

PKC binds active G alpha (z)

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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: 82

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

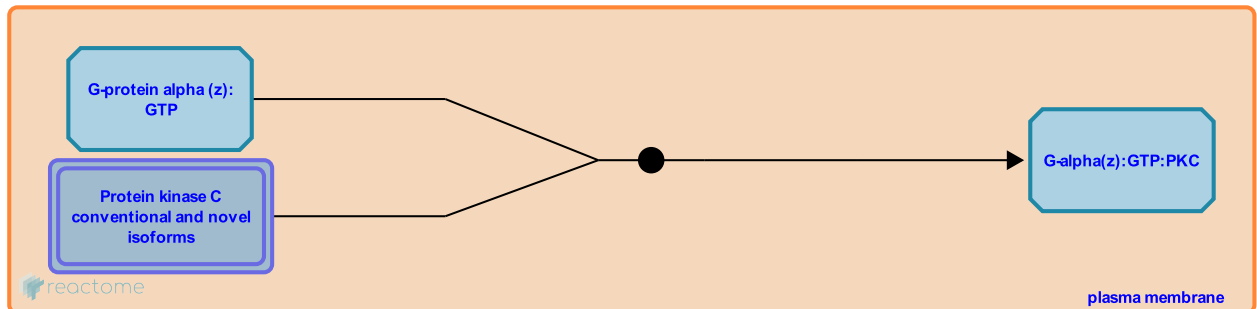
PKC binds active G alpha (z) ↗

Stable identifier: R-HSA-8982703

Type: binding

Compartments: plasma membrane

Inferred from: PKC (cow) binds G alpha z (rat) (Bos taurus)



G alpha z (Lounsbury et al. 1991) and G alpha 12 (Kozasa & Gilman, 1996) are excellent in vitro substrates for all three subtypes of protein kinase C (PKC). Activation of PKC in intact platelets by agents such as thrombin, thromboxane A2 (TXA2) analogues and phorbol esters leads to rapid and near-stoichiometric phosphorylation of G alpha z (Carlson et al. 1989). PKC can bind to G alpha z and facilitate its phosphorylation at Ser-27 (Lounsbury et al. 1993). This phosphorylation blocks the interaction of G alpha z with Gbeta:gamma suggesting that it is a regulatory mechanism for attenuating signalling by preventing subunit reassociation.

Literature references

Lounsbury, KM., Manning, DR., Casey, PJ., Brass, LF. (1991). Phosphorylation of Gz in human platelets. Selectivity and site of modification. *J Biol Chem*, 266, 22051-6. ↗

Casey, PJ., Fields, TA. (1995). Phosphorylation of Gz alpha by protein kinase C blocks interaction with the beta gamma complex. *J. Biol. Chem.*, 270, 23119-25. ↗

Editions

2010-05-18	Authored	Jupe, S.
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