AMP + H2O => IMP + NH4+ (AMPD)

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01/10/2020

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).

Literature references

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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. ↗

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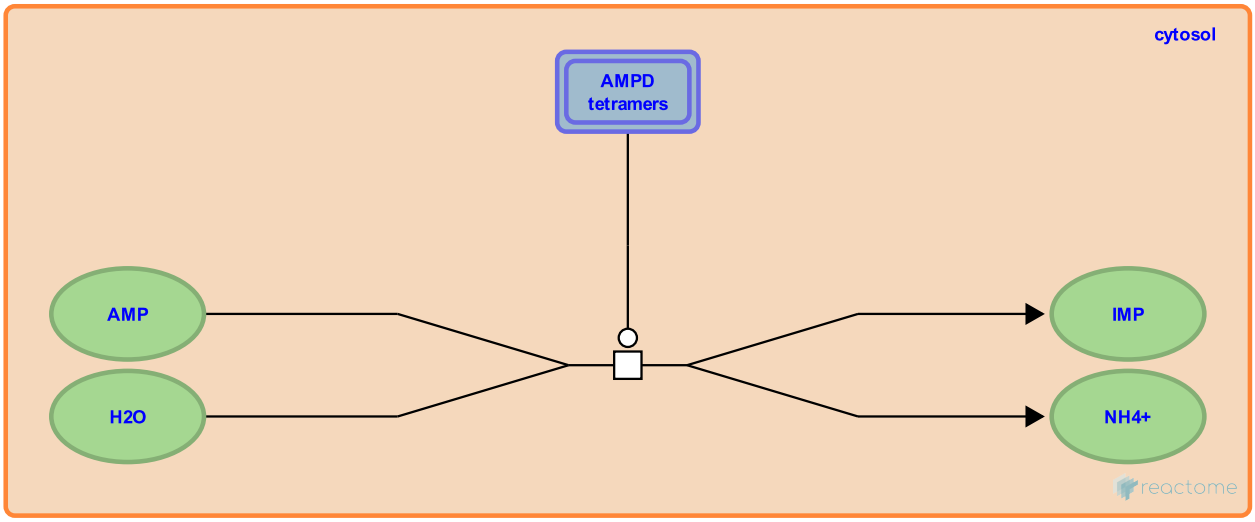
Stable identifier: R-HSA-76590

Type: transition

Compartments: cytosol



Cytosolic AMP deaminase (AMPD) catalyzes the hydrolysis of AMP to yield IMP and ammonia. Three isoforms of AMPD, E, L, and M, have been identified that differ in their expression patterns in the body. All occur as tetramers and all have qualitatively the same catalytic activity, however (Bausch-Jurken et al. 1992; Mahnke-Zizelman et al. 1998).

Literature references

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Mahnke-Zizelman, DK., Tullson, PC., Sabina, RL. (1998). Novel aspects of tetramer assembly and N-terminal domain structure and function are revealed by recombinant expression of human AMP deaminase isoforms. *J Biol Chem, 273*, 35118-25.

Editions

2010-02-06	Revised	D'Eustachio, P.