carbovir diphosphate + ATP => carbovir triphosphate + ADP

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20/09/2019

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

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. ↗

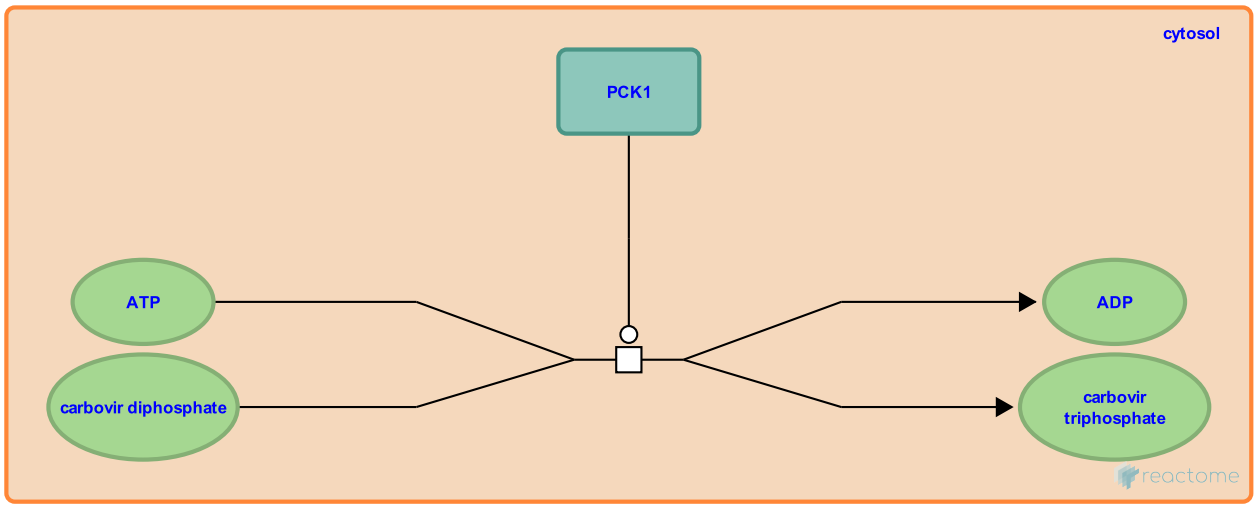
carbovir diphosphate + ATP => carbovir triphosphate + ADP ↗

Stable identifier: R-HSA-2162096

Type: transition

Compartments: cytosol

Inferred from: carbovir diphosphate + ATP => carbovir triphosphate + ADP (Rattus norvegicus)



Cytosolic PCK1 (phosphoenolpyruvate carboxykinase 1) catalyzes the reaction of carbovir diphosphate and ATP to form carbovir triphosphate and ADP. The activity of human PCK1 and relative inactivity of human nucleoside diphosphate kinase are inferred from the properties of the purified rat and bovine enzymes in vitro (Miller et al. 1992).

Literature references

Miller, WH., Daluge, SM., Garvey, EP., Hopkins, S., Reardon, JE., Boyd, FL. et al. (1992). Phosphorylation of carbovir enantiomers by cellular enzymes determines the stereoselectivity of antiviral activity. *J Biol Chem, 267*, 21220-4. ↗

Editions

2012-03-14	Authored	D'Eustachio, P.
2012-03-16	Edited	D'Eustachio, P.
2012-03-16	Reviewed	Jassal, B.