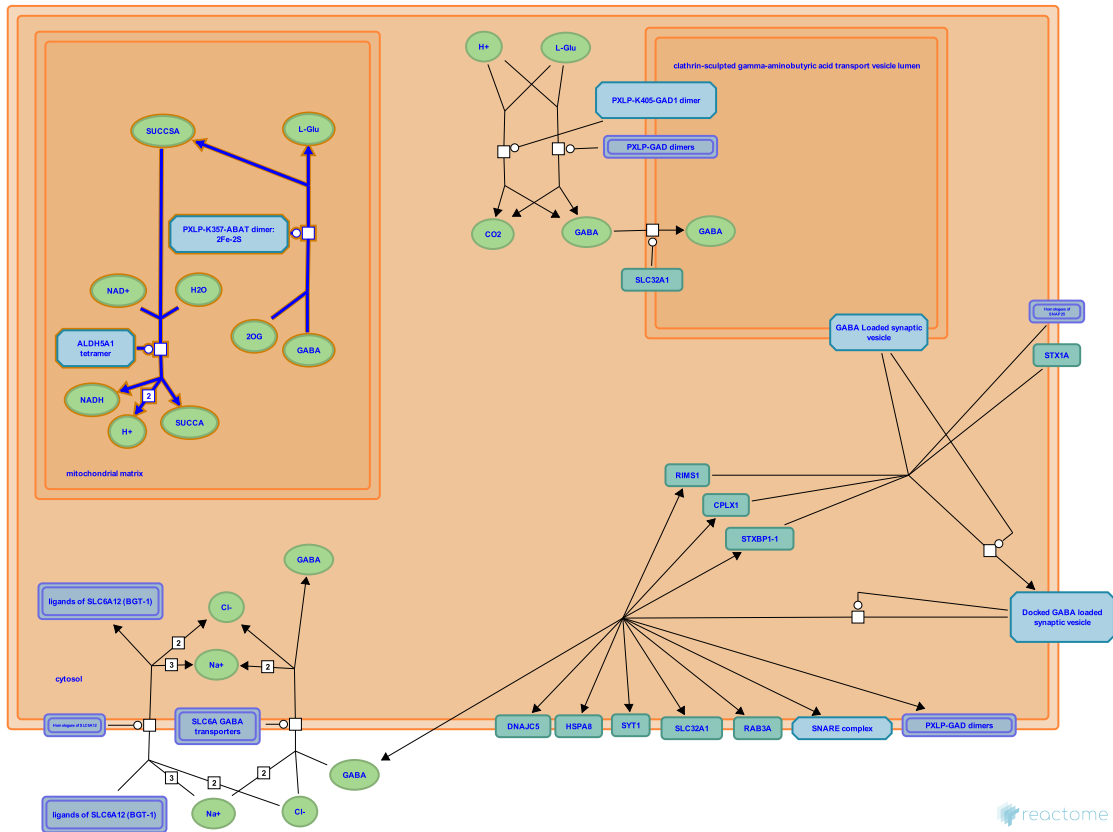


Degradation of GABA



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

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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

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Reactome database release: 70

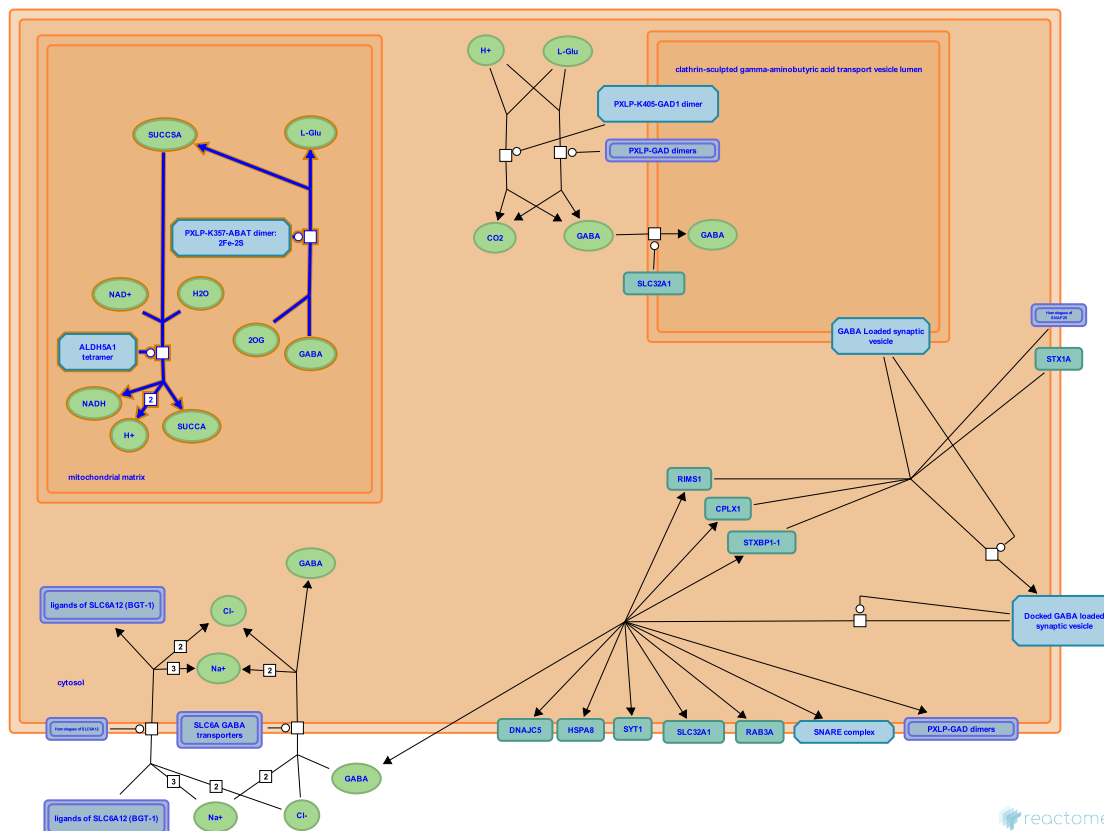
This document contains 1 pathway and 2 reactions ([see Table of Contents](#))

Degradation of GABA ↗

Stable identifier: R-CEL-916853

Compartments: cytosol, mitochondrial matrix

Inferred from: Degradation of GABA (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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

PXLP-K357-ABAT dimer:2Fe-2S transforms GABA to SUCCSA ↗

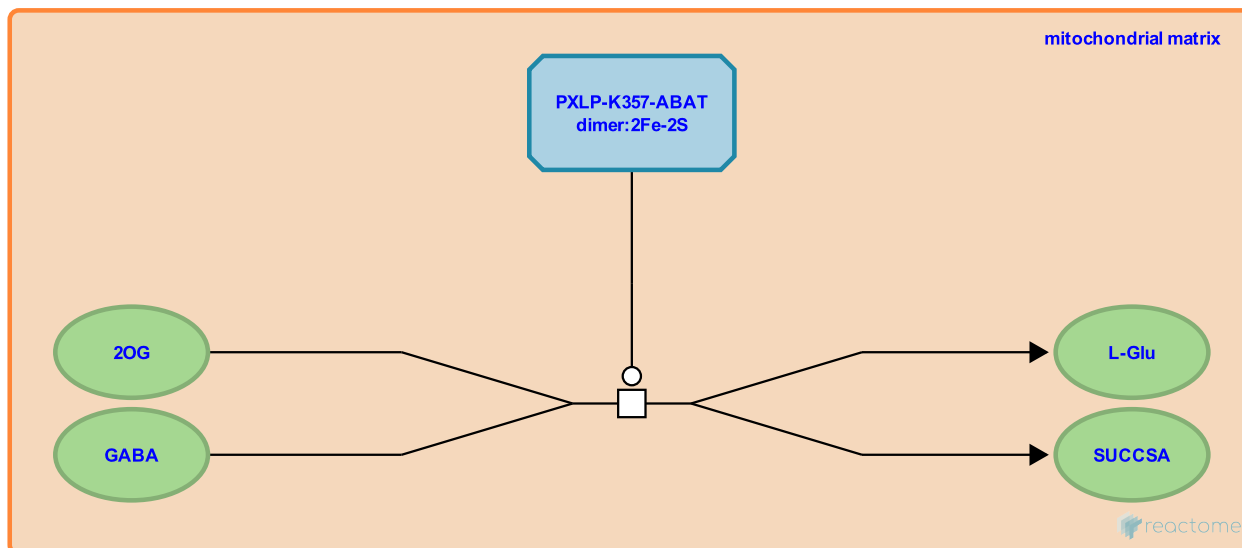
Location: [Degradation of GABA](#)

Stable identifier: R-CEL-916855

Type: transition

Compartments: mitochondrial matrix

Inferred from: [PXLP-K357-ABAT dimer:2Fe-2S transforms GABA to SUCCSA \(Homo sapiens\)](#)



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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Followed by: [ALDH5A1 dehydrogenates SUCCSA to SUCCA](#)

ALDH5A1 dehydrogenates SUCCSA to SUCCA ↗

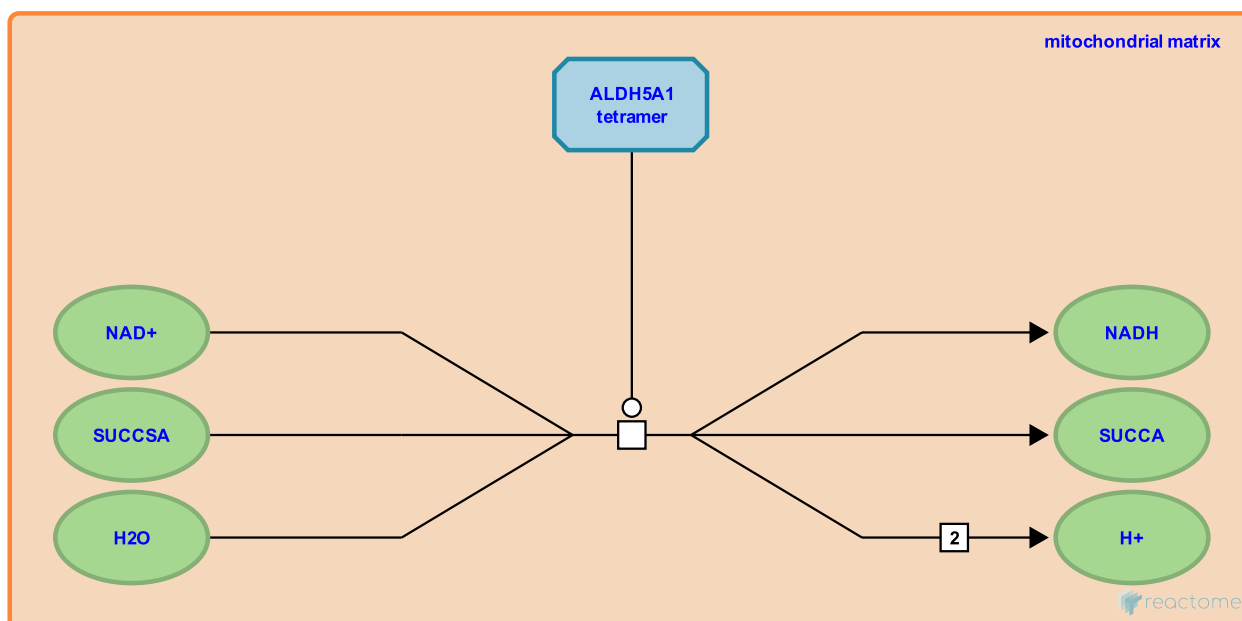
Location: [Degradation of GABA](#)

Stable identifier: R-CEL-888548

Type: transition

Compartments: mitochondrial matrix

Inferred from: [ALDH5A1 dehydrogenates SUCCSA to SUCCA \(Homo sapiens\)](#)



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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [PXLK-K357-ABAT dimer:2Fe-2S transforms GABA to SUCCSA](#)

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