K63polyUb-TAK1 autophosphorylates

Garapati, P V., Geijtenbeek, TB.

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

04/05/2024

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

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Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

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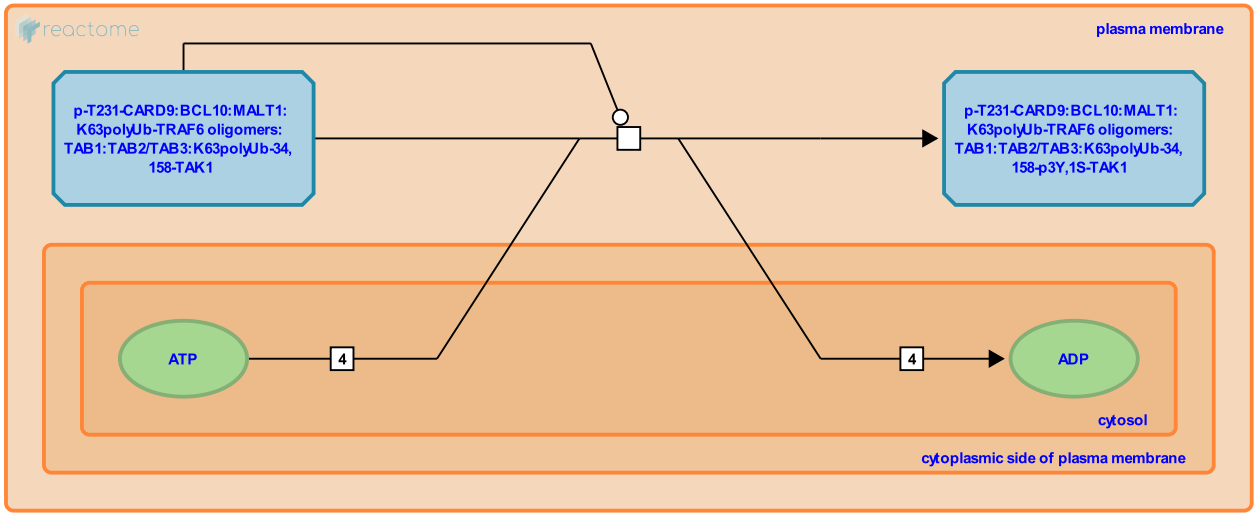
Stable identifier: R-HSA-5607732

Type: transition

Compartments: plasma membrane, cytosol



TAK1-binding protein 1 (TAB1) is a TAK1-interacting protein and induces TAK1 (Transforming growth factor beta-associated kinase 1) kinase activity through promoting autophosphorylation of key serine/threonine sites of the kinase activation loop. There are four phosphorylation sites in the activation loop and analysis of these site mutants indicate that autophosphorylation of S192, is followed by sequential phosphorylation of T178, T187, and finally T184 (Scholz et al. 2010).

Literature references

Thali, RF., Scholz, R., Neumann, D., Sidler, CL., Winssinger, N., Cheung, PC. (2010). Autoactivation of transforming growth factor beta-activated kinase 1 is a sequential bimolecular process. *J. Biol. Chem., 285*, 25753-66.

Editions

2014-07-14	Authored, Edited	Garapati, P V.
2014-09-02	Reviewed	Geijtenbeek, TB.