ALDOB tetramer cleaves Fru-1-P to GA and DHAP

Cameselle, JC., D'Eustachio, P., Hill, DP., Jassal, B., Ribeiro, JM.

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

21/05/2024

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. ↗

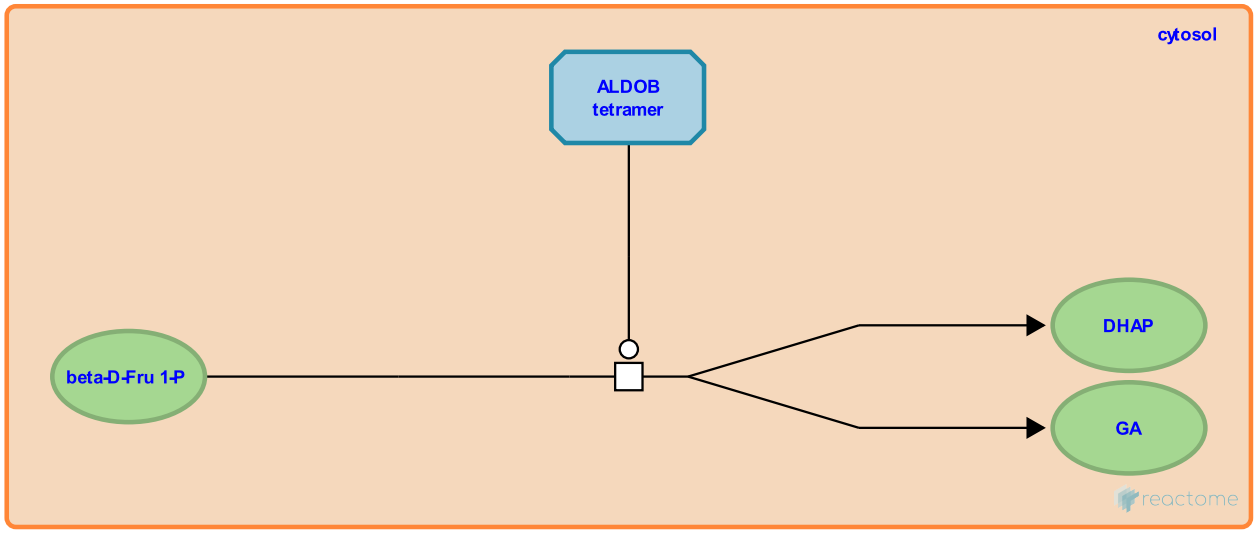
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

ALDOB tetramer cleaves Fru-1-P to GA and DHAP ↗

Stable identifier: R-HSA-70342

Type: transition

Compartments: cytosol



Cytosolic aldolase B (ALDOB) catalyzes the reaction of D-fructose 1-phosphate (Fru 1-P) to form dihydroxyacetone phosphate (DHAP) and D-glyceraldehyde (GA) (Hers & Kusaka 1953; Schapira 1975). The active form of the enzyme is a tetramer (Dalby et al. 2001). Deficiencies in the enzyme are associated with hereditary fructose intolerance in vivo (e.g., Tolan 1995; Ali et al. 1998).
ALDOB is the same aldolase isoform that catalyzes the reversible cleavage of fructose-1,6-bisphosphate in glycolysis. This isoform, found in liver, kidney, and intestine, is approximately equally active with fructose 1 phosphate and fructose 1,6 bisphosphate as substrates at saturating concentrations, while the muscle and brain isoforms (ALDOA and ALDOC, respectively), have little activity with fructose-1-phosphate (Lebherz & Rutter 1969; Penhoet et el. 1969).

Literature references

Tolan, DR. (1995). Molecular basis of hereditary fructose intolerance: mutations and polymorphisms in the human aldolase B gene. *Hum Mutat, 6*, 210-8. ↗

Kochman, M., Rutter, WJ., Penhoet, EE. (1969). Isolation of fructose diphosphate aldolases A, B, and C. *Biochemistry, 8*, 4391-5. ↗

Littlechild, JA., Tolan, DR., Dalby, AR. (2001). The structure of human liver fructose-1,6-bisphosphate aldolase. *Acta Crystallogr D Biol Crystallogr, 57*, 1526-33. ↗

Hers, HG., Kusaka, T. (1953). [The metabolism of fructose-1-phosphate in the liver.]. *Biochim Biophys Acta, 11*, 427-37. ↗

Rutter, WJ., Lebherz, HG. (1969). Distribution of fructose diphosphate aldolase variants in biological systems. *Biochemistry, 8*, 109-21. ↗

Editions

2010-01-25	Revised	D'Eustachio, P.
2014-11-29	Edited	D'Eustachio, P.
2015-01-29	Revised	D'Eustachio, P.
2015-01-29	Reviewed	Jassal, B.
2015-08-28	Authored	Ribeiro, JM., Cameselle, JC.
2023-05-16	Reviewed	Hill, DP.