



## Editorial

*Somnath Dutta and Tanweer Hussain\**

Knowledge of the three-dimensional structure of cellular macromolecules plays a crucial role in understanding its function. In the last few years, the field of structural biology has witnessed significant advancements including those in cryo-electron microscopy (cryo-EM) using which near-atomic resolution of macromolecules can be obtained. Hence, it is timely that the journal of Indian Institute of Science has decided to bring out a special issue on 'Recent Advances in Structural Biology'.

This issue is a collection of reviews that aims to bring out the recent developments in various approaches of structural biology, namely X-ray crystallography, nuclear magnetic resonance (NMR) spectroscopy, electron microscopy, biophysical tools and computational methods. Dutta reviews the progress in single-particle cryo-EM and cryo-electron tomography (cryo-TM) including the newly developed technologies that have been implemented in cryo-EM to obtain maps at molecular details. Ghosh and Das present an overview of bacteriophages as a model system for the structural studies done using negative stains in the early days to the current approach of using cryo-EM. The above reviews present a glimpse of how the recent advances in cryo-EM have revolutionized structural biology.

Kinatukara and Sankaranarayanan review enzymes called fatty acyl-AMP ligases, their mechanism of action and how the enzyme-substrate complex structures determined by X-ray crystallography have been employed to deduce substrate specificity. It is interesting to note that few proteins crystallize *in vivo*. The review by Banerjee et al. discusses *in vivo*-grown protein

microcrystals and the new approaches towards microcrystallography to determine structures from crystals of very small size. Majumder et al. reviews the mechanism of functioning of ion-coupled transporters. Since crystallization of membrane proteins is often very challenging, this review also presents other biophysical tools and methods that are employed to understand these transporters.

Nuclear Magnetic Resonance (NMR) Spectroscopy is also an important technique to determine structures and study dynamics of macromolecules. In this issue, Rai et al. review the advances in isotope labeling and its advantages over the conventional one in NMR spectroscopy. Apart from experimental methods, computational methods can also be used to probe structures of biological macromolecules. Haider discusses G-quadruplex structures and the various computational tools that can be used to study G-quadruplex-ligand interactions.

We are pleased to be invited to be the guest editors of this issue. We thank the authors for their contributions, the reviewers for their timely reports, the Editor-in-Chief Prof. Guru Row, and the editorial teams at Archives and Publication Cell of the Indian Institute of Science as well as Springer for their cooperation. We also thank Ayushi A. Datey and Priyabrata Nag from the Department of Molecular Reproduction, Development and Genetics, Indian Institute of Science for the cover image.

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Indian Institute  
of Science, Bangalore,  
India.

\*hussain@iisc.ac.in;  
somnath@iisc.ac.in



**Dr. Somnath Dutta** joined IISc as an Assistant Professor in April 2016 and started his cryo-EM lab at Molecular Biophysics Unit. He pursued his Ph.D. degree from National Institute of Cholera and Enteric Diseases, Kolkata (Jadavpur University) in

2010. Subsequently, he moved to University of Michigan, Ann Arbor, USA, for his post-doctoral training. He was later a research investigator at the University of Michigan. Finally, he moved to India and started his own research group at Indian Institute of Science, Bangalore. He is currently working on structural characterization of biomolecules using single-particle cryo-electron microscopy.



**Dr. Tanweer Hussain** is an Assistant Professor in the Department of Molecular Reproduction, Development and Genetics, Indian Institute of Science. He obtained his PhD degree from Centre for Cellular and Molecular Biology, Hyderabad, in 2011. He

then moved to MRC Laboratory of Molecular Biology, Cambridge, UK, for his post-doctoral research. In December 2016, he returned back to India to start his research group in Indian Institute of Science. His research interest lies in understanding protein synthesis and its regulation.