AKT phosphorylates MKRN1

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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. ↗

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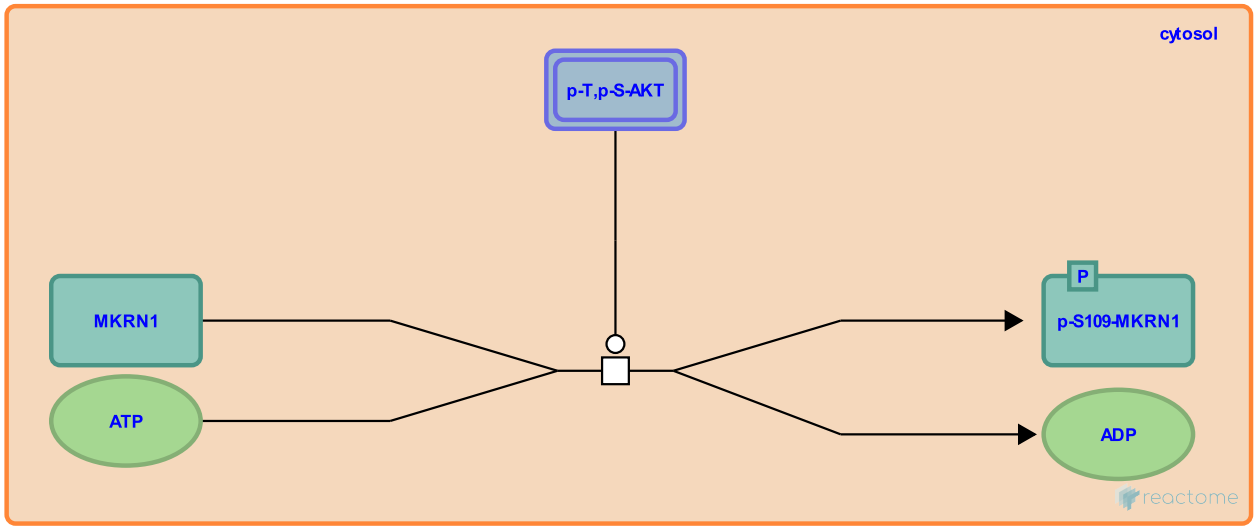
Stable identifier: R-HSA-8948757

Type: transition

Compartments: cytosol



AKT1 (and possibly AKT2 and AKT3), activated in response to EGF treatment, phosphorylates MKRN1, an E3 ubiquitin ligase, on serine residue S109. AKT-mediated phosphorylation results in stabilization of MKRN1, protecting it from ubiquitination and proteasome-mediated degradation (Lee et al. 2015).

Literature references

Hewitt, SM., Han, HJ., Lee, MS., Lee, C., Chung, JY., Kim, JH. et al. (2015). PI3K/AKT activation induces PTEN ubiquitination and destabilization accelerating tumourigenesis. *Nat Commun, 6*, 7769. ↗

Editions

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