Hydrolysis of ATP and release of folded actin from CCT/TriC

Cowan, NJ., Matthews, L.
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


Reactome database release: 83

This document contains 1 reaction (see Table of Contents)
**Hydrolysis of ATP and release of folded actin from CCT/TriC**

**Stable identifier:** R-NUL-391437

**Type:** dissociation

**Compartments:** cytosol

TriC/CCT-mediated beta-actin folding involves rapid ATP-independent formation of a binary complex, followed by a slower ATP-dependent release of the native product (Gao et al., 1992). Group II chaperonins enclose substrate proteins following substrate binding through the formation of a "built-in" lid over the central cavity. Upon ATP binding, lid formation is triggered by the transition state of ATP hydrolysis (Meyer, et al., 2003).

**Literature references**


**Editions**

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