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Structure of the Topoisomerase Domain of a Novel Archaeal type IB Topoisomerase at 2.25 Å Resolution.

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Topoisomerases are ubiquitous enzymes that resolve the topological problems associated with cellular cycles of replication, transcription, recombination and cellular condensation. They are classified into types I and II depending on the transient cleavage in one (type I) or both (type II) DNA strands. DNA topoisomerase V of *Methanopyrus kandleri*, a 112 kDa protein, is the first type IB topoisomerase found in prokaryotes. The structure of the amino-terminus 60 kDa domain of *M. kandleri* topoisomerase V (consisting of the core topoisomerase subdomain and 8 HhH motifs) has now been solved. The 60kDa domain possesses topoisomerase activity, as judged by its ability to relax supercoiled DNA. The protein crystallized in the orthorhombic space group P2₁2₁2₁ with unit cell dimension of $a=70.7$, $b=89.8$ and $c=189.1$ and two molecules in the asymmetric unit. The structure was solved by SAD and phasing calculations were carried out using SOLVE and SHARP. The structure of topoisomerase V represents a novel all-alpha fold. Details of the structure and insights into the possible mechanistic cycle will be presented.