Autophosphorylation and activation of MEKK1

Garapati, P V., Niarakis, A., Roncagalli, R.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

05/05/2024

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. ↗

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

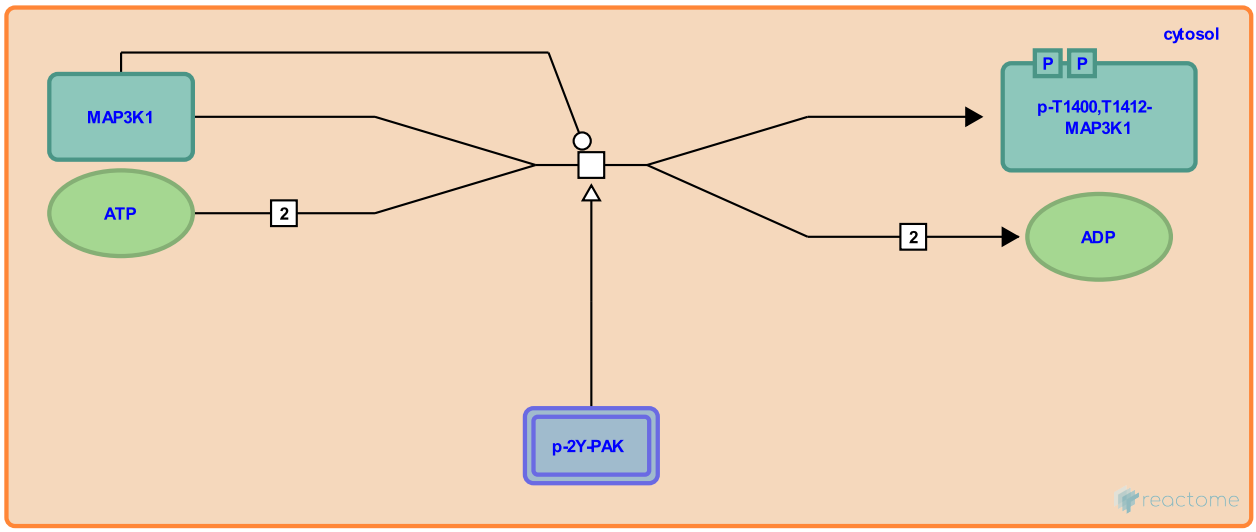
Autophosphorylation and activation of MEKK1 ↗

Stable identifier: R-HSA-2730887

Type: transition

Compartments: cytosol

Inferred from: Autophosphorylation and activation of Mekk1 (Mus musculus)



FCERI aggregation has been shown to activate JNK as well as protein kinases upstream of JNK, such as MEKK1 (Mitogen-activated protein kinase/ERK Kinase Kinase-1) and JNK kinase (JNKK). PAK has been shown to be the upstream kinase involved in the activation of MEKK1, however no direct phosphorylation of MEKK1 by PAK is observed. Two threonine residues at positions 1400 and 1412 (analogous to 1381 and 1393 in mouse) in the activation loop of MEKK1 between the kinase subdomains VII and VIII are essential for its catalytic activity. The catalytic domain of MEKK1 is able to autophosphorylate these residues, enhancing its own activity.

Editions

2012-08-22	Edited	Garapati, P V.
2012-12-21	Authored	Niarakis, A.
2013-02-13	Reviewed	Roncagalli, R.