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Crystal Structure of the Ligand-bound Saccharopine Reductase from *Saccharomyces cerevisiae*. Babak Andi, Paul F. Cook, Ann H. West, Dept. of Chemistry and Biochemistry, The Univ. of Oklahoma, 620 Parrington Oval, Norman, OK 73019.

Saccharopine reductase (SR) is the penultimate enzyme of the unique α -amino adipate pathway for the biosynthesis of lysine in fungi important for developing new specific antimycotic agents. The enzyme catalyzes the NADPH-dependent condensation reaction of the α -amino adipate δ -semialdehyde with glutamate to make saccharopine. The crystal structure of the apo-SR has been previously solved in space group $P3_121$ with unit cell dimensions of $a = b = 85.28 \text{ \AA}$, $c = 141.98 \text{ \AA}$ from crystals grown in ammonium sulfate. Recent studies show that the apo-SR crystals can also be obtained using PEG-MME 2000 as a precipitant, which was used to obtain a structure of ligand-bound SR. In this study, the crystal structures of the ligand-bound SR obtained from the crystals grown in ammonium sulfate and PEG-MME 2000 are compared.

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