

# PI3P is dephosphorylated to PI by the Mtmr2:Sbf2 tetramer at the plasma membrane

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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.

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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: 74

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

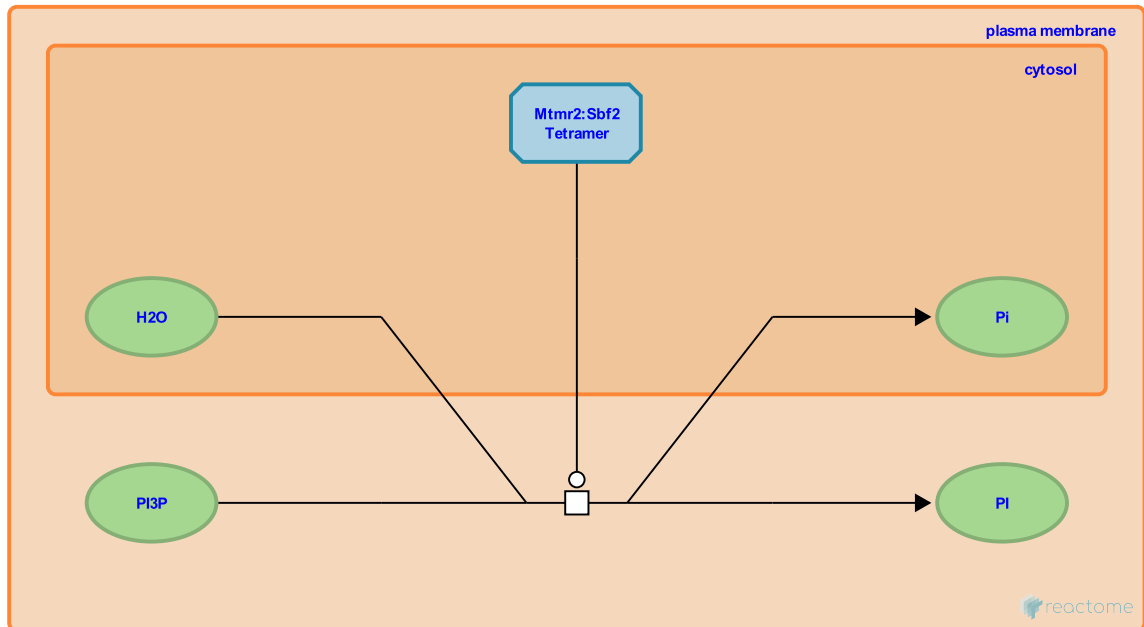
## PI3P is dephosphorylated to PI by the Mtmr2:Sbf2 tetramer at the plasma membrane



**Stable identifier:** R-MMU-6809977

**Type:** transition

**Compartments:** plasma membrane, cytosol



Formation of the complex with Sbf2 (Mtmr13) dramatically increases phosphatidylinositol-3-phosphatase catalytic activity of mouse Mtmr2 (Berger et al. 2006).

### Literature references

Berger, P., Berger, I., Schaffitzel, C., Tersar, K., Volkmer, B., Suter, U. (2006). Multi-level regulation of myotubularin-related protein-2 phosphatase activity by myotubularin-related protein-13/set-binding factor-2. *Hum. Mol. Genet.*, 15, 569-79. [↗](#)

### Editions

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