

# PP1 dephosphorylates TGFBR1

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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. [↗](#)
- 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: 77

This document contains 1 reaction ([see Table of Contents](#))

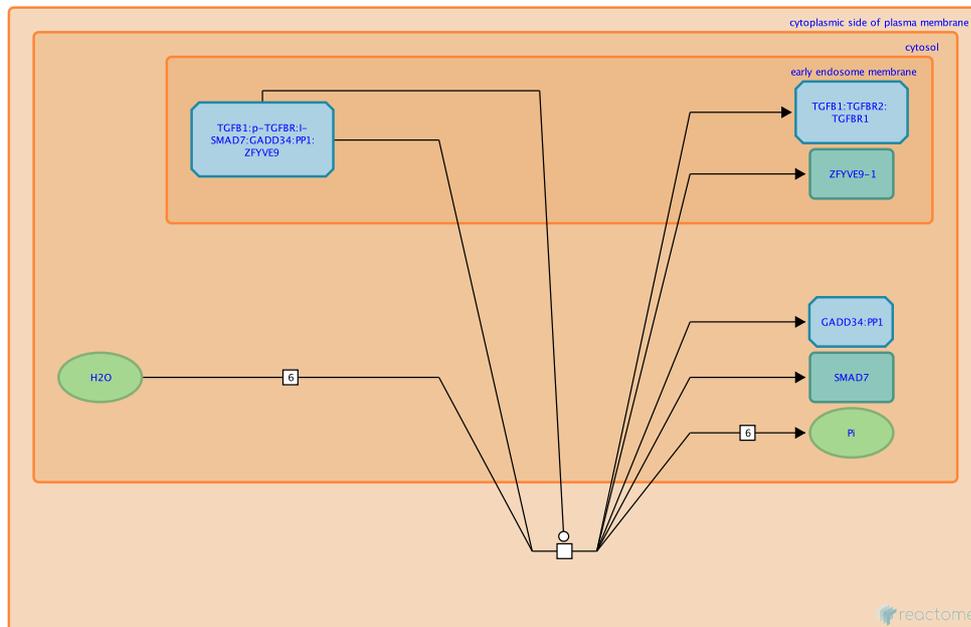
## PP1 dephosphorylates TGFBR1 ↗

**Stable identifier:** R-HSA-178178

**Type:** transition

**Compartments:** cytoplasmic side of plasma membrane

**Inferred from:** PP1CC dephosphorylates TGFBR1 (Homo sapiens)



PP1 dephosphorylates TGF-beta receptor-1 (TGFBR1), thereby inhibiting TGF-beta signaling. It has not been precisely examined whether PP1 dephosphorylates all TGFBR1 serine and threonine residues phosphorylated by TGFBR2 (Shi et al. 2004). This was inferred from experiments that used a recombinant mouse Smad7 and recombinant human TGFBR1, TGFBR2 and PP1.

### Literature references

Shi, W., Sun, C., He, B., Xiong, W., Shi, X., Yao, D. et al. (2004). GADD34-PP1c recruited by Smad7 dephosphorylates TGFbeta type I receptor. *J Cell Biol*, 164, 291-300. ↗

### Editions

2006-02-02	Authored	Jassal, B., Heldin, CH., Moustakas, A., Huminiecki, L.
2012-04-05	Revised	Orlic-Milacic, M.
2012-04-10	Edited	Jassal, B.
2012-05-14	Reviewed	Huang, T.