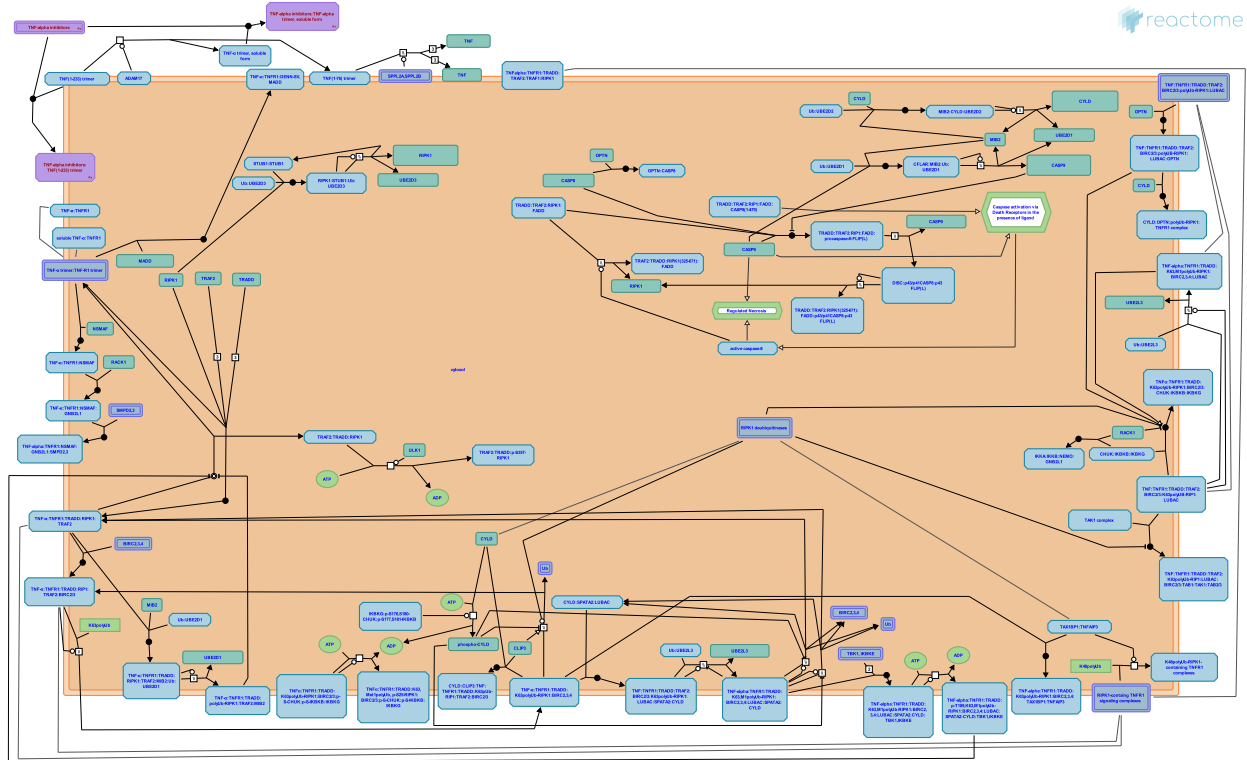


TNF signaling



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/).

03/05/2024

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

- 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., 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. [↗](#)

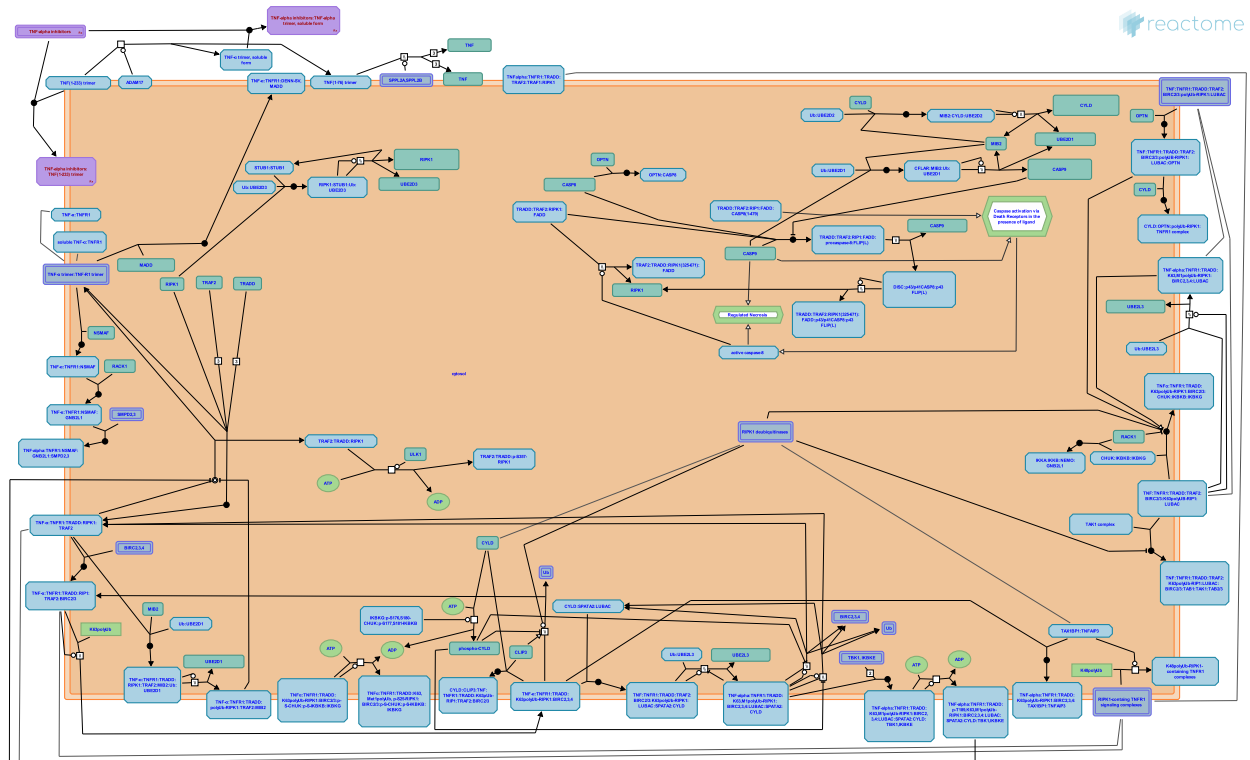
Reactome database release: 88

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

TNF signaling ↗

Stable identifier: R-CFA-75893

Inferred from: TNF 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.reactome.org) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

TNF- α is cleaved by ADAM17 (TACE) ↗

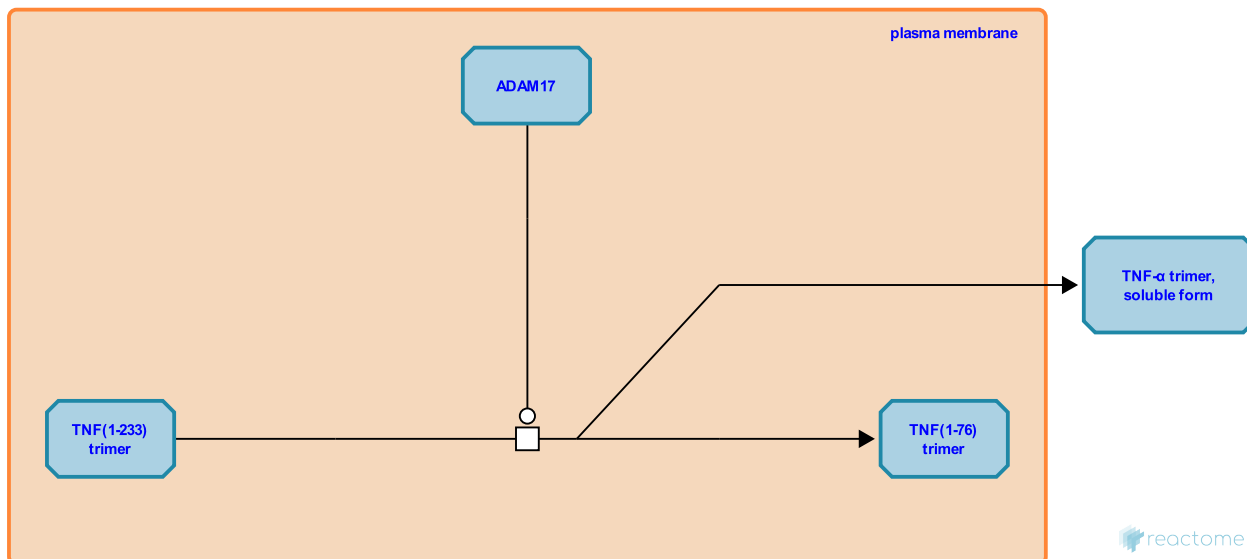
Location: [TNF signaling](#)

Stable identifier: R-CFA-3371385

Type: transition

Compartments: plasma membrane, extracellular region

Inferred from: [TNF- \$\alpha\$ is cleaved by ADAM17 \(TACE\) \(Homo sapiens\)](#)



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: [TNF-alpha inhibitors bind to TNF\(1-233\) trimer](#), [TNF-alpha inhibitors bind to soluble TNF trimer](#)

TNF-alpha inhibitors bind to soluble TNF trimer ↗

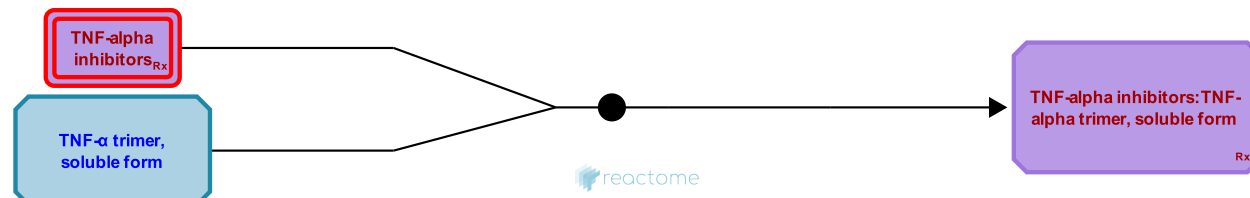
Location: [TNF signaling](#)

Stable identifier: R-CFA-9714924

Type: binding

Compartments: extracellular region

Inferred from: [TNF-alpha inhibitors bind to soluble TNF 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>

Preceded by: [TNF-α is cleaved by ADAM17 \(TACE\)](#)

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

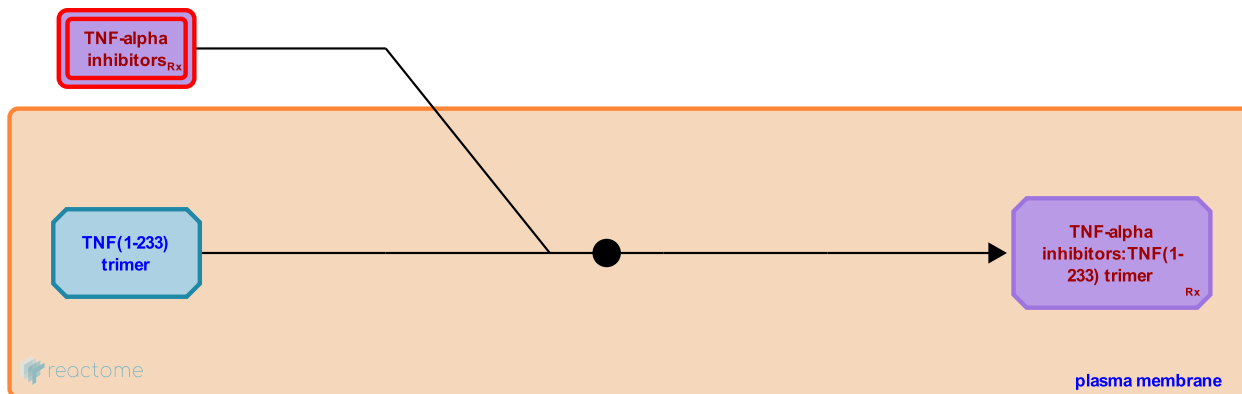
Location: [TNF signaling](#)

Stable identifier: R-CFA-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>

Preceded by: [TNF- \$\alpha\$ is cleaved by ADAM17 \(TACE\)](#)

TNF:TNFR1 binds TRADD, TRAF2 and RIPK1 ↗

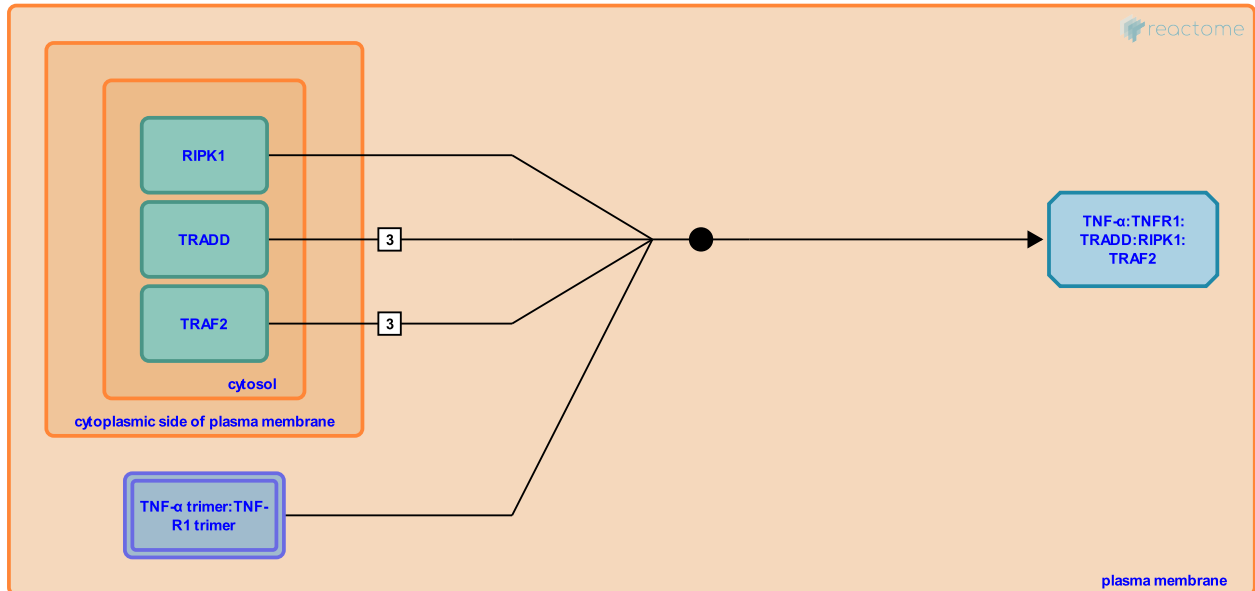
Location: TNF signaling

Stable identifier: R-CFA-83656

Type: binding

Compartments: plasma membrane, cytosol

Inferred from: TNF:TNFR1 binds TRADD, TRAF2 and 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.

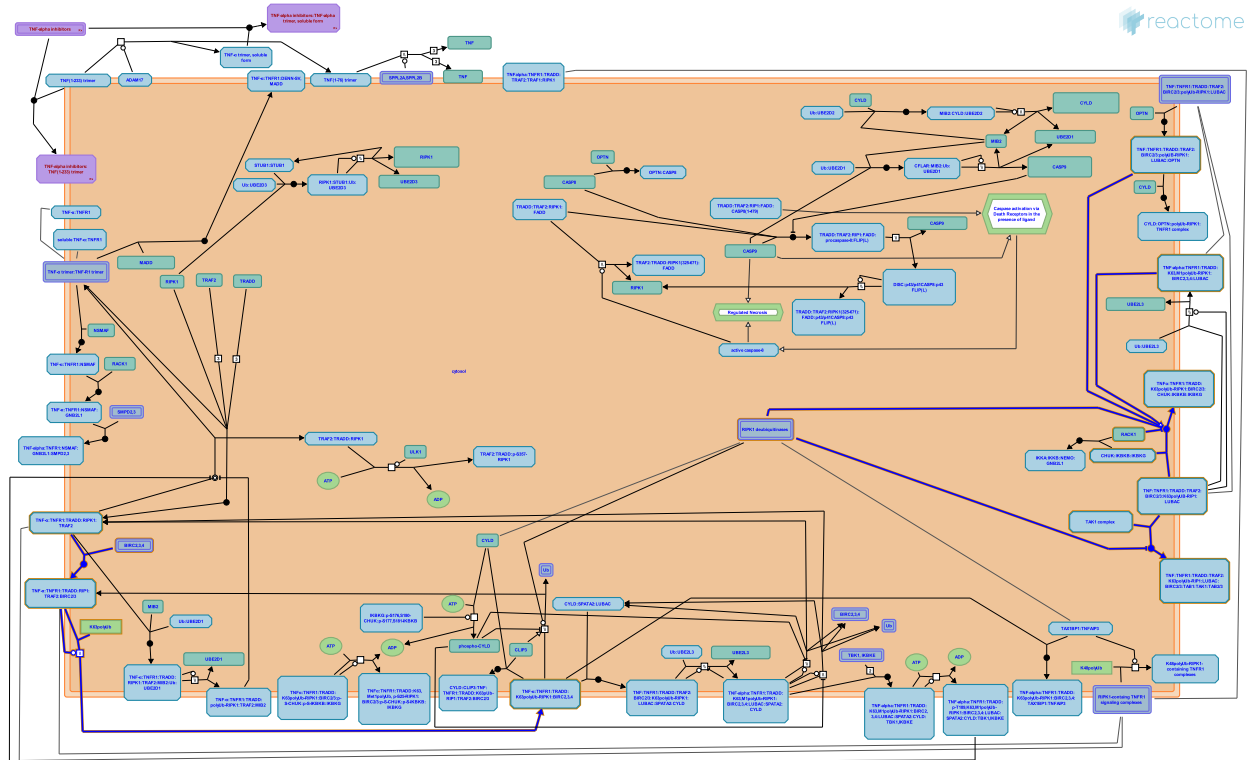
[More details and caveats of the event inference in Reactome.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

TNFR1-induced NF-kappa-B signaling pathway ↗

Location: TNF signaling

Stable identifier: R-CFA-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.

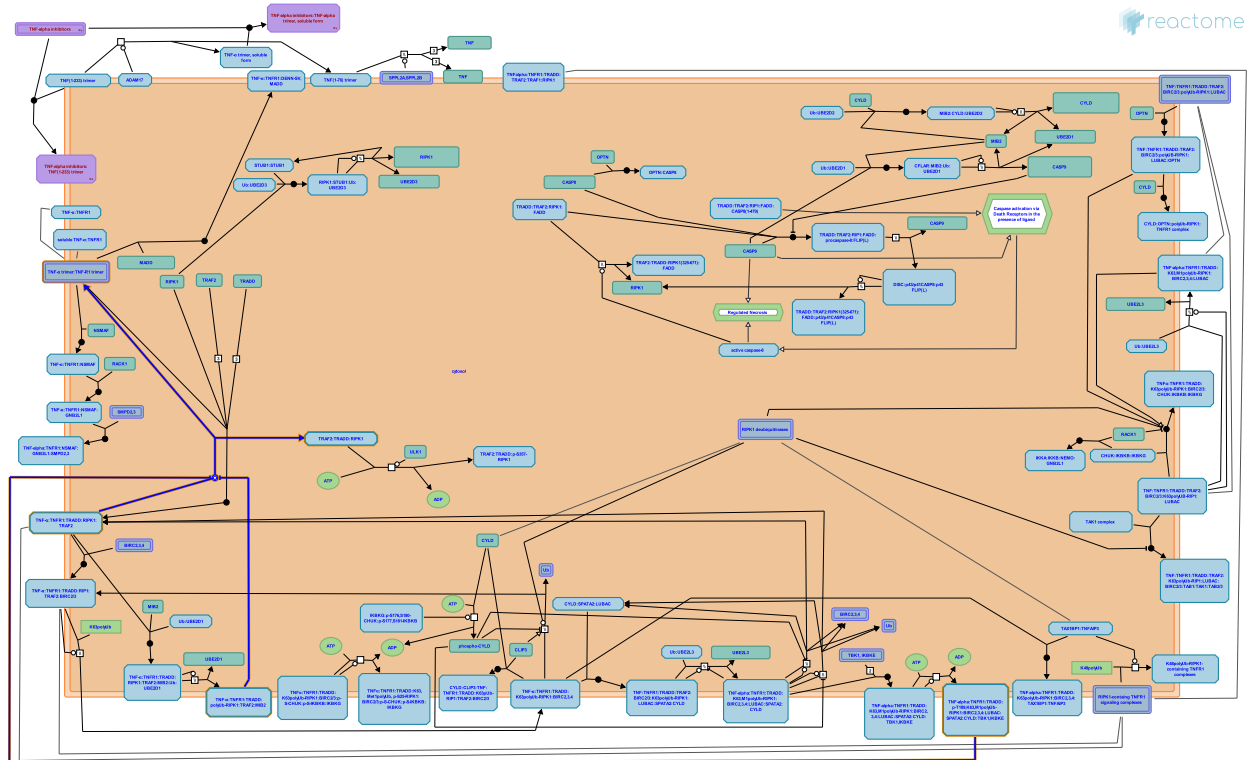
[More details and caveats of the event inference in Reactome.](http://www.reactome.org) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

TNFR1-induced proapoptotic signaling ↗

Location: TNF signaling

Stable identifier: R-CFA-5357786

Inferred from: TNFR1-induced proapoptotic 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.

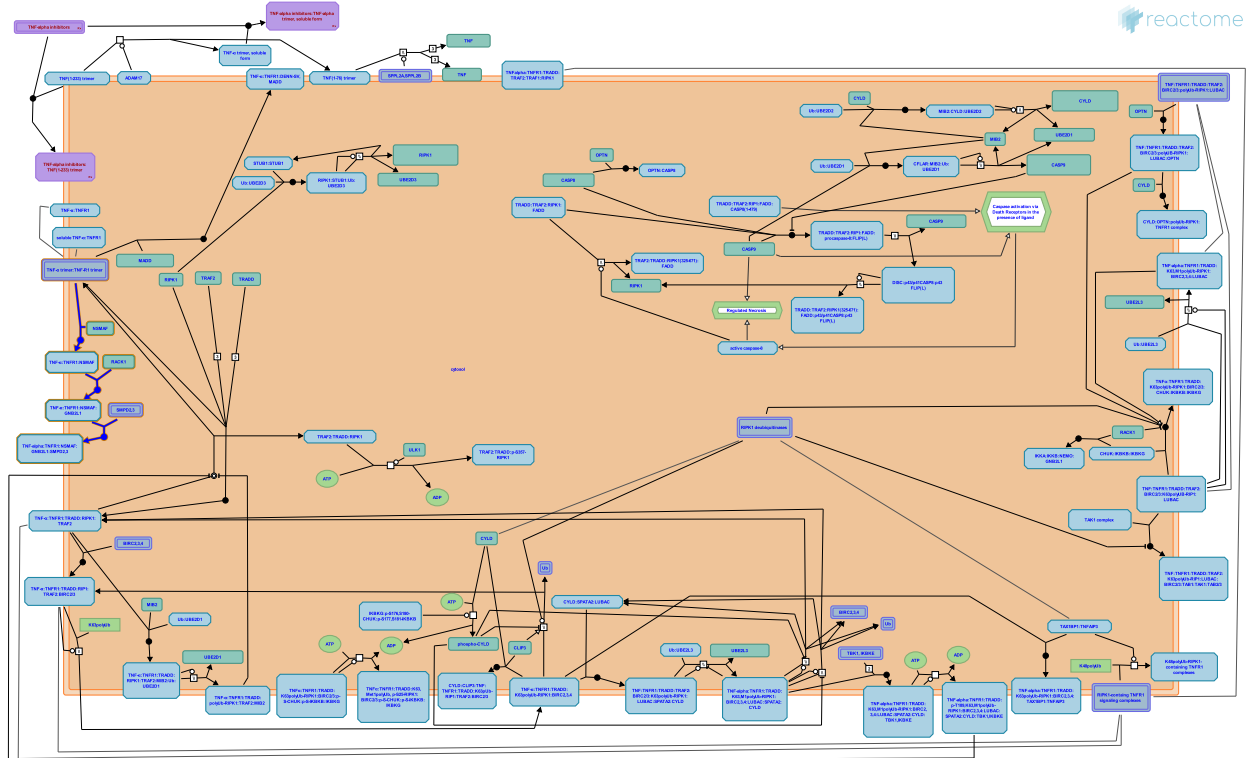
[More details and caveats of the event inference in Reactome.](http://www.reactome.org) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

TNFR1-mediated ceramide production ↗

Location: TNF signaling

Stable identifier: R-CFA-5626978

Inferred from: TNFR1-mediated ceramide production (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.

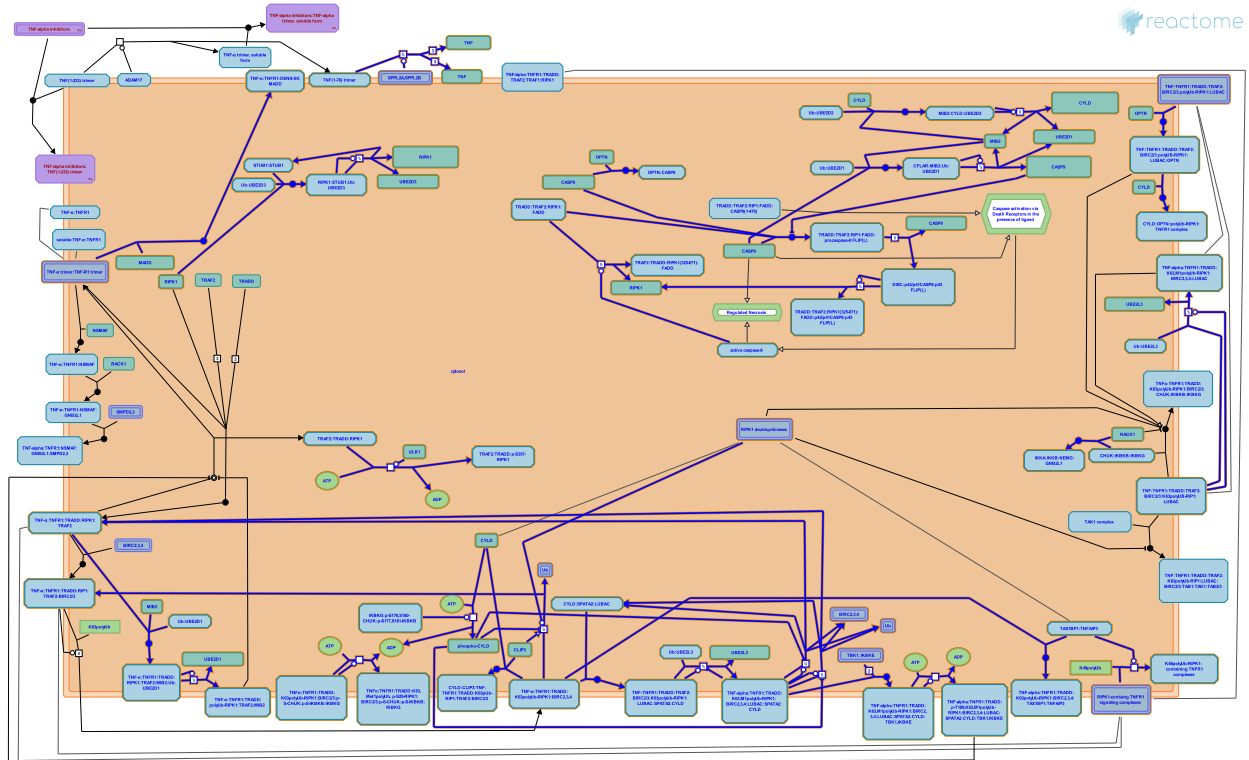
[More details and caveats of the event inference in Reactome.](http://www.reactome.org) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Regulation of TNFR1 signaling ↗

Location: TNF signaling

Stable identifier: R-CFA-5357905

Inferred from: Regulation of TNFR1 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.reactome.org) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Table of Contents

Introduction	1
❖ TNF signaling	2
➤ TNF- α is cleaved by ADAM17 (TACE)	3
➤ TNF-alpha inhibitors bind to soluble TNF trimer	4
➤ TNF-alpha inhibitors bind to TNF(1-233) trimer	5
➤ TNF:TNFR1 binds TRADD, TRAF2 and RIPK1	6
❖ TNFR1-induced NF-kappa-B signaling pathway	7
❖ TNFR1-induced proapoptotic signaling	8
❖ TNFR1-mediated ceramide production	9
❖ Regulation of TNFR1 signaling	10
Table of Contents	11