

CAMK2 binds MAP3K7

Kikuchi, A., Matthews, L., Rothfels, K.

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

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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. [↗](#)

Reactome database release: 74

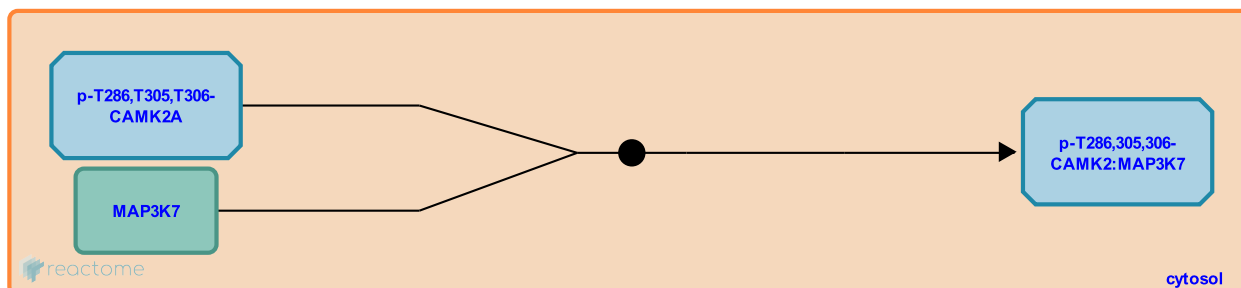
This document contains 1 reaction ([see Table of Contents](#))

CAMK2 binds MAP3K7 [↗](#)

Stable identifier: R-HSA-4332356

Type: binding

Compartments: cytosol



Several studies in *C. elegans* and vertebrates suggest that a TAK1-NLK kinase cascade regulates the activity of the canonical WNT signaling pathway (Ishitani et al, 1999; Meneghini et al, 1999; Shin et al, 1999; Rocheleau et al, 1999). Activation of this MAPK cascade depends on CAMK2 activity downstream of WNT5a non-canonical signaling (Ishitani et al, 2003a, b). CAMK2 co-precipitates with TAK1/MAP3K7 upon co-transfection in HEK293 cells and calcium signaling activates MAP3K7 in a CAMK2-dependent manner (Ishitani et al, 2003a).

Literature references

- Rocheleau, CE., Yasuda, J., Shin, TH., Lin, R., Sawa, H., Okano, H. et al. (1999). WRM-1 activates the LIT-1 protein kinase to transduce anterior/posterior polarity signals in *C. elegans*. *Cell*, 97, 717-26. [↗](#)
- Ishitani, T., Kishida, S., Hyodo-Miura, J., Ueno, N., Yasuda, J., Waterman, M. et al. (2003). The TAK1-NLK mitogen-activated protein kinase cascade functions in the Wnt-5a/Ca(2+) pathway to antagonize Wnt/beta-catenin signaling. *Mol. Cell. Biol.*, 23, 131-9. [↗](#)
- Ishitani, T., Ninomiya-Tsuji, J., Matsumoto, K. (2003). Regulation of lymphoid enhancer factor 1/T-cell factor by mitogen-activated protein kinase-related Nemo-like kinase-dependent phosphorylation in Wnt/beta-catenin signaling. *Mol. Cell. Biol.*, 23, 1379-89. [↗](#)
- Shin, TH., Yasuda, J., Rocheleau, CE., Lin, R., Soto, M., Bei, Y. et al. (1999). MOM-4, a MAP kinase kinase kinase-related protein, activates WRM-1/LIT-1 kinase to transduce anterior/posterior polarity signals in *C. elegans*. *Mol. Cell*, 4, 275-80. [↗](#)
- Meneghini, MD., Ishitani, T., Carter, JC., Hisamoto, N., Ninomiya-Tsuji, J., Thorpe, CJ. et al. (1999). MAP kinase and Wnt pathways converge to downregulate an HMG-domain repressor in *Caenorhabditis elegans*. *Nature*, 399, 793-7. [↗](#)

Editions

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