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Crystal Structure of the Hypothetical Protein Xcc0516 from *Xanthomonas campestris*: A Novel Quaternary Structure Assembled by Five Four-Helix Bundles. Li-Ying Lin, Chung-Lun Ching, Ko-Hsin Chin, Shan-Ho Chou, and Nei-Li Chan, L.-Y. Lin and C.-L. Ching contributed equally to this work, Inst. of Biochemistry, College of Life Sciences, National Chung Hsing Univ., Taichung 402, TAIWAN.

The crystal structure of Xcc0516 (SwissProt accession number: Q8PD29), a 14.6-kDa conserved hypothetical cytosolic protein from plant pathogen *Xanthomonas campestris*, has been determined at 2.5 Å resolution by the multiwavelength anomalous diffraction method. Xcc0516 was selected as a target for structural determination because it exhibits no apparent sequence homology to any structure in the Protein Data Bank. While it turns out that the Xcc0516 monomer adopts a common four-helix bundle fold with a typical up-down-up-down arrangement of helices, interestingly, five monomers associate to form a pentameric ring structure with C5 symmetry. To our knowledge, this is the first example of a pentameric toroid formed by non-transmembrane four-helix bundle domain. Self-association of four-helix bundles into a toroid-like oligomer is predominantly achieved by aligning the principle (pseudo-4-fold) axis of individual subunit approximately along the main oligomer axis. In contrast, the Xcc0516 monomer tilts by ~50 degree about the C5 axis. A BLAST search revealed that Xcc0516 can be aligned over its entire length with the bacterial 23S rRNA proteins of the Ribosomal_S23p protein family (Pfam domain PF05635), with *E* values around e-36. Since residues involved in Xcc0516 pentamer formation are highly conserved among Ribosomal_S23p family members, they are likely to adopt a similar quaternary architecture.