

PI(3,5)P2 is dephosphorylated to PI3P by FIG4 at the early endosome 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

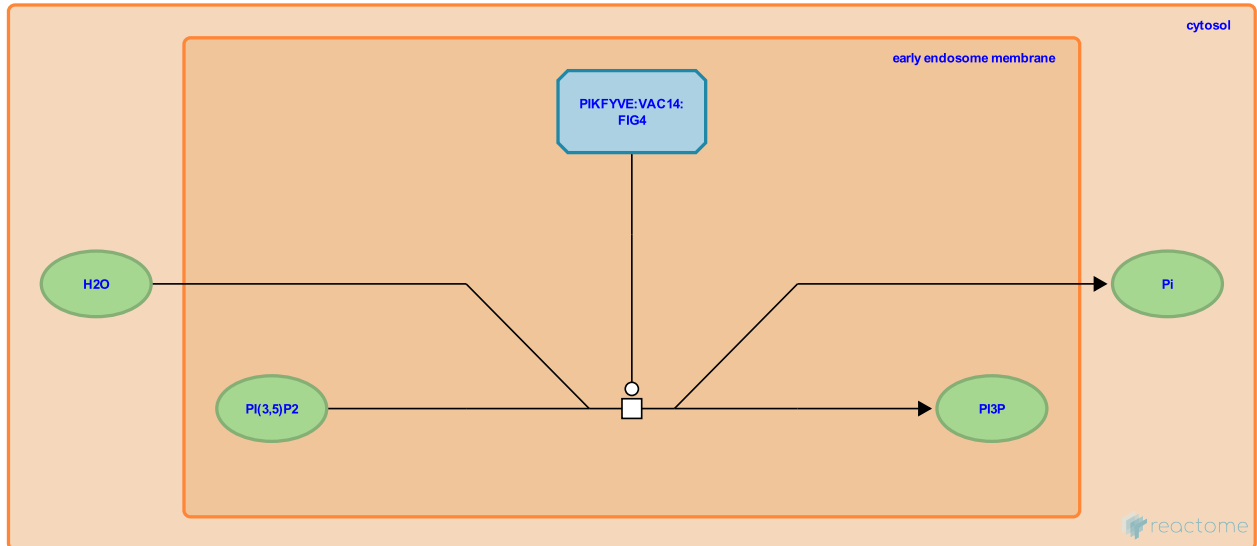
This document contains 1 reaction ([see Table of Contents](#))

PI(3,5)P2 is dephosphorylated to PI3P by FIG4 at the early endosome membrane [↗](#)

Stable identifier: R-HSA-1676174

Type: transition

Compartments: early endosome membrane, cytosol



At the early endosome membrane, the PAS complex, consisting of FYVE finger-containing phosphoinositide kinase (PIKFYVE), yeast VAC14 homologue (VAC14), and polyphosphoinositide phosphatase aka SAC3 (FIG4), binds to the membrane via PIKFYVE's FYVE finger. The FIG4 phosphatase component dephosphorylates phosphatidylinositol 3,5-bisphosphate (PI(3,5)P2) to phosphatidylinositol 3-phosphate (PI3P) (Sbrissa et al. 2007, Sbrissa et al. 2008).

Literature references

Sbrissa, D., Ikononov, OC., Fu, Z., Ijuin, T., Gruenberg, J., Takenawa, T. et al. (2007). Core protein machinery for mammalian phosphatidylinositol 3,5-bisphosphate synthesis and turnover that regulates the progression of endosomal transport. Novel Sac phosphatase joins the ArPIKfyve-PIKfyve complex. *J Biol Chem*, 282, 23878-91. [↗](#)

Sbrissa, D., Ikononov, OC., Fenner, H., Shisheva, A. (2008). ArPIKfyve homomeric and heteromeric interactions scaffold PIKfyve and Sac3 in a complex to promote PIKfyve activity and functionality. *J Mol Biol*, 384, 766-79. [↗](#)

Editions

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