

26 MAY Sun

- 13:00 - 14:00 Registration
- 14:00 - 14:30 Opening ceremony
- 14:30 - 15:45 **Nobel Talk 1, Chair: John Johnson (Scripps Research Institute)**
(NT-1) Thomas Steitz (Yale University, USA)
From the Structure and Function of the Ribosome to New Antibiotics
- 15:45 - 16:15 Break
- 16:15 - 18:00 Session (1) **Synchrotron radiation and free electron lasers**
Chair: Shinichi Adachi (KEK) and John Helliwell (University of Manchester)
(O1-1) Thomas Schneider (EMBL Hamburg, Germany)
EMBL beamlines for macromolecular crystallography at PETRA III
(O1-2) Yoshinori Nishino (Hokkaido University, Japan)
Coherent imaging with X-ray free-electron lasers
(O1-3) Thomas Irving (Illinois Institute of Technology, USA)
Sub-millisecond solution scattering at the BioCAT facility at the Advanced Photon Source
- 18:00 - 18:15 Break
- 18:15 - 19:45 Welcome party at the View Room, 9th Floor

27 MAY Mon

- 9:15 - 10:15 **Plenary Lecture 1, Chair: Leann Tilley (University of Melbourne)**
(PL-1) Yoshinori Fujiyoshi (Nagoya University, Japan)
Structural physiology of channels
- 10:15 - 10:45 Break
- 10:45 - 12:30 **Session (2) New methodology and instrumentation**
Chair: Atsushi Nakagawai (Osaka University) and Min Yao (Hokkaido University)
(O2-1) Randy Read (University of Cambridge, UK):
Extending the limits of molecular replacement
(O2-2) Andrea Thorn (University of Cambridge, UK)
Pushing the boundaries of phasing with SHELXC/D/E
(O2-3) Leonard Chavas (High Energy Accelerator Research Organization (KEK), Japan)
New methodologies at PF AR-NW12A: implementation of high-pressure MX
(O2-4) Noriyoshi Sakabe (High Energy Accelerator Research Organization (KEK) and Foundation for Advanced International Science (FAIS), Japan)
"U-shape rotating anticathode compact X-ray generator:" 20 times stronger than a commercially available X-ray source
- 12:30 - 13:30 **Sponsored Lunch at Meeting room No. 3 (4F) by Agilent Technologies Japan, Ltd.**
- 13:30 - 15:00 Poster display session (odd number)

15:00 – 19:00 **Sessions (3 and 4) Drug design**
Chair: Midori Takimoto-Kamimura (Teijin Pharma) and Roderick Hubbard
(O3&4-1) Roderick Hubbard (York University & Vernalis, UK)
Current perspectives in fragment-based drug discovery
(O3&4-2) Gerhard Klebe (Marburg University, Germany)
Structure-thermodynamics correlation: a guideline for the optimization of fragments to leads
(O3&4-3) Tom Davies (ASTEX, UK)
Fragment-based drug discovery using X-ray crystallography
(O3&4-4) Miles Congreve (Heptares Therapeutics Limited,UK)
Fragment and structure based drug discovery for G protein-coupled receptors
(O3&4-5) Tsuyoshi Inoue (Osaka University, Japan)
Novel crystallization method and structure-based design of recombinant antibody fragments
(O3&4-6) Osamu Nureki (University of Tokyo., Japan)
Structural basis for a novel drug extrusion mechanism by MATE multidrug transporter and its inhibitor design

28 MAY Tue

9:15 - 10:15 **Plenary Lecture 2, Chair: Nobuo Niimura (Ibaraki University)**
(PL-2) Paul Langan (Oak Ridge National laboratory, USA)
Seeing the chemistry in biology with neutrons

10:15 - 10:45 Break

10:45 - 12:30 **Session (5) Electron microscopy, Chair: Takuo Yasunaga (Kyushu Institute of Technology, Japan) and Atsuo Miyazawa (University of Hyogo)**
(O5-1) Yifan Cheng (University of California, San Francisco, USA)
Attempting high-resolution single particle cryoEM of small proteins: combining biochemistry and hardware
(O5-2) Masahide Kikkawa (University of Tokyo, Japan)
High-resolution imaging of axonemal motors
(O5-3) Naoyuki Miyazaki (National Institute for Physiological Sciences, Japan)
Cryo-electron tomography: towards revealing the viral life cycle of Rice dwarf virus
(O5-4) Takashi Fujii (RIKEN Quantitative Biology Center, Japan)
High resolution structural analysis of helical filaments by cryoEM

12:30 - 13:30 Group Photo at the Main Hall (Conference Room) at 7th floor and Lunch

13:30 - 15:00 Poster display session (even number)

15:00 – 16:45 **Session (6) Tomography and Imaging**
Chair: Kazuhiro Aoyama (FEI Company) and Atsuo Miyazawa (University of Hyogo)

(O6-1) Paul Matsudaira (National University of Singapore, Singapore)

Imaging protein in water at room temperature by TEM

(O6-2) Marc Storms (FEI Company, Netherlands)

Latest developments in cryo-TEM: FEI Arctica and Falcon II™

(O6-3) Takuo Yasunaga (Kyushu Institute of Technology, Japan)

Applications of image processing system, Eos, to three-dimensional electron microscopy

(O6-4) Yoshitaka Kimori (National Institutes of Natural Sciences, Japan)

Morphological image processing for quantitative shape analysis of biomedical structures

16:45 - 17:15 Break

17:15 - 18: 15 **Plenary Lecture 3, Chair: Midori Takimoto-Kamimura (Teijin Phrama)**

(PL-3) Ian Wilson (Scripps Research Institute, USA)

Structure-based vaccine design

18:15 - 18:30 Break

18:30 - 21:00 Banquette at the View Room, 9th Floor

29 MAY Wed

9:15 - 10:30 **Nobel Talk 2, Chair: So Iwata (Kyoto University)**

(NT-2) Brian Kobilka (Stanford University, USA)

Structural insights into G protein coupled receptor activation.

10:30 – 11:00 Break

11:00 - 12:45 **Session (7), Neutron diffraction and hydration structure**

Chair: Nobuo Niimura (Ibaraki University) and Alberto Podjarny (IGBMC)

(O7-1) Andrey Kovalevsky (Oak Ridge National laboratory, USA)

Mechanistic enzymology with neutrons and quantum biochemistry

(O7-2) Andreas Ostermann (Technische Universität München, Germany)

Macromolecular neutron diffraction at the FRM II neutron source

(O7-3) Takeshi Yokoyama (University of Toyama, Japan)

Hydrogen-bond network and pH sensitivity in human transthyretin

(O7-4) Kazuo Kurihara (JAEA, Japan)

Detailed structure analysis of active Site of β -lactamase TOHO-1

12:45 - 13:45 Lunch

13:45 - 15:30 **Session (8) Membrane proteins and macromolecular complexes**

Chair: Nobuo Kamiya and Brian Kobilka

(O8-1) So Iwata (Kyoto University, Japan)

Crystallisation of mammalian membrane proteins using antibody fragments.

(O8-2) Genji Kurisu (Osaka University, Japan)

Structure of the cytoplasmic dynein motor domain

(O8-3) Nobuo Kamiya (Osaka City University, Japan)

Oxygen evolution mechanism of photosystem II predicted from its 1.9 Å resolution structure

15:30 – 16:00

Break

16:00 - 17:45

Session (9) Protein structure and dynamics

Chair: Mamoru Sato and Giuseppe Zaccai

(O9-1) Mamoru Sato (Yokohama City University, Japan)

SAXS and MD simulation to investigate protein flexibility in solution

(O9-2) Giuseppe Zaccai (ILL, France)

Neutrons reveal the ecology of protein and water dynamics

(O9-3) Masaaki Sugiyama (Kyoto University, Japan)

Small-angle neutron scattering for subunit kinetics of protein complex in solution

17:45 – 18:00

Closing ceremony