About SOR1 and SOR2 SOR1 encodes a NAD-dependent sorbitol dehydrogenase that is part of the polyol dehydrogenase branch of the medium-chain dehydrogenase/reductasesuperfamily of enzymes. It is not expressed under most laboratory conditions but is induced when cells are grown in media containing sorbitol, a hexose carbohydrate similar to fructose. It is also induced when cells are grown on xylose, a pentose sugar found in lignocellulose, though S. cerevisiae cannot effectively utilize xylose as a carbon source. In vitro, Sor1p has been demonstrated to have activity on sorbitol and xylitol, but not on mannitol or the primary alcohol ethanol. SOR2 encodes an enzyme almost identical to SOR1. It has also been predicted to be involved in metabolism of hexoses by computational analysis of protein interaction networks.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