COMMDs displace CAND1 from cytosolic CRL E3 ubiquitin ligase complexes

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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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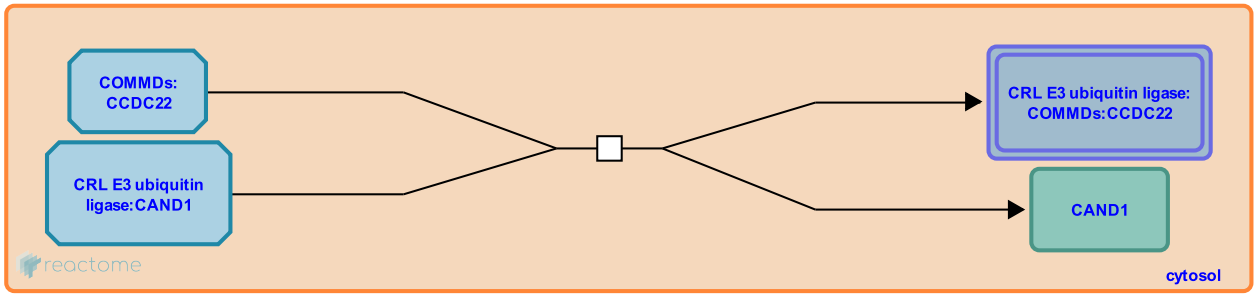
Stable identifier: R-HSA-8955289

Type: transition

Compartments: cytosol



COMMD1 is a member of a family of 10 copper metabolism MURR1 domain-containing proteins that have pleiotropic roles in copper metabolism, NF kappa beta-mediated transcription, the hypoxic response and electrolyte transport (Burstein et al, 2005; reviewed in Maine and Burstein, 2007). COMMD proteins have differential tissue and expression levels, but appear to have partially overlapping function and form homo- and heterodimers through the shared COMM domain (Burstein et al, 2005). COMMD1 and other family members interact with the cullin subunit of CRL E3 ubiquitin ligase complexes, as well as with CCDC22, a protein implicated in X-linked intellectual disability that may regulate COMMD localization. Together, COMMD proteins and CCDC22 activate the ubiquitin ligase activity of CRL complexes by displacing the CAND1 inhibitor (Burstein et al, 2005; Maine et al, 2007; Mao et al, 2011; Starokadomskyy et al, 2013;Phillips-Krawczak et al, 2015). The specificity of interaction between various COMMD and CUL family members may serve to fine tune the regulation of CRL activation, although these details remain to be determined.

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Editions

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