ESRF

ESRF	**Experiment title:** *Escherichia coli* 1-deoxy-D-xylulose-5-phosphate reductoisomerase	**Experiment number**: LS-1912
Beamline: ID14-1, ID14-4	**Date of experiment**: from: 25.04.2001 to: 26.04.2001	**Date of report**: 19.03.2003
Shifts: 1, 3	**Local contact(s)**: Dr. Joanne McCarthy, Dr. Bill Shepard	*Received at ESRF:*

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Report:

We have solved the 2.5 Å crystal structure of 1-deoxy-d-xylulose-5-phosphate (DOXP) reductoisomerase, an enzyme involved in the mevalonate-independent 2-C-methyl-D-erythritol-4-phosphate (MEP) pathway of isoprenoid biosynthesis. The structure reveals that the enzyme is present as a homodimer. Each monomer displays a V like shape and is composed of an amino terminal dinucleotide binding domain, a connective domain and a carboxy terminal four helix bundle domain. The connective domain is responsible for dimerisation and harbours most of the active site. The strictly conserved acidic residues Asp150, Glu152, Glu231 and Glu234 are clustered at the putative active site and are

probably involved in the binding of divalent cations mandatory for enzyme activity. The connective and four helix bundle domains show significant mobility upon superposition of the dinucleotide binding domains of the three conformational states present in the asymmetric unit of the crystal. A still more pronounced flexibility is observed for a loop spanning residues 186 to 216, which adopts two completely different conformations within the three protein conformers. A possible involvement of this loop in an induced fit during substrate binding is discussed.

Reuter, K., Sanderbrand, S., Jomaa, H., Wiesner, J., Steinbrecher, I., Beck, E., Hintz, M., Klebe, G., and Stubbs, M.T. 2002. Crystal structure of 1-deoxy-D-xylulose-5-phosphate reductoisomerase, a crucial enzyme in the non-mevalonate pathway of isoprenoid biosynthesis. *J. Biol. Chem.* 277: 5378-5384.