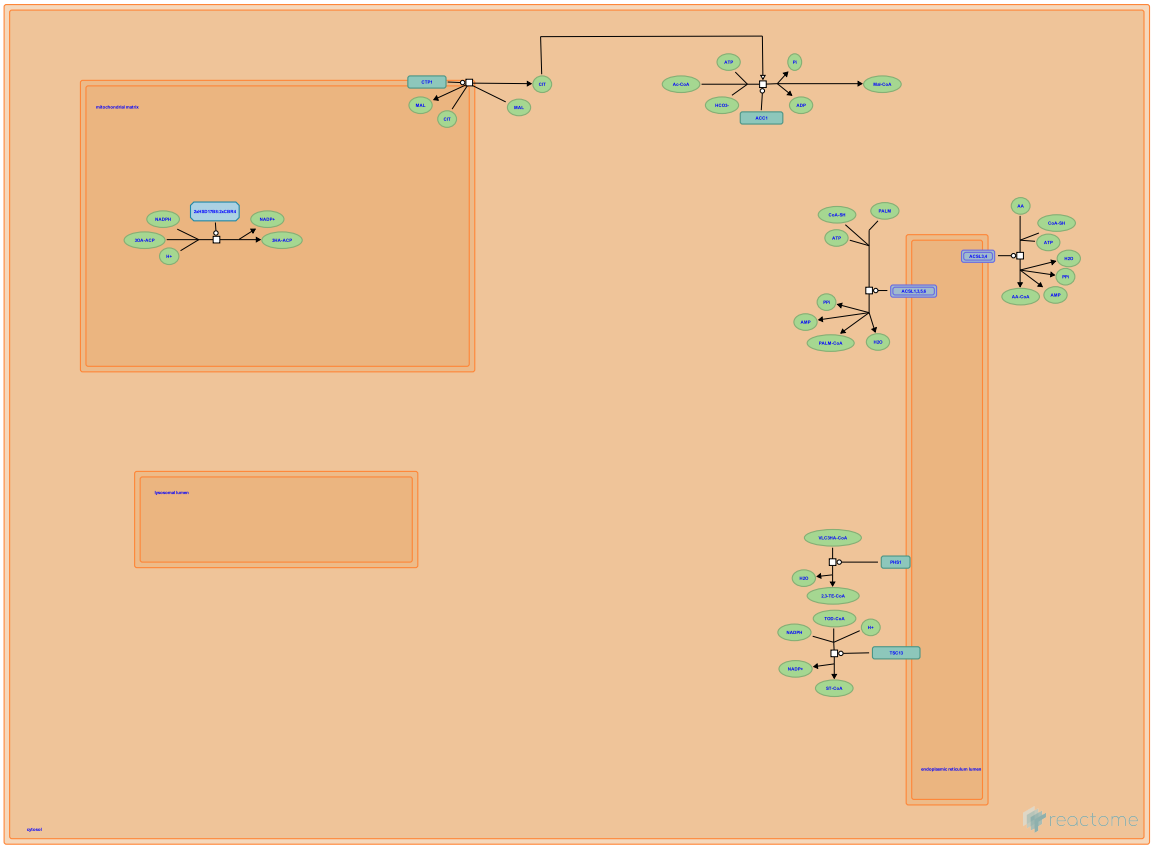
Fatty acyl-CoA biosynthesis ↗

Location: Fatty acid metabolism

Stable identifier: R-SCE-75105

Compartments: cytosol, endoplasmic reticulum membrane

Inferred from: Fatty acyl-CoA biosynthesis (Homo sapiens)



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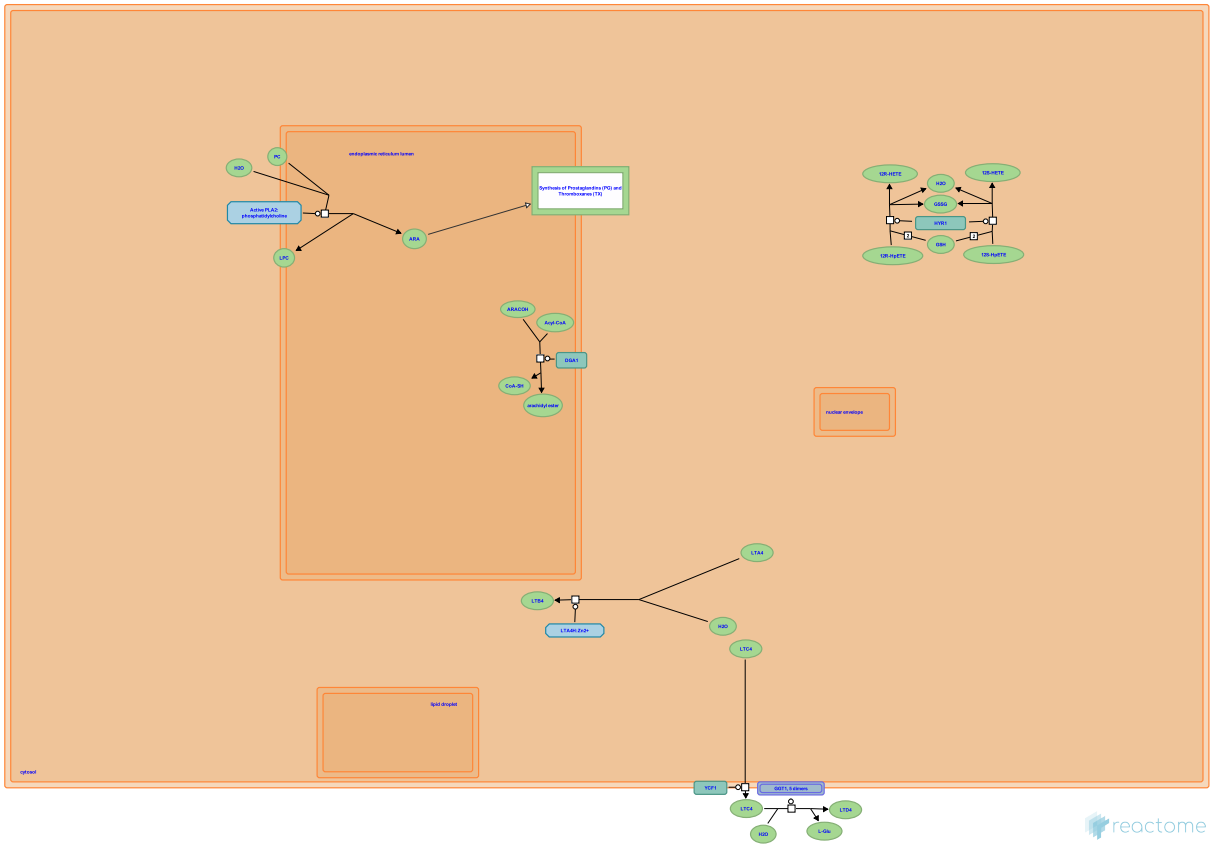
Arachidonic acid metabolism ↗

Location: Fatty acid metabolism

Stable identifier: R-SCE-2142753

Inferred from: Arachidonic acid metabolism (Homo sapiens)



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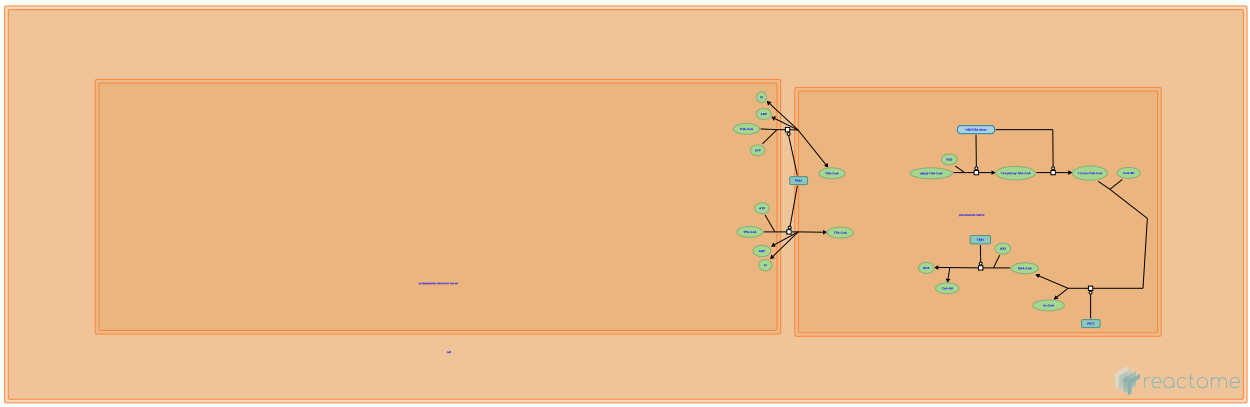
alpha-linolenic (omega3) and linoleic (omega6) acid metabolism ↗

Location: Fatty acid metabolism

Stable identifier: R-SCE-2046104

Compartments: endoplasmic reticulum lumen, endoplasmic reticulum membrane, peroxisomal matrix, peroxisomal membrane

Inferred from: alpha-linolenic (omega3) and linoleic (omega6) acid metabolism (Homo sapiens)



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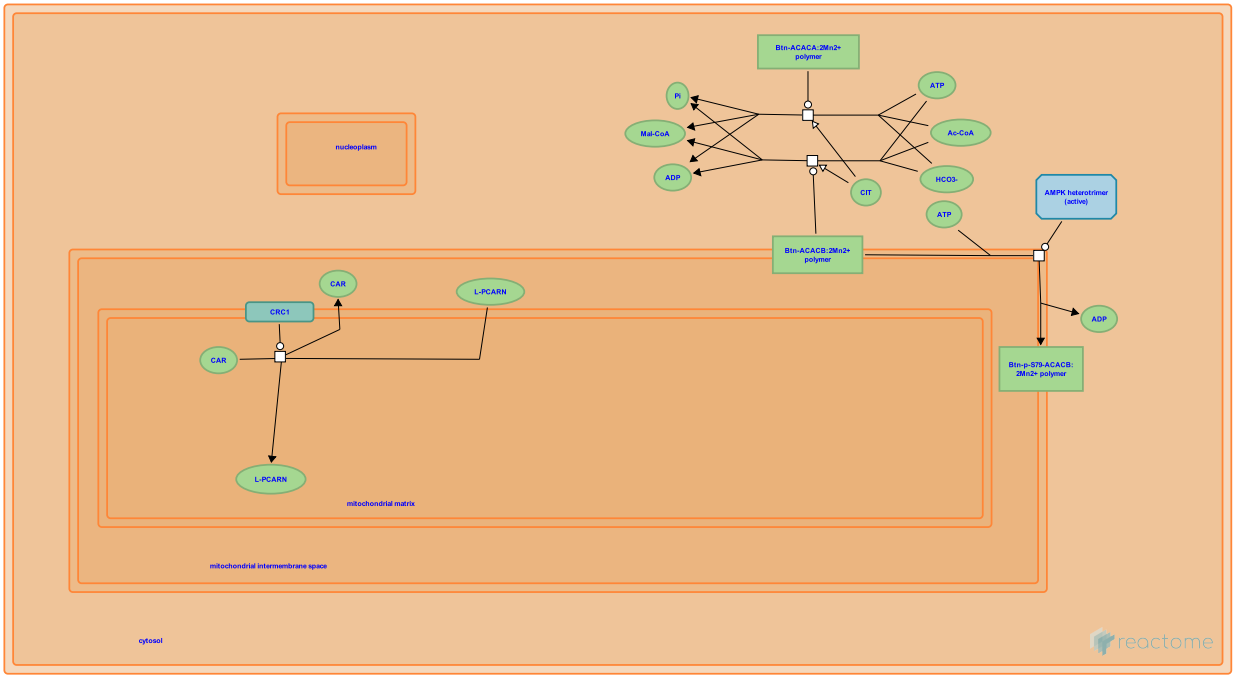
Carnitine metabolism ↗

Location: Fatty acid metabolism

Stable identifier: R-SCE-200425

Compartments: mitochondrion, cytosol

Inferred from: Carnitine metabolism (Homo sapiens)



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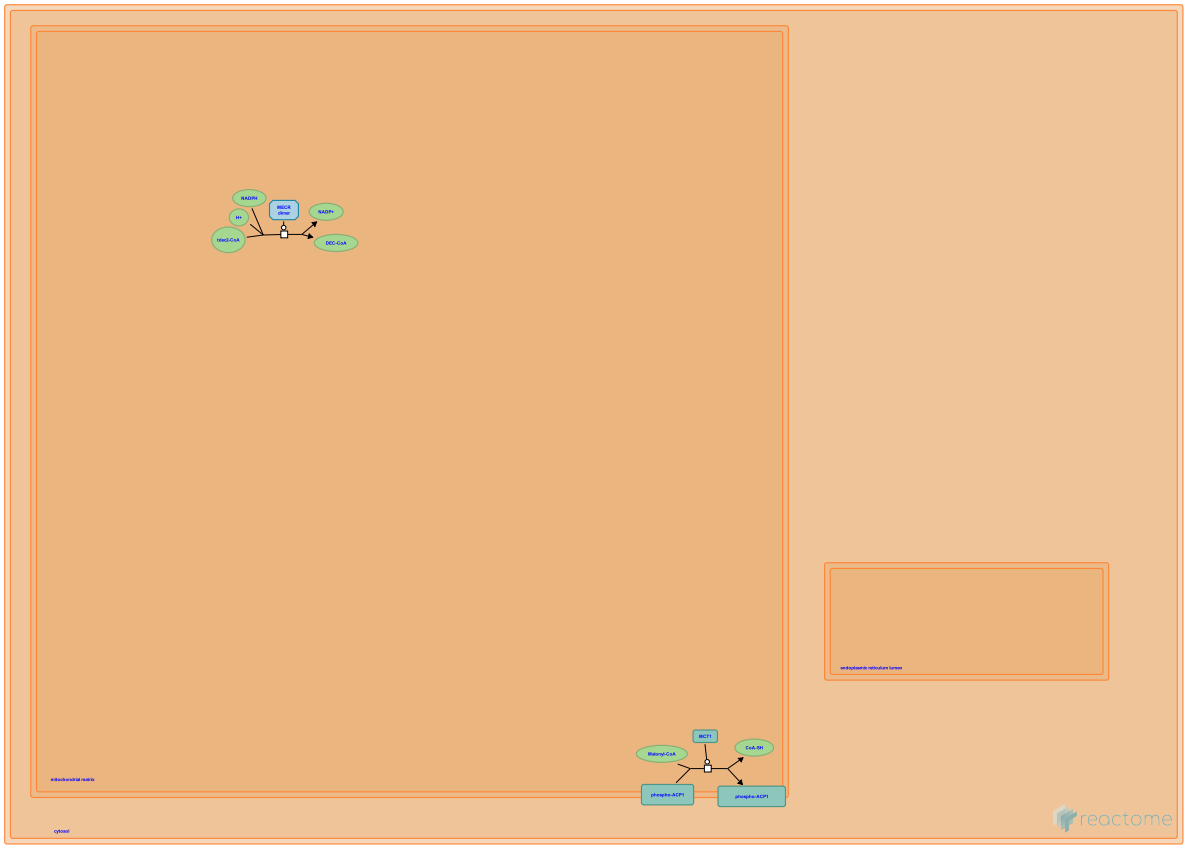
Mitochondrial Fatty Acid Beta-Oxidation ↗

Location: Fatty acid metabolism

Stable identifier: R-SCE-77289

Compartments: mitochondrial matrix

Inferred from: Mitochondrial Fatty Acid Beta-Oxidation (Homo sapiens)



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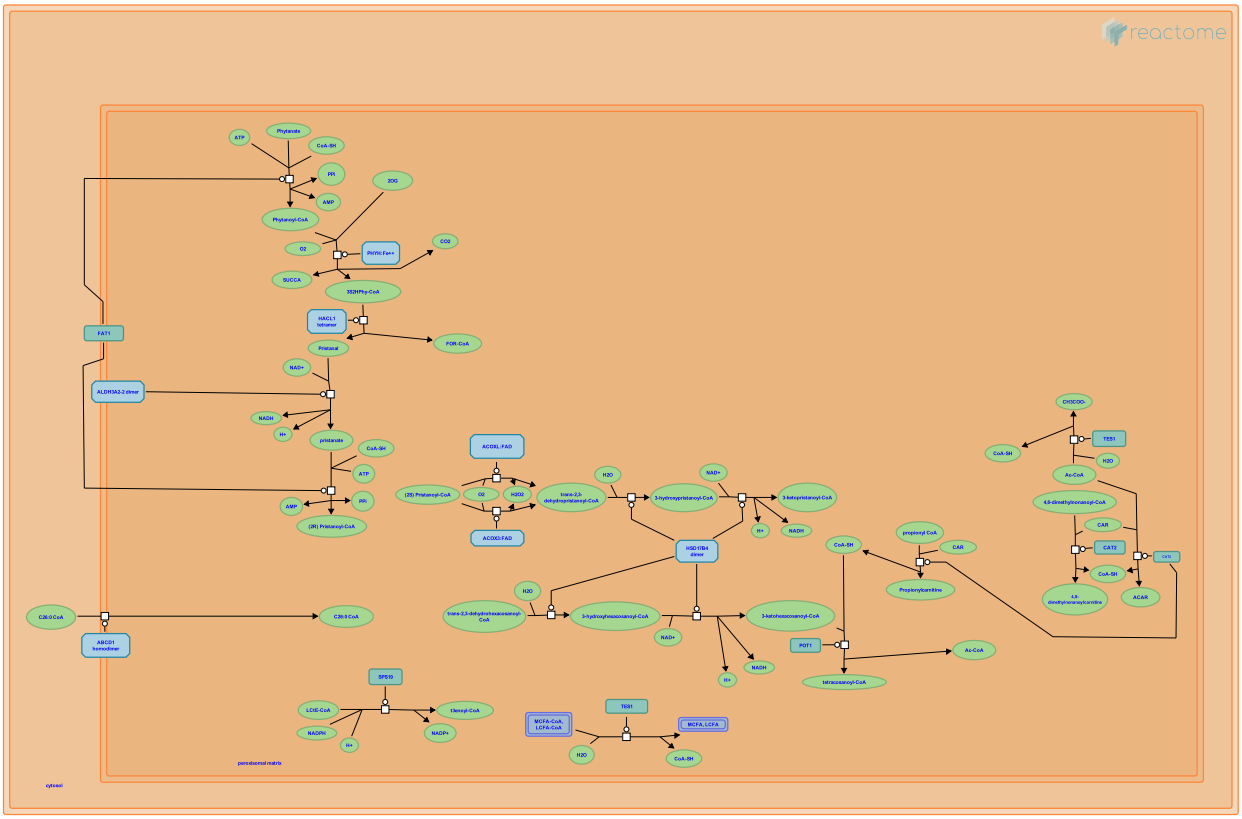
Peroxisomal lipid metabolism ↗

Location: Fatty acid metabolism

Stable identifier: R-SCE-390918

Inferred from: Peroxisomal lipid metabolism (Homo sapiens)



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