

aspartate + alpha-ketoglutarate (2-oxoglutarate) \rightleftharpoons oxaloacetate + glutamate

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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. [↗](#)

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. [↗](#)

Reactome database release: 88

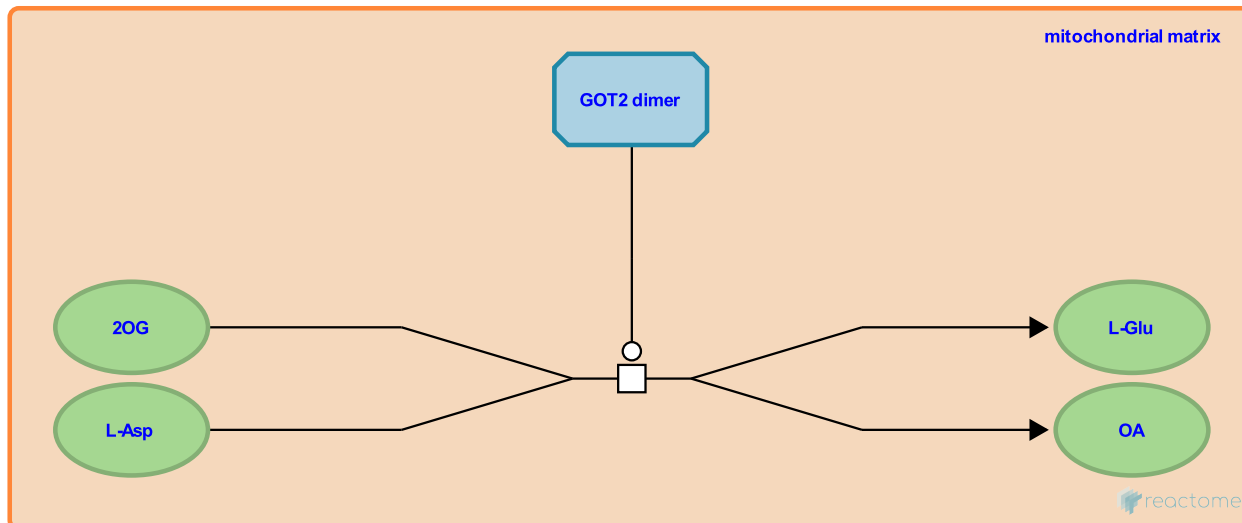
This document contains 1 reaction ([see Table of Contents](#))

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

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 active 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.
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