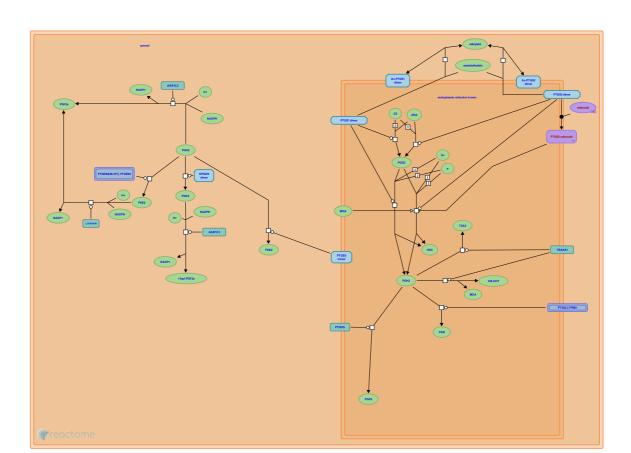


Synthesis of Prostaglandins (PG) and Thromboxanes (TX)



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.

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).

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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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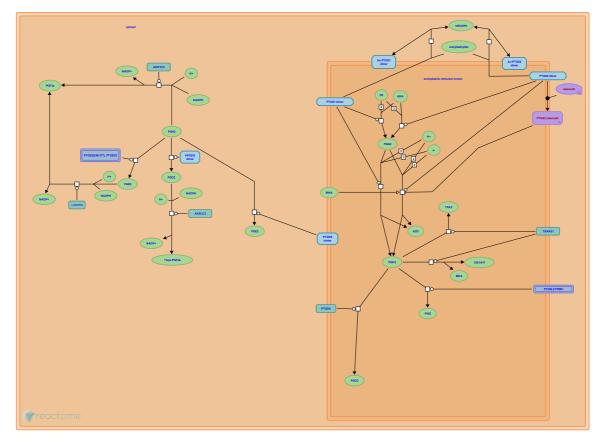
Reactome database release: 74

This document contains 1 pathway and 17 reactions (see Table of Contents)

Synthesis of Prostaglandins (PG) and Thromboxanes (TX)

Stable identifier: R-CFA-2162123

Inferred from: Synthesis of Prostaglandins (PG) and Thromboxanes (TX) (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.

PTGS2 dimer binds celecoxib **→**

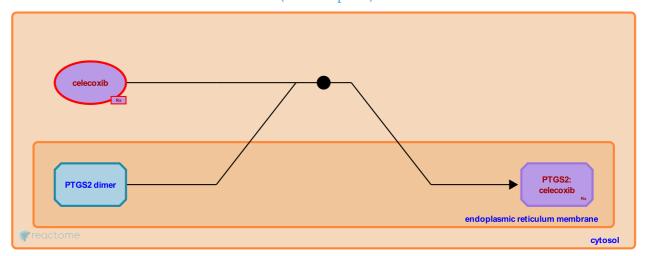
Location: Synthesis of Prostaglandins (PG) and Thromboxanes (TX)

Stable identifier: R-CFA-2309779

Type: binding

Compartments: cytosol, endoplasmic reticulum membrane

Inferred from: PTGS2 dimer binds celecoxib (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.

Aspirin acetylates PTGS1

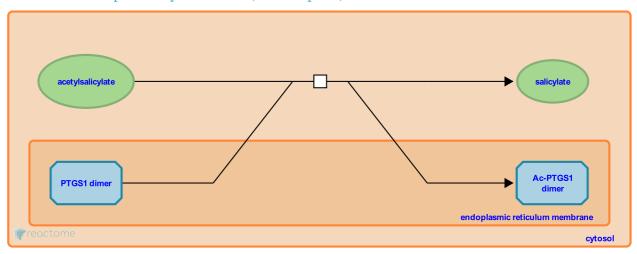
Location: Synthesis of Prostaglandins (PG) and Thromboxanes (TX)

Stable identifier: R-CFA-2314678

Type: transition

Compartments: cytosol, endoplasmic reticulum membrane

Inferred from: Aspirin acetylates PTGS1 (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.

Aspirin acetylates PTGS2

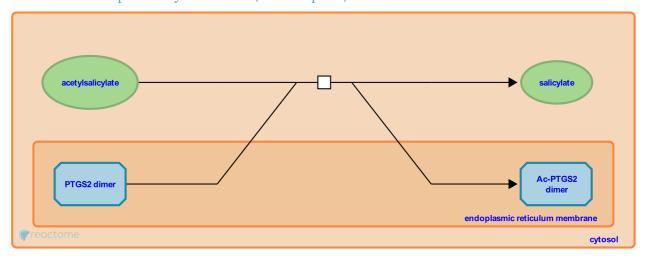
Location: Synthesis of Prostaglandins (PG) and Thromboxanes (TX)

Stable identifier: R-CFA-2314686

Type: transition

Compartments: cytosol, endoplasmic reticulum membrane

Inferred from: Aspirin acetylates PTGS2 (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.

Arachidonic acid is oxidised to PGG2 by PTGS1

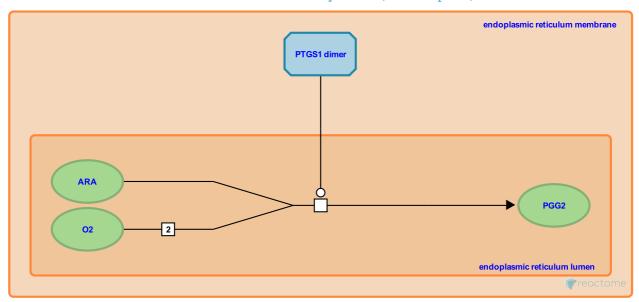
Location: Synthesis of Prostaglandins (PG) and Thromboxanes (TX)

Stable identifier: R-CFA-140355

Type: transition

Compartments: endoplasmic reticulum lumen, endoplasmic reticulum membrane

Inferred from: Arachidonic acid is oxidised to PGG2 by PTGS1 (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: PGG2 is reduced to PGH2 by PTGS1

Arachidonic acid is oxidised to PGG2 by PTGS2

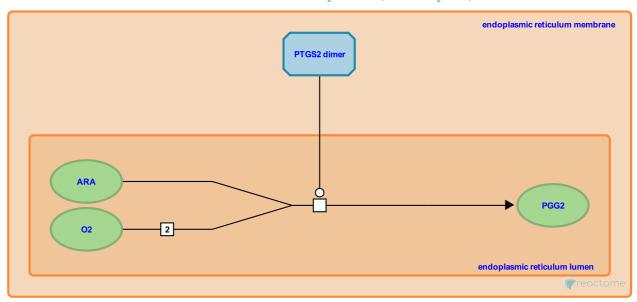
Location: Synthesis of Prostaglandins (PG) and Thromboxanes (TX)

Stable identifier: R-CFA-2309787

Type: transition

Compartments: endoplasmic reticulum lumen, endoplasmic reticulum membrane

Inferred from: Arachidonic acid is oxidised to PGG2 by PTGS2 (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: PGG2 is reduced to PGH2 by PTGS2

PGG2 is reduced to PGH2 by PTGS1 >

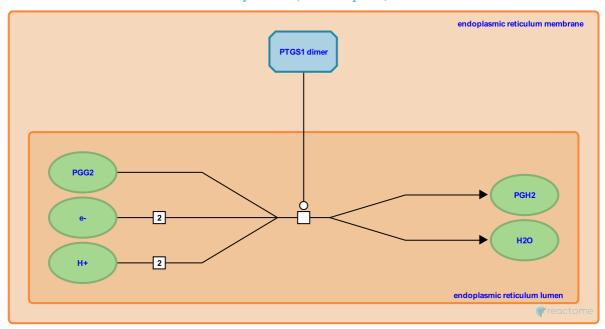
Location: Synthesis of Prostaglandins (PG) and Thromboxanes (TX)

Stable identifier: R-CFA-140359

Type: transition

Compartments: endoplasmic reticulum lumen, endoplasmic reticulum membrane

Inferred from: PGG2 is reduced to PGH2 by PTGS1 (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: Arachidonic acid is oxidised to PGG2 by PTGS1

Followed by: PGH2 is degraded to 12S-HHT and MDA by TBXAS1, PGH2 is isomerised to PGD2 by PTGDS, TBXAS1 isomerises PGH2 to TXA2, PTGIS, CYP8A1 isomerise PGH2 to PGI2

PGG2 is reduced to PGH2 by PTGS2 >

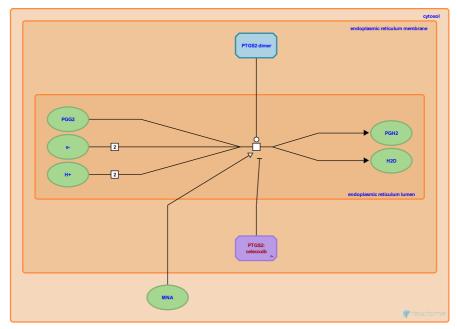
Location: Synthesis of Prostaglandins (PG) and Thromboxanes (TX)

Stable identifier: R-CFA-2309773

Type: transition

Compartments: endoplasmic reticulum lumen, endoplasmic reticulum membrane

Inferred from: PGG2 is reduced to PGH2 by PTGS2 (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: Arachidonic acid is oxidised to PGG2 by PTGS2

Followed by: PGH2 is degraded to 12S-HHT and MDA by TBXAS1, PGH2 is isomerised to PGD2 by PTGDS, TBXAS1 isomerises PGH2 to TXA2, PTGIS, CYP8A1 isomerise PGH2 to PGI2

PGH2 is reduced to PGF2a by AKR1C3 >

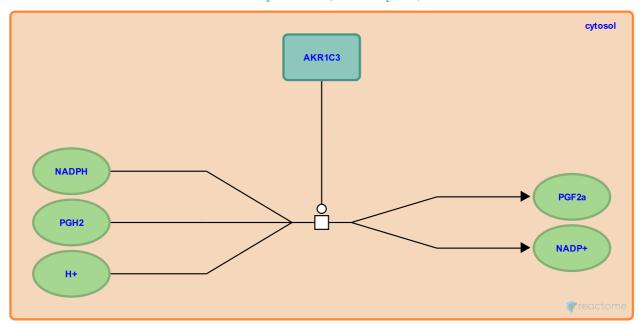
Location: Synthesis of Prostaglandins (PG) and Thromboxanes (TX)

Stable identifier: R-CFA-2161549

Type: transition

Compartments: cytosol

Inferred from: PGH2 is reduced to PGF2a by AKR1C3 (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.

PGH2 is isomerised to PGE2 by PTGES **对**

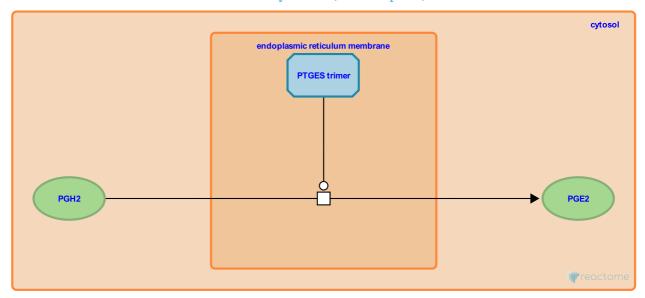
Location: Synthesis of Prostaglandins (PG) and Thromboxanes (TX)

Stable identifier: R-CFA-2161660

Type: transition

Compartments: endoplasmic reticulum membrane, cytosol

Inferred from: PGH2 is isomerised to PGE2 by PTGES (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.

Prostaglandin E synthase isomerizes PGH2 to PGE2 7

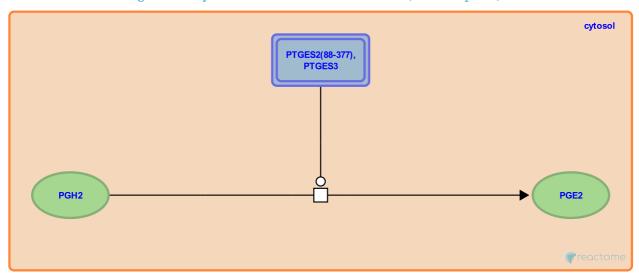
Location: Synthesis of Prostaglandins (PG) and Thromboxanes (TX)

Stable identifier: R-CFA-265295

Type: transition

Compartments: cytosol

Inferred from: Prostaglandin E synthase isomerizes PGH2 to PGE2 (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.

PGE2 is converted to PGF2a by CBR1 >

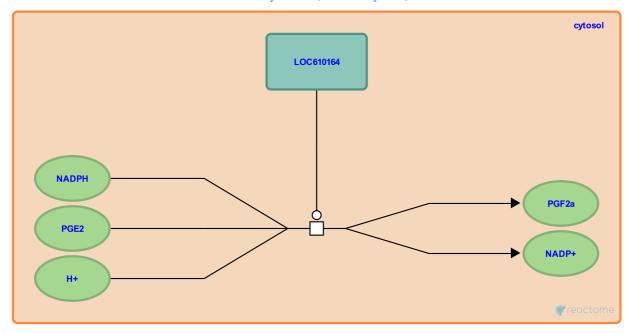
Location: Synthesis of Prostaglandins (PG) and Thromboxanes (TX)

Stable identifier: R-CFA-2161651

Type: transition

Compartments: cytosol

Inferred from: PGE2 is converted to PGF2a by CBR1 (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.

PGH2 is isomerised to PGD2 by PTGDS >

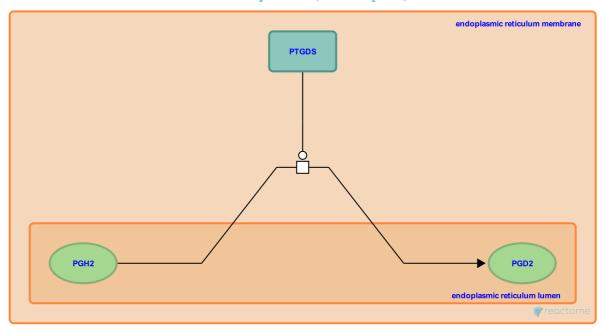
Location: Synthesis of Prostaglandins (PG) and Thromboxanes (TX)

Stable identifier: R-CFA-2161620

Type: transition

Compartments: endoplasmic reticulum membrane, endoplasmic reticulum lumen

Inferred from: PGH2 is isomerised to PGD2 by PTGDS (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

PGH2 is isomerised to PGD2 by HPGDS

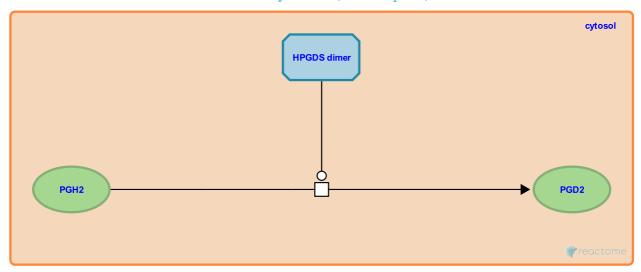
Location: Synthesis of Prostaglandins (PG) and Thromboxanes (TX)

Stable identifier: R-CFA-2161701

Type: transition

Compartments: cytosol

Inferred from: PGH2 is isomerised to PGD2 by HPGDS (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: PGD2 is reduced to 11-epi-PGF2a by AKRIC3

PGD2 is reduced to 11-epi-PGF2a by AKRIC3 **→**

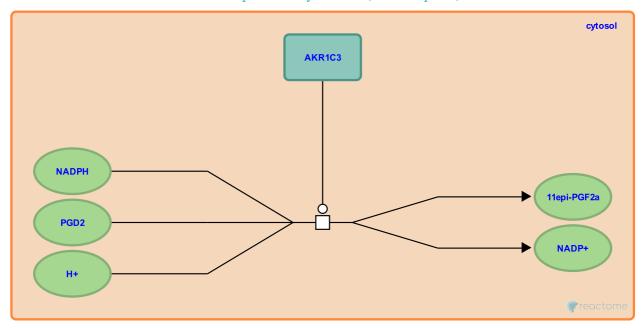
Location: Synthesis of Prostaglandins (PG) and Thromboxanes (TX)

Stable identifier: R-CFA-2161614

Type: transition

Compartments: cytosol

Inferred from: PGD2 is reduced to 11-epi-PGF2a by AKRIC3 (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: PGH2 is isomerised to PGD2 by HPGDS

PTGIS, CYP8A1 isomerise PGH2 to PGI2 7

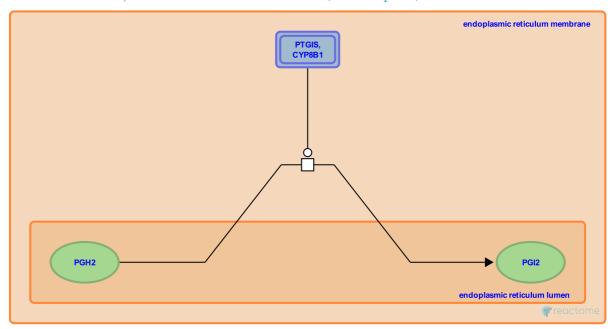
Location: Synthesis of Prostaglandins (PG) and Thromboxanes (TX)

Stable identifier: R-CFA-76496

Type: transition

Compartments: endoplasmic reticulum membrane, endoplasmic reticulum lumen

Inferred from: PTGIS, CYP8A1 isomerise PGH2 to PGI2 (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

TBXAS1 isomerises PGH2 to TXA2

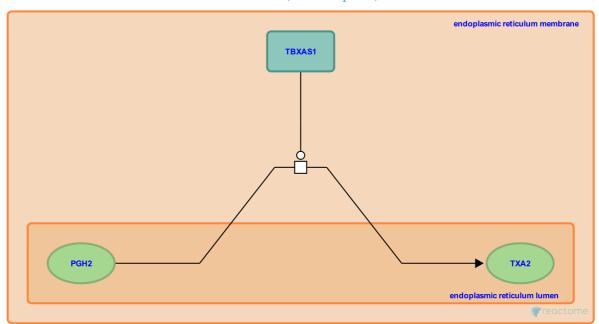
Location: Synthesis of Prostaglandins (PG) and Thromboxanes (TX)

Stable identifier: R-CFA-76500

Type: transition

Compartments: endoplasmic reticulum membrane, endoplasmic reticulum lumen

Inferred from: TBXAS1 isomerises PGH2 to TXA2 (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

PGH2 is degraded to 12S-HHT and MDA by TBXAS1

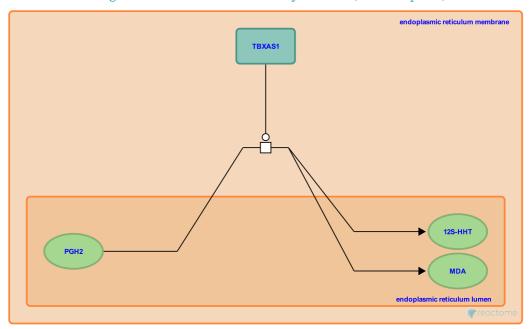
Location: Synthesis of Prostaglandins (PG) and Thromboxanes (TX)

Stable identifier: R-CFA-2161613

Type: transition

Compartments: endoplasmic reticulum membrane, endoplasmic reticulum lumen

Inferred from: PGH2 is degraded to 12S-HHT and MDA by TBXAS1 (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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