Phosphoenolpyruvate + H2O <=> 2-Phospho-D-glycerate

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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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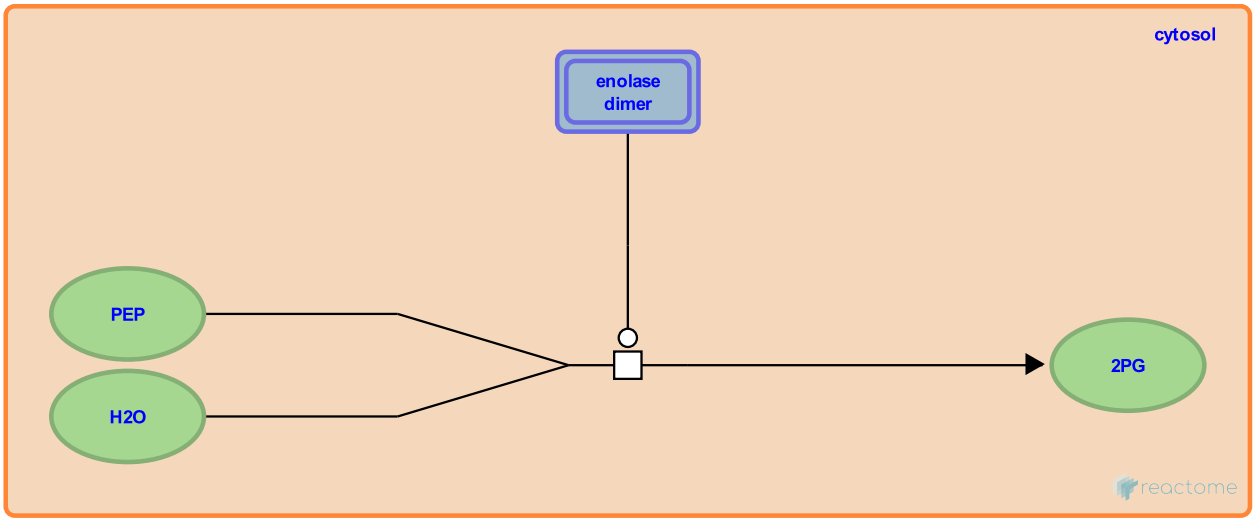
Stable identifier: R-HSA-70494

Type: transition

Compartments: cytosol



Cytosolic enolase dimer catalyzes the reversible reaction of phosphoenolpyruvate and water to form 2-phosphoglycerate. Three enolase isozymes have been purified and biochemically characterized. The alpha isoform is widely expressed (Giallongo et al. 1986). The beta isoform is expressed in muscle. Evidence for its function in vivo in humans comes from studies of a patient in whom a point mutation in the gene encoding the enzyme was associated specifically with reduced enolase activity in muscle extracts, and with other symptoms consistent with a defect in glycolysis (Comi et al. 2001). The gamma isoform of human enolase is normally expressed in neural tissue. It is not known to have distinctive biochemical functions, but is of possible clinical interest as a marker of some types of neuroendocrine and lung tumors (McAleese et al. 1988). Verma and Kurl (1993) identifed a possible fourth isoform, a "lung-specific" enolase whose expression is increased in response to dexamethasone treatment. The protein has not been biochemically characterized, however, nor have the levels of mRNA and protein in other tissues been examined. Thus, the observation that this protein is particularly similar in its predicted amino acid sequence to a duck crystallin (Wistow et al. 1988) raises the possibility that its normal function is unrelated to glycolysis.

Literature references

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Editions

2008-09-10	Reviewed	Harris, RA.