TRiC/CCT binds unfolded G-protein beta subunit

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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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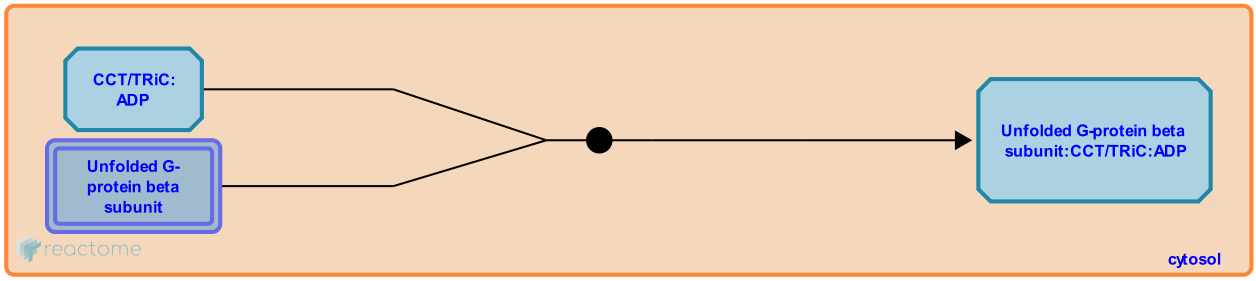
Stable identifier: R-HSA-6814119

Type: binding

Compartments: cytosol



The TRiC/CCT chaperonin complex binds nascent, unfolded, G-protein beta subunit (GNB1, GNB2, GNB3, GNB4 or GNB5) (Wells et al. 2006). G-beta reaches a near-native state in the folding cavity of TRiC, except that TRiC cannot mediate the folding of the seven-bladed beta propeller of the G-protein beta to a stable conformation (Plimpton et al. 2015).

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Editions

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