

2007/2/15

## 国際ワークショップ (International Workshop on Perspectives on Stable Isotope Aided NMR Methods for Protein Structural Analysis) のご案内

千里ライフサイエンスセンター（大阪）にて、国際ワークショップ（<http://www.sailnmr.org/workshop/>）が開催されます。本ワークショップでは、主に NMR 安定同位体法の応用や、SAIL法の発展および普及を目的とした討議を行います。参加費は無料ですので、ふるってご参加ください。

プログラムは 3 ページ以降にありますので、参照してください。

日時：2007 年 3 月 30-31 日

会場：千里ライフサイエンスセンター（大阪）

組織委員：甲斐荘正恒（名大）、嶋田一夫（東大）、藤原敏道（阪大）、阿久津秀雄（阪大）、稲垣冬彦（北大）、西村善文（横市大）、Peter Güntert（理研 GSC）

また、本ワークショップでは、ポスター発表を募集いたします。発表を希望される方は、2 月 28 日（水）までに、下記メールアドレスまで、要旨をご送付ください。要旨は、次ページのテンプレートを参考にして、MS ワード形式、A4 用紙 1 枚以内、英文にて作成してください。ポスターは、A0（841 x 1189 mm）以内の大きさにて作成してください。

要旨送付先：[kainosho@nmr.chem.metro-u.ac.jp](mailto:kainosho@nmr.chem.metro-u.ac.jp)

## **International Workshop on Perspectives on Stable Isotope Aided NMR Methods for Protein Structural Analysis**

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We would like to invite you to participate in the International Workshop on Perspectives on Stable Isotope Aided NMR Methods for Protein Structural Analysis, which will be held at the Senri Life Science Center in Osaka on March 30-31, 2007. This workshop is intended to solicit for advice and support from the biological NMR community to develop the SAIL and related methods, in order to make them available to all of us. Because of this specific task, we would be very glad if you will be able to emphasize the importance of optimization of samples, especially their isotope labeling patterns, in your presentations. Any advice along this line would be most welcome. The specific aims of the Workshop are: (i) To explore advanced isotope-aided NMR methodology, including SAIL and cell-free protein synthesis, for structural studies of larger proteins, protein complexes, and membrane proteins. (ii) To extend optimal isotope labeling methods to solid-state NMR, especially targeting membrane proteins. (iii) To develop fully automated structural analysis of stable isotope labeled proteins. (iv) To discuss applications of optimal isotope labeling for NMR investigations of ligand binding (drug discovery). The workshop features lectures by eminent NMR spectroscopists, as well as poster presentations and a panel discussion on Sample Optimization Methods for Protein NMR. We are looking forward to meeting you at the International Workshop on Perspectives on Stable Isotope Aided NMR Methods for Protein Structural Analysis in Osaka.

Draft Program for the International Workshop on: "Perspectives on Stable Isotope Aided NMR Methods for Protein Structural Analysis"

Date: March 30-31, 2007

Venue: Senri Bioscience Center, Osaka, Japan

Organizing Committee: Masatsune Kainosho (Nagoya Univ.), Ichio Shimada (Tokyo Univ.), Toshimichi Fujiwara (PRI, Osaka Univ.), Hideo Akutsu (PRI, Osaka Univ.), Fuyuhiko Inagaki (Hokkaido Univ.), Yoshifumi Nishimura (Yokohama City Univ.), Peter Güntert (RIKEN)

All long talks will be 30 min including 5 min for discussion, except the keynote lecture by Prof. Wüthrich, that will be allocated 10 more min. All short talks shown with \* will be 20 min including 5 min for discussion.

March 30, 2007 (Friday)

Opening remark (9:00-9:10)

Masatsune Kainosho (Nagoya Univ.)

Keynote Lecture (9:10-9:50)

Kurt Wüthrich (Scripps, ETH): APSY-NMR- Present state and outlook

Session Ia- New Methodologies I (9:50-10:50):

Convener: Masatsune Kainosho (Nagoya Univ.)

Ad Bax (NIH) : High precision dipolar couplings on isotopically labeled proteins to address the dynamics question

Peter Güntert (RIKEN): Automated protein structure determination with SAIL-FLYA

Session Ib- New Methodologies II (10:50-12:00):

Convener: Peter Güntert (RIKEN)

Martin Billeter (Göteborg Univ.): Analysis of NMR data from fast spectroscopy

Yutaka Ito\* (Tokyo Metropolitan Univ.): Application of nonlinear sampling and maximum entropy reconstruction to "difficult" protein samples

Shin-ichi Tate\* (Hiroshima Univ.): Molecular alignment determination only using orientation dependent TROSY shift changes

Lunch break 12:00-13:30 (poster presentation)

Session IIa - Protein/Nucleic Acids Structure I (13:30-15:30)

Convener: Hideo Akutsu (Osaka Univ.)

Peter E. Wright (Scripps): Intrinsically disordered proteins: New challenges for NMR

Yoshifumi Nishimura (Yokohama City Univ.): NMR dynamics in the PhoB DNA-binding domain and the intrinsically disordered domain of the neural repressor

Fuyuhiko Inagaki (Hokkaido Univ.): Structural basis on the inhibition of CrkII activity by phosphorylation

Ichio Shimada (Tokyo Univ.): NMR study on protein-protein interactions using paramagnetic probe

Coffee break 15:30-16:00 (poster presentation)

Session IIb - Protein/Nucleic Acids Structure II (16:00-18:00)

Convener: Fuyuhiko Inagaki (Hokkaido Univ.)

Juli Feigon (UCLA) Structural studies of RNA processing and modification

Masato Katahira\* (Yokohama City Univ.): The structure of human telomeric DNA and the interactions of hnRNP A1/hnRNP D proteins with telomeric DNA

Rolf Boelens (Univ. Utrecht): Structure and dynamics in gene regulation and DNA repair

Masahiro Shirakawa\* (Kyoto Univ.): Structural studies of ubiquitin-like modifier proteins

Chojiro Kojima\* (NAIST): NMR structure of a protein complex beyond 25 kDa - possibility and limitation of uniform labeling approach

March 31, 2007(Saturday)

Session III – Sample preparation/labeling (9:00-11:40)

Convener: Ichio Shimada (Tokyo Univ.)

Masatsune Kainosho (Nagoya Univ.): Perspective of further optimization for isotope labeling methods in biological NMR spectroscopy

Mitsu Ikura(Toronto Univ.):Optimization of NMR samples for the investigation of protein-protein complexes

Koichi Kato\* (Nagoya City Univ.): Stable-isotope-assisted NMR analyses of post-translational modifications

Gottfried Otting (Australian National Univ.): Protein samples for NMR: cell-free protein synthesis and lanthanide labeling

John L. Markley (Univ. Wisconsin-Madison): Experience with a wheat germ cell-free protein system for preparing labeled eukaryotic proteins for NMR analysis

Takanori Kigawa\* (RIKEN) Cell-free protein synthesis for stable-isotope aided NMR

Lunch break 11:40-13:10 (poster presentation)

Session III - Membrane proteins solid/solution-state NMR (13:10-15:10)

Convener: Toshimichi Fujiwara (Osaka Univ.)

Stanley J. Opella (UCSD): Co-development of isotopic labeling schemes and pulse sequences for structure determination of membrane proteins

Hartmut Oschkinat (FMP Berlin): Protein structure determination by MAS solid-state NMR: application to fibrils and membrane proteins

Volker Dötsch (Frankfurt Univ.): Structure determination of integral membrane proteins by NMR spectroscopy

Hideo Akutsu (Osaka Univ.): NMR Investigation of Energy Conversion Systems

Session IV – Protein-ligand/protein-protein interactions- Drug discovery (15:10-16:30)

Convener: Yoshifumi Nishimura (Yokohama City Univ.)

Gerhard Wagner (Harvard Medical School): Use of isotope labels in NMR-based drug discovery

Christian Griesinger (MPI): New methods and applications for the study of protein ligand interactions

Daisuke Kohda\* (Kyushu Univ): Relaxation study reveals a dual-mode interaction mechanism for mitochondrial presequence recognition by Tom20

Coffee break 16:30-17:00 (poster presentation)

Session V. Panel Discussion on Sample Optimization Methods (17:00-18:30)

Each one presents a short presentation (~10 min) to stimulate discussion

Convener: Kurt Wüthrich

Panelist: Opella, Oschkinat, Markley, Kainosho, Wagner, others.

Concluding Remark by Kurt Wüthrich