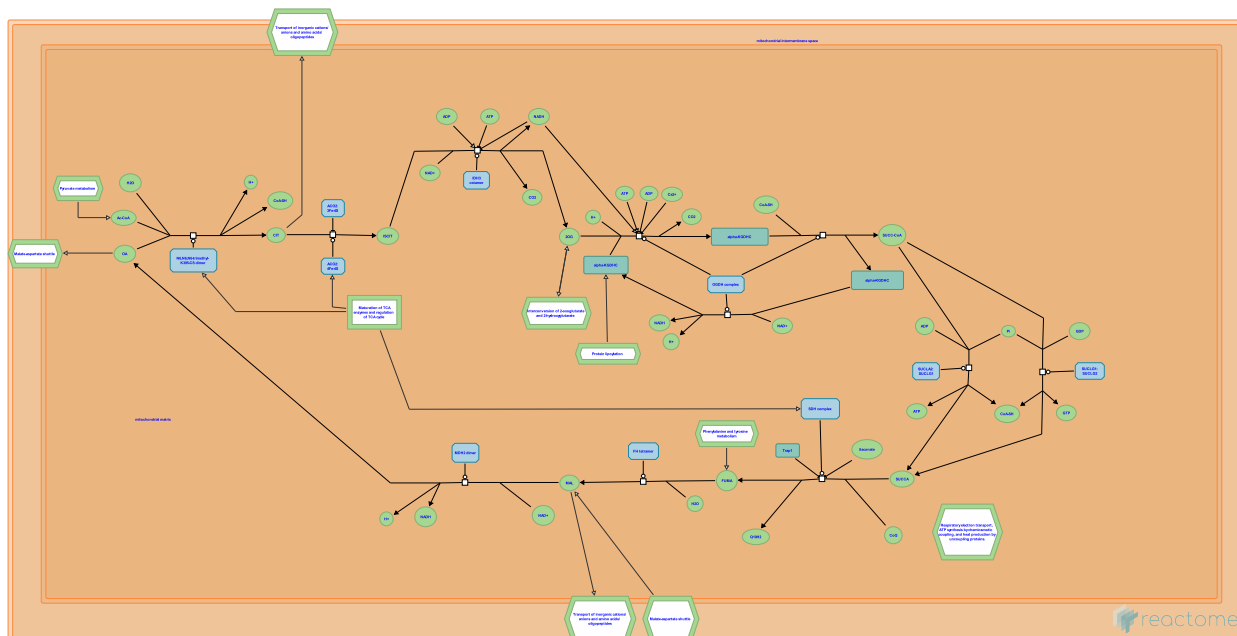


# Citric acid cycle (TCA cycle)



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

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This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the [Reactome Textbook](https://reactome.org/textbook).

06/05/2024

## 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

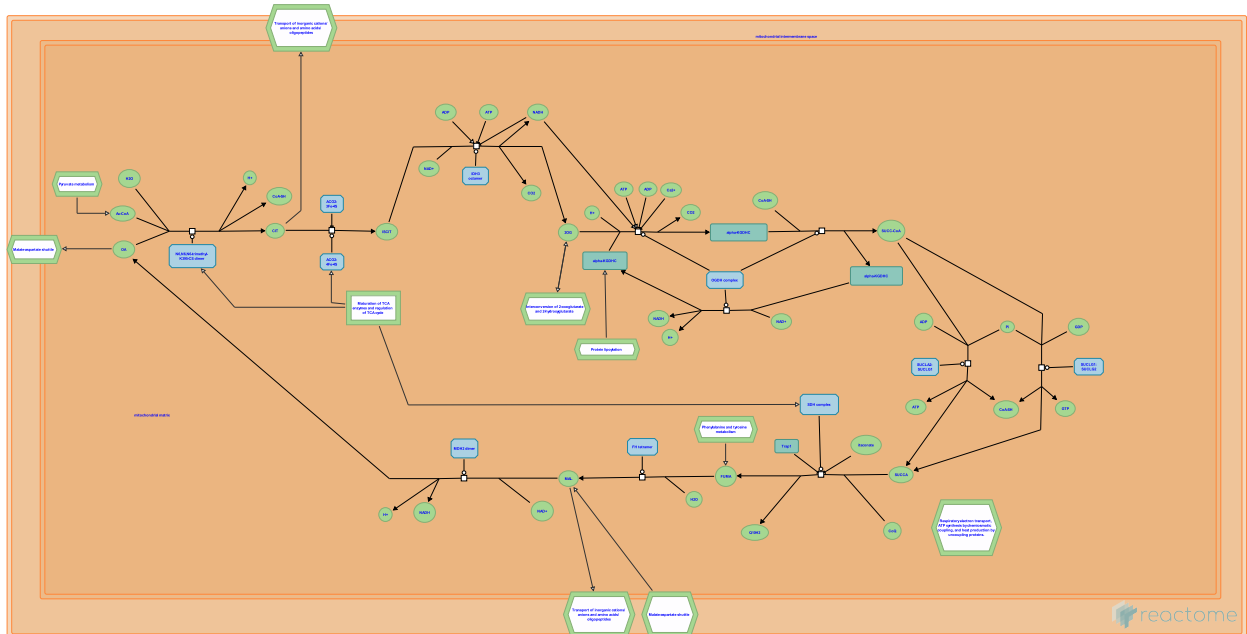
This document contains 3 pathways and 8 reactions ([see Table of Contents](#))

## Citric acid cycle (TCA cycle) ↗

**Stable identifier:** R-DME-71403

**Compartments:** mitochondrion

**Inferred from:** Citric acid cycle (TCA cycle) (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>

## CS acetylates OA to citrate ↗

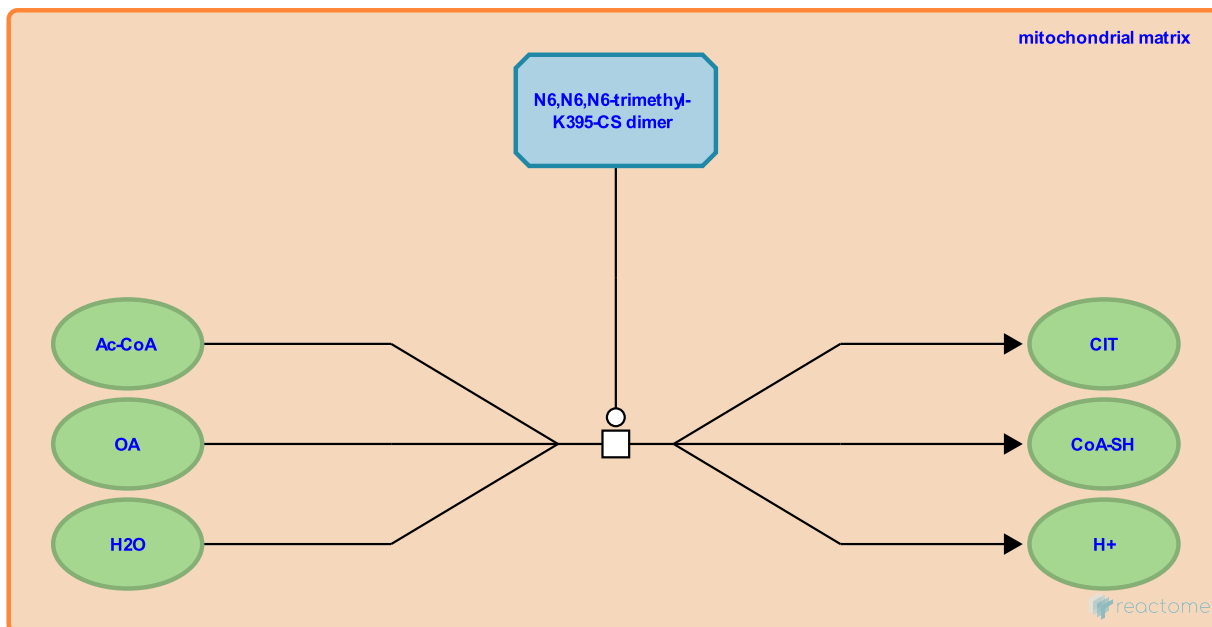
**Location:** Citric acid cycle (TCA cycle)

**Stable identifier:** R-DME-70975

**Type:** transition

**Compartments:** mitochondrial matrix

**Inferred from:** CS acetylates OA to citrate (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:** MDH2 dimer dehydrogenates MAL

**Followed by:** ACO2 isomerizes citrate

## ACO2 isomerizes citrate ↗

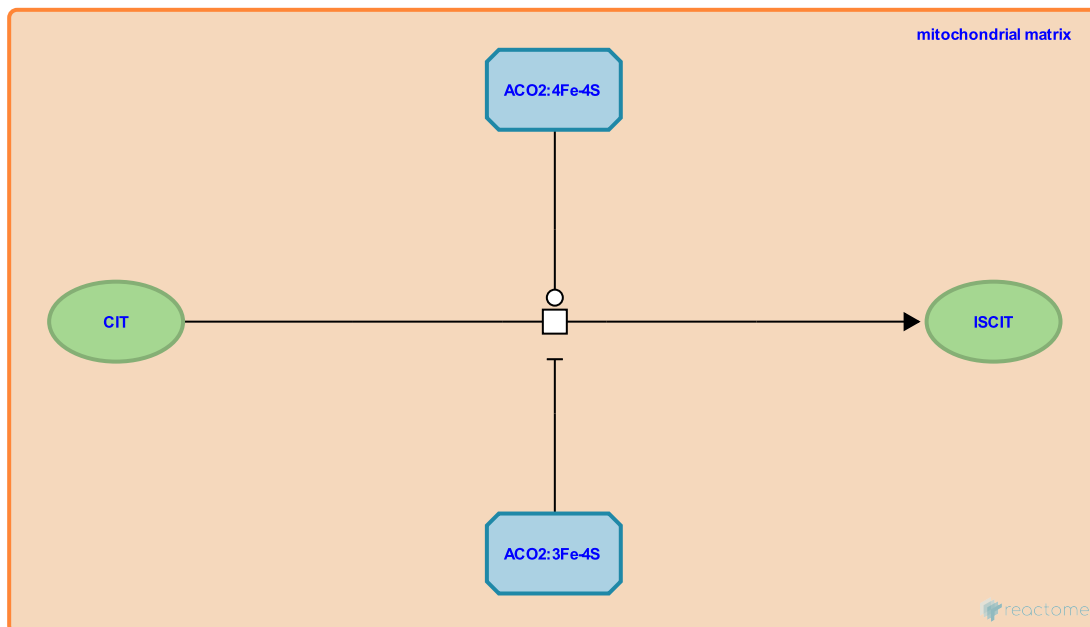
**Location:** Citric acid cycle (TCA cycle)

**Stable identifier:** R-DME-70971

**Type:** transition

**Compartments:** mitochondrial matrix

**Inferred from:** ACO2 isomerizes citrate (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:** CS acetylates OA to citrate

**Followed by:** IDH3 complex decarboxylates isocitrate

## IDH3 complex decarboxylates isocitrate ↗

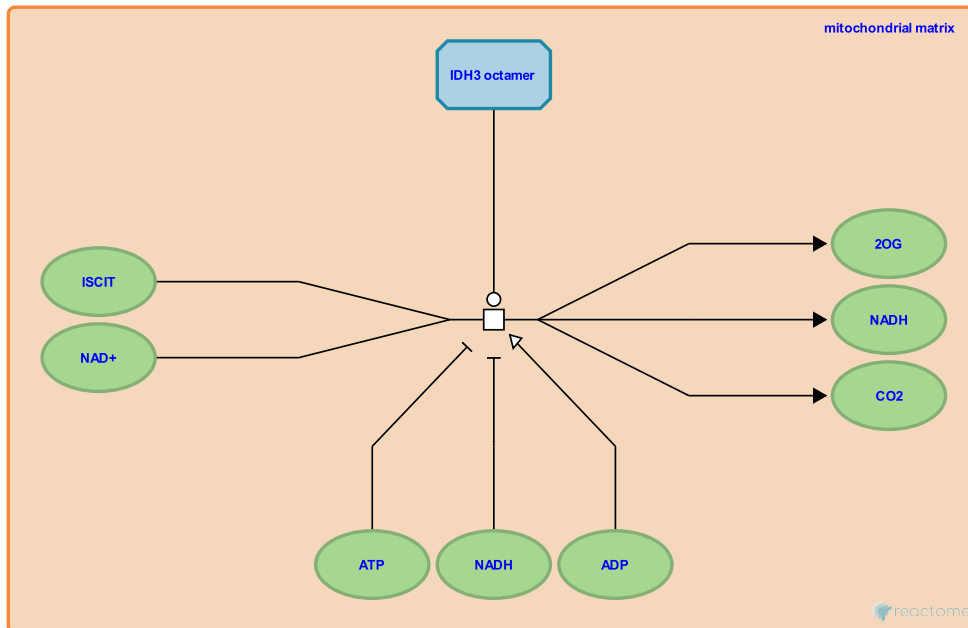
**Location:** Citric acid cycle (TCA cycle)

**Stable identifier:** R-DME-70967

**Type:** transition

**Compartments:** mitochondrial matrix

**Inferred from:** IDH3 complex decarboxylates isocitrate (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:** ACO2 isomerizes citrate

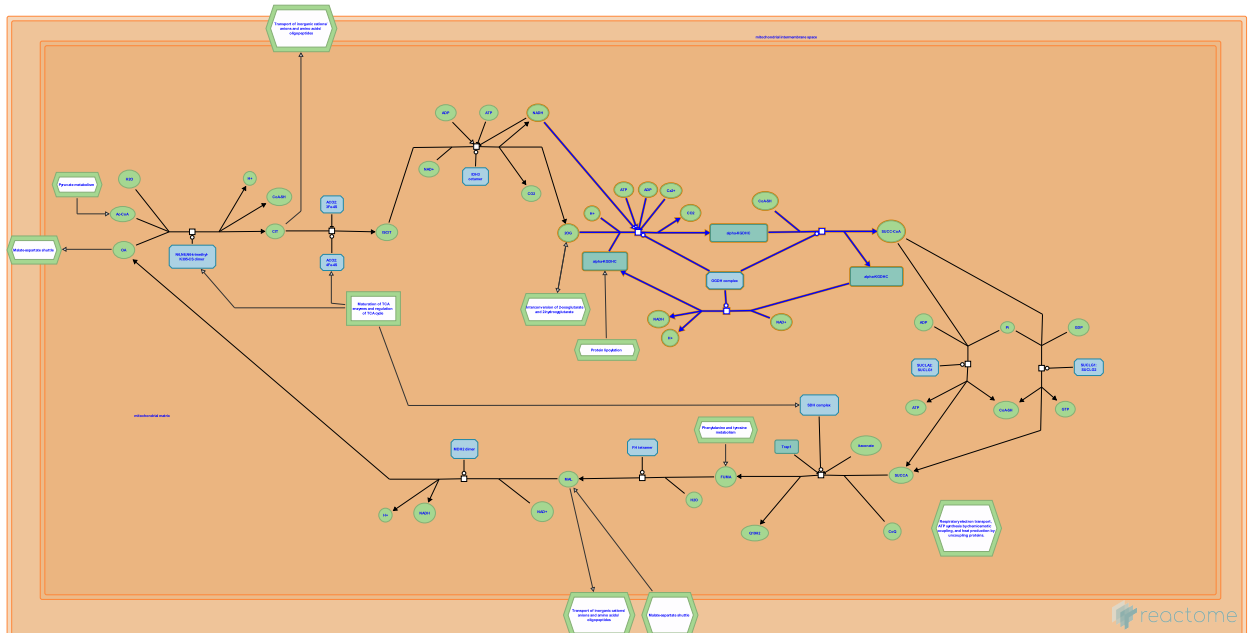
## OGDH complex synthesizes succinyl-CoA from 2-OG ↗

**Location:** Citric acid cycle (TCA cycle)

**Stable identifier:** R-DME-9853506

**Compartments:** mitochondrial matrix

**Inferred from:** OGDH complex synthesizes succinyl-CoA from 2-OG (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.](https://www.reactome.org) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## SUCLG1/A2 cleaves succinyl-CoA ↗

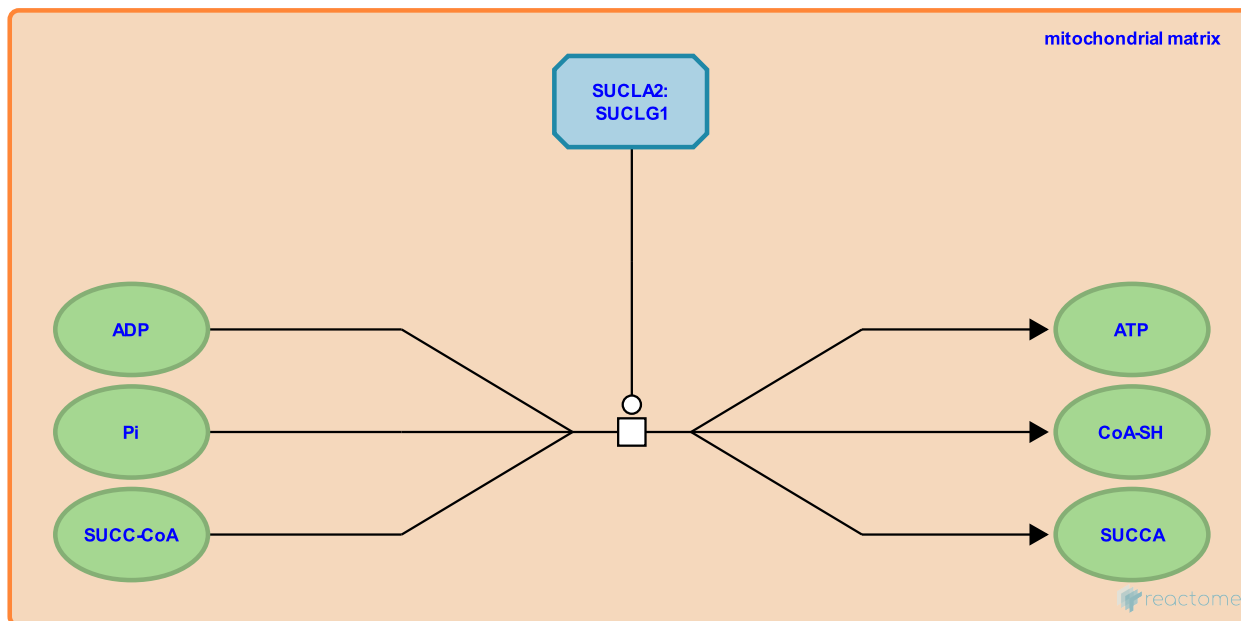
**Location:** Citric acid cycle (TCA cycle)

**Stable identifier:** R-DME-70997

**Type:** transition

**Compartments:** mitochondrial matrix

**Inferred from:** SUCLG1/A2 cleaves succinyl-CoA (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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**Followed by:** SDH complex dehydrogenates succinate



## SUCLG1/G2 cleaves succinyl-CoA ↗

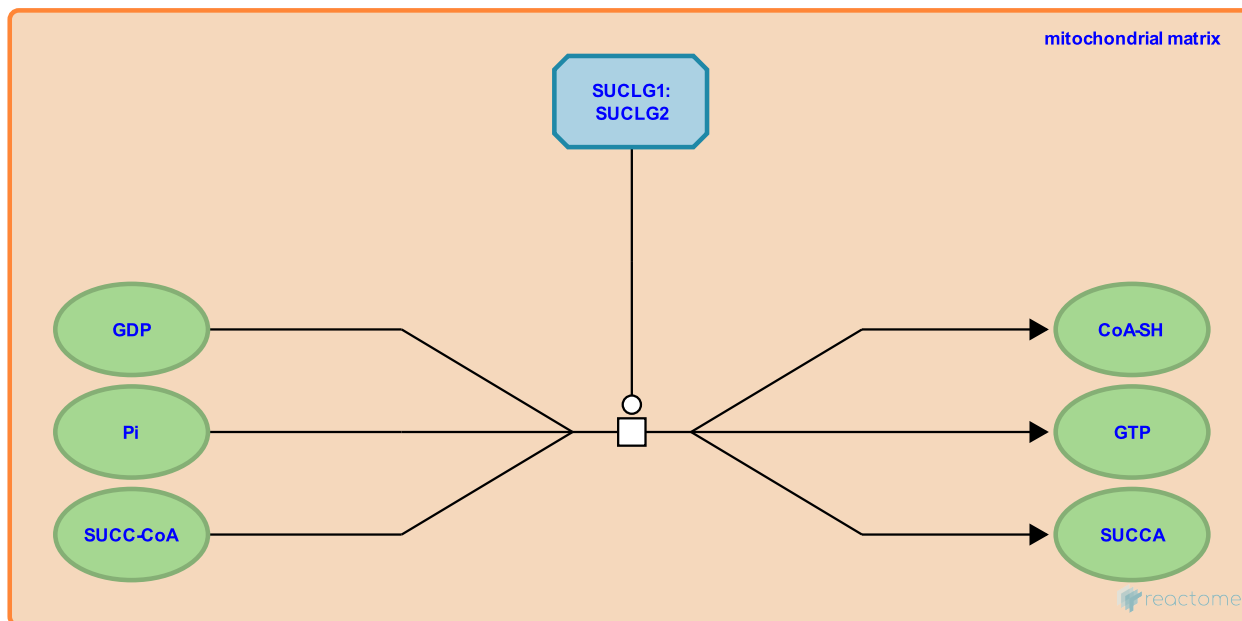
**Location:** Citric acid cycle (TCA cycle)

**Stable identifier:** R-DME-71775

**Type:** transition

**Compartments:** mitochondrial matrix

**Inferred from:** SUCLG1/G2 cleaves succinyl-CoA (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>

**Followed by:** SDH complex dehydrogenates succinate

## SDH complex dehydrogenates succinate ↗

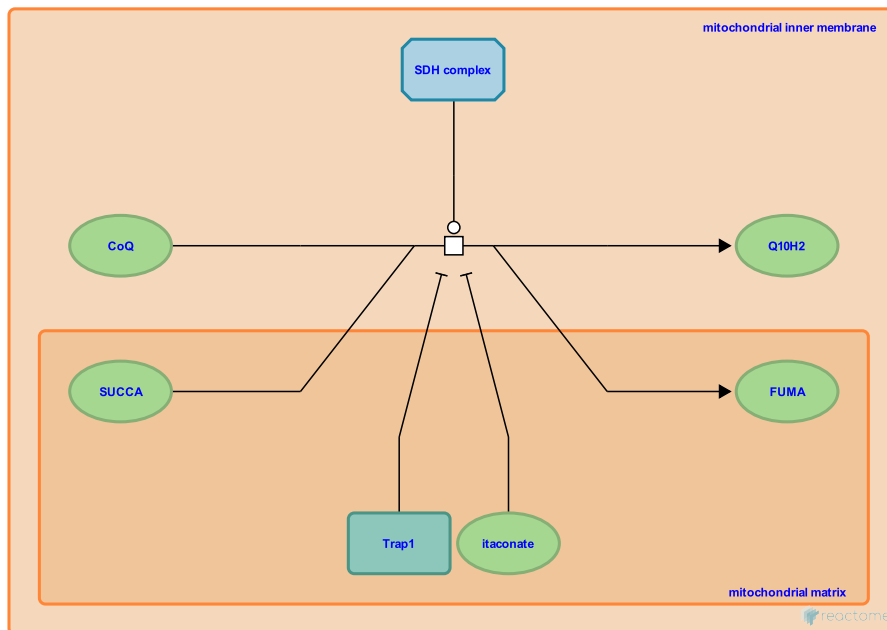
**Location:** Citric acid cycle (TCA cycle)

**Stable identifier:** R-DME-70994

**Type:** transition

**Compartments:** mitochondrial inner membrane, mitochondrial matrix

**Inferred from:** SDH complex dehydrogenates succinate (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:** [SUCLG1/A2 cleaves succinyl-CoA](#), [SUCLG1/G2 cleaves succinyl-CoA](#)

**Followed by:** [FH tetramer hydrates fumarate to L-malate](#)

## FH tetramer hydrates fumarate to L-malate ↗

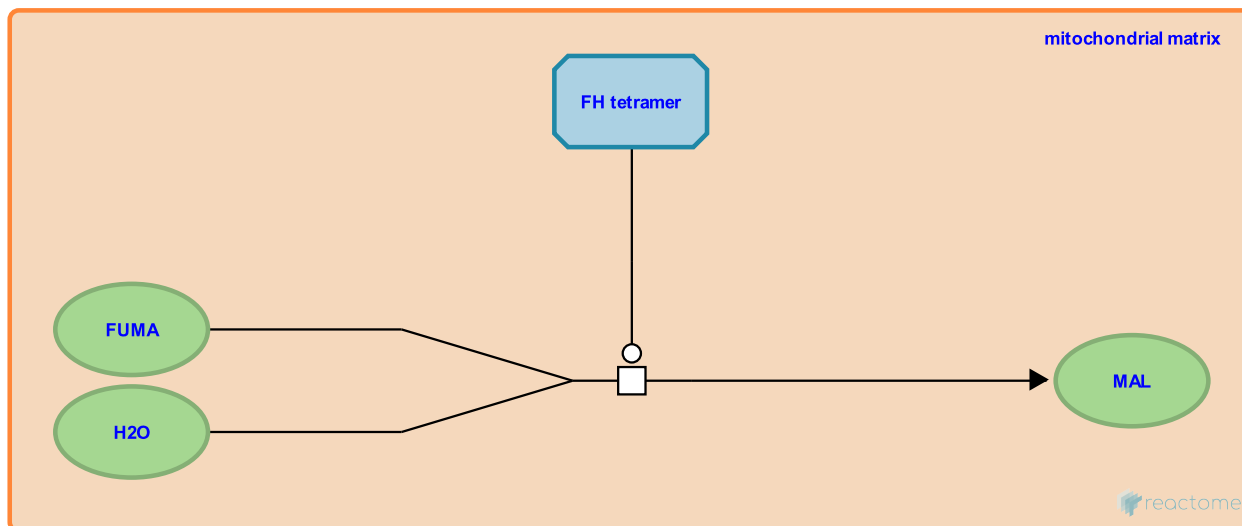
**Location:** Citric acid cycle (TCA cycle)

**Stable identifier:** R-DME-70982

**Type:** transition

**Compartments:** mitochondrial matrix

**Inferred from:** FH tetramer hydrates fumarate to L-malate (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:** SDH complex dehydrogenates succinate

**Followed by:** MDH2 dimer dehydrogenates MAL

## MDH2 dimer dehydrogenates MAL ↗

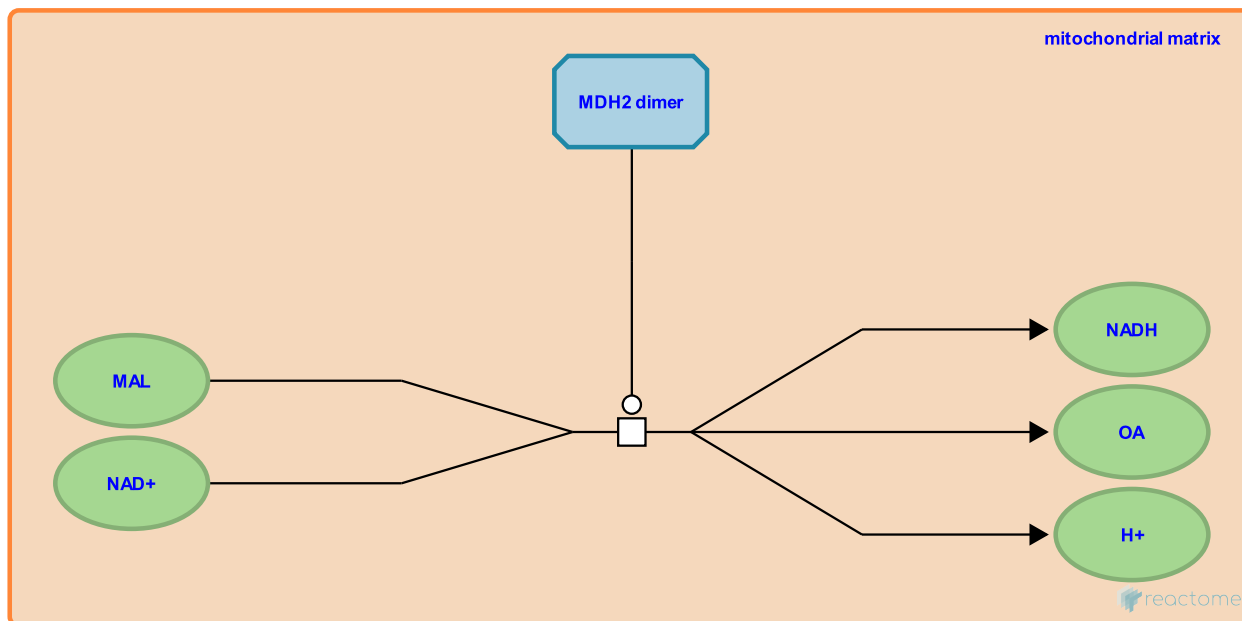
**Location:** Citric acid cycle (TCA cycle)

**Stable identifier:** R-DME-70979

**Type:** transition

**Compartments:** mitochondrial matrix

**Inferred from:** MDH2 dimer dehydrogenates MAL (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:** FH tetramer hydrates fumarate to L-malate

**Followed by:** CS acetylates OA to citrate



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