

Activation of PLC beta-1

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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: 88

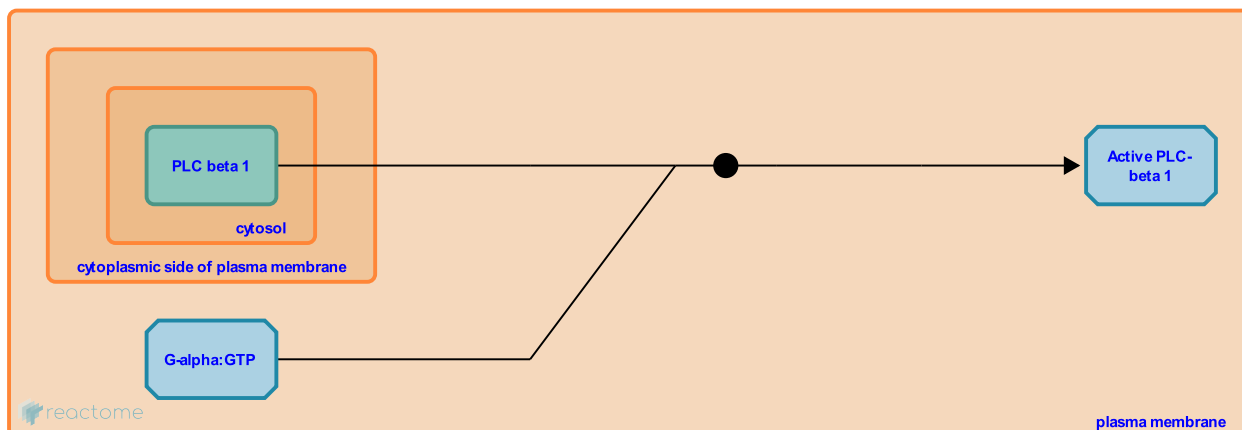
This document contains 1 reaction ([see Table of Contents](#))

Activation of PLC beta-1 [↗](#)

Stable identifier: R-BTA-374858

Type: binding

Compartments: cytosol, plasma membrane



The active form of G protein alpha subunit q (Gq-alpha) was found to activate phospholipase C beta-1 (PLC-beta1), in investigations using bovine membranes. Subsequently, all 4 human isoforms have been shown to be activated by Gq, though activation of PLCbeta-4 is limited. In recombinant assays, several activated rat G alpha q family members were found to stimulate human PLC-beta isoforms with the same rank order of decreasing potency. PLC-beta1 stimulation was slightly more than for PLC-beta3; PLC-beta3 stimulation was 10-fold greater than for beta-2. PLC-beta2 is expressed specifically in hematopoietic cells. PLC-beta acts directly on Gq to accelerate hydrolysis of bound GTP, thus PLC-betas are GTPase activating proteins (GAPs). The crystal structure of the C-terminal region from Turkey PLC-beta, revealed a novel fold composed almost entirely of three long helices forming a coiled-coil that dimerizes along its long axis in an antiparallel orientation. The extent of the dimer interface and gel exclusion chromatography data suggest that PLC-betas are functionally dimeric.

Literature references

- Smrcka, AV., Sternweis, PC., Hepler, JR., Brown, KO. (1991). Regulation of polyphosphoinositide-specific phospholipase C activity by purified Gq. *Science*, 251, 804-7. [↗](#)
- Zhou, CJ., Abdel-Latif, AA., Akhtar, RA. (1994). Identification of phosphoinositide-specific phospholipase C-beta 1 and GTP-binding protein, Gq alpha, in bovine iris sphincter membranes: characteristics of the phospholipase and its coupling to cholinergic muscarinic receptors. *Exp Eye Res*, 59, 377-84. [↗](#)
- Rhee, SG., Jhon, DY., Blank, JL., Berstein, G., Ross, EM., Exton, JH. (1992). Phospholipase C-beta 1 is a GTPase-activating protein for Gq/11, its physiologic regulator. *Cell*, 70, 411-8. [↗](#)
- Rhee, SG., Taylor, SJ., Chae, HZ., Exton, JH. (1991). Activation of the beta 1 isozyme of phospholipase C by alpha subunits of the Gq class of G proteins. *Nature*, 350, 516-8. [↗](#)

Editions

2004-03-31	Authored	Jassal, B., Le Novere, N.
2009-06-03	Reviewed	Akkerman, JW.