Spry regulation of FGF signaling

22/09/2020

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.

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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. ↗
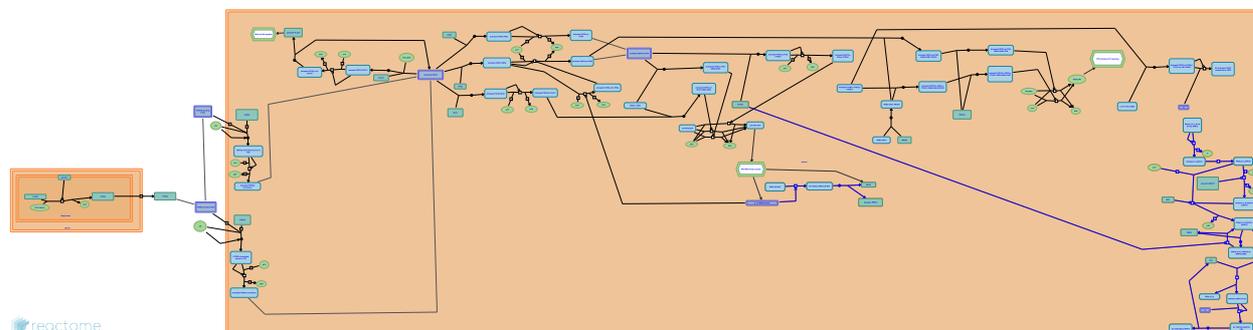
Reactome database release: 73

This document contains 1 pathway and 11 reactions ([see Table of Contents](#))

Spry regulation of FGF signaling ↗

Stable identifier: R-CFA-1295596

Compartments: cytosol, plasma membrane

Inferred from: Spry regulation of FGF 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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp
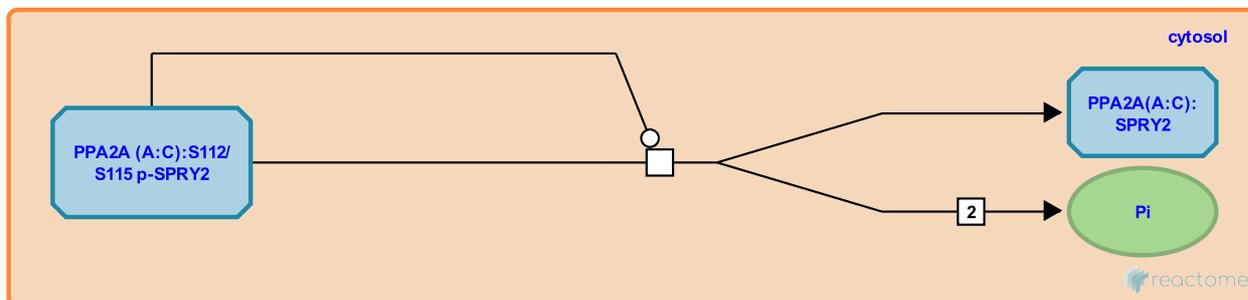
PPA2A dephosphorylates SPRY2 ↗

Location: Spry regulation of FGF signaling

Stable identifier: R-CFA-1295632

Type: transition

Compartments: cytosol

Inferred from: PPA2A dephosphorylates SPRY2 (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: SPRY2 translocates to the plasma membrane

SPRY2 translocates to the plasma membrane ↗
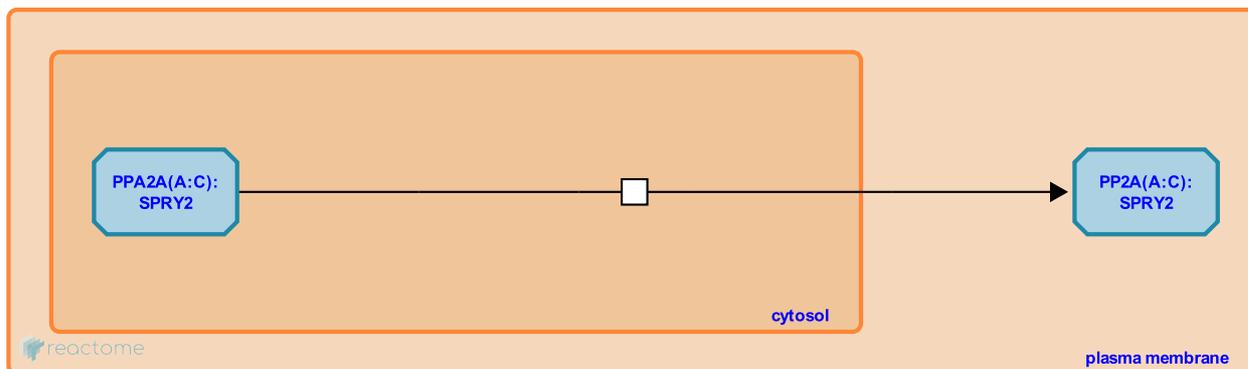
Location: Spry regulation of FGF signaling

Stable identifier: R-CFA-1295599

Type: transition

Compartments: cytosol, plasma membrane

Inferred from: SPRY2 translocates to the plasma 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.

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Preceded by: PPA2A dephosphorylates SPRY2

Followed by: SPRY2 is phosphorylated by phosphorylated MNK1, SRC phosphorylates SPRY2 on Y55 and Y227

SRC phosphorylates SPRY2 on Y55 and Y227 ↗
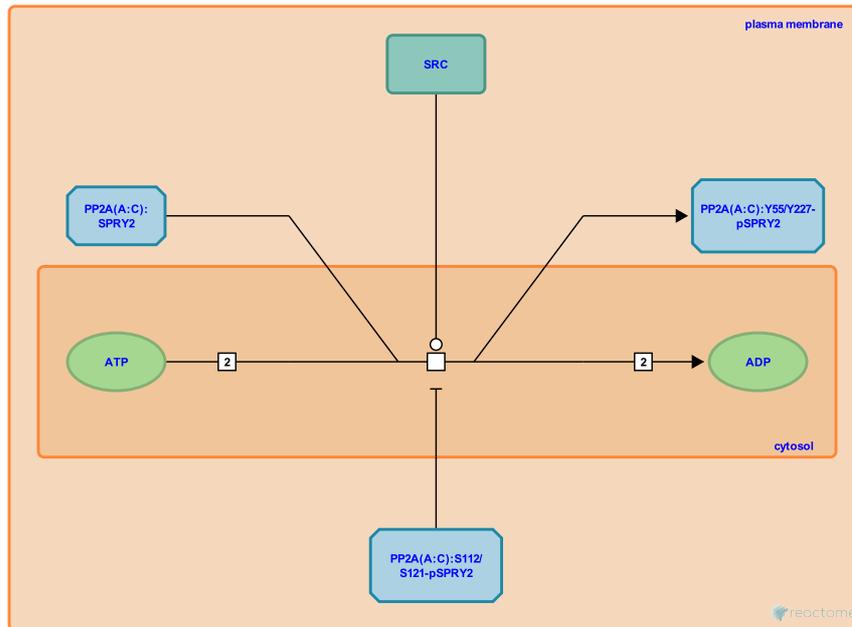
Location: Spry regulation of FGF signaling

Stable identifier: R-CFA-1295609

Type: transition

Compartments: cytosol, plasma membrane

Inferred from: SRC phosphorylates SPRY2 on Y55 and Y227 (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: SPRY2 translocates to the plasma membrane

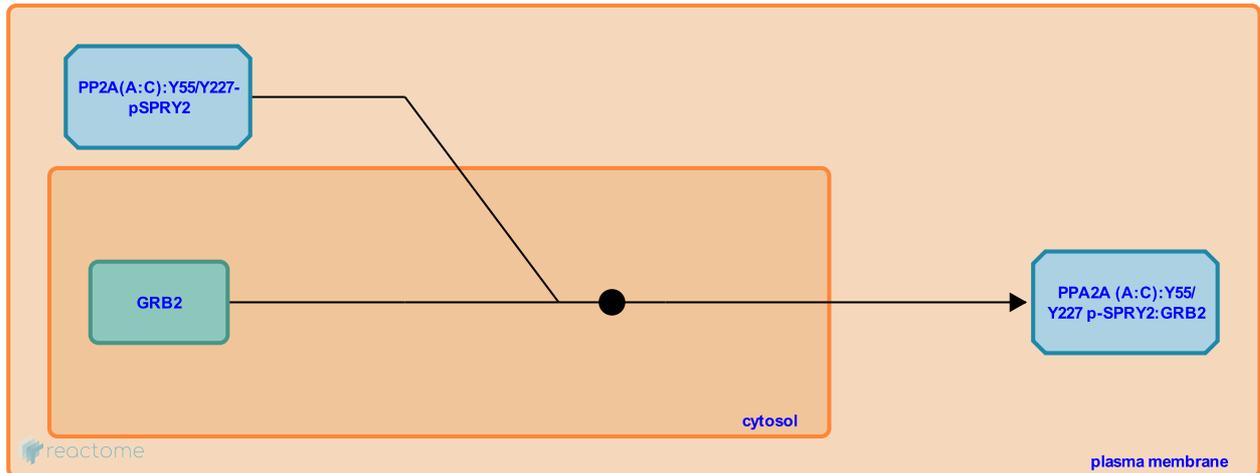**Followed by:** SPRY2 binds GRB2, SPRY2 binds CBL

SPRY2 binds GRB2 ↗

Location: Spry regulation of FGF signaling

Stable identifier: R-CFA-1295613

Type: binding

Compartments: cytosol, plasma membrane

Inferred from: SPRY2 binds 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.

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Preceded by: SRC phosphorylates SPRY2 on Y55 and Y227

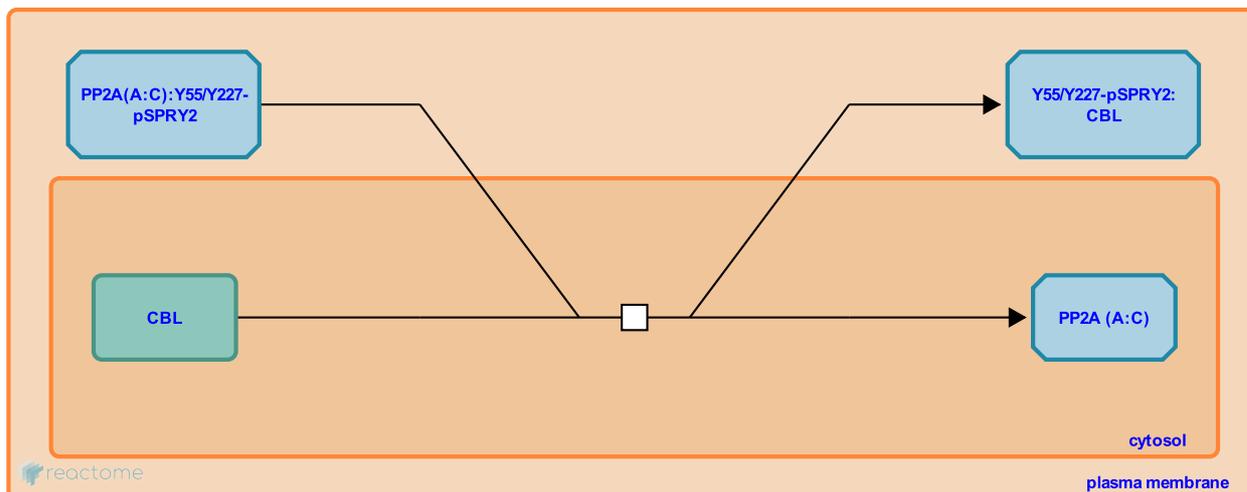**Followed by:** PPTN11 dephosphorylates SPRY2

SPRY2 binds CBL ↗

Location: Spry regulation of FGF signaling

Stable identifier: R-CFA-1295622

Type: transition

Compartments: cytosol, plasma membrane

Inferred from: SPRY2 binds 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: SRC phosphorylates SPRY2 on Y55 and Y227

Followed by: Phosphorylated SPRY2 is ubiquitinated by CBL
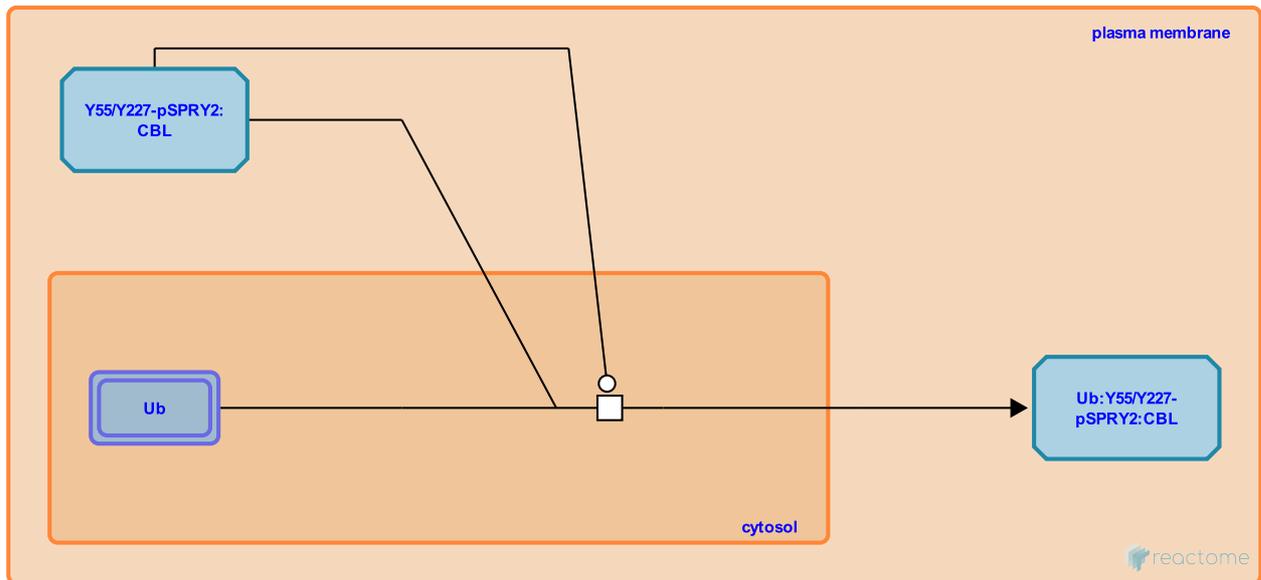
Phosphorylated SPRY2 is ubiquitinated by CBL ↗

Location: Spry regulation of FGF signaling

Stable identifier: R-CFA-934604

Type: transition

Compartments: cytosol, plasma membrane

Inferred from: Phosphorylated SPRY2 is ubiquitinated by 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: SPRY2 binds CBL

Followed by: CBL dissociates from ubiquitinated p-SPRY2
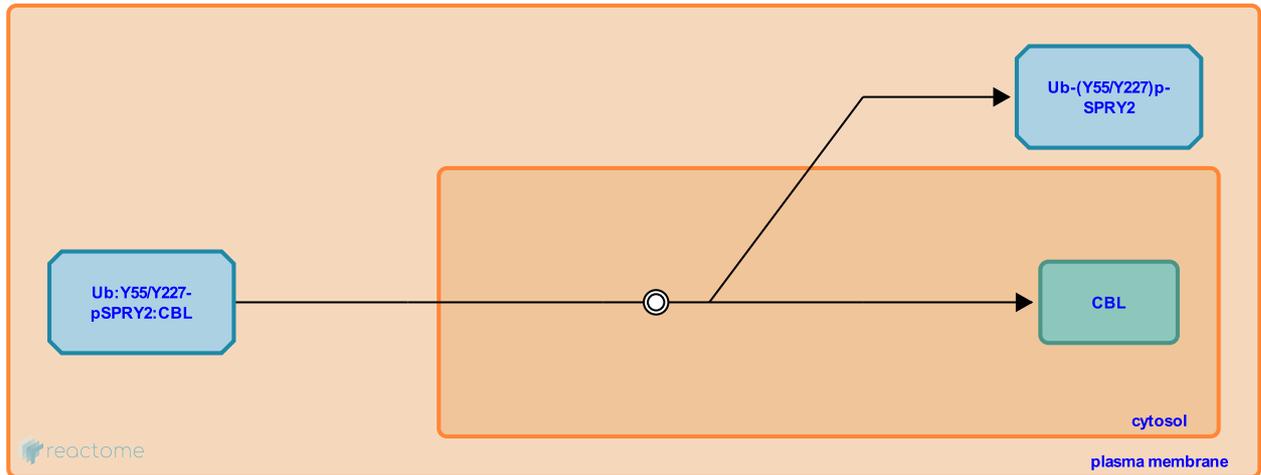
CBL dissociates from ubiquitinated p-SPRY2 ↗

Location: Spry regulation of FGF signaling

Stable identifier: R-CFA-1295621

Type: dissociation

Compartments: cytosol, plasma membrane

Inferred from: CBL dissociates from ubiquitinated p-SPRY2 (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: Phosphorylated SPRY2 is ubiquitinated by CBL
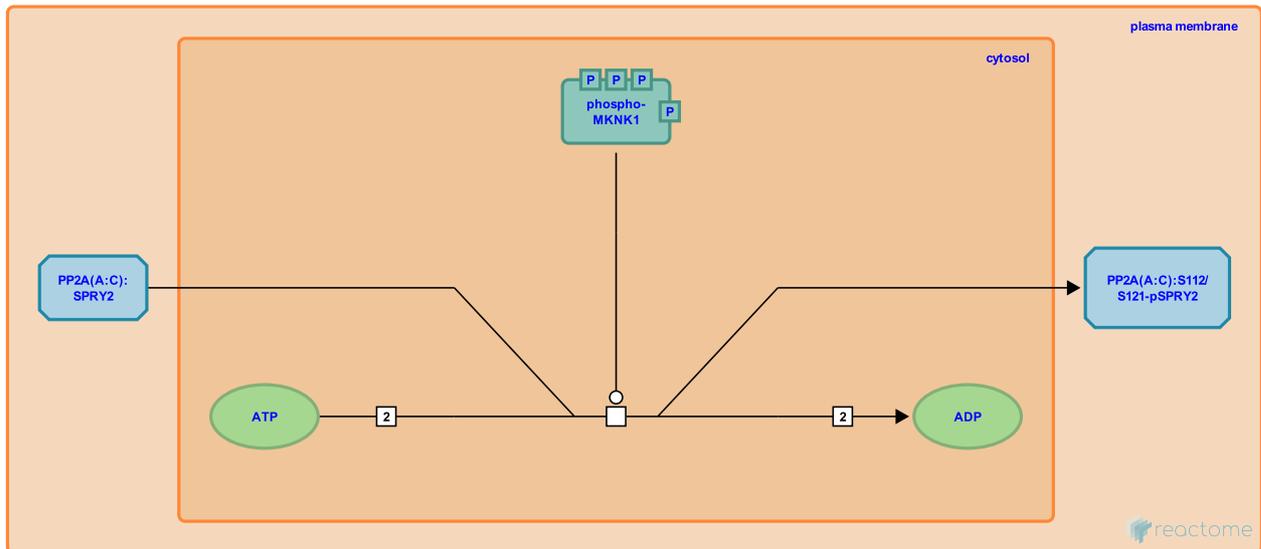
SPRY2 is phosphorylated by phosphorylated MNK1 ↗

Location: Spry regulation of FGF signaling

Stable identifier: R-CFA-934559

Type: transition

Compartments: cytosol, plasma membrane

Inferred from: SPRY2 is phosphorylated by phosphorylated MNK1 (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: SPRY2 translocates to the plasma membrane

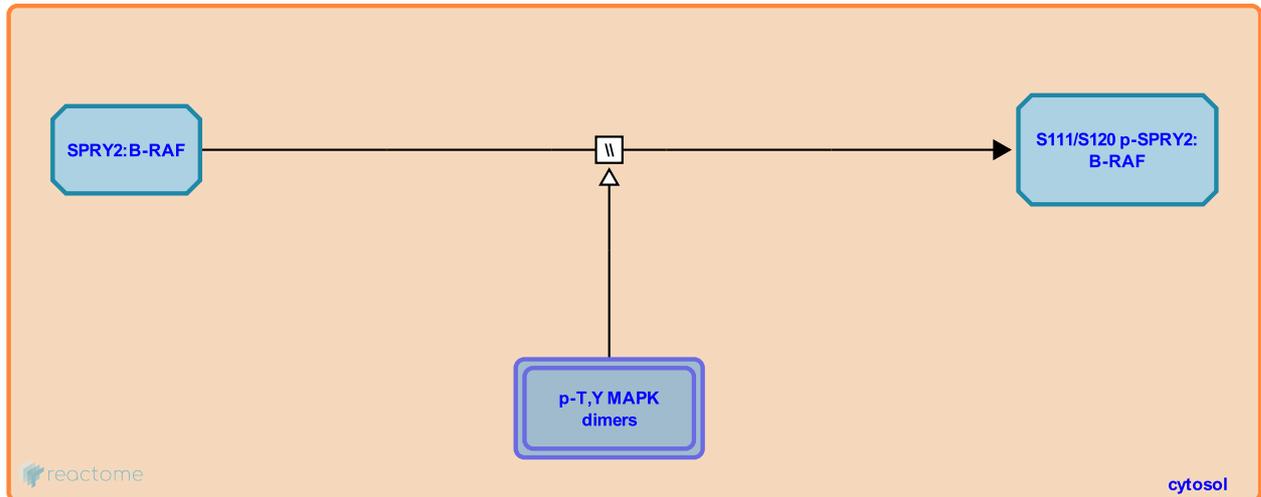## SPRY2 is serine phosphorylated in response to MAPK activation ↗

Location: Spry regulation of FGF signaling

Stable identifier: R-CFA-1295634

Type: omitted

Compartments: cytosol

Inferred from: SPRY2 is serine phosphorylated in response to MAPK 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.

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Followed by: B-RAF dissociates from S111/S120 p-SPRY2

B-RAF dissociates from S111/S120 p-SPRY2 ↗

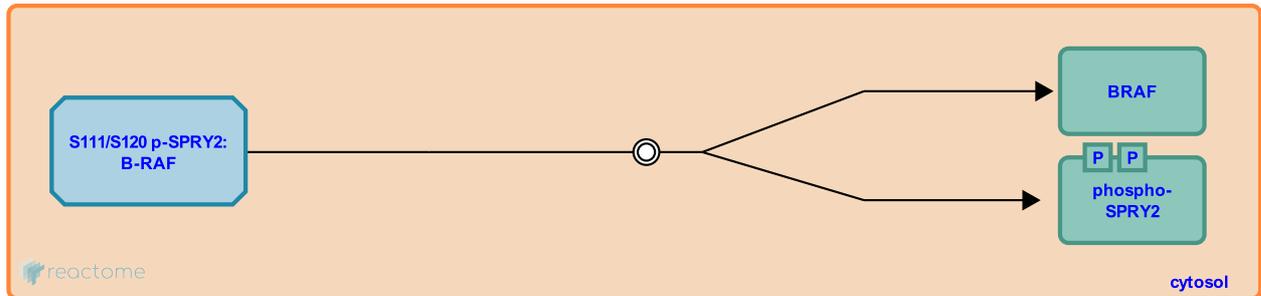**Location:** Spry regulation of FGF signaling

Stable identifier: R-CFA-1295604

Type: dissociation

Compartments: cytosol

Inferred from: B-RAF dissociates from S111/S120 p-SPRY2 (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: SPRY2 is serine phosphorylated in response to MAPK activation
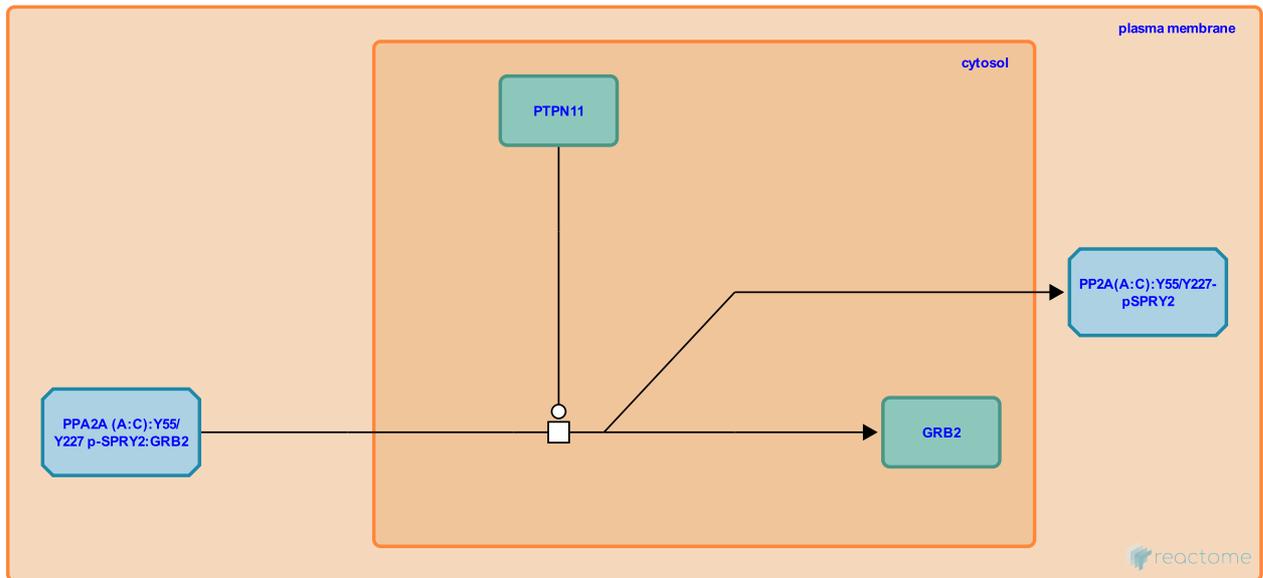
PPTN11 dephosphorylates SPRY2 ↗

Location: Spry regulation of FGF signaling

Stable identifier: R-CFA-1549564

Type: transition

Compartments: cytosol, plasma membrane

Inferred from: PPTN11 dephosphorylates SPRY2 (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: SPRY2 binds GRB2

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