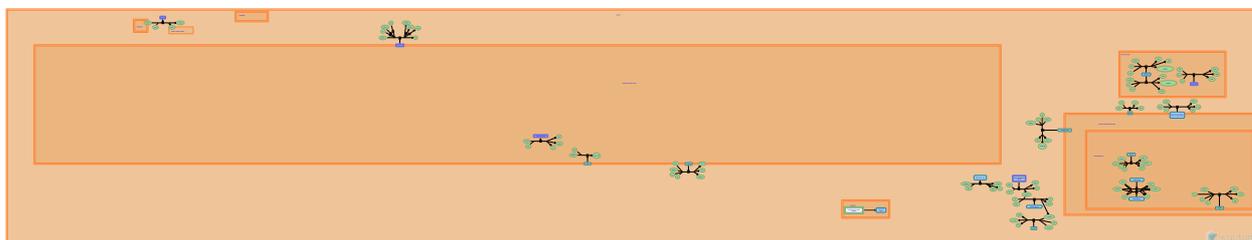


Phase I - Functionalization of compounds



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.

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Literature references

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Reactome database release: 70

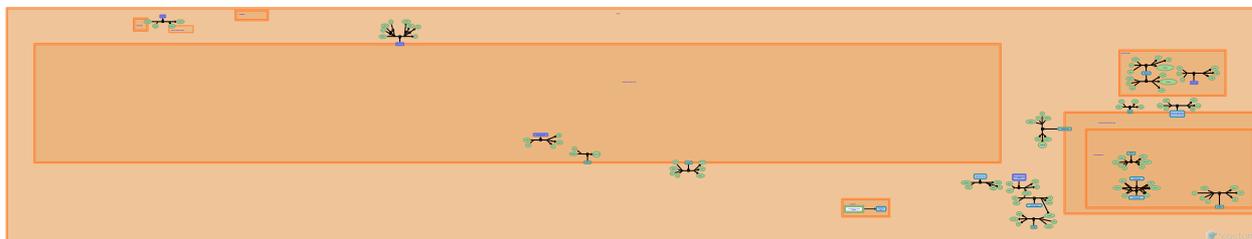
This document contains 5 pathways and 5 reactions ([see Table of Contents](#))

Phase I - Functionalization of compounds ↗

Stable identifier: R-DME-211945

Compartments: cytosol, mitochondrial inner membrane, mitochondrial outer membrane, mitochondrial matrix, endoplasmic reticulum membrane, endoplasmic reticulum lumen

Inferred from: [Phase I - Functionalization of compounds \(Homo sapiens\)](#)



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>

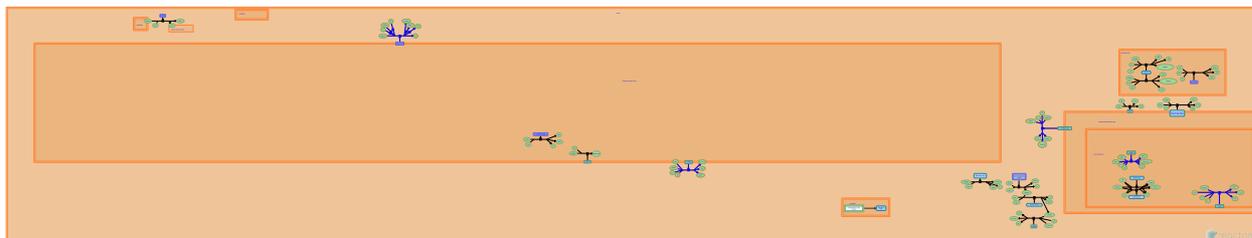
Cytochrome P450 - arranged by substrate type [↗](#)

Location: [Phase I - Functionalization of compounds](#)

Stable identifier: R-DME-211897

Compartments: endoplasmic reticulum membrane, cytosol, mitochondrial inner membrane, mitochondrial matrix

Inferred from: [Cytochrome P450 - arranged by substrate type \(Homo sapiens\)](#)



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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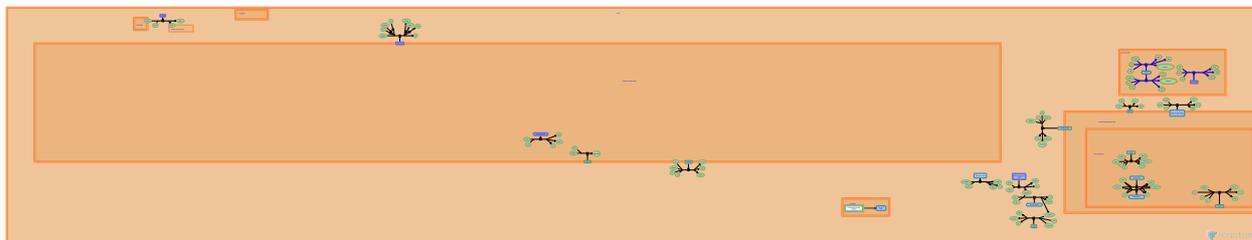
Amine Oxidase reactions ↗

Location: [Phase I - Functionalization of compounds](#)

Stable identifier: R-DME-140179

Compartments: mitochondrial outer membrane, peroxisomal matrix

Inferred from: [Amine Oxidase reactions \(Homo sapiens\)](#)



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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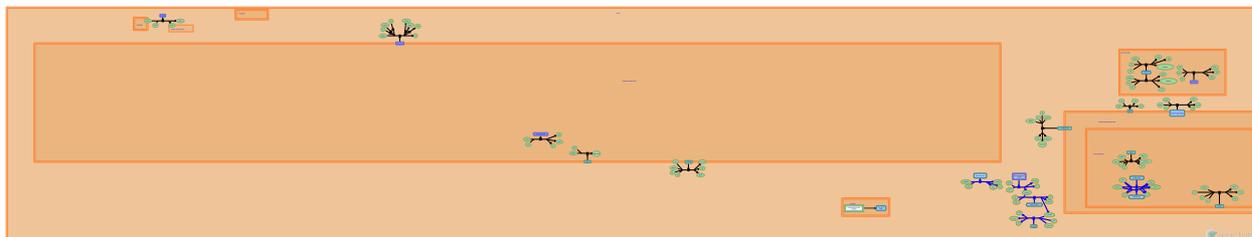
Ethanol oxidation ↗

Location: [Phase I - Functionalization of compounds](#)

Stable identifier: R-DME-71384

Compartments: cytosol, mitochondrial matrix

Inferred from: [Ethanol oxidation \(Homo sapiens\)](#)



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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CES1 trimer.CES2 hydrolyse COCN to BEG ↗

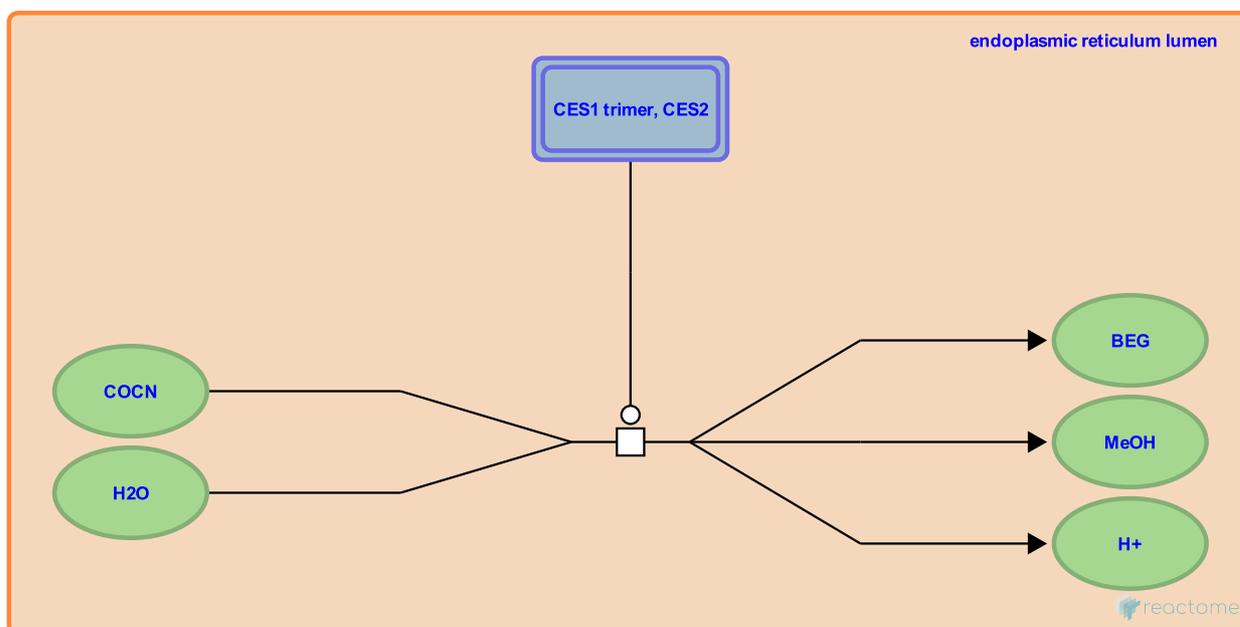
Location: Phase I - Functionalization of compounds

Stable identifier: R-DME-5693691

Type: transition

Compartments: endoplasmic reticulum lumen

Inferred from: [CES1 trimer.CES2 hydrolyse COCN to BEG \(Homo sapiens\)](#)



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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EPHX1 hydrates BaP4,5O to BaP4,5-DHD ↗

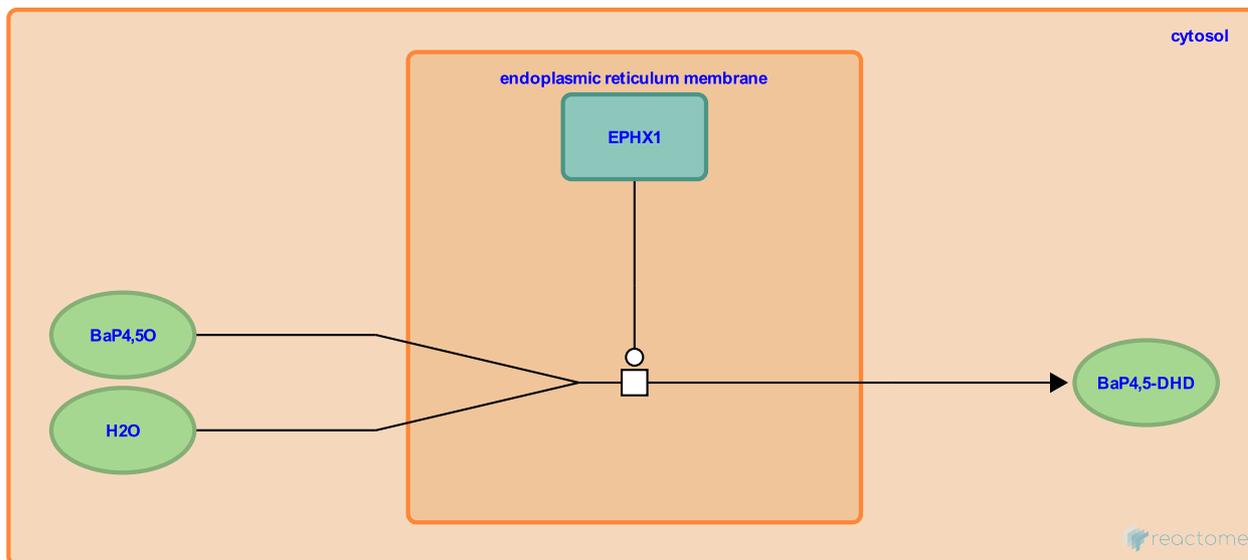
Location: [Phase I - Functionalization of compounds](#)

Stable identifier: R-DME-5694077

Type: transition

Compartments: endoplasmic reticulum membrane, cytosol

Inferred from: [EPHX1 hydrates BaP4,5O to BaP4,5-DHD \(Homo sapiens\)](#)



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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BPHL hydrolyses VACV to ACV ↗

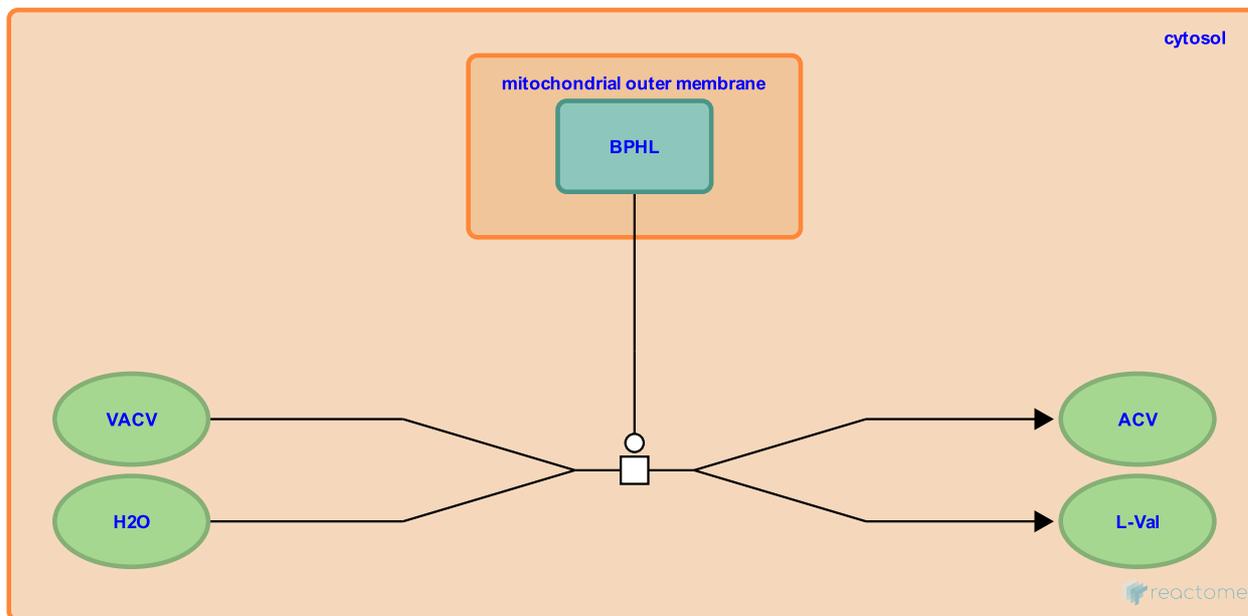
Location: Phase I - Functionalization of compounds

Stable identifier: R-DME-6784959

Type: transition

Compartments: cytosol, mitochondrial outer membrane

Inferred from: BPHL hydrolyses VACV to ACV (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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MARC1,MARC2 reduce N-hydroxylated compounds ↗

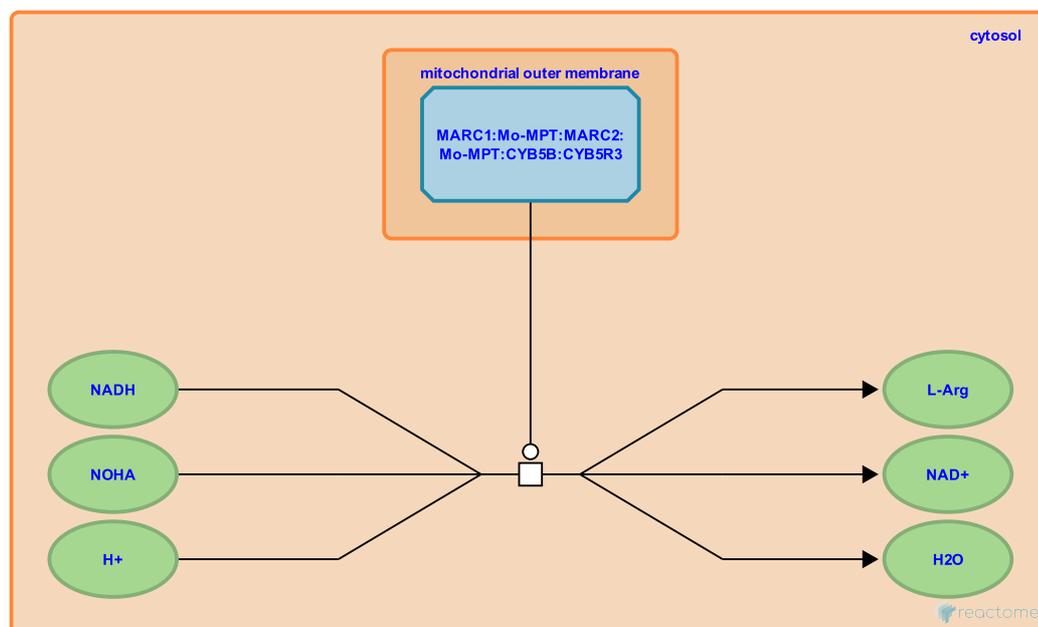
Location: Phase I - Functionalization of compounds

Stable identifier: R-DME-8936442

Type: transition

Compartments: cytosol, mitochondrial outer membrane

Inferred from: [MARC1,MARC2 reduce N-hydroxylated compounds \(Homo sapiens\)](#)



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>

CES3 hydrolyses CHEST to CHOL and LCFA(-) ↗

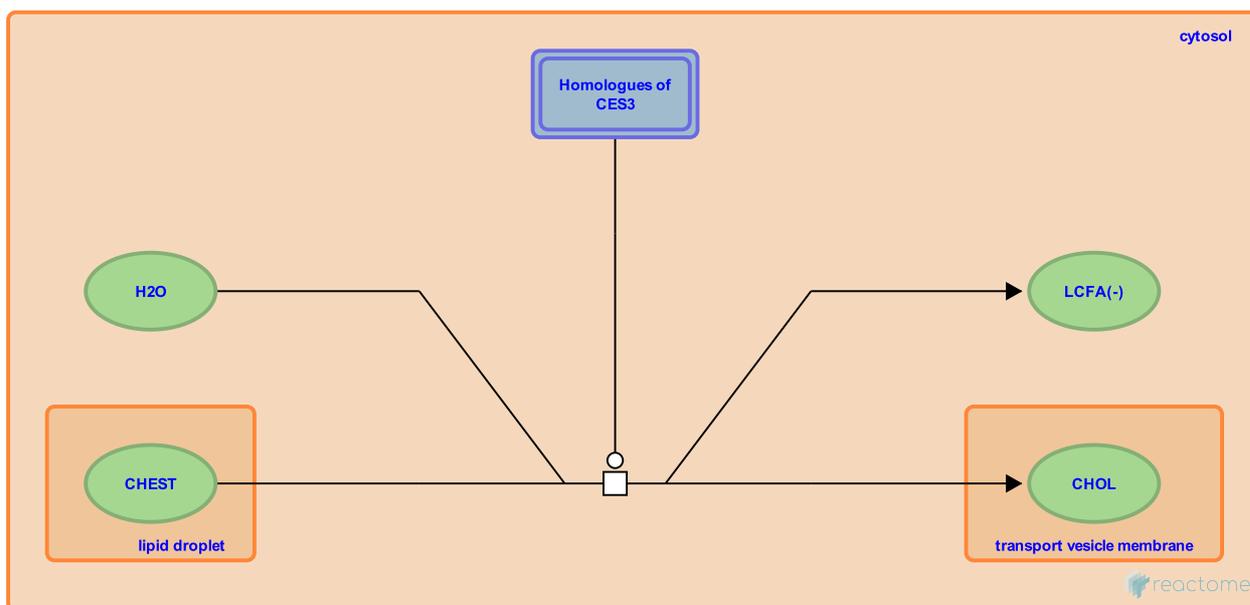
Location: Phase I - Functionalization of compounds

Stable identifier: R-DME-8937442

Type: transition

Compartments: cytosol, lipid droplet, transport vesicle membrane

Inferred from: CES3 hydrolyses CHEST to CHOL and LCFA(-) (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.

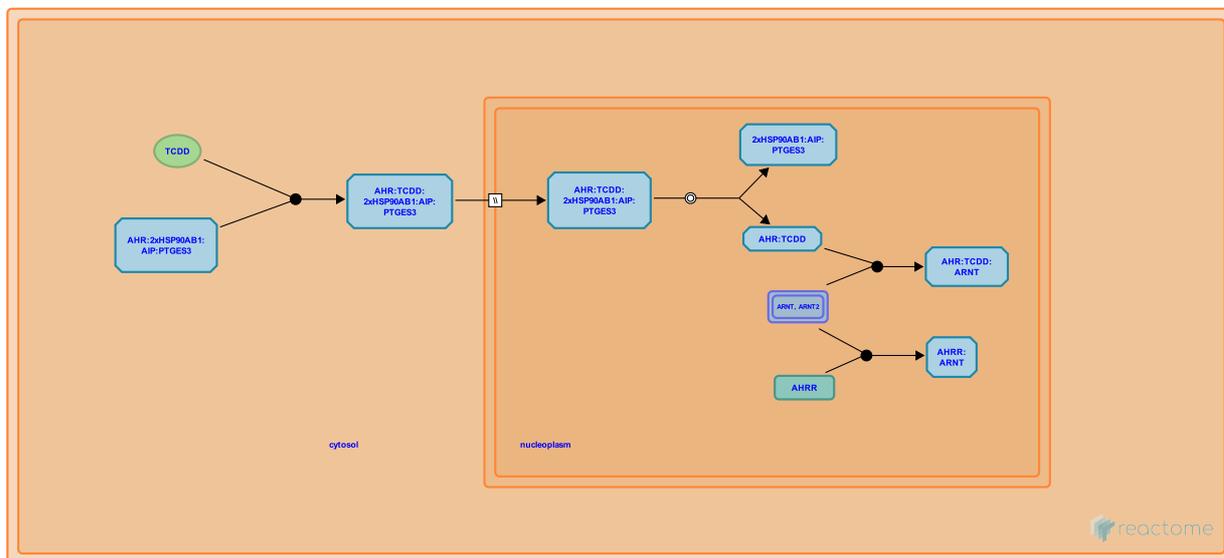
[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Aryl hydrocarbon receptor signalling ↗

Location: Phase I - Functionalization of compounds

Stable identifier: R-DME-8937144

Inferred from: Aryl hydrocarbon receptor signalling (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>

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