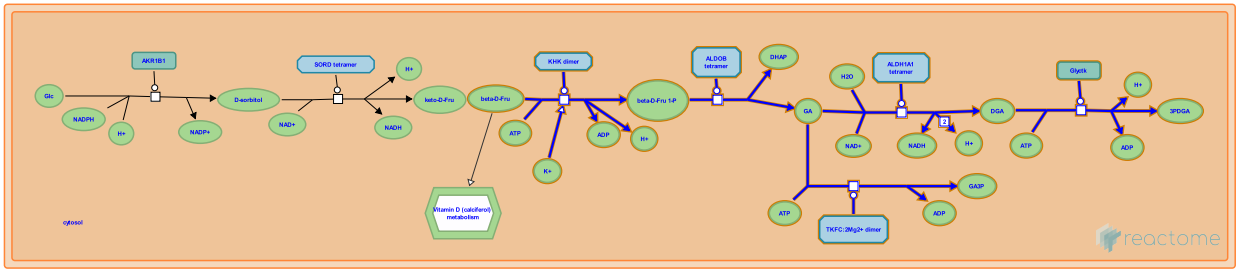
Fructose catabolism



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

19/05/2024

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. ↗

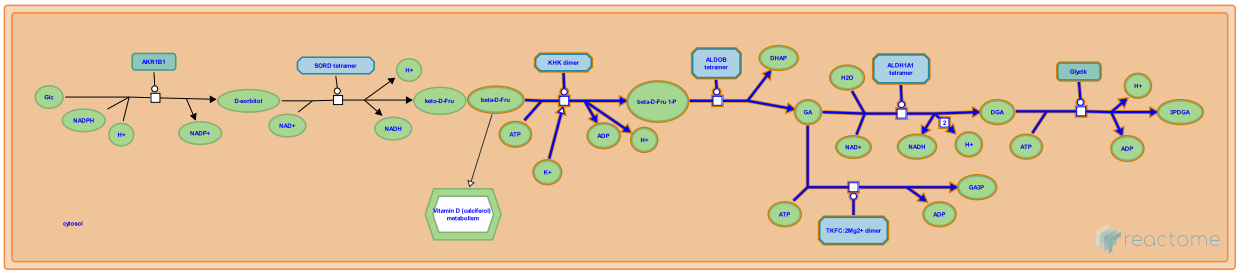
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

Fructose catabolism ↗

Stable identifier: R-RNO-70350

Inferred from: Fructose catabolism (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

KHK dimer phosphorylates Fru to Fru 1-P ↗

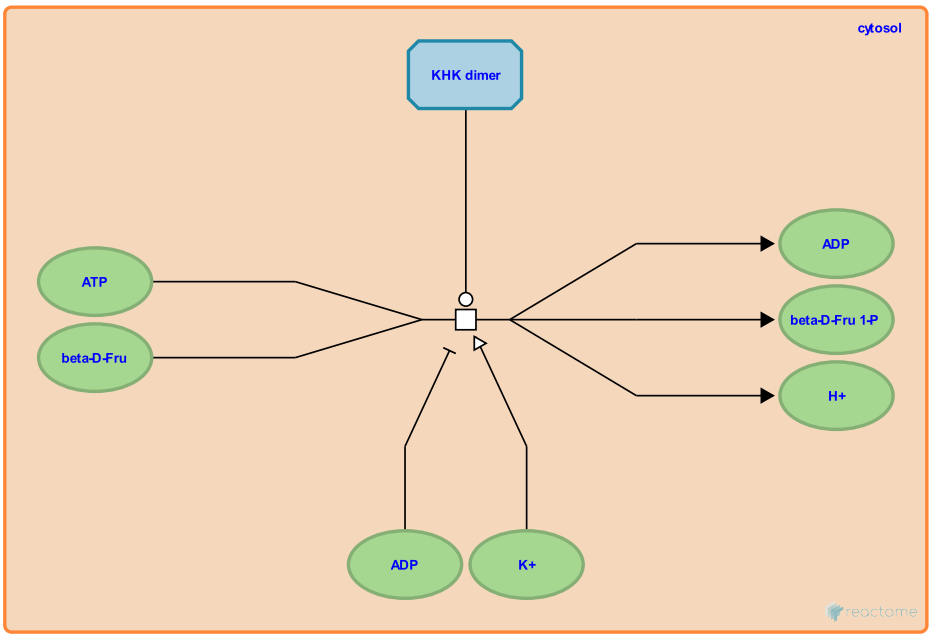
Location: Fructose catabolism

Stable identifier: R-RNO-70333

Type: transition

Compartments: cytosol

Inferred from: KHK dimer phosphorylates Fru to Fru 1-P (Homo sapiens)



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Followed by: ALDOB tetramer cleaves Fru-1-P to GA and DHAP

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

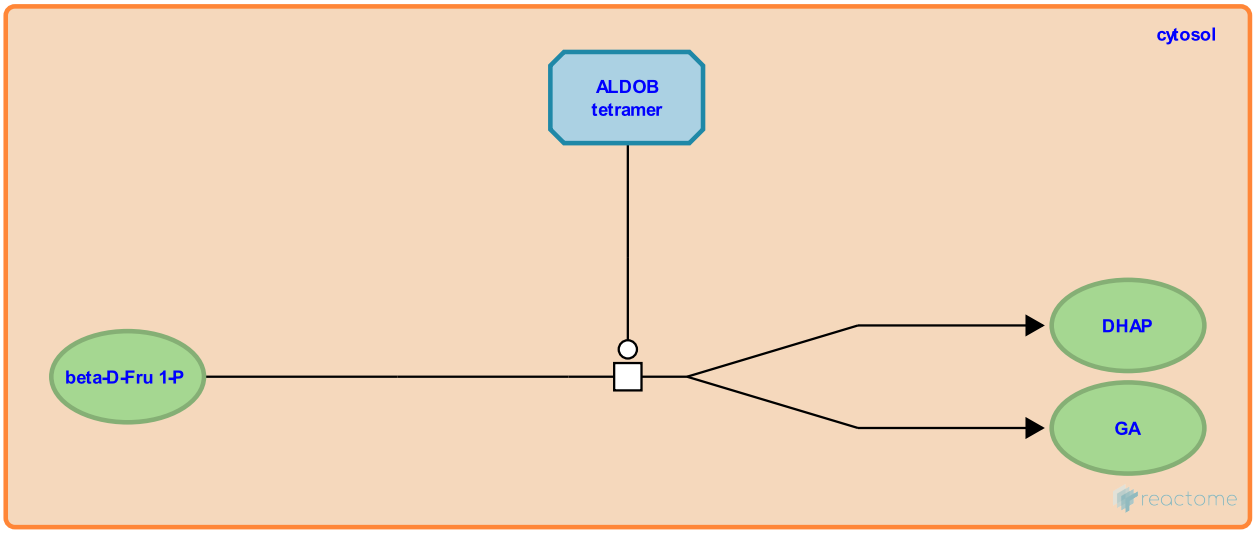
Location: Fructose catabolism

Stable identifier: R-RNO-70342

Type: transition

Compartments: cytosol

Inferred from: ALDOB tetramer cleaves Fru-1-P to GA and DHAP (Homo sapiens)



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Preceded by: KHK dimer phosphorylates Fru to Fru 1-P

Followed by: ALDH1A1 oxidises GA to DGA, DAK dimer phosphorylates D-glyceraldehyde to form D-glyceraldehyde 3-phosphate

DAK dimer phosphorylates D-glyceraldehyde to form D-glyceraldehyde 3-phosphate

↗

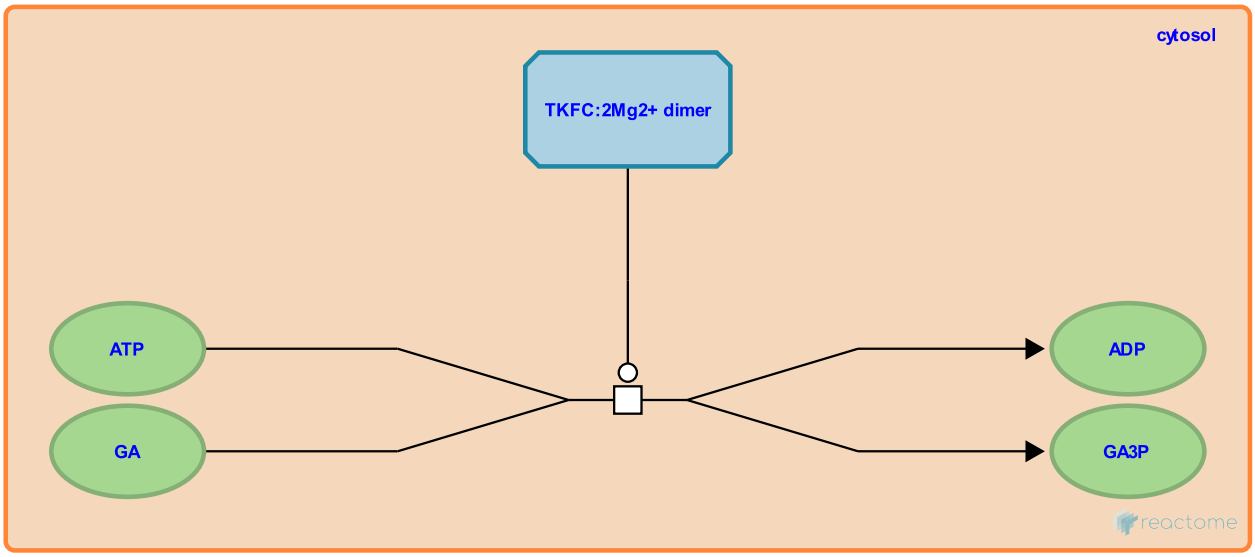
Location: Fructose catabolism

Stable identifier: R-RNO-70349

Type: transition

Compartments: cytosol

Inferred from: DAK dimer phosphorylates D-glyceraldehyde to form D-glyceraldehyde 3-phosphate (Homo sapiens)



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Preceded by: ALDOB tetramer cleaves Fru-1-P to GA and DHAP

ALDH1A1 oxidises GA to DGA ↗

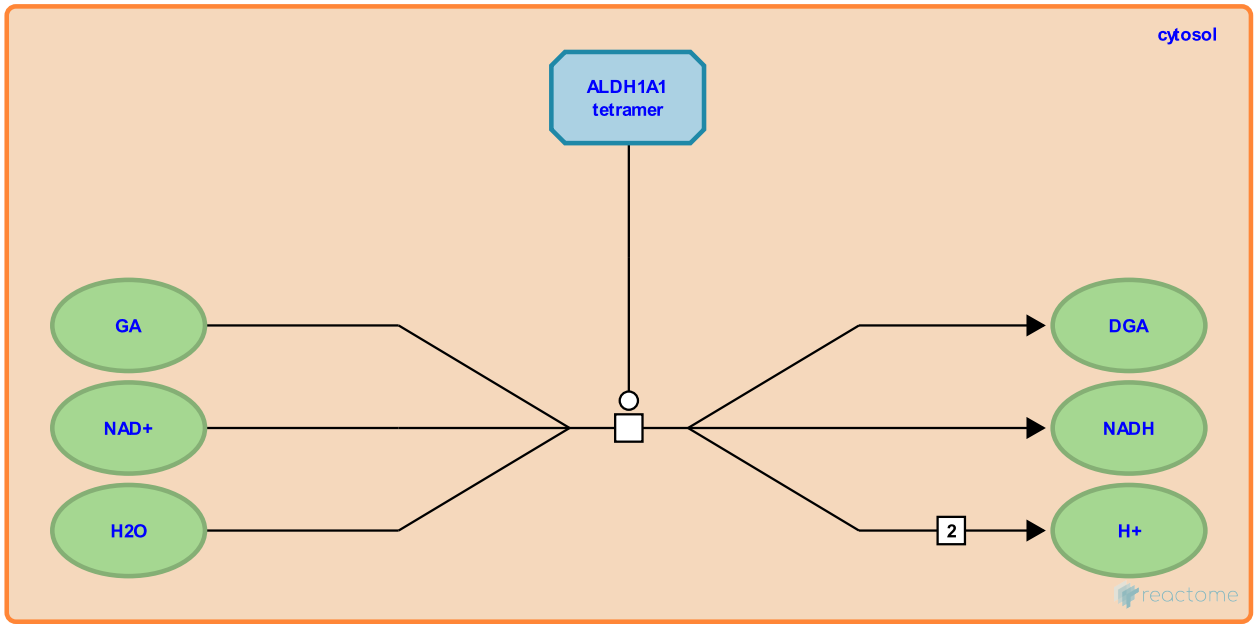
Location: Fructose catabolism

Stable identifier: R-RNO-6813749

Type: transition

Compartments: cytosol

Inferred from: ALDH1A1 oxidises GA to DGA (Homo sapiens)



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More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: ALDOB tetramer cleaves Fru-1-P to GA and DHAP

Followed by: GLYCTK phosphorylates DGA to 3PDGA

GLYCTK phosphorylates DGA to 3PDGA ↗

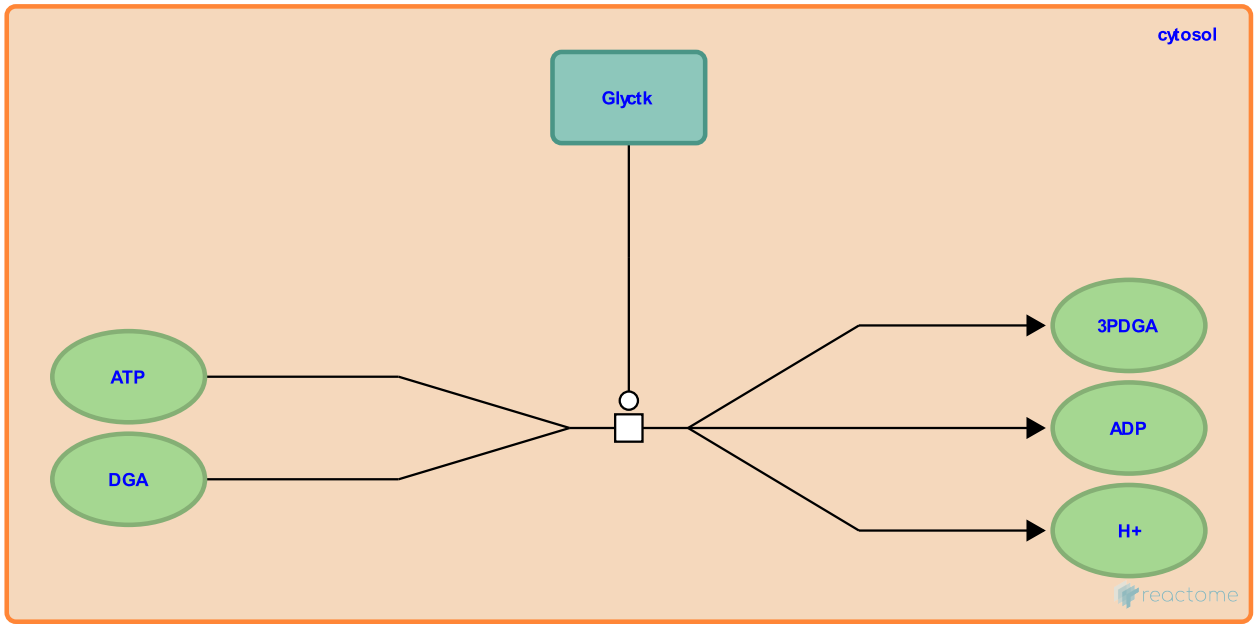
Location: Fructose catabolism

Stable identifier: R-RNO-6799495

Type: transition

Compartments: cytosol

Inferred from: GLYCTK phosphorylates DGA to 3PDGA (Homo sapiens)



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Preceded by: ALDH1A1 oxidises GA to DGA

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