



## 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. [↗](#)
- 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 database: Efficient access to complex pathway data. *PLoS computational biology*, 14, e1005968. [↗](#)

Reactome database release: 82

This document contains 4 pathways and 2 reactions ([see Table of Contents](#))



## AWAT1 transfers acyl group from acyl-CoA to ARACOH, forming wax esters ↗

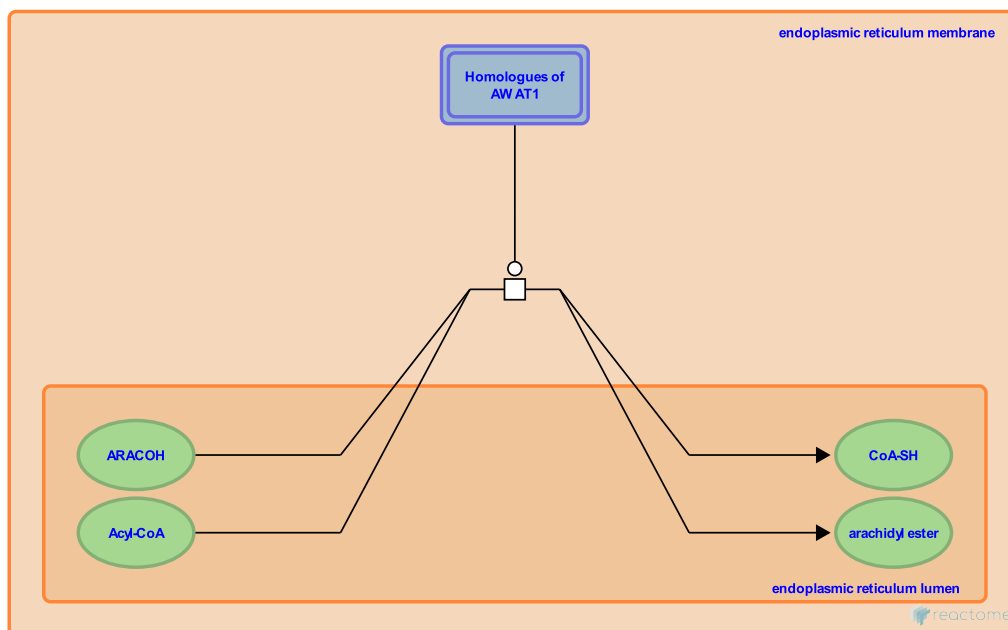
**Location:** [Arachidonic acid metabolism](#)

**Stable identifier:** R-DME-5696424

**Type:** transition

**Compartments:** endoplasmic reticulum membrane, endoplasmic reticulum lumen

**Inferred from:** [AWAT1 transfers acyl group from acyl-CoA to ARACOH, forming wax esters \(Homo sapiens\)](#)



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>

## FAAH2 hydrolyses AEA to AA and ETA ↗

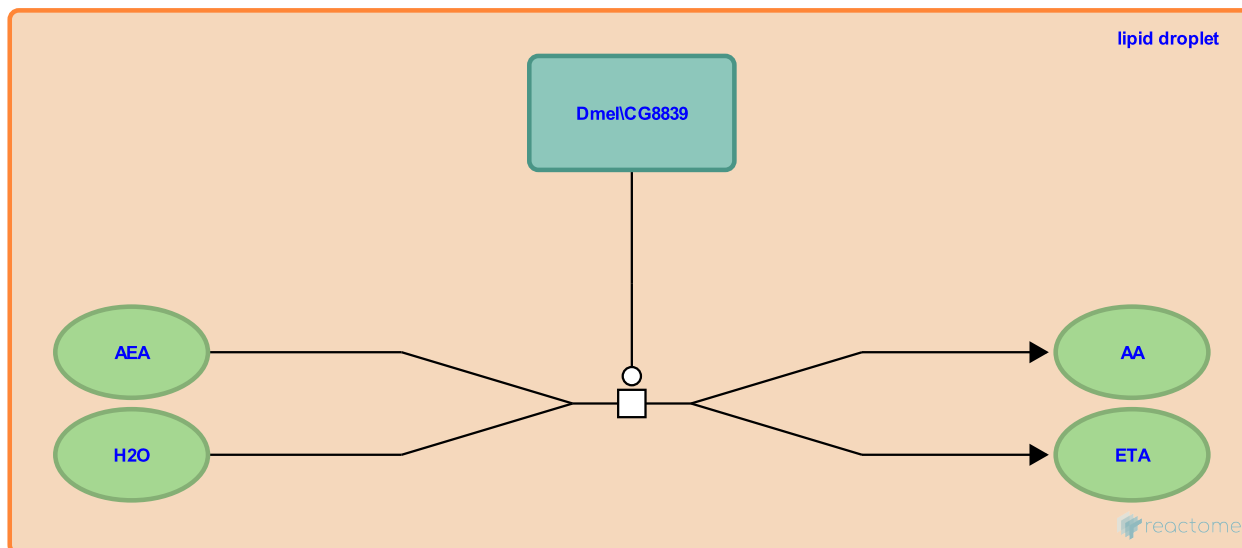
**Location:** [Arachidonic acid metabolism](#)

**Stable identifier:** R-DME-5693751

**Type:** transition

**Compartments:** lipid droplet

**Inferred from:** [FAAH2 hydrolyses AEA to AA and ETA \(Homo sapiens\)](#)



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.

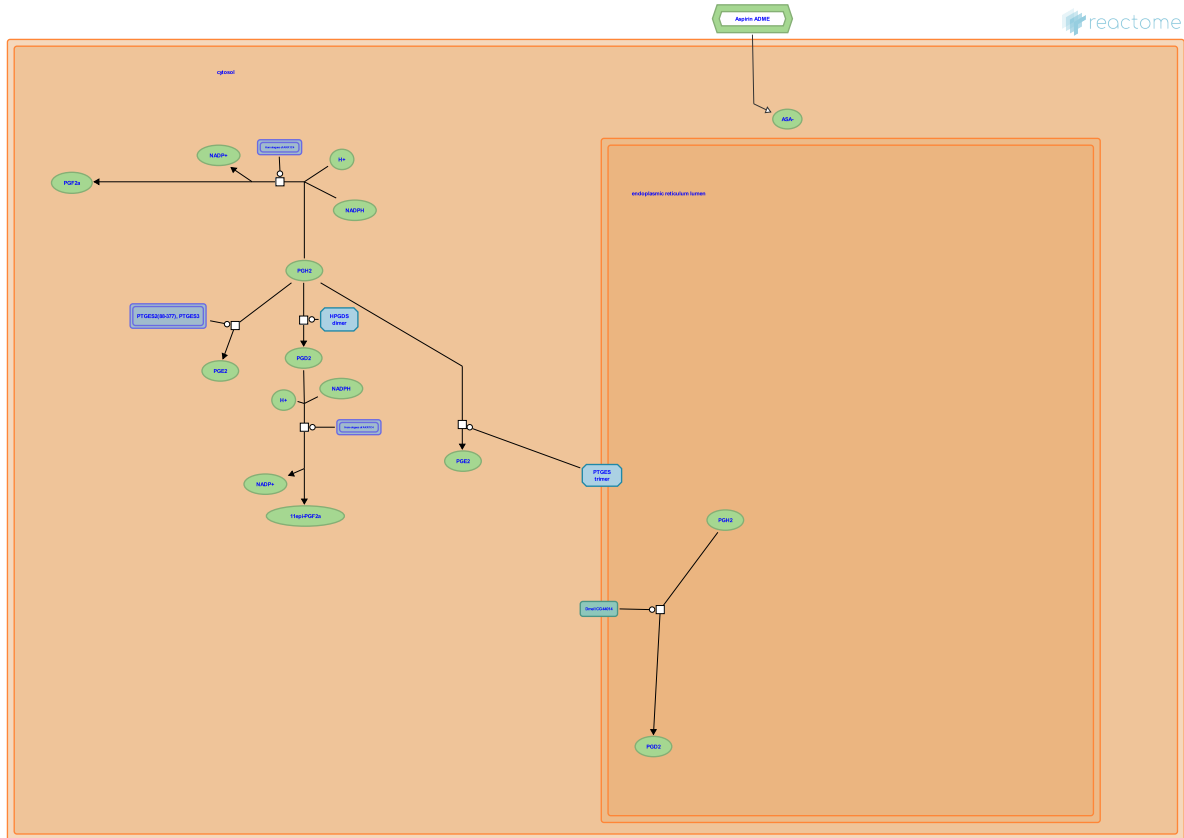
[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## Synthesis of Prostaglandins (PG) and Thromboxanes (TX) ↗

**Location:** Arachidonic acid metabolism

**Stable identifier:** R-DME-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.

[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>







# Table of Contents

Introduction	1
☒ Arachidonic acid metabolism	2
↳ AWAT1 transfers acyl group from acyl-CoA to ARACOH, forming wax esters	3
↳ FAAH2 hydrolyses AEA to AA and ETA	4
☒ Synthesis of Prostaglandins (PG) and Thromboxanes (TX)	5
☒ Synthesis of Leukotrienes (LT) and Eoxins (EX)	6
☒ Synthesis of (16-20)-hydroxyeicosatetraenoic acids (HETE)	7
Table of Contents	8