TGF-beta receptor signaling activates SMADs

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.

31/10/2022
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


Reactome database release: 82

This document contains 2 pathways and 6 reactions (see Table of Contents)

https://reactome.org
TGF-beta receptor signaling activates SMADs

Stable identifier: R-CEL-2173789

Inferred from: TGF-beta receptor signaling activates SMADs (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
Latent TGF-beta-1 is cleaved by FURIN

Location: TGF-beta receptor signaling activates SMADs

Stable identifier: R-CEL-170844

Type: transition

Compartments: Golgi lumen, Golgi membrane

Inferred from: Latent TGF-beta-1 is cleaved by FURIN (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><a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp</a>

Followed by: Secretion and activation of the latent large complex of TGF-beta-1
**Secretion and activation of the latent large complex of TGF-beta-1**

**Location:** TGF-beta receptor signaling activates SMADs

**Stable identifier:** R-CEL-177107

**Type:** omitted

**Compartments:** Golgi lumen, extracellular region

**Inferred from:** Secretion and activation of the latent large complex of TGF-beta-1 (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:** Latent TGF-beta-1 is cleaved by FURIN
Latent TGF-beta-3 binds integrins

Location: TGF-beta receptor signaling activates SMADs

Stable identifier: R-CEL-2396029

Type: binding

Compartments: plasma membrane

Inferred from: Latent TGF-beta-3 binds integrins (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
Activated type I receptor phosphorylates SMAD2/3 directly

**Location:** TGF-beta receptor signaling activates SMADs

**Stable identifier:** R-CEL-170868

**Type:** transition

**Compartments:** early endosome membrane

**Inferred from:** Activated type I receptor phosphorylates SMAD2/3 directly (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:** Phosphorylated SMAD2/3 dissociates from TGFBR
Phosphorylated SMAD2/3 dissociates from TGFBR

Location: TGF-beta receptor signaling activates SMADs

Stable identifier: R-CEL-170850

Type: dissociation

Compartments: early endosome

Inferred from: Phosphorylated SMAD2/3 dissociates from TGFBR (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: Activated type I receptor phosphorylates SMAD2/3 directly

Followed by: Phosphorylated SMAD2 and SMAD3 form a complex with SMAD4
**Phosphorylated SMAD2 and SMAD3 form a complex with SMAD4**

**Location:** TGF-beta receptor signaling activates SMADs

**Stable identifier:** R-CEL-170847

**Type:** transition

**Compartments:** cytosol

**Inferred from:** Phosphorylated SMAD2 and SMAD3 form a complex with SMAD4 (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:** Phosphorylated SMAD2/3 dissociates from TGFB

https://reactome.org
**Downregulation of TGF-beta receptor signaling**

**Location:** TGF-beta receptor signaling activates SMADs

**Stable identifier:** R-CEL-2173788

**Inferred from:** Downregulation of TGF-beta receptor 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](http://www.pantherdb.org/about.jsp)
Table of Contents

Introduction 1

- TGF-beta receptor signaling activates SMADs 2
  - Latent TGF-beta-1 is cleaved by FURIN 3
  - Secretion and activation of the latent large complex of TGF-beta-1 4
- Latent TGF-beta-3 binds integrins 5
- Activated type I receptor phosphorylates SMAD2/3 directly 6
- Phosphorylated SMAD2/3 dissociates from TGFBR 7
- Phosphorylated SMAD2 and SMAD3 form a complex with SMAD4 8
- Downregulation of TGF-beta receptor signaling 9

Table of Contents 10