

[GLS]

D'Eustachio, P., Inga, A., Zaccara, S.

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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://reactome.org/licenses/).

05/05/2024

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. [↗](#)

Reactome database release: 88

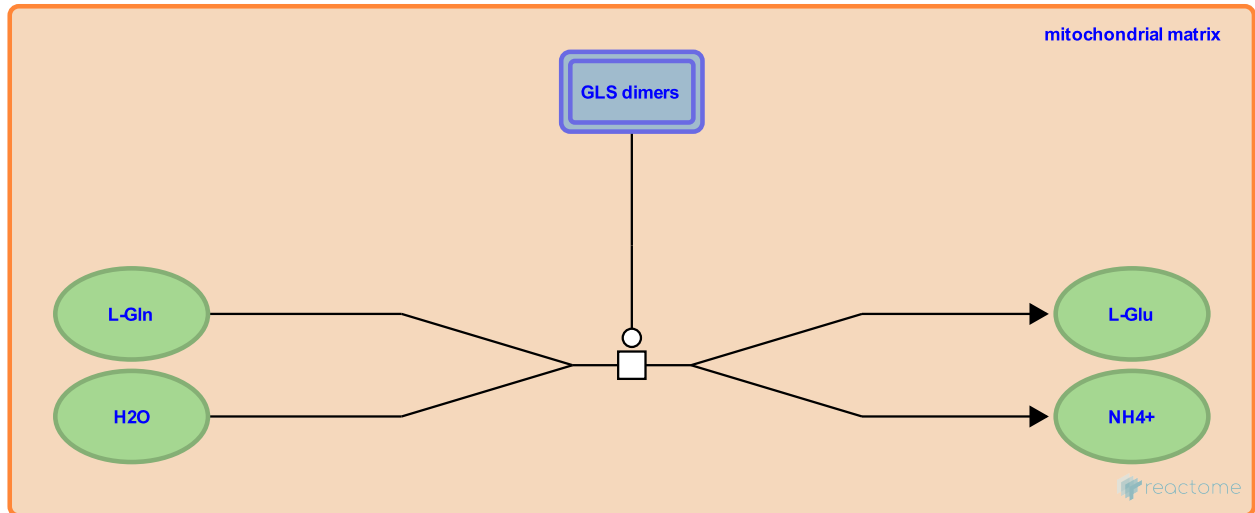
This document contains 1 reaction ([see Table of Contents](#))

glutamine + H2O => glutamate + NH4+ [GLS] ↗

Stable identifier: R-HSA-70609

Type: transition

Compartments: mitochondrial matrix



Mitochondrial glutaminase (GLS) catalyzes the hydrolysis of glutamine to yield glutamate and ammonia. Two GLS enzymes have been identified, one abundantly expressed in the liver (GLS - Elgadi et al. 1999) and one abundantly expressed in kidney (GLS2 - Gomez-Fabre et al. 2000). Their biochemical properties are similar. The enzymes are inferred to function as dimers based on unpublished crystallographic data for GLS (PDB 3CZD) and studies of glutaminase enzyme purified from Ehrlich Ascites cells (Quesada et al. 1988).

Literature references

Aledo, JC., Alonso, FJ., Gomez-Fabre, PM., Nunez De Castro, I., Marquez, J., Campos, JA. et al. (2000). Molecular cloning, sequencing and expression studies of the human breast cancer cell glutaminase. *Biochem J*, 345, 365-75. ↗

Medina, MA., Nunez De Castro, I., Marquez, J., Quesada, AR., Sánchez-Jiménez, F., Perez-Rodriguez, J. (1988). Purification of phosphate-dependent glutaminase from isolated mitochondria of Ehrlich ascites-tumour cells. *Biochem J*, 255, 1031-5. ↗

Souba, WW., Elgadi, KM., Qian, M., Meguid, RA., Abcouwer, SF. (1999). Cloning and analysis of unique human glutaminase isoforms generated by tissue-specific alternative splicing. *Physiol Genomics*, 1, 51-62. ↗

Editions

2003-05-04	Authored	D'Eustachio, P.
2010-04-30	Edited	D'Eustachio, P.
2016-02-04	Reviewed	Inga, A., Zaccara, S.