

International Symposium on Stable Isotope Aided Biological NMR

May 2 (Mon) and 3 (Tue), 2005

Tokyo Garden Palace (1-7-5 Yushima, Bunkyo-ku, Tokyo 113-003, Japan)

Admission free. Everybody is welcome.

May 2 (Mon), 2005

10:00-10:05

Opening remark

10:05-11:55

Mitsu Ikura (University of Toronto)

Application of heteronuclear multidimensional NMR to protein-protein complexes

Fuyuhiko Inagaki (Hokkaido University)*

NMR studies on phagocyte oxidation system

G. C. K. Roberts (University of Leicester)

Unfolding for binding: talin-vinculin interaction

Angela M. Gronenborn (University of Pittsburgh)

Structural and functional studies on cyanovirin-N, a potent HIV-inactivating protein

11:55-13:20 Lunch

13:20-15:00

Juli Feigon (UCLA)

Structural and functional studies of human telomerase and Yeast RNase III

Yoshifumi Nishimura (Yokohama City University) *

Structural biology of chromatin-related proteins

Robert Kaptein (Utrecht University)

How regulatory proteins interact with DNA: The lac repressor system

Kouseke Morikawa (BERI)*

Structural view of the clamp loading mechanism onto DNA

15:00-15:30 Coffee break

15:30-17:00

Ad Bax (NIH)

Weak alignment offers new opportunities in NMR structure determination.

Peter Güntert (Riken)*

Automated structure determination of SAIL- and other proteins

Masatsune Kainosho (Tokyo Metropolitan University)**

Optimal isotope labeling for NMR protein structure determination – The SAIL method

17:30-19:30 Banquet

May 3 (Tue), 2005

10:00-11:50

Peter E. Wright (Research Institute of Scripps Clinic)

Dissecting protein folding pathways

Yutaka Ito (Riken)*

NMR approaches for the study of larger proteins

Tai-Huang Huang (Academia Sinica, Taipei)

Domain-swapping as a mechanism for regulating heparin binding affinity and the function of the human hepatoma-derived growth factor

John L. Markley (University of Wisconsin)

Automation in protein NMR spectroscopy

11:50-13:20 Lunch

13:20-15:20

Heinz Rüterjans (University of Frankfurt)

Some advantages of NMR for the description of protein structures

Masahiro Shirakawa (Kyoto University)*

Structure and recognition of ubiquitination signals

Flemming M. Poulsen (University of Copenhagen)

Formation of native and non-native-like interactions in protein folding

Bong-Jin Lee (Seoul National University)*

Structural characterization of the nickel-binding properties of bacillus pasteurii urease accessory protein UreE in solution

Heisaburo Shindo (Tokyo University of Pharmacy & Life Science) *

Structure and interactions of the SAP domain of SUMO-ligase PIAS1

15:20-15:50 Coffee break

15:50-17:30

Hideo Akutsu (Osaka University)*

A challenge for investigation of H⁺-ATP synthase by NMR

Stanley J. Opella (UCSD)

Structure determination of membrane proteins by NMR spectroscopy

Ichio Shimada (University of Tokyo)*

NMR study of membrane protein-ligand interaction

Kurt Wüthrich (ETH, Research Institute of Scripps Clinic)

Reminiscences of stable isotope events in biomolecular NMR

17:30-17:35

Closing remark

*20 min, **40 min, otherwise 30 min talk including 5-min discussion

Organizing Committee:

Hideo Akutsu, Yoji Arata, Mitsu Ikura, Ichio Shimada, and Hisaburo Shindo

Contact: Hideo Akutsu, akutsu@protein.osaka-u.ac.jp