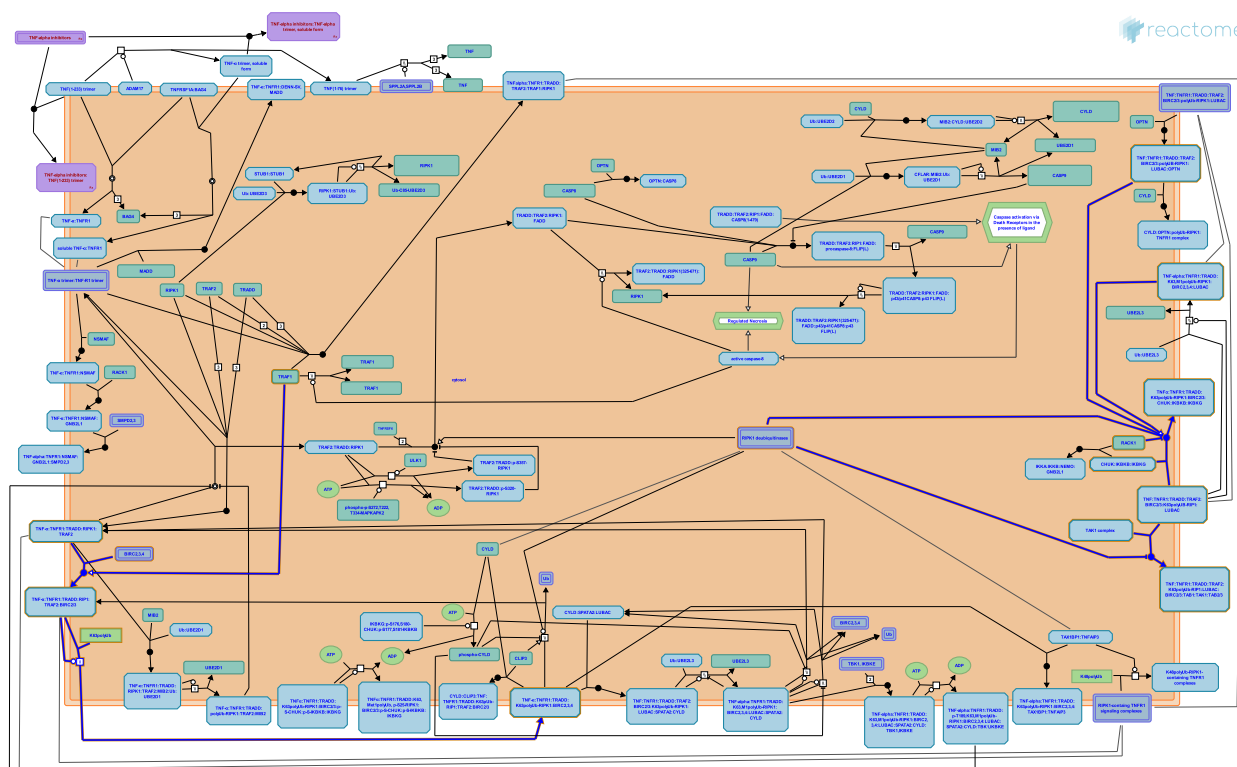


TNFR1-induced NF-kappa-B signaling pathway



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).

19/05/2024

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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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. [↗](#)

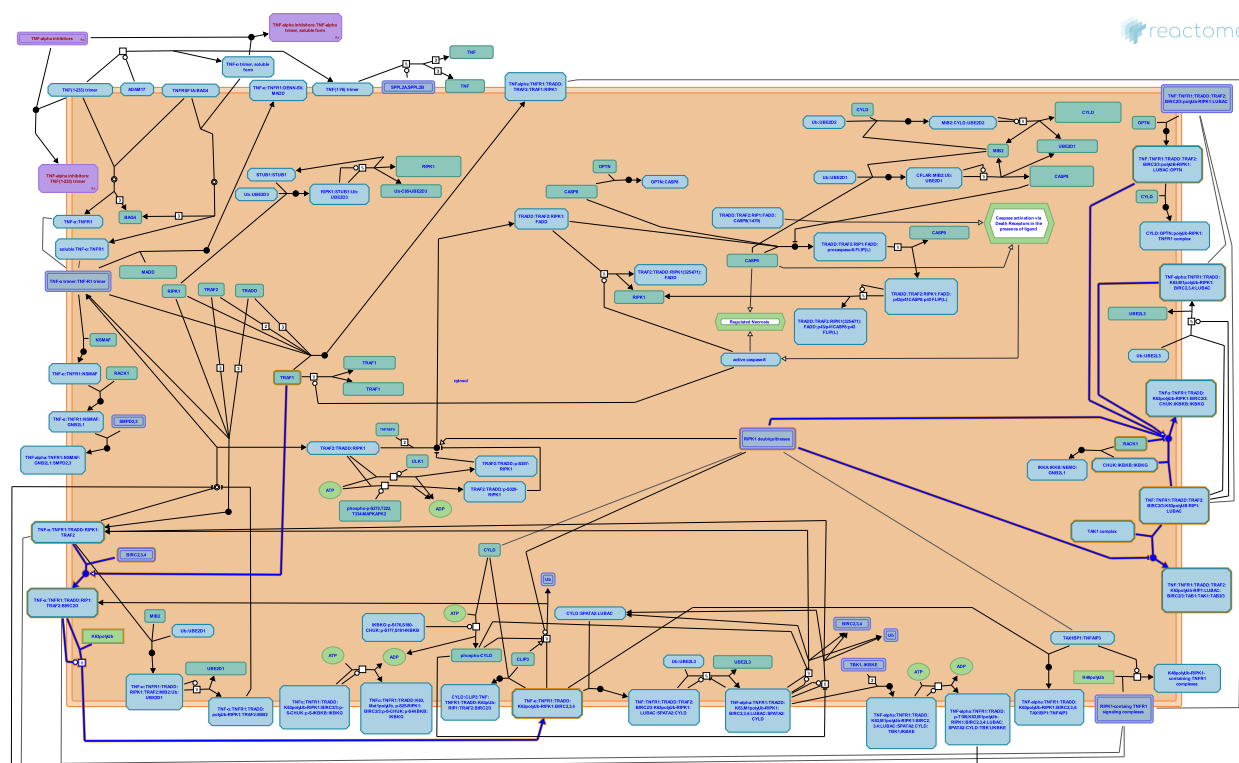
Reactome database release: 88

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

TNFR1-induced NF-kappa-B signaling pathway ↗

Stable identifier: R-SSC-5357956

Inferred from: TNFR1-induced NF-kappa-B signaling 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>

TNF:TNFR1:TRADD:TRAF2:RIPK1 recruits BIRC2/3 (cIAP1/2) ↗

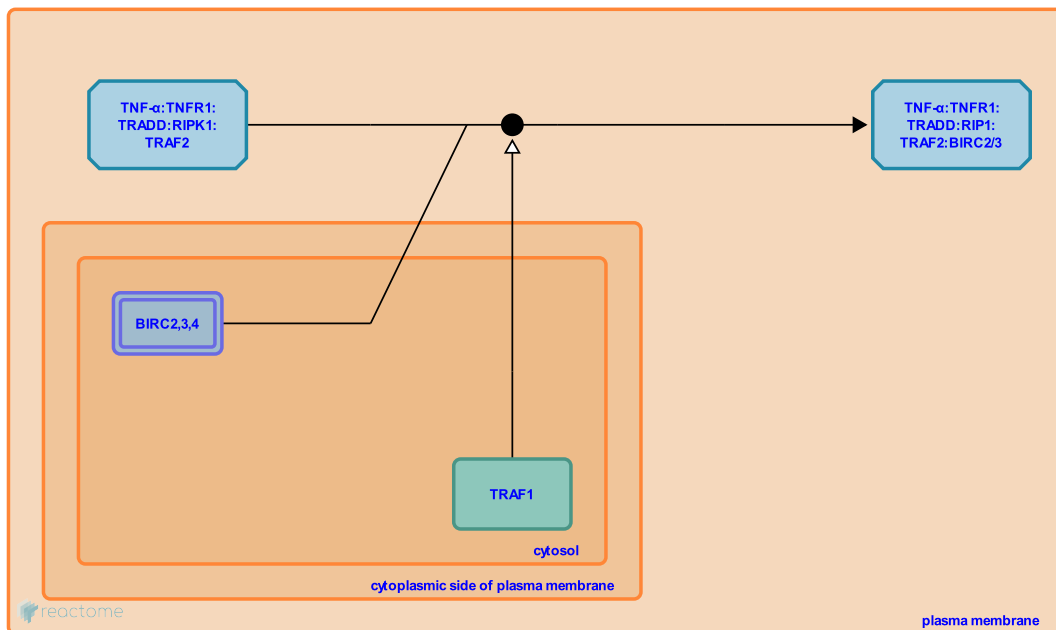
Location: TNFR1-induced NF-kappa-B signaling pathway

Stable identifier: R-SSC-5357780

Type: binding

Compartments: plasma membrane, cytosol

Inferred from: TNF:TNFR1:TRADD:TRAF2:RIPK1 recruits BIRC2/3 (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Followed by: BIRC(cIAP1/2) ubiquitinates RIPK1

BIRC(cIAP1/2) ubiquitinates RIPK1 ↗

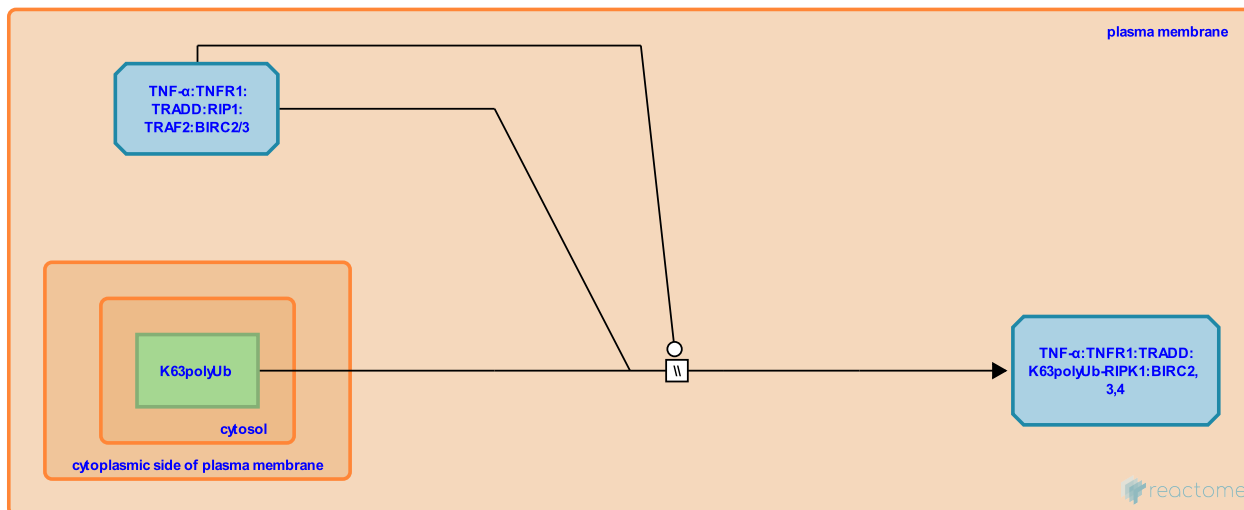
Location: TNFR1-induced NF-kappa-B signaling pathway

Stable identifier: R-SSC-5357757

Type: omitted

Compartments: plasma membrane, cytosol

Inferred from: BIRC(cIAP1/2) ubiquitinates RIPK1 (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.](https://www.reactome.org/docs/event_inference.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: TNF:TNFR1:TRADD:TRAF2:RIPK1 recruits BIRC2/3 (cIAP1/2)

Followed by: TNF:TNFR1:TRADD:TRAF2:K63polyUb-RIPK1:BIRC2/3:LUBAC recruits TAK1 complex

TNF:TNFR1:TRADD:TRAF2:K63polyUb-RIPK1:BIRC2/3:LUBAC recruits TAK1 complex ↗

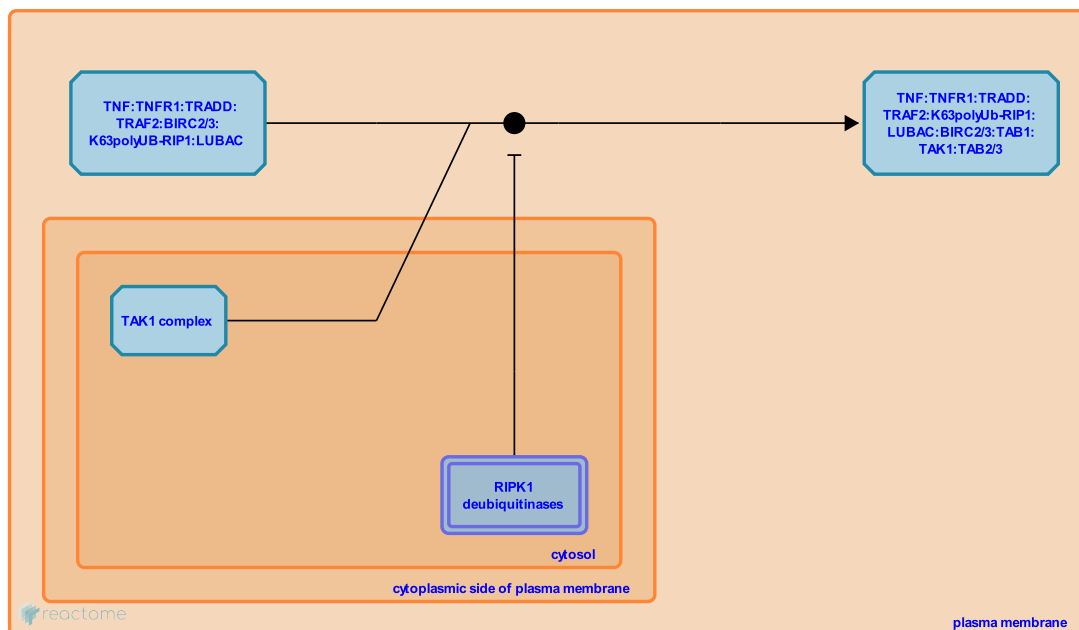
Location: TNFR1-induced NF-kappa-B signaling pathway

Stable identifier: R-SSC-5357860

Type: binding

Compartment: plasma membrane, cytosol

Inferred from: TNF:TNFR1:TRADD:TRAF2:K63polyUb-RIPK1:BIRC2/3:LUBAC recruits TAK1 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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: BIRC(cIAP1/2) ubiquitinates RIPK1

TNF:TNFR1:TRADD:TRAF2:K63polyUb-RIPK1:BIRC2,3:LUBAC recruits IKKA:IKB-KB:IKBKKG ↗

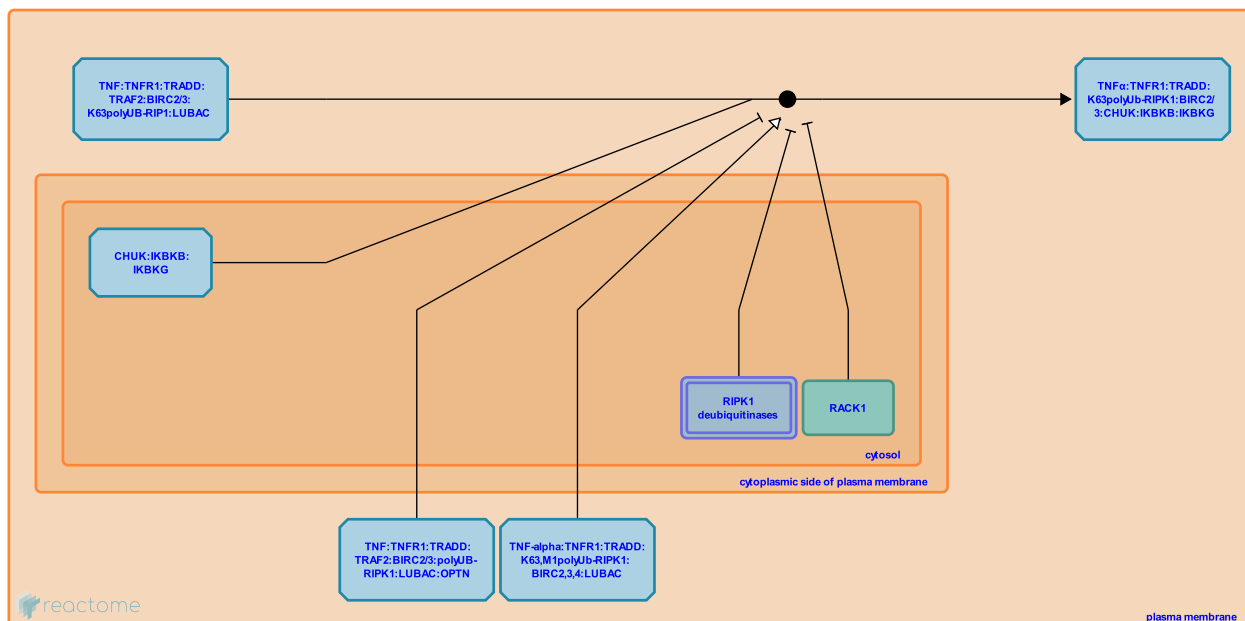
Location: TNFR1-induced NF-kappa-B signaling pathway

Stable identifier: R-SSC-5357776

Type: binding

Compartments: plasma membrane, cytosol

Inferred from: TNF:TNFR1:TRADD:TRAF2:K63polyUb-RIPK1:BIRC2,3:LUBAC recruits IKKA:IKBKB:IKB-KG (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>

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