Phosphorylation and activation of PLCG due to FCGR3A effect

Gregory, DJ., Murillo, JI.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

06/05/2024

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. ↗

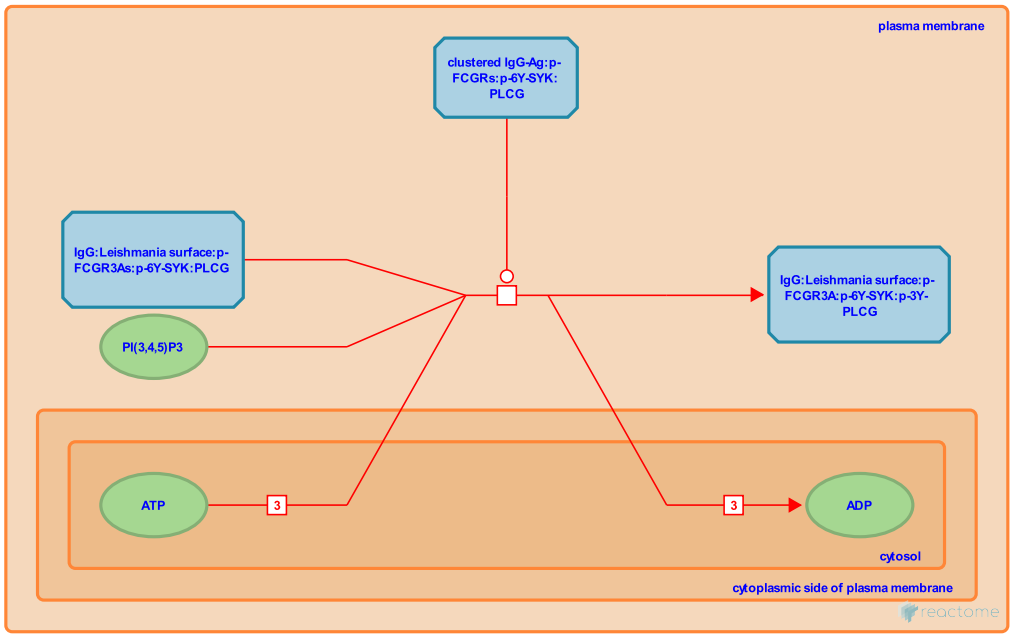
Phosphorylation and activation of PLCG due to FCGR3A effect ↗

Stable identifier: R-HSA-9664278

Type: transition

Compartments: plasma membrane, cytosol, extracellular region

Diseases: cutaneous leishmaniasis



PLCG is tyrosine phosphorylated by either SYK or Src kinases on three tyrosine residues and this phosphorylation enhances the activity of PLCG. Although maximal activation requires binding of PLCG to PIP3 with its plecstrin homology (PH) domain.

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 phosphotyrosyl residues in the linker region of Syk and is a substrate for Syk. *Mol Cell Biol, 16*, 1305-15. ↗

Kim, YJ., Rhee, SG., Sekiya, F., Poulin, B. (2004). Mechanism of tyrosine phosphorylation and activation of phospholipase C-gamma 1. Tyrosine 783 phosphorylation is not sufficient for lipase activation. *J Biol Chem, 279*, 32181-90. ↗

Editions

2020-02-04	Reviewed	Gregory, DJ.
2020-02-05	Authored, Edited	Murillo, JI.