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The Structure of *Thermatoga Maritima* S-Adenosylmethionine Decarboxylase: Evidence for Gene Duplication and Fusion in the Evolution of Adometdcs. Angela V. Toms¹, Cynthia Kinsland¹, Anthony E. Pegg², Steven E. Ealick¹, ¹Dept. of Chemistry & Chemical Biology, Cornell Univ., Ithaca, NY 14853, ²Dept. of Cellular & Molecular Physiology, The Milton S. Hershey Medical Center, Pennsylvania State Univ. College of Medicine, Hershey, PA 17033.

S-adenosylmethionine decarboxylase (AdoMetDC) is a critical regulatory enzyme in the polyamine biosynthetic pathway. The AdoMetDC decarboxylation reaction depends upon a pyruvoyl cofactor generated via an autocatalytic proenzyme self-cleavage reaction. Although both the prokaryotic and eukaryotic AdoMetDCs undergo the same self-maturation process, they have very limited sequence homology.

The structure of the *T. maritima* AdoMetDC proenzyme has been determined to 1.6 Å resolution using MAD phasing methods. The structure of the *T. maritima* AdoMetDC proenzyme provides further evidence of an ancient gene duplication event in the evolution of the eukaryotic AdoMetDCs. Several key active site residues involved in substrate binding, catalysis or proenzyme processing that were identified in the human AdoMetDC (Eckstrom *et al.*, 2001; Tolbert *et al.*, 2001) are readily recognized in the *T. maritima* AdoMetDC even though the sequence homology is less than 10%.