PXLP-K278-PHYKPL tetramer hydrolyses 5PHL

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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. ↗

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. ↗

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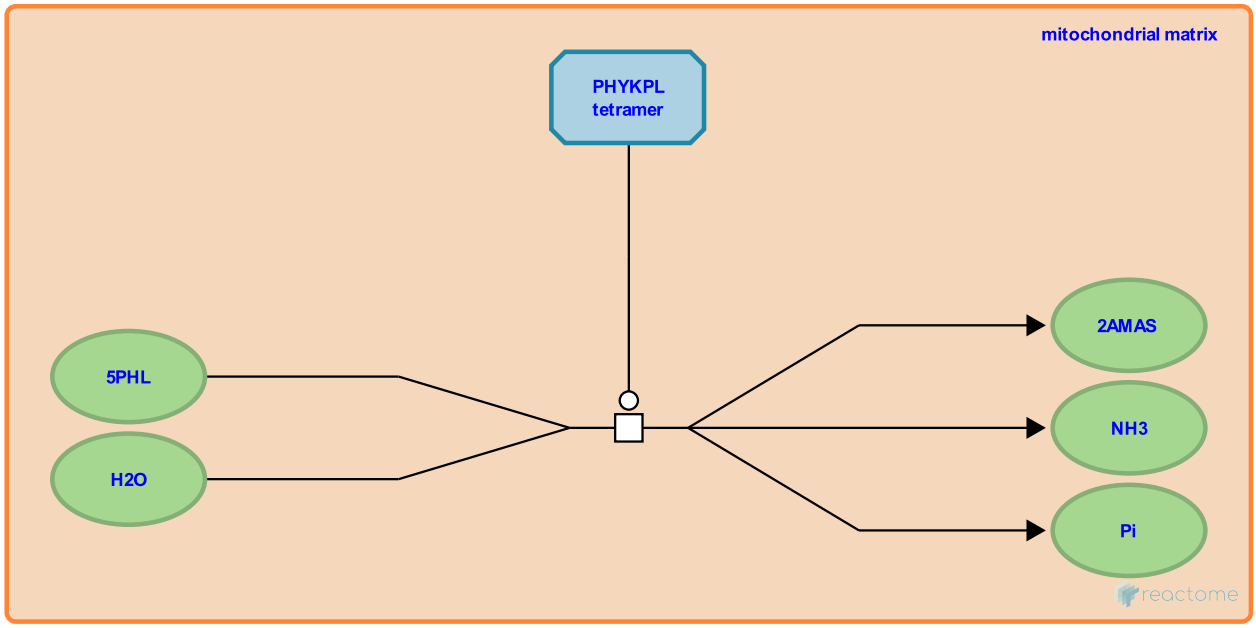
Stable identifier: R-HSA-5696408

Type: transition

Compartments: mitochondrial matrix



In mitochondria, ethanolamine-phosphate phospho-lyase and 5-phosphohydroxy-L-lysine phospho-lyase (ETNPPL and PHYKPL respectively) are two closely related pyridoxal-phosphate-dependent, homotetrameric ammoniophospholyases that hydrolyse phosphoethanolamine (PETA) and 5-phosphohydroxylysine (5PHL) respectively (Veiga-da-Cunha et al. 2012). PETA is a component and a precursor of phospholipids whereas 5PHL is a breakdown product of collagen. ETNPPL utilises one pyridoxal 5'-phosphate (PXLP) as cofactor per subunit.

Literature references

Stroobant, V., Balligand, T., Veiga-da-Cunha, M., Van Schaftingen, E., Hadi, F. (2012). Molecular identification of hydroxylysine kinase and of ammoniophospholyases acting on 5-phosphohydroxy-L-lysine and phosphoethanolamine. *J. Biol. Chem., 287*, 7246-55. ↗

Editions

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