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Pyridoxal 5'-phosphate binding induces conformational changes

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**Structural studies on the decameric *S. typhimurium* arginine decarboxylase (ADC):  
pyridoxal 5'-phosphate binding induces conformational changes.**

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**Abstract**

Enteric pathogens such as *Salmonella typhimurium* colonize the human gut in spite of the lethal acidic pH environment (pH <2.5) due to the activation of inducible acid tolerance response (ATR) systems. The pyridoxal 5'-phosphate (PLP)-dependent enzyme, biodegradative arginine decarboxylase (ADC, encoded by *AdiA*), is a component of an ATR system. The enzyme consumes a cytoplasmic proton in the process of arginine degradation to agmatine. Arginine-agmatine antiporter (*AdiC*) exchanges the product agmatine for arginine. In this manuscript, we describe structural of *Salmonella typhimurium* ADC (*StADC*). The decameric structure assembled from five dimers related by a non crystallographic 5-fold symmetry represents the first apo-form of the enzyme. The structure suggests that PLP-binding is not a prerequisite for oligomerization. Comparison with *E. coli* ADC reveals that PLP-binding is accompanied by the movement and ordering of two loops (residues 150-159 and 191-197) and a few active site residues such as His256 and Lys257. A number of residues important for substrate binding are

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