タンパク質結晶構造解析

Crystal structure of APE0912, a short-chain dehydrogenase/reductase family protein from *Aeropyrum pernix* K1 with a unique catalytic triad

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Short-chain dehydrogenases/reductases (SDRs), ca. 250-residue long, are enzymes that catalyze NAD(P)(H)-dependent oxidation/reduction of various substrates such as alcohols, sugars, steroids, aromatic compounds, and xenobiotics.

The APE0912 gene of hyperthermophilic archaea *Aeropyrum pernix* K1 encodes a SDR family protein with an unknown function. X-ray diffraction data of the APE0912 crystal were obtained on the KEK beamline NW12, and the crystal structure was determined at 1.8-Å resolution. APE0912 exists as a mixture of dimmer and tetramer in solution, and the protomer contained seven β-strands, nine α-helices, and four 3_{10}-helices. Although APE0912 has an NAD(P)-binding Rossmann-fold composed of a parallel β-sheet sandwiched between two arrays of parallel α-helices, no electron density for NADPH was observed even when the protein solution containing 5 mM NADPH was used for crystallization.

All members of the SDR family reported to date have a catalytic triad of Ser-Tyr-Lys, but APE0912 did not have the catalytic triad residues characteristic of the SDR family. Instead, APE0912 had Ser144, Ser157, and Arg161 at the corresponding positions. Furthermore, the two molecules in the asymmetric unit exhibited open and closed forms that alter the accessibility of substrates and cofactors to the Ser-Ser-Arg triad. Although both the open and closed forms of SDR family protein have already been reported, the positional alteration of the α-helix found in APE0912 is unique among SDR family members.