

PCK2 phosphorylates OA to yield PEP

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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

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- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph data-base: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968.

Reactome database release: 88

This document contains 1 reaction (see Table of Contents)

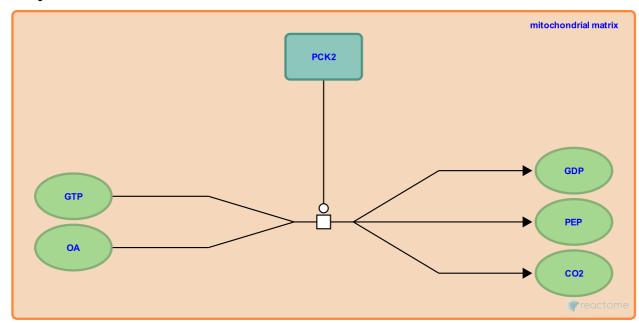
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PCK2 phosphorylates OA to yield PEP **对**

Stable identifier: R-HSA-372819

Type: transition

Compartments: mitochondrial matrix



PCK2 (phosphoenolcarboxykinase), located in the mitochondrial matrix, catalyzes the physiologically irreversible reaction of oxaloacetate (OA) and GTP to form phosphoenolpyruvate (PEP), GDP, and CO2 (Modaressi et al. 1996, 1998).

Literature references

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Brechtel, K., Christ, B., Modaressi, S., Jungermann, K. (1998). Human mitochondrial phosphoenolpyruvate carboxykinase 2 gene. Structure, chromosomal localization and tissue-specific expression. *Biochem J*, 333, 359-66.

Editions

2008-09-10	Reviewed	Harris, RA.
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