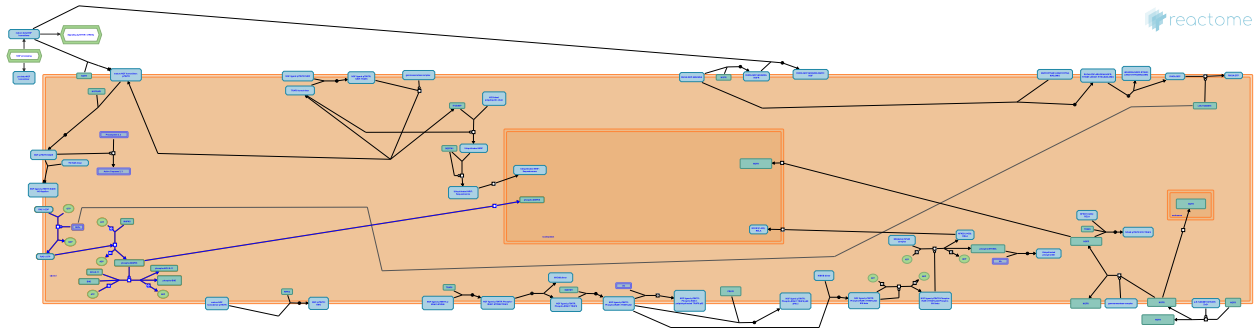


NRAGE signals death through JNK



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/).

08/05/2024

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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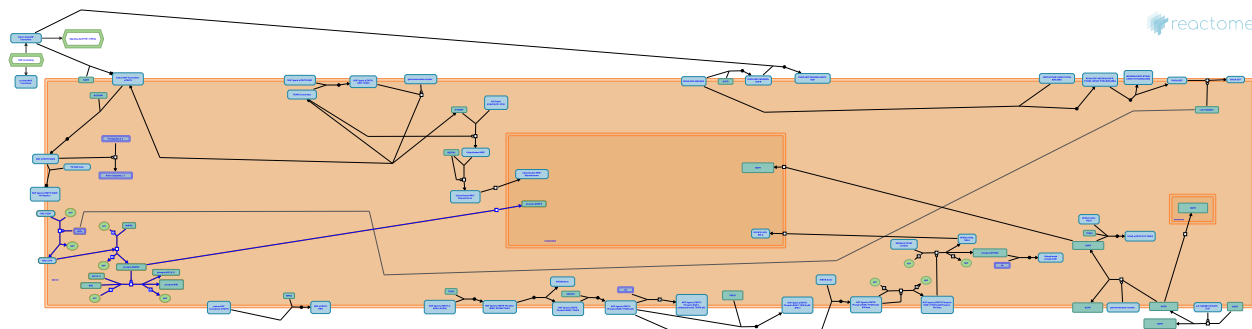
Reactome database release: 88

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

NRAGE signals death through JNK ↗

Stable identifier: R-BTA-193648

Inferred from: NRAGE signals death through JNK (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) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

p75NTR indirectly activates RAC and Cdc42 via a guanyl-nucleotide exchange factor



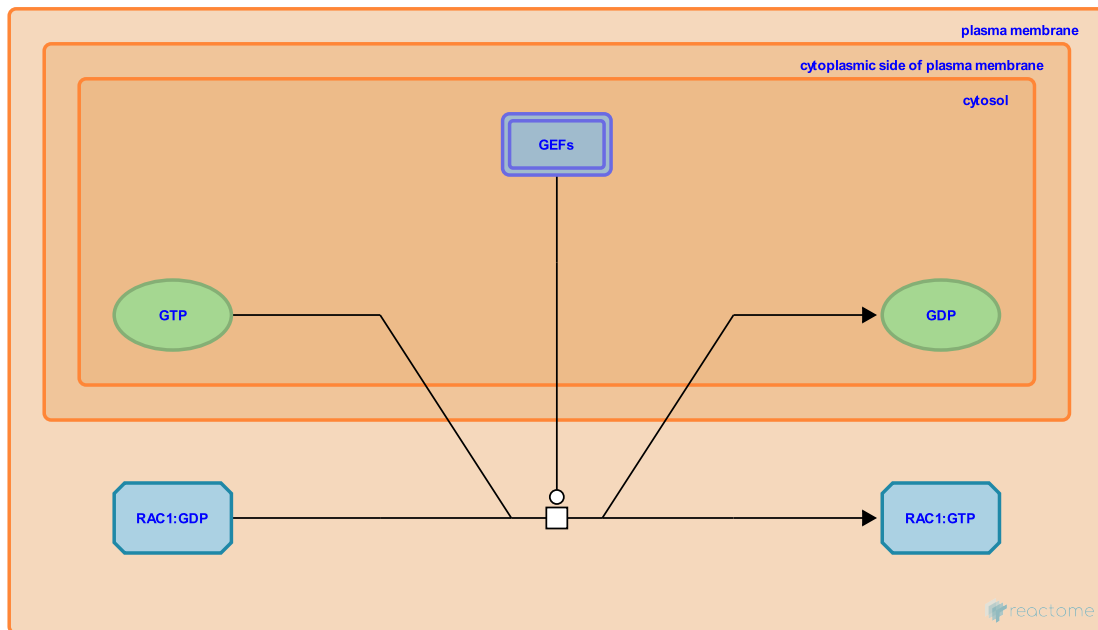
Location: NRAGE signals death through JNK

Stable identifier: R-BTA-205039

Type: transition

Compartments: plasma membrane, cytosol

Inferred from: p75NTR indirectly activates RAC and Cdc42 via a guanyl-nucleotide exchange factor (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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GTP-bound RAC contributes to JNK activation ↗

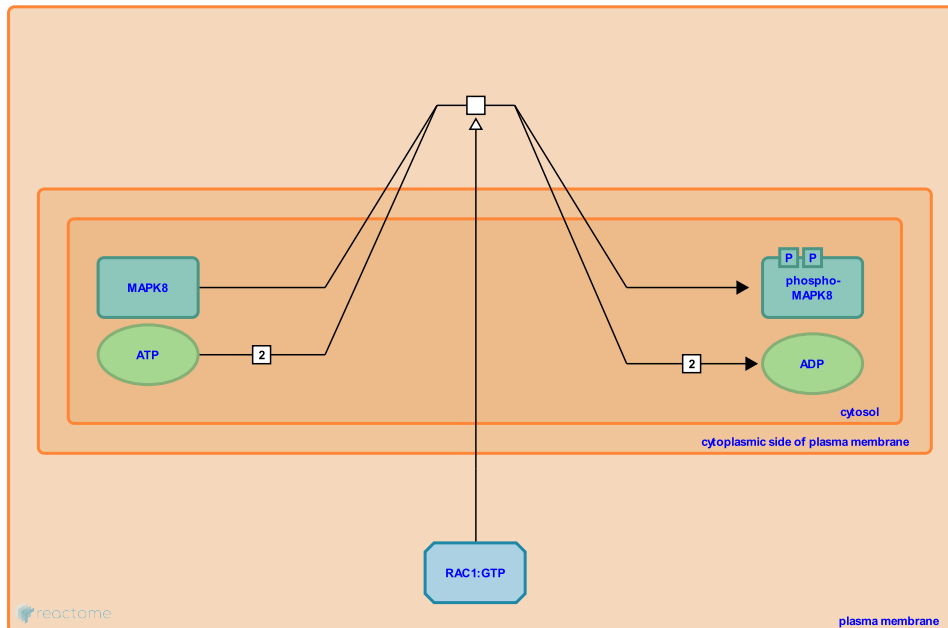
Location: NRAGE signals death through JNK

Stable identifier: R-BTA-205136

Type: transition

Compartments: plasma membrane, cytosol

Inferred from: GTP-bound RAC contributes to JNK 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.

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

Followed by: JNK phosphorylates BIM, BAD and other targets

JNK phosphorylates BIM, BAD and other targets ↗

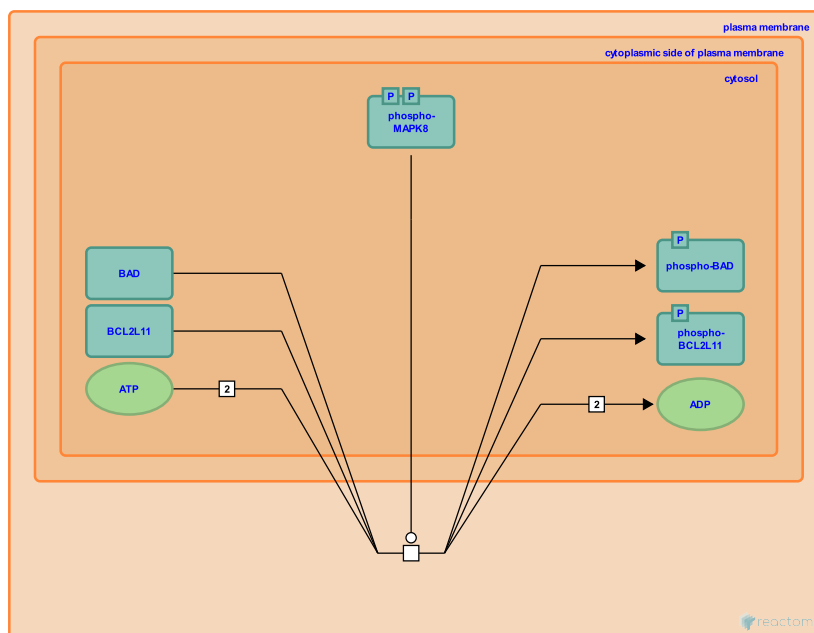
Location: NRAGE signals death through JNK

Stable identifier: R-BTA-205075

Type: transition

Compartments: plasma membrane, cytosol

Inferred from: JNK phosphorylates BIM, BAD and other targets (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) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: GTP-bound RAC contributes to JNK activation

Active JNK moves to the nucleus and phosphorylates different transcription factors



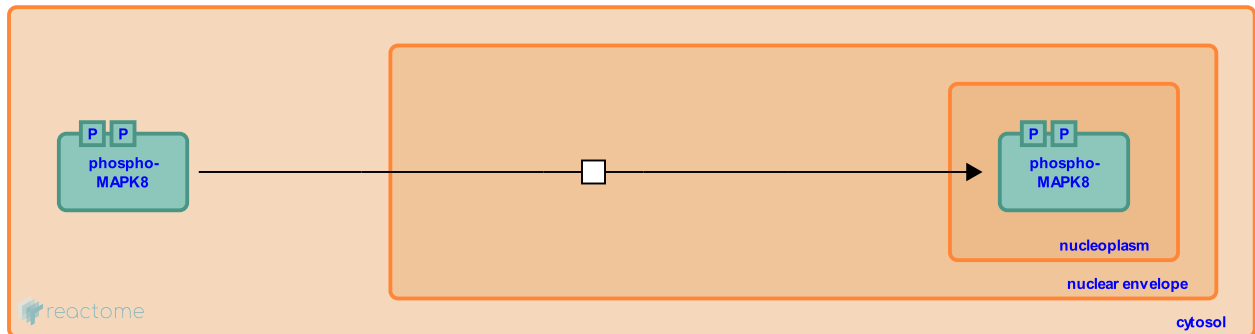
Location: NRAGE signals death through JNK

Stable identifier: R-BTA-193666

Type: transition

Compartments: nuclear envelope

Inferred from: Active JNK moves to the nucleus and phosphorylates different transcription factors (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.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

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