PDCL binds G-protein beta and TRiC/CCT

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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

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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. ↗

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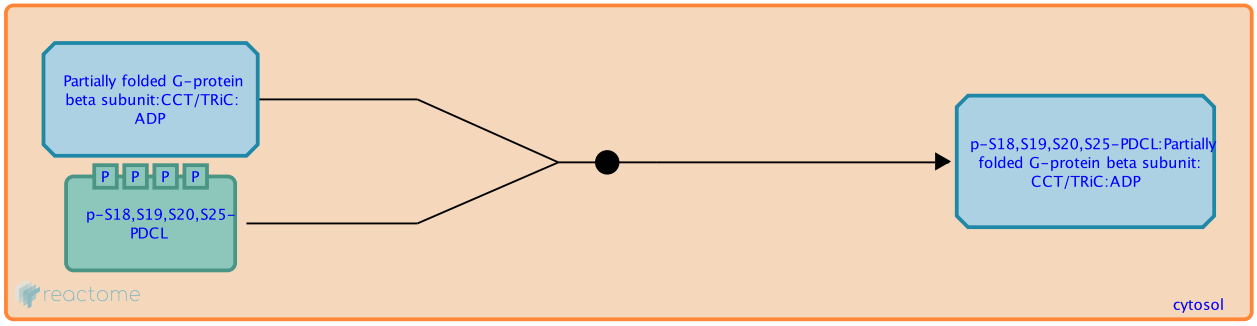
Stable identifier: R-HSA-6814121

Type: binding

Compartments: cytosol



PDCL (PhLP1), phosphorylated by the casein kinase II complex (CK2), simultaneously binds to the unfolded G-protein beta subunit and the TRiC/CCT chaperonin (Lukov et al. 2005, Lukov et al. 2006, Plimpton et al. 2015). Phosphorylation is not a prerequisite for PDCL binding to TRiC/CCT and the unfolded G-protein beta, but is necessary for PDCL-mediated release of folded G-protein beta from TRiC/CCT (Lukov et al. 2006).

Literature references

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Editions

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