

# **TAB2 binds to ubiquitinated IAP2:BEN:UEV1A E3 ligase complex and activates TAK1 kinase**

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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: 88

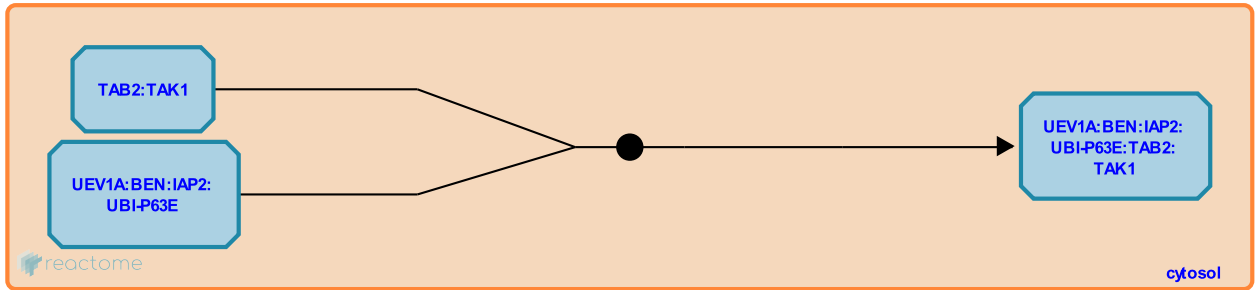
This document contains 1 reaction ([see Table of Contents](#))

**TAB2 binds to ubiquitinated IAP2:BEN:UEV1A E3 ligase complex and activates TAK1 kinase** ↗

**Stable identifier:** R-DME-209289

**Type:** binding

**Compartments:** cytosol



TAB2 in complex with TAK1 kinase binds to the ubiquitin chains emanating from the Apoptosis 2 Inhibitor (IAP2):Bendless (BEN):UEV1A E3 ligase complex. The formation of an E3 ligase:TAB2:TAK1 complex may cause conformational changes to the catalytic domain of TAK1 thus inducing its kinase activity.

**Literature references**

Liao, DS., Silverman, N., Chung, Y., Hong, M., Zhou, R., Chen, ZJ. et al. (2005). The role of ubiquitination in Drosophila innate immunity. *J Biol Chem*, 280, 34048-55. ↗

Leulier, F., Lhocine, N., Lemaitre, B., Meier, P. (2006). The Drosophila inhibitor of apoptosis protein DIAP2 functions in innate immunity and is essential to resist gram-negative bacterial infection. *Mol Cell Biol*, 26, 7821-31. ↗

**Editions**

2007-07-11	Authored	Williams, MG.
2008-06-20	Reviewed	Lemaitre, B., Silverman, N.
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