Activated phosphorylated TAK1 kinase phosphorylates and activates IRD5

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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. ↗

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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. ↗

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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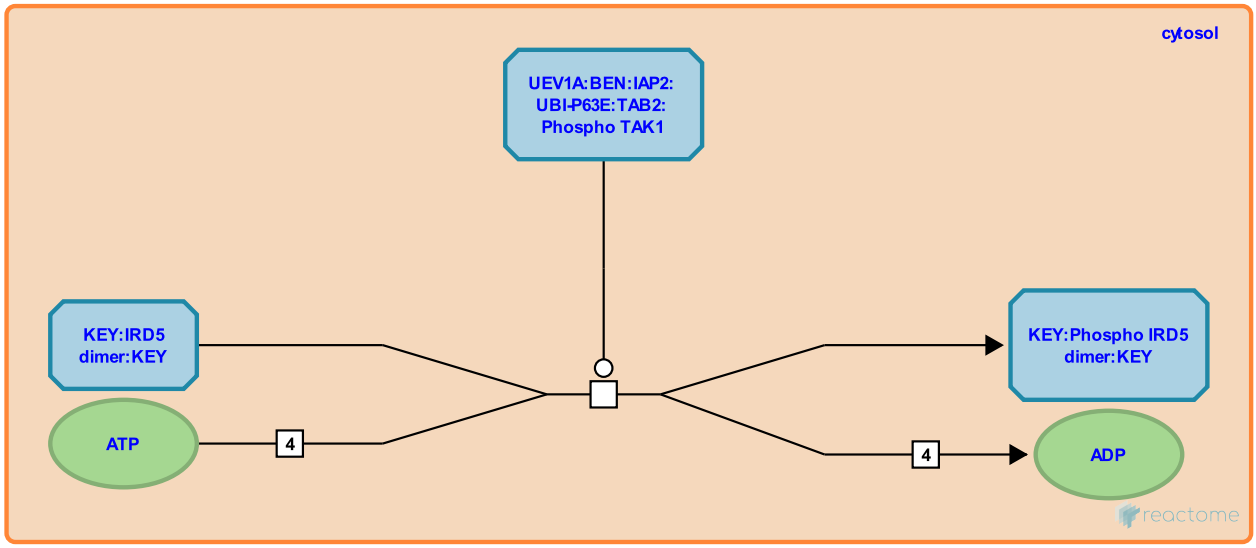
Stable identifier: R-DME-209240

Type: transition

Compartments: cytosol



IRD5 is phosphorylated and activated by phosphorylated TAK1 kinase at residues Thr217 and Ser221 in the activation loop.

Literature references

Schneider, D., Silverman, N., Erlich, RL., Bernstein, E., Zhou, R., Hunter, M. et al. (2003). Immune activation of NF-kappaB and JNK requires Drosophila TAK1. *J Biol Chem, 278*, 48928-34. ↗

Editions

2007-07-11	Authored	Williams, MG.
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