Association of CCT/TriC with other substrates during biosynthesis (unknown chaperone)

Cowan, NJ., Matthews, L.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

21/09/2024

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).

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. ↗

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

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. ↗

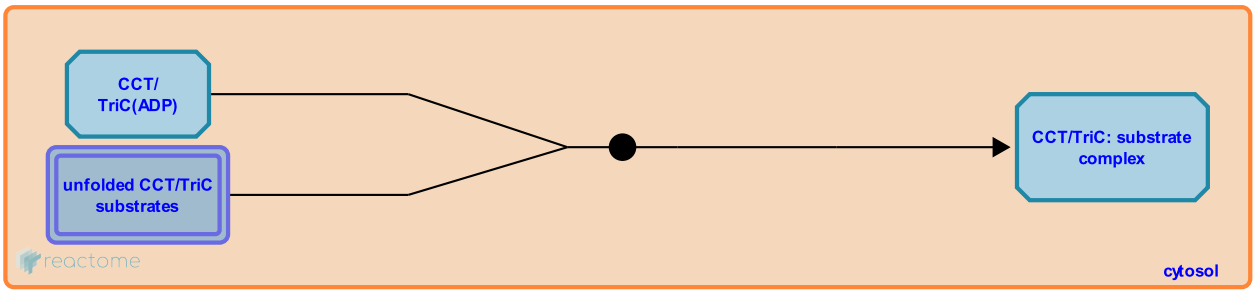
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

Association of CCT/TriC with other substrates during biosynthesis (unknown chaperone)

Stable identifier: R-NUL-391979

Type: binding

Compartments: cytosol



A combination of proteomic and bioinformatics analyses of TRiC substrates has revealed that they have complex topologies that are slow folding and aggregation prone (Yam et al., 2008). These substrates are also enriched in proteins that belong to oligomeric assemblies suggesting that TRiC plays a role in promoting complex assembly (Yam et al., 2008). Two possible mechanisms describing the role of TriC have been suggested (Yam et al., 2008). The processes of TRiC-mediated folding and assembly could be directly coupled, or TRiC could fold monomeric subunits and hold them in an assembly-competent state until they associate with the appropriate partner subunits. The complete list of TriC subsrates is not yet known. Many of its substrates that are targeted during biosynthesis are conserved between mammals and yeast (Yam et al. 2008).

Literature references

Lin, HT., Burlingame, A., Frydman, J., Xia, Y., Gerstein, M., Yam, AY. (2008). Defining the TRiC/CCT interactome links chaperonin function to stabilization of newly made proteins with complex topologies. *Nat Struct Mol Biol, 15*, 1255-62.

Editions

2009-01-21	Reviewed	Cowan, NJ.
2009-02-06	Authored	Matthews, L.
2009-02-21	Edited	Matthews, L.