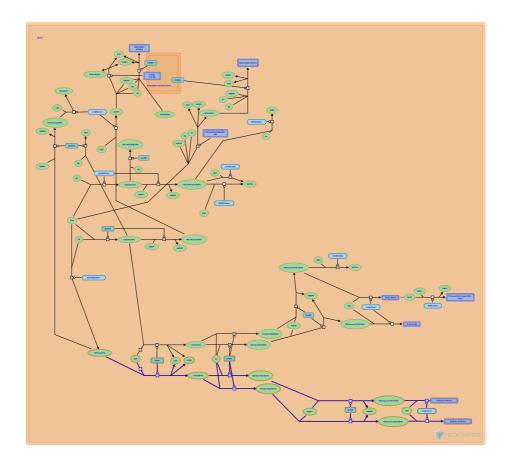


Biosynthesis of aspirin-triggered D-series

resolvins



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.

12/05/2024

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 data-base: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968.

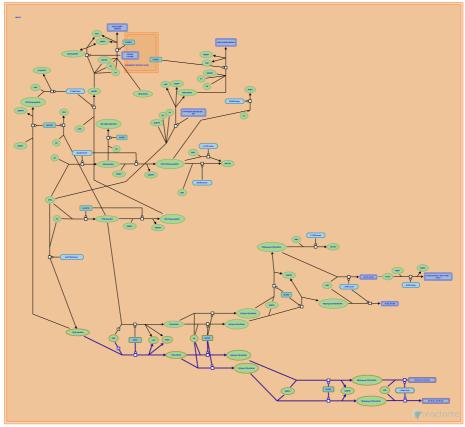
Reactome database release: 88

This document contains 1 pathway and 7 reactions (see Table of Contents)

Biosynthesis of aspirin-triggered D-series resolvins

Stable identifier: R-BTA-9020265

Inferred from: Biosynthesis of aspirin-triggered D-series resolvins (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

GPX4-2 reduces 17(R)-Hp-DHA to 17(R)-HDHA →

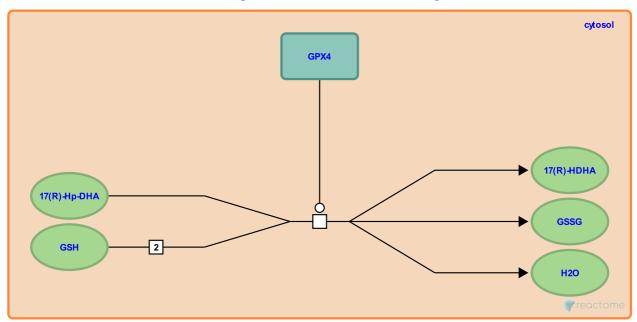
Location: Biosynthesis of aspirin-triggered D-series resolvins

Stable identifier: R-BTA-9020271

Type: transition

Compartments: cytosol

Inferred from: GPX4-2 reduces 17(R)-Hp-DHA to 17(R)-HDHA (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: ALOX5 oxidises 17(R)-HDHA to 4(S)-Hp-17(R)-HDHA, ALOX5 oxidises 17(R)-HDHA to 7(S)-Hp-17(R)-HDHA

ALOX5 oxidises 17(R)-HDHA to 4(S)-Hp-17(R)-HDHA

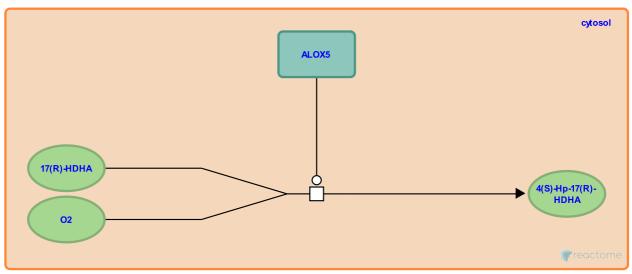
Location: Biosynthesis of aspirin-triggered D-series resolvins

Stable identifier: R-BTA-9020259

Type: transition

Compartments: cytosol

Inferred from: ALOX5 oxidises 17(R)-HDHA to 4(S)-Hp-17(R)-HDHA (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: GPX4-2 reduces 17(R)-Hp-DHA to 17(R)-HDHA

Followed by: ALOX5 dehydrogenates 4(S)-Hp-17(R)-HDHA to 4S(5)-epoxy-17(R)-HDHA

ALOX5 oxidises 17(R)-HDHA to 7(S)-Hp-17(R)-HDHA

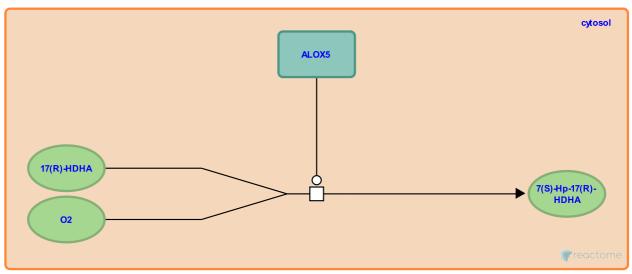
Location: Biosynthesis of aspirin-triggered D-series resolvins

Stable identifier: R-BTA-9020251

Type: transition

Compartments: cytosol

Inferred from: ALOX5 oxidises 17(R)-HDHA to 7(S)-Hp-17(R)-HDHA (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: GPX4-2 reduces 17(R)-Hp-DHA to 17(R)-HDHA

Followed by: ALOX5 dehydrogenates 7(S)-Hp-17R-HDHA to 7S(8)-epoxy-17R-HDHA

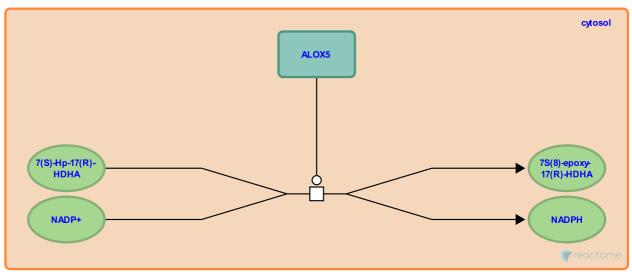
Location: Biosynthesis of aspirin-triggered D-series resolvins

Stable identifier: R-BTA-9020256

Type: transition

Compartments: cytosol

Inferred from: ALOX5 dehydrogenates 7(S)-Hp-17R-HDHA to 7S(8)-epoxy-17R-HDHA (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: ALOX5 oxidises 17(R)-HDHA to 7(S)-Hp-17(R)-HDHA

Followed by: LTA4H:Zn2+ hydrolyses 7S(8)-epoxy-17(R)-HDHA to AT-RvD1 or AT-RvD2

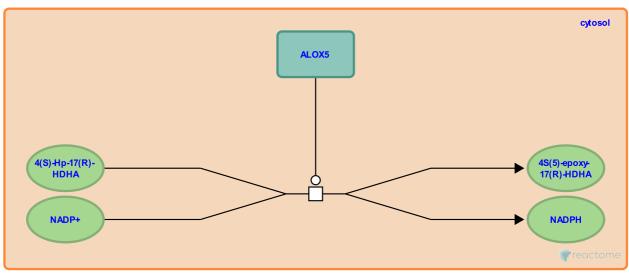
Location: Biosynthesis of aspirin-triggered D-series resolvins

Stable identifier: R-BTA-9020278

Type: transition

Compartments: cytosol

Inferred from: ALOX5 dehydrogenates 4(S)-Hp-17(R)-HDHA to 4S(5)-epoxy-17(R)-HDHA (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: ALOX5 oxidises 17(R)-HDHA to 4(S)-Hp-17(R)-HDHA

Followed by: LTA4H:Zn2+ hydrolyses 4S(5)-epoxy-17(R)-HDHA to AT-RvD3 or AT-RvD4

LTA4H:Zn2+ hydrolyses 7S(8)-epoxy-17(R)-HDHA to AT-RvD1 or AT-RvD2 7

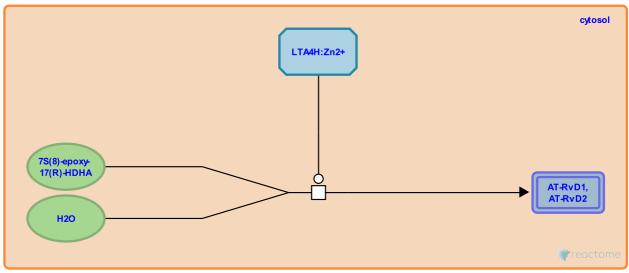
Location: Biosynthesis of aspirin-triggered D-series resolvins

Stable identifier: R-BTA-9020252

Type: transition

Compartments: cytosol

Inferred from: LTA4H:Zn2+ hydrolyses 7S(8)-epoxy-17(R)-HDHA to AT-RvD1 or AT-RvD2 (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: ALOX5 dehydrogenates 7(S)-Hp-17R-HDHA to 7S(8)-epoxy-17R-HDHA

LTA4H:Zn2+ hydrolyses 4S(5)-epoxy-17(R)-HDHA to AT-RvD3 or AT-RvD4 7

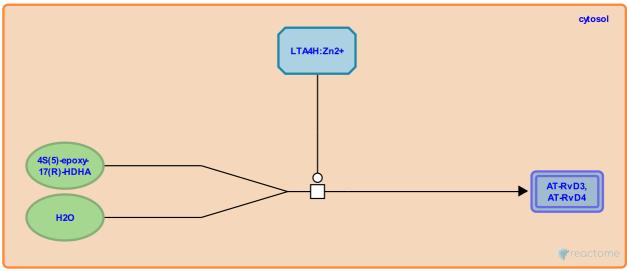
Location: Biosynthesis of aspirin-triggered D-series resolvins

Stable identifier: R-BTA-9020270

Type: transition

Compartments: cytosol

Inferred from: LTA4H:Zn2+ hydrolyses 4S(5)-epoxy-17(R)-HDHA to AT-RvD3 or AT-RvD4 (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: ALOX5 dehydrogenates 4(S)-Hp-17(R)-HDHA to 4S(5)-epoxy-17(R)-HDHA

Table of Contents

Introduction	1
Biosynthesis of aspirin-triggered D-series resolvins	2
GPX4-2 reduces 17(R)-Hp-DHA to 17(R)-HDHA	3
ALOX5 oxidises 17(R)-HDHA to 4(S)-Hp-17(R)-HDHA	4
ALOX5 oxidises 17(R)-HDHA to 7(S)-Hp-17(R)-HDHA	5
ALOX5 dehydrogenates 7(S)-Hp-17R-HDHA to 7S(8)-epoxy-17R-HDHA	6
ALOX5 dehydrogenates 4(S)-Hp-17(R)-HDHA to 4S(5)-epoxy-17(R)-HDHA	7
LTA4H:Zn2+ hydrolyses 7S(8)-epoxy-17(R)-HDHA to AT-RvD1 or AT-RvD2	8
LTA4H:Zn2+ hydrolyses 4S(5)-epoxy-17(R)-HDHA to AT-RvD3 or AT-RvD4	9
Table of Contents	10