

THE STRUCTURE OF *XANTHOMONAS AXONOPODIS* PV. CITRI YAEQ  
REVEALS NEW COMPACT PROTEIN FOLD BUILT AROUND A VARIATION OF  
THE PD-(D/E)XK NUCLEASE MOTIF

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The YaeQ family of proteins are found in many Gram-negative and a few Gram-positive bacteria. We have determined the first structure of a member of the YaeQ family by X-ray crystallography. The YaeQ fold consists of a central  $\alpha$ -helix surround by two curved  $\beta$ -sheets in which most of the central  $\alpha$ -helix is hidden from the solvent. The top face of the YaeQ structure displays several loops that contain the well conserved AXHPSE motif, the acidic DEP(D/E) motif as well as strictly conserved G85 and R148 residues. Comparisons with other structures indicate that YaeQ represents a new compact protein fold built around a variation of the PD-(D/E)XK nuclease motif found in type II endonucleases and enzymes involved in DNA replication, repair, and recombination. We present a comparative analysis that shows that catalytically important residues in the PD-(D/E)XK nuclease superfamily are spatially conserved in YaeQ and other highly conserved YaeQ residues may be poised to interact with nucleic acid structures. While specific YaeQ function is unknown, these results point towards a probable role in a specific process involving recognition and/or cleavage of nucleic acids.