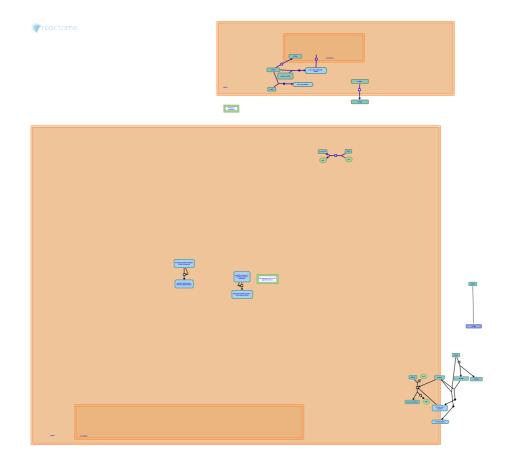


Interleukin-37 signaling



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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of Creative Commons Attribution 4.0 International (CC BY 4.0)
License. For more information see our License.

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.

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

- 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.
- 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

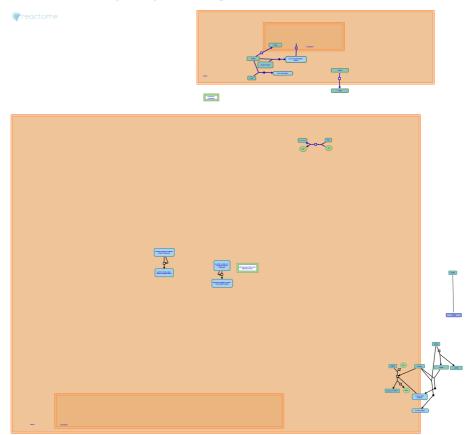
This document contains 1 pathway and 6 reactions (see Table of Contents)

Interleukin-37 signaling 对

Stable identifier: R-DRE-9008059

Compartments: cytosol, plasma membrane, extracellular region

Inferred from: Interleukin-37 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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

IL37(?-218) translocates from the cytosol to the nucleus 7

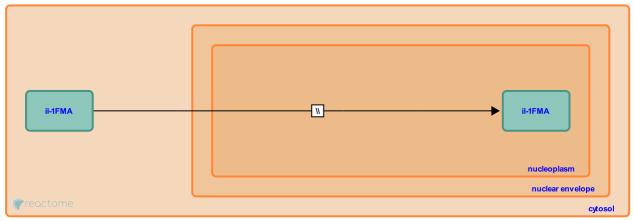
Location: Interleukin-37 signaling

Stable identifier: R-DRE-9008696

Type: omitted

Compartments: nucleoplasm, cytosol

Inferred from: IL37(?-218) translocates from the cytosol to the 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.

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

IL37(?-218) binds p-S423,S425-SMAD3 7

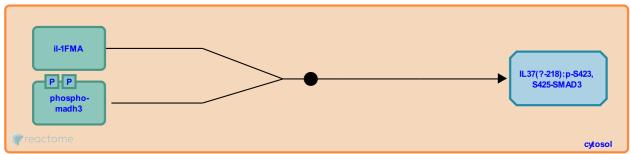
Location: Interleukin-37 signaling

Stable identifier: R-DRE-9009910

Type: binding

Compartments: cytosol

Inferred from: IL37(?-218) binds p-S423,S425-SMAD3 (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: IL37(?-218) binds SMAD3, IL37(?-218):p-S423,S425-SMAD3 translocates to the nucleus

IL37(?-218):p-S423,S425-SMAD3 translocates to the nucleus 7

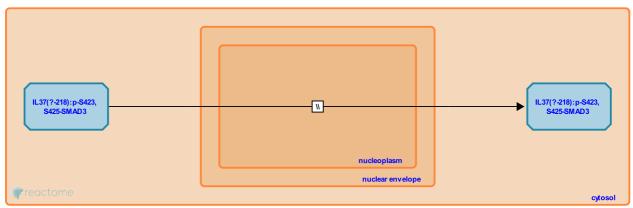
Location: Interleukin-37 signaling

Stable identifier: R-DRE-9008928

Type: omitted

Compartments: nucleoplasm, cytosol

Inferred from: IL37(?-218):p-S423,S425-SMAD3 translocates to the 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.

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

Preceded by: IL37(?-218) binds p-S423,S425-SMAD3

IL37(?-218) binds SMAD3 **对**

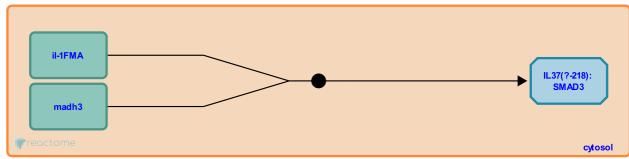
Location: Interleukin-37 signaling

Stable identifier: R-DRE-9008692

Type: binding

Compartments: cytosol

Inferred from: IL37(?-218) binds SMAD3 (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: IL37(?-218) binds p-S423,S425-SMAD3

IL37, IL37(?-218) translocates from cytosol to extracellular region **₹**

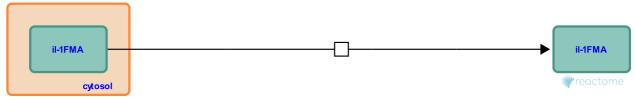
Location: Interleukin-37 signaling

Stable identifier: R-DRE-9008694

Type: transition

Compartments: extracellular region, cytosol

Inferred from: IL37, IL37(?-218) translocates from cytosol to extracellular region (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

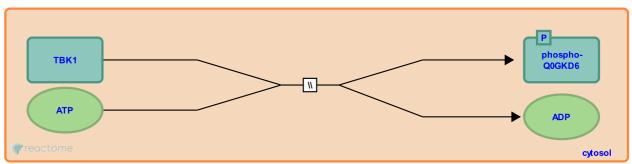
Location: Interleukin-37 signaling

Stable identifier: R-DRE-9008684

Type: omitted

Compartments: cytosol

Inferred from: TBK1 phosphorylation (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

Table of Contents

Introduction	1
Interleukin-37 signaling	2
IL37(?-218) translocates from the cytosol to the nucleus	3
► IL37(?-218) binds p-S423,S425-SMAD3	4
IL37(?-218):p-S423,S425-SMAD3 translocates to the nucleus	5
→ IL37(?-218) binds SMAD3	6
▶ IL37, IL37(?-218) translocates from cytosol to extracellular region	7
TBK1 phosphorylation	8
Table of Contents	9