

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. [↗](#)

Reactome database release: 70

This document contains 1 pathway and 9 reactions ([see Table of Contents](#))

CYP3A4,5 hydroxylates AFB1 to AFQ1 ↗

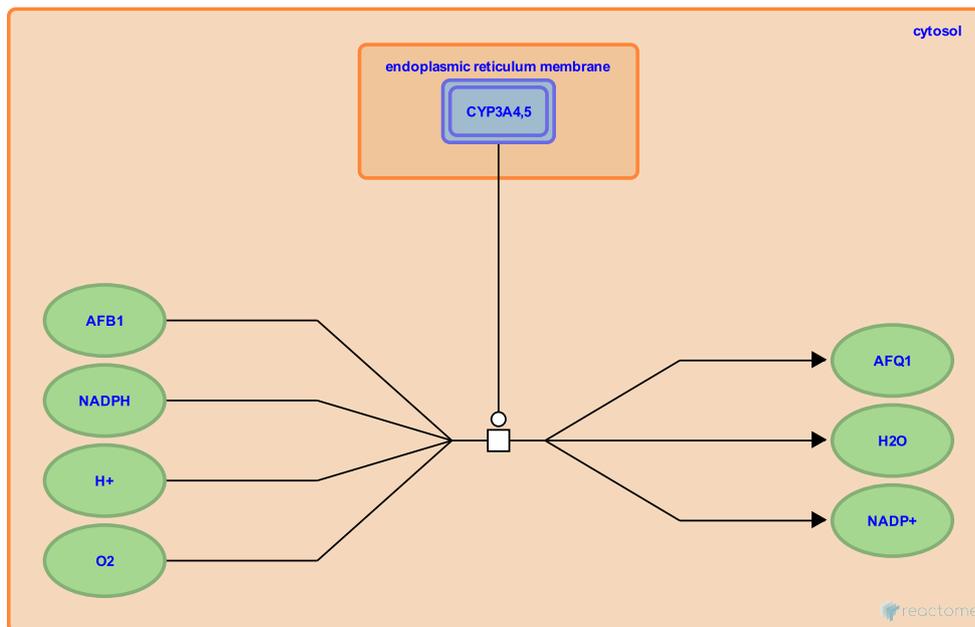
Location: [Aflatoxin activation and detoxification](#)

Stable identifier: R-GGA-5423664

Type: transition

Compartments: cytosol, endoplasmic reticulum membrane

Inferred from: [CYP3A4,5 hydroxylates AFB1 to AFQ1 \(Homo sapiens\)](#)



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>

CYP1A2 hydroxylates AFB1 to AFM1 ↗

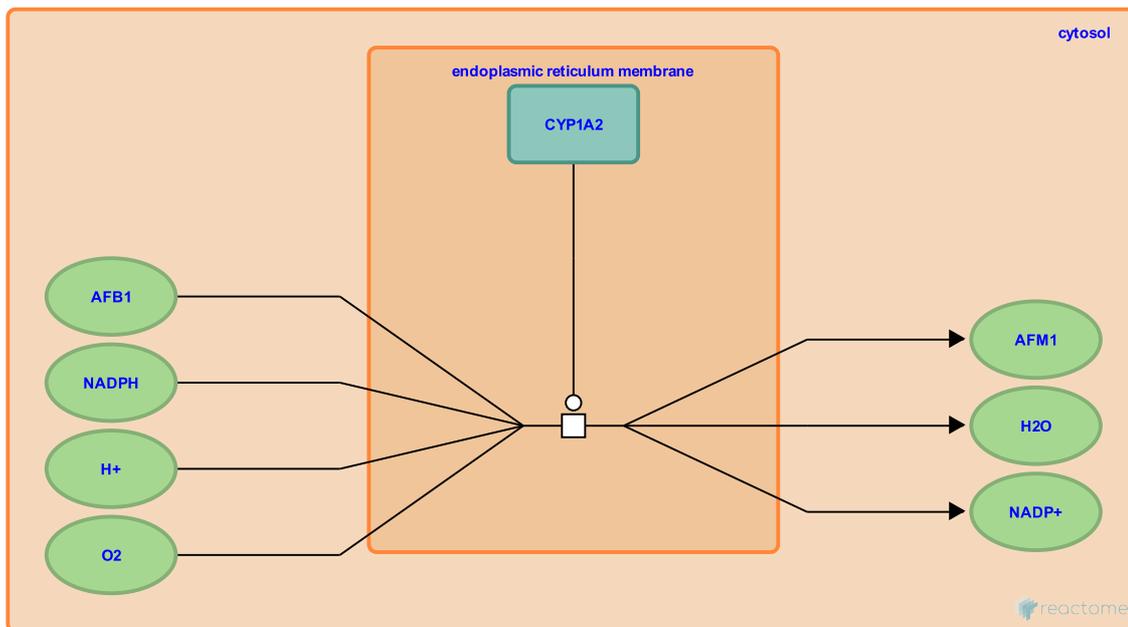
Location: [Aflatoxin activation and detoxification](#)

Stable identifier: R-GGA-5423678

Type: transition

Compartments: endoplasmic reticulum membrane, cytosol

Inferred from: [CYP1A2 hydroxylates AFB1 to AFM1 \(Homo sapiens\)](#)



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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CYP1A2,3A4,3A5,2A13 oxidise AFB1 to AFXBO ↗

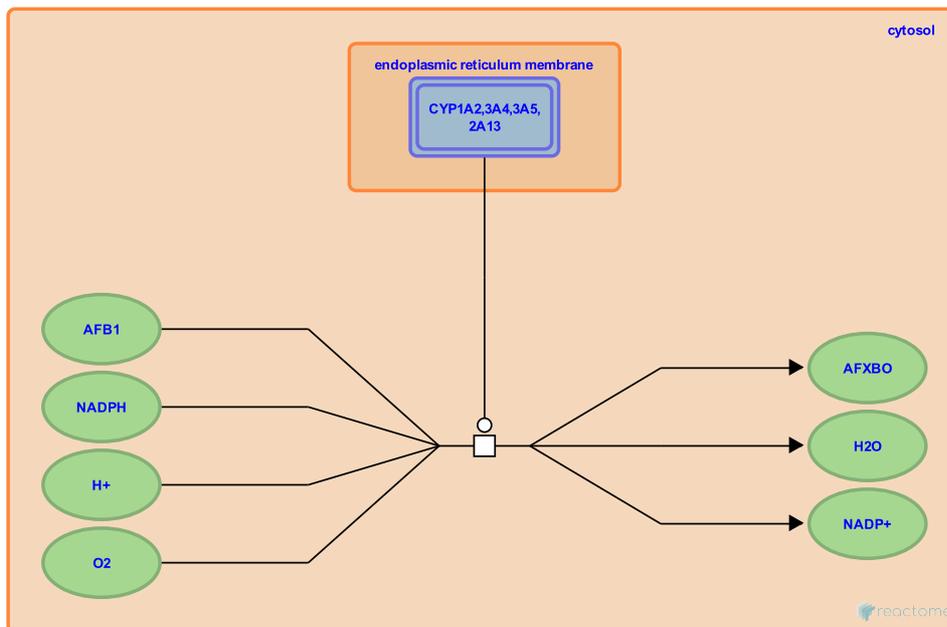
Location: [Aflatoxin activation and detoxification](#)

Stable identifier: R-GGA-156526

Type: transition

Compartments: cytosol, endoplasmic reticulum membrane

Inferred from: [CYP1A2,3A4,3A5,2A13 oxidise AFB1 to AFXBO \(Homo sapiens\)](#)



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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Followed by: [MGST trimers transfer GS from GSH to AFXBO and AFNBO](#)

CYP1A2, 3A4 oxidise AFB1 to AFNBO ↗

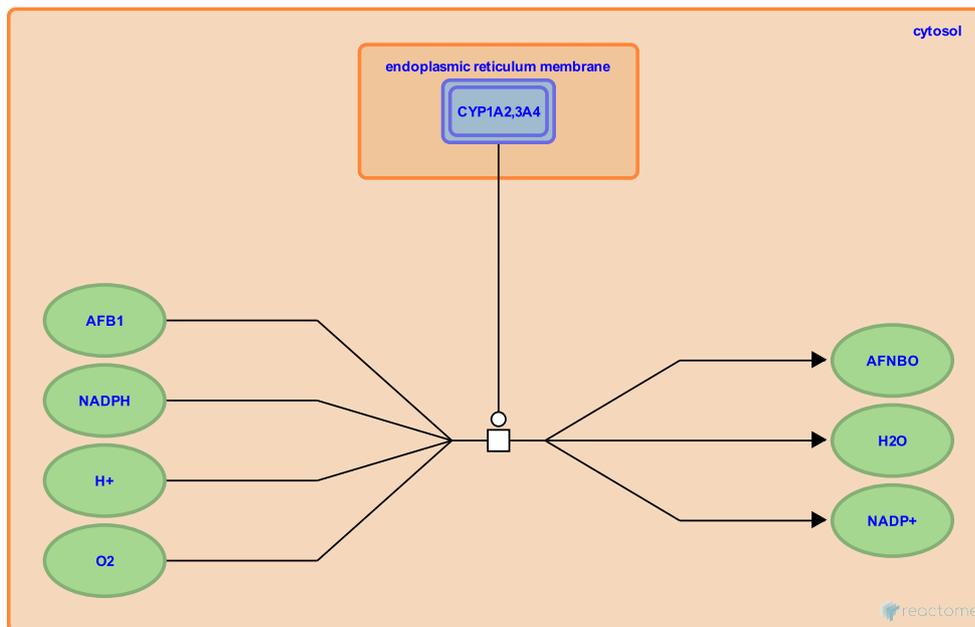
Location: [Aflatoxin activation and detoxification](#)

Stable identifier: R-GGA-5423672

Type: transition

Compartments: cytosol, endoplasmic reticulum membrane

Inferred from: [CYP1A2, 3A4 oxidise AFB1 to AFNBO \(Homo sapiens\)](#)



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>

Followed by: [MGST trimers transfer GS from GSH to AFXBO and AFNBO](#)

MGST trimers transfer GS from GSH to AFXBO and AFNBO ↗

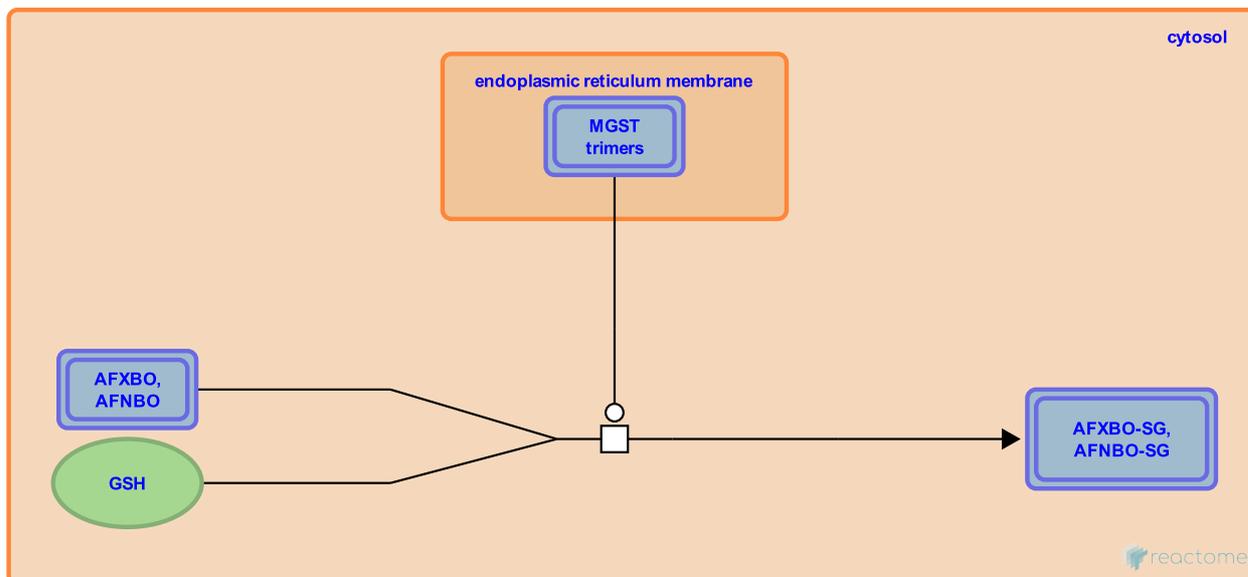
Location: [Aflatoxin activation and detoxification](#)

Stable identifier: R-GGA-5423653

Type: transition

Compartments: cytosol, endoplasmic reticulum membrane

Inferred from: [MGST trimers transfer GS from GSH to AFXBO and AFNBO \(Homo sapiens\)](#)



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: [CYP1A2,3A4,3A5,2A13 oxidise AFB1 to AFXBO](#), [CYP1A2, 3A4 oxidise AFB1 to AFNBO](#)

GGTs hydrolyse glutamate from AFXBO-SG, AFNBO-SG ↗

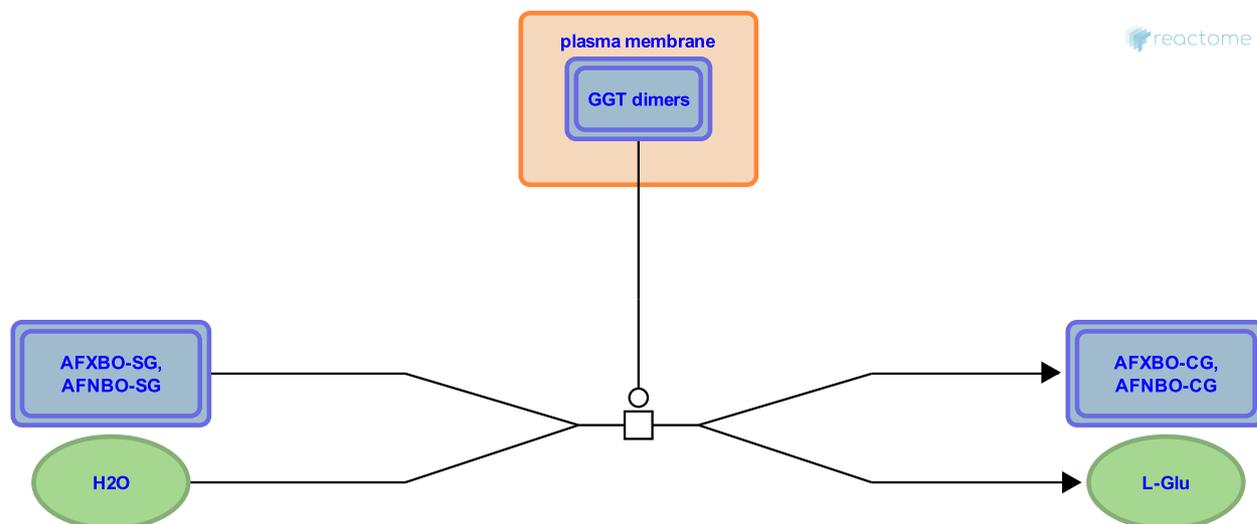
Location: [Aflatoxin activation and detoxification](#)

Stable identifier: R-GGA-5433072

Type: transition

Compartments: extracellular region, plasma membrane

Inferred from: [GGTs hydrolyse glutamate from AFXBO-SG, AFNBO-SG \(Homo sapiens\)](#)



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>

Followed by: [DPEPs hydrolyse glycine from AFXBO-CG, AFNBO-CG](#)

DPEPs hydrolyse glycine from AFXBO-CG, AFNBO-CG ↗

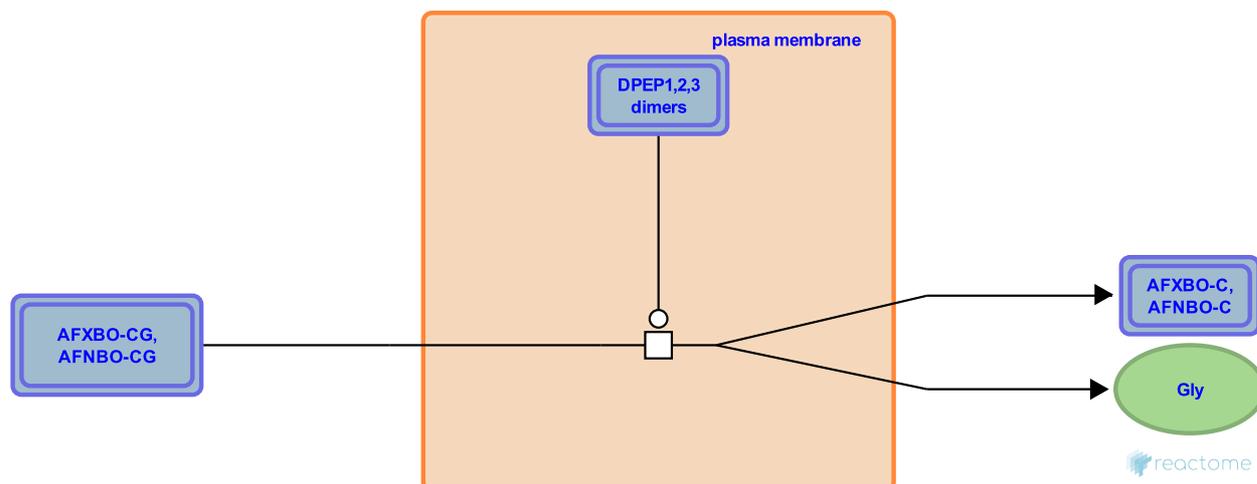
Location: [Aflatoxin activation and detoxification](#)

Stable identifier: R-GGA-5433067

Type: transition

Compartments: plasma membrane, extracellular region

Inferred from: [DPEPs hydrolyse glycine from AFXBO-CG, AFNBO-CG \(Homo sapiens\)](#)



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>

Preceded by: [GGTs hydrolyse glutamate from AFXBO-SG, AFNBO-SG](#)

ACY1:Zn²⁺ dimer hydrolyses mercapturic acids ↗

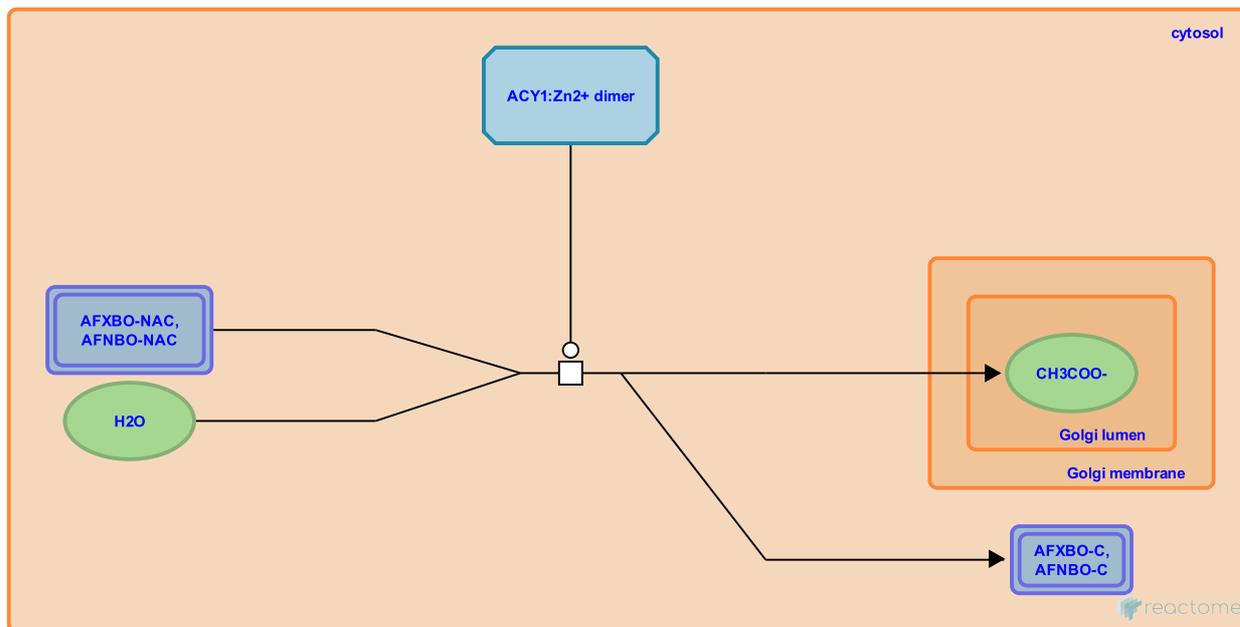
Location: [Aflatoxin activation and detoxification](#)

Stable identifier: R-GGA-5433074

Type: transition

Compartments: cytosol

Inferred from: [ACY1:Zn²⁺ dimer hydrolyses mercapturic acids \(Homo sapiens\)](#)



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>

AKR dimers reduce AFB₂DHO to AFB₂DOH ↗

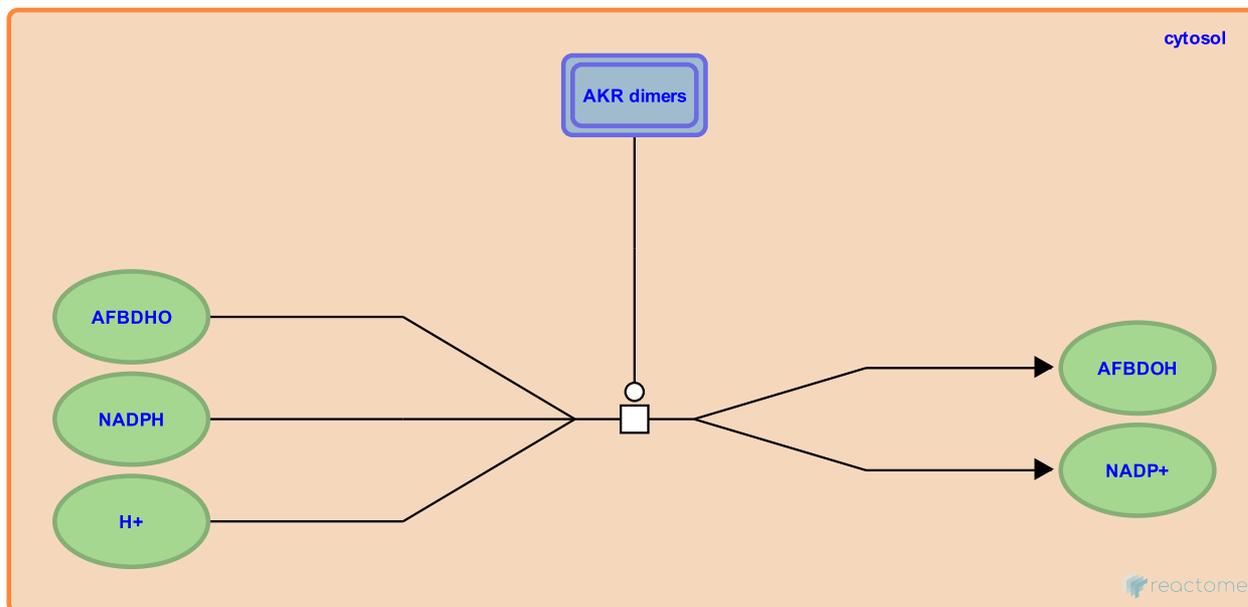
Location: [Aflatoxin activation and detoxification](#)

Stable identifier: R-GGA-5423637

Type: transition

Compartments: cytosol

Inferred from: [AKR dimers reduce AFB₂DHO to AFB₂DOH \(Homo sapiens\)](#)



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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