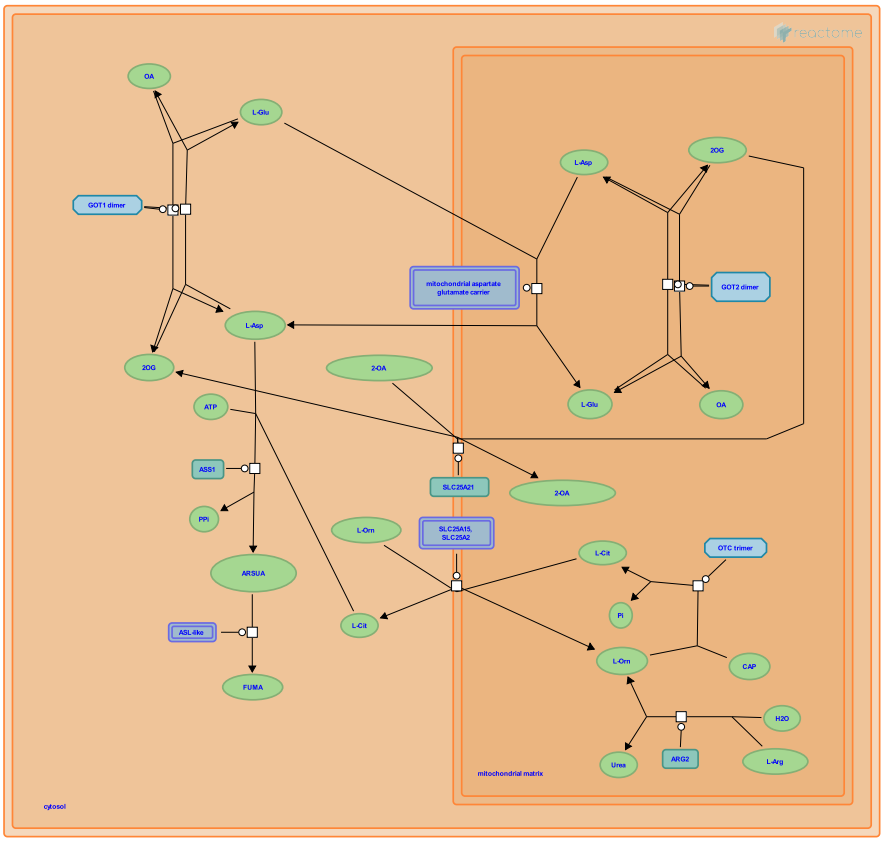
Amino acid metabolism



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26/04/2024

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. ↗

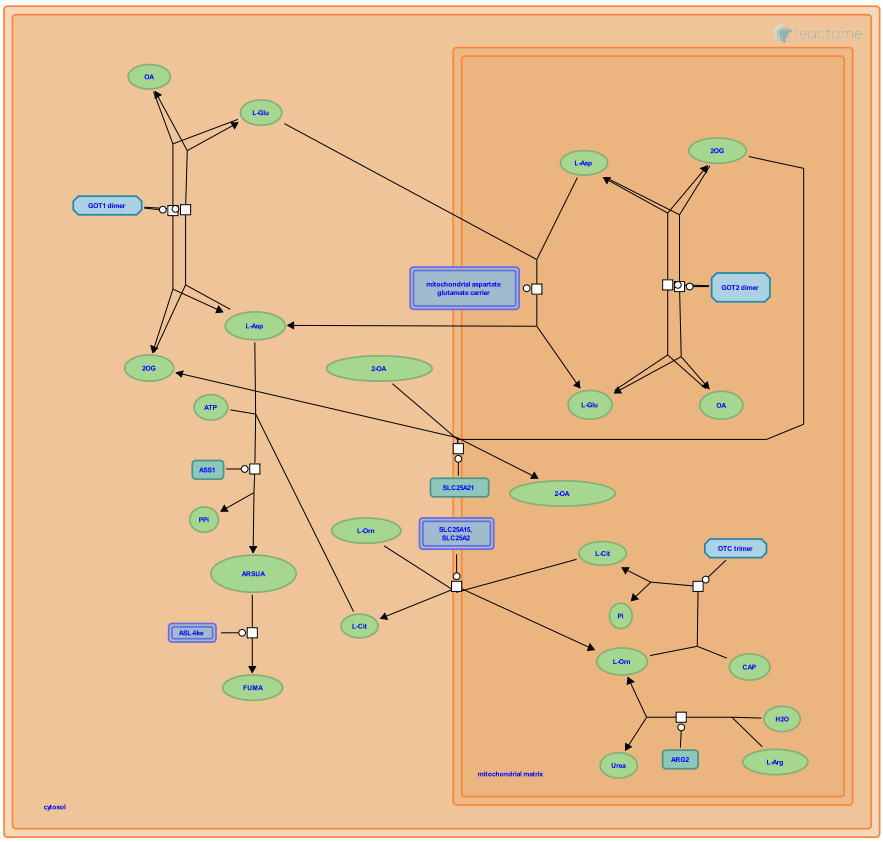
Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

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. ↗

Amino acid metabolism ↗

Stable identifier: R-GGA-372568



Several intracellular transport processes and transamination reactions that are components of amino acid metabolism are also needed for gluconeogenesis. These reactions are listed here together with four reactions associated with arginine metabolism.

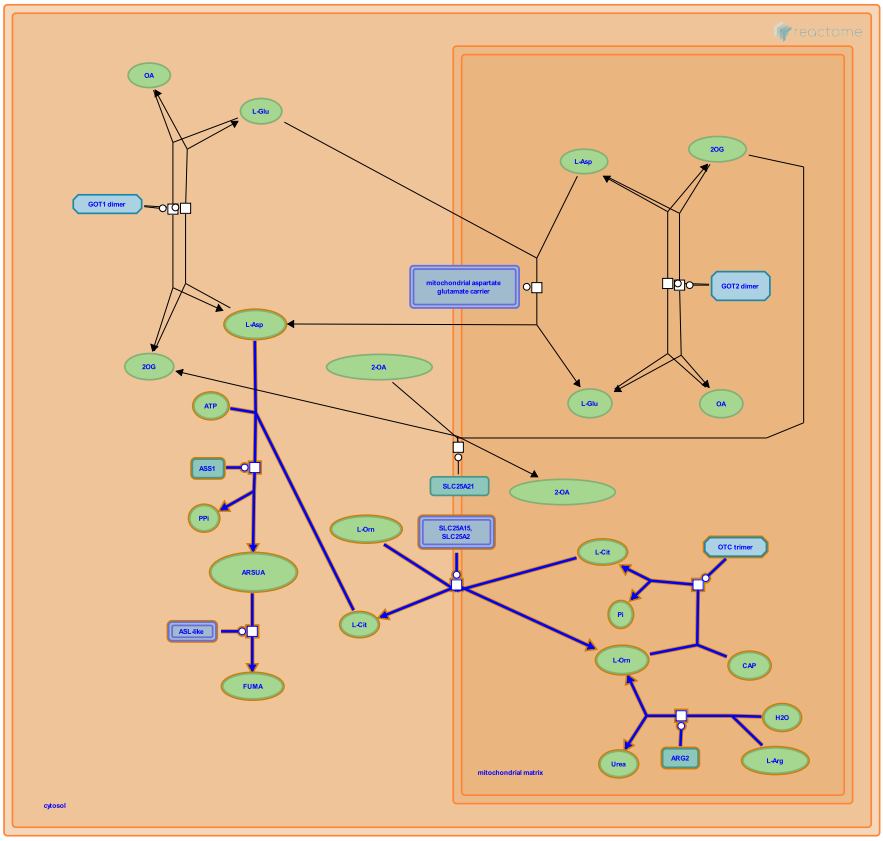
Editions

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

Arginine metabolism ↗

Location: Amino acid metabolism

Stable identifier: R-GGA-187630



Arginine is an essential amino acid in chickens. Citrulline, but not ornithine, can substitute for at least part of this nutritional requirement, and enzymes capable of converting cirulline to agininosuccinate, and the latter molecule to arginine and fumarate have been found in chicken kidney tissue, albeit not in liver. A mitochondrial enzyme that catalyzes the hydrolysis of arginine to ornithine and urea has also been found and biochemically characterized (Tamir and Ratner 1963a, b). It may play a role in polyamine biosynthesis (Grillo et al. 1983).

Biochemical studies and searches of the chicken genomic DNA sequence for open reading frames encoding proteins with homology to known human ones suggest that two additional reactions may occur in chickens that are related to arginine metabolism and the urea cycle in human. Their roles in normal chicken physiology are unknown. A chicken protein with ornithine transcarbamylase activity has been identified (Tsuji 1983), although conversion of ornithine to citrulline is undetectable in vivo (Tamir and Ratner 1963a). Transporters capable of exchanging ornithine and citrulline across the inner mitochondrial membrane have been inferred to exist from genome analysis.

Literature references

Fossa, T., Dianzani, U., Grillo, MA. (1983). Arginase, ornithine decarboxylase and S-adenosylmethionine decarboxylase in chicken brain and retina. *Int J Biochem, 15*, 1081-4. ↗

Ratner, S., Tamir, H. (1963). Enzymes of arginine metabolism in chicks. *Arch Biochem Biophys, 102*, 249-58. ↗

Tsuji, S. (1983). Chicken ornithine transcarbamylase: purification and some properties. *J Biochem, 94*, 1307-15. ↗

Ratner, S., Tamir, H. (1963). A study of ornithine, citrulline and arginine synthesis in growing chicks. *Arch Biochem Biophys, 102*, 259-69. ↗

Editions

2006-09-20	Authored	Schmidt, C.
2008-09-10	Edited, Reviewed	D'Eustachio, P.

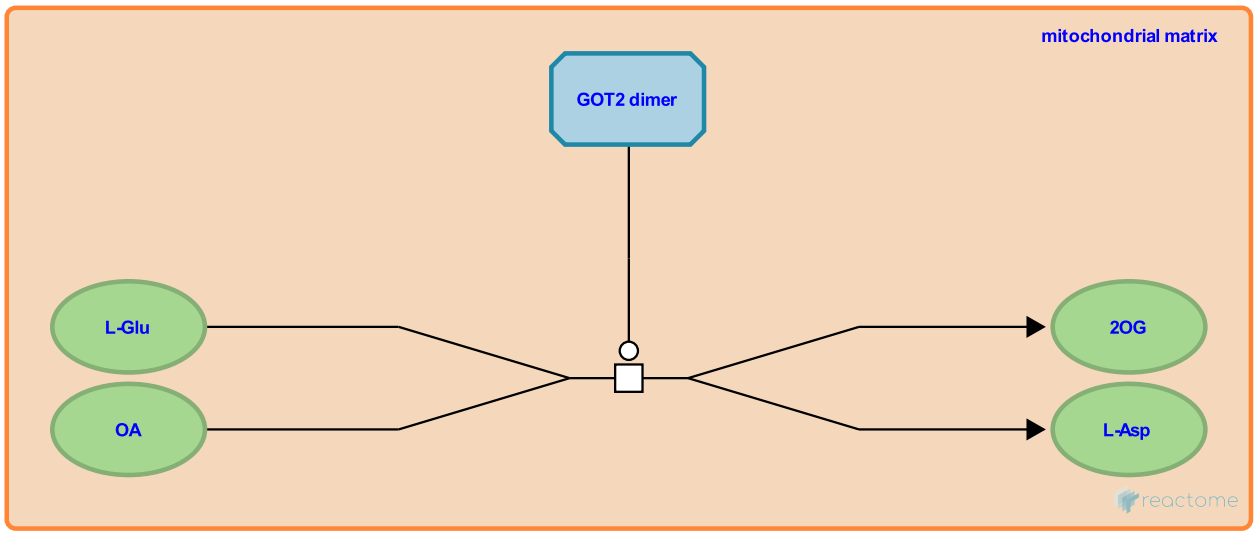
oxaloacetate + glutamate <=> aspartate + alpha-ketoglutarate (2-oxoglutarate) ↗

Location: Amino acid metabolism

Stable identifier: R-GGA-372564

Type: transition

Compartments: mitochondrial matrix



Mitochondrial GOT2 catalyzes the reversible transamination of oxaloacetate and glutamate to form aspartate and alpha-ketoglutarate (2-oxoglutarate). The active form of the enzyme is a homodimer, with one molecule of pyridoxal phosphate bound to each enzyme monomer (Graf-Hausner et al. 1983; McPhalen et al. 1992).

Followed by: aspartate [mitochondrial matrix] + glutamate [cytosol] <=> aspartate [cytosol] + glutamate [mitochondrial matrix]

Literature references

Wilson, KJ., Christen, P., Graf-Hausner, U. (1983). The covalent structure of mitochondrial aspartate aminotransferase from chicken. Identification of segments of the polypeptide chain invariant specifically in the mitochondrial isoenzyme. *J Biol Chem, 258*, 8813-26. ↗

Vincent, MG., Jansonius, JN., McPhalen, CA. (1992). X-ray structure refinement and comparison of three forms of mitochondrial aspartate aminotransferase. *J Mol Biol, 225*, 495-517. ↗

Editions

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

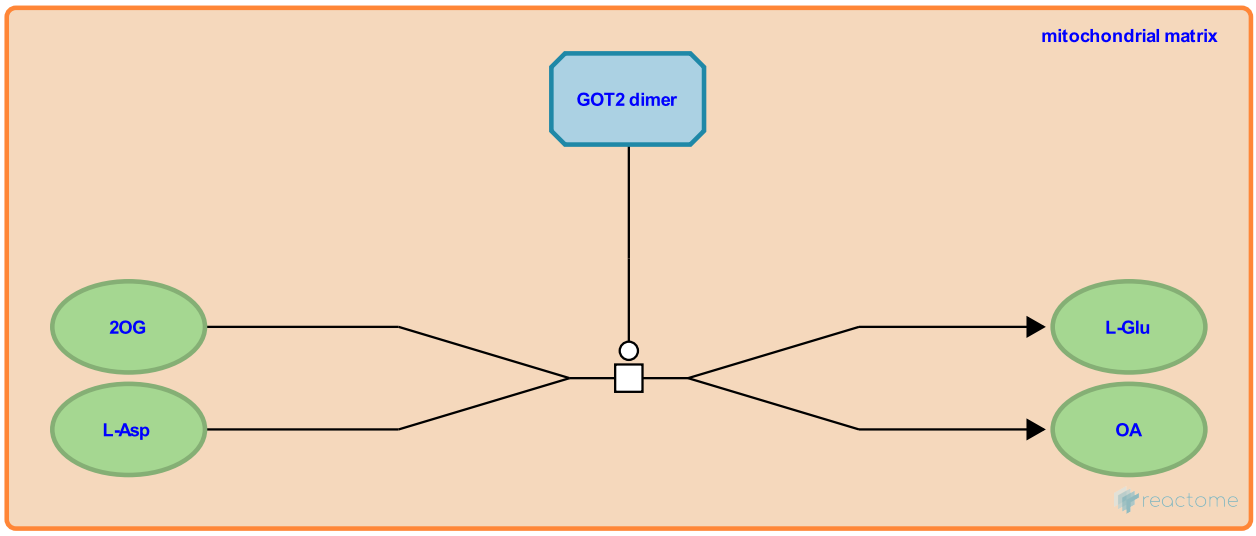
aspartate + alpha-ketoglutarate (2-oxoglutarate) <=> oxaloacetate + glutamate ↗

Location: Amino acid metabolism

Stable identifier: R-GGA-372559

Type: transition

Compartments: mitochondrial matrix



Mitochondrial GOT2 catalyzes the reversible transamination of aspartate and alpha-ketoglutarate (2-oxoglutarate) to form oxaloacetate and glutamate. The acrtive form of the enzyme is a homodimer, with one molecule of pyridoxal phosphate bound to each enzyme monomer (McPhalen et al. 1992).

Literature references

Vincent, MG., Jansonius, JN., McPhalen, CA. (1992). X-ray structure refinement and comparison of three forms of mitochondrial aspartate aminotransferase. *J Mol Biol, 225*, 495-517. ↗

Editions

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

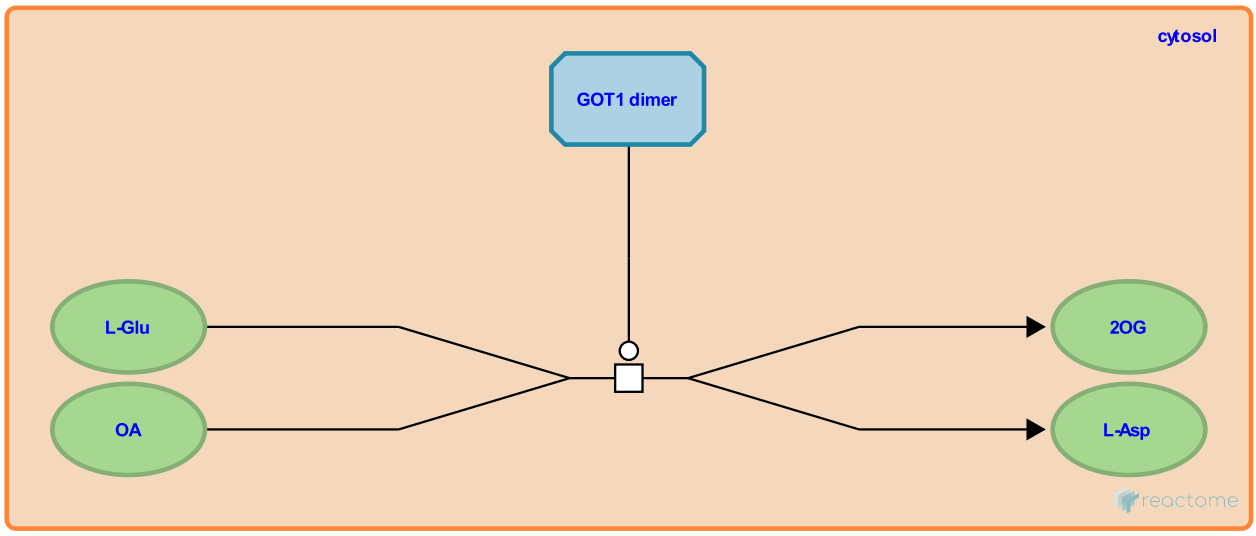
oxaloacetate + glutamate <=> aspartate + alpha-ketoglutarate (2-oxoglutarate) ↗

Location: Amino acid metabolism

Stable identifier: R-GGA-372717

Type: transition

Compartments: cytosol



Cytosolic GOT1 catalyzes the reversible transamination of oxaloacetate and glutamate to form aspartate and alpha-ketoglutarate (2-oxoglutarate). The active form of the enzyme is a homodimer, with one molecule of pyridoxal phosphate bound to each enzyme monomer (Shlyapnikov et al. 1979).

Literature references

Myasnikov, AN., Myagkova, MA., Shlyapnikov, SV., Severin, ES., Braunstein, AE., Torchinsky, YM. (1979). Primary structure of cytoplasmic aspartate aminotransferase from chicken heart and its homology with pig heart isoenzymes. *FEBS Lett, 106*, 385-8. ↗

Editions

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

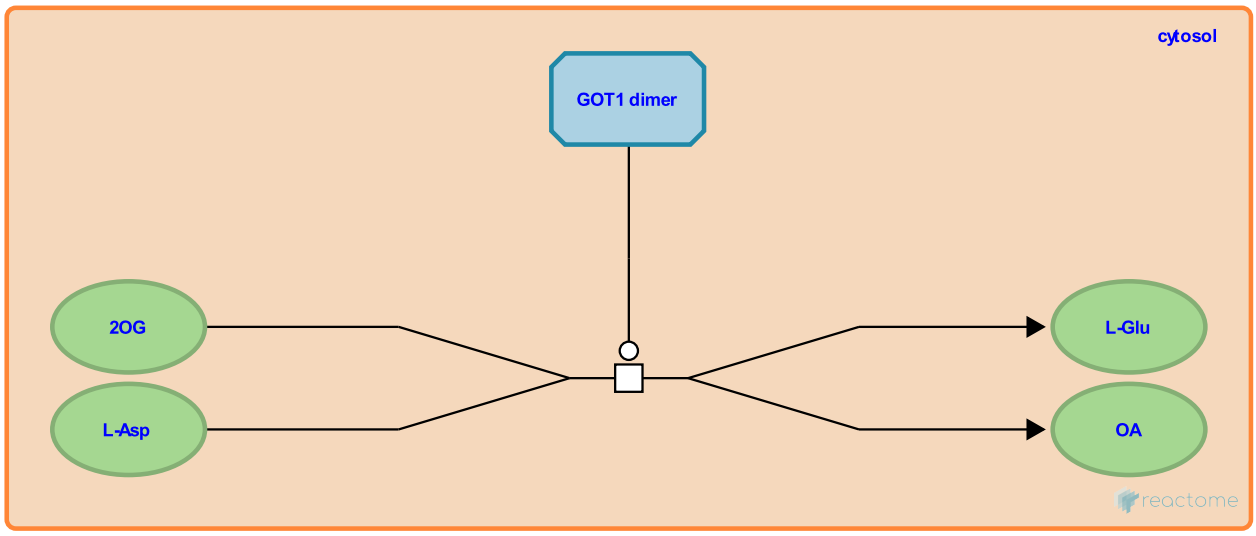
aspartate + alpha-ketoglutarate (2-oxoglutarate) <=> oxaloacetate + glutamate ↗

Location: Amino acid metabolism

Stable identifier: R-GGA-372719

Type: transition

Compartments: cytosol



Cytosolic GOT1 catalyzes the reversible transamination of aspartate and alpha-ketoglutarate (2-oxoglutarate) to form oxaloacetate and glutamate. The active form of the enzyme is a homodimer, with one molecule of pyridoxal phosphate bound to each enzyme monomer (Shlyapnikov et al. 1979).

Preceded by: 2-oxoglutarate [mitochondrial matrix] + 2-oxoadipate [cytosol] <=> 2-oxoglutarate [cytosol] + 2-oxoadipate [mitochondrial matrix], aspartate [mitochondrial matrix] + glutamate [cytosol] <=> aspartate [cytosol] + glutamate [mitochondrial matrix]

Literature references

Myasnikov, AN., Myagkova, MA., Shlyapnikov, SV., Severin, ES., Braunstein, AE., Torchinsky, YM. (1979). Primary structure of cytoplasmic aspartate aminotransferase from chicken heart and its homology with pig heart isoenzymes. *FEBS Lett, 106,* 385-8. ↗

Editions

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

2-oxoglutarate [mitochondrial matrix] + 2-oxoadipate [cytosol] <=> 2-oxoglutarate [cytosol] + 2-oxoadipate [mitochondrial matrix] ↗

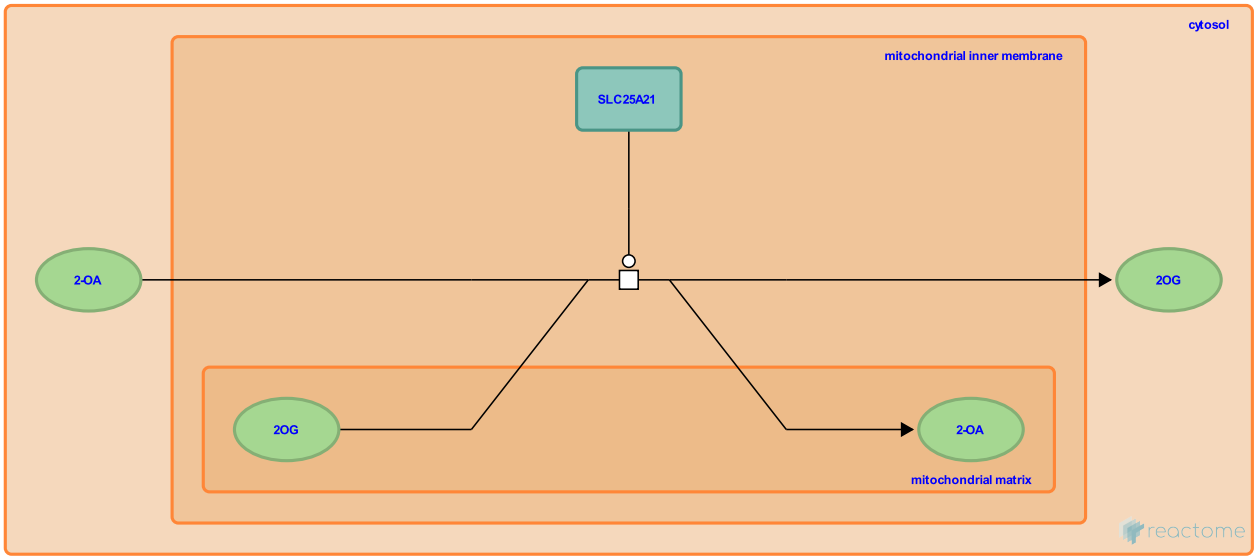
Location: Amino acid metabolism

Stable identifier: R-GGA-372742

Type: transition

Compartments: mitochondrial inner membrane, cytosol, mitochondrial matrix

Inferred from: 2-oxoglutarate [mitochondrial matrix] + 2-oxoadipate [cytosol] <=> 2-oxoglutarate [cytosol] + 2-oxoadipate [mitochondrial matrix] (Homo sapiens)



SLC25A21, the mitochondrial 2-oxodicarboxylate carrier, mediates the exchange of 2-oxoadipate and 2-oxoglutarate across the inner mitochondrial membrane. No chicken transport protein capable of mediating this reaction has been identified, although an open reading frame capable of encoding a protein closely similar to authentic human SLC25A21 has been identified computationally in the ENSEMBL chicken gene set. This reaction is inferred from its human counterpart.

Followed by: aspartate + alpha-ketoglutarate (2-oxoglutarate) <=> oxaloacetate + glutamate

Editions

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

aspartate [mitochondrial matrix] + glutamate [cytosol] <=> aspartate [cytosol] + glutamate [mitochondrial matrix] ↗

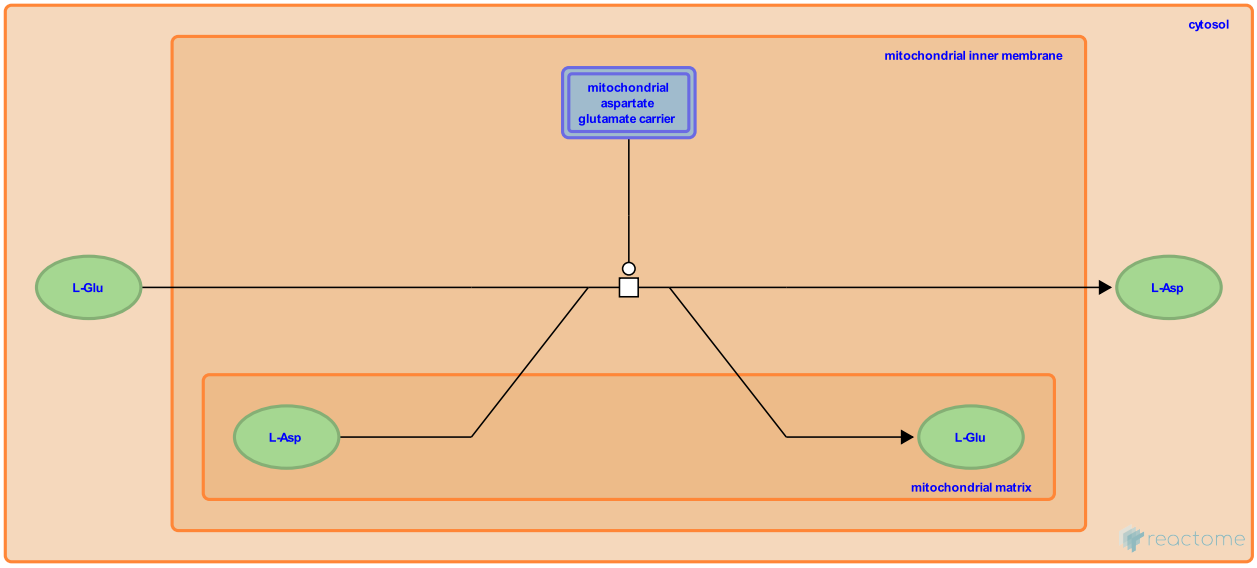
Location: Amino acid metabolism

Stable identifier: R-GGA-372726

Type: transition

Compartments: mitochondrial inner membrane, mitochondrial matrix, cytosol

Inferred from: SLC25A12,13 exchange L-Glu and L-Asp (Homo sapiens)



SLC25A12 and SLC25A13 each mediate the exchange of cytosolic aspartate and mitochondrial glutamate. Both transport proteins are localized in the inner mitochondrial membrane. No chicken transport proteins capable of mediating this reaction has been identified, although open reading frames capable of encoding a protein closely similar to authentic human SLC25A12 and SLC25A13 have been identified computationally in the ENSEMBL chicken gene set. This reaction is inferred from its human counterpart.

Preceded by: oxaloacetate + glutamate <=> aspartate + alpha-ketoglutarate (2-oxoglutarate)

Followed by: aspartate + alpha-ketoglutarate (2-oxoglutarate) <=> oxaloacetate + glutamate

Editions

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

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