

# K63polyUb-TRAF6 ubiquitinates TAK1

Garapati, P V., Geijtenbeek, TB.

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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](#). For more information see our [license](#).

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

- 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

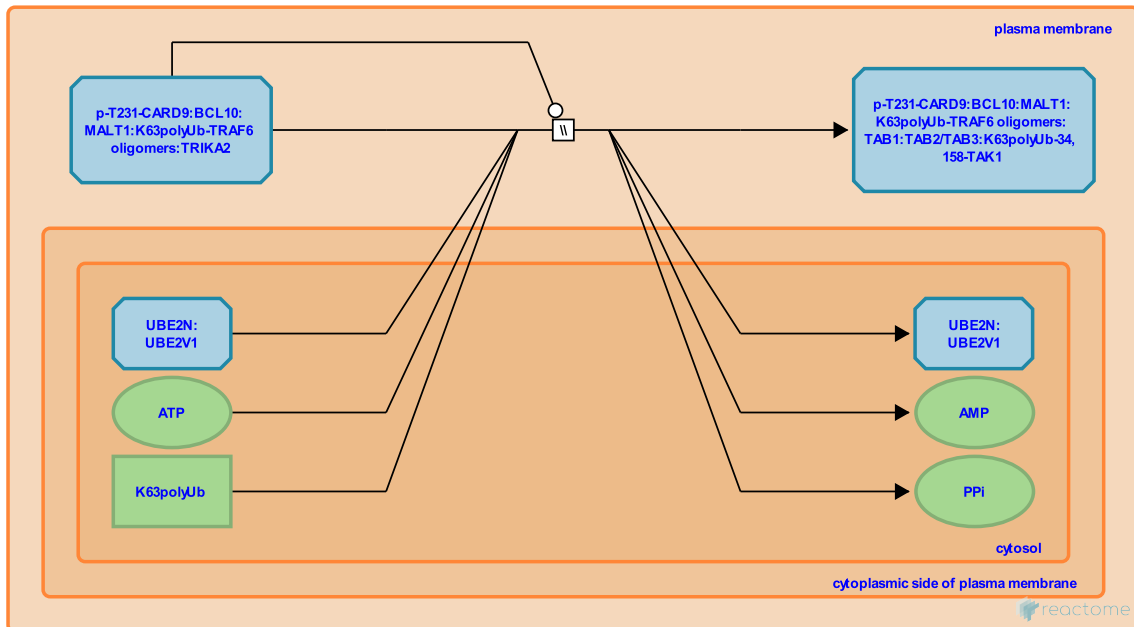
This document contains 1 reaction ([see Table of Contents](#))

## K63polyUb-TRAF6 ubiquitinates TAK1 ↗

**Stable identifier:** R-HSA-5607757

**Type:** omitted

**Compartments:** plasma membrane, cytosol



TAK1-binding protein 2 (TAB2), or its homologue TAB3, binds preferentially to K63-linked polyubiquitin chains in TRAF6 and links TRAF6 (TNF receptor-associated factor 6) to TAK1 (Transforming growth factor beta-associated kinase 1). TRAF6 ubiquitinates TAK1 on K34 and K158 and this triggers conformational changes in TAK1 that lead to autophosphorylation and activation (Fan et al. 2010, Hamidi et al. 2011).

### Literature references

Landström, M., Barluenga, S., von Bulow, V., Winssinger, N., Hamidi, R., Heldin, CH. et al. (2012). Polyubiquitination of transforming growth factor  $\beta$  (TGF $\beta$ )-associated kinase 1 mediates nuclear factor- $\kappa$ B activation in response to different inflammatory stimuli. *J. Biol. Chem.*, 287, 123-33. ↗

Xie, M., Fan, Y., Fu, S., Zhang, H., Shi, Y., Mao, R. et al. (2010). Lysine 63-linked polyubiquitination of TAK1 at lysine 158 is required for tumor necrosis factor alpha- and interleukin-1beta-induced IKK/NF-kappaB and JNK/AP-1 activation. *J. Biol. Chem.*, 285, 5347-60. ↗

### Editions

2014-07-14

Authored, Edited

Garapati, P V.

2014-09-02

Reviewed

Geijtenbeek, TB.