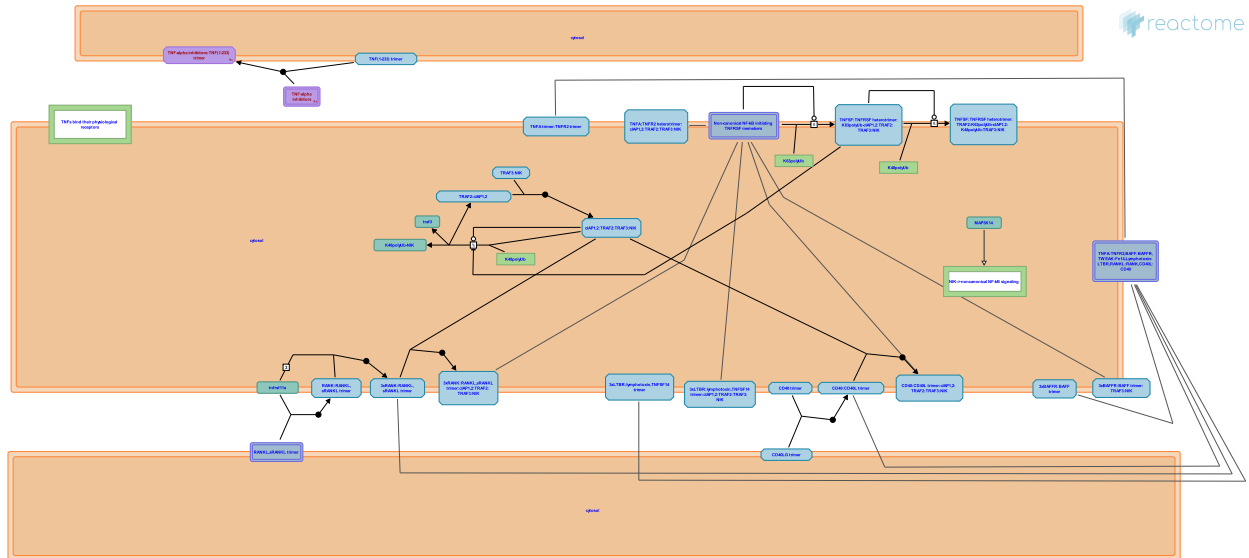


TNFR2 non-canonical NF-kB pathway



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

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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).

06/05/2024

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

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- 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

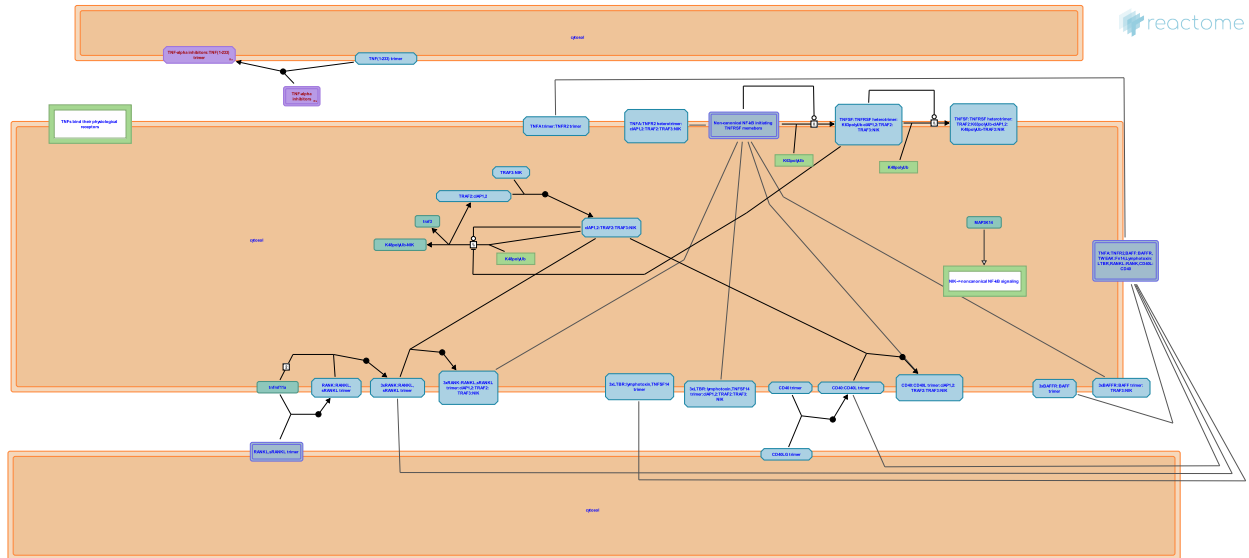
This document contains 4 pathways and 5 reactions ([see Table of Contents](#))

TNFR2 non-canonical NF-kB pathway ↗

Stable identifier: R-XTR-5668541

Compartments: plasma membrane, nucleoplasm

Inferred from: TNFR2 non-canonical NF-kB pathway (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

TRAF3:NIK binds TRAF2:cIAP1/2 ↗

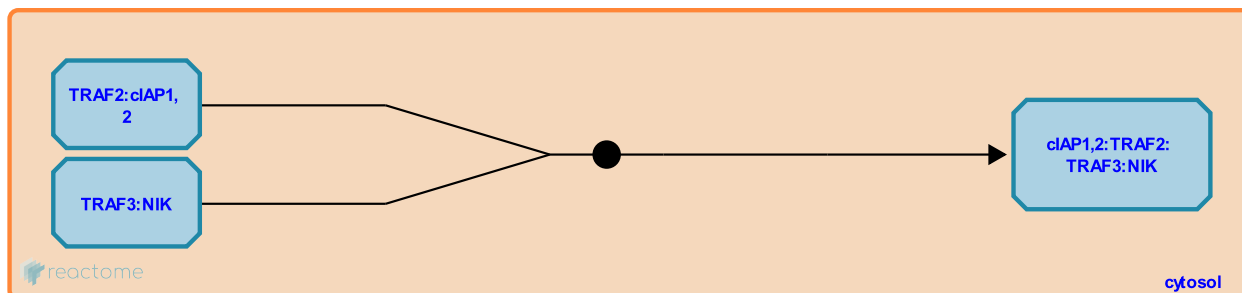
Location: TNFR2 non-canonical NF-kB pathway

Stable identifier: R-XTR-5668543

Type: binding

Compartments: cytosol

Inferred from: TRAF3:NIK binds TRAF2:cIAP1/2 (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.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Followed by: cIAP1,2 ubiquitinates NIK in cIAP1,2:TRAF2::TRAF3:NIK

cIAP1,2 ubiquitinates NIK in cIAP1,2:TRAF2::TRAF3:NIK ↗

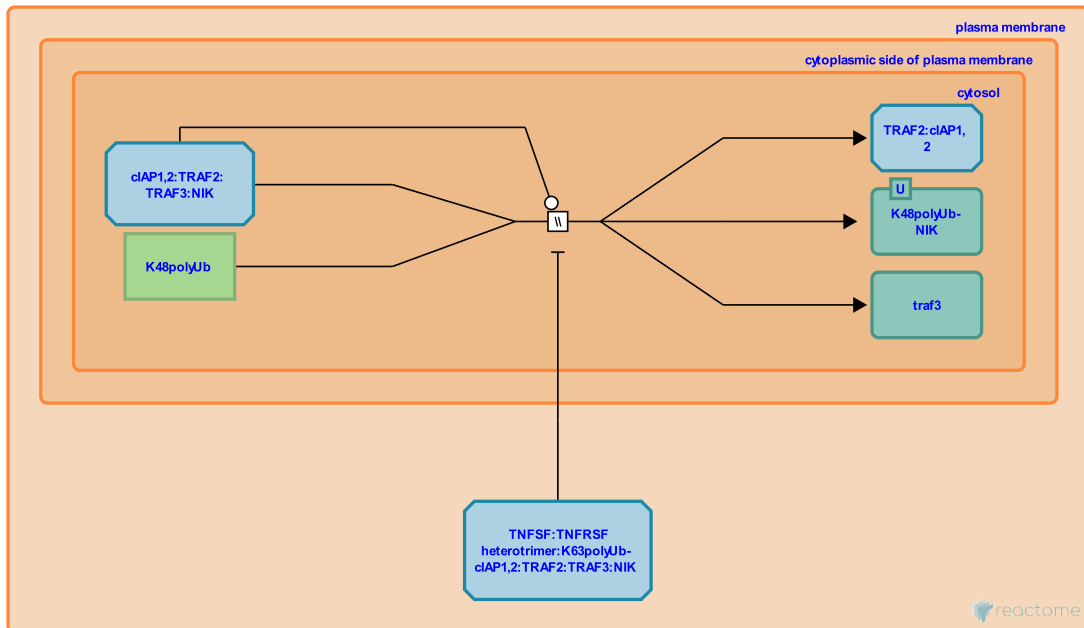
Location: TNFR2 non-canonical NF-κB pathway

Stable identifier: R-XTR-5668534

Type: omitted

Compartments: cytosol

Inferred from: cIAP1,2 ubiquitinates NIK in cIAP1,2:TRAF2::TRAF3:NIK (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: TRAF3:NIK binds TRAF2:cIAP1/2

TNF-alpha inhibitors bind to TNF(1-233) trimer ↗

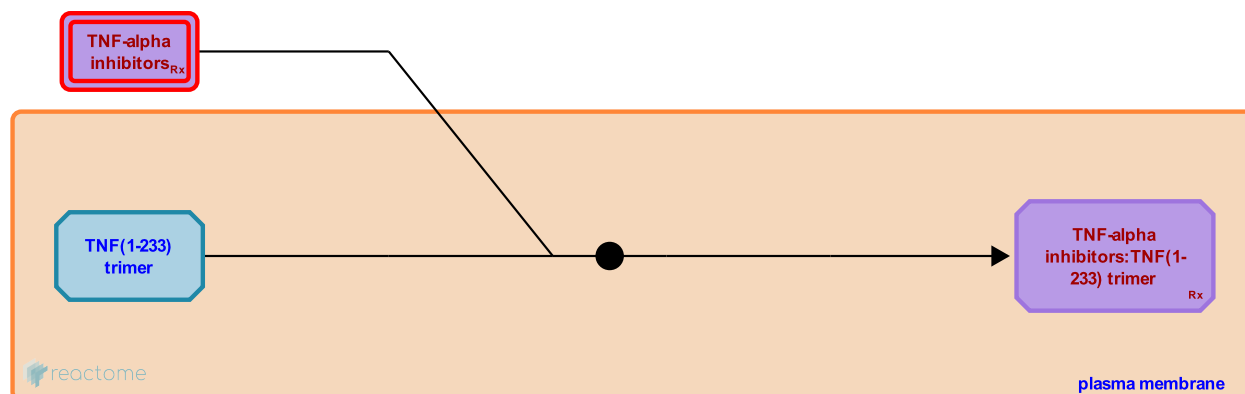
Location: [TNFR2 non-canonical NF-kB pathway](#)

Stable identifier: R-XTR-9714959

Type: binding

Compartments: plasma membrane

Inferred from: [TNF-alpha inhibitors bind to TNF\(1-233\) trimer \(Homo sapiens\)](#)



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.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

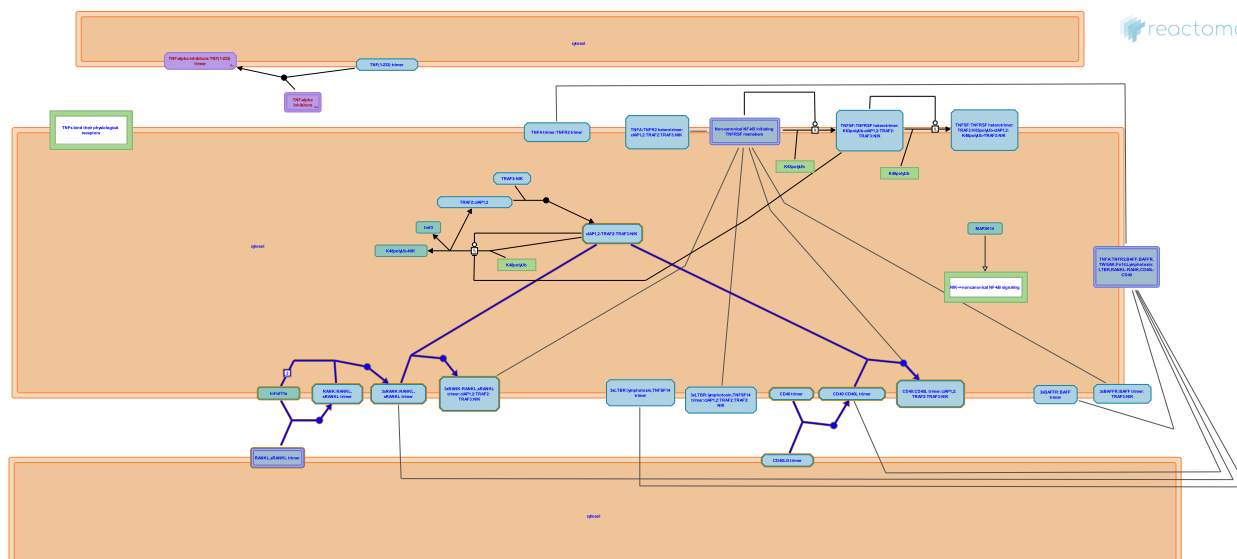
TNF receptor superfamily (TNFSF) members mediating non-canonical NF- κ B pathway ↗

Location: TNFR2 non-canonical NF- κ B pathway

Stable identifier: R-XTR-5676594

Compartments: plasma membrane, extracellular region, cytosol

Inferred from: TNF receptor superfamily (TNFSF) members mediating non-canonical NF- κ B pathway (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

TRAF2 ubiquitinates cIAP1,2 in cIAP1,2:TRAF1:TRAF2:TRAF3:NIK ↗

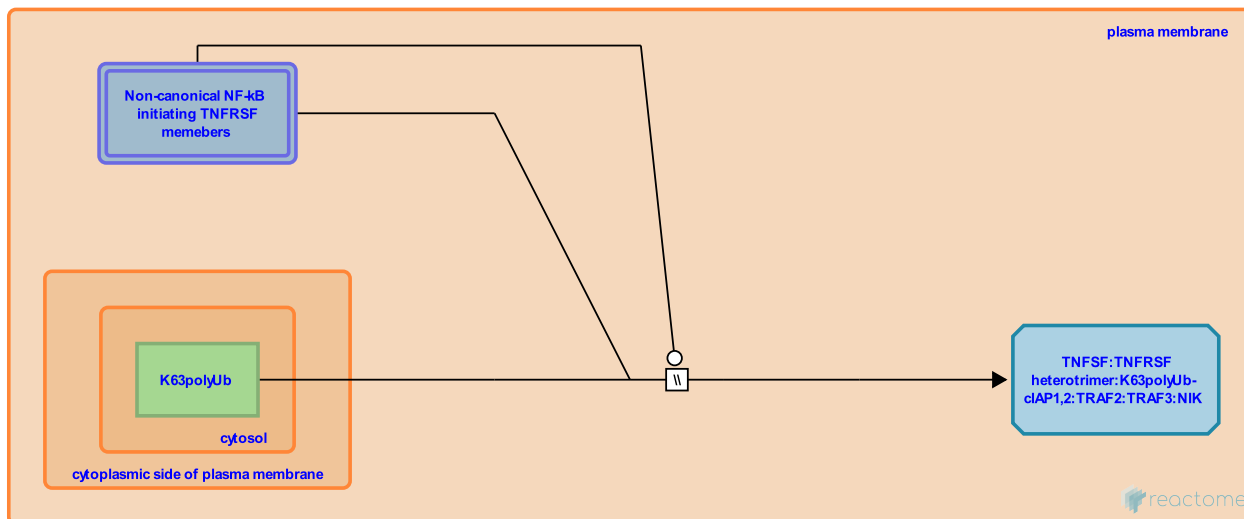
Location: TNFR2 non-canonical NF- κ B pathway

Stable identifier: R-XTR-5668414

Type: omitted

Compartments: plasma membrane, cytosol

Inferred from: TRAF2 ubiquitinates cIAP1,2 in cIAP1,2:TRAF1:TRAF2:TRAF3:NIK (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Followed by: K63polyUb-cIAP1,2 ubiquitinates TRAF3

K63polyUb-cIAP1,2 ubiquitinates TRAF3 ↗

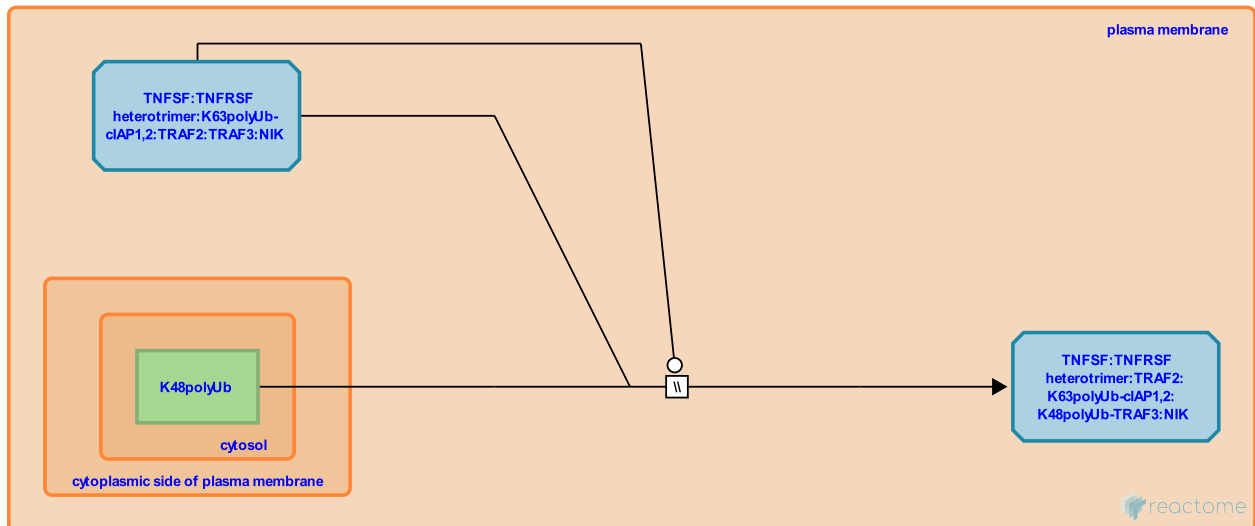
Location: TNFR2 non-canonical NF-κB pathway

Stable identifier: R-XTR-5668454

Type: omitted

Compartments: plasma membrane, cytosol

Inferred from: K63polyUb-cIAP1,2 ubiquitinates TRAF3 (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: TRAF2 ubiquitinates cIAP1,2 in cIAP1,2:TRAF1:TRAF2:TRAF3:NIK

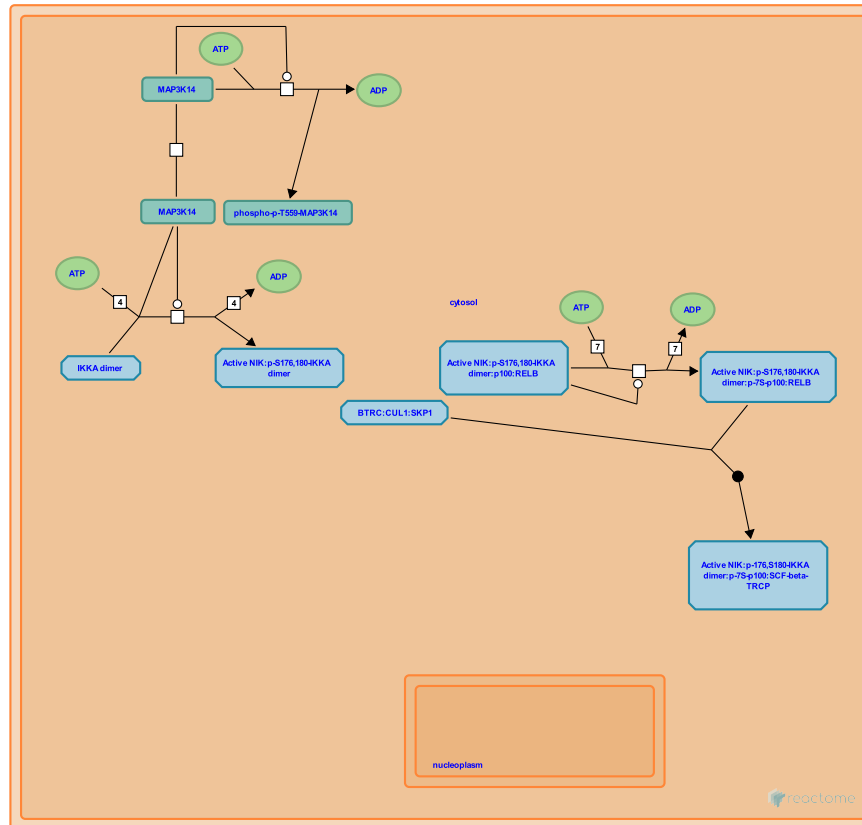
NIK-->noncanonical NF-kB signaling ↗

Location: TNFR2 non-canonical NF-kB pathway

Stable identifier: R-XTR-5676590

Compartments: nucleoplasm, cytosol

Inferred from: NIK-->noncanonical NF-kB 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.

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

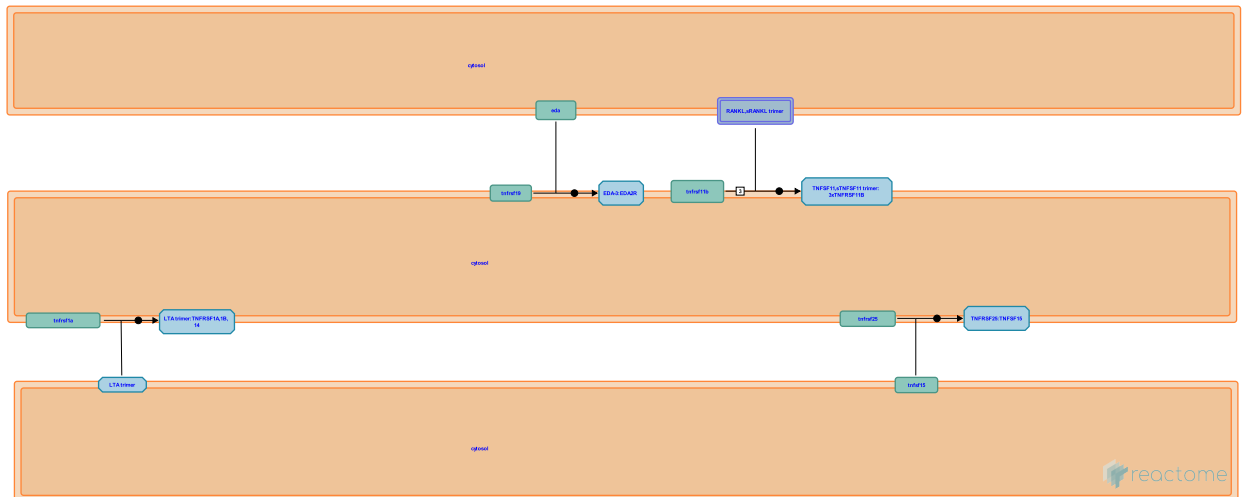
TNFs bind their physiological receptors ↗

Location: TNFR2 non-canonical NF- κ B pathway

Stable identifier: R-XTR-5669034

Compartments: plasma membrane

Inferred from: TNFs bind their physiological receptors (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.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

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