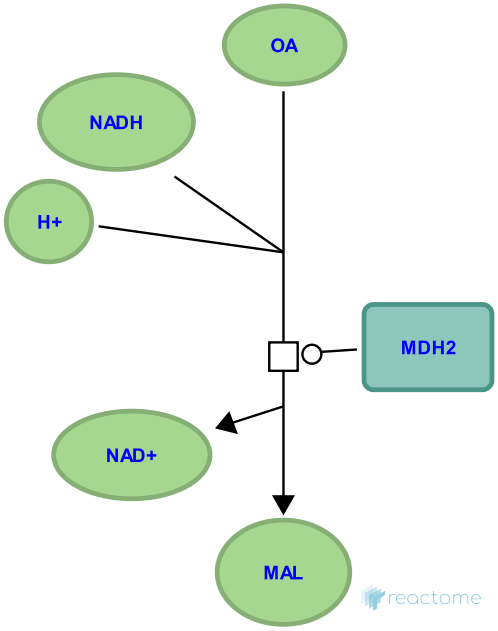
Lipid metabolism



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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. ↗

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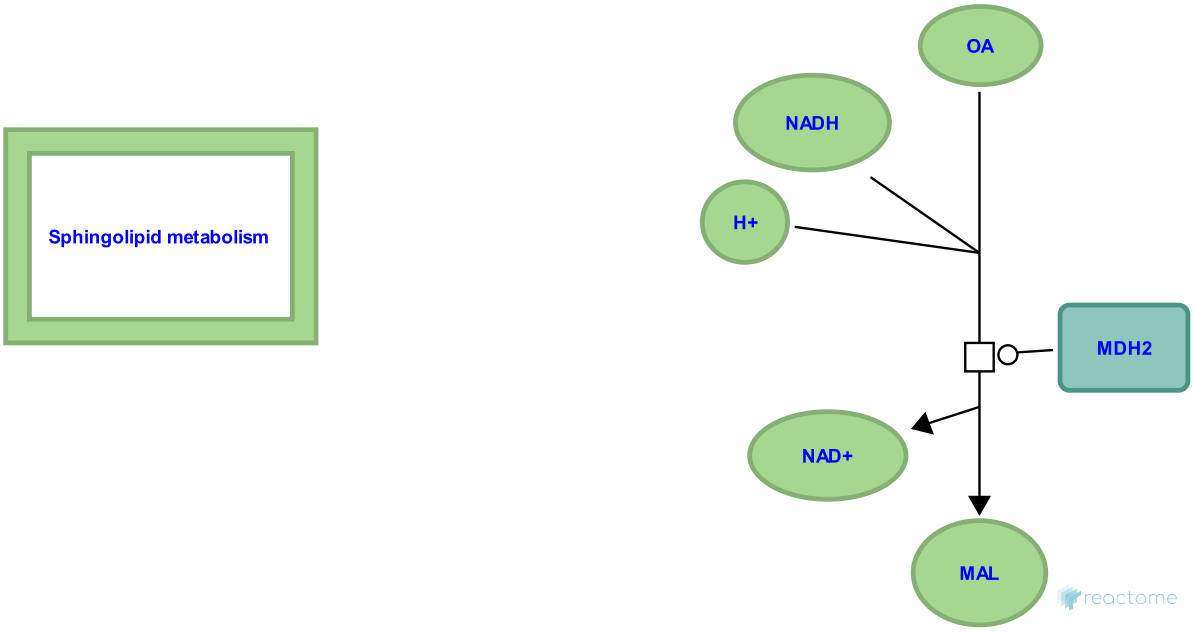
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

Lipid metabolism ↗

Stable identifier: R-GGA-372442



The reduction of oxaloacetate to malate is a reaction in common between pathways of lipid and carbohydrate metabolism. Aspects of reactions involved in sphingolipid synthesis have been inferred from the known properties of the orthologous human enzymes.

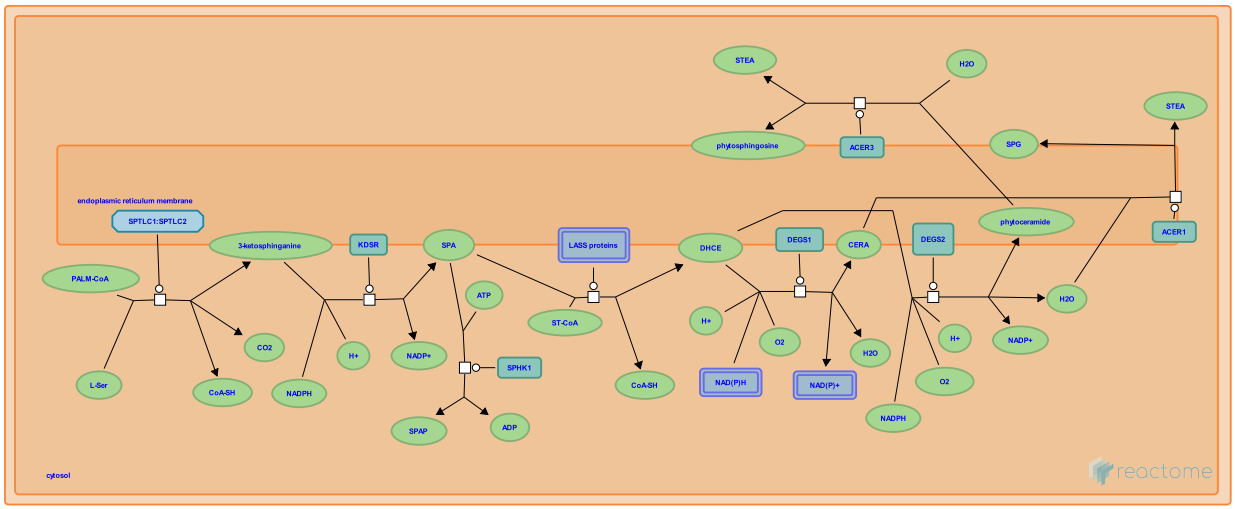
Editions

2008-09-10	Authored	D'Eustachio, P.

Sphingolipid metabolism ↗

Location: Lipid metabolism

Stable identifier: R-GGA-433584



Sphingolipids are derivatives of sphingosine (trans-1,3-dihydroxy 2-amino-4-octadecene), an 18-carbon unsaturated amino alcohol. Amide linkage of a fatty acid to sphingosine yields ceramides. Esterification of choline to ceramides yields sphingomyelin, and ceramide glycosylation yields gangliosides. These molecules appear to be essential components of cell membranes, and intermediates in the pathways of sphingolipid synthesis and breakdown modulate processes including apoptosis.

De novo synthesis proceeds in four steps: the reaction of palmitoyl-CoA and serine to form 3-dehydrosphinganine, the reduction of 3-dehydrosphinganine to sphinganine, the reaction of sphinganine and a long-chain fatty acyl CoA to form dihydroceramide, and the desaturation of dihydroceramide to form ceramide.

Other sphingolipids involved in signaling are derived from ceramide and its biosynthetic intermediates. These include sphinganine (dihydrosphingosine) 1-phosphate, phytoceramide, sphingosine, and sphingosine 1-phosphate.

Sphingomyelin is synthesized in a single step in the membrane of the Golgi apparatus from ceramides generated in the endoplasmic reticulum (ER) membrane and transferred to the Golgi by CERT (ceramide transfer protein), an isoform of COL4A3BP that is associated with the ER membrane as a complex with PPM1L (protein phosphatase 1-like) and VAPA or VAPB (VAMP-associated proteins A or B). Sphingomyelin synthesis appears to be regulated primarily at the level of this transport process through the reversible phosphorylation of CERT.

These processes have not been experimentally studied in chickens, but are inferred here from their human counterparts.

Editions

2009-08-22	Authored, Edited, Reviewed	D'Eustachio, P.

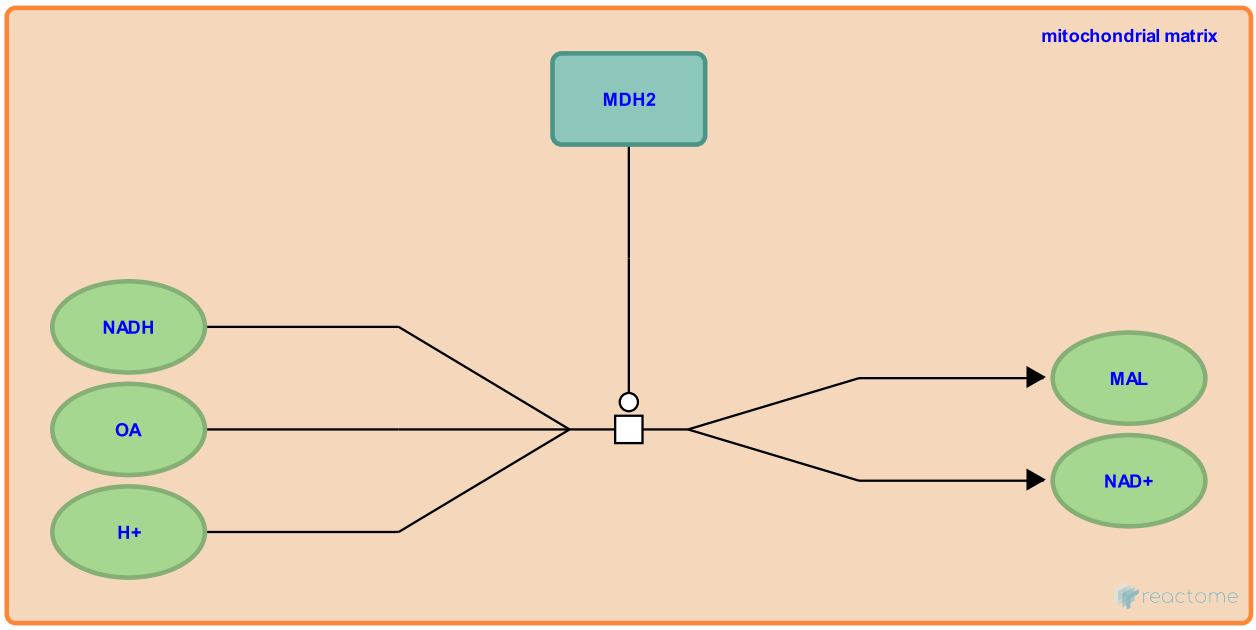
oxaloacetate + NADH + H+ <=> malate + NAD+ ↗

Location: Lipid metabolism

Stable identifier: R-GGA-372422

Type: transition

Compartments: mitochondrial matrix



Oxaloacetate is reversibly reduced by NADH + H+ to form malate and NAD+. No chicken enzyme capable of catalyzing this reaction has been identified, although an open reading frame capable of encoding a protein closely similar to authentic human mitochondrial malate dehydrogenase (MDH2) has been identified computationally in the ENSEMBL chicken gene set. This reaction is inferred from the known properties of mammalian MDH2 (Wolfe & Neilands 1956).

Editions

2008-09-10	Authored, Edited	D'Eustachio, P.
2008-09-10	Reviewed	Harris, RA.

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