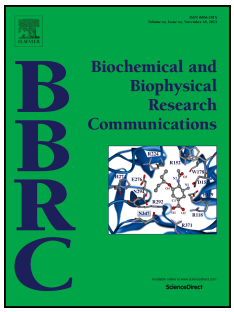
Accepted Manuscript



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

G. Deka, S.R. Bharath, H.S. Savithri, M.R.N. Murthy

PII: S0006-291X(17)31374-8

DOI: 10.1016/j.bbrc.2017.07.032

Reference: YBBRC 38138

To appear in: *Biochemical and Biophysical Research Communications*

Received Date: 4 July 2017

Accepted Date: 6 July 2017

Please cite this article as: G. Deka, S.R. Bharath, H.S. Savithri, M.R.N. Murthy, Structural studies on the decameric *S. typhimurium* arginine decarboxylase (ADC): Pyridoxal 5'-phosphate binding induces conformational changes, *Biochemical and Biophysical Research Communications* (2017), doi: 10.1016/j.bbrc.2017.07.032.

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

G. Deka[1], S.R. Bharath [1], H.S. Savithri [2] and M.R.N. Murthy [1*].

[1] Molecular Biophysics Unit, Indian Institute of Science, Bangalore 560012, India

[2] Biochemistry Department, Indian Institute of Science, Bangalore 560012, India

**Correspondence e-mail: mrn@mbu.iisc.ernet.in*

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 (*St*ADC). 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