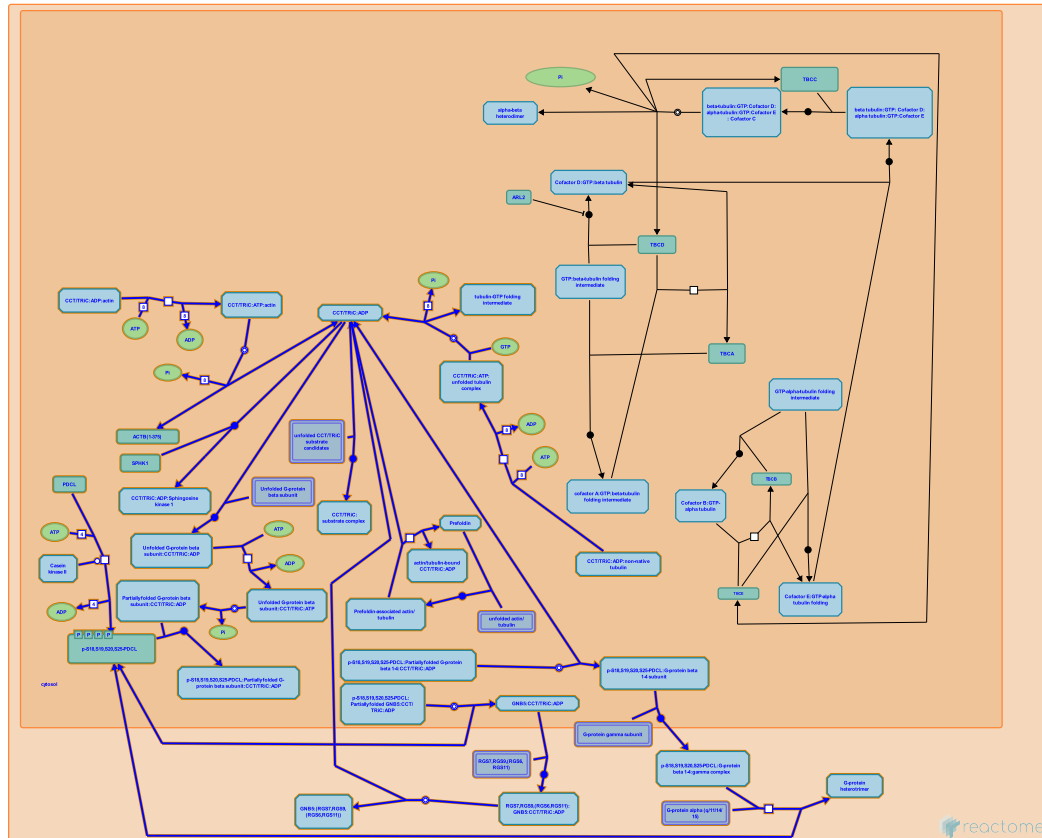


# Chaperonin-mediated protein folding



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This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the [Reactome Textbook](https://reactome.org).

30/04/2024

## 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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

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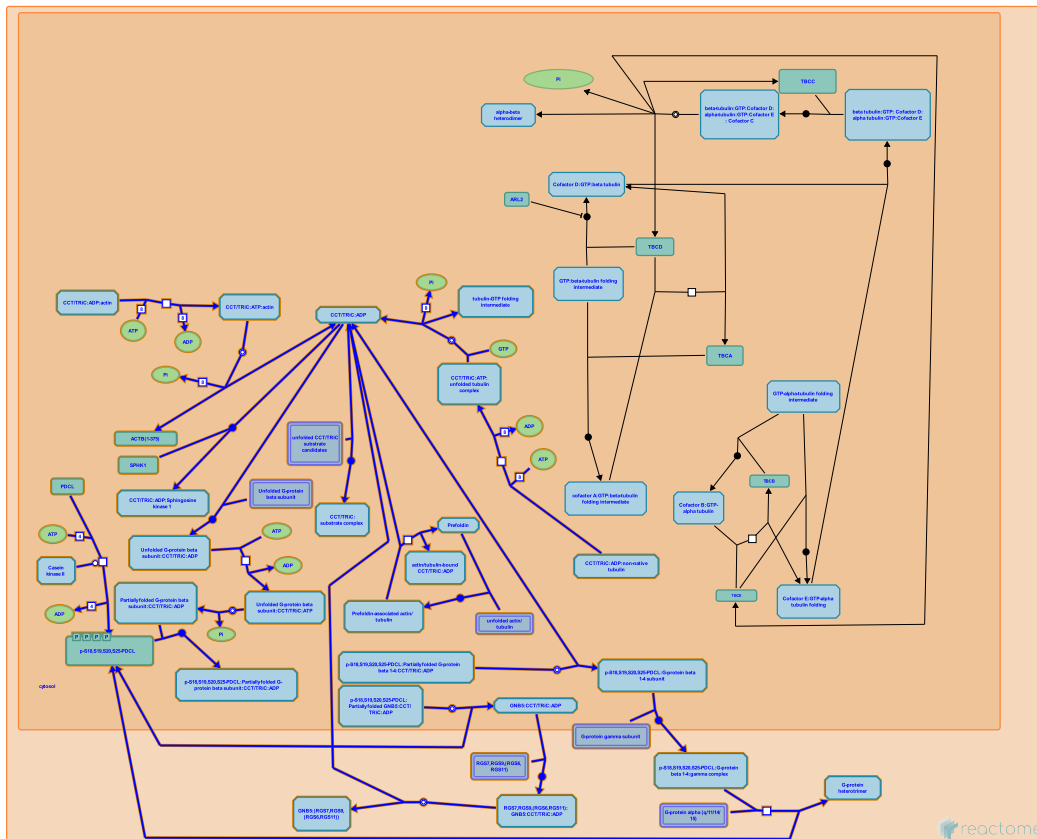
Reactome database release: 88

This document contains 4 pathways ([see Table of Contents](#))

# Chaperonin-mediated protein folding ↗

Stable identifier: R-HSA-390466

Compartments: cytosol



The eukaryotic chaperonin TCP-1 ring complex (TRiC/ CCT) plays an essential role in the folding of a subset of proteins prominent among which are the actins and tubulins (reviewed in Altschuler and Willison, 2008). CCT/TRiC is an example of a type II chaperonin, defined (in contrast to type I) as functioning in the absence of a cochaperonin. TriC/CCT is a multisubunit toroidal complex that forms a cylinder containing two back-to-back stacked rings enclosing a cavity where substrate folding occurs in an ATP dependent process (reviewed in Altschuler and Willison, 2008 ). CCT/TriC contains eight paralogous subunits that are conserved throughout eukaryotic organisms (Leroux and Hartl 2000; Archibald et al. 2001; Valpuesta et al. 2002). CCT-mediated folding of non-native substrate protein involves capture through hydrophobic contacts with multiple chaperonin subunits followed by transfer of the protein into the central ring cavity where it folds. Although folding is initiated within this central cavity, only 5%-20% of proteins that are released have partitioned to the native state. The remaining portion is then recaptured by other chaperonin molecules (Cowan and Lewis 2001). This cycling process may be repeated multiple times before a target protein partitions to the native state. In the cell, binding to CCT occurs via presentation of target protein bound to upstream chaperones. During translation, the emerging polypeptide chain may be transferred from the ribosome to CCT via the chaperone Prefoldin (Vainberg et al., 1998) or the Hsp70 chaperone machinery (Melville et al., 2003). While the majority of CCT substrates ultimately partition to the native state as soluble, monomeric proteins, alpha and beta tubulin are unusual in that they require additional cofactors that are required to assemble the tubulin heterodimer (Cowan and Lewis 2001).

## Literature references

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## Editions

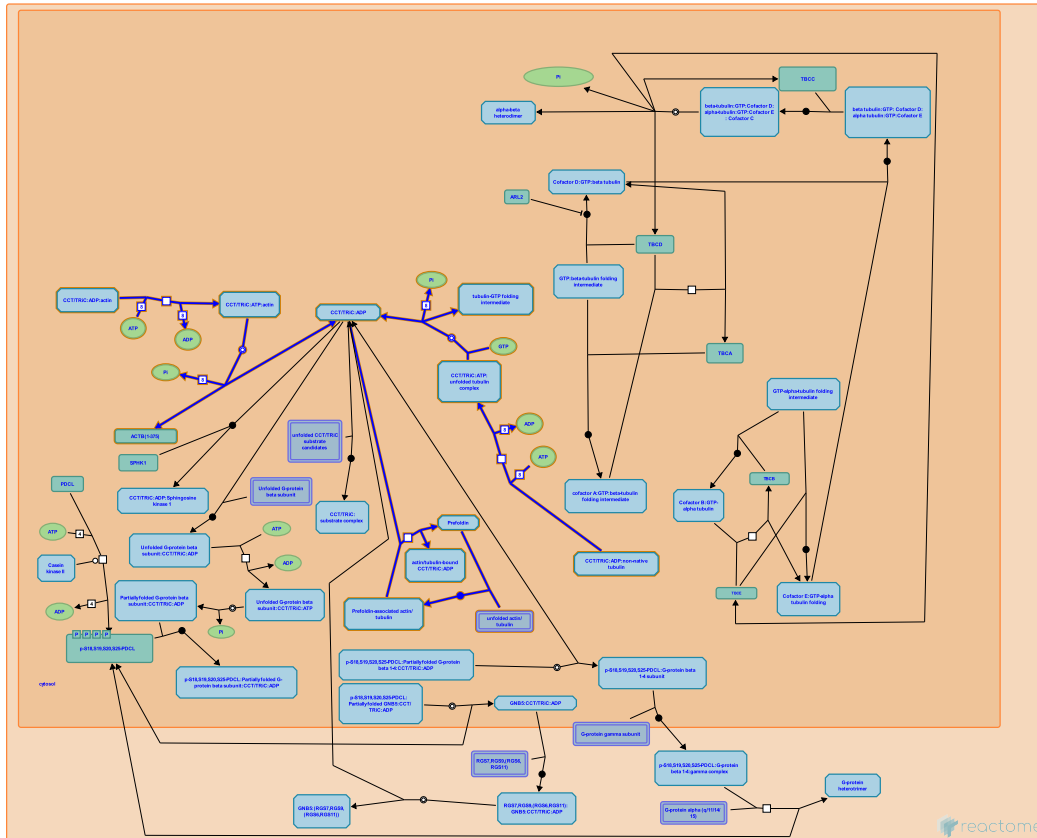
2008-12-01	Authored	Matthews, L.
2009-01-21	Reviewed	Cowan, NJ.
2009-02-21	Edited	Matthews, L.

# Cooperation of Prefoldin and TriC/CCT in actin and tubulin folding [↗](#)

**Location:** [Chaperonin-mediated protein folding](#)

**Stable identifier:** R-HSA-389958

**Compartments:** cytosol



In the case of actin and tubulin folding, and perhaps other substrates, the emerging polypeptide chain is transferred from the ribosome to TRiC via Prefoldin (Vainberg et al., 1998).

## Literature references

Klein, HL., Rommelaere, H., Vandekerckhove, J., Lewis, SA., Cowan, NJ., Ampe, C. et al. (1998). Prefoldin, a chaperone that delivers unfolded proteins to cytosolic chaperonin. *Cell*, 93, 863-73. [↗](#)

## Editions

2008-12-01	Authored	Matthews, L.
2009-01-21	Reviewed	Cowan, NJ.
2009-02-21	Edited	Matthews, L.





Thulin, CD., Lukov, GL., Ludtke, PJ., Hu, T., Carter, MD., Baker, CM. et al. (2006). Mechanism of assembly of G protein betagamma subunits by protein kinase CK2-phosphorylated phosducin-like protein and the cytosolic chaperonin complex. *J. Biol. Chem.*, 281, 22261-74. [↗](#)

## **Editions**

2015-11-30	Authored, Edited	Orlic-Milacic, M.
2015-12-22	Reviewed	Willardson, BM.



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