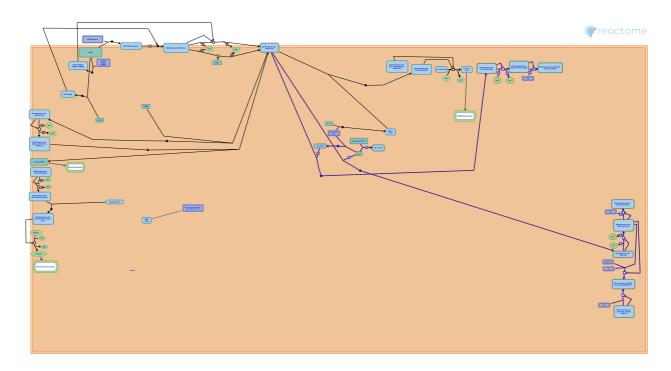


EGFR downregulation



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.

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

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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.

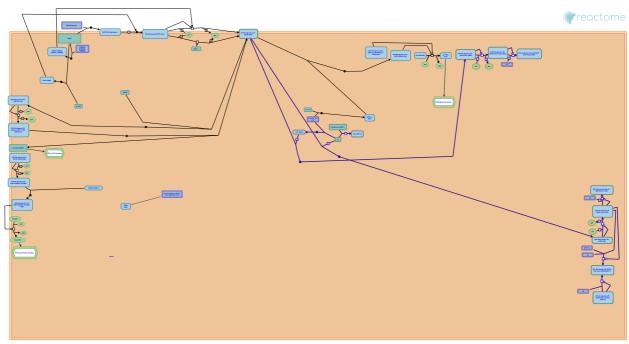
Reactome database release: 88

This document contains 1 pathway and 10 reactions (see Table of Contents)

EGFR downregulation

Stable identifier: R-DRE-182971

Inferred from: EGFR downregulation (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

Binding of CBL to EGFR ↗

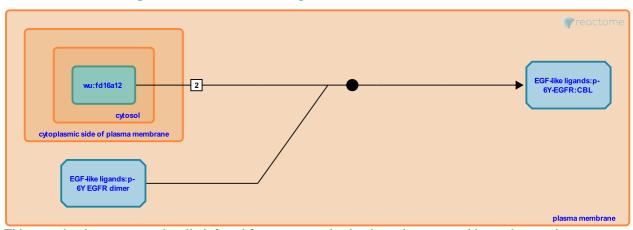
Location: EGFR downregulation

Stable identifier: R-DRE-183055

Type: binding

Compartments: plasma membrane, extracellular region

Inferred from: Binding of CBL to EGFR (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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Followed by: Phosphorylation of CBL (EGFR:CBL)

Phosphorylation of CBL (EGFR:CBL) **对**

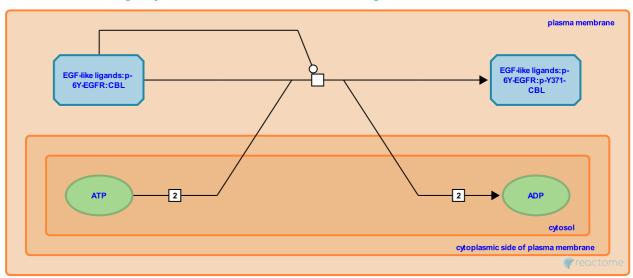
Location: EGFR downregulation

Stable identifier: R-DRE-182969

Type: transition

Compartments: plasma membrane, cytosol

Inferred from: Phosphorylation of CBL (EGFR:CBL) (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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Preceded by: Binding of CBL to EGFR

Followed by: Ubiquitination of stimulated EGFR (CBL), CBL binds and ubiquitinates phosphorylated Sprouty

CBL binds and ubiquitinates phosphorylated Sprouty →

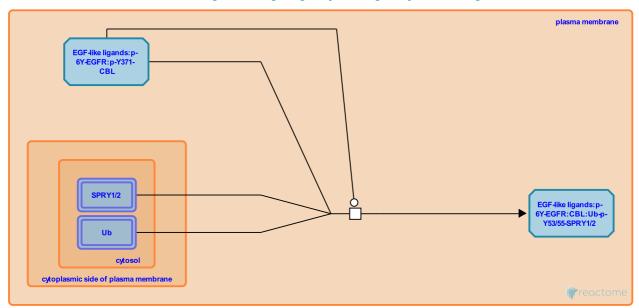
Location: EGFR downregulation

Stable identifier: R-DRE-183089

Type: transition

Compartments: plasma membrane, cytosol

Inferred from: CBL binds and ubiquitinates phosphorylated Sprouty (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: Phosphorylation of CBL (EGFR:CBL)

Ubiquitination of stimulated EGFR (CBL) 对

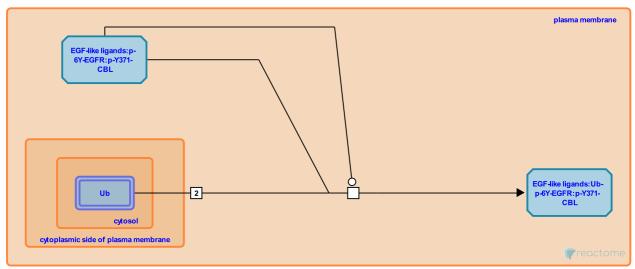
Location: EGFR downregulation

Stable identifier: R-DRE-182993

Type: transition

Compartments: plasma membrane, cytosol

Inferred from: Ubiquitination of stimulated EGFR (CBL) (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.

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

Preceded by: Phosphorylation of CBL (EGFR:CBL)

CBL binds to GRB2 对

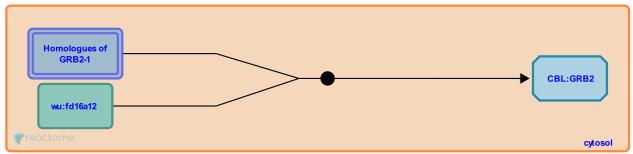
Location: EGFR downregulation

Stable identifier: R-DRE-183052

Type: binding

Compartments: cytosol

Inferred from: CBL binds to GRB2 (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: Localization of CBL:GRB2 to the membrane

Localization of CBL:GRB2 to the membrane

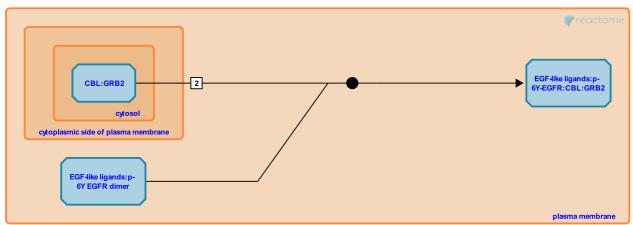
Location: EGFR downregulation

Stable identifier: R-DRE-183067

Type: binding

Compartments: plasma membrane, extracellular region, cytosol

Inferred from: Localization of CBL:GRB2 to the membrane (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: CBL binds to GRB2

Followed by: Phosphorylation of CBL (EGFR:GRB2:CBL)

Phosphorylation of CBL (EGFR:GRB2:CBL) **→**

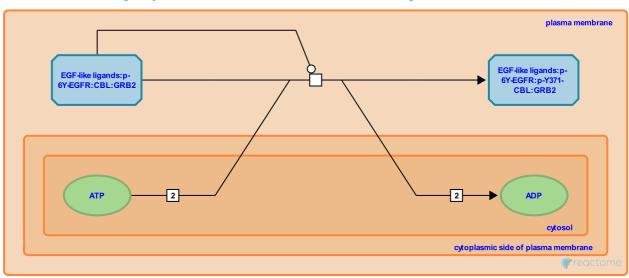
Location: EGFR downregulation

Stable identifier: R-DRE-183058

Type: transition

Compartments: plasma membrane, cytosol

Inferred from: Phosphorylation of CBL (EGFR:GRB2:CBL) (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: Localization of CBL:GRB2 to the membrane

Followed by: Ubiquitination of stimulated EGFR (CBL:GRB2)

Ubiquitination of stimulated EGFR (CBL:GRB2) 对

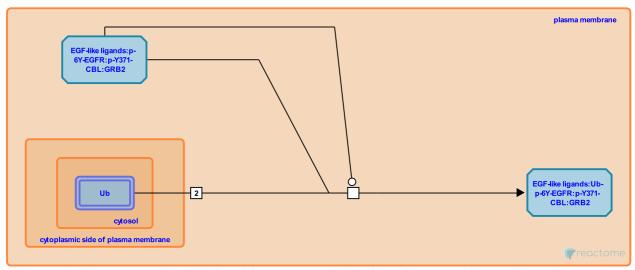
Location: EGFR downregulation

Stable identifier: R-DRE-183036

Type: transition

Compartments: plasma membrane, cytosol

Inferred from: Ubiquitination of stimulated EGFR (CBL:GRB2) (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.

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

Preceded by: Phosphorylation of CBL (EGFR:GRB2:CBL)

Sprouty lures CBL away from EGFR **↗**

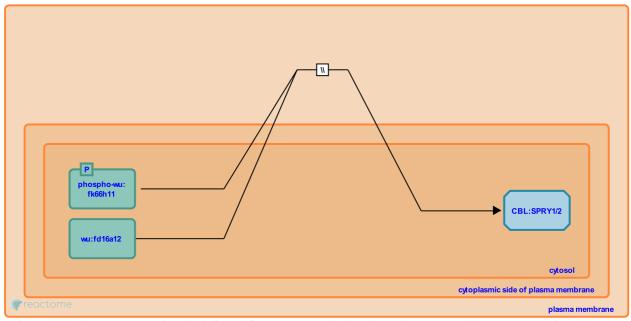
Location: EGFR downregulation

Stable identifier: R-DRE-182988

Type: omitted

Compartments: plasma membrane

Inferred from: Sprouty lures CBL away from EGFR (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

CBL ubiquitinates Sprouty

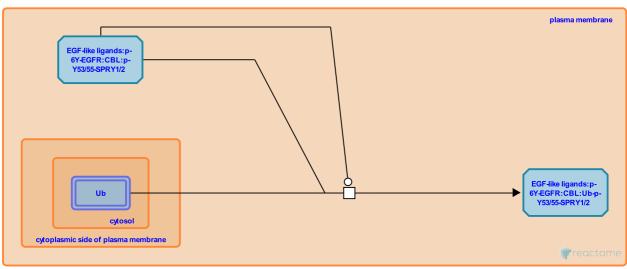
Location: EGFR downregulation

Stable identifier: R-DRE-183051

Type: transition

Compartments: plasma membrane, cytosol

Inferred from: CBL ubiquitinates Sprouty (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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