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#### SOLUTE BINDING PROTEINS AND THEIR COGNATE LIGANDS: STRUCTURE, FUNCTION AND THEIR ROLE IN FUNCTIONAL ANNOTATION

BIOGRAPHY

Umesh Yadava has started his career as Lecturer at MGPG College, Gorakhpur in 2001. He joined Department of Physics, DDU Gorakhpur University in 2003. He is the recipient of DST Young Scientist under FAST Track Scheme, and UGC Raman Fellowship awards. He has one-year postdoctoral research experience at AECOM, New York, USA.

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he uptake of exogenous solutes is mediated by transport systems embedded in the plasma membrane and drive active transport even at µM to nM solute concentrations. In many of these systems a periplasmic Solute-Binding Protein (SBP) is utilized to bind their cognate ligands with high affinity and deliver them to the membrane bound translocator subunits. Active transport systems with SBP components are traditionally divided into three main families based on their energetic coupling mechanism, primary sequence and subunit composition: tripartite ATP-independent periplasmic transporters (TRAP), ATP binding cassette transporters (ABC) and tripartite tricarboxylate transporters (TTT). Knowledge of the cognate ligand for the SBP component of the transporter can provide crucial data for functional assignment of co-located or co-regulated genes. In the present study, the structural and functional characterizations of several solute binding proteins have been carried out. Proteins were cloned from genomic DNA, expressed by autoinduction and purified by a combination of Ni-NTA and size exclusion chromatography. The purified SBPs were screened using differential scanning fluorometry (DSF) and a >400 compounds ligand library. Two of the SBPs exhibited DSF hits that were novel for their respective transport family. Crystallization trials of proteins have been conducted with their respective DSF ligand hits. Those SBPs that have structures determined and their respective interactions with co-crystallized ligands will be presented. Cocrystallization with DSF determined ligands resulted in structures of Avi\_5305 in complex with D-glucosamine and D-galactosamine, the first structure of an ABC SBP with an amino sugar.

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