

# SapM dephosphorylates PI3P

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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

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- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
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Reactome database release: 88

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

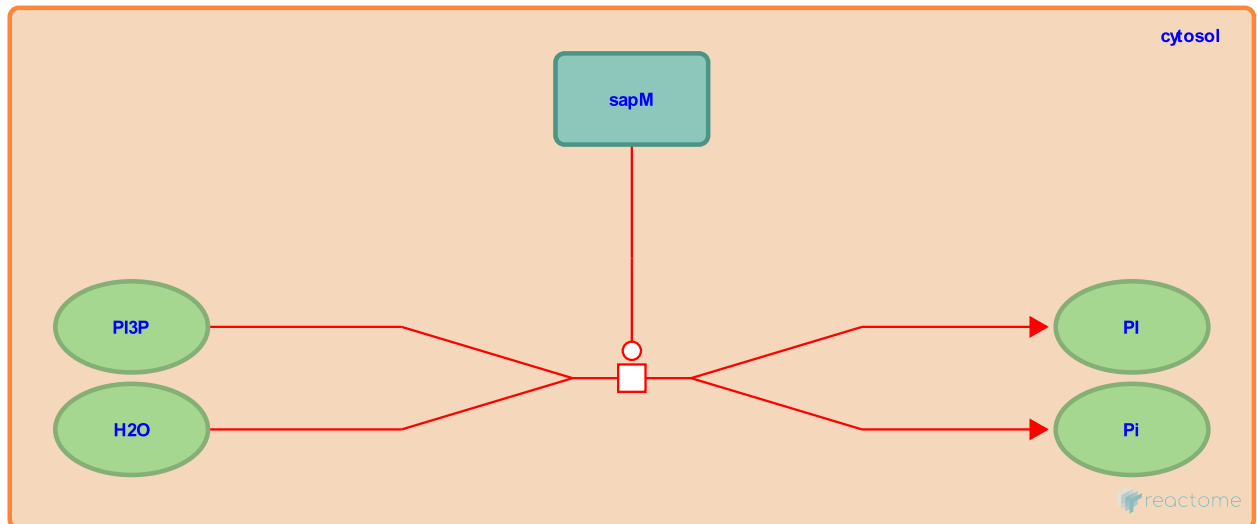
## SapM dephosphorylates PI3P [↗](#)

**Stable identifier:** R-HSA-9636457

**Type:** transition

**Compartments:** cytosol

**Diseases:** tuberculosis



Phosphatidylinositol-3-phosphatase (SapM) catalyzes the dephosphorylation of phosphatidylinositol 3-phosphate (PI3P) to phosphatidylinositol (PI) (Vergne et al. 2005).

### Literature references

Deretic, V., Belisle, J., Lucas, M., Vergne, I., Lee, HH., Chua, J. (2005). Mechanism of phagolysosome biogenesis block by viable *Mycobacterium tuberculosis*. *Proc. Natl. Acad. Sci. U.S.A.*, 102, 4033-8. [↗](#)

### Editions

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