FAAH hydrolyses AEA to AA and ETA

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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

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. ↗

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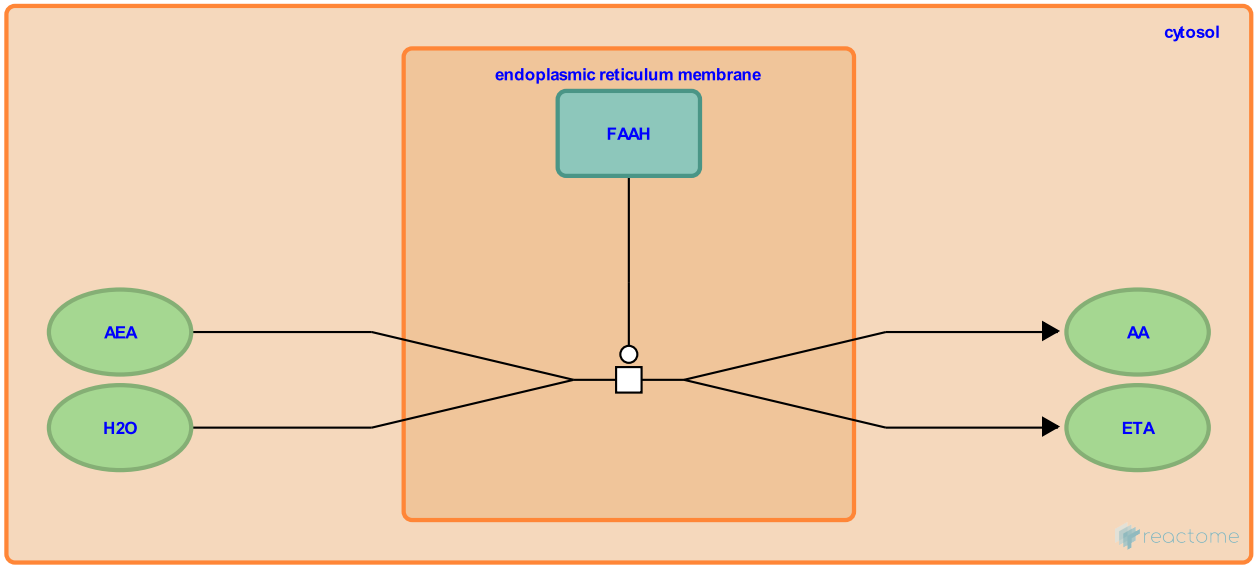
Stable identifier: R-HSA-5693742

Type: transition

Compartments: endoplasmic reticulum membrane, cytosol



Fatty acid amides are a class of lipid transmitters that include the endogenous cannabinoid anandamide (AEA) and the sleep-inducing chemical oleamide. The magnitude and duration of their signalling are controlled by enzymatic hydrolysis mediated by fatty-acid amide hydrolases 1 and 2 (FAAH, H2). Hydrolysis of AEA is described here (Wei et al. 2006). FAAH is localised to the ER membrane whereas FAAH2 is localised to lipid droplets (Kaczocha et al. 2010).

Literature references

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Editions

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