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## Structure of arginine decarboxylases from *Salmonella typhimurium* and ordering of loops close to the active site upon PLP-binding

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**S**almonella typhimurium colonizes in the human gastro-intestinal tract due to its ability to withstand high acidic pH (pH<2.5). Its acid tolerance response (ATR) is due to lysine decarboxylase (LDC) and arginine decarboxylase (ADC) systems, which maintains the internal pH of the bacterium close to 4. ADC consumes one proton from the cytoplasm while decarboxylating an arginine to agmatine. The arginine-agmatine antiporter (AdiC) exchanges an internal agmatine with an external arginine. Thus, together, ADC and AdiC reduces the proton concentration within the cell. Here, we present the X-ray crystal structure of the inducible StADC (AdiA) at 3.1 Å resolutions. The crystal asymmetric unit contains a decamer (MW ~800 kDa) constitute of five homodimers related by a non-crystallographic five-fold axis of symmetry. The structure represents the apo-form of the enzyme while the earlier reported structure of the *E. coli* enzyme corresponds to the holo-form. Binding of PLP converts two disordered loops close to the active site into ordered confirmations. These conformational transitions may be important for substrate entry and product release. A large number of acidic residues are found on the surface of StADC. As proposed earlier, low pH may neutralize surface charges in homodimers that are catalytically inactive and promote the formation of functionally active decamers. Comparison of StADC with other members of group III decarboxylases shows that these enzymes are likely to follow similar catalytic mechanisms.

## Biography

G Deka joined the Department of Biological Sciences at the Indian Institute of Science as an Integrated PhD student in 2010 and earned her MS degree in 2012. Currently, she is pursuing her PhD under Prof. M.R.N. Murthy. She is attempting to understand the catalytic mechanism of a subset of PLP-dependent enzymes using mutagenesis, X- ray crystallography and enzyme kinetics studies. Apart from her PhD research work, she has gained experience in computational protein design and in the development of rapid diagnostic tools for early detection of malaria. Her curiosity to understand important biological problems motivate her to explore new areas in biology.

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