

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. [↗](#)

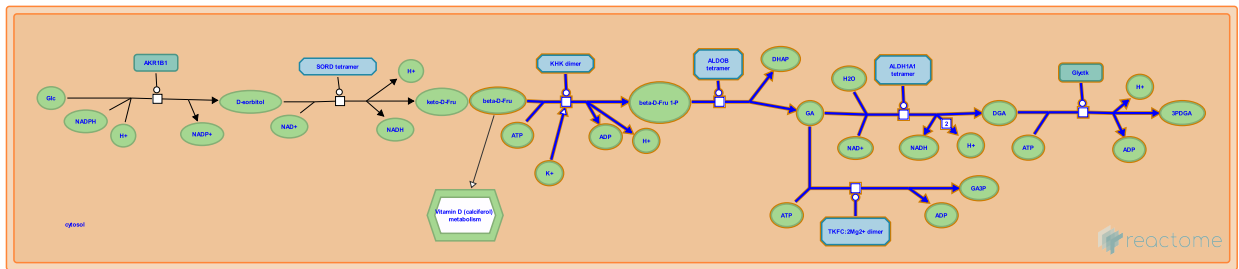
Reactome database release: 88

This document contains 1 pathway and 5 reactions ([see Table of Contents](#))

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 ↗

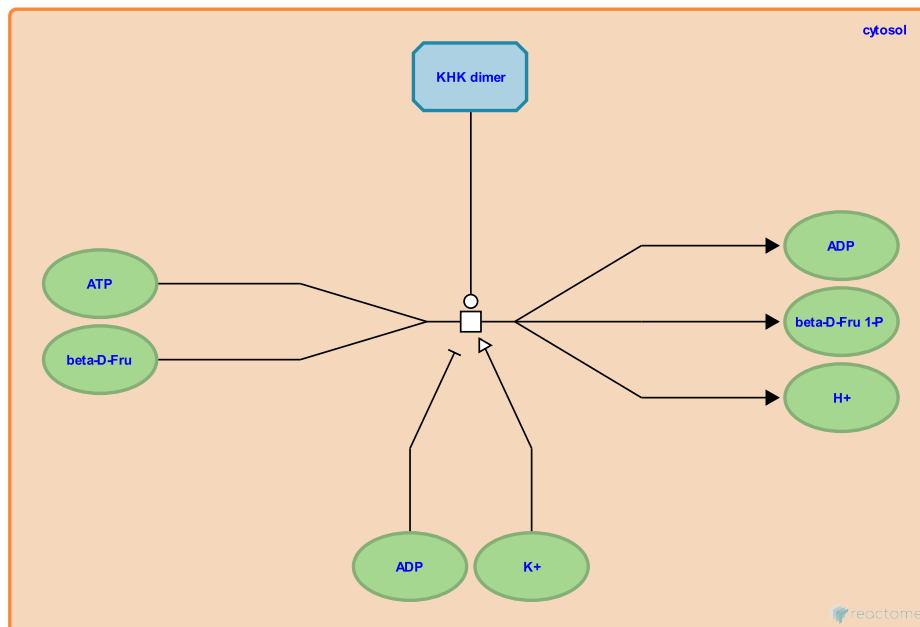
Location: [Fructose catabolism](#)

Stable identifier: R-RNO-70333

Type: transition

Compartments: cytosol

Inferred from: [KHK dimer phosphorylates Fru to Fru 1-P \(Homo sapiens\)](#)



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

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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 ↗

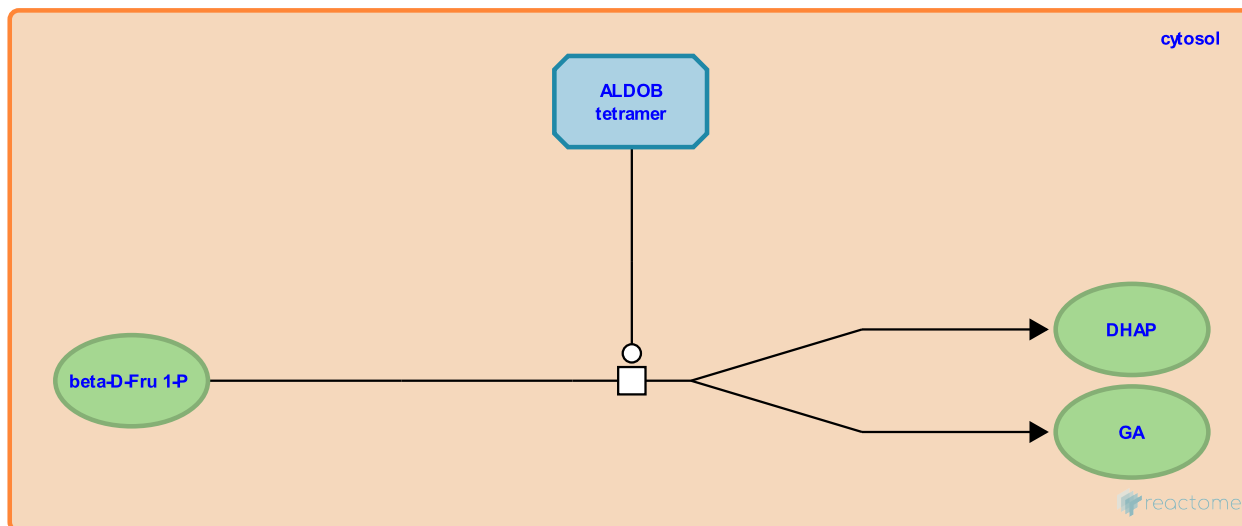
Location: [Fructose catabolism](#)

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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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.

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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



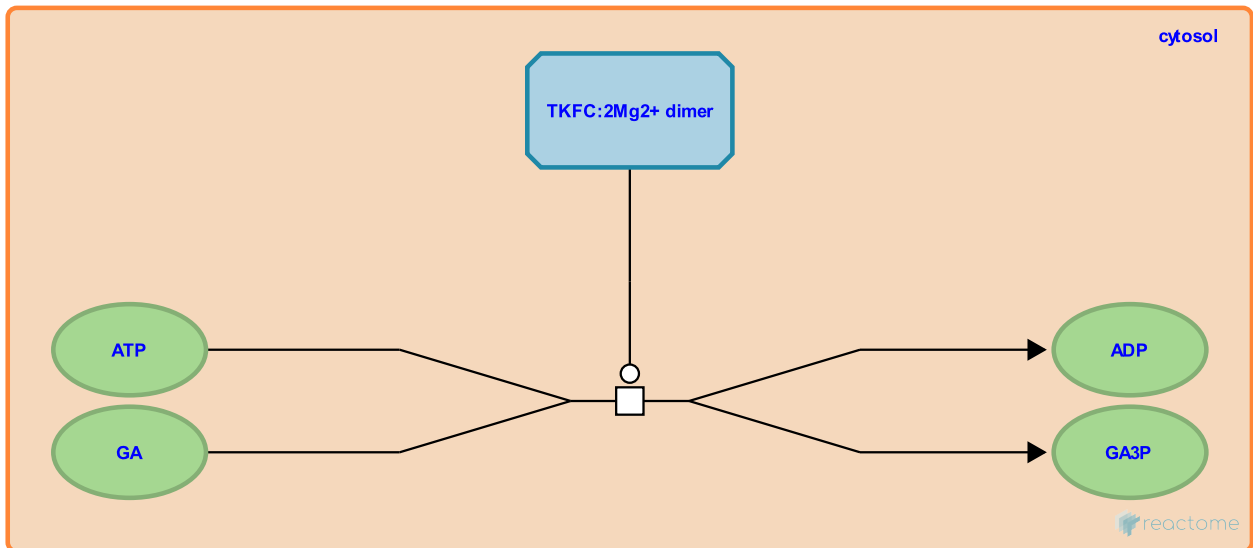
Location: [Fructose catabolism](#)

Stable identifier: R-RNO-70349

Type: transition

Compartments: cytosol

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



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.

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Preceded by: [ALDOB tetramer cleaves Fru-1-P to GA and DHAP](#)

ALDH1A1 oxidises GA to DGA ↗

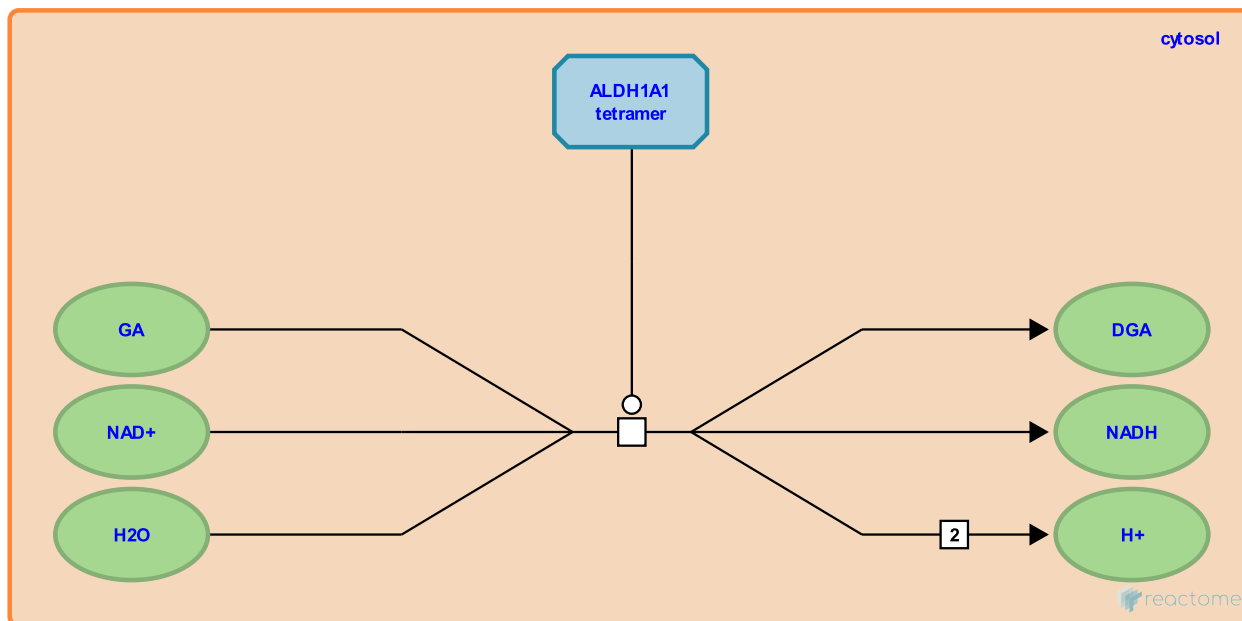
Location: Fructose catabolism

Stable identifier: R-RNO-6813749

Type: transition

Compartments: cytosol

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



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.](http://www.pantherdb.org/about.jsp) 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 ↗

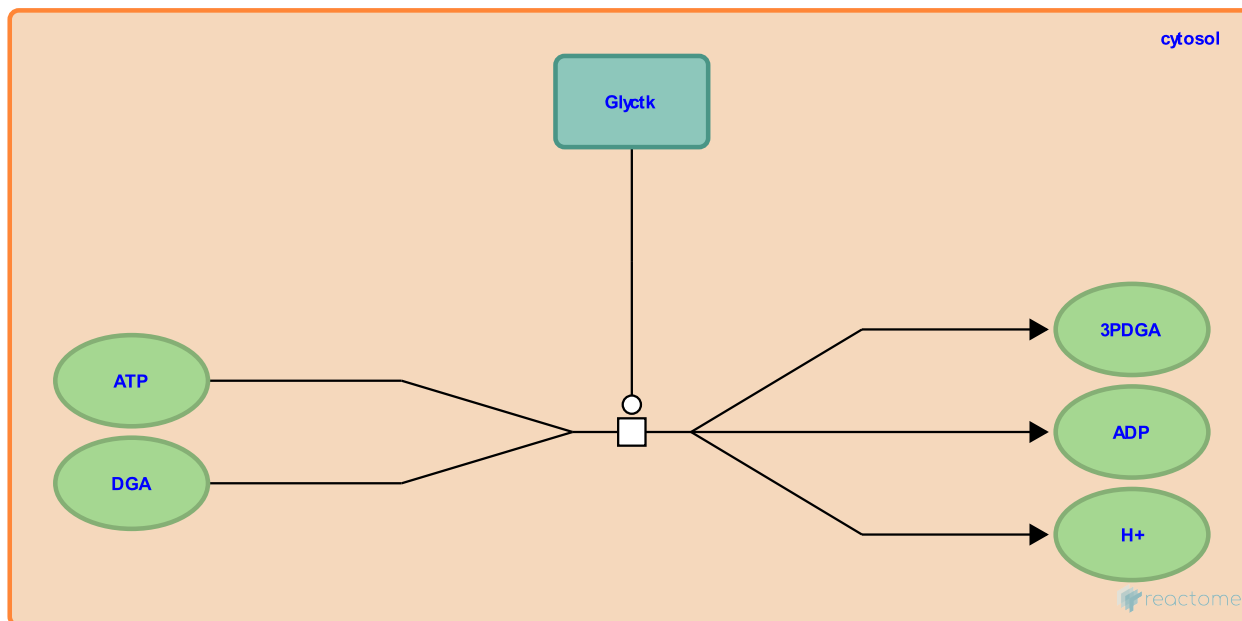
Location: [Fructose catabolism](#)

Stable identifier: R-RNO-6799495

Type: transition

Compartments: cytosol

Inferred from: [GLYCTK phosphorylates DGA to 3PDGA \(Homo sapiens\)](#)



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>

Preceded by: [ALDH1A1 oxidises GA to DGA](#)

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