MAP2K6 phosphorylates PIP4K2B

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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., 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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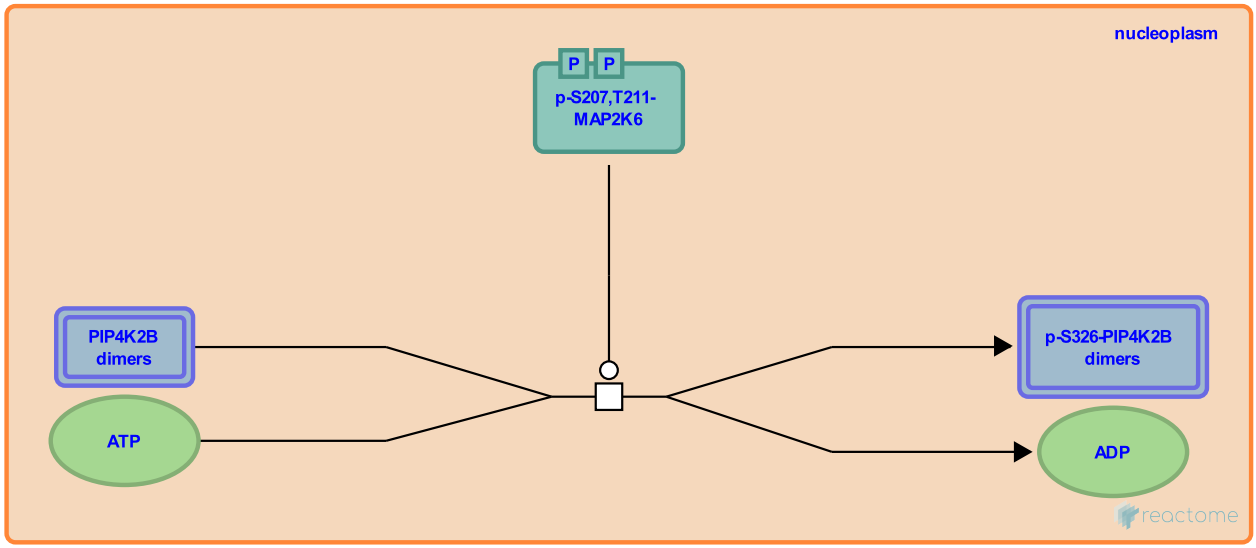
Stable identifier: R-HSA-8877691

Type: transition

Compartments: nucleoplasm



Under conditions of cellular stress, such as increased level of reactive oxygen species, MAP2K6 (MKK6), and possibly other kinases of the p38 MAPK family, phosphorylates PIP4K2B at serine residue S326. Threonine residue T322 of PIP4K2B is also phosphorylated under stress conditions, but the responsible kinase is not known. MAP2K6 may also phosphorylate PIP4K2A, but not PIP4K2C (Kuene et al. 2012).

Literature references

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Editions

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