OKAZAKI CONFERENCE

Okazaki COE Conference

Okazaki IMS Conference 2002
"Search for Frontier of Biomolecular Science"

The series of conferences which had been called "IMS COE Conference" until last year, is renamed henceforth to "Okazaki IMS Conference, (year)." The series of international conferences will be held once a year with a focus on some selected area of molecular science. This year the organization of the conference was left to Profs. Kazuhiko Kinosita, Yoshihito Watanabe (moved to Nagoya Univ. afterward), and Teizo Kitagawa of Center for Integrative Bioscience. Accordingly, they organized a symposium on "Dynamical Structures and Molecular Design of Metalloproteins," which was held on November 19 through 21, 2002 at Okazaki Conference Center. Twenty one invited talks including nine oversea lecturers, and thirty-five poster presentations were involved. The number of registered participants were 114 including 22 foreigners.

An amino acid sequence of a given protein is determined by gene and idividual proteins adopt a specific three dimensional structure to perform their physiological functions. The characteristics of proteins include that they are flexible macromolecules whose structures are dynamical and that the structure itself changes with a progress of reaction in the case of enzymes. It is the purpose of this conference to discuss the dynamical structures of proteins determined with time-resolved techniques in nano- or pico-second time regimes and their relations with physiological functions. The discussion is further extended to design an arrangement of amino acid residues so that nonactive protein could be converted to an active enzyme along a given reaction.

The symposium started from a sonorous lecture by Prof. S. G. Sligar, who covered comprehensively heme enzymes. Structure and reaction mechanism of cytochrome P450 attracted attention and it was demonstrated that myoglobin, an oxygen carrier protein, can be converted to cytochrome P450 with a specific enzymatic activity by using site-directed mutagenesis. Various enzymatic activities were generated by different site-directed mutations to a single protein and these facts led us to reconsider the idea that protein functions were developed with evolution of organisms. Bioenergetic sessions involved a coupling mechanism of electron/proton transfers in terminal oxidases and an active biomotor movement of ATPase. The latter was demonstrated as a movie of a single molecule. Thus, the cutting-edge results were introduced in this conference and young participants were stimulated greatly. The program was as follows;

PROGRAM

November 18 (Monday)
15:00–18:30 Registration
18:30–20:00 Get-Together Party

November 19 (Tuesday)
9:00– 9:10 Welcome Greeting
K. Kaya (Director, IMS)
Opening Remarks
T. Kitagawa (Center for Integrative Bioscience)

Chair: M. Ikeda-Saito (Tohoku University)
9:10– 9:50
S. G. Sligar (University of Illinois, Urbana):
The Cytochrome P450 Dynamic Landscape: A Case of Complex Adaptive Matter
9:50–10:30
Y. Watanabe (Nagoya University):
Introduction of P450, Peroxidase, and Catalase Activities into Myoglobin by Site-Directed Mutagenesis

10:30–10:50 Coffee Break

Chair: Y. Shiro (RIKEN)
10:50–11:30
V. Srajer (Argonne National Laboratory):
Nanosecond Time-Resolved X-Ray Diffraction Study of Protein Relaxation and Ligand Migration in Myoglobin and *Scapharca* Hemoglobin
11:30–12:10
M. Nakasako (Keio University):
Hydration Structure of Proteins

12:10–13:30 Lunch
13:30–15:00 Poster Discussion

Chair: K. Akasaka (Kinki University)
15:00–15:40
H. Kandori (Nagoya Institute of Technology):
Internal Water Molecules of Rhodopsins at Work
15:40–16:20
R. B. Dyer (Los Alamos National Laboratory):
The Role of Fast Protein Motions in Enzymatic Catalysis
16:20–16:40 Coffee Break

Chair: Y. Naruta (Kyushu University)
16:40–17:20
I. Hamachi (Kyushu University):
Bioorganic Engineering of Native Proteins
17:20–18:00
D. B. Goodin (Scripps Research Institute):
Engineering Heme Enzymes to Bind Novel Ligands, Substrates and Molecular Wires

November 20 (Wednesday)
Chair: T. Hase (Osaka University)
9:00– 9:40
S. Yoshikawa (Himeji Institute of Technology):
The Reaction Mechanism of Cytochrome *c* Oxidase
9:40–10:20
Y. Lu (University of Illinois, Urbana):
Designing a Cytochrome *c* Oxidase: Structural and Kinetic Study of Cu_A and Heme-Cu_B Model Proteins

10:20–10:40 Coffee Break

Chair: N. Go (Institute of Atomic Energy)
10:40–11:20
Y. Okamoto (IMS):
Molecular Simulations of Protein Folding.
11:20–12:00
S. Hayward (University of East Anglia):
A Database Approach to Understanding and Predicting Functional Domain Movements in Proteins

12:00–13:20 Lunch
13:20–14:50 Poster Discussion

Chair: K. Yoshihara (JAIST)
14:50–15:30
M. Terazima (Kyoto University):
New Time-resolved Detections on Energy and Protein Structures of Some Photoactive Proteins
15:30–16:10
R. J. D. Miller (University of Toronto):
Advent of Few Cycle Optical Pulses: Mapping the Transduction of Reaction Forces from the Quantum to Mesoscale Motions of Protein Functions

16:10–16:30 Coffee Break

Chair: K. Nagayama (Center for Integrative Bioscience)
16:30 – 17:10
A. Ikai, M. T. Alam, R. Afrin and H. Arakawa
(Tokyo Institute of Technology):
Force Spectroscopy of Metallo-protein Dynamics
17:10–17:50
K. Kinosita Jr. (Center for Integrative Bioscience):
Single-Molecule Physiology under an Optical Microscope: How Molecular Machines May Work

18:30–20:30 Banquet: Okazaki New Grand Hotel

November 21 (Thursday)
Chair: M. Go (Nagoya University)
9:00– 9:40
I. Morishima (Kyoto University):
Module as the Structural and Functional Unit in Hemoproteins and Its Application to Design of Novel Hemoproteins
9:40– 10:20
T. Yomo (Osaka University):
Experimental Evolution of Function from Random Sequences

10:20–10:40 Coffee Break

Chair: T. Iizuka (Hosei University)
10:40–11:20
L. -L. Wong (Oxford University):
Molecular Recognition in Catalysis by Cytochrome P450cam
11:20–12:00
T. Kitagawa (Center for Integrative Bioscience):
Time-Resolved Resonance Raman Study on Vibrational and Structural Relaxations of Carbonmonoxy Myoglobin
12:00–12:40
P. Anfinrud (National Institutes of Health):
Watching a Protein as Its Functions with Picosecond Time-Resolved X-Ray Crystallography and Femtosecond Time-Resolved IR Spectroscopy

12:40–12:45 Concluding Remarks
K. Kinosita Jr. (Center for Integrative Bioscience)