

Recruitment of PLCgamma to membrane

Garapati, P V., Rosales, C.

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/).

08/05/2024

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

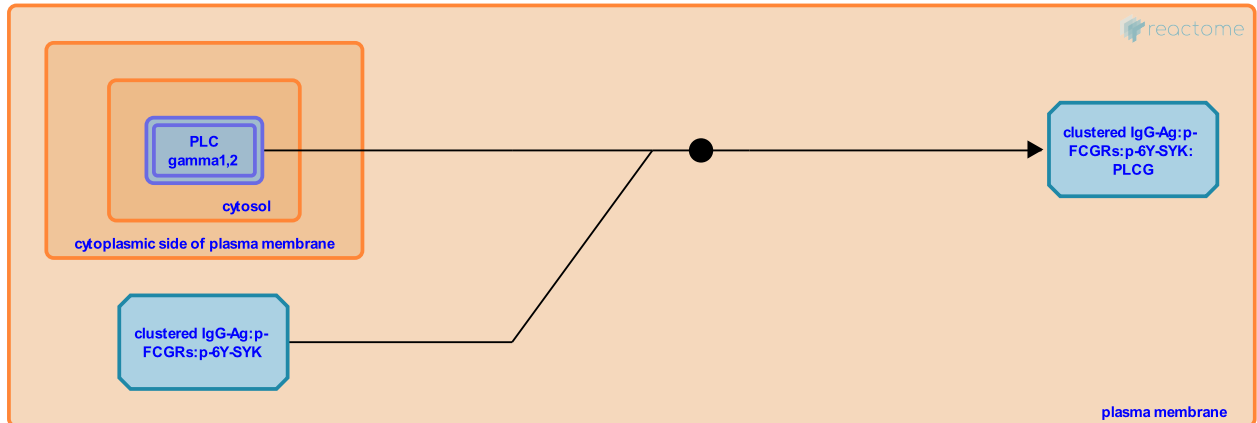
This document contains 1 reaction ([see Table of Contents](#))

Recruitment of PLCgamma to membrane [↗](#)

Stable identifier: R-HSA-2029270

Type: binding

Compartments: plasma membrane, cytosol, extracellular region



PLCgamma (PLCG) is recruited to FCGR and the phosphorylated Y342 and Y346 in SYK have been reported to be involved in the interaction of PLCG (Law et al. 1996). PLCG accumulates at the phagocytic cup during FCGR, but the exact role of PLCG in the regulation of phagocytosis is not clear. It may be involved in FCGR signaling by activating PKC through DAG production (Garcia-Garcia & Rosales 2002)

Literature references

- Dusi, S., Donini, M., Della Bianca, V., Rossi, F. (1994). Tyrosine phosphorylation of phospholipase C-gamma 2 is involved in the activation of phosphoinositide hydrolysis by Fc receptors in human neutrophils. *Biochem Biophys Res Commun*, 201, 1100-8. [↗](#)
- Chandran, KA., Law, CL., Clark, EA., Sidorenko, SP. (1996). Phospholipase C-gamma1 interacts with conserved phosphoryl residues in the linker region of Syk. *Mol Cell Biol*, 16, 1305-15. [↗](#)

Editions

2012-01-04	Authored, Edited	Garapati, P V.
2012-05-15	Reviewed	Rosales, C.