Casein kinase II phosphorylates PTEN

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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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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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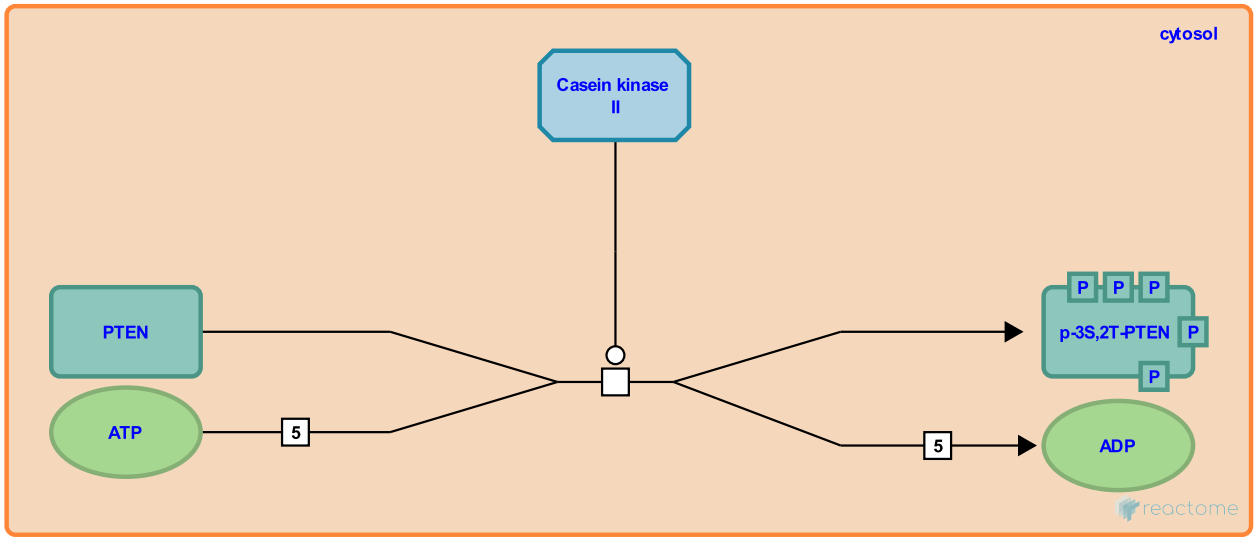
Stable identifier: R-HSA-8850945

Type: transition

Compartments: cytosol



Casein kinase II (CK2) constitutively phosphorylates the C-terminal tail of PTEN on serine and threonine residues S370, S380, T382, T383 and S385. S370 and S385 are the main CK2 phosphorylation sites in PTEN (Torres and Pulido 2001, Miller et al. 2002). CK2-mediated phosphorylation increases PTEN protein stability (Torres and Pulido 2001) but results in ~30% reduction in PTEN lipid phosphatase activity (Miller et al. 2002).

Literature references

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Lane, WS., Miller, SJ., Seldin, DC., Neel, BG., Lou, DY. (2002). Direct identification of PTEN phosphorylation sites. *FEBS Lett., 528*, 145-53. ↗

Editions

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