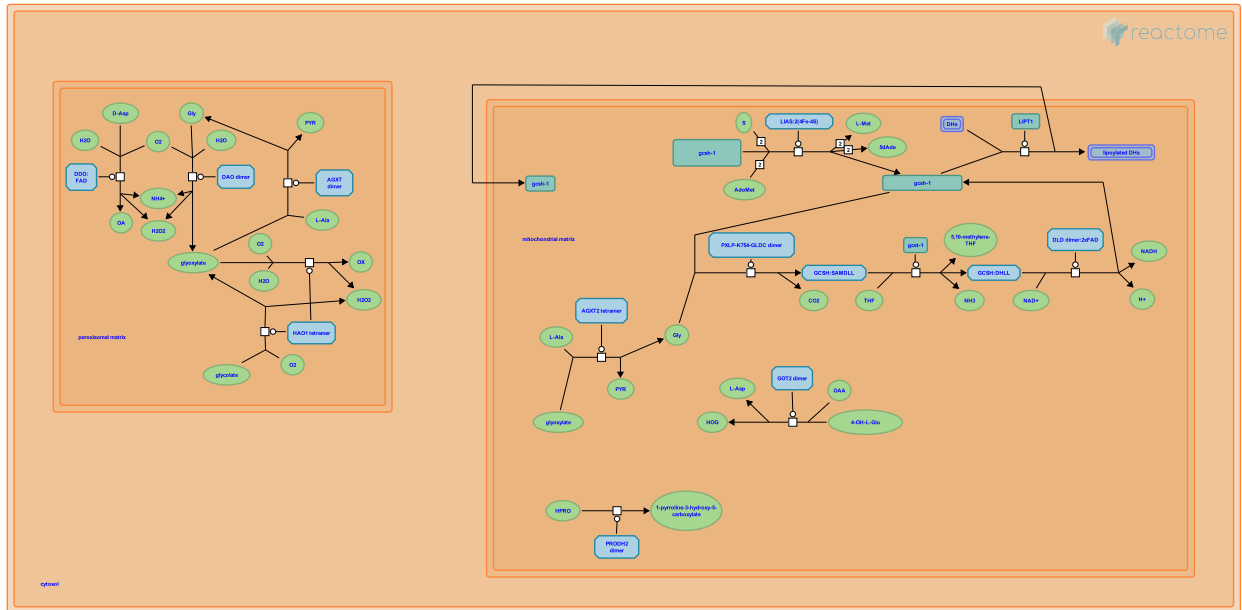


Glyoxylate metabolism and glycine degradation



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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://creativecommons.org/licenses/by/4.0/).

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. [↗](#)

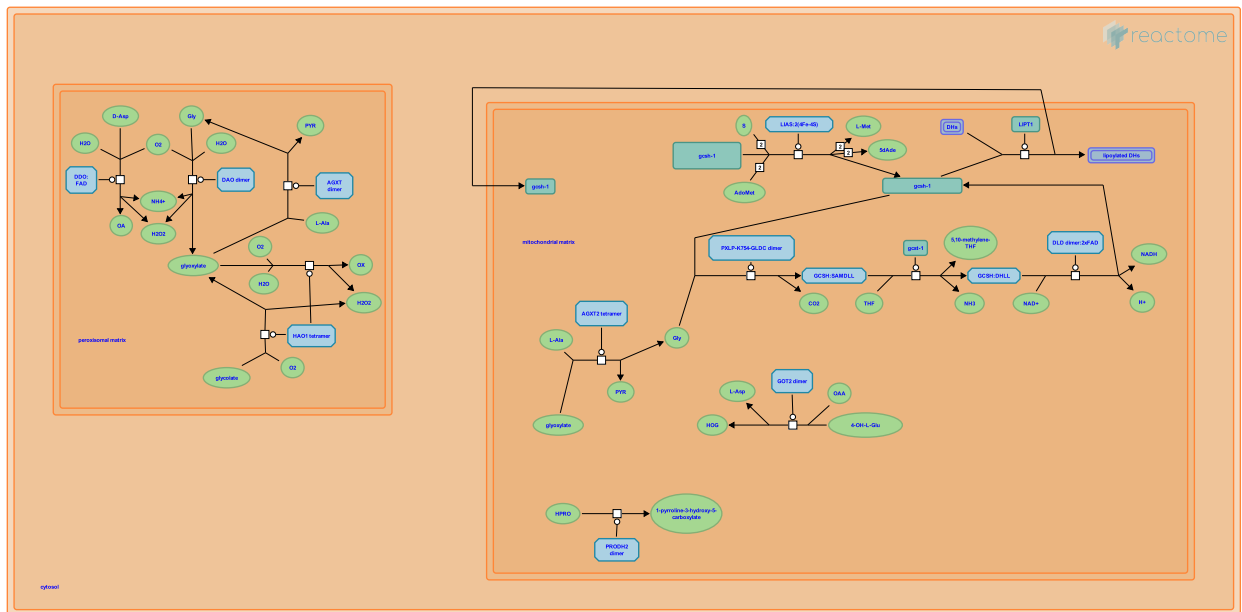
Reactome database release: 74

This document contains 2 pathways and 10 reactions ([see Table of Contents](#))

Glyoxylate metabolism and glycine degradation ↗

Stable identifier: R-CEL-389661

Inferred from: Glyoxylate metabolism and glycine degradation (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>

PRODH2:FAD dimer dehydrogenates HPRO to 1-pyrroline-3-hydroxy-5-carboxylate



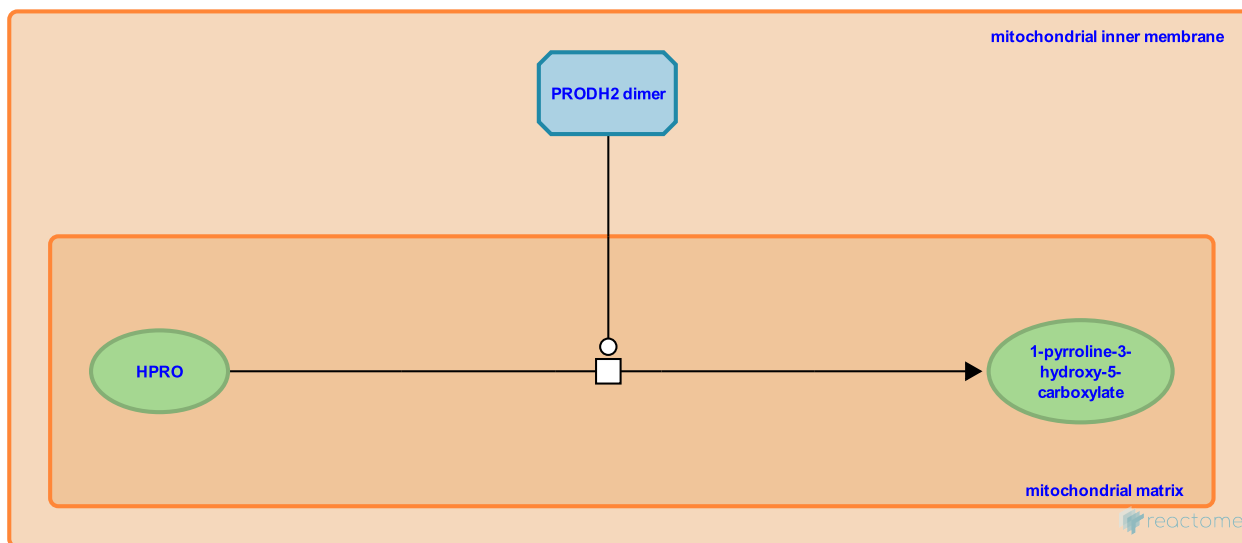
Location: Glyoxylate metabolism and glycine degradation

Stable identifier: R-CEL-6784224

Type: transition

Compartments: mitochondrial matrix, mitochondrial inner membrane

Inferred from: [PRODH2:FAD dimer dehydrogenates HPRO to 1-pyrroline-3-hydroxy-5-carboxylate \(Homo sapiens\)](#)



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-K279-GOT2 dimer transaminates 4-OH-L-glutamate to 4-hydroxy-2-oxoglutarate (HOG) ↗

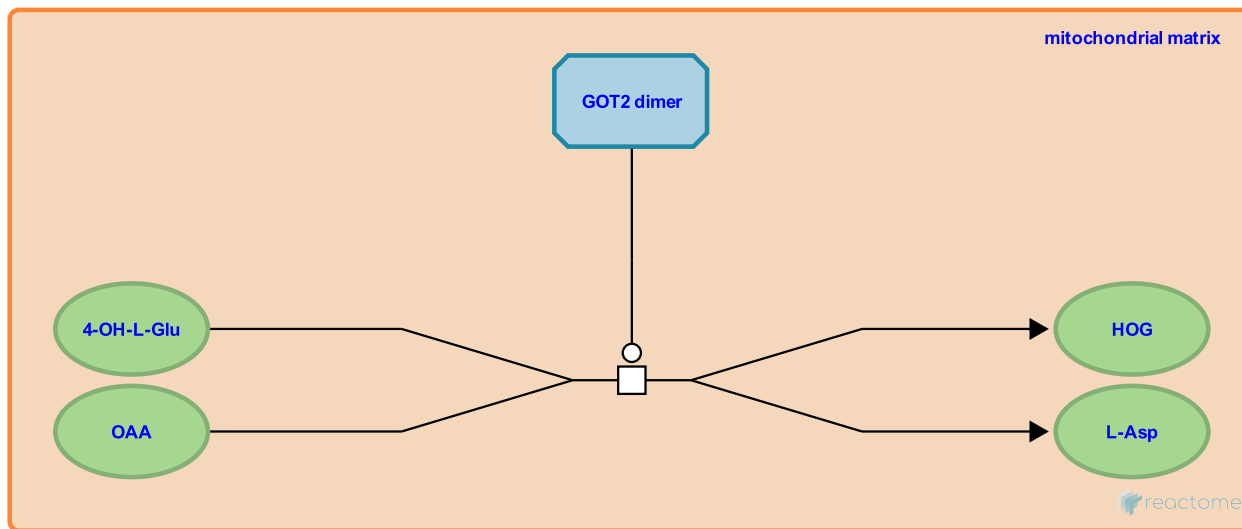
Location: Glyoxylate metabolism and glycine degradation

Stable identifier: R-CEL-6784393

Type: transition

Compartments: mitochondrial matrix

Inferred from: PXLP-K279-GOT2 dimer transaminates 4-OH-L-glutamate to 4-hydroxy-2-oxoglutarate (HOG) (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>

Mitochondrial AGXT2 tetramer transaminates glyoxylate and alanine to glycine and pyruvate ↗

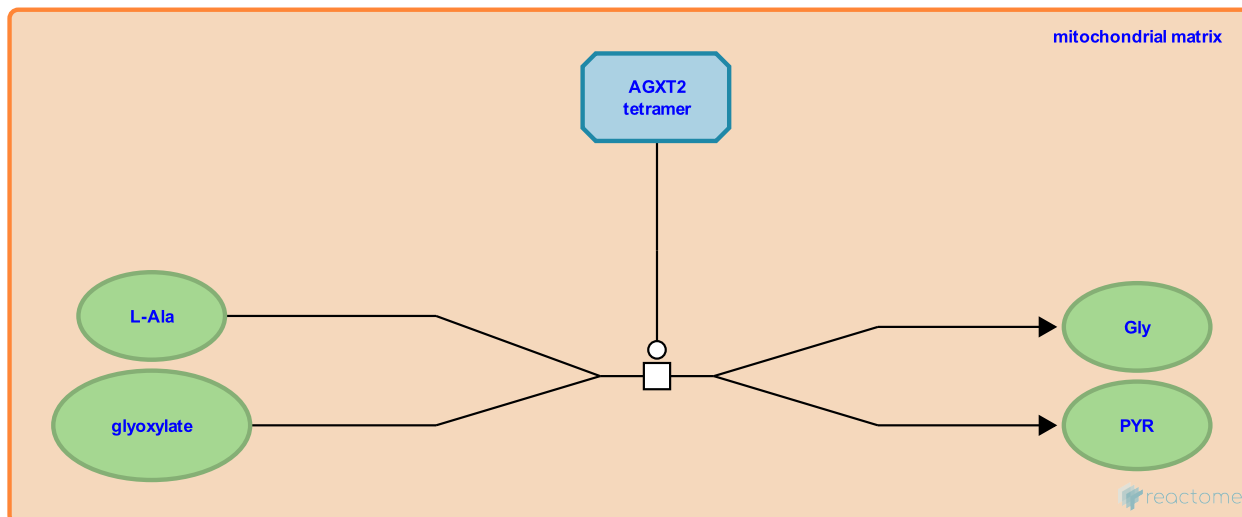
Location: [Glyoxylate metabolism and glycine degradation](#)

Stable identifier: R-CEL-904864

Type: transition

Compartments: mitochondrial matrix

Inferred from: [Mitochondrial AGXT2 tetramer transaminates glyoxylate and alanine to glycine and pyruvate \(Homo sapiens\)](#)



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>

glycine + O2 => glyoxylate + H2O2 + NH4+ ↗

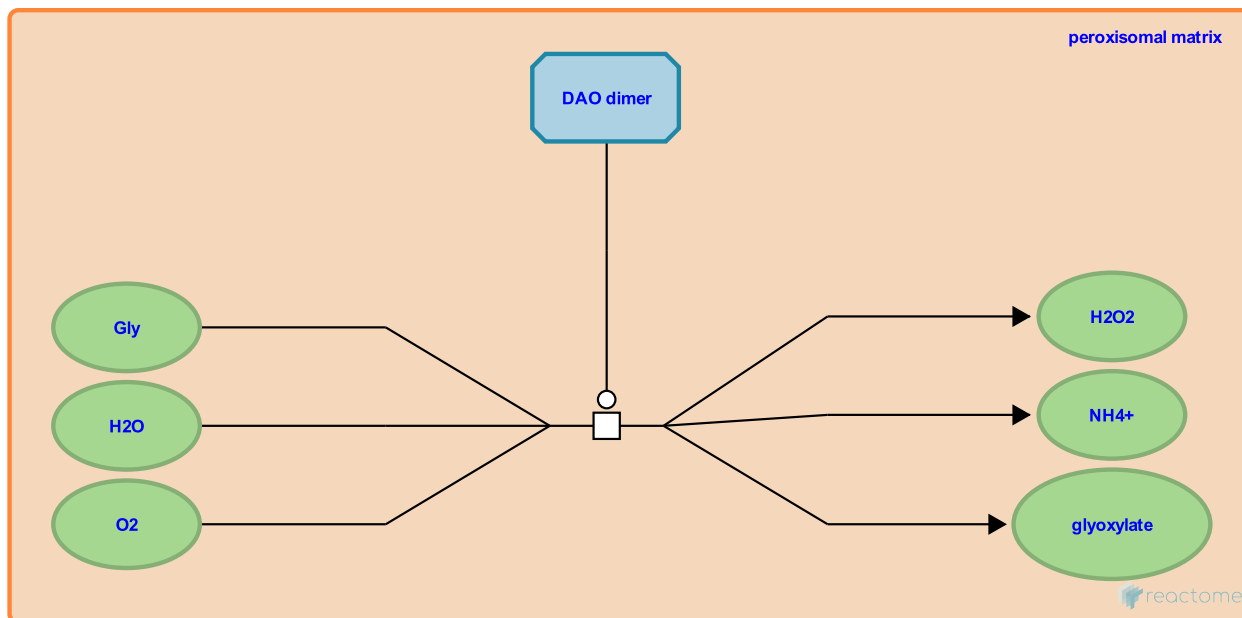
Location: Glyoxylate metabolism and glycine degradation

Stable identifier: R-CEL-389821

Type: transition

Compartments: peroxisomal matrix

Inferred from: glycine + O2 => glyoxylate + H2O2 + NH4+ (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: [glyoxylate + alanine => glycine + pyruvate \[peroxisome\]](#)

Followed by: [Conversion of glyoxylate to oxalate](#), [glyoxylate + alanine => glycine + pyruvate \[peroxisome\]](#)

DDO oxidizes D-Asp to OA [↗](#)

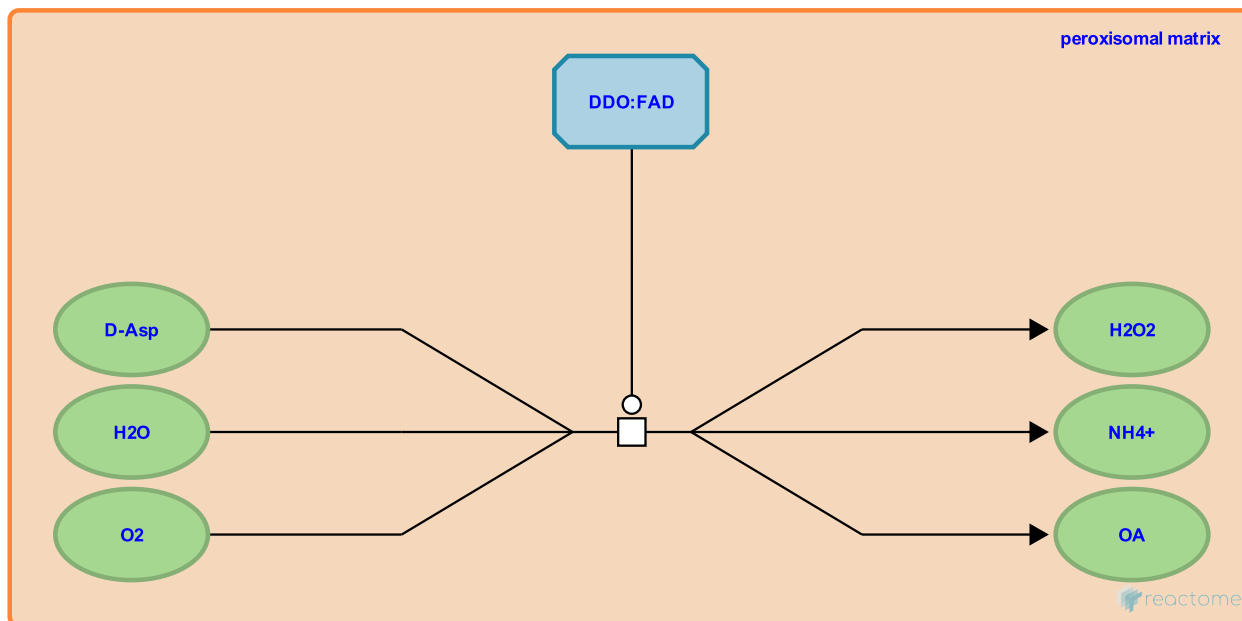
Location: [Glyoxylate metabolism and glycine degradation](#)

Stable identifier: R-CEL-6810076

Type: transition

Compartments: peroxisomal matrix

Inferred from: [DDO oxidizes D-Asp to OA \(Homo sapiens\)](#)



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>

glyoxylate + alanine => glycine + pyruvate [peroxisome] ↗

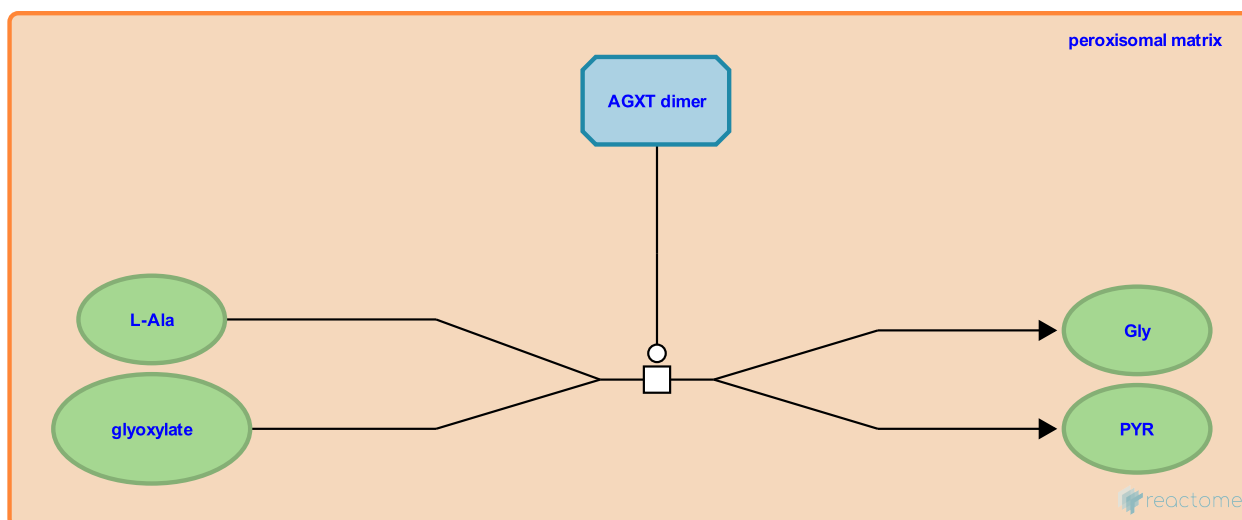
Location: [Glyoxylate metabolism and glycine degradation](#)

Stable identifier: R-CEL-389684

Type: transition

Compartments: peroxisomal matrix

Inferred from: [glyoxylate + alanine => glycine + pyruvate \[peroxisome\]](#) (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: [glycine + O2 => glyoxylate + H2O2 + NH4+](#), [HAO1 tetramer oxidizes glycolate to glyoxylate](#)

Followed by: [glycine + O2 => glyoxylate + H2O2 + NH4+](#)

HAO1 tetramer oxidizes glycolate to glyoxylate ↗

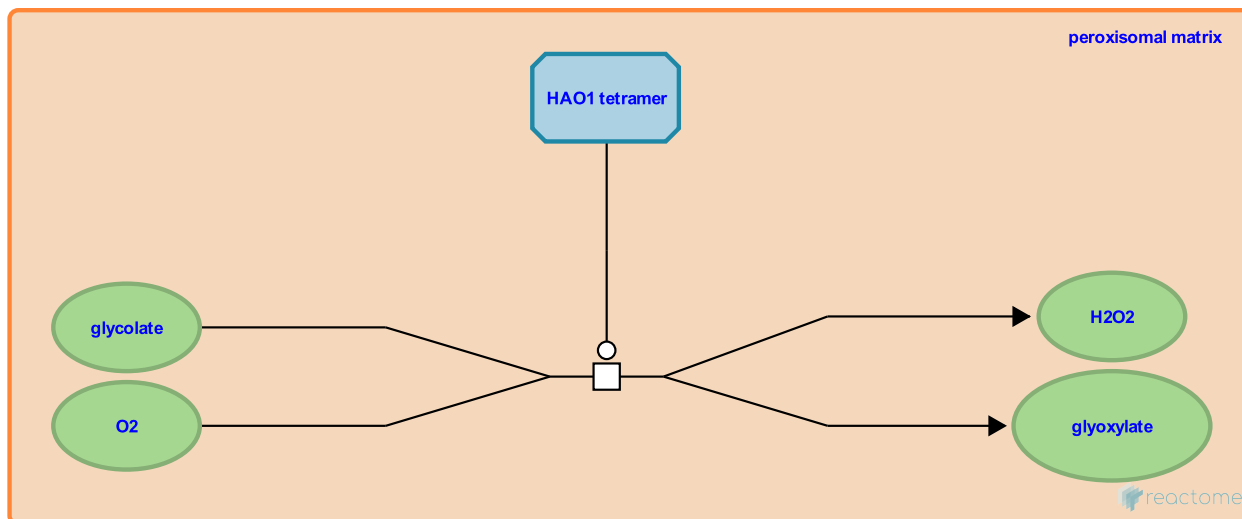
Location: [Glyoxylate metabolism and glycine degradation](#)

Stable identifier: R-CEL-389842

Type: transition

Compartments: peroxisomal matrix

Inferred from: [HAO1 tetramer oxidizes glycolate to glyoxylate \(Homo sapiens\)](#)



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: [Conversion of glyoxylate to oxalate](#), [glyoxylate + alanine => glycine + pyruvate \[peroxisome\]](#)

Conversion of glyoxylate to oxalate ↗

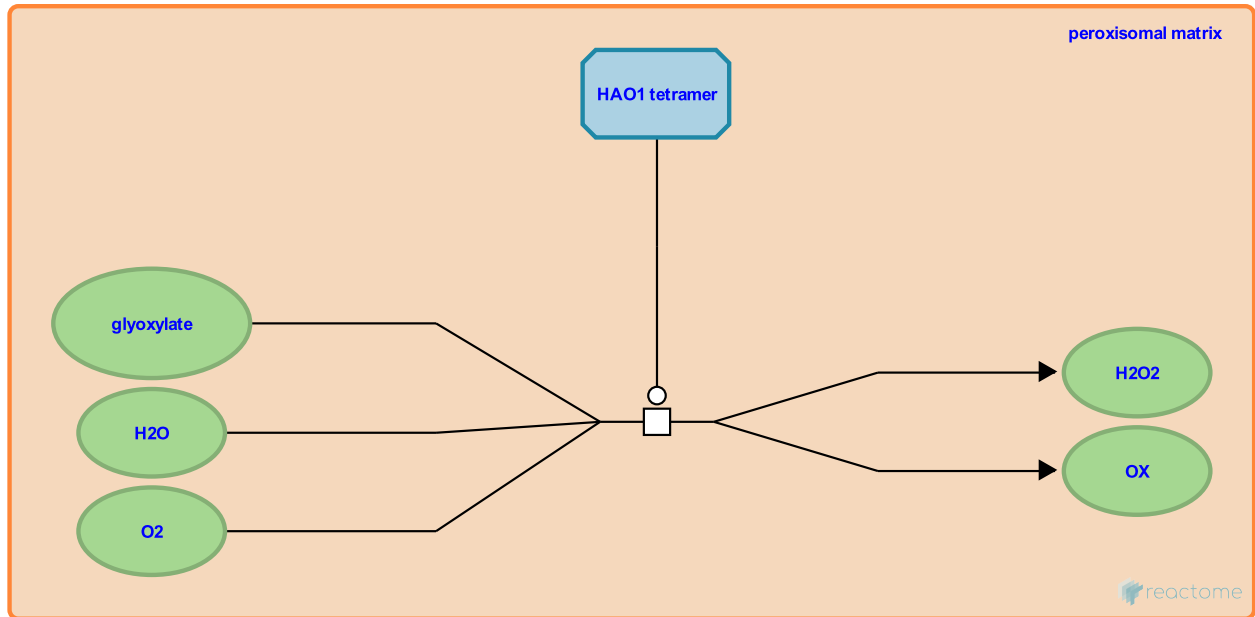
Location: Glyoxylate metabolism and glycine degradation

Stable identifier: R-CEL-389862

Type: transition

Compartments: peroxisomal matrix

Inferred from: Conversion of glyoxylate to oxalate (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>

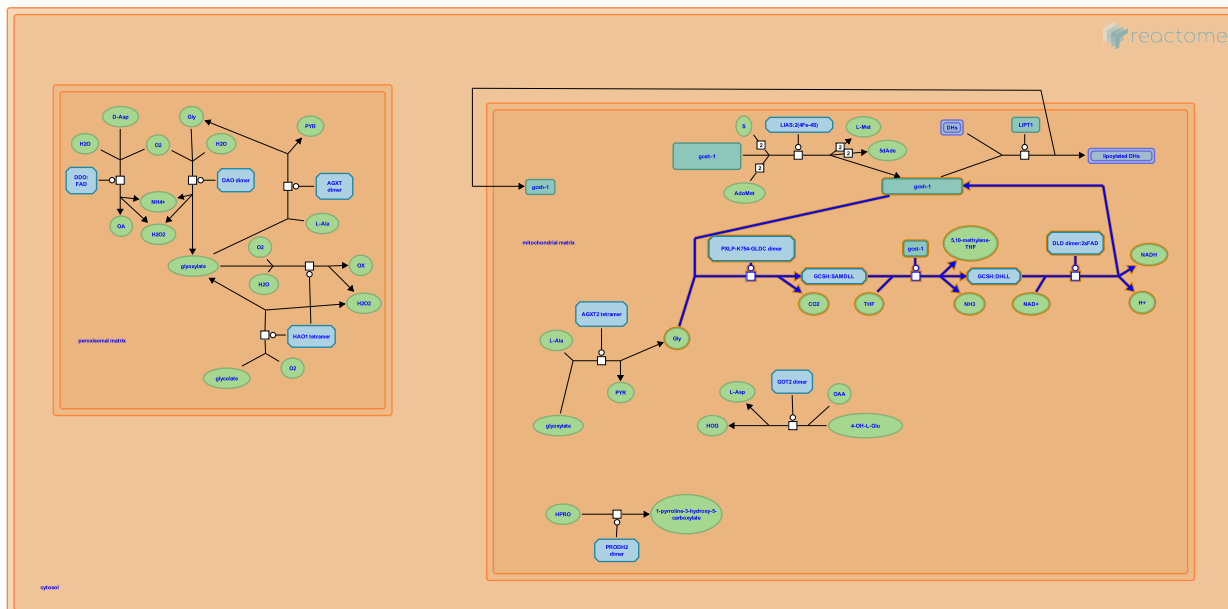
Preceded by: [glycine + O2 => glyoxylate + H2O2 + NH4+](#), [HAO1 tetramer oxidizes glycolate to glyoxylate](#)

Glycine degradation ↗

Location: Glyoxylate metabolism and glycine degradation

Stable identifier: R-CEL-6783984

Inferred from: Glycine degradation (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>

LIAS:2(4Fe-4S) transforms octanoyl-K107-GCSH to lipoyl-K107-GCSH ↗

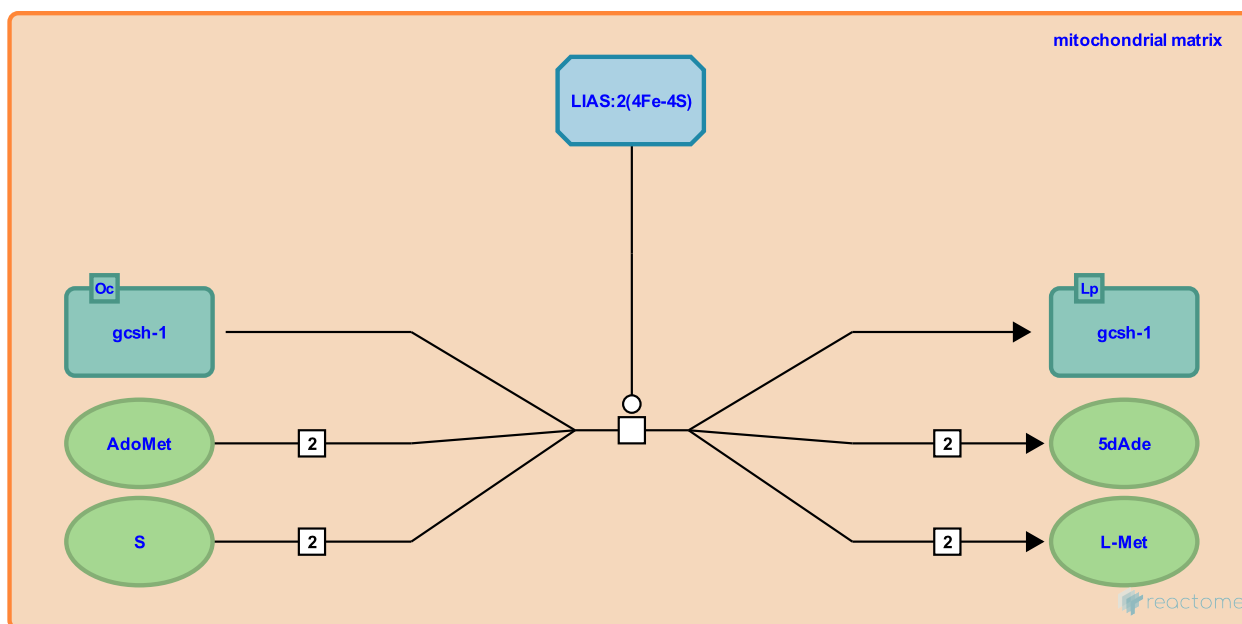
Location: Glyoxylate metabolism and glycine degradation

Stable identifier: R-CEL-6793591

Type: transition

Compartments: mitochondrial matrix

Inferred from: LIAS:2(4Fe-4S) transforms octanoyl-K107-GCSH to lipoyl-K107-GCSH (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: LIPT1 transfers lipoyl group from lipoyl-GCSH to DHs

LIPT1 transfers lipoyl group from lipoyl-GCSH to DHs ↗

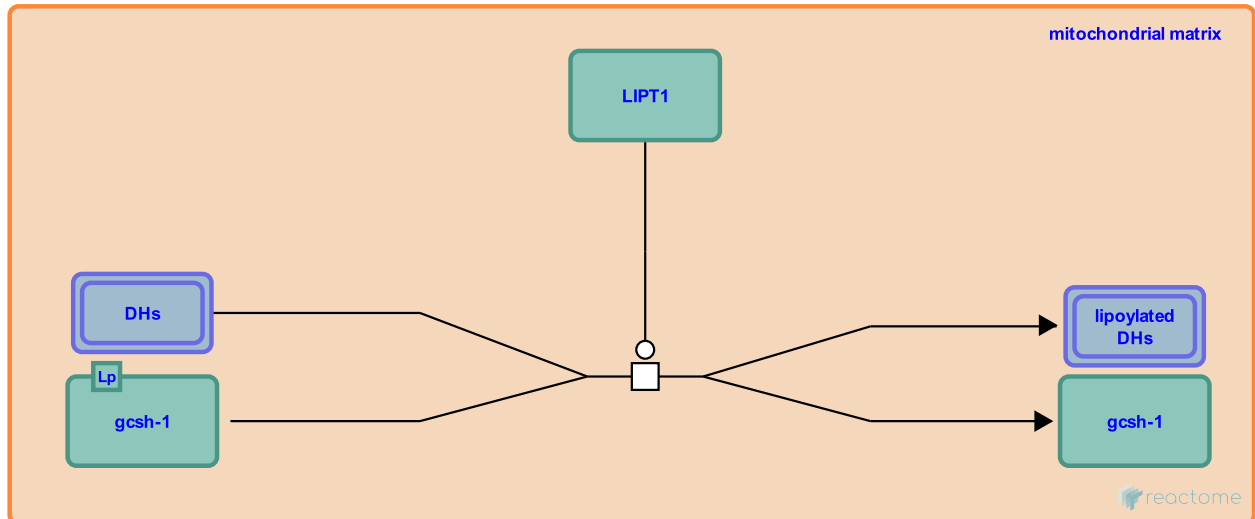
Location: [Glyoxylate metabolism and glycine degradation](#)

Stable identifier: R-CEL-6792572

Type: transition

Compartments: mitochondrial matrix

Inferred from: [LIPT1 transfers lipoyl group from lipoyl-GCSH to DHs \(Homo sapiens\)](#)



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: [LIAS:2\(4Fe-4S\) transforms octanoyl-K107-GCSH to lipoyl-K107-GCSH](#)

Table of Contents

Introduction	1
☒ Glyoxylate metabolism and glycine degradation	2
↳ PRODH2:FAD dimer dehydrogenates HPRO to 1-pyrroline-3-hydroxy-5-carboxylate	3
↳ PXLK-K279-GOT2 dimer transaminates 4-OH-L-glutamate to 4-hydroxy-2-oxoglutarate (HOG)	4
↳ Mitochondrial AGXT2 tetramer transaminates glyoxylate and alanine to glycine and pyruvate	5
↳ glycine + O ₂ => glyoxylate + H ₂ O ₂ + NH ₄ ⁺	6
↳ DDO oxidizes D-Asp to OA	7
↳ glyoxylate + alanine => glycine + pyruvate [peroxisome]	8
↳ HAO1 tetramer oxidizes glycolate to glyoxylate	9
↳ Conversion of glyoxylate to oxalate	10
☒ Glycine degradation	11
↳ LIAS:2(4Fe-4S) transforms octanoyl-K107-GCSH to lipoyl-K107-GCSH	12
↳ LIPT1 transfers lipoyl group from lipoyl-GCSH to DHs	13
Table of Contents	14