Tpl2 phosphorylates Mek1, Sek1

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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 database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

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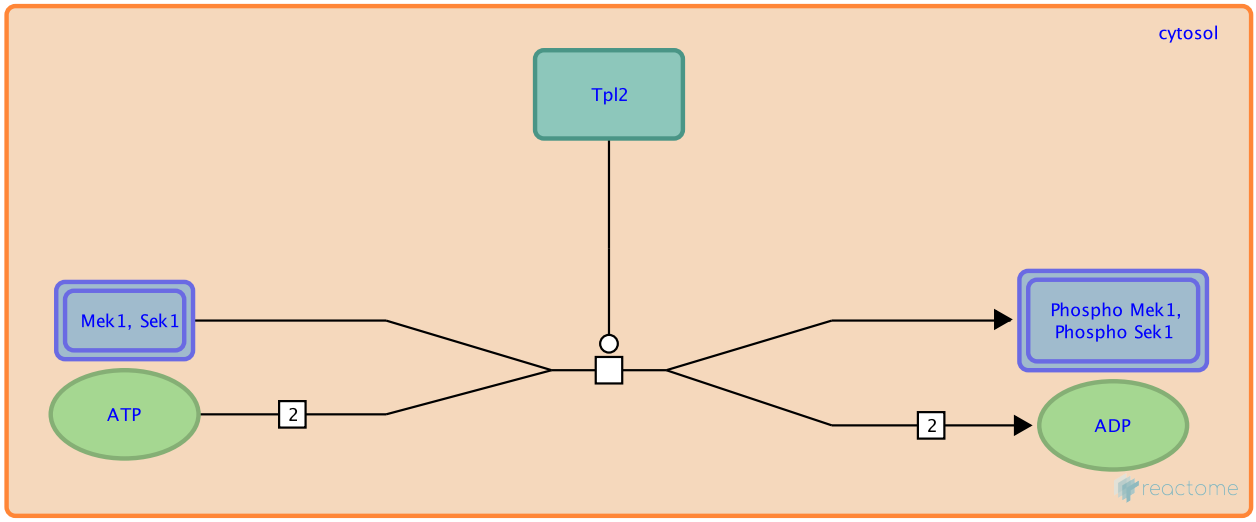
Stable identifier: R-NUL-451681

Type: transition

Compartments: cytosol



Tpl2 (also known as Cot, officially known as MAP3K8) is constitutively bound to NFKB p105 (p105) which inhibits its MEK kinase activity in resting cells. Proteolysis of p105 frees Tpl2 from p105 and allows subsequent phosphorylation and activation of MEK1. Tpl2 can also activate SEK1 (MAP2K4). Phosphorylation of Tpl-2 is believed to play a role in its activation (Cho et al, 2005; Robinson et al. 2007).

Positions of phosphorylations represented here are inferred from general experimental data (Zheng & Guan, 1994).

Literature references

Salmeron, A., Ahmad, TB., Carlile, GW., Pappin, D., Narsimhan, RP., Ley, SC. (1996). Activation of MEK-1 and SEK-1 by Tpl-2 proto-oncoprotein, a novel MAP kinase kinase kinase. *EMBO J, 15*, 817-26. ↗

Editions

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