AKT1 E17K mutant phosphorylates caspase-9

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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. ↗

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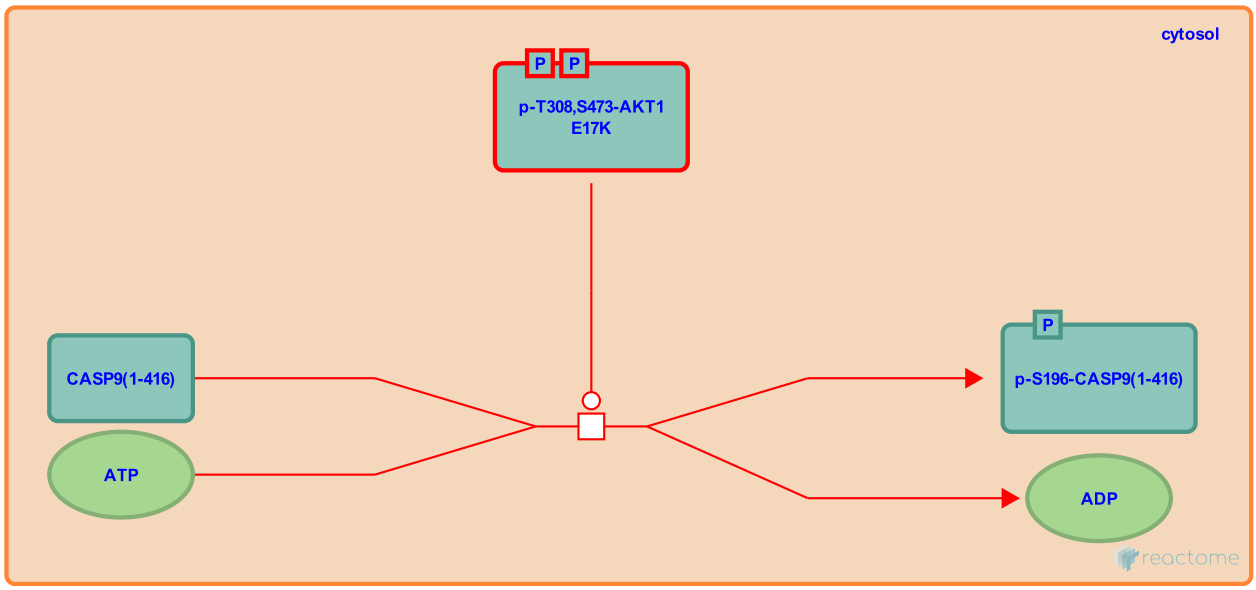
Stable identifier: R-HSA-2399985

Type: transition

Compartments: cytosol

Diseases: cancer



AKT1 E17K gain-of-function mutant is expected to phosphorylate caspase-9 (CASP9), like the wild-type AKT (Cardone et al. 1998), but this has not been experimentally tested.

Literature references

Cardone, MH., Roy, N., Stennicke, HR., Salvesen, GS., Franke, TF., Stanbridge, E. et al. (1998). Regulation of cell death protease caspase-9 by phosphorylation. *Science, 282*, 1318-21. ↗

Editions

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