兵庫県立大学大学院 生命理学研究科
Graduate School of Life Science, University of Hyogo

グローバル COE プログラム
Global COE Program

「ピコバイオロジー：原子レベルの生命科学」
Picobiology: Life Science at the Atomic Level

International Symposium on Membrane Proteins and High Resolution X-ray Structural Analysis

日時: 2008年 9月 1日 (月)

場所: 先端科学技術支援センター・セミナー室１（兵庫県 赤穂郡 上郡町 光都）

PROGRAM

(Organized by T. Tsukihara and S. Yoshikawa)

9:00-9:05 Opening remarks (Tomitake Tsukihara)

9:05-9:35 Koji Inaka (Maruwa Foods, Japan)
Sample preparation for high quality protein crystals.

9:35-10:20 Andrea Schmidt (EMBL, Germany)
Structural enzymology at atomic resolution on the example of hydroxynitrile lyase from *Hevea brasiliensis*.

10:20-10:35 Coffee break

10:35-11:05 Atsushi Nakagawa (Osaka Univ., Japan)
High-resolution x-ray crystallographic study of bovine H-protein of glycine cleavage system.

11:05-11:50 Christian Jelsch (CNRS UHP, France)
Ultra high resolution refinement: MoPro refinement program.

11:50-13:00 Lunch

13:00-13:45 Alberto Podjany (Univ. of Strasburg, France)
Quantum model of catalysis based on subatomic resolution X-ray and neutron diffraction studies of fully deuterated human aldose reductase.

13:45-14:15 Yoshiki Higuchi (Univ. of Hyogo, Japan)
X-ray structural study of [NiFe] hydrogenase - Consideration of the relationship between intensity data and electron density map.

14:15-14:30 Coffee break

14:30- 15:15 Jean-Luc Popot (CNRS and Université Paris-7, France)
Amphipols: Synthetic polymers that turn membrane proteins into soluble ones. Applications to folding and immobilization.

15:15-15:45 Shoji Maeda (Osaka Univ., Japan)
Low-resolution analysis of gap junction.

15:45-16:00 Coffee break

16:00-16:45 Di Xia (NIH, USA)
How to separate a pair of electrons: The mechanism of cytochrome bc_1 function.

16:45-17:15 Midori Murakami (Nagoya Univ., Japan)
X-ray structure of squid rhodopsin.

17:15-17:45 Tomitake Tsukihara (Univ. of Hyogo, Japan)
X-ray structural analysis of bovine cytochrome *c* oxidase.

Closing remarks (Shinya Yosikawa)

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