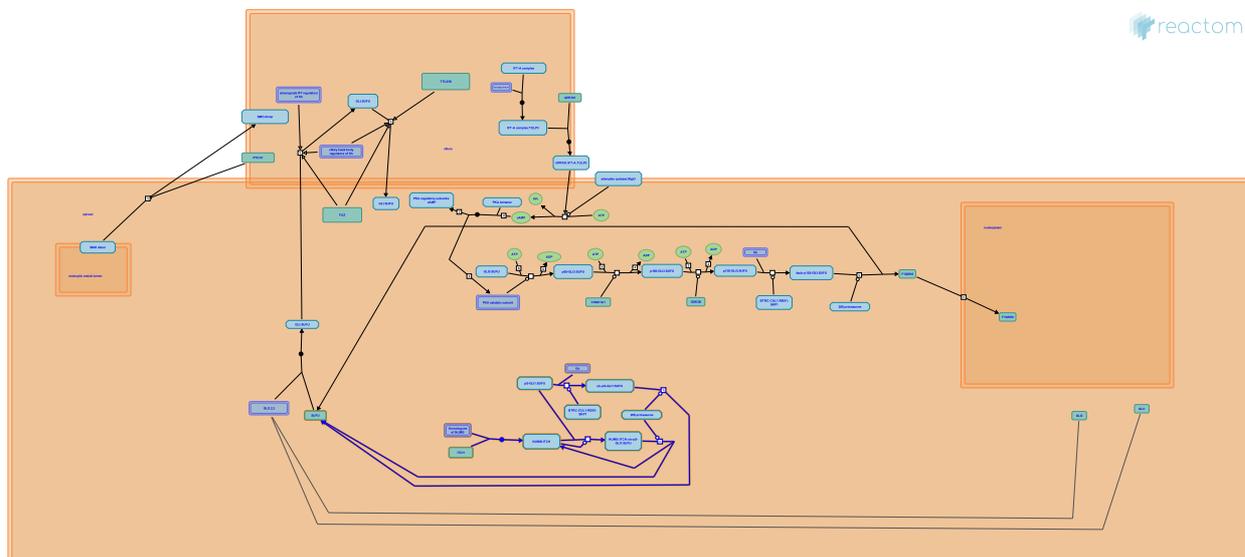


# Degradation of GLI1 by the proteasome



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

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## 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. [↗](#)
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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. [↗](#)

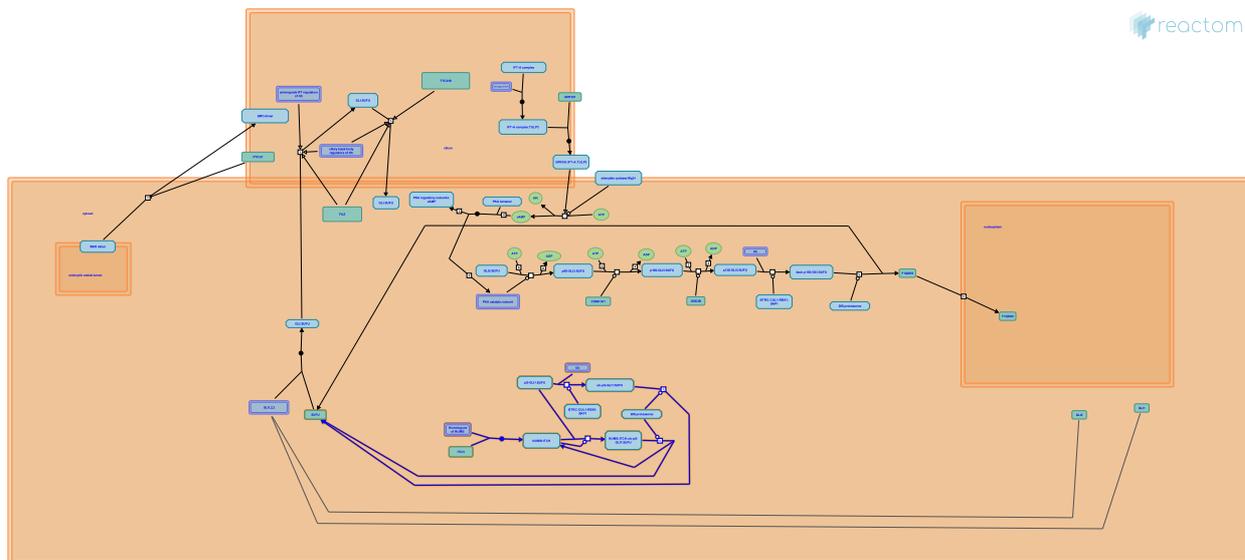
Reactome database release: 70

This document contains 1 pathway and 5 reactions ([see Table of Contents](#))

## Degradation of GLI1 by the proteasome ↗

**Stable identifier:** R-DRE-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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## SCF(beta-TrCP) ubiquitinates p-GLI1 [↗](#)

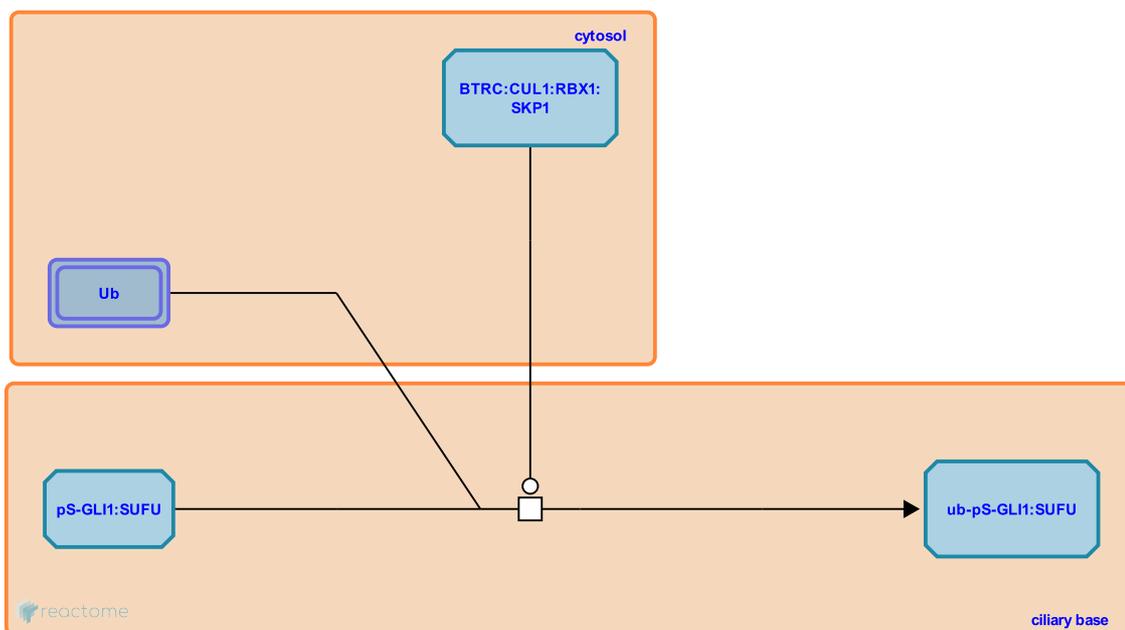
**Location:** [Degradation of GLI1 by the proteasome](#)

**Stable identifier:** R-DRE-5610742

**Type:** transition

**Compartments:** ciliary base

**Inferred from:** [SCF\(beta-TrCP\) ubiquitinates p-GLI1 \(Homo sapiens\)](#)



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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Followed by:** [GLI1 is degraded by the proteasome after ubiquitination by beta-TrCP](#)

## GLI1 is degraded by the proteasome after ubiquitination by beta-TrCP ↗

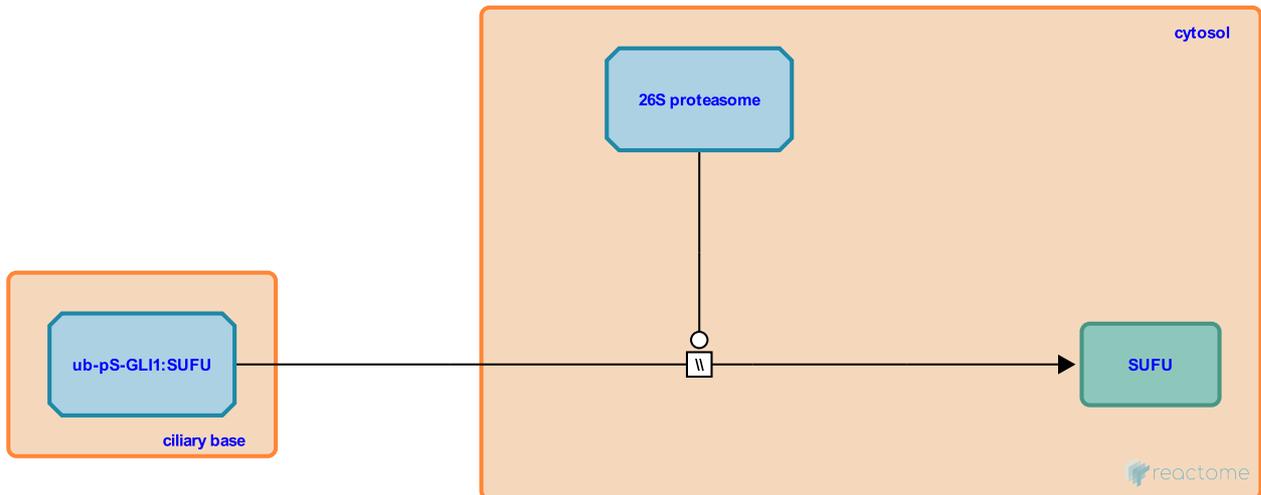
**Location:** [Degradation of GLI1 by the proteasome](#)

**Stable identifier:** R-DRE-5610758

**Type:** omitted

**Compartments:** cytosol

**Inferred from:** [GLI1 is degraded by the proteasome after ubiquitination by beta-TrCP \(Homo sapiens\)](#)



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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [SCF\(beta-TrCP\) ubiquitinates p-GLI1](#)

## NUMB binds ITCH ↗

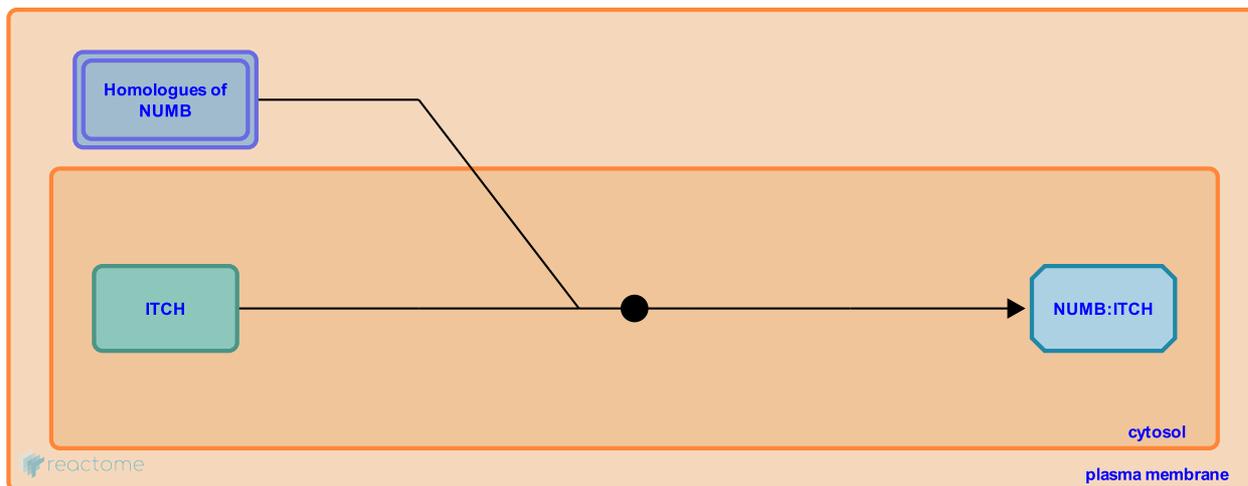
**Location:** [Degradation of GLI1 by the proteasome](#)

**Stable identifier:** R-DRE-5610735

**Type:** binding

**Compartments:** cytosol

**Inferred from:** [NUMB binds ITCH \(Homo sapiens\)](#)



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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Followed by:** [NUMB:ITCH bind and ubiquitnate GLI1](#)

## NUMB:ITCH bind and ubiquitnate GLI1 ↗

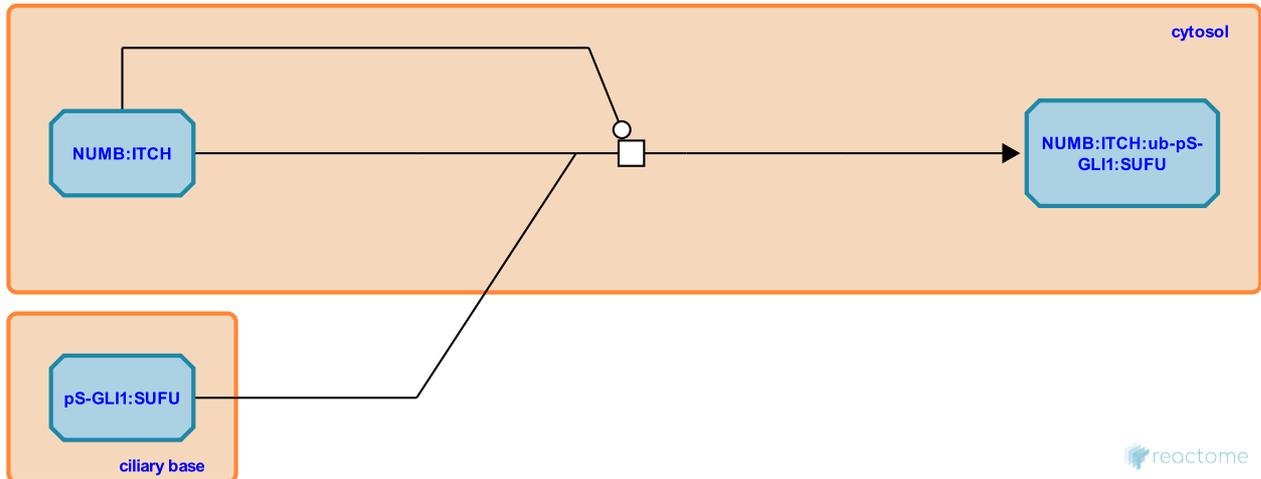
**Location:** [Degradation of GLI1 by the proteasome](#)

**Stable identifier:** R-DRE-5610737

**Type:** transition

**Compartments:** cytosol

**Inferred from:** [NUMB:ITCH bind and ubiquitnate GLI1 \(Homo sapiens\)](#)



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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [NUMB binds ITCH](#)

**Followed by:** [GLI1 is degraded by the proteasome after ubiquitination by ITCH](#)

## GLI1 is degraded by the proteasome after ubiquitination by ITCH ↗

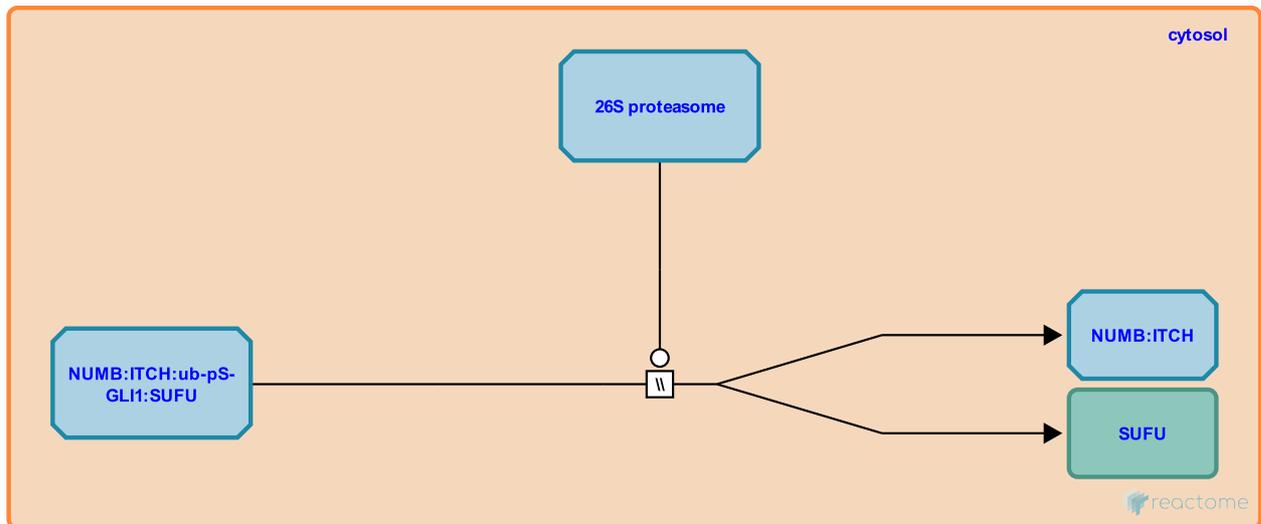
**Location:** [Degradation of GLI1 by the proteasome](#)

**Stable identifier:** R-DRE-5610760

**Type:** omitted

**Compartments:** cytosol

**Inferred from:** [GLI1 is degraded by the proteasome after ubiquitination by ITCH \(Homo sapiens\)](#)



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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [NUMB:ITCH bind and ubiquitnate GLI1](#)

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