Hedgehog 'off' state

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.

17/05/2024

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.

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. ↗
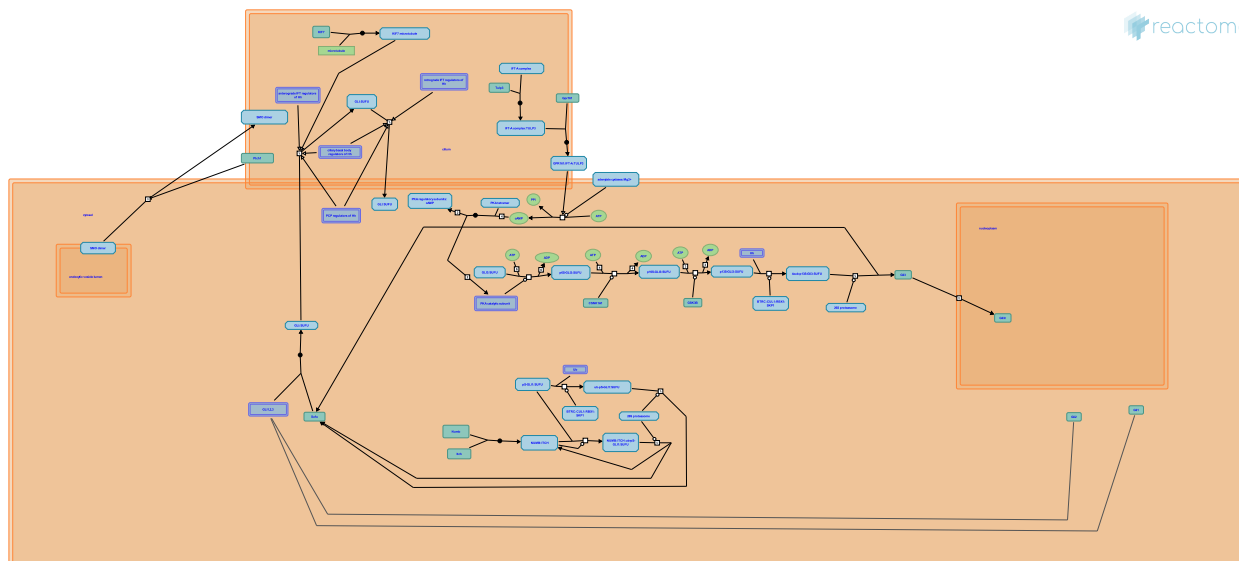
Reactome database release: 88

This document contains 3 pathways and 10 reactions (see Table of Contents)

Hedgehog 'off' state ↗

Stable identifier: R-MMU-5610787

Inferred from: Hedgehog 'off' state (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

PTCH1 inhibits accumulation of SMO in the primary cilium in the absence of Hh signal ↗
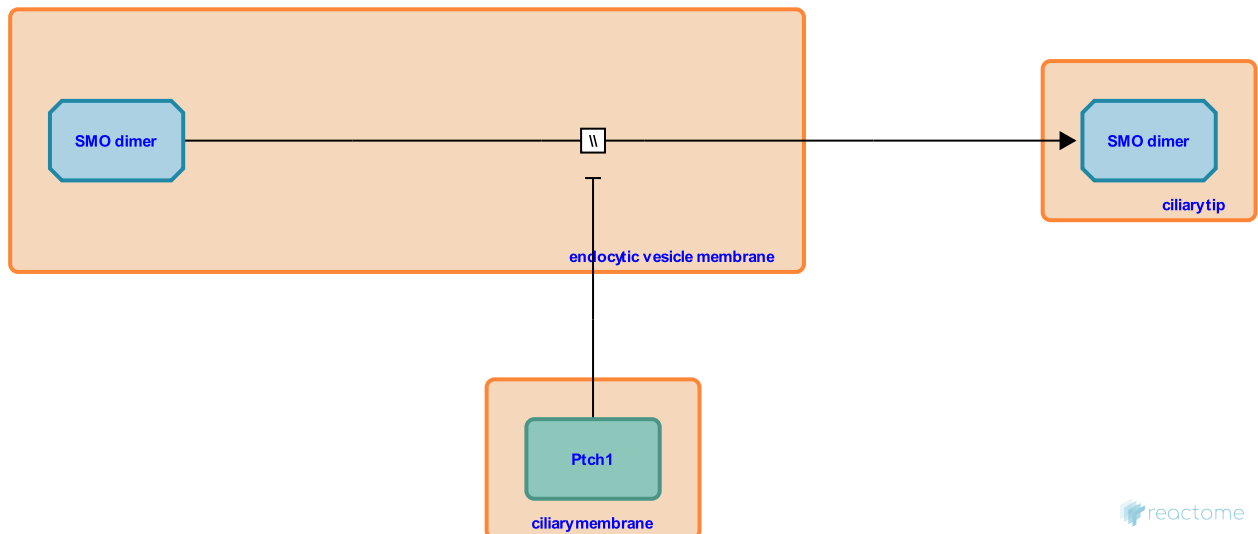
Location: Hedgehog 'off' state

Stable identifier: R-MMU-5610763

Type: omitted

Compartments: endocytic vesicle membrane

Inferred from: PTCH1 inhibits accumulation of SMO in the primary cilium in the absence of Hh signal (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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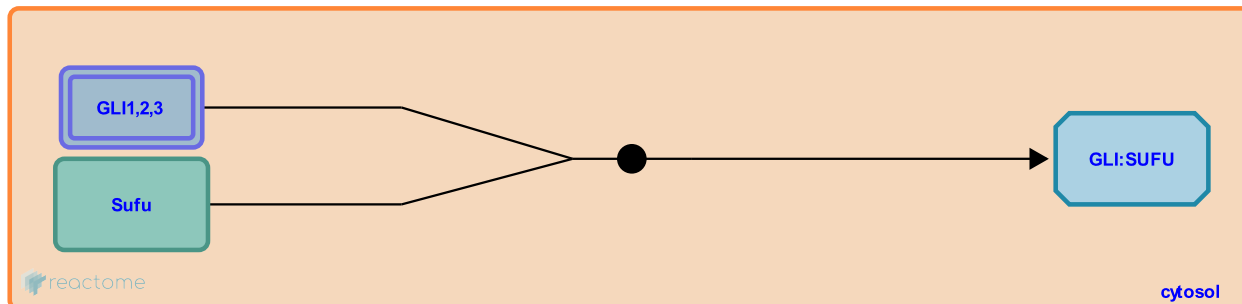
GLI proteins bind SUFU ↗

Location: Hedgehog 'off' state

Stable identifier: R-MMU-5610723

Type: binding

Compartments: cytosol

Inferred from: GLI proteins bind SUFU (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

KIF7 is recruited to the ciliary tip through interaction with axonemal microtubules ↗
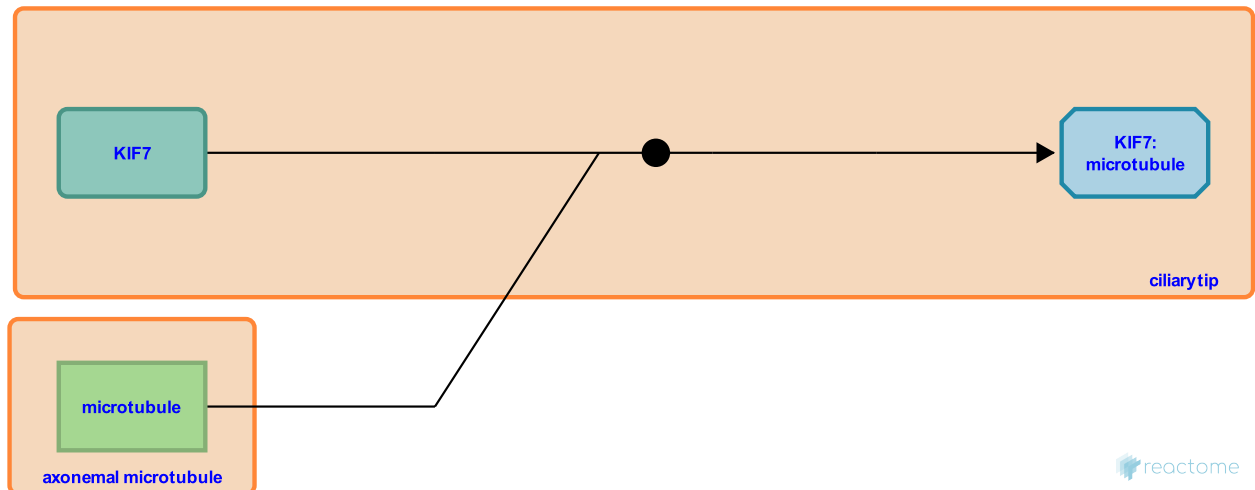
Location: Hedgehog 'off' state

Stable identifier: R-MMU-5610733

Type: binding

Compartments: ciliary tip

Inferred from: KIF7 is recruited to the ciliary tip through interaction with axonemal microtubules (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

The intraflagellar transport B (IFT-B) complex is required for the transit of GLI:SUFU complexes to the ciliary tip ↗
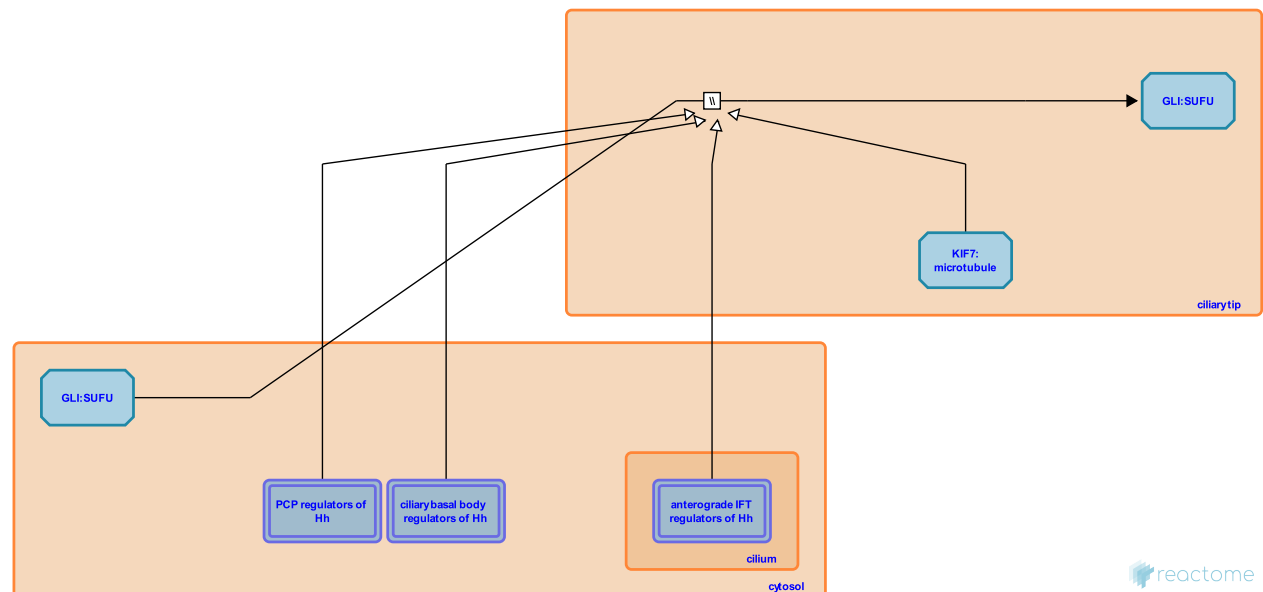
Location: Hedgehog 'off' state

Stable identifier: R-MMU-5610767

Type: omitted

Compartments: ciliary tip

Inferred from: The intraflagellar transport B (IFT-B) complex is required for the transit of GLI:SUFU complexes to the ciliary tip (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

The intraflagellar transport A (IFT-A) complex is required for the transit of GLI:SUFU complexes to the ciliary base ↗
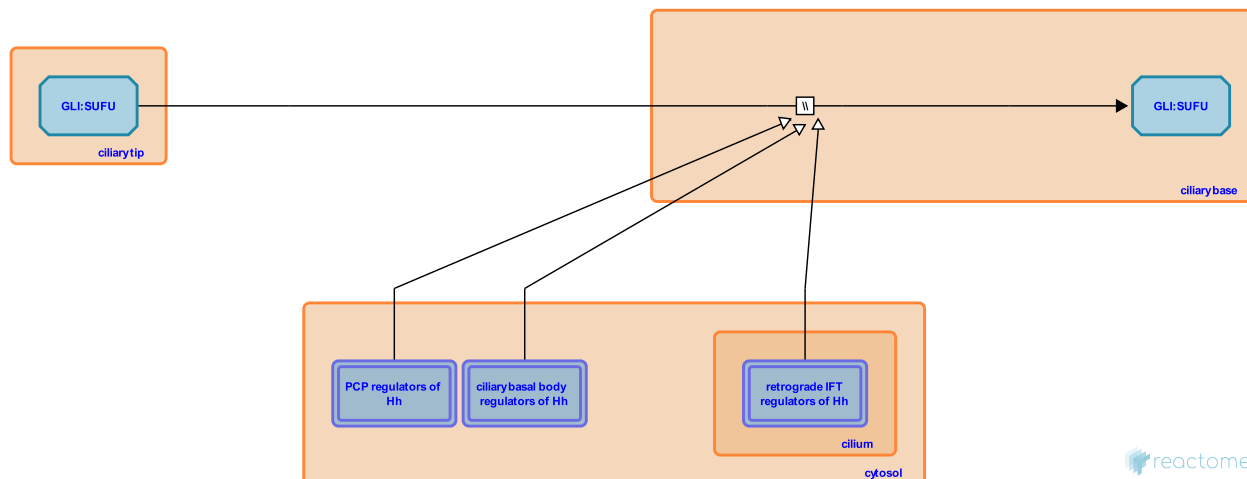
Location: Hedgehog 'off' state

Stable identifier: R-MMU-5610766

Type: omitted

Compartments: ciliary base

Inferred from: The intraflagellar transport A (IFT-A) complex is required for the transit of GLI:SUFU complexes to the ciliary base (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

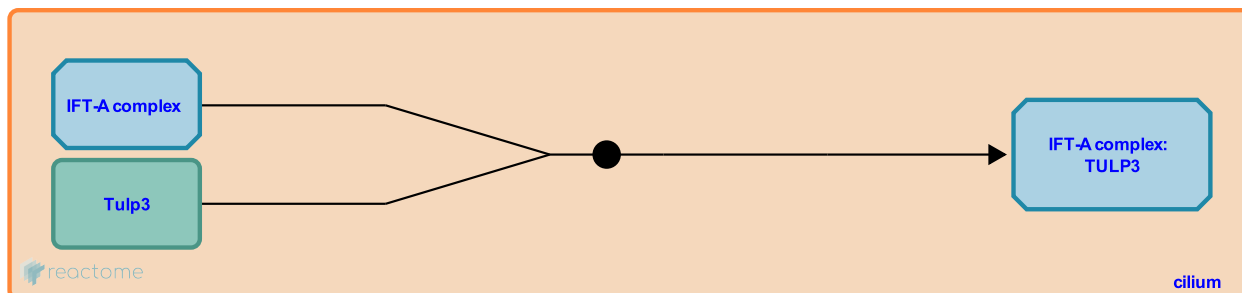## The IFT-A complex recruits TULP3 ↗

Location: Hedgehog 'off' state

Stable identifier: R-MMU-5610726

Type: binding

Compartments: cilium

Inferred from: The IFT-A complex recruits TULP3 (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: TULP3 is required for GPR161 localization in the cilium

TULP3 is required for GPR161 localization in the cilium ↗

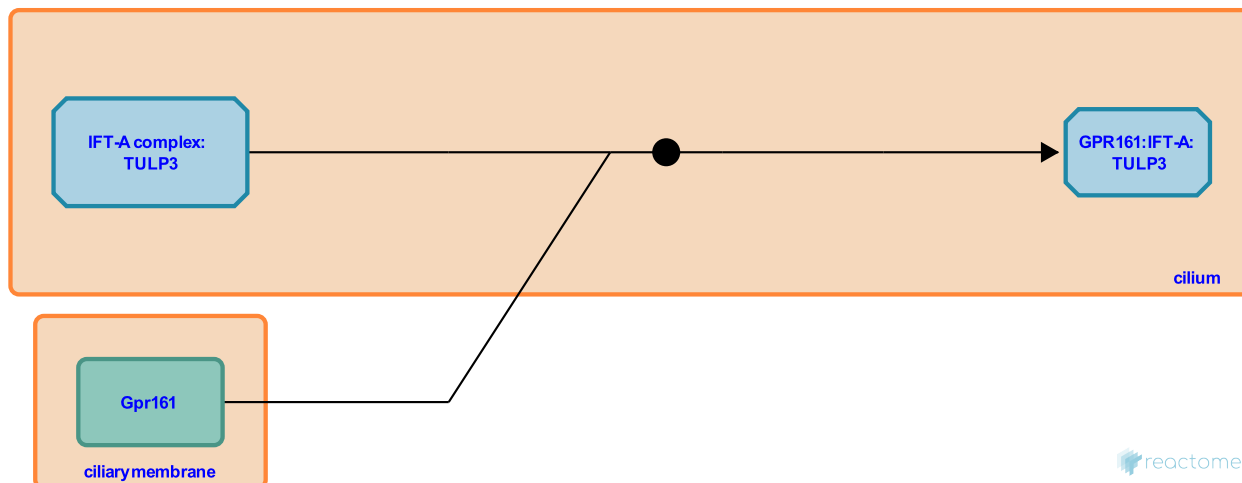**Location:** Hedgehog 'off' state

Stable identifier: R-MMU-5610725

Type: binding

Compartments: cilium

Inferred from: TULP3 is required for GPR161 localization in the cilium (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: The IFT-A complex recruits TULP3

Followed by: GPR161 promotes cAMP production in a G alpha(s)-dependent manner

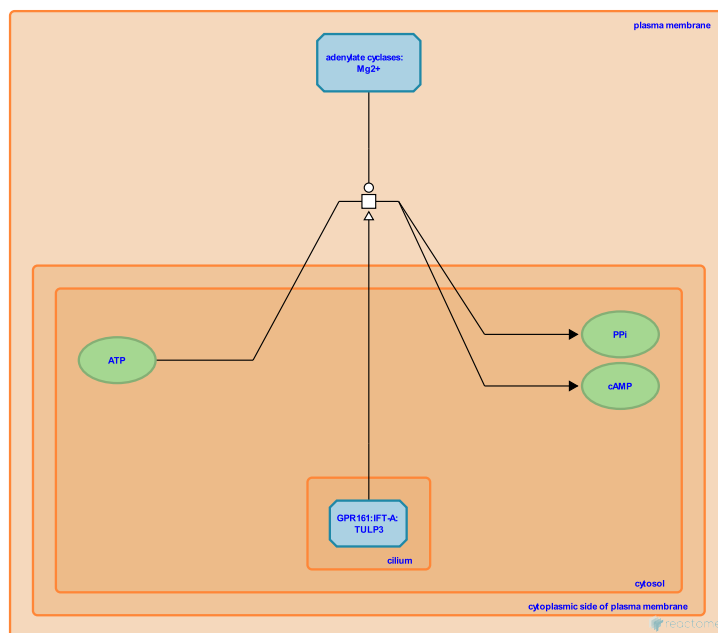# GPR161 promotes cAMP production in a G alpha(s)-dependent manner ↗

Location: Hedgehog 'off' state

Stable identifier: R-MMU-5610727

Type: transition

Compartments: plasma membrane

Inferred from: GPR161 promotes cAMP production in a G alpha(s)-dependent manner (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: TULP3 is required for GPR161 localization in the cilium

Followed by: cAMP dissociates PKA, promoting GLI processing
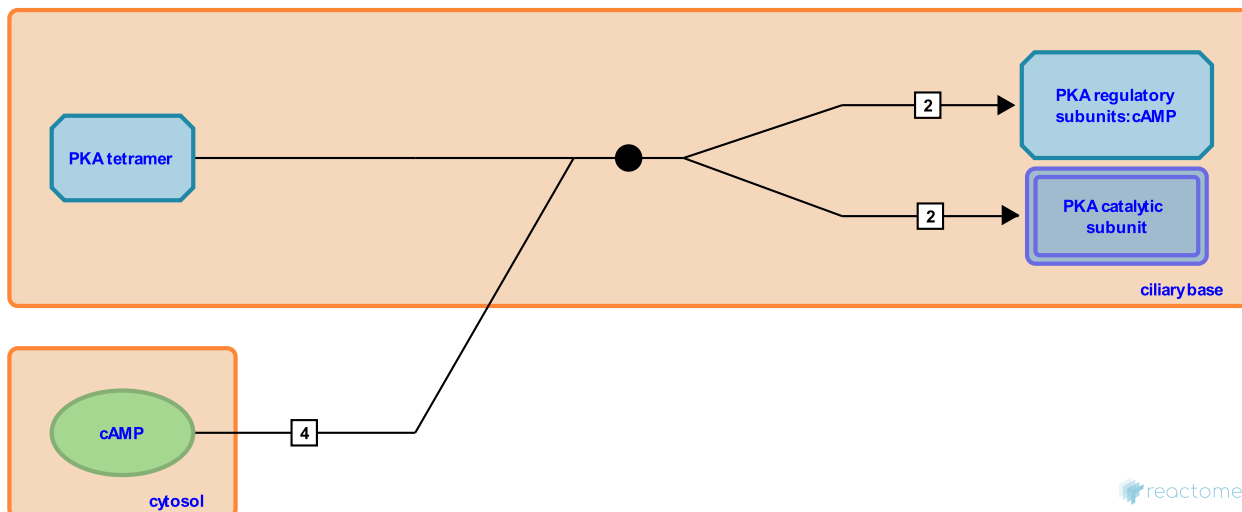
cAMP dissociates PKA, promoting GLI processing ↗

Location: Hedgehog 'off' state

Stable identifier: R-MMU-5610749

Type: binding

Compartments: ciliary base

Inferred from: cAMP dissociates PKA, promoting GLI processing (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: GPR161 promotes cAMP production in a G alpha(s)-dependent manner

GLI3 is processed to GLI3R by the proteasome ↗

Location: Hedgehog 'off' state

Stable identifier: R-MMU-5610785

Inferred from: GLI3 is processed to GLI3R by the proteasome (Homo sapiens)
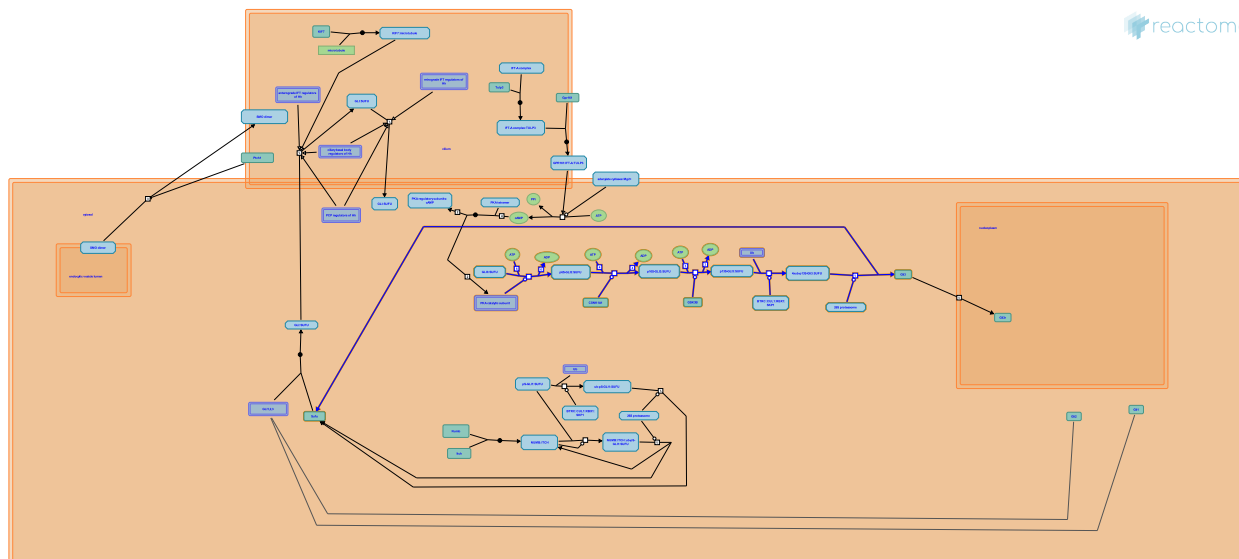
This event has been computationally inferred from an event that has been demonstrated in another species.

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

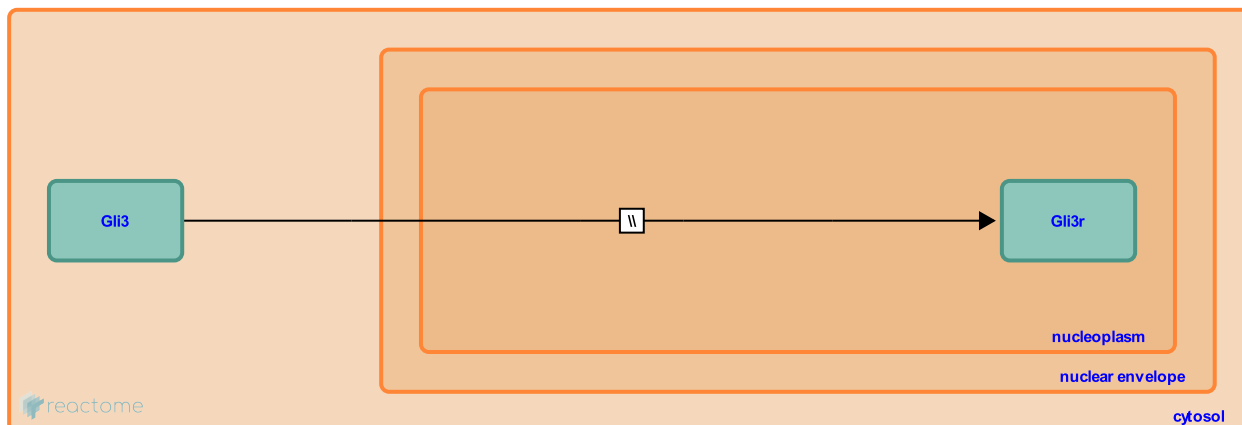## GLI3R translocates to the nucleus ↗

Location: Hedgehog 'off' state

Stable identifier: R-MMU-5610752

Type: omitted

Compartments: nucleoplasm, cytosol

Inferred from: GLI3R 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.
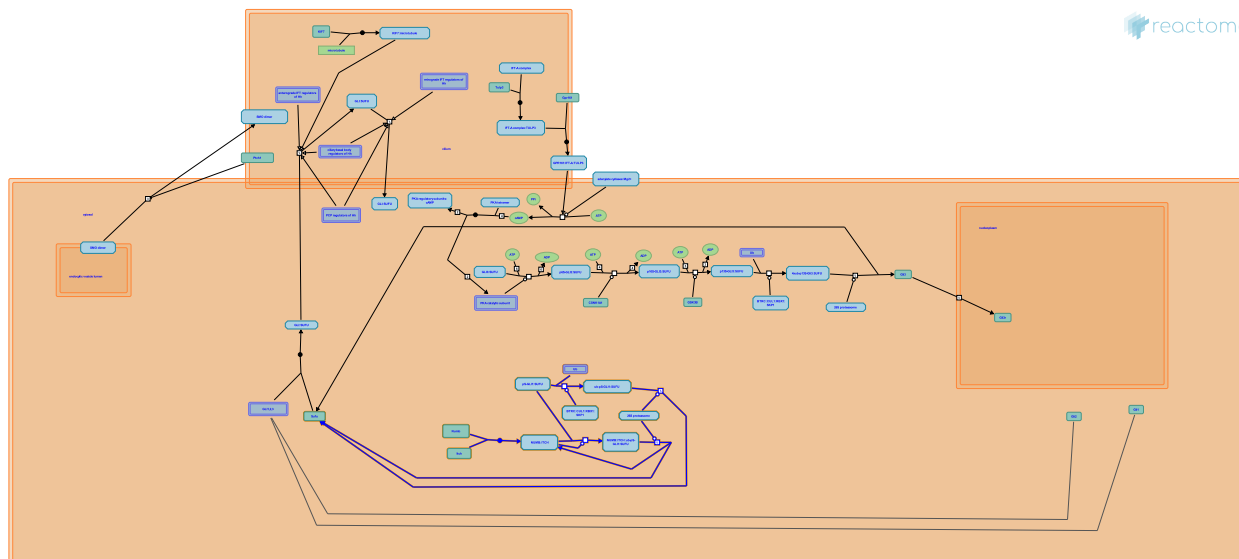
More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Degradation of GLI1 by the proteasome ↗

Location: Hedgehog 'off' state

Stable identifier: R-MMU-5610780

Inferred from: Degradation of GLI1 by the proteasome (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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