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Structural Flexibility of *E. coli* Peptide Deformylase Deduced from Multiple Independent Crystal Lattices.

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Deformylation of newly synthesized proteins is an essential step in bacterial protein production. As this pathway is present in bacteria but absent in higher organisms, peptide deformylase (PDF), the enzyme that catalyzes the reaction, has been studied as a potential target for a novel antibiotic. In the course of a program aimed at identifying such an antibiotic, the crystal structure of *E. coli* peptide deformylase was determined.

PDF was found to be an exceptionally easy protein to crystallize. Using standard commercial screens, crystals useful for data collection were obtained in more than 25% of the crystallization wells. Each of the crystals obtained in these screens was characterized crystallographically, and five unique crystal forms were identified. Subsequently a sixth crystal lattice was identified, one that grew under the same conditions as one of the original five lattices, and later a seventh lattice was obtained in complex with an inhibitor.

Crystallization conditions were optimized for each of the seven lattices to produce the best possible diffraction quality crystals. Eventually a monoclinic lattice was used to determine phases for the structure using the heavy atom isomorphous replacement method. Using a refined model for the structure obtained in the monoclinic system, the structures of the protein in the other six lattices were determined by the molecular replacement method.

This rich source of independent structural data has allowed us to compare the structure of PDF in a number of truly independent crystalline environments. To this set of structures, the structure of a C-terminally truncated short form of the enzyme was later added. The greatest structural flexibility is found in the C-terminal alpha helix; small but significant structural plasticity is found in other regions of the protein.