

PI3K alpha, beta, gamma convert PIP2 to PIP3

Akkerman, JW., Harper, MT., Jones, ML., Jupe, S., Poole, AW.

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](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://reactome.org/licenses/).

30/04/2024

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: 88

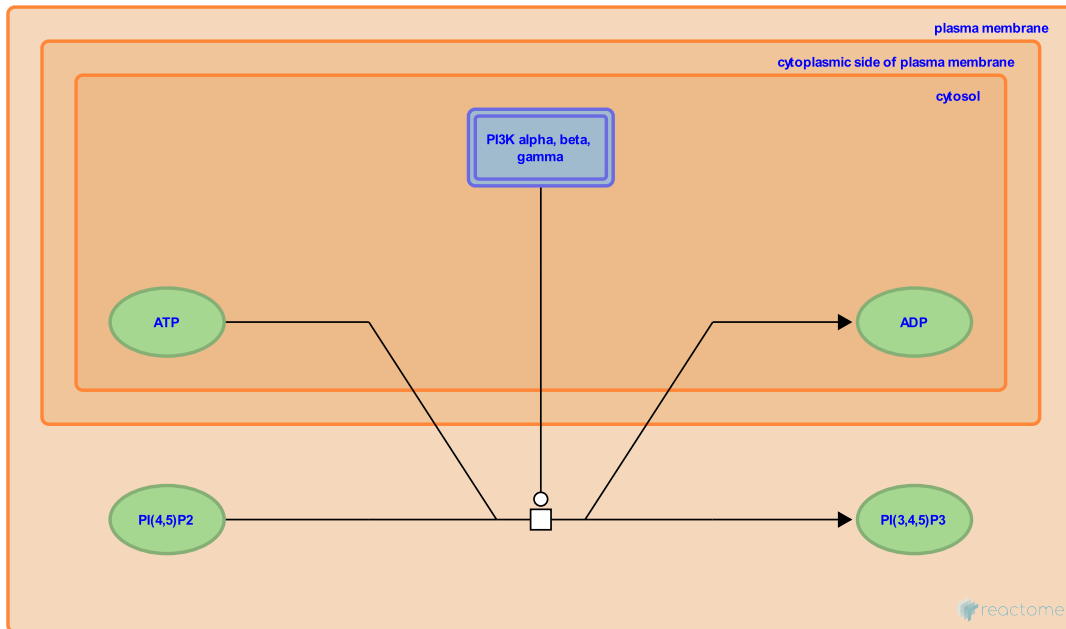
This document contains 1 reaction ([see Table of Contents](#))

PI3K alpha, beta, gamma convert PIP2 to PIP3 [↗](#)

Stable identifier: R-HSA-437162

Type: transition

Compartments: cytosol, plasma membrane



Class I Phosphoinositide 3-kinases (PI3Ks) are heterodimeric proteins, each having a catalytic subunit of 110-120 kDa and an associated regulatory subunit. PI3Ks alpha, beta and delta share a common regulatory p85 subunit, PI3K gamma has a p101 regulatory subunit. All the class I PI3Ks are able to phosphorylate PtdIns, PtdIns-4-P, or PtdIns-4,5-P2 (PIP2) on the free 3-position, and have a strong preference for PIP2. They are activated by receptor tyrosine kinases and by Ras and Rho family GTPases.

Literature references

Schlessinger, J., Mondino, A., Hu, P., Skolnik, EY. (1993). Cloning of a novel, ubiquitously expressed human phosphatidylinositol 3-kinase and identification of its binding site on p85. *Mol Cell Biol*, 13, 7677-88. [↗](#)

Malek, D., Nurnberg, B., Dhand, R., Vanhaesebroeck, B., Volinia, S., Loubtchenkov, M. et al. (1995). Cloning and characterization of a G protein-activated human phosphoinositide-3 kinase. *Science*, 269, 690-3. [↗](#)

Editions

2009-09-04	Authored	Akkerman, JW.
2009-11-02	Reviewed	Poole, AW., Jones, ML., Harper, MT.
2009-11-03	Edited	Jupe, S.