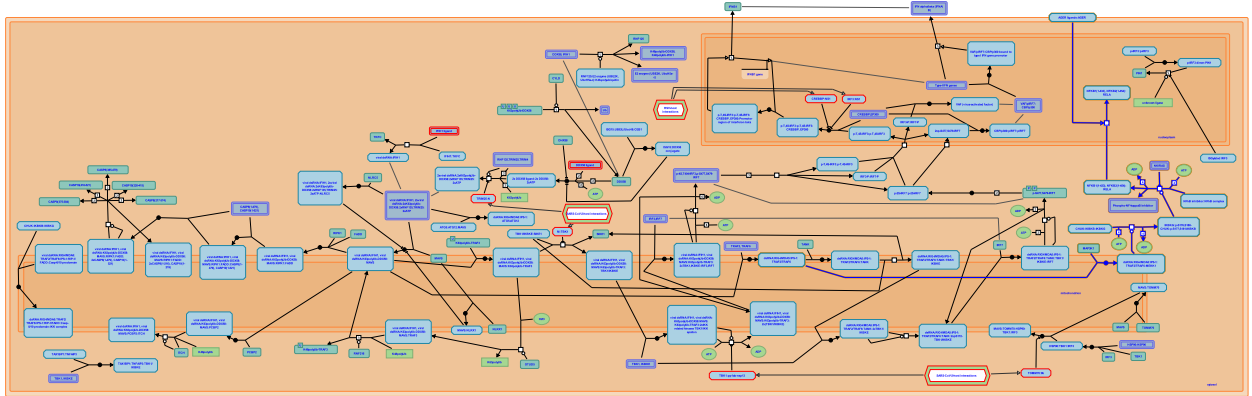


TRAF6 mediated NF- κ B activation



Akira, S., D'Eustachio, P., Fitzgerald, KA., Garapati, P V., Jin, L., Kawai, T., Mocarski, ES.,
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This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the [Reactome Textbook](https://reactome.org/textbook/).

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.

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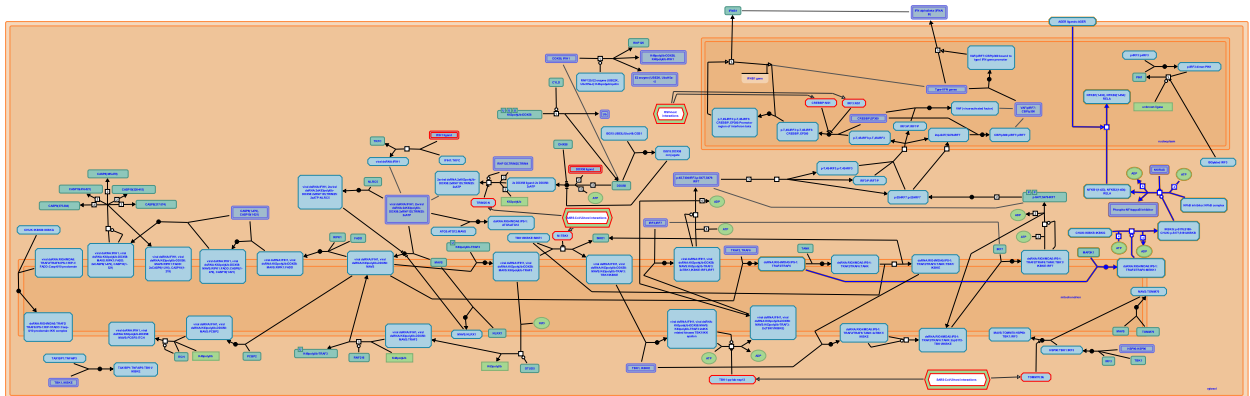
Reactome database release: 88

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

TRAF6 mediated NF-kB 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-κB 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-κB and MAP Kinases for optimal induction of type I IFNs.

Literature references

Kobayashi, T., Kawai, T., Yoshioka, T., Yoshida, H., Takaesu, G., Yoshida, R. 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 ↗

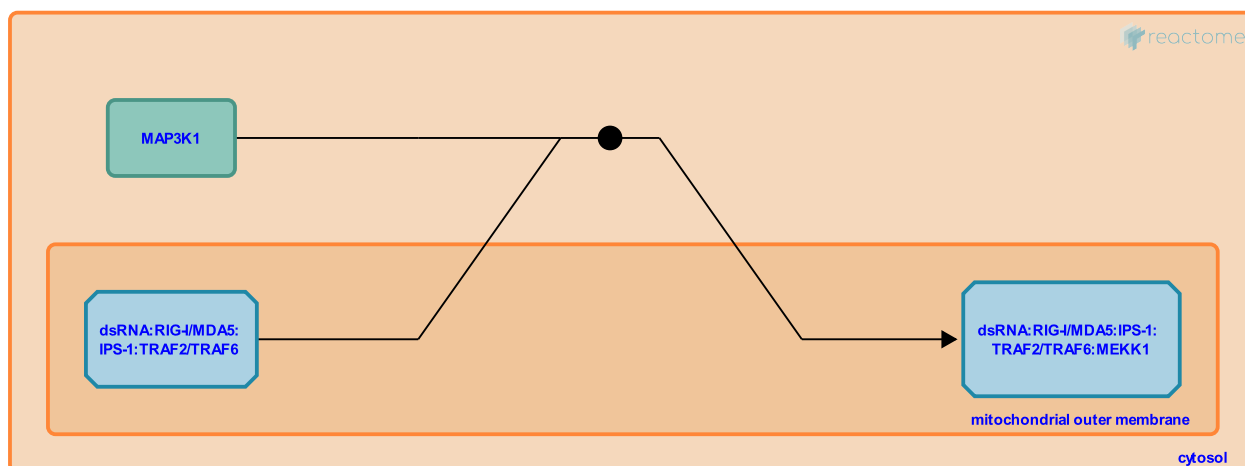
Location: [TRAF6 mediated NF-kB activation](#)

Stable identifier: R-HSA-933528

Type: binding

Compartments: cytosol, mitochondrial outer membrane

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



TRAF6 requires MEKK1 (MAP3K1) to activate NF-kB and MEKK1 may interact with TRAF6, which in turn contributes to the activation of IKK and MAPKK, leading to the activation of NF-kB and AP-1. (Yoshida et al)

Followed by: [Activation of IKK by MEKK1](#)

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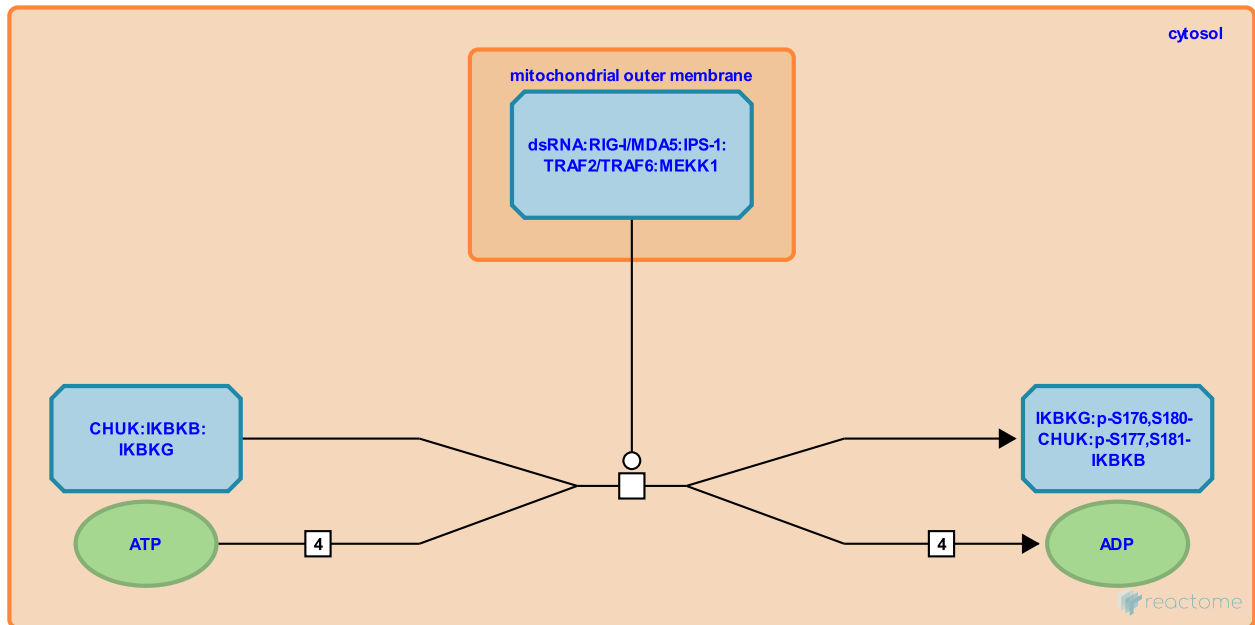
Activation of IKK by MEKK1 ↗

Location: TRAF6 mediated NF- κ B activation

Stable identifier: R-HSA-933530

Type: transition

Compartments: cytosol, mitochondrial outer membrane



In Human, IKKs - I κ B kinase (IKK) complex serves as the master regulator for the activation of NF- κ B by various stimuli. It contains two catalytic subunits, IKK alpha and IKK beta, and a regulatory subunit, IKKgamma/NEMO. The activation of IKK complex and NF κ B mediated antiviral response are dependent on the phosphorylation of IKK alpha/beta at its activation loop and the ubiquitination of NEMO.[Solt et al 2009]; [Li et al 2002]. NEMO ubiquitination by TRAF6 is required for optimal activation of IKKalpha/beta; it's remained unclear if NEMO subunit undergoes K63-linked or linear ubiquitination.

This basic trimolecular complex is referred to as the IKK complex. Each catalytic IKK subunit has a N-term kinase domain a leucine zipper (LZ) motifs, a helix-loop-helix (HLH) and a C-ter NEMO binding domain (NBD). IKK catalytic subunits are dimerized through their LZ motifs.

IKK beta is the major IKK catalytic subunit for NF- κ B activation. MEKK1 can activate both IKK-alpha (IKKA) and IKK-beta (IKKB) in vivo. MEKK1 phosphorylates Ser-176 and Ser-180 in IKKA and Ser-177 and Ser-181 in IKKB activation loop and thus activate the IKK kinase activity, leading to the I κ B alpha phosphorylation and NF- κ B activation.

Preceded by: [Interaction of MEKK1 with TRAF6](#)

Followed by: [Active IKK Complex phosphorylates NF-kappa-B inhibitor](#)

Literature references

- Marcu, KB., Li, X., Hanidu, A., Savitt, A., Aro, P., Mische, S. et al. (2002). IKKalpha, IKKbeta, and NEMO/IKKgamma are each required for the NF-kappa B-mediated inflammatory response program. *J Biol Chem*, 277, 45129-40. ↗
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Editions

2010-08-02	Authored, Edited	Garapati, P V.
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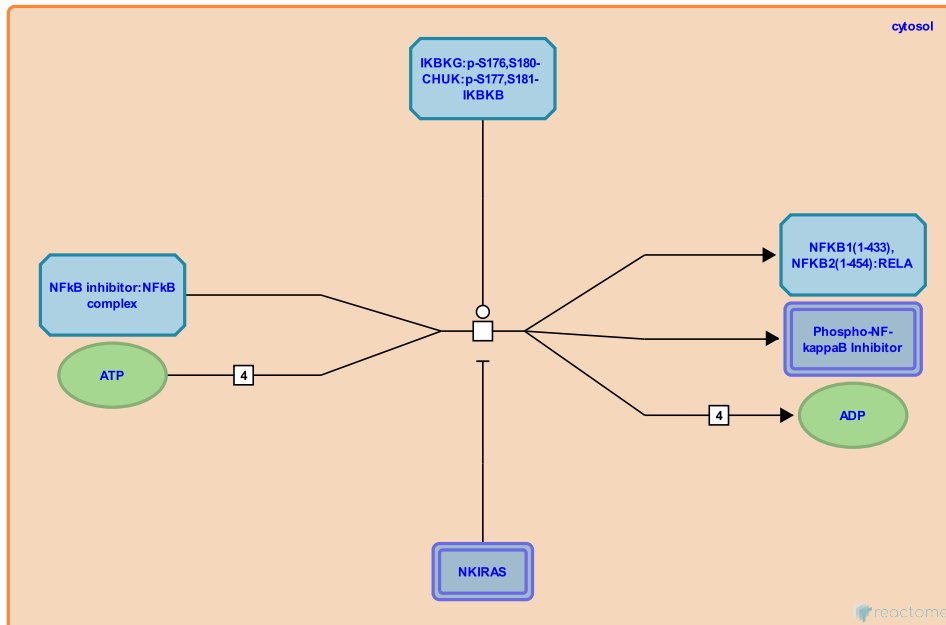
Active IKK Complex phosphorylates NF-kappa-B inhibitor ↗

Location: TRAF6 mediated NF-kB activation

Stable identifier: R-HSA-168140

Type: transition

Compartments: cytosol



In human, IκBs (NFKBIA, NFKBIB or NFKBIE) are inhibitory proteins that sequesters NF-kappa-B in the cytoplasm, by masking a nuclear localization signal, located just at the C-terminal end of the RelA (p65) subunit of the RelA:NFKB1 heterodimer.

A key event in NF-kappa-B activation involves phosphorylation of IκB by an IκB kinase (IKK). The phosphorylation and ubiquitination of IκB kinase complex is mediated by two distinct pathways, either the classical or alternative pathway. In the classical NF-kappa-B signaling pathway, the activated IKK (IκB kinase) complex, predominantly acting through IKK beta (IKKb, IKBKB) in an IKK gamma (IKKγ, NEMO)-dependent manner, catalyzes the phosphorylation of IκBs (at sites equivalent to Ser32 and Ser36 of human NFKBIA (IκB-alpha) or Ser19 and Ser22 of NFKBIB (IκB-beta)). Once phosphorylated, IκB undergoes ubiquitin-mediated degradation, releasing NF-kappa-B.

Preceded by: Activation of IKK by MEKK1

Followed by: NF-kappa-B complex is transported from cytosol to nucleus

Literature references

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Editions

2009-09-29	Revised	Shamovsky, V.
2009-12-16	Edited	Shamovsky, V.
2011-12-08	Reviewed	D'Eustachio, P.
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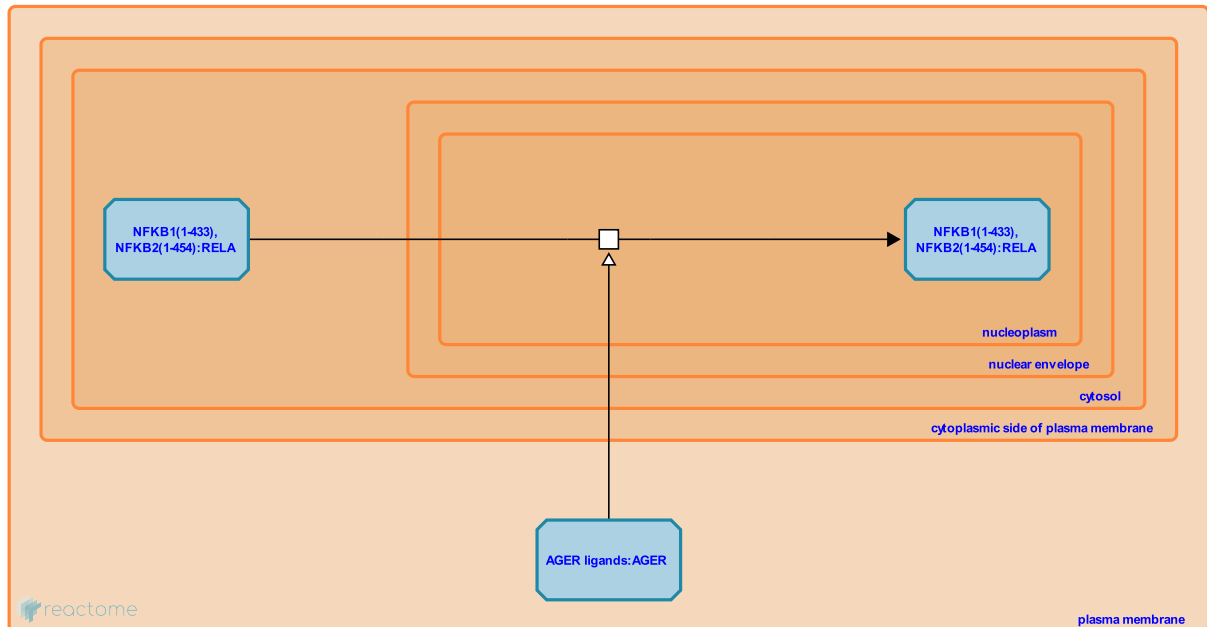
NF-kappa-B complex is transported from cytosol to nucleus ↗

Location: TRAF6 mediated NF-kB activation

Stable identifier: R-HSA-168166

Type: transition

Compartments: nucleoplasm, cytosol



Though the signaling cascade is unclear, several pieces of experimental data suggest that activation of AGER leads to sustained activation and upregulation of NFkappaB, measured as NFkappaB translocation to the nucleus, and increased levels of de novo synthesized NFkappaB.

NFkB is a family of transcription factors that play pivotal roles in immune, inflammatory, and antiapoptotic responses. There are five NF-kB/Rel family members, p65 (RelA), RelB, c-Rel, p50/p105 (NF-kappa-B1) and p52/p100 (NF-kappa-B2). All members of the NFkB family contain a highly conserved DNA-binding and dimerization domain called Rel-homology region (RHR). The RHR is responsible for homo- or heterodimerization. Therefore, NF-kappa-B exists in unstimulated cells as homo- or heterodimers; the most common heterodimer is p65/p50. NF-kappa-B is sequestered in the cytosol of unstimulated cells through the interactions with a class of inhibitor proteins called IkbBs, which mask the nuclear localization signal of NF-kB and prevent its nuclear translocation. Various stimuli induce the activation of the IkbB kinase (IKK) complex, which then phosphorylates IkbBs. The phosphorylated IkbBs are ubiquitinated and then degraded through the proteasome-mediated pathway. The degradation of IkbBs releases NF-kappa-B and it can be transported into nucleus where it induces the expression of target genes.

Preceded by: Active IKK Complex phosphorylates NF-kappa-B inhibitor

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2012-11-13	Reviewed	Fitzgerald, KA.
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2013-05-17	Edited	Shamovsky, V.
2013-05-22	Reviewed	Jin, L., Wu, J.
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