MAPKs phosphorylate PP2A

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02/05/2024

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. ↗

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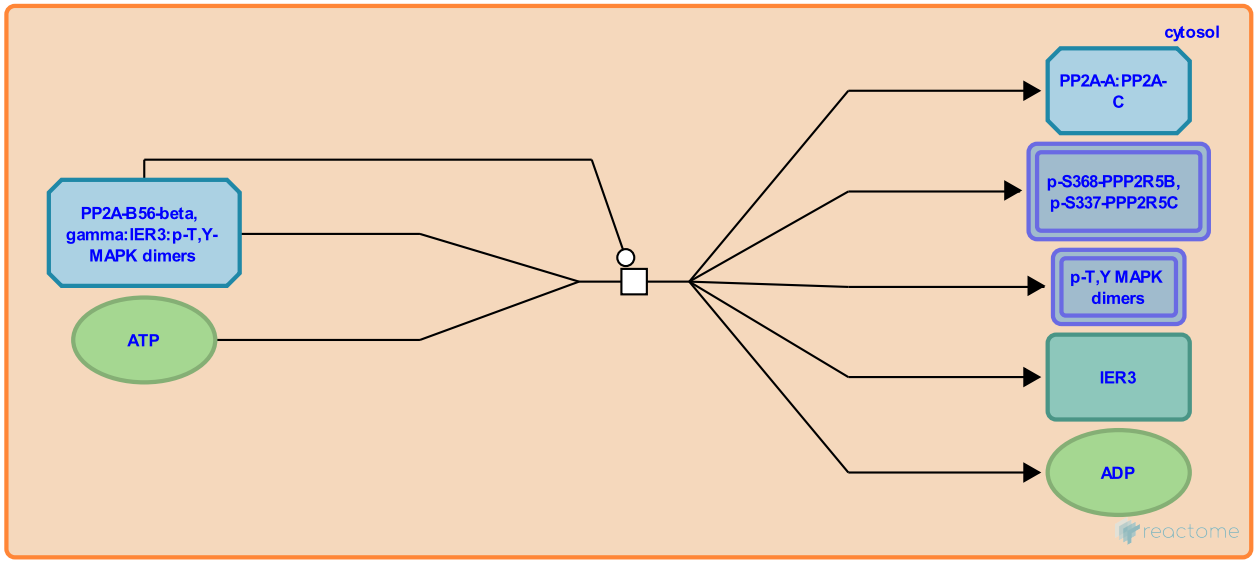
Stable identifier: R-HSA-6811454

Type: transition

Compartments: cytosol



Activated MAPK1 (ERK2) or MAPK3 (ERK1), recruited to the PP2A complex through IER3 (IEX-1), phosphorylate the regulatory subunit PPP2R5B (B56-beta) or PPP2R5C (B56-gamma) of the PP2A complex on serine residue S368 or S337, respectively. ERK-mediated phosphorylation of the PP2A regulatory subunits causes dissociation of the PP2A complex and prevents PP2A-mediated dephosphorylation of AKT1 (Letourneux et al. 2006, Rocher et al. 2007).

Literature references

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Editions

2015-12-22	Authored, Edited	Orlic-Milacic, M.
2016-02-08	Reviewed	Porteu, F.