Cdd1p is a cytidine deaminasecapable of deaminating cytidine into cytosine, which is important for the pyrimidine salvage pathway. Null mutants are viable and display weak 5-fluorocytidine resistance, which indicates a partial impairment in cytidine metabolism. The active enzyme is a homotetramer. Thus the enzyme complex contains four active sites, each of which is complexed with Zn2+. It is found in both the cytoplasm and the nucleus.Cdd1p has been shown to deaminate cytidine to uridine in an ectopically expressed fragment of human apolipoprotein BmRNA, which suggests that mRNA C>U editing may exist in Saccharomyces cerevisiae. However, native substrates for Cdd1p-dependent RNA editing have not been identified, thus it is not clear if this activity is biologically relevant. Cdd1p has also been shown to deaminate deoxycytidine in vitro, but the biological significance of this has also not been established.The Cdd1 protein has similarity to a number of proteins from other species, from bacteria to mammals. Cdd1p is similar to mouse activation-induced cytidine deaminase, human activation-induced deaminase proteinand to human RNA-editing enzyme apolipoprotein B editing catalytic subunit 1 protein. Mutations in the AICDA protein have been detected in humans with hyper-IgM type 2 syndrome. Cdd1p contains a tertiary fold with high structural homology to the catalytic domains of Escherichia coli cytidine deaminase and Bacillus subtilis cytidine deaminase. Cdd1p also contains putative ZDD motifs that align with regions in various proteins including S. cerevisiae Dcd1p, Erv1p, Fcy1p, Rib2p, Tad1p, Tad2p, and Tad3p, Trypanosoma cruzi ADAT1h, Caenorhabditis elegans ADAR, rat APOBEC-1, mouse APOBEC-2, and human 605257>AICDA, APOBEC1, APOBEC2, APOBEC3B, ADAR; ADARB1, and GFER proteins.