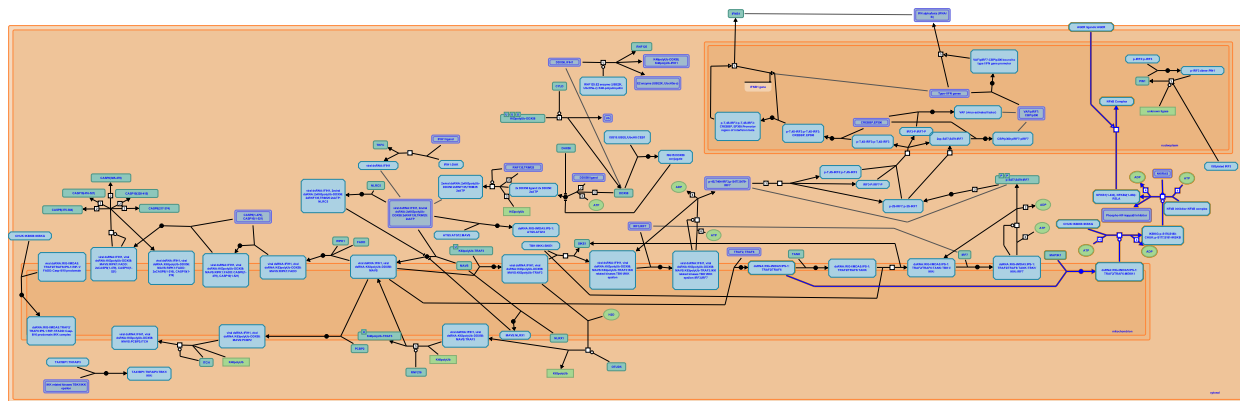


TRAF6 mediated NF- κ B activation



Akira, S., D'Eustachio, P., Fitzgerald, KA., Garapati, P V., Jin, L., Kawai, T., Mocarski, ES.,
Napetschnig, J., Shamovsky, V., Upton, JW., Wu, J.

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 Inter-
national \(CC BY 4.0\) License](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://creativecommons.org/licenses/by/4.0/).

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. [↗](#)

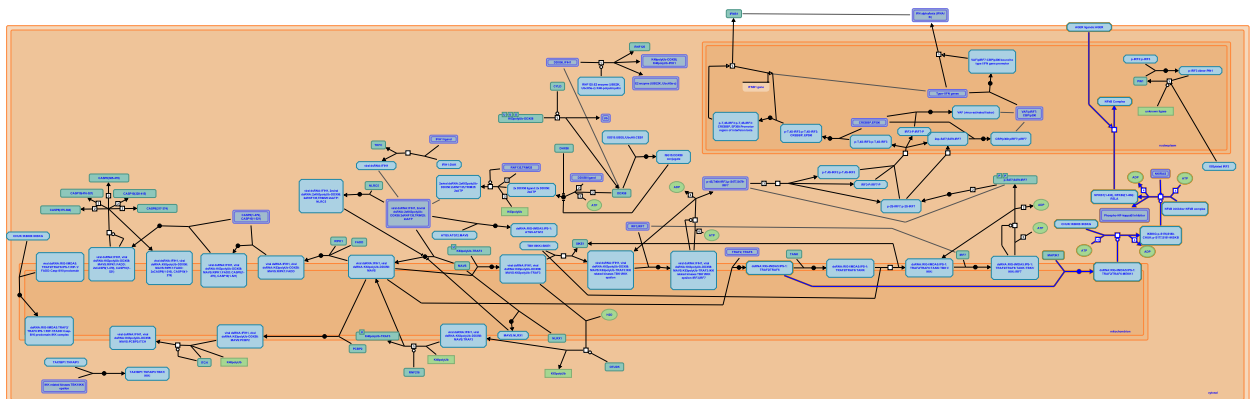
Reactome database release: 71

This document contains 1 pathway and 4 reactions ([see Table of Contents](#))

TRAF6 mediated NF- κ B activation ↗

Stable identifier: R-HSA-933542

Compartments: mitochondrial outer membrane, cytosol



reactome

The TRAF6/TAK1 signal activates a canonical IKK complex, resulting in the activation of NF- κ B as well as MAPK cascades leading to the activation of AP-1. Although TRAF6/TAK1 has been implicated in Toll like receptor (TLR) mediated cytokine production, the involvement of these molecules in the regulation of type I IFN induction mediated by RIG-I/MDA5 pathway is largely unknown. According to the study done by Yoshida et al RIG-I/IPS-1 pathway requires TRAF6 and MAP3K, MEKK1 to activate NF- κ B and MAP Kinases for optimal induction of type I IFNs.

Literature references

Yoshida, R., Takaesu, G., Yoshida, H., Okamoto, F., Yoshioka, T., Choi, Y. et al. (2008). TRAF6 and MEKK1 play a pivotal role in the RIG-I-like helicase antiviral pathway. *J Biol Chem*, 283, 36211-20. ↗

Editions

2010-08-02	Authored, Edited	Garapati, P V.
2010-10-30	Reviewed	Akira, S., Kawai, T.

Interaction of MEKK1 with TRAF6 ↗

Location: [TRAF6 mediated NF-kB activation](#)

Stable identifier: R-HSA-933528

Type: binding

Compartments: cytosol, mitochondrial outer membrane

Inferred from: [Interaction of MEKK1 with TRAF6 \(Mus musculus\)](#)