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Crystal Structure of a Bacterial Antitoxin Reveals a Conserved Fold Found in Both Toxin and Antitoxin Molecules. Mark A. Arbing, Min Su, John F. Hunt, Dept. of Biological Sciences, Columbia Univ., New York, NY 10027.

Prokaryotic toxin-antitoxin systems encode a stable toxin and an unstable antitoxin that regulate bacterial growth in response to environmental stress. The *E. coli* YeeUV system has an as yet undetermined physiological role but YeeV toxicity and the ability of YeeU to abrogate it has been demonstrated. We have determined the crystal structure of the *E. coli* antidote protein YeeU at 2.2 Å resolution by Se-Met SAD. In contrast to known antidote structures which are predominantly unfolded proteins lacking a hydrophobic core YeeU consists of a stably-folded domain. The YeeU structure consists of a non-continuous five stranded antiparallel β-sheet with a kinked α-helix inserted between strands two and three. In addition to its having a compact folded structure a DALI search revealed that YeeU has significant structural homology to the toxins RelE and YoeB of the RelBE and YefM-YoeB toxin-antitoxin systems, respectively. YeeU shares only 7 percent sequence identity with both toxins but the conserved structural features include three strands of the β-sheet and the α-helix. A lack of conservation of the RelE and YoeB active site residues in comparable positions in the YeeU structure is consistent with its predicted antitoxin function.