Glyoxylate metabolism and glycine degradation

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.

29/03/2025

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., Fabregat, A., Fabregat, A., Fabregat, A., Fabregat, A., Fabregat, A. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics, 18*, 142. ↗

Sidiropoulos, K., Sidiropoulos, K., Sidiropoulos, K., Sidiropoulos, K., Sidiropoulos, K., Sidiropoulos, K. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

Fabregat, A., Fabregat, A., Fabregat, A., Fabregat, A., Fabregat, A., Fabregat, A. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

Fabregat, A., Fabregat, A., Fabregat, A., Fabregat, A., Fabregat, A., Fabregat, A. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗
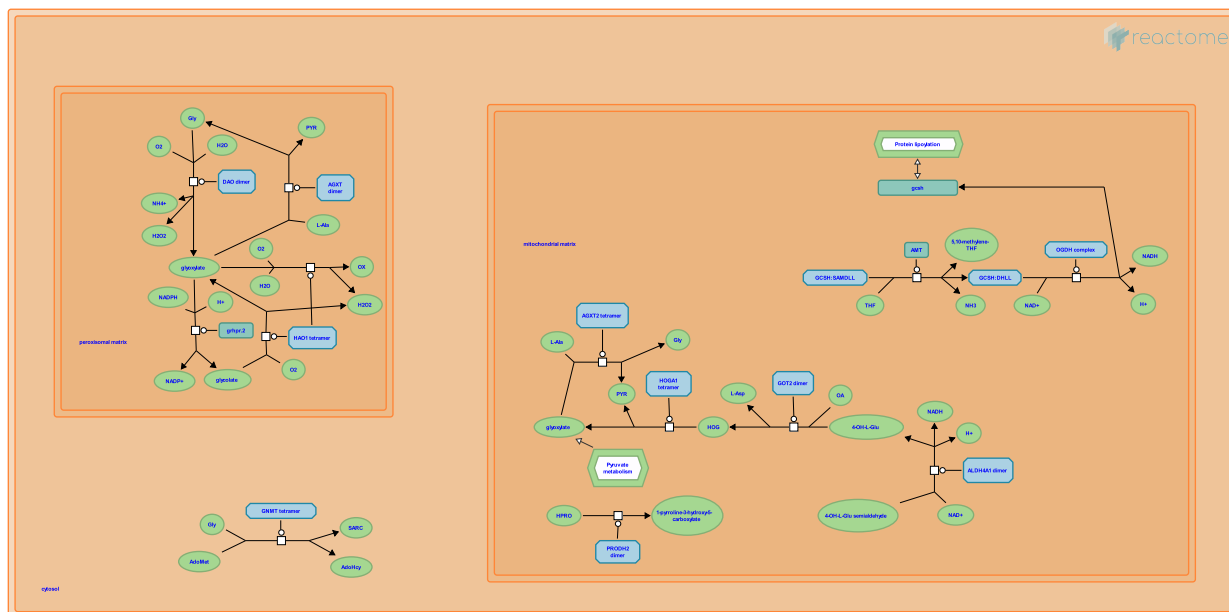
Reactome database release: 91

This document contains 2 pathways and 11 reactions (see Table of Contents)

Glyoxylate metabolism and glycine degradation ↗

Stable identifier: R-XTR-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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

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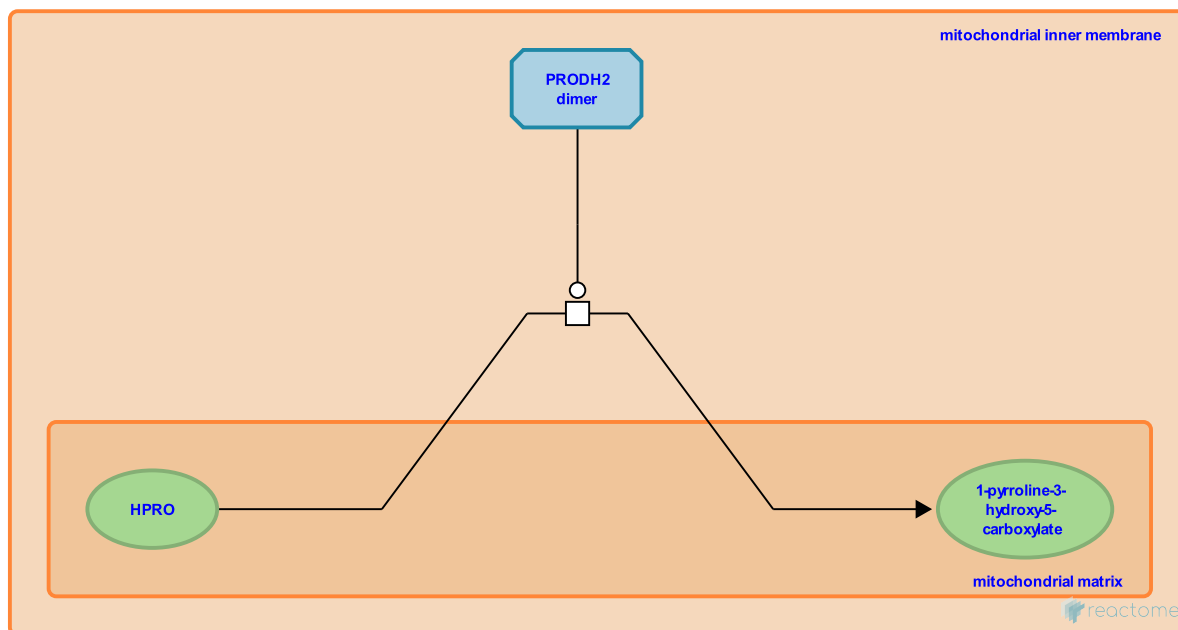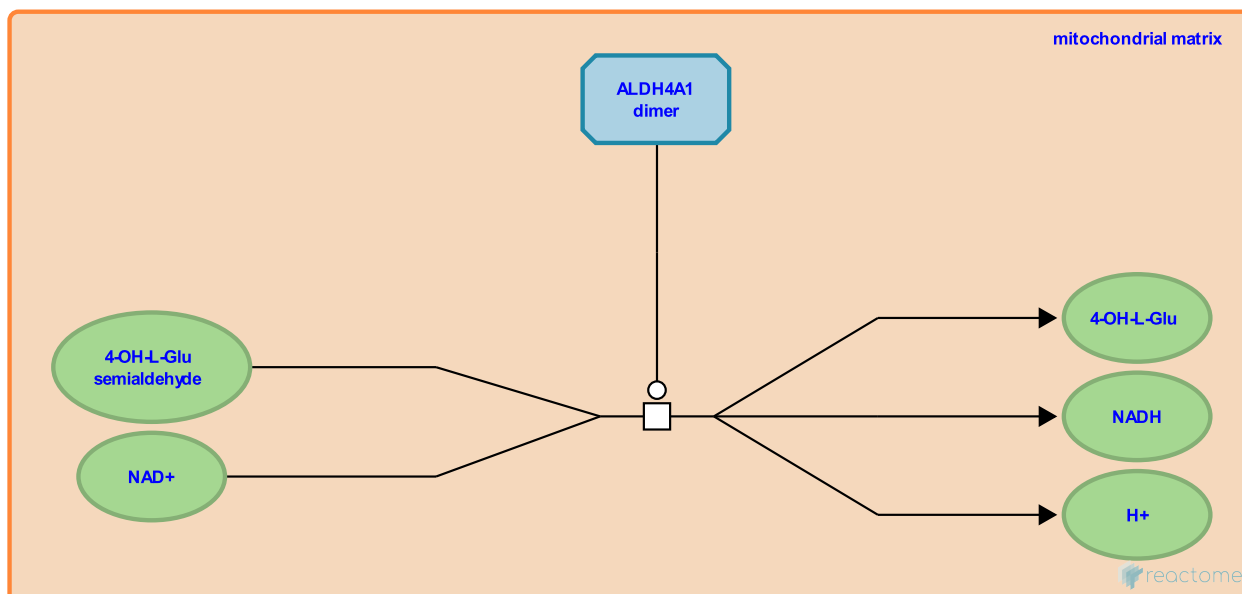
↗

Location: Glyoxylate metabolism and glycine degradation

Stable identifier: R-XTR-6784224

Type: transition

Compartments: mitochondrial inner membrane, mitochondrial matrix

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.

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ALDH4A1 dimer dehydrogenates 4-OH-L-glutamate semialdehyde to 4-OH-L-glutamate ↗

Location: Glyoxylate metabolism and glycine degradation

Stable identifier: R-XTR-6784399

Type: transition

Compartments: mitochondrial matrix

Inferred from: ALDH4A1 dimer dehydrogenates 4-OH-L-glutamate semialdehyde to 4-OH-L-glutamate (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

Followed by: PXLP-K279-GOT2 dimer transaminates 4-OH-L-glutamate to 4-hydroxy-2-oxoglutarate (HOG)

PXLP-K279-GOT2 dimer transaminates 4-OH-L-glutamate to 4-hydroxy-2-oxoglutarate (HOG) ↗
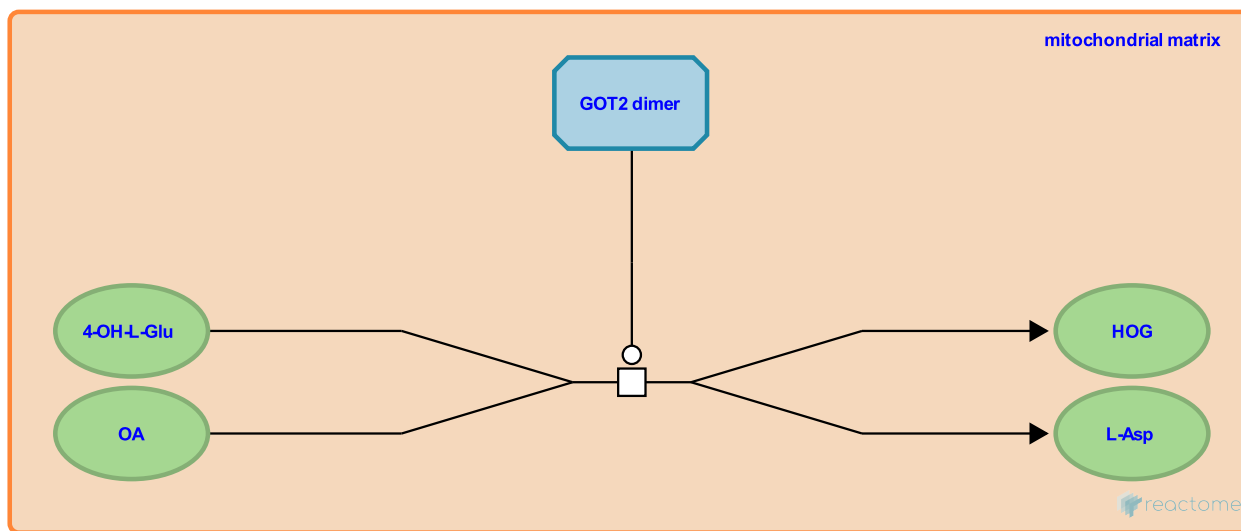
Location: Glyoxylate metabolism and glycine degradation

Stable identifier: R-XTR-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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: ALDH4A1 dimer dehydrogenates 4-OH-L-glutamate semialdehyde to 4-OH-L-glutamate

Followed by: HOGA1 tetramer aldol-cleaves 4-OH-2-oxoglutarate (HOG) to glyoxylate and pyruvate

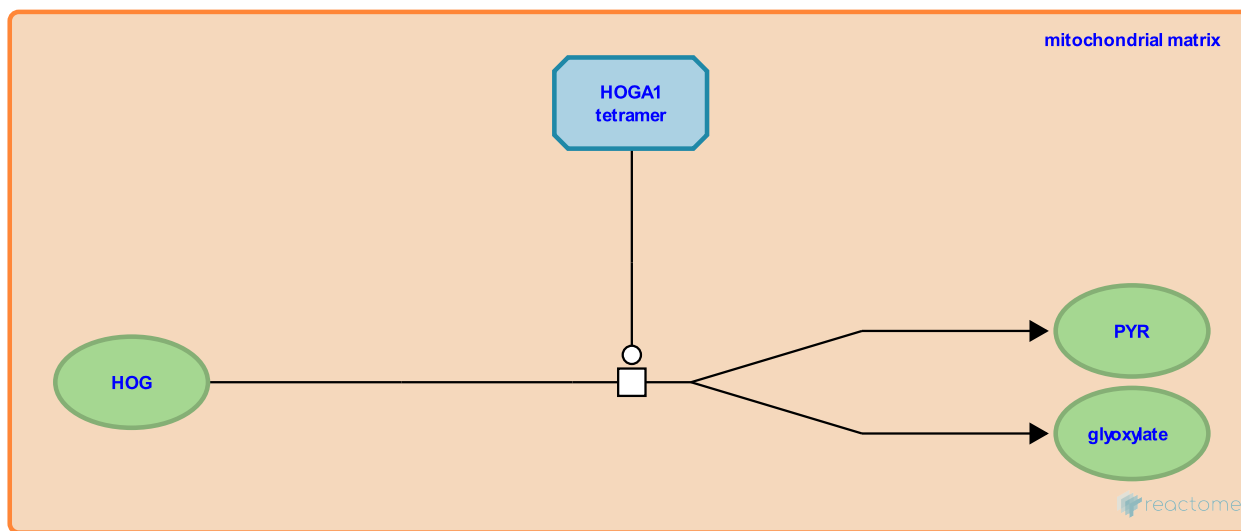## HOGA1 tetramer aldol-cleaves 4-OH-2-oxoglutarate (HOG) to glyoxylate and pyruvate ↗

Location: Glyoxylate metabolism and glycine degradation

Stable identifier: R-XTR-6784423

Type: transition

Compartments: mitochondrial matrix

Inferred from: HOGA1 tetramer aldol-cleaves 4-OH-2-oxoglutarate (HOG) to glyoxylate 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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: PXLP-K279-GOT2 dimer transaminates 4-OH-L-glutamate to 4-hydroxy-2-oxoglutarate (HOG)

Followed by: Mitochondrial AGXT2 tetramer transaminates glyoxylate and alanine to glycine and pyruvate

Mitochondrial AGXT2 tetramer transaminates glyoxylate and alanine to glycine and pyruvate ↗
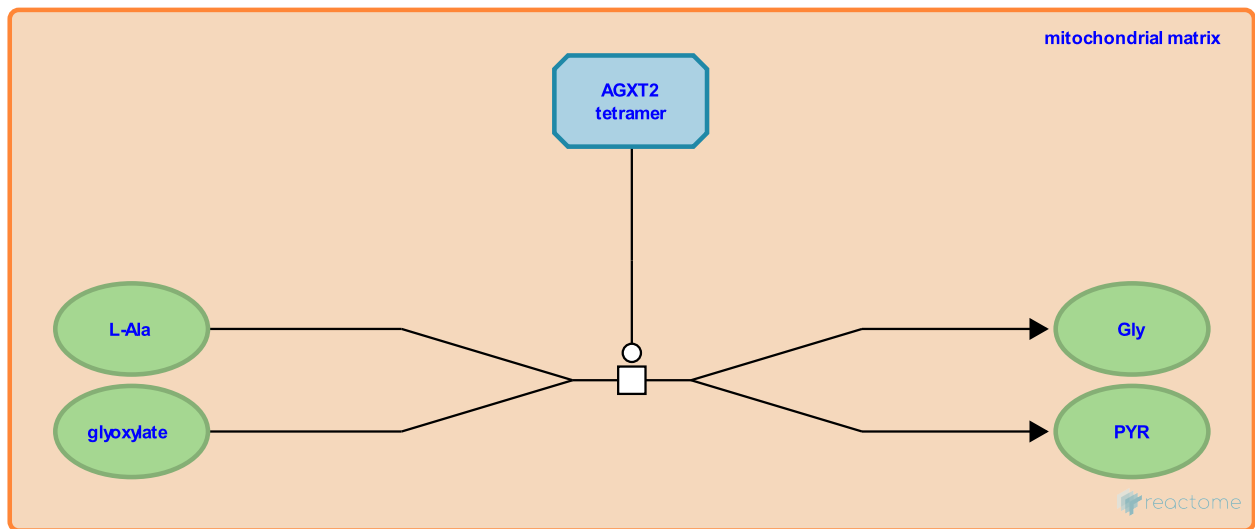
Location: Glyoxylate metabolism and glycine degradation

Stable identifier: R-XTR-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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: HOGA1 tetramer aldol-cleaves 4-OH-2-oxoglutarate (HOG) to glyoxylate and pyruvate

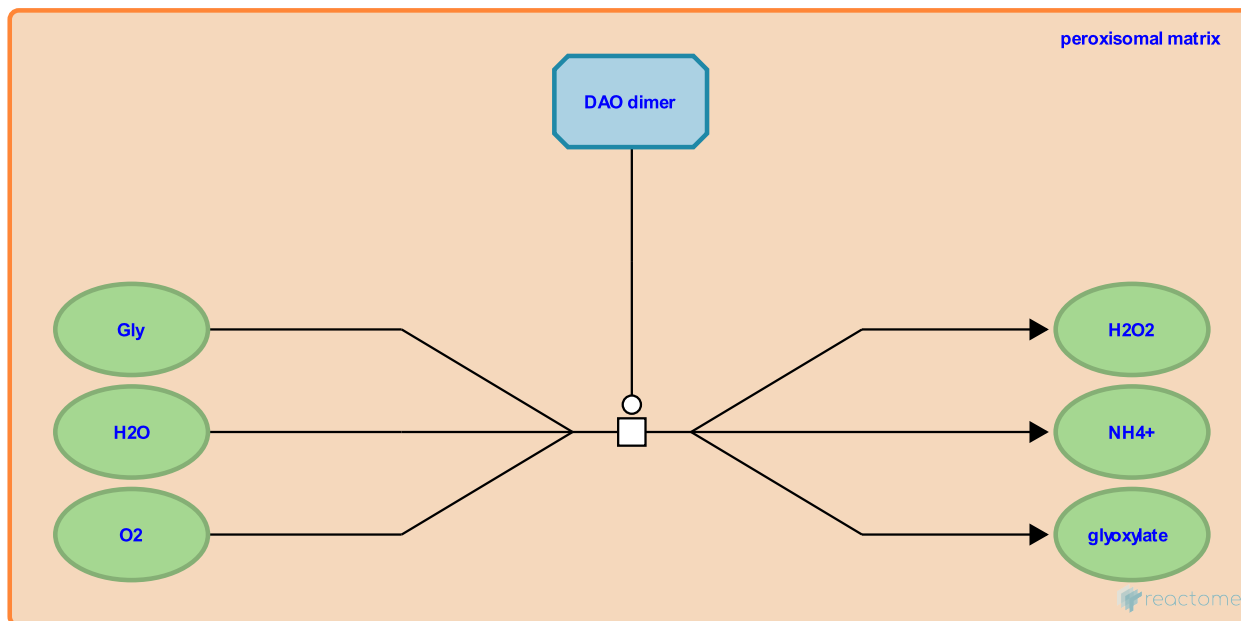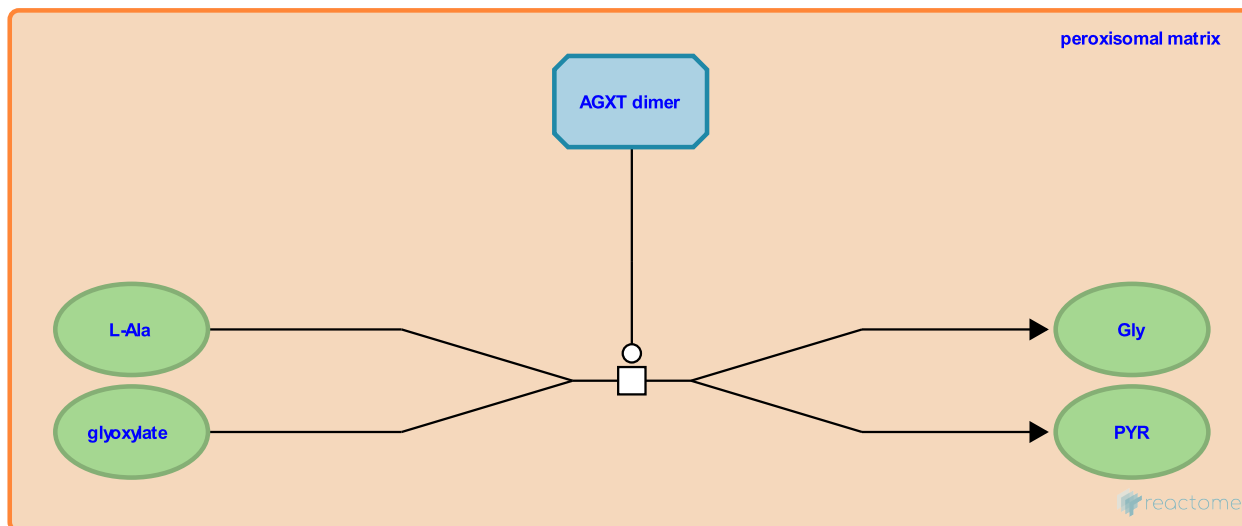# glycine + O2 => glyoxylate + H2O2 + NH4+ ↗

Location: Glyoxylate metabolism and glycine degradation

Stable identifier: R-XTR-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. 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 + NADPH + H+ => glycolate + NADP+, glyoxylate + alanine => glycine + pyruvate [peroxisome]

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

Location: Glyoxylate metabolism and glycine degradation

Stable identifier: R-XTR-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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: HAO1 tetramer oxidizes glycolate to glyoxylate, glycine + O2 => glyoxylate + H2O2 + NH4+

Followed by: glycine + O2 => glyoxylate + H2O2 + NH4+

glyoxylate + NADPH + H+ => glycolate + NADP+ ↗

Location: Glyoxylate metabolism and glycine degradation

Stable identifier: R-XTR-389826

Type: transition

Compartments: peroxisomal matrix

Inferred from: glyoxylate + NADPH + H+ => glycolate + NADP+ (Homo sapiens)
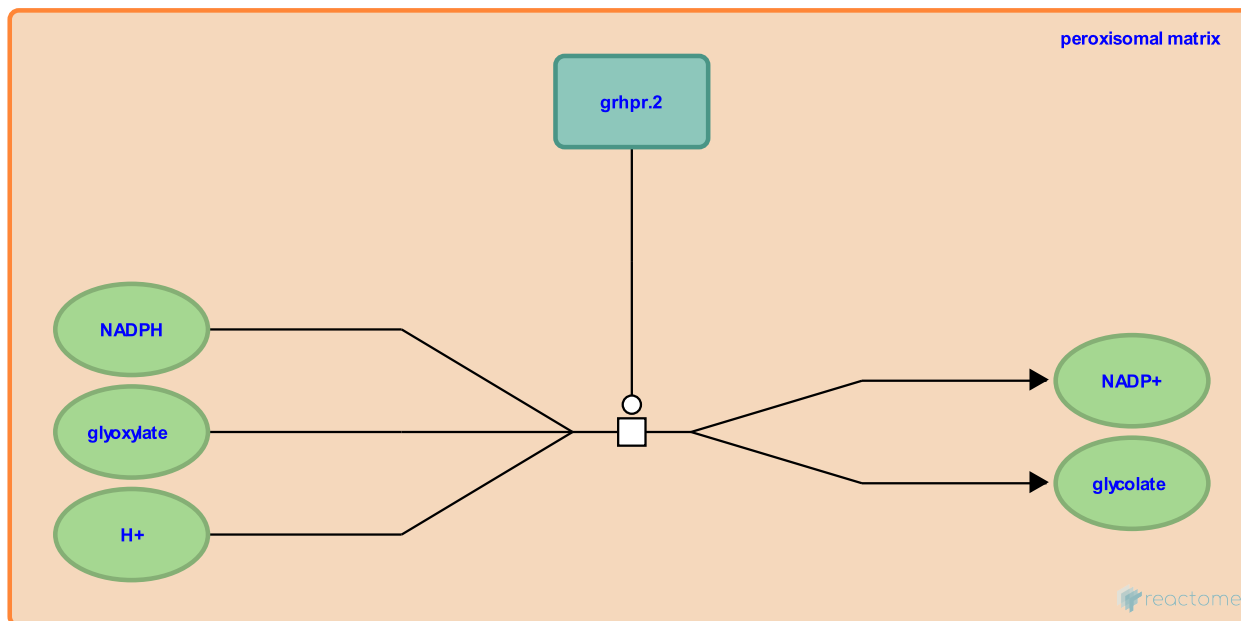
This event has been computationally inferred from an event that has been demonstrated in another species.

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

Followed by: HAO1 tetramer oxidizes glycolate to glyoxylate
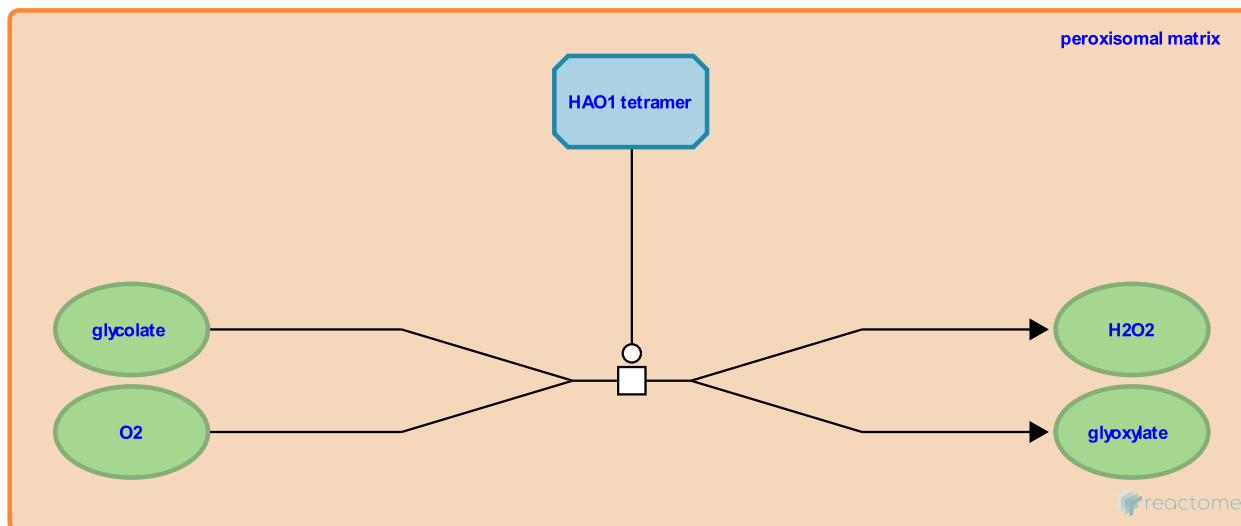
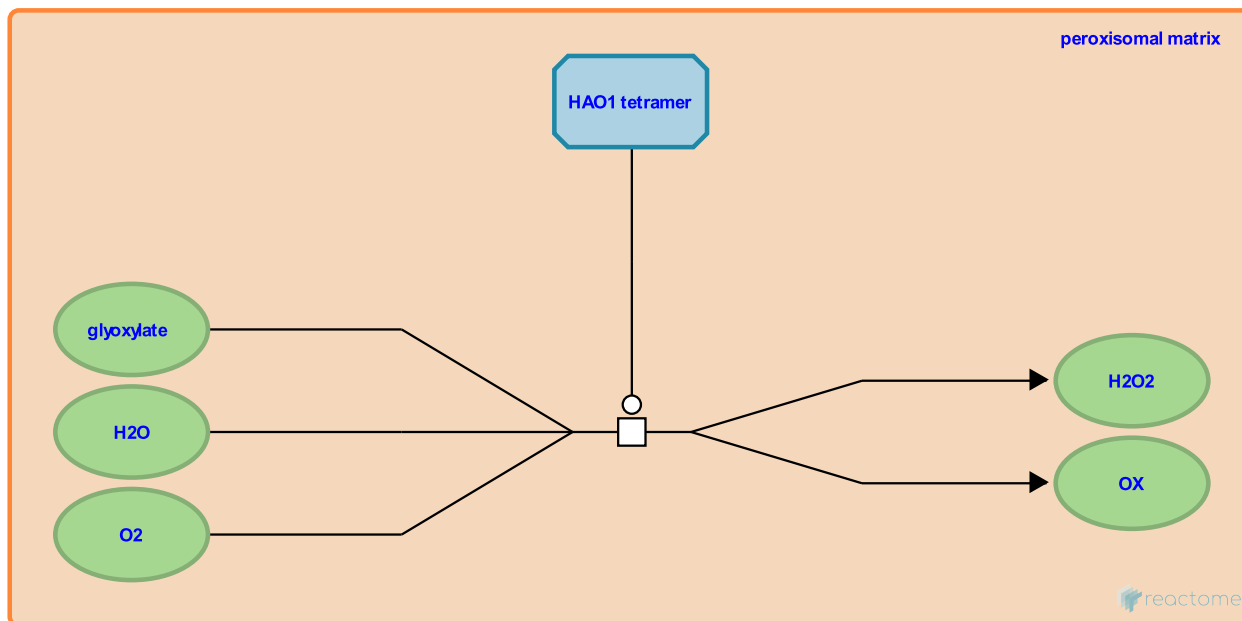# HAO1 tetramer oxidizes glycolate to glyoxylate ↗

Location: Glyoxylate metabolism and glycine degradation

Stable identifier: R-XTR-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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: glyoxylate + NADPH + H+ => glycolate + NADP+

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-XTR-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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp
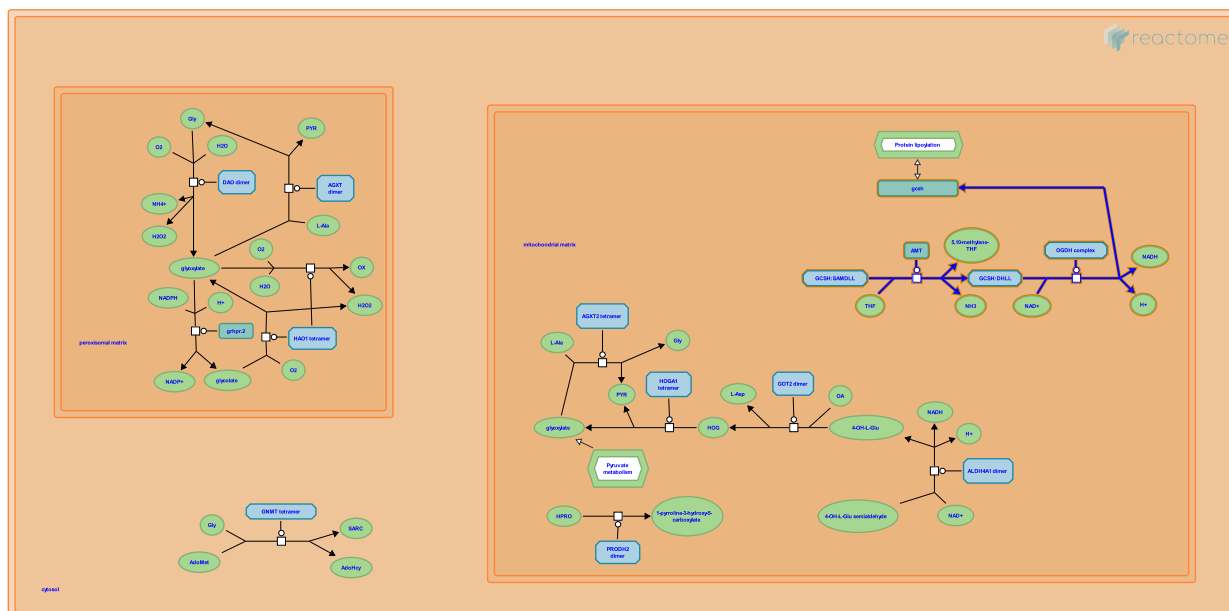
Preceded by: HAO1 tetramer oxidizes glycolate to glyoxylate, glycine + O2 => glyoxylate + H2O2 + NH4+

Glycine degradation ↗

Location: Glyoxylate metabolism and glycine degradation

Stable identifier: R-XTR-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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

GNMT tetramer transfers methyl group from AdoMet to Gly to form AdoHyc and SARC ↗
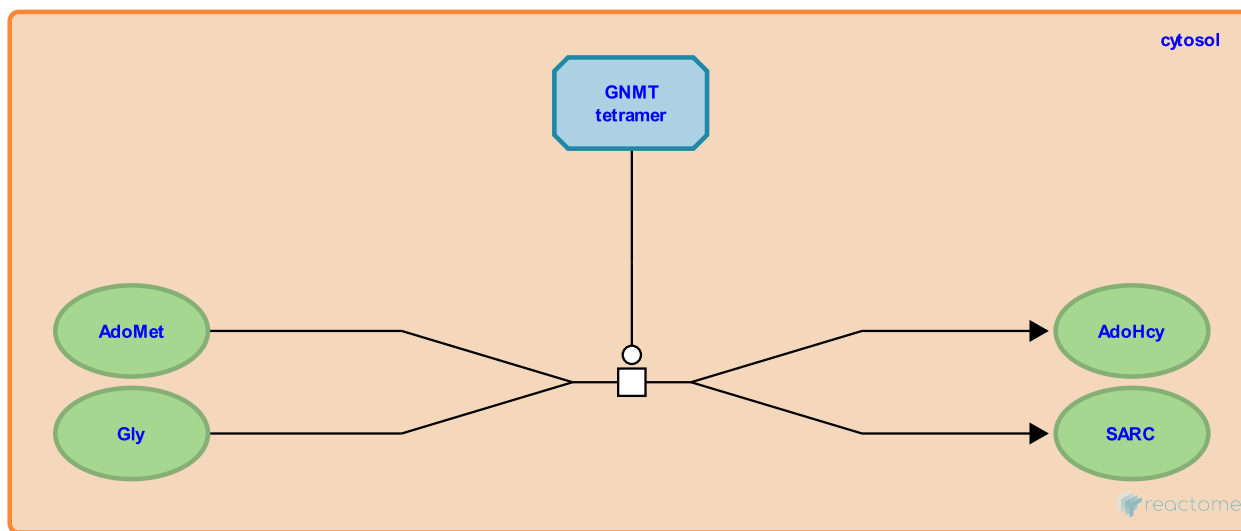
Location: Glyoxylate metabolism and glycine degradation

Stable identifier: R-XTR-6798317

Type: transition

Compartments: cytosol

Inferred from: GNMT tetramer transfers methyl group from AdoMet to Gly to form AdoHyc and SARC (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

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