

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. [↗](#)
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- 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: 82

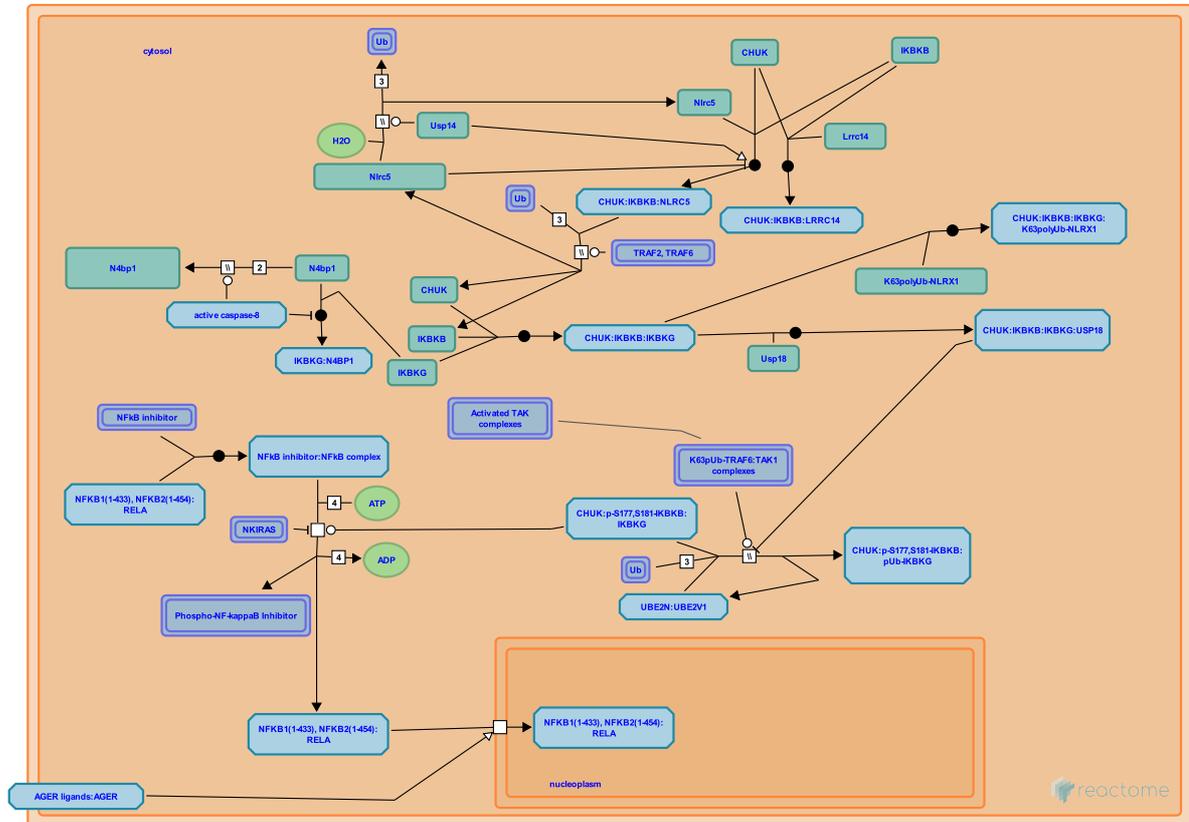
This document contains 2 pathways and 5 reactions ([see Table of Contents](#))

TAK1-dependent IKK and NF-kappa-B activation [↗](#)

Stable identifier: R-RNO-445989

Compartments: cytosol, nucleoplasm

Inferred from: [TAK1-dependent IKK and NF-kappa-B activation](#) (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

/electronic_inference_compara.html target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <http://www.pantherdb.org/about.jsp> target='NEW'><http://www.pantherdb.org/about.jsp>

CHUK, IKBKB and IKBKG form IKK complex ↗

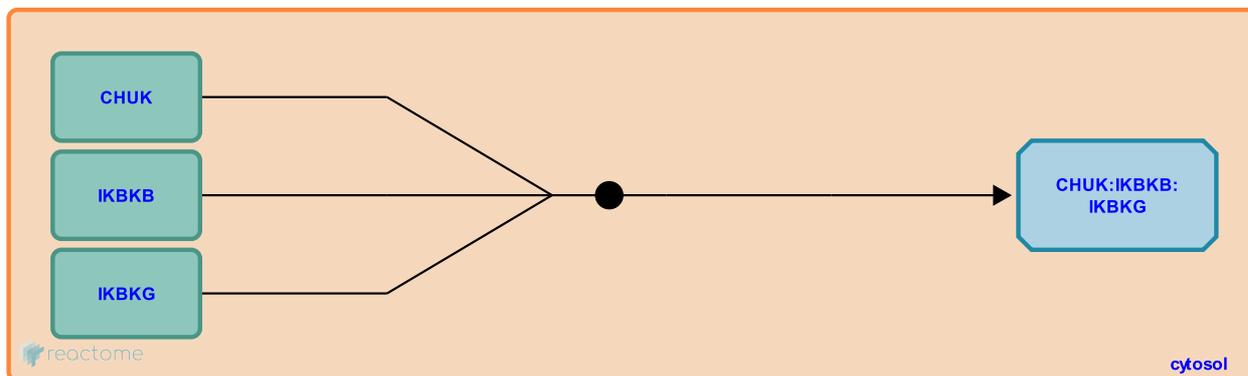
Location: [TAK1-dependent IKK and NF-kappa-B activation](#)

Stable identifier: R-RNO-5609665

Type: binding

Compartments: cytosol

Inferred from: [CHUK, IKBKB and IKBKG form IKK complex \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

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Ubiquitination of IKBKG by TRAF6 ↗

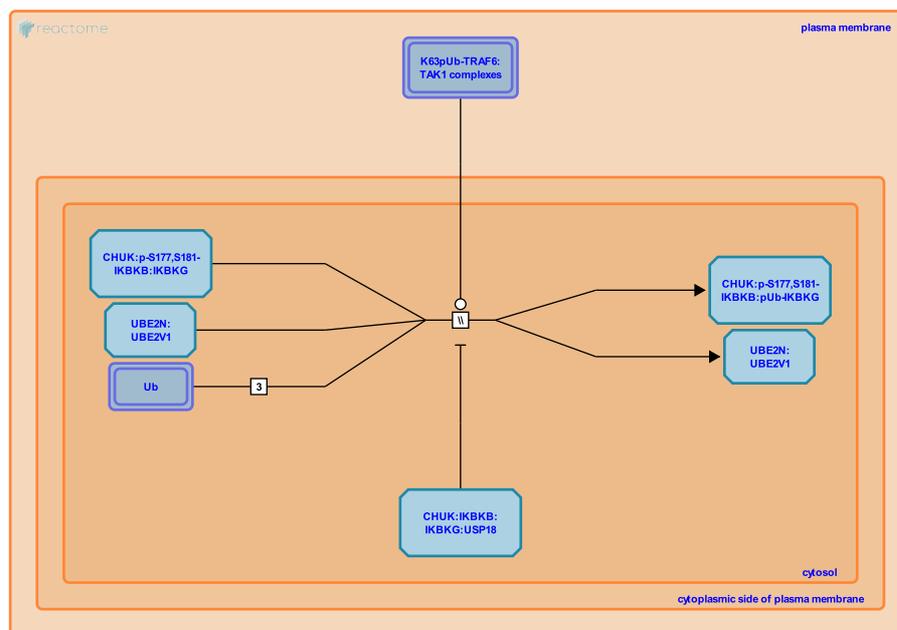
Location: TAK1-dependent IKK and NF-kappa-B activation

Stable identifier: R-RNO-9758604

Type: omitted

Compartments: cytosol

Inferred from: Ubiquitination of IKBKG by TRAF6 (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

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NF-kappa-B inhibitor binds NF-kappa-B complex ↗

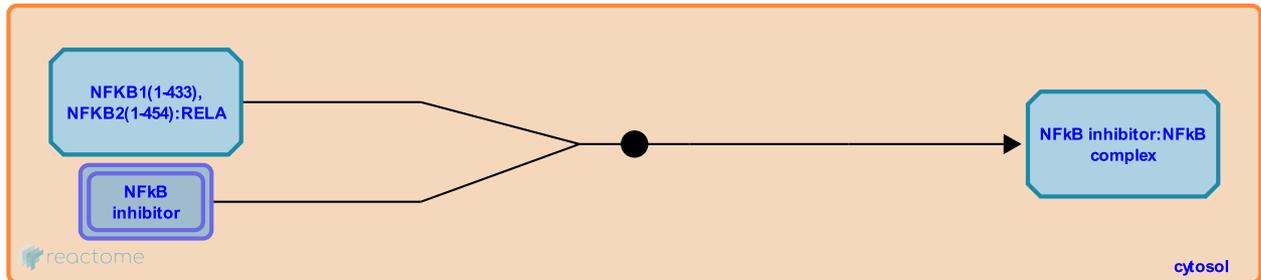
Location: [TAK1-dependent IKK and NF-kappa-B activation](#)

Stable identifier: R-RNO-9630923

Type: binding

Compartments: cytosol

Inferred from: [NF-kappa-B inhibitor binds NF-kappa-B complex \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

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

Active IKKKB phosphorylates NF-kappa-B inhibitor ↗

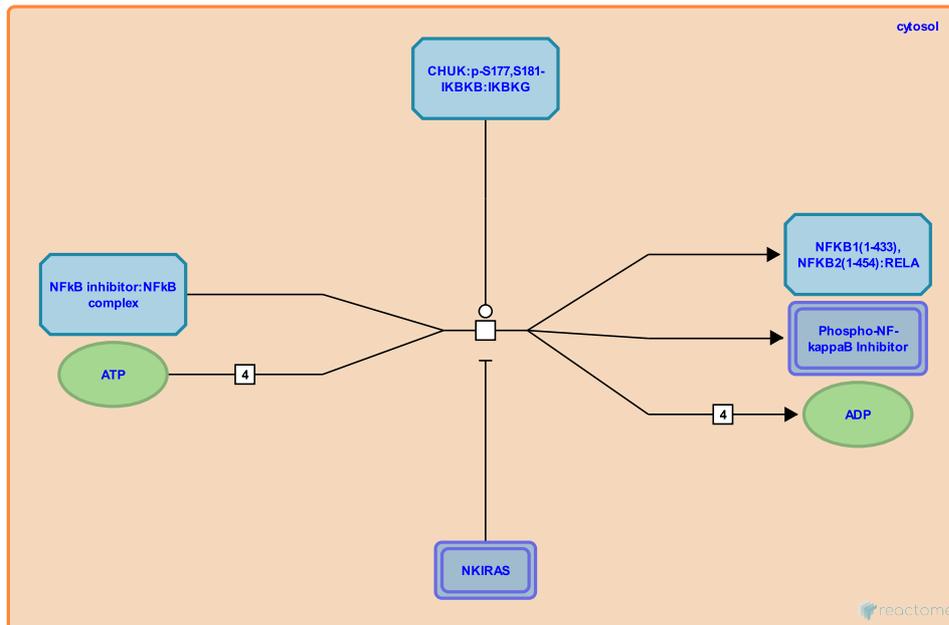
Location: TAK1-dependent IKK and NF-kappa-B activation

Stable identifier: R-RNO-9773803

Type: transition

Compartments: cytosol

Inferred from: Active IKKKB phosphorylates NF-kappa-B inhibitor (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

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Preceded by: [NF-kappa-B inhibitor binds NF-kappa-B complex](#)

Followed by: [NF-kappa-B complex is transported from cytosol to nucleus](#)

NF-kappa-B complex is transported from cytosol to nucleus ↗

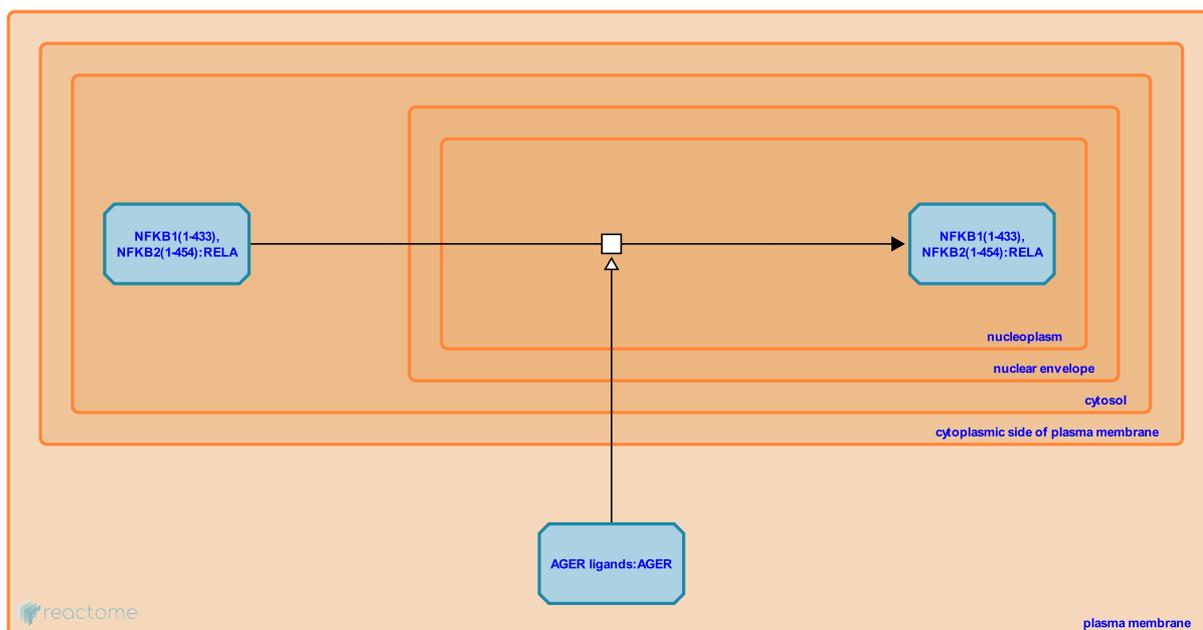
Location: TAK1-dependent IKK and NF-kappa-B activation

Stable identifier: R-RNO-168166

Type: transition

Compartments: nucleoplasm, cytosol

Inferred from: NF-kappa-B complex is transported from cytosol to nucleus (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

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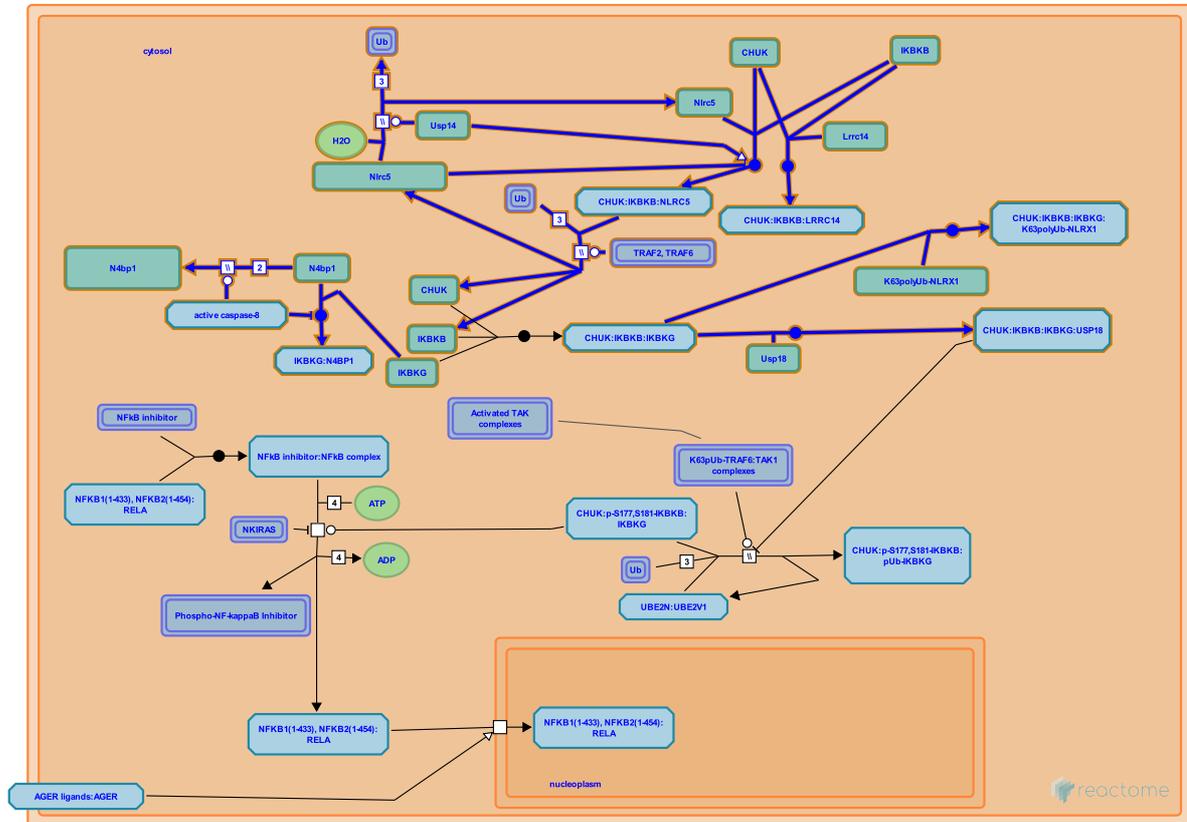
Preceded by: Active IKBKB phosphorylates NF-kappa-B inhibitor

Regulation of NF-kappa B signaling ↗

Location: TAK1-dependent IKK and NF-kappa-B activation

Stable identifier: R-RNO-9758274

Inferred from: Regulation of NF-kappa B signaling (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

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