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Crystal Structure of ACMSD a Metal-Dependent Non-Oxidative Decarboxylase from *Pseudomonas fluorescens*. Dariusz Martynowski¹, Yvonne Eyobo¹, Kun Yang¹, Aimin Liu², Hong Zhang¹,
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The enzyme 2-amino-3-carboxymuconate-6-semialdehyde (ACMSD) plays an important role in two metabolic events: the tryptophan kynurenine pathway present primarily in mammals and the 2-nitrobenzoic acid pathway in microorganisms. The step catalyzed by ACMSD determines the flow of metabolic intermediates to either acetyl CoA or quinolinic acid in these pathways. ACMSD is a new member in aminohydrolase superfamily with a TIM-barrel fold, representing a new metal-dependent enzymatic activity. Crystal structure of the protein from *Pseudomonas fluorescens* was determined by X-ray crystallography experiment and solved using selenomethionine MAD phasing method. Derivative and native datasets were collected to 2.7Å and 1.8Å respectively. The structure revealed the presence of a single zinc ion in the active site, which is liganded to several residues that are invariant in the superfamily.