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Structure of the C-terminal Domain of Prokaryotic Topoisomerase II: A Novel beta-Propeller Implies How Gyrase Wraps DNA. Nei-Li Chan, Tung-Ju Hsieh, Inst. of Biochemistry, College of Life Sciences, National Chung Hsing Univ., Taichung City, Taiwan.

The highly conserved type IIA topoisomerases alter the topological state of DNA by catalyzing ATP-dependent passage of DNA duplexes through one another. In bacteria, two homologous type IIA enzymes, DNA gyrase and topoisomerase IV (TopIV), have been identified. Although these two bacterial enzymes share a high degree of similarity, yet they appear to have distinct cellular functions. Gyrase is responsible for introducing negative supercoil into bacterial genome, while TopIV is the decatenating enzyme required for the segregation of linked daughter chromosomes. It has been shown that the supercoiling capability of gyrase can be attributed to the DNA binding activity of its C-terminal domain (CTD). Interestingly, despite clear sequence homology, no such activity was found for the TopIV-CTD. To characterize the differences between these domains, we have cloned, purified, and crystallized the 36 kDa TopIV-CTD from *Bacillus stearo-thermophilus*. And the 2.0 Å crystal structure of TopIV-CTD has been determined by Se-MAD approach. Preliminary analysis indicated that the TopIV-CTD belongs to a novel type of beta-propeller fold. Details on structural determination and analysis will be presented.