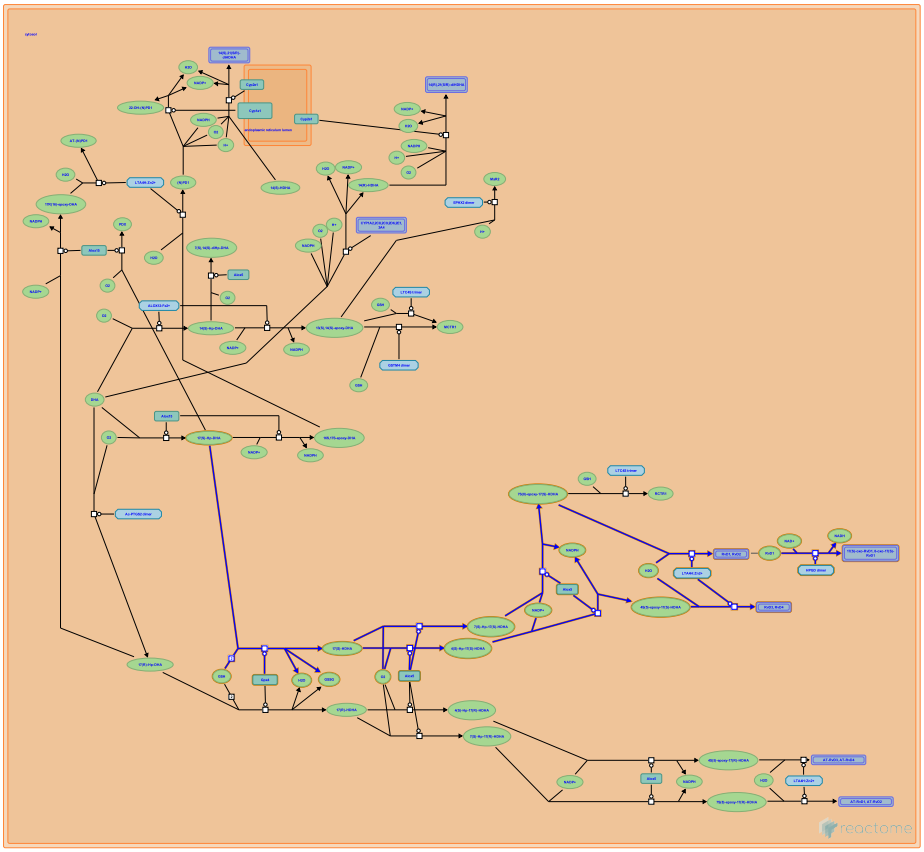
Biosynthesis of D-series resolvins



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

31/10/2020

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., 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. ↗

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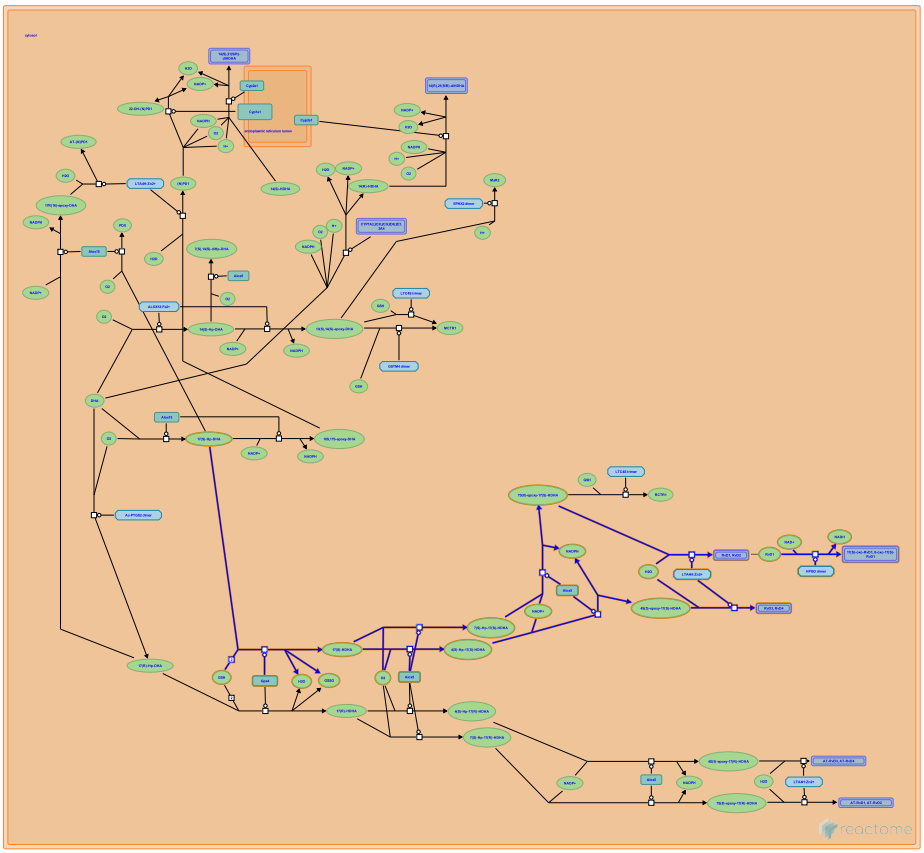
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

Biosynthesis of D-series resolvins ↗

Stable identifier: R-MMU-9018676

Inferred from: Biosynthesis of 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.

<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

GPX4-2 reduces 17(S)-Hp-DHA to 17(S)-HDHA ↗

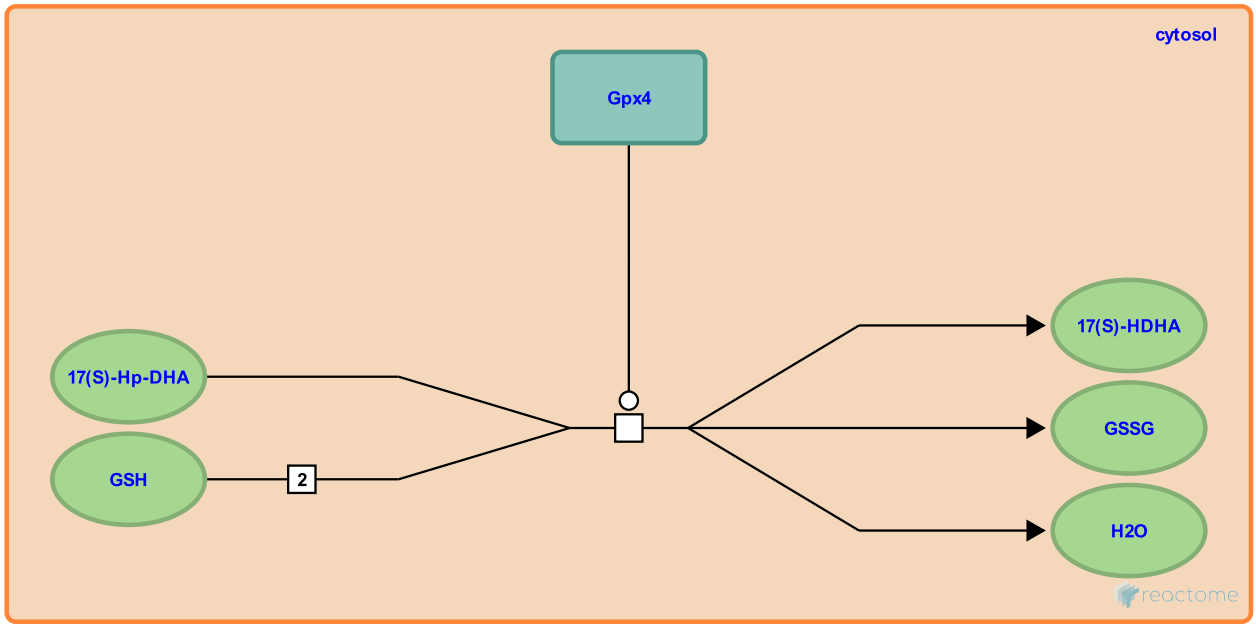
Location: Biosynthesis of D-series resolvins

Stable identifier: R-MMU-9020273

Type: transition

Compartments: cytosol

Inferred from: GPX4-2 reduces 17(S)-Hp-DHA to 17(S)-HDHA (Homo sapiens)



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Followed by: ALOX5 oxidises 17(S)-HDHA to 7(S)-Hp-17(S)-HDHA, ALOX5 oxidises 17(S)-HDHA to 4(S)-Hp-17(S)-HDHA

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

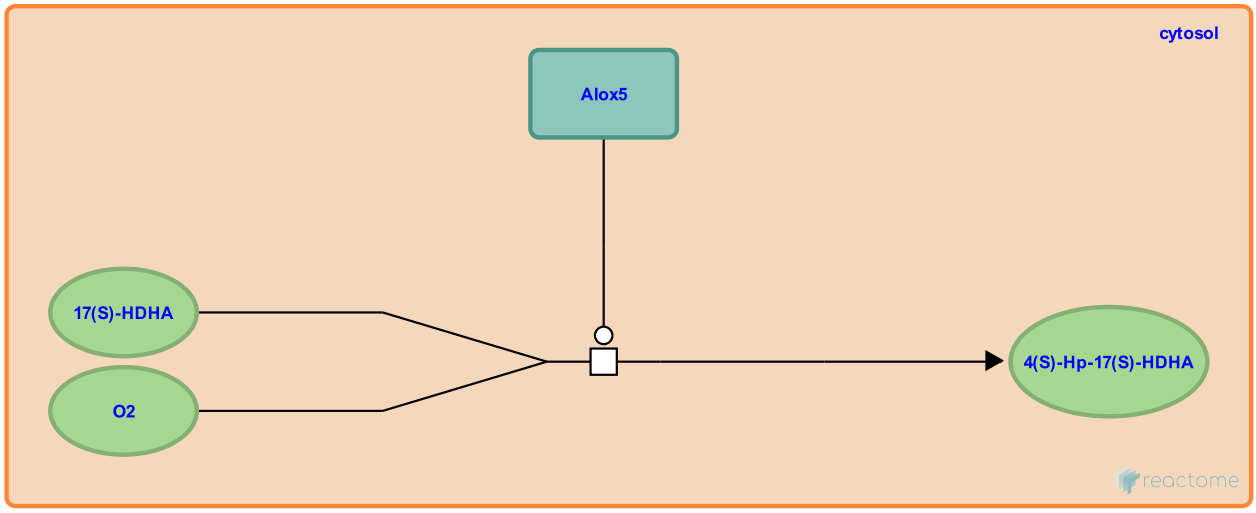
Location: Biosynthesis of D-series resolvins

Stable identifier: R-MMU-9020264

Type: transition

Compartments: cytosol

Inferred from: ALOX5 oxidises 17(S)-HDHA to 4(S)-Hp-17(S)-HDHA (Homo sapiens)



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Preceded by: GPX4-2 reduces 17(S)-Hp-DHA to 17(S)-HDHA

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

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

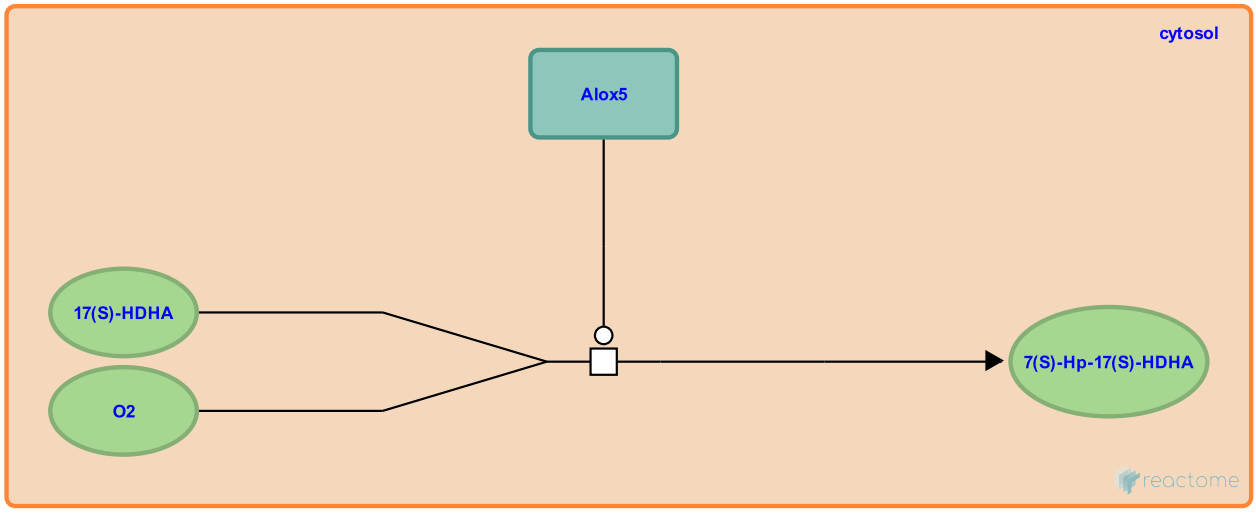
Location: Biosynthesis of D-series resolvins

Stable identifier: R-MMU-9020282

Type: transition

Compartments: cytosol

Inferred from: ALOX5 oxidises 17(S)-HDHA to 7(S)-Hp-17(S)-HDHA (Homo sapiens)



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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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Preceded by: GPX4-2 reduces 17(S)-Hp-DHA to 17(S)-HDHA

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

ALOX5 dehydrogenates 7(S)-Hp-17(S)-HDHA to 7S(8)-epoxy-17S-HDHA ↗

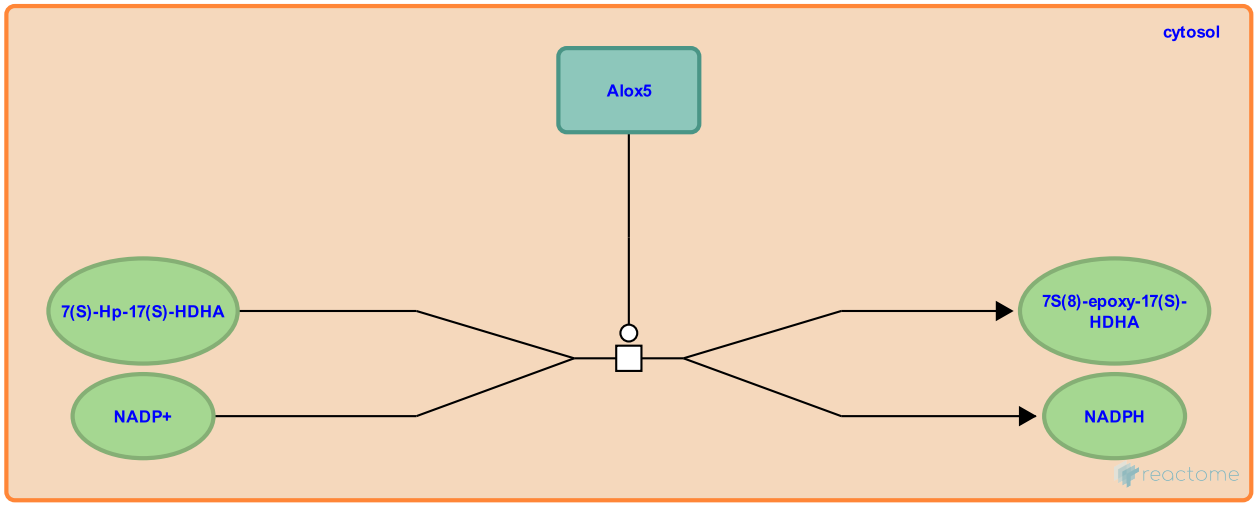
Location: Biosynthesis of D-series resolvins

Stable identifier: R-MMU-9020255

Type: transition

Compartments: cytosol

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

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Preceded by: ALOX5 oxidises 17(S)-HDHA to 7(S)-Hp-17(S)-HDHA

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

ALOX5 dehydrogenates 4(S)-Hp-17(S)-HDHA to 4S(5)-epoxy-17(S)-HDHA ↗

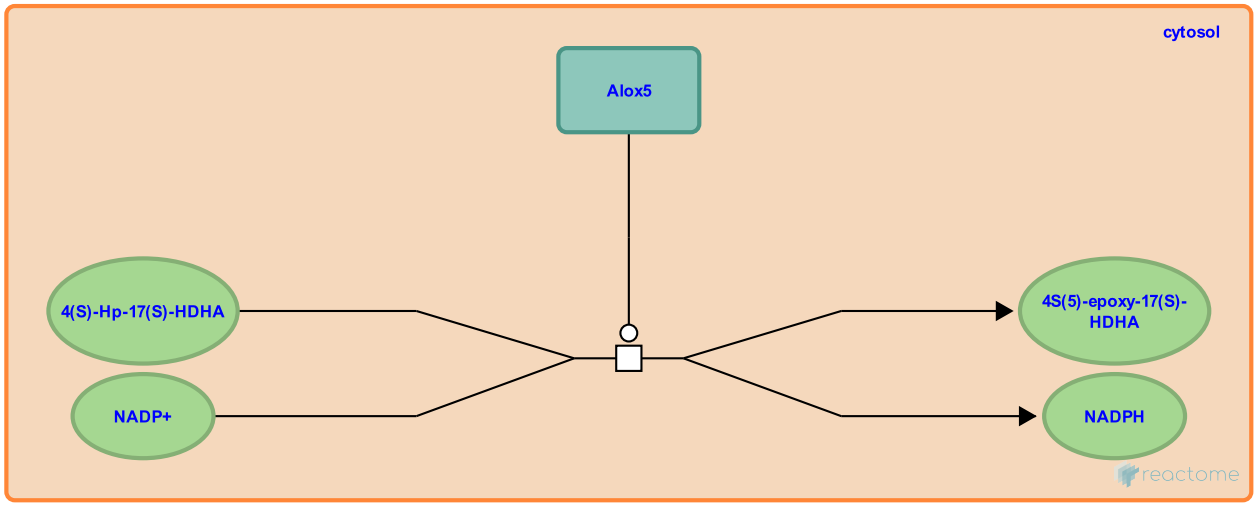
Location: Biosynthesis of D-series resolvins

Stable identifier: R-MMU-9020277

Type: transition

Compartments: cytosol

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

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Preceded by: ALOX5 oxidises 17(S)-HDHA to 4(S)-Hp-17(S)-HDHA

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

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

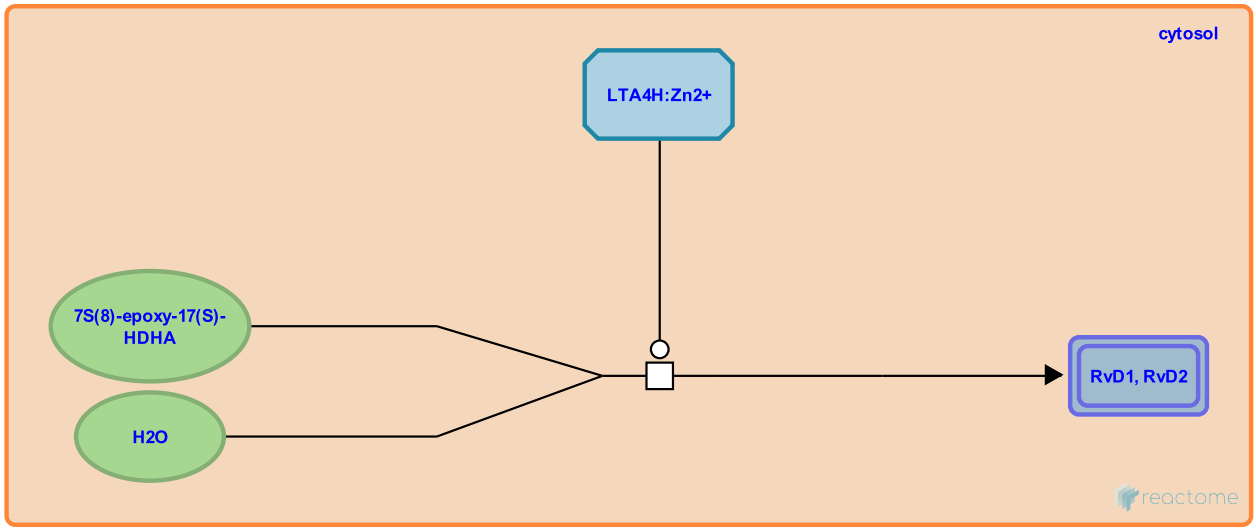
Location: Biosynthesis of D-series resolvins

Stable identifier: R-MMU-9020258

Type: transition

Compartments: cytosol

Inferred from: LTA4H:Zn2+ hydrolyses 7S(8)-epoxy-17(S)-HDHA to RvD1 or 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.

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

Followed by: HPGD dimer oxidises RvD1 to 17(S)-oxo-RvD1 and 8-oxo-17(S)-RvD1

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

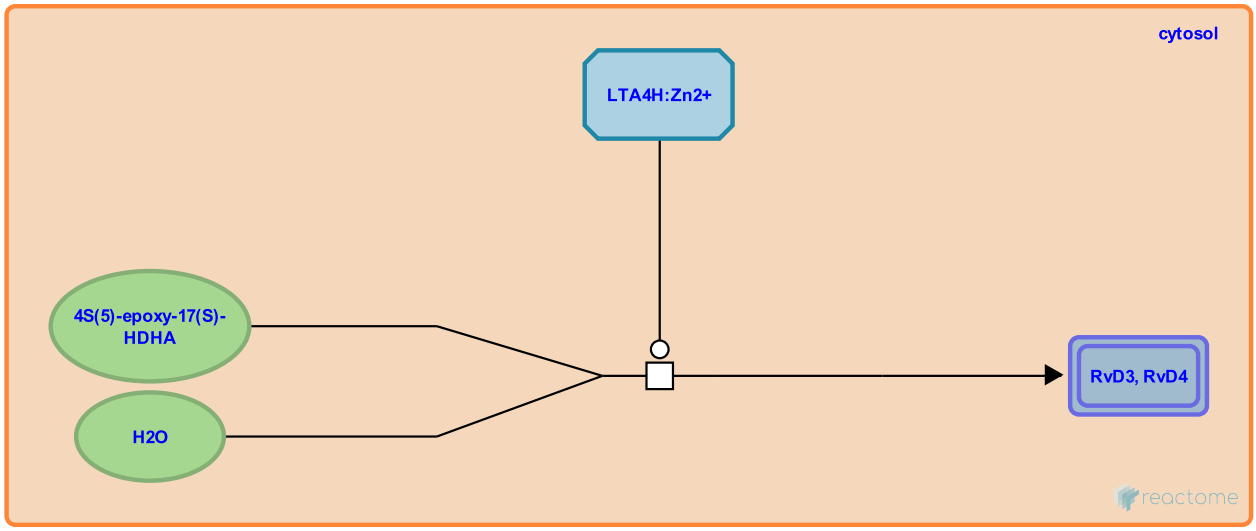
Location: Biosynthesis of D-series resolvins

Stable identifier: R-MMU-9020253

Type: transition

Compartments: cytosol

Inferred from: LTA4H:Zn2+ hydrolyses 4S(5)-epoxy-17(S)-HDHA to RvD3 or 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.

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

HPGD dimer oxidises RvD1 to 17(S)-oxo-RvD1 and 8-oxo-17(S)-RvD1 ↗

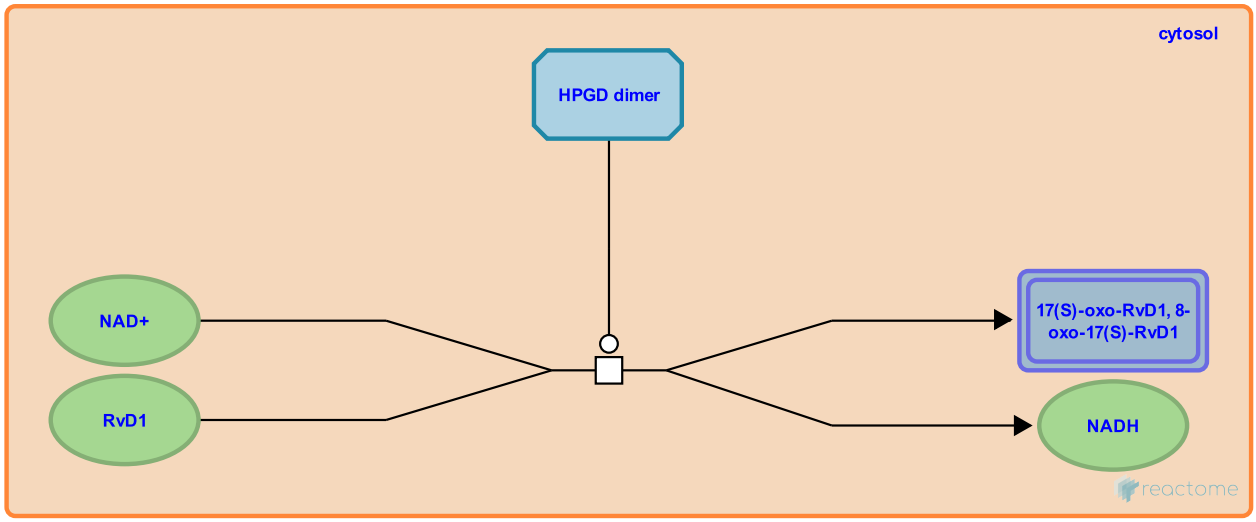
Location: Biosynthesis of D-series resolvins

Stable identifier: R-MMU-9024766

Type: transition

Compartments: cytosol

Inferred from: HPGD dimer oxidises RvD1 to 17(S)-oxo-RvD1 and 8-oxo-17(S)-RvD1 (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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Preceded by: LTA4H:Zn2+ hydrolyses 7S(8)-epoxy-17(S)-HDHA to RvD1 or RvD2

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