

Phosphorylated MAPKs phosphorylate

ATF-2

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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.
- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph data-base: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968.

Reactome database release: 88

This document contains 1 reaction (see Table of Contents)

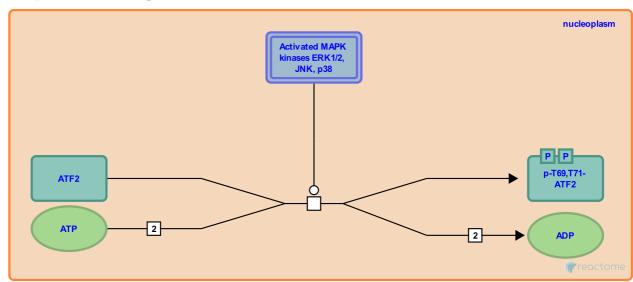
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Stable identifier: R-HSA-168053

Type: transition

Compartments: nucleoplasm



the Raf-MEK-ERK pathway induces phosphorylation of ATF2 Thr71, whereas subsequent ATF2 Thr69 phosphorylation requires the Ral-RalGDS-Src-p38 pathway. Cooperation between ERK and p38 was found to be essential for ATF2 activation by these mitogens; the activity of p38 and JNK/SAPK in growth factor-stimulated fibroblasts is insufficient to phosphorylate ATF2 Thr71 or Thr69 + 71 significantly by themselves, while ERK cannot dual phosphorylate ATF2 Thr69 + 71 efficiently.

At the beginning of this reaction, 1 molecule of 'ATP', and 1 molecule of 'ATF-2' are present. At the end of this reaction, 1 molecule of 'ADP', and 1 molecule of 'ATF-2-P' are present.

This reaction is mediated by the 'protein kinase activity' of 'MAPK1-P'.

Literature references

Editions

2005-11-10	Authored	Luo, F.
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2009-12-16	Edited, Revised	Shamovsky, V.