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Structure of A Novel Acetylcitrulline Deacetylase from *Xanthomonas campestris*. D. Shi, X. Yu, L. Roth, M. Tuchman and N. M. Allewell, Children's National Medical Center, Washington, DC 20010, USA, College of Chemical and Life Sciences, Univ. of Maryland, College Park, MD 20742, USA.

The structures of a novel *N*-acetylcitrulline deacetylase from a plant pathogen *Xanthomonas campestris* have been solved using a three-wavelength dataset collected from a single crystal of SeMet protein. Six selenium sites were found using SOLVE and 82% of the polypeptide chain was automatically traced using RESOLVE. Refinement was carried out using CNS with 1.75 Å datasets to a crystallographic R factor of 19.8% and a free R factor of 22.4%. The structure of the monomer consists of two domains. The catalytic domain provides ligands for the metal ions in the active site. The other domain forms the dimer interface through hydrophobic interactions between helices and hydrogen bonding between two β strands forming a continuous β sheet across the dimer. The polypeptide fold of the monomer is similar to the fold of *Pseudomonas* sp. carboxypeptidase G2 and *Neisseria meningitidis* succinyl diaminopimelate desuccinylase. The availability of three-dimensional structures of this protein allows us to identify the residues that are important to the substrate binding and catalytic reaction.