The Structure of Yersinia pestis Dehydroquinase

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Type II dehydroquinase (EC 4.2.1.10) catalyzes the third step in the shikimate pathway by dehydrating 3-dehydroquinate to dehydroshikimate. *Y. pestis* dehydroquinase is formed by monomers of 150 amino acid residues that assemble as dodecamers. The enzyme was purified by size-exclusion and ion-exchange chromatography and crystallized using 16% PEG 3350. The crystals diffracted to 2.9Å resolution and belong to space group I4₁ (a=b= 132.4 Å, c = 187.2 Å) with six monomers in the crystallographic asymmetric unit. The dodecamer is built up by a crystallographic operators. The structure was determined by molecular replacement techniques and refined. The monomers display a typical flavodoxin-like fold with a central parallel β -sheet connected by helices. The active site is on the C-terminal end of the parallel β -sheet, at the trimer interface, and near the external surface of the dodecamer.

The structure of the active site is similar to that reported for the enzyme in other species. A peculiar feature of the enzyme is a loop, residues 18 to 29, that closes down on the active site when substrates and inhibitors are bound, and is often ordered only in such cases. Loop residue Tyr 28 (24 in *M. tuberculosis* numbering) is critical in the dehydration step according to the proposed mechanism. In the *Y. pestis* enzyme the loop is ordered in only one out of six subunits, and is in a completely open conformation with a displacement of main chain atoms of up to 11 Å, relative to the closed state.

Keywords: shikimate pathway, Type II dehydroquinase, Y. pestis