ADH6 and ADH7 are non-essential genes that encode the only S. cerevisiae members of the cinnamyl alcohol dehydrogasefamily. CADs are a subgroup of medium-chain zinc-containing alcohol dehydrogenases that were originally identified in plants where they are involved in the biosynthesis of lignin. However, since lignin biosynthesis does not occur in yeast, in S. cerevisiae these enzymes are instead thought to participate in lignin degradation, the synthesis of fusel alcohols, and NADPH homeostasis. Although their kinetic properties differ slightly, both Adh6p and Adh7p use the cofactor NADPH and have a broad substrate specificity. Adh6p and Adh7p share 64% sequence identity and each forms homodimers made up of 40 kDa subunits. The crystal structure of Adh6p shows that its two subunits are structurally dissimilar with one subunit in the apoand the other in the holoconformation. Additonally, two zinc atoms are found per Adh6p subunit and only one cofactor molecule binds per dimer. ADH6 is induced when galactose is the sole source of carbon in the media. Yeast strains overexpressing ADH6 are able to grow under toxic concentrations of veratraldehyde, and cell lysates from overexpressing strains are able to support the use of both NADPH and NADH as co-factors during the conversion of 5-hydroxymethyl furfural to 5-hydroxymethylfurfuryl alcohol.About the medium-chain dehydrogenase/reductasefamily Medium-chain dehydrogenase/reductases, sometimes referred to as long-chain dehydrogenases, constitute an ancient and widespread enzyme superfamily with members found in Bacteria, Archaea, and Eukaryota. Many MDR members are basic metabolic enzymes acting on alcohols or aldehydes, and thus these enzymes may have roles in detoxifying alcohols and related compounds, protecting against environmental stresses such as osmotic shock, reduced or elevated temperatures, or oxidative stress. The family also includes the mammalian zeta-crystallin lens protein, which may protect the lens against oxidative damage and enzymes which produce lignocellulose in plants. MDR enzymes typically have subunits of about 350 aa residues and are two-domain proteins, with a catalytic domain and a second domain for binding to the nicotinamide cofactor, either NADor NADP. They contain 0, 1, or 2 zinc atoms. When zinc is present, it is involved in catalysis at the active site. Based on phylogenetic and sequence analysis, the members of the MDR superfamily can be further divided into more closely related subgroups. In families which are widespread from prokaryotes to eukaryotes, some members appear conserved across all species, while others appear to be due to lineage specific duplications. Some subgroups are only found in certain taxa. S. cerevisiae contains fifteenor twenty-onemembers of the MDR superfamily, listed below. The difference in number is due to six sequences that were included as members of the quinone oxidoreductase family by Riveros-Rosas et al.but not by Nordling et al.. Zinc-containing enzyme groups: - PDH; \"polyol\" dehydrogenase family - BDH1, BDH2, SOR1, SOR2, XYL2 - ADH; class III alcohol dehydrogenase family - SFA1 - Y-ADH; \"yeast\" alcohol dehydrogenase family - ADH1, ADH2, ADH3, ADH5 - CADH; cinnamyl alcohol dehydrogenase family - ADH6, ADH7 Non-zinc-containing enzyme groups: - NRBP; nuclear receptor binding proteinor MRF; mitochondrial respiratory functionfamily - ETR1 - QOR; quinone oxidoreductase family - ZTA1, AST1, AST2, YCR102C, YLR460C, YMR152W, YNL134C- LTD; leukotriene B4 dehydrogenases - YML131W - ER; enoyl reductasesor ACR; acyl-CoA reductasefamily - no members in S. cerevisiae