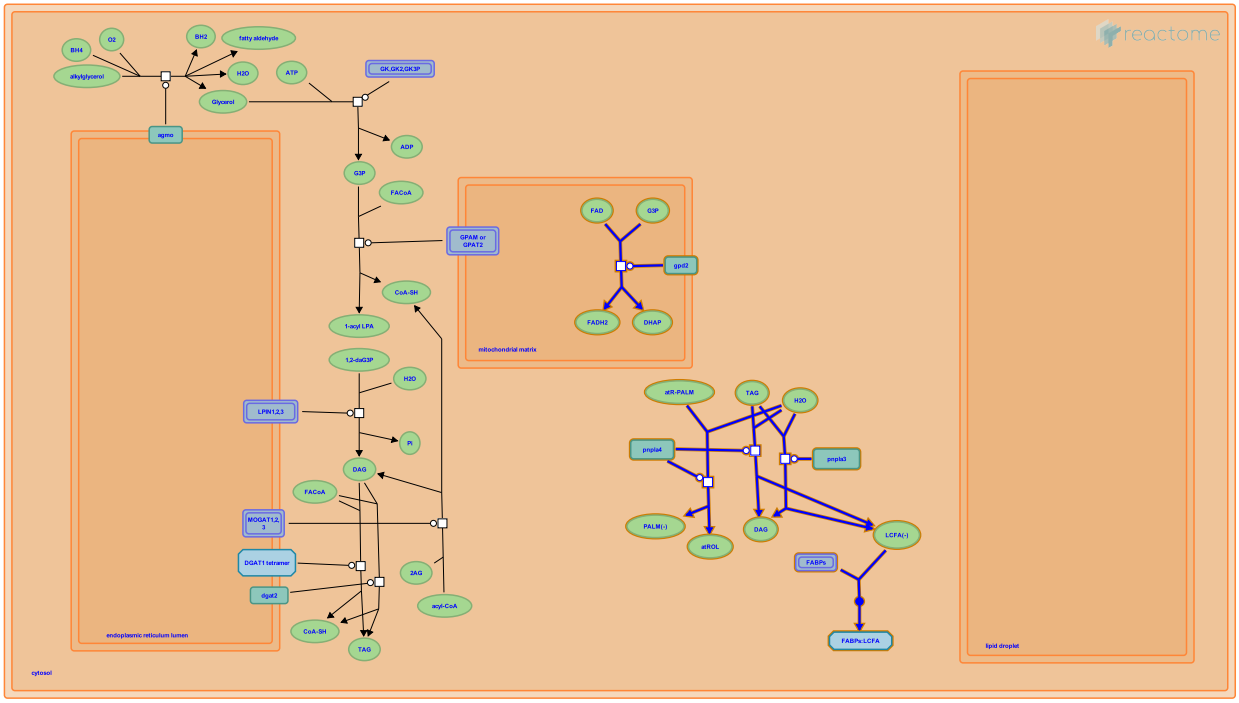
Triglyceride catabolism



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.

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. ↗

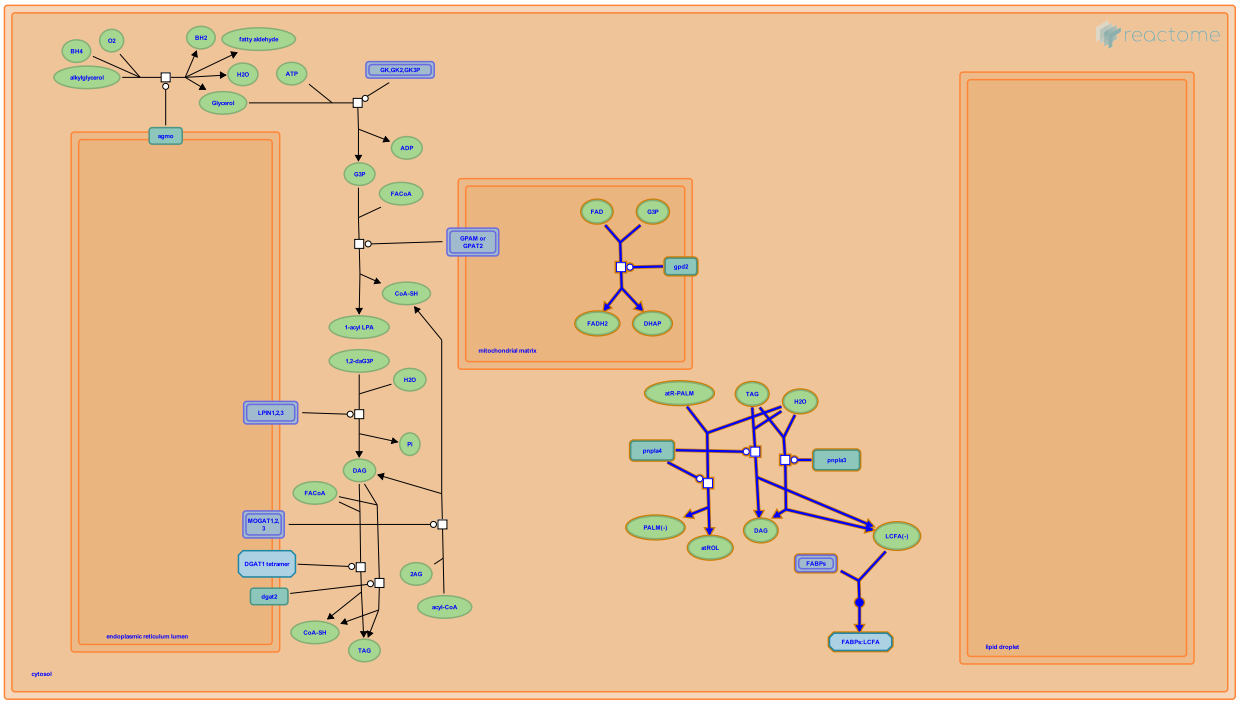
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

Triglyceride catabolism ↗

Stable identifier: R-DRE-163560

Inferred from: Triglyceride catabolism (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

FABPs bind LCFAs ↗

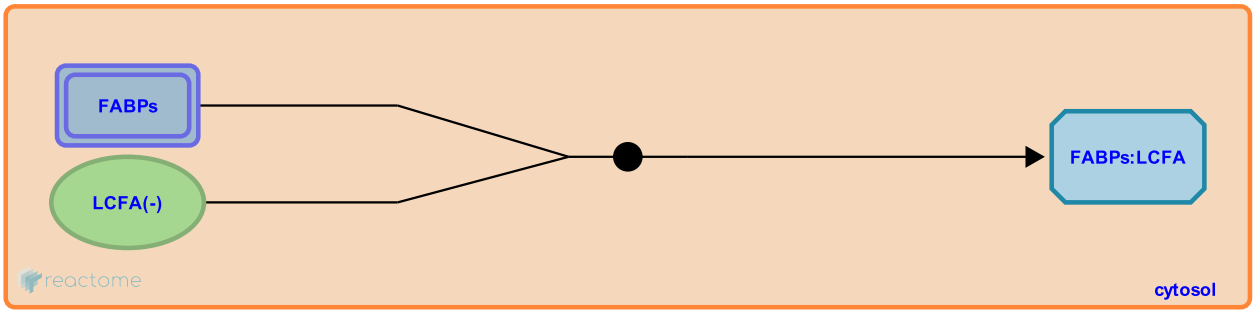
Location: Triglyceride catabolism

Stable identifier: R-DRE-5334794

Type: binding

Compartments: cytosol

Inferred from: FABPs bind LCFAs (Homo sapiens)



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PNPLA4 hydrolyzes TAG ↗

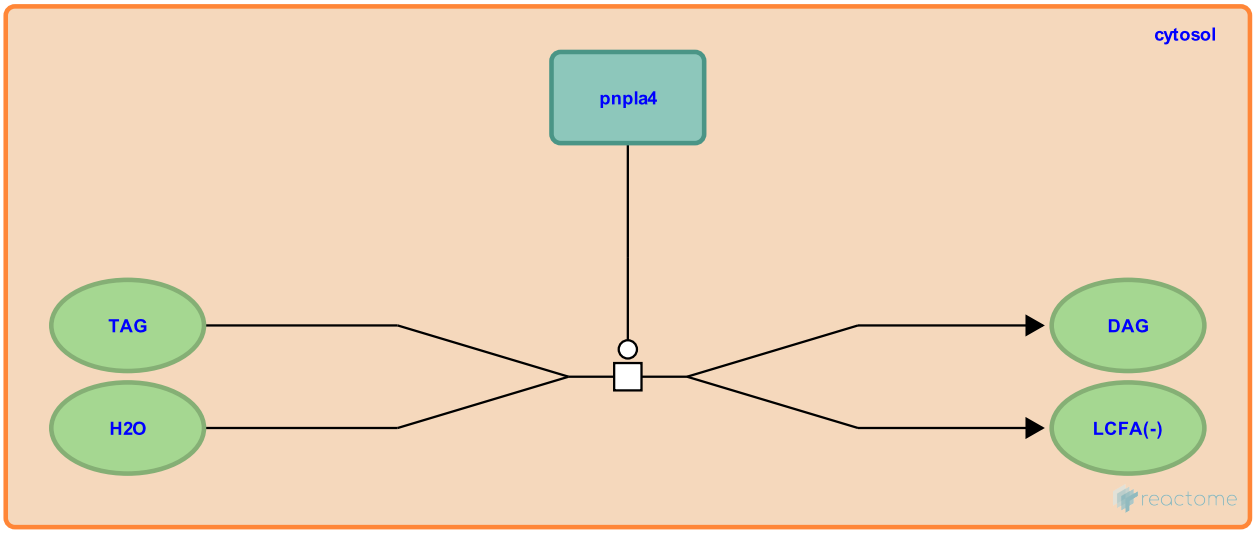
Location: Triglyceride catabolism

Stable identifier: R-DRE-8848338

Type: transition

Compartments: cytosol, endoplasmic reticulum membrane

Inferred from: PNPLA4 hydrolyzes TAG (Homo sapiens)



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PNPLA4 hydrolyzes retinyl palmitate ↗

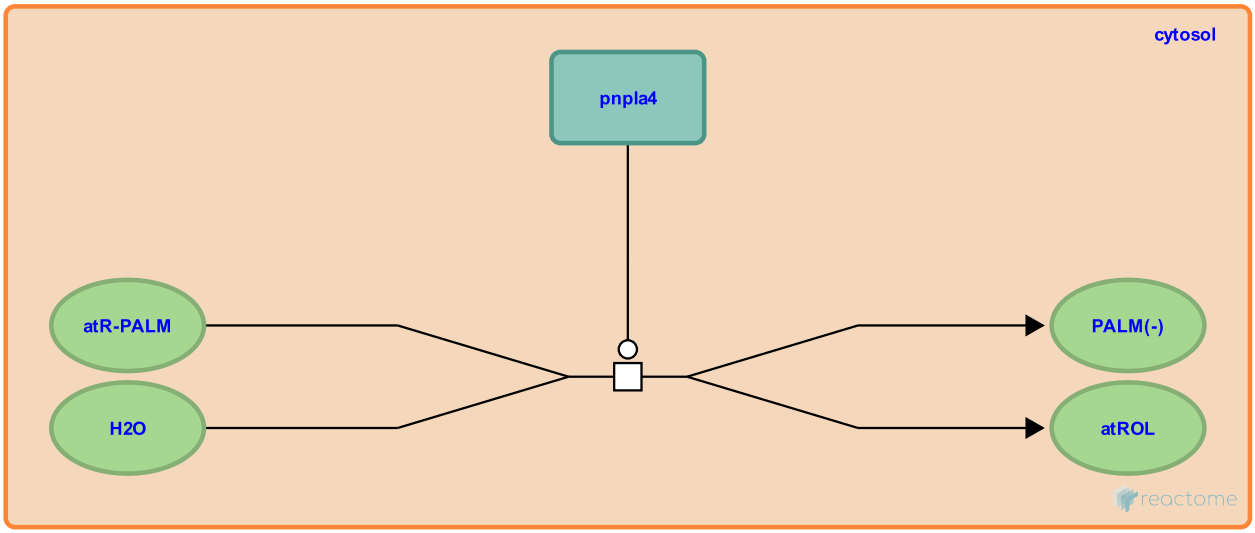
Location: Triglyceride catabolism

Stable identifier: R-DRE-8848355

Type: transition

Compartments: cytosol

Inferred from: PNPLA4 hydrolyzes retinyl palmitate (Homo sapiens)



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PNPLA5 hydrolyzes TAG ↗

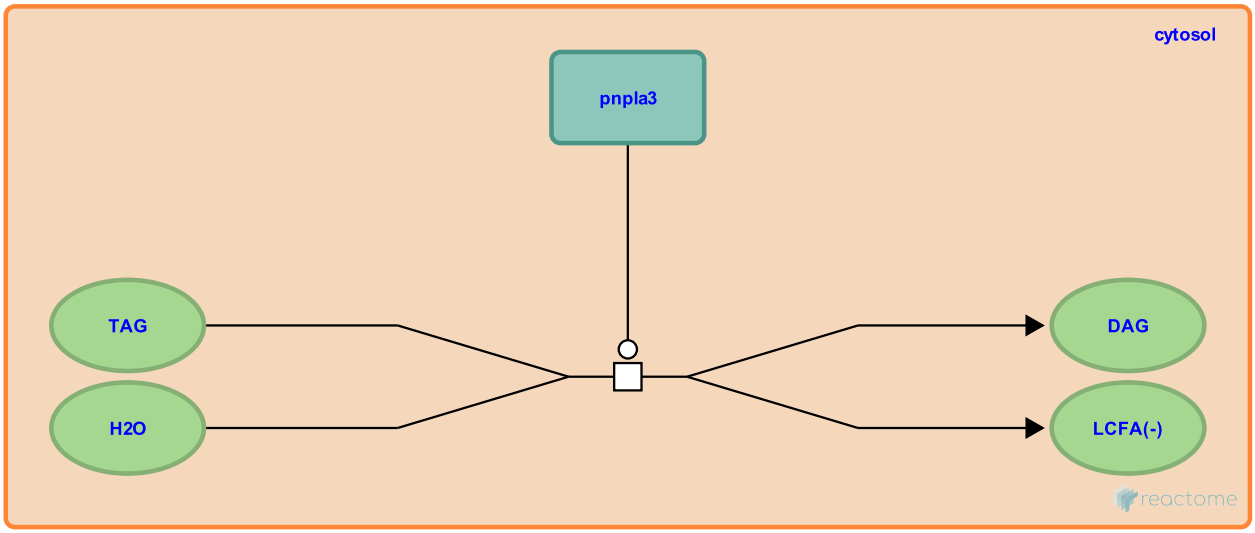
Location: Triglyceride catabolism

Stable identifier: R-DRE-8848339

Type: transition

Compartments: cytosol, endoplasmic reticulum membrane

Inferred from: PNPLA5 hydrolyzes TAG (Homo sapiens)



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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

Gly-3-P+FAD->DHAP+FADH2 (catalyzed by mitochondrial Gly-Phos dehydrogenase)

↗

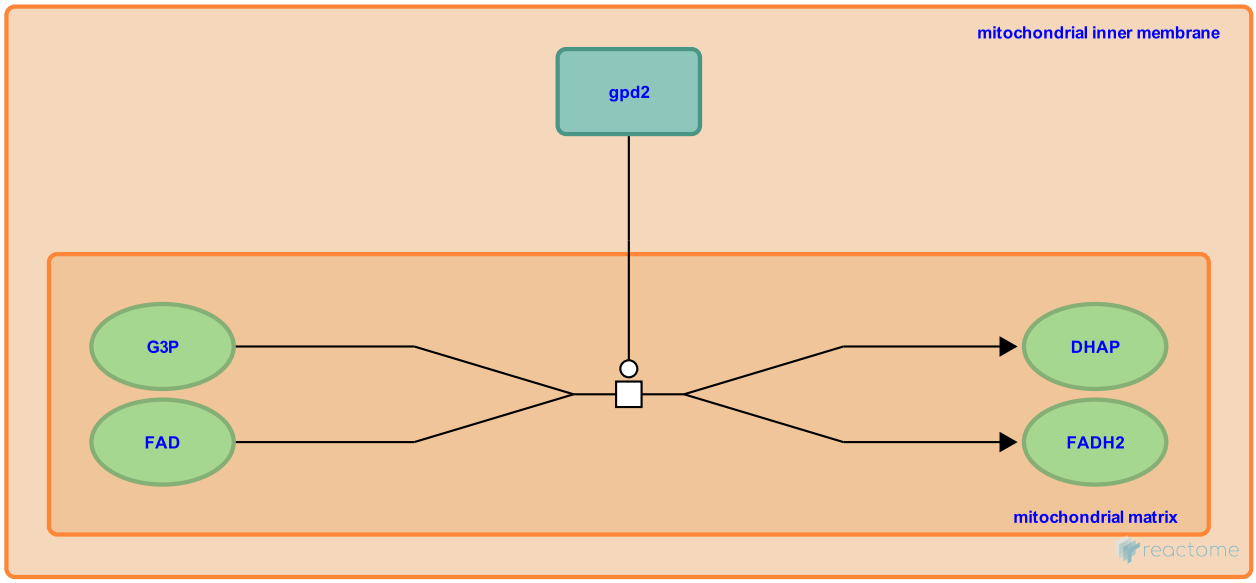
Location: Triglyceride catabolism

Stable identifier: R-DRE-188467

Type: transition

Compartments: mitochondrial matrix, mitochondrial inner membrane

Inferred from: Gly-3-P+FAD->DHAP+FADH2 (catalyzed by mitochondrial Gly-Phos dehydrogenase) (Homo sapiens)



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

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