NANYANG TECHNOLOGICAL UNIVERSITY

School of Biological Sciences

SBS Seminar Announcement

Surmounting the Speed, Size and 'Foldedness' barriers in solution-state Protein NMR

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Abstract

Biological function is a complex interplay of structure, dynamics and interaction of different types of biological molecules, small & big, folded & unfolded, and rigid & flexible in part or in full. Nuclear Magnetic Resonance (NMR) spectroscopy has emerged during the last two decades as the most powerful technique to address these issues and continues to undergo unparalleled development. Much of this in the recent years has been driven by applications to proteins. New methodological developments are continuously happening pushing the frontiers further and further.

We have been developing NMR methods and protocols for rapid chemical shift assignment of protein backbone ($^{1}H^{N}$, ^{15}N, $^{13}C\alpha$, and $^{13}C'$) resonances. The protocol has been automated and the algorithm has been named as AUTOBA. The NMR methods and the AUTOBA protocol enable backbone fold determination in a matter of two days, enable elucidation of complete equilibrium folding pathways, and also enable structural characterization of large protein aggregates in solution. This talk will summarize those accomplishments. I will also show how these can be helpful in gaining functional insights.

Dr. Ramakrishna V Hosur is the Professor at the Tata Institute of Fundamental Research, Mumbai, India. He made important contributions in the area of Biomolecular NMR, Structural Biology and Biophysical Chemistry. He developed new multidimensional NMR techniques, novel strategies and software packages for quantitative macromolecular structure determination. These have led to determination of atomic resolution solution structures of important nucleic acid segments. In addition DNA duplexes containing cognate sites of specific proteins and unusual DNA forms have been investigated. He is presently working on the structures and dynamics of large proteins, protein-protein complexes and multistranded nucleic acid structures by NMR and other spectroscopic methods.

Tuesday, 10 June 2014 11.00am to 12.00pm SBS Classroom 7 (SBS-B1n-17)

Host: A/Prof Konstantin Pervushin

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