

W0131

Crystal Structures of Δ^1 -pyrroline-2-carboxylate Reductase from *Pseudomonas*. Masaru Goto, Hisashi Muramatsu, Hisaaki Mihara, Tatsuo Kurihara, Nobuyoshi Esaki, Rie Omi, Ikuko Miyahara, Ken Hirotsu, Dept. of Biochemistry, Osaka Medical College, Takatuki City OSAKA 569-8686, Japan.

Δ^1 -Piperideine-2-carboxylate/ Δ^1 -pyrroline-2-carboxylate reductase from *Pseudomonas syringae* pv. tomato belongs to a novel subclass in a large family of NAD(P)H-dependent oxidoreductases distinct from the conventional MDH/LDH superfamily characterized by the Rossmann fold. We have determined the structures of the following three forms of the enzyme: the unliganded form, the complex with NADPH, and the complex with NADPH and pyrrole-2-carboxylate at 1.55, 1.8, and 1.7 Å resolutions, respectively. The enzyme exists as a dimer, and the subunit consists of three domains, domain I, domain II (NADPH binding domain), and domain III. The core of the NADPH binding domain consists of a SEven-Stranded predominantly Antiparallel β -Sheet, which is called "SESAS", fold characteristic of the new oxidoreductase family. The enzyme's preference for NADPH over NADH is explained by the cofactor binding site architecture. A comparison of the overall structures revealed that the mobile domains I and III change their conformations to produce the catalytic form. This conformational change plays important roles in substrate recognition and the catalytic process.