# G-protein alpha releases G-protein hetero-trimer from PDCL

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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. ↗

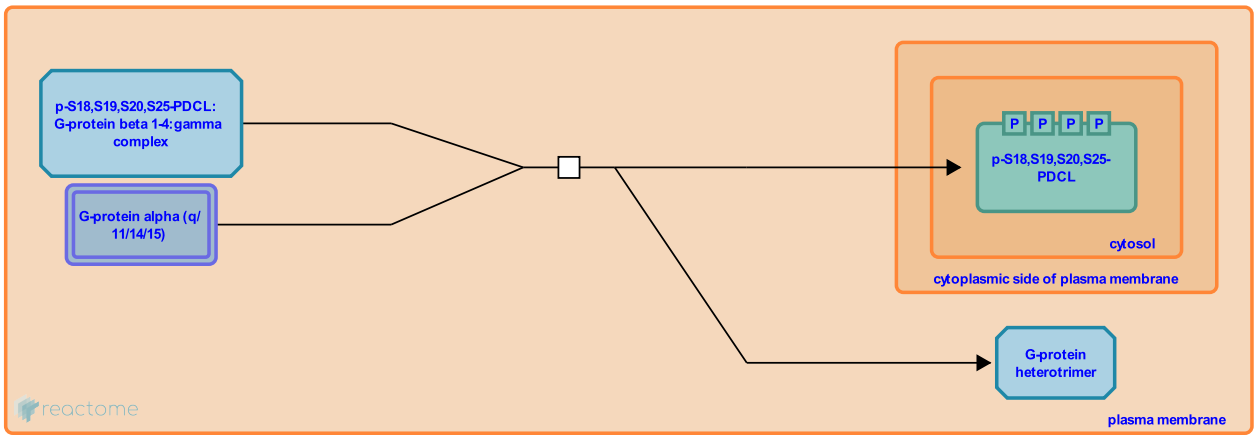
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

## G-protein alpha releases G-protein heterotrimer from PDCL ↗

**Stable identifier:** R-HSA-8850560

**Type:** transition

**Compartments:** cytosol, plasma membrane




G-protein alpha associates with G-protein beta:gamma dimers bound to PDCL (PhLP1), resulting in release of the G-protein heterotrimer from PDCL co-chaperone (Lukov et al. 2005, Plimpton et al. 2015).

## Literature references


Lukov, GL., Hu, T., Hamm, HE., McLaughlin, JN., Willardson, BM. (2005). Phosducin-like protein acts as a molecular chaperone for G protein betagamma dimer assembly. *EMBO J., 24*, 1965-75. ↗

Makaju, A., Lai, CW., Prince, JT., Carrascosa, JL., Plimpton, RL., Cuellar, J. et al. (2015). Structures of the Gβ-CCT and PhLP1-Gβ-CCT complexes reveal a mechanism for G-protein β-subunit folding and Gβγ dimer assembly. *Proc. Natl. Acad. Sci. U.S.A., 112*, 2413-8. ↗


## Editions

| | | |
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