

# ATP binds G-protein beta associated 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

- 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. 7
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. A
- 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: 77

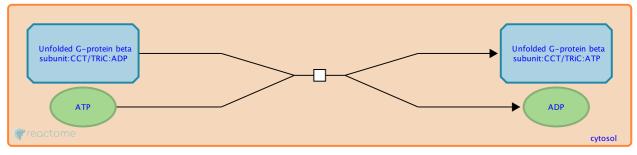
This document contains 1 reaction (see Table of Contents)

# ATP binds G-protein beta associated TRiC/CCT 7

#### Stable identifier: R-HSA-6814124

#### Type: transition

#### Compartments: cytosol



Based on structural studies of the TRiC/CCT chaperonin complex, the exchange of ADP for ATP enables conformational change of the chaperonin complex needed for folding of substrate proteins. It is assumed that TRiC/CCT-mediated folding of the G-protein beta subunit follows this universal pattern of TRiC/CCT functioning (Melki et al. 1997).

## Literature references

Melki, R., Batelier, G., Soulié, S., Williams RC, Jr. (1997). Cytoplasmic chaperonin containing TCP-1: structural and functional characterization. *Biochemistry*, *36*, 5817-26.

### **Editions**

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