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Structural Studies of Pyruvoyl-Dependent Arginine Decarboxylase from *Methanococcus jannaschii*. Erika Soriano, Steve E. Ealick, Dept. of Chemistry & Chemical Biology, Cornell Univ., Ithaca, NY 14853.

Arginine decarboxylase (ArgDC) is a pyruvoyl-dependent polyamine biosynthetic enzyme found in a variety of organisms. The pyruvoyl group of arginine decarboxylase is generated by an internal serinolysis reaction at a highly conserved serine residue in the proenzyme, resulting in two polypeptide chains. The pyruvoyl group is at the N-terminus of the second chain and serves as an electron sink for the decarboxylation reaction. Based on the native structure of trimeric ArgDC from *Methanococcus jannaschii* we proposed that the highly conserved residues Asn47 and Glu109 are involved in the self-processing reaction. These mutants were prepared and activity assays for both mutants showed very slow processing rates. Three-dimensional structures were determined at 2.0 Å resolution. The structure of the N47A mutant showed the enzyme to be partially processed. Mutating the asparagine to an alanine resulted in a loss of hydrogen bonding to backbone of Ile54, leading to a shift in the residues involved in the pyruvoyl formation. In contrast, the structure of the E109Q mutant contained a pyruvoyl group at each active site.