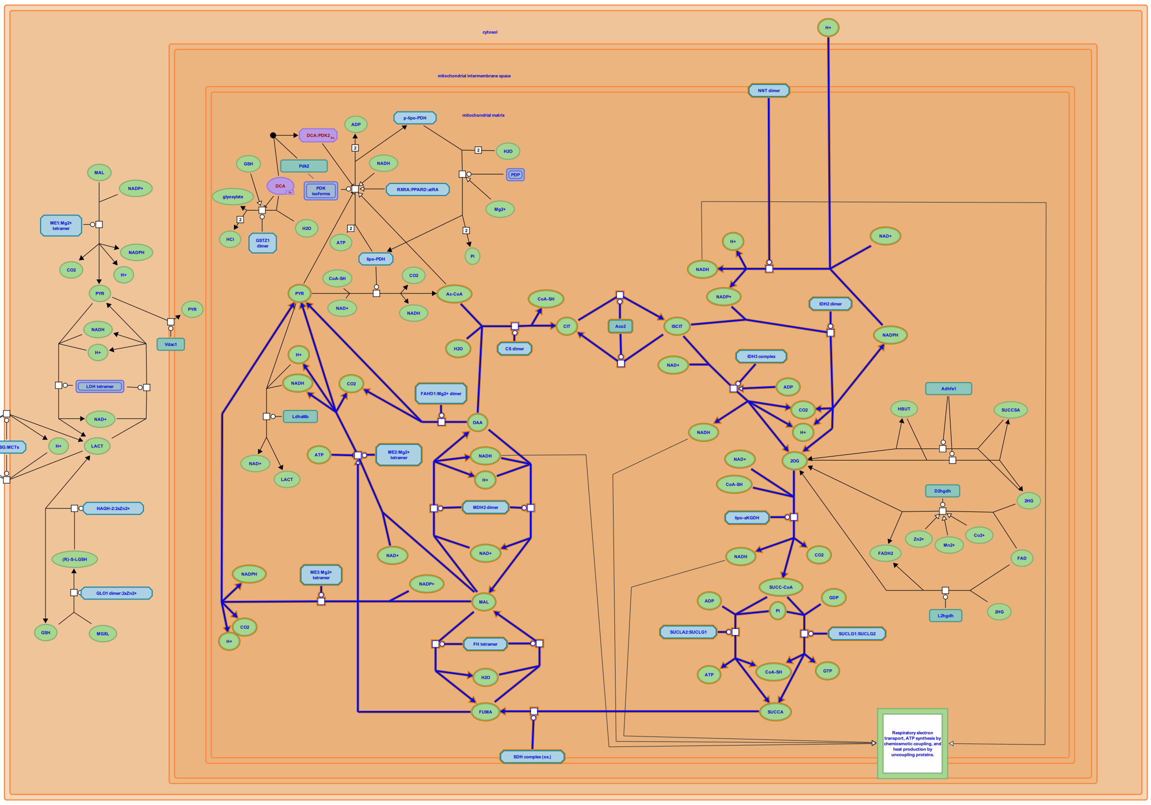
Citric acid cycle (TCA cycle)



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

28/07/2021

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: 77

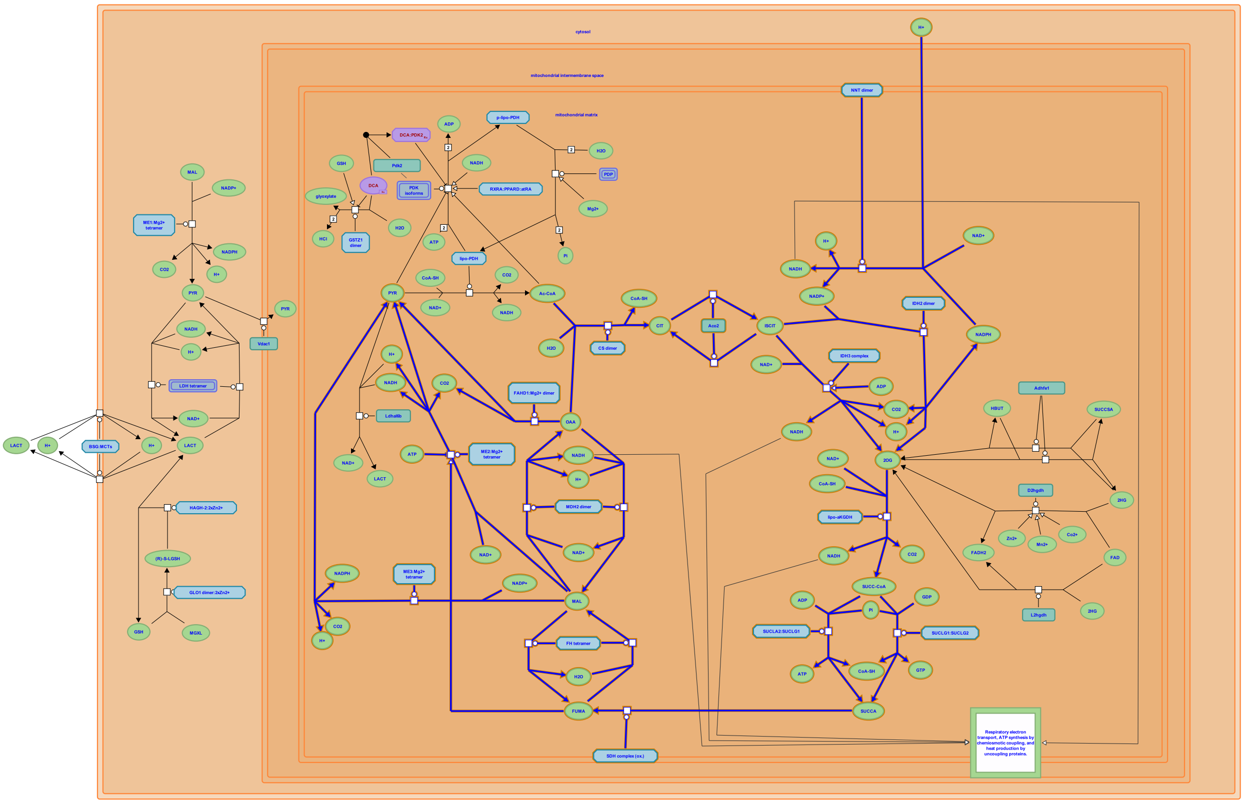
This document contains 1 pathway and 17 reactions (see Table of Contents)

Citric acid cycle (TCA cycle) ↗

Stable identifier: R-MMU-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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Acetyl-CoA + H2O + Oxaloacetate => Citrate + CoA ↗

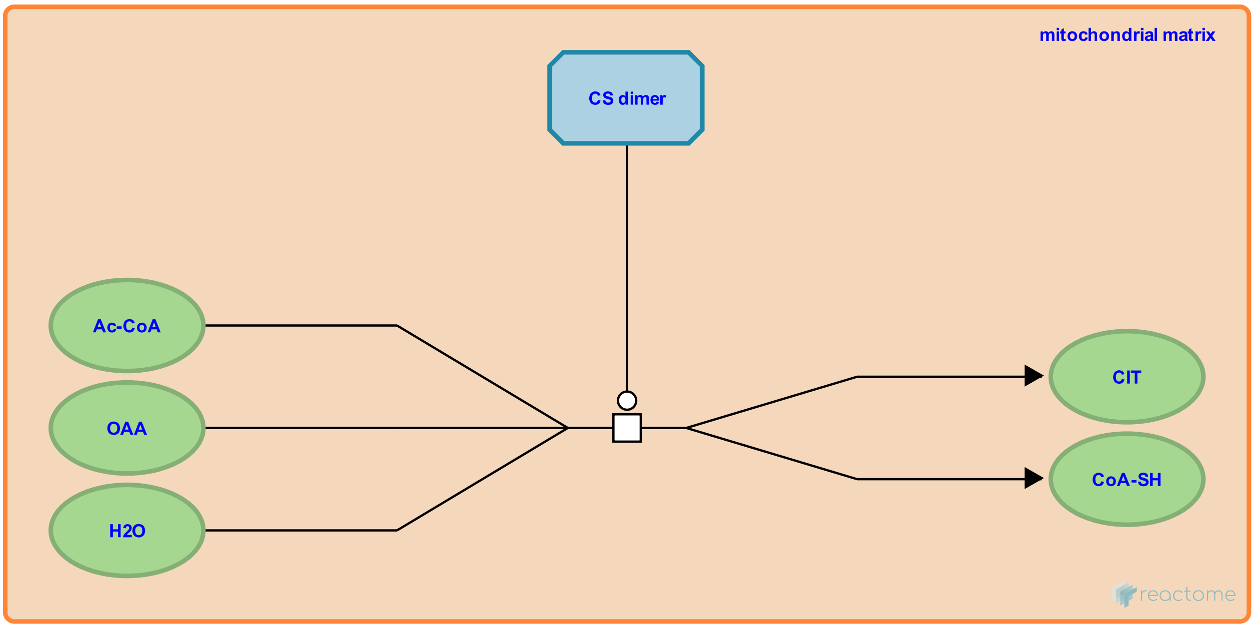
Location: Citric acid cycle (TCA cycle)

Stable identifier: R-MMU-70975

Type: transition

Compartments: mitochondrial matrix

Inferred from: Acetyl-CoA + H2O + Oxaloacetate => Citrate + 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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Preceded by: (S)-Malate + NAD+ <=> Oxaloacetate + NADH + H+

Followed by: citrate <=> isocitrate

citrate <=> isocitrate ↗

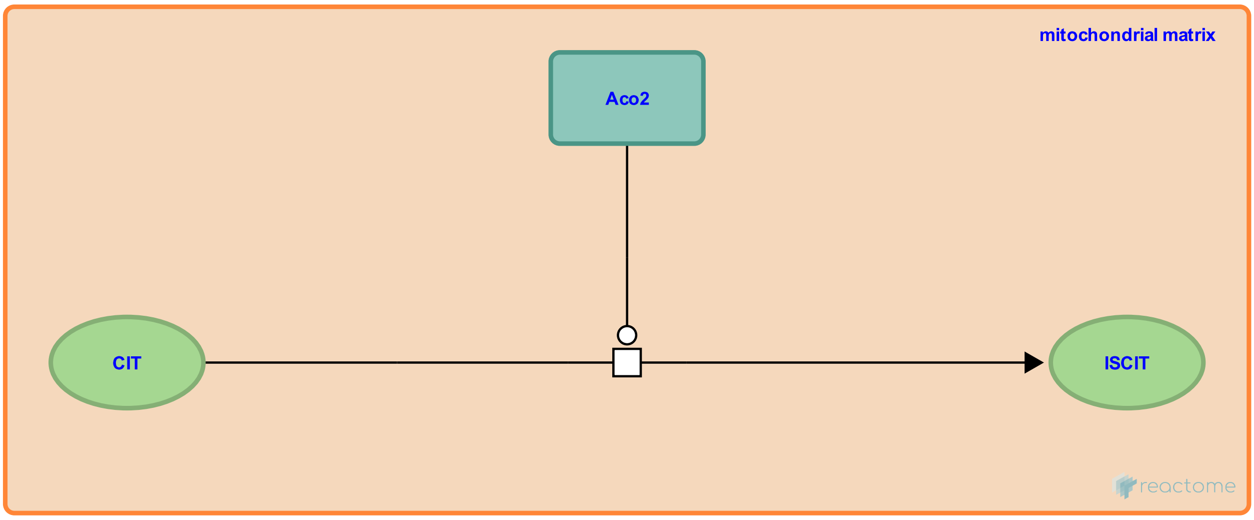
Location: Citric acid cycle (TCA cycle)

Stable identifier: R-MMU-70971

Type: transition

Compartments: mitochondrial matrix

Inferred from: citrate <=> 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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Preceded by: Acetyl-CoA + H2O + Oxaloacetate => Citrate + CoA

Followed by: isocitrate + NADP+ => alpha-ketoglutarate + CO2 + NADPH + H+ [IDH2], isocitrate + NAD+ => alpha-ketoglutarate + CO2 + NADH + H+ [IDH3]

isocitrate <=> citrate ↗

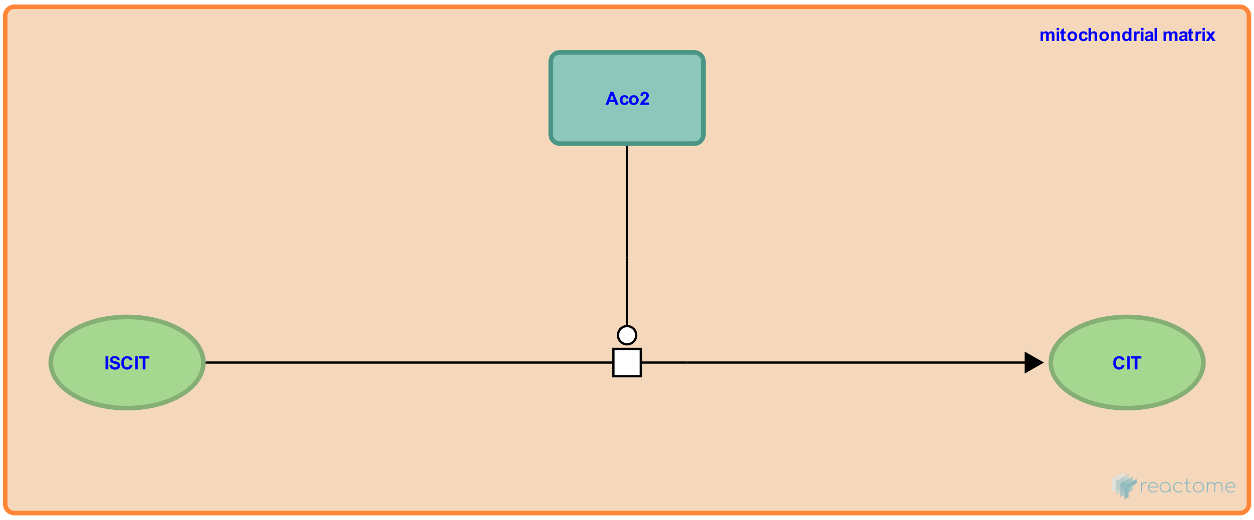
Location: Citric acid cycle (TCA cycle)

Stable identifier: R-MMU-450975

Type: transition

Compartments: mitochondrial matrix

Inferred from: isocitrate <=> 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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

isocitrate + NAD+ => alpha-ketoglutarate + CO2 + NADH + H+ [IDH3] ↗

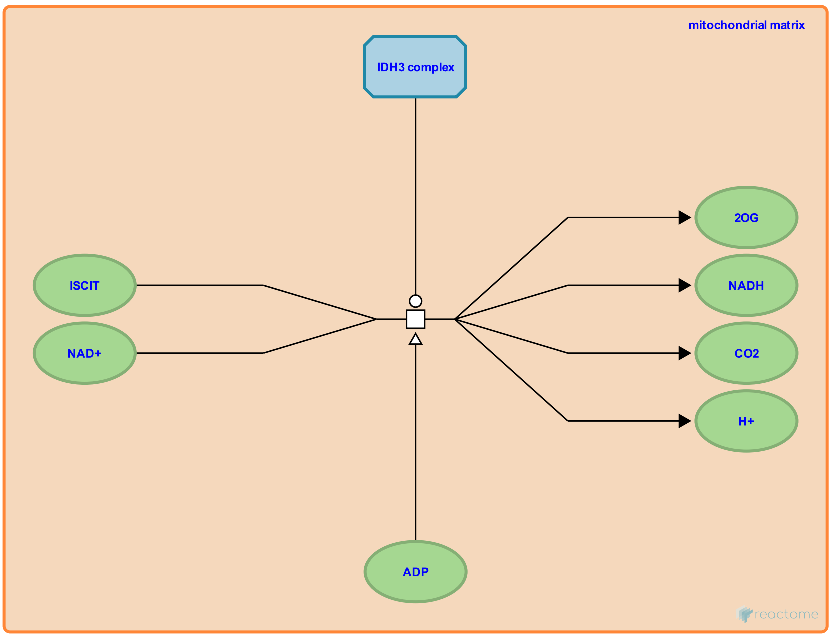
Location: Citric acid cycle (TCA cycle)

Stable identifier: R-MMU-70967

Type: transition

Compartments: mitochondrial matrix

Inferred from: isocitrate + NAD+ => alpha-ketoglutarate + CO2 + NADH + H+ [IDH3] (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Preceded by: citrate <=> isocitrate

Followed by: alpha-ketoglutarate + CoASH + NAD+ => succinyl-CoA + CO2 + NADH + H+

isocitrate + NADP+ => alpha-ketoglutarate + CO2 + NADPH + H+ [IDH2] ↗

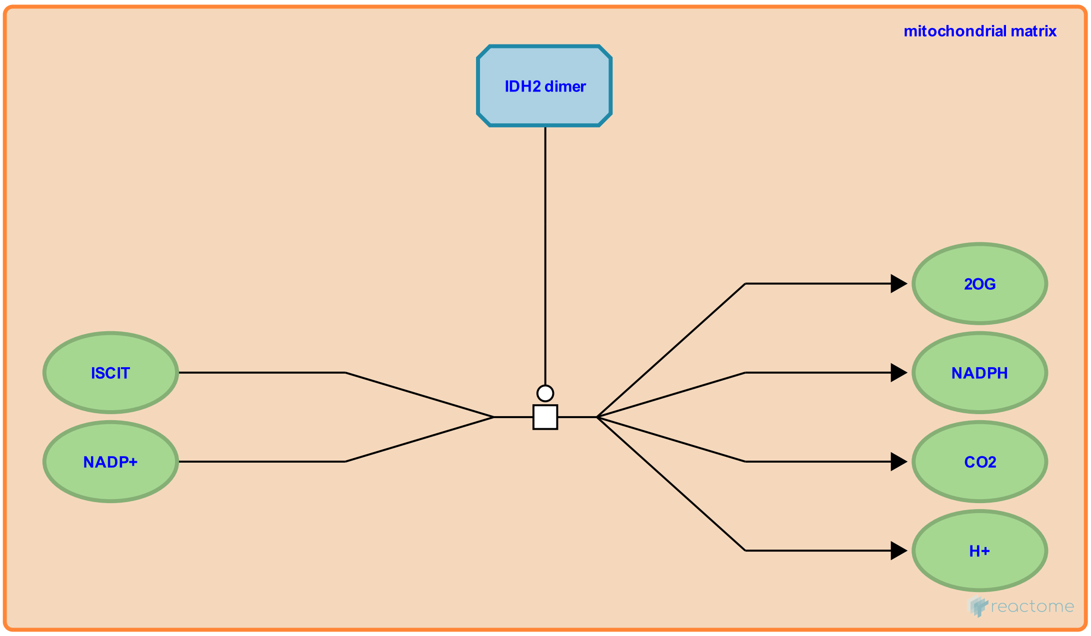
Location: Citric acid cycle (TCA cycle)

Stable identifier: R-MMU-450984

Type: transition

Compartments: mitochondrial matrix

Inferred from: isocitrate + NADP+ => alpha-ketoglutarate + CO2 + NADPH + H+ [IDH2] (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Preceded by: citrate <=> isocitrate

Followed by: NADPH + NAD+ + H+ [cytosol] => NADP+ + NADH + H+ [mitochondrial matrix]

NADPH + NAD+ + H+ [cytosol] => NADP+ + NADH + H+ [mitochondrial matrix] ↗

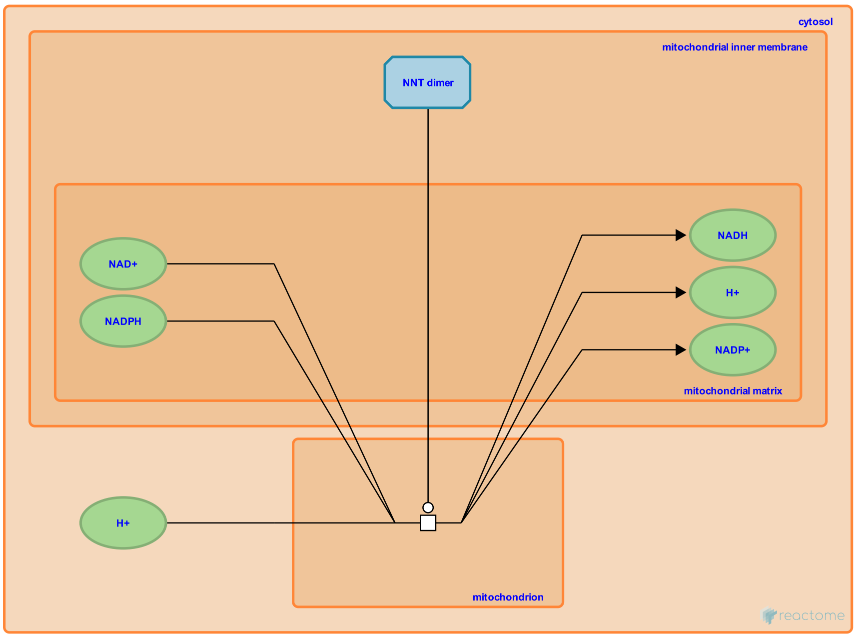
Location: Citric acid cycle (TCA cycle)

Stable identifier: R-MMU-450971

Type: transition

Compartments: mitochondrion

Inferred from: NADPH + NAD+ + H+ [cytosol] => NADP+ + NADH + H+ [mitochondrial matrix] (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Preceded by: isocitrate + NADP+ => alpha-ketoglutarate + CO2 + NADPH + H+ [IDH2]

alpha-ketoglutarate + CoASH + NAD+ => succinyl-CoA + CO2 + NADH + H+ ↗

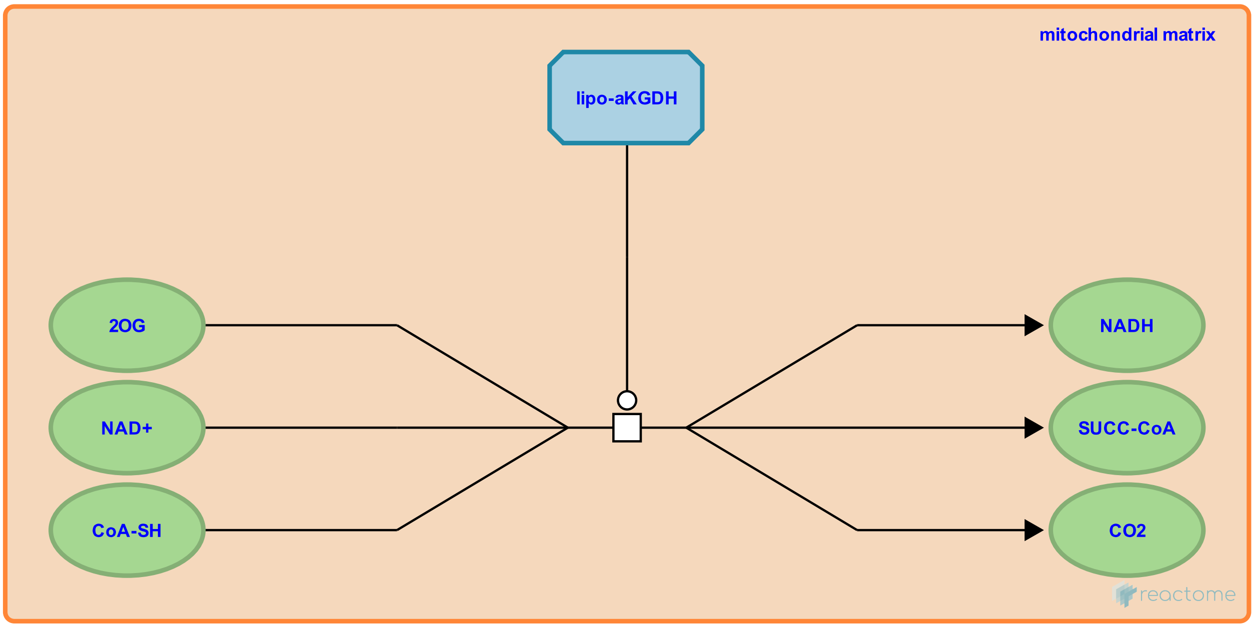
Location: Citric acid cycle (TCA cycle)

Stable identifier: R-MMU-71401

Type: transition

Compartments: mitochondrial matrix

Inferred from: alpha-ketoglutarate + CoASH + NAD+ => succinyl-CoA + CO2 + NADH + H+ (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Preceded by: isocitrate + NAD+ => alpha-ketoglutarate + CO2 + NADH + H+ [IDH3]

Followed by: ADP + Orthophosphate + Succinyl-CoA <=> ATP + Succinate + CoA, GDP + Orthophosphate + Succinyl-CoA <=> GTP + Succinate + CoA

GDP + Orthophosphate + Succinyl-CoA <=> GTP + Succinate + CoA ↗

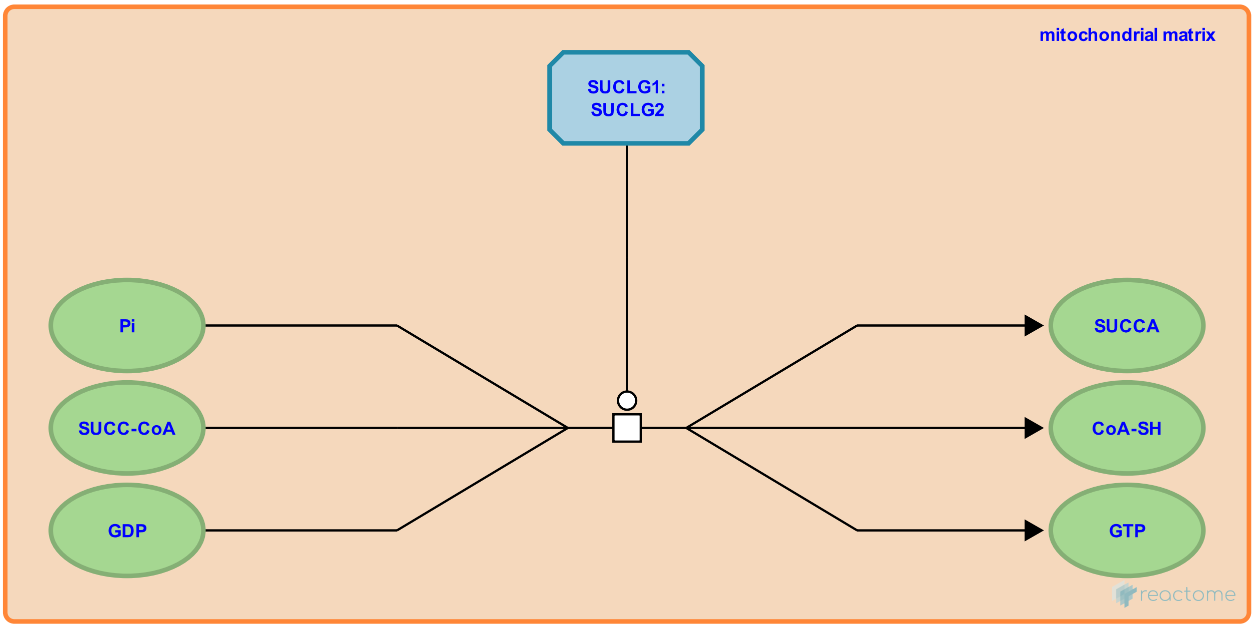
Location: Citric acid cycle (TCA cycle)

Stable identifier: R-MMU-71775

Type: transition

Compartments: mitochondrial matrix

Inferred from: GDP + Orthophosphate + Succinyl-CoA <=> GTP + Succinate + 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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Preceded by: alpha-ketoglutarate + CoASH + NAD+ => succinyl-CoA + CO2 + NADH + H+

Followed by: Succinate <=> Fumarate (with FAD redox reaction on enzyme)

ADP + Orthophosphate + Succinyl-CoA <=> ATP + Succinate + CoA ↗

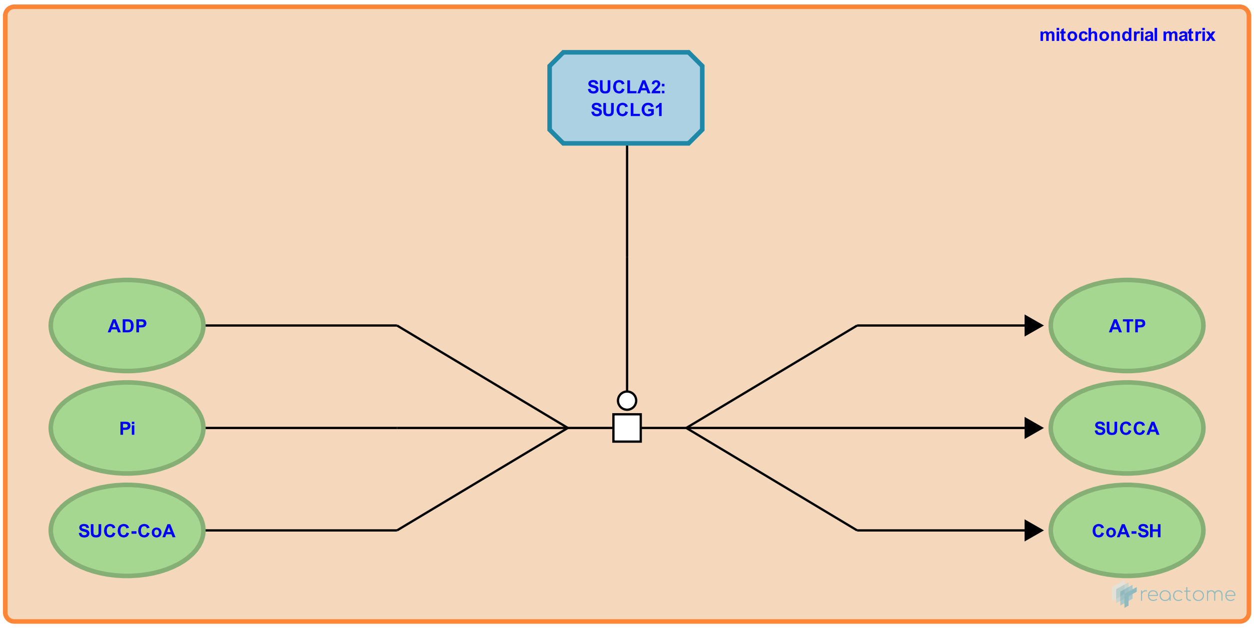
Location: Citric acid cycle (TCA cycle)

Stable identifier: R-MMU-70997

Type: transition

Compartments: mitochondrial matrix

Inferred from: ADP + Orthophosphate + Succinyl-CoA <=> ATP + Succinate + 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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Preceded by: alpha-ketoglutarate + CoASH + NAD+ => succinyl-CoA + CO2 + NADH + H+

Followed by: Succinate <=> Fumarate (with FAD redox reaction on enzyme)

Succinate <=> Fumarate (with FAD redox reaction on enzyme) ↗

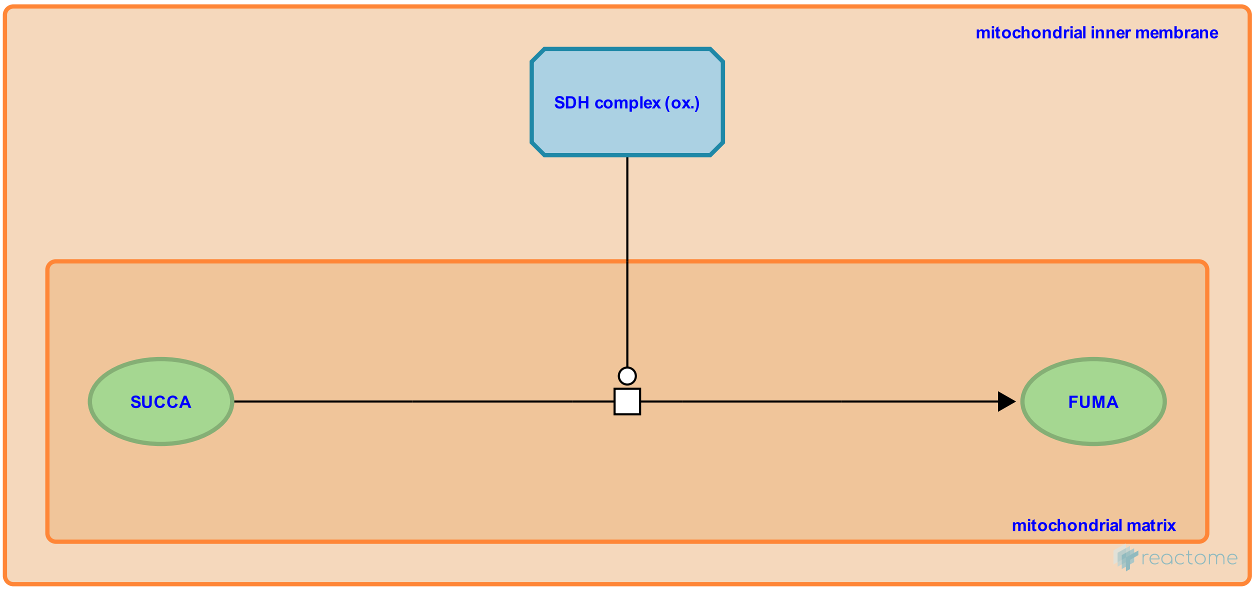
Location: Citric acid cycle (TCA cycle)

Stable identifier: R-MMU-70994

Type: transition

Compartments: mitochondrial matrix, mitochondrial inner membrane

Inferred from: Succinate <=> Fumarate (with FAD redox reaction on enzyme) (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Preceded by: ADP + Orthophosphate + Succinyl-CoA <=> ATP + Succinate + CoA, GDP + Orthophosphate + Succinyl-CoA <=> GTP + Succinate + CoA

Followed by: Fumarate + H2O <=> (S)-Malate

Fumarate + H2O <=> (S)-Malate ↗

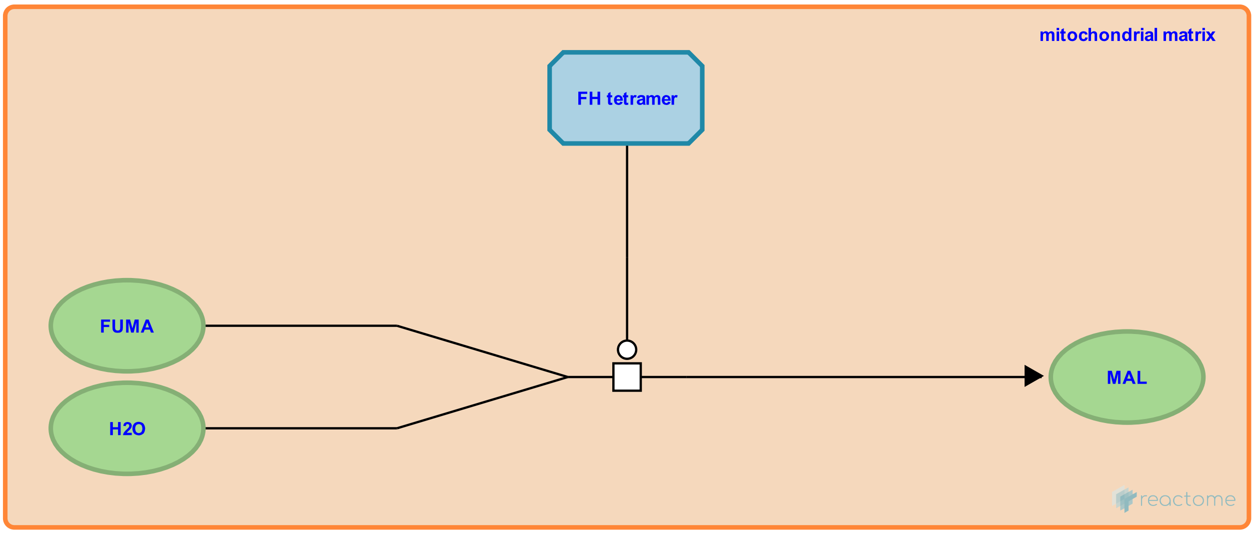
Location: Citric acid cycle (TCA cycle)

Stable identifier: R-MMU-70982

Type: transition

Compartments: mitochondrial matrix

Inferred from: Fumarate + H2O <=> (S)-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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Preceded by: Succinate <=> Fumarate (with FAD redox reaction on enzyme)

Followed by: (S)-Malate + NAD+ <=> Oxaloacetate + NADH + H+, ME3:Mg2+ tetramer oxidatively decarboxylates MAL to PYR, ME2:Mg2+ tetramer oxidatively decarboxylates MAL to PYR

(S)-Malate <=> Fumarate + H2O ↗

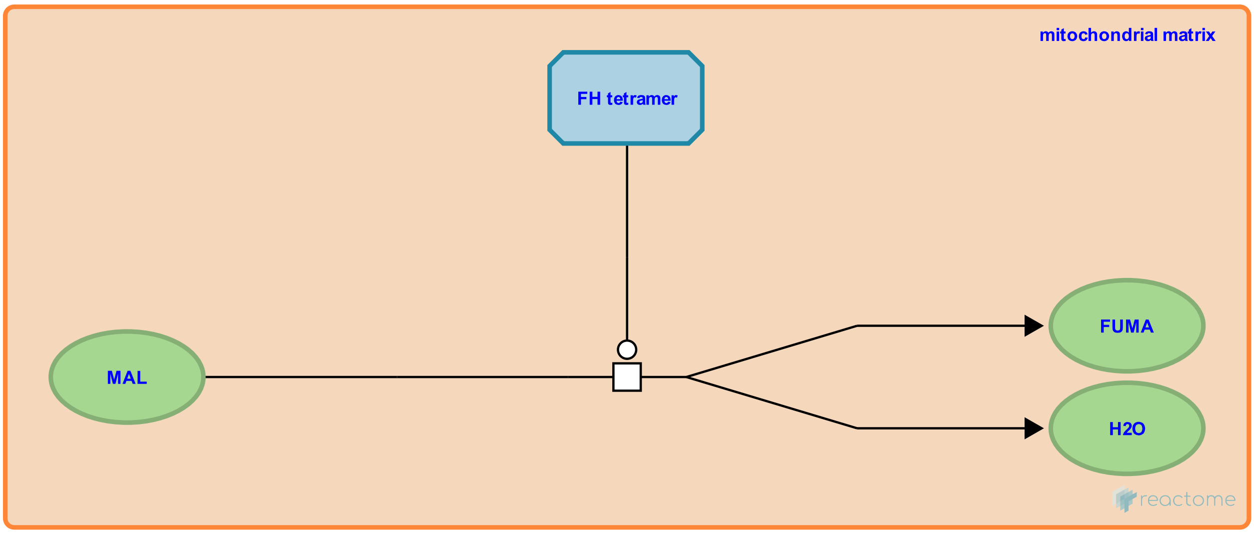
Location: Citric acid cycle (TCA cycle)

Stable identifier: R-MMU-451033

Type: transition

Compartments: mitochondrial matrix

Inferred from: (S)-Malate <=> Fumarate + H2O (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

(S)-Malate + NAD+ <=> Oxaloacetate + NADH + H+ ↗

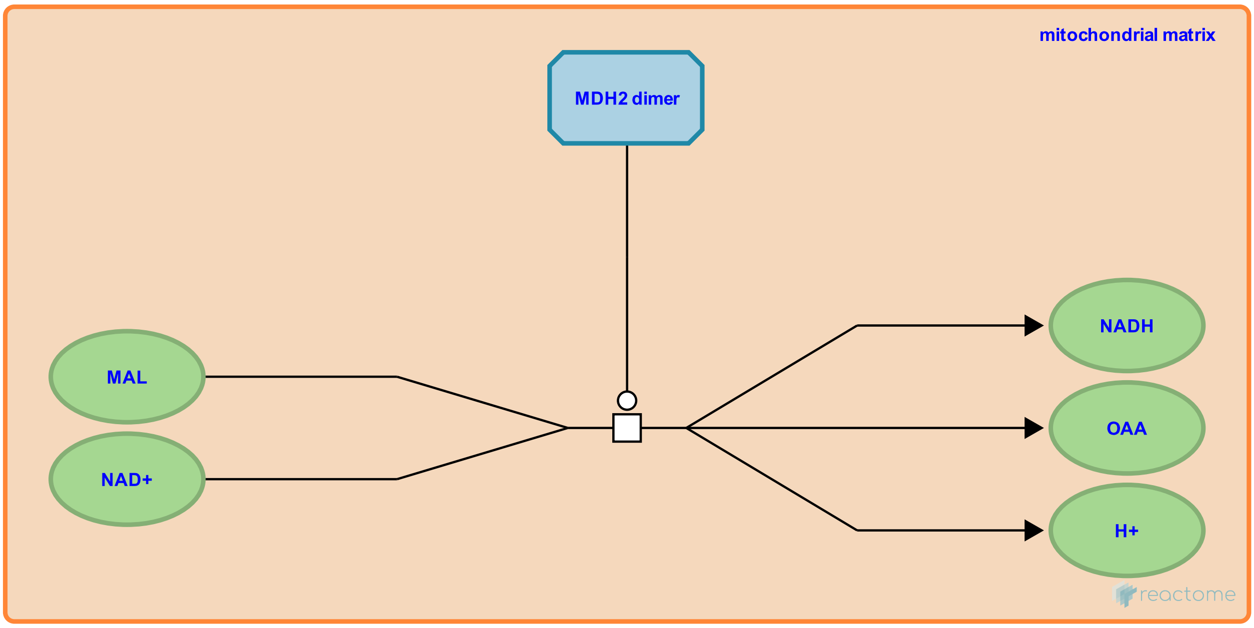
Location: Citric acid cycle (TCA cycle)

Stable identifier: R-MMU-70979

Type: transition

Compartments: mitochondrial matrix

Inferred from: (S)-Malate + NAD+ <=> Oxaloacetate + NADH + H+ (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Preceded by: Fumarate + H2O <=> (S)-Malate

Followed by: FAHD1:Zn2+ dimer hydrolyses OA to PYR, Acetyl-CoA + H2O + Oxaloacetate => Citrate + CoA

Oxaloacetate + NADH + H+ <=> (S)-Malate + NAD+ ↗

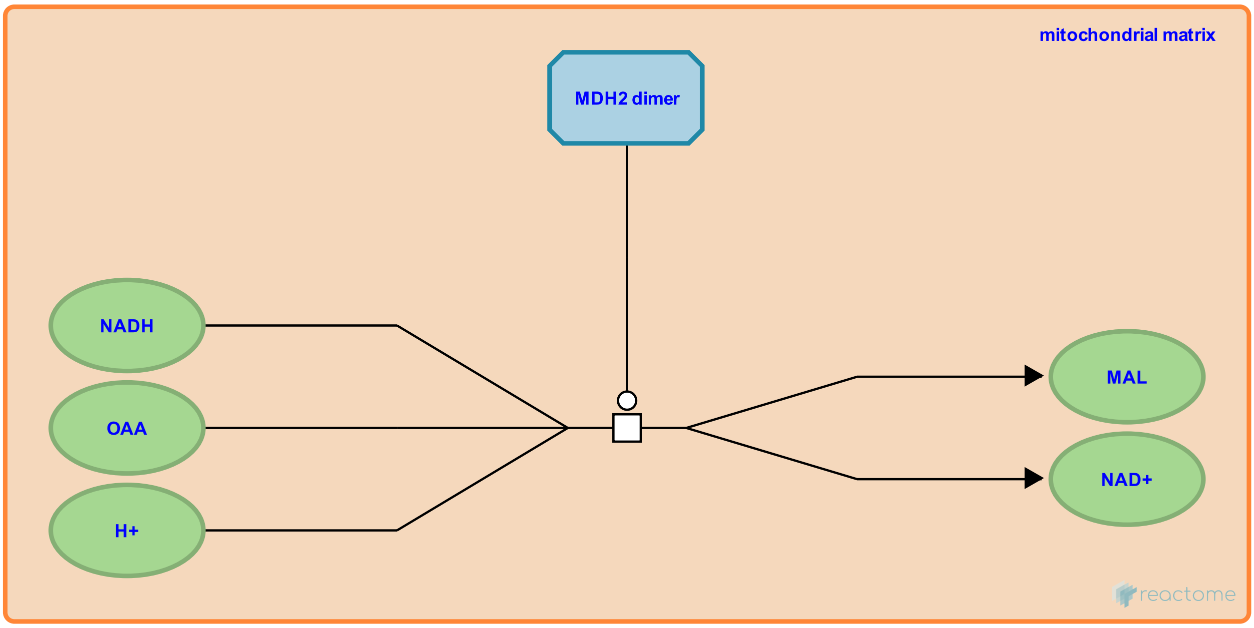
Location: Citric acid cycle (TCA cycle)

Stable identifier: R-MMU-71783

Type: transition

Compartments: mitochondrial matrix

Inferred from: Oxaloacetate + NADH + H+ <=> (S)-Malate + NAD+ (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Followed by: ME3:Mg2+ tetramer oxidatively decarboxylates MAL to PYR, ME2:Mg2+ tetramer oxidatively decarboxylates MAL to PYR

FAHD1:Zn2+ dimer hydrolyses OA to PYR ↗

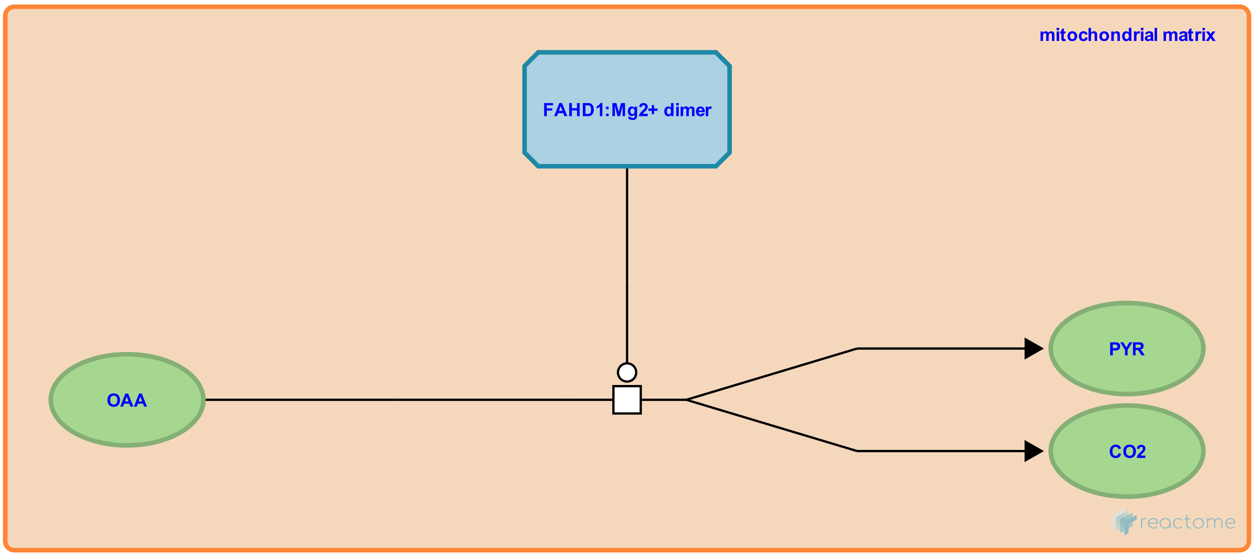
Location: Citric acid cycle (TCA cycle)

Stable identifier: R-MMU-9012016

Type: transition

Compartments: mitochondrial matrix

Inferred from: FAHD1:Zn2+ dimer hydrolyses OA to PYR (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Preceded by: (S)-Malate + NAD+ <=> Oxaloacetate + NADH + H+

ME2:Mg2+ tetramer oxidatively decarboxylates MAL to PYR ↗

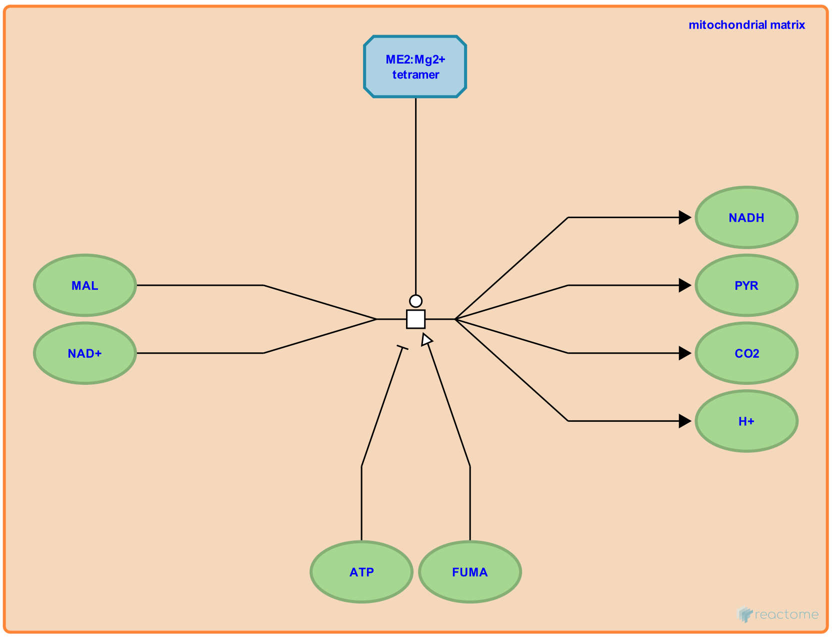
Location: Citric acid cycle (TCA cycle)

Stable identifier: R-MMU-9012268

Type: transition

Compartments: mitochondrial matrix

Inferred from: ME2:Mg2+ tetramer oxidatively decarboxylates MAL to PYR (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Preceded by: Oxaloacetate + NADH + H+ <=> (S)-Malate + NAD+, Fumarate + H2O <=> (S)-Malate

ME3:Mg2+ tetramer oxidatively decarboxylates MAL to PYR ↗

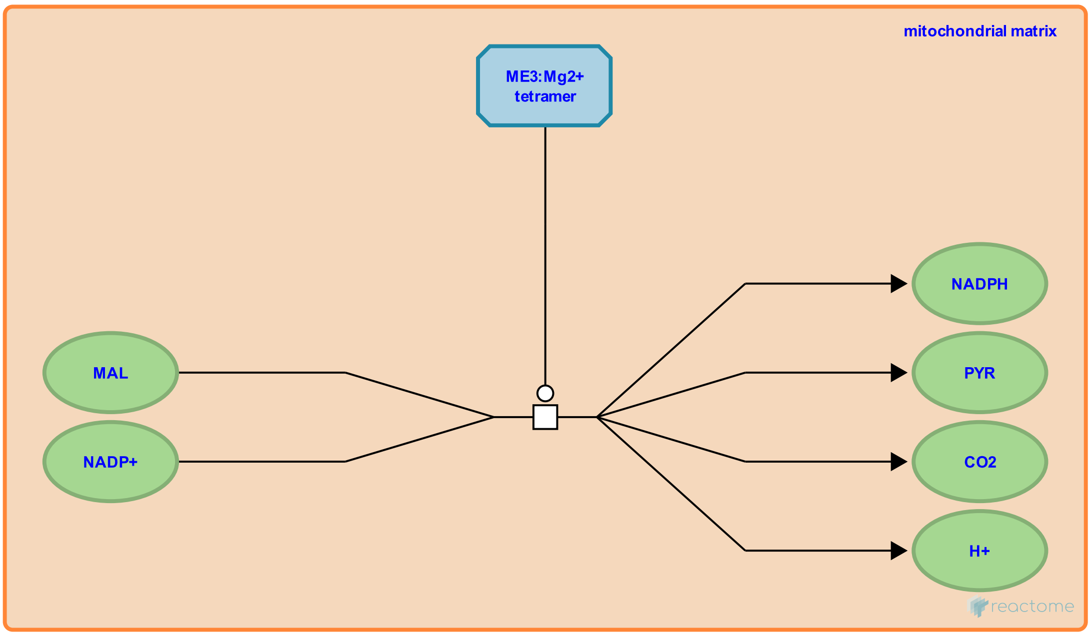
Location: Citric acid cycle (TCA cycle)

Stable identifier: R-MMU-9012349

Type: transition

Compartments: mitochondrial matrix

Inferred from: ME3:Mg2+ tetramer oxidatively decarboxylates MAL to PYR (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Preceded by: Oxaloacetate + NADH + H+ <=> (S)-Malate + NAD+, Fumarate + H2O <=> (S)-Malate

Table of Contents