

6th International Symposium on Diffraction Structural Biology: ISDSB2019

Osaka University Hall, Osaka University Toyonaka Campus, October 17-20, 2019

17 October 2019

13:00	13:15	Opening Remarks		Atsushi Nakagawa	Osaka Univ., Japan
Plenary Talk 1 (Chair: So Iwata)					
13:15	14:00	PL-01	Structure-based design of novel therapeutics against influenza virus	Ian Wilson	Scripps Research Inst., USA
14:00	14:20	Coffee Break			
Session 1 MX facilities 1 (Chair: Atsushi Nakagawa, Takashi Yamane) Nobuhisa Watanabe Memorial Session					
14:20	14:50	O-01	Making molecular movies	So Iwata	Kyoto Univ., Japan
14:50	15:20	O-02	Macromolecular crystallography at SPring-8	Masaki Yamamoto	RIKEN SPring-8 Center, Japan
15:20	15:50	O-03	Structural biology and time-resolved X-ray studies at the Photon Factory	Sin-ichi Adachi	IMSS, KEK, Japan
15:50	16:20	O-04	Mixed-valence state of the oxygen-evolving complex in photosystem II, determined by utilization of X-ray anomalous dispersion effect	Nobuo Kamiya	Osaka City Univ., Japan
16:20	16:35	O-05	An overview of X-rays, neutrons and electrons as experimental probes in structural biology	John R Helliwell	Univ. Manchester, UK
Welcome Reception					
16:35	17:05	Transfer			
17:05	18:35	Reception			

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Session 2 MX facilities 2 (Chair: Yukio Morimoto, Leighton Coates)					
9:00	9:30	O-06	Opportunities for structural biologists at the ALBA synchrotron: current status and perspectives	Roeland Boer	ALBA Synchrotron, Spain
9:30	9:45	O-07	Status and development of structural biology beamlines at the Canadian Light Source	Pawel Grochulski	Canadian Light Source, Canada
9:45	10:15	O-08	Status of the MX beamlines at the first MBA-based Synchrotron MAX IV	Marjorlein Thunnissen	Max IV, Lund Univ., Sweden
10:15	10:30	O-09	XChem: an 'in-crystal' fragment screening facility at Diamond Light Source	Alice Douangamath	Diamond Light Source, UK
10:30	10:50	Coffee Break			
Plenary Talk 2 (Chair: Takayuki Katoh)					
10:50	11:35	PL-02	Structure-guided drug development by cryo-EM	Yoshinori Fujiyoshi	Tokyo Med. & Dent. Univ., Japan
11:35	13:05	Lunch (Buffet for invited attendees) / Poster viewing			
Session 3 Macromolecular Crystallography 1 (Chair: Chwan-Deng Hsiao, Takayoshi Kinoshita)					
13:05	13:35	O-10	Application of rigid linkers in structural biology	Jie-Oh Lee	KAIST, Korea
13:35	13:50	O-11	Antagonist-inactivation Mechanism of Innate Immune Receptor TLR8 Revealed by X-ray Crystal Structure Analysis.	Kentaro Sakaniwa	Univ. Tokyo, Japan
13:50	14:20	O-12	Transient partial dehydration of potassium ions facilitates permeation through Kir channels	Jacqui Gulbis	The Walter and Eliza Hall Inst., Australia
14:20	14:35	O-13	An embrace: Structural basis of the human endoglin-BMP9 interaction	Marcel Bokhove	Fukushima Medical Univ., Japan
14:35	16:05	Poster Session 1 with Coffee			
Session 4 Macromolecular Crystallography 2 (Chair: Taro Tamada, Katsuhiko Kusaka)					
16:05	16:35	O-14	Anomalous X-ray diffraction studies of ion transport in K ⁺ channels	Leighton Coates	Oak Ridge Natl., Lab., USA
16:35	16:50	O-15	O ₂ -activation and unidirectional proton-pump mechanisms of cytochrome <i>c</i> oxidase elucidated by X-ray structures of its catalytic intermediates	Tomitake Tsukihara	Univ. Hyogo, Japan
16:50	17:20	O-16	Structure and function of chloroplast tail-anchored membrane protein recognition by ArsA1	Chwan-Deng Hsiao	Academia Sinica, Taiwan
17:20	17:35	O-17	Serial nano-beam electron diffraction of protein nano-crystals	Pascal Hogan-Lamarre	Univ. Toronto, Canada

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Nobel Lecture (Chair: John E. Johnson)						
9:00	10:00	NL	Single-particle cryo-electron microscopy: visualization of biological molecules in their native states	Joachim Frank	Columbia Univ., USA	
10:00	10:10	Group Photo				
Session 5 Cryo-TEM (Keiichi Namba, Akihiro Kawamoto)						
10:10	10:40	O-18	Structural basis for the assembly and energy transfer in maize PSI-LHCI-LHCII supercomplex	Mei Li	Chinese Academy of Science, China	
10:40	11:10	O-19	Structure of the Ebola virus core by single-particle cryo-EM	Yukihiko Sugita	Osaka Univ., Japan	
11:10	11:30	Coffee Break				
11:30	12:00	O-20	CryoEM structure of the PA28/20S proteasome complex from <i>Plasmodium falciparum</i> with implications for proteostasis and antimalarial drug development	Leann Tilley	Univ. Melbourne, Australia	
12:00	12:30	O-21	MicroED: conception, practice and future opportunities	Tamir Gonen	UCLA, USA	
12:30	14:00	Lunch (Buffet for invited attendees) / Poster viewing				
14:00	15:30	Poster Session 2 with Coffee				
Session 6 Sponsored Session (Thermo Fisher Scientific)						
15:30	16:30	SS-01	Cryo-EM structures capture the transport cycle of the P4-ATPase flippase	Masahiro Hiraizumi	Mitsubishi Tanabe Pharma Corporation / The University of Tokyo	
16:30	16:50	Transfer				
16:50	18:50	Q&A session in Banquet				

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Plenary Talk 3 (Chair: Genji Kurisu)						
9:00	9:45	PL-03	How structural biologists and the Protein Data Bank contributed to recent US Food and Drug Administration new drug approvals	Stephen K. Burley	RCSB Protein Data Bank, Rutgers University and UC San Diego, USA	
9:45	10:05	Coffee Break				
Session 7 Software and databases (Min Yao, John R. Helliwell)						
10:05	10:35	O-22	Software developments for jointly improving diffraction data collection, processing and quality evaluation	Gerard Bricogne	Global Phasing, UK	
10:35	10:50	O-23	Automated data processing for microcrystallography	Keitaro Yamashita	Univ. Tokyo, Japan	
10:50	11:20	O-24	The Crystallographic Information Management System (CRIMS); Enabling fully automated, remote controlled protein to structure pipelines for drug design	Jose A. Marquez	EMBL Grenoble, France	
11:20	11:35	O-25	From two-dimensional crystal serial diffraction to a three-dimensional intensity set: paving the way to the time-resolved study of large-scale movements in membrane proteins	Cecilia Casadei	Paul Scherrer Inst., Switzerland	
11:35	13:05	Lunch (Buffet for invited attendees)				
Session 8 Drug Discovery 1 (Chair: Midori Kamimura, Terese Bergfors)						
13:05	13:35	O-26	Structure based design enabled for membrane protein drug targets by advances in X-FEL and cryo-EM sciences	Michael Hennig	LeadXpro, Switzerland	
13:35	14:05	O-27	Recent advances in structure and fragment based lead discovery	Roderick E. Hubbard	York Univ., UK	
14:05	14:35	O-28	Dissecting GPCR structure and dynamics with X-ray lasers	Vadim Cherezov	Univ. Southern California, USA	
14:35	14:50	O-29	Discovery of Molecular-Targeted Drugs by X-ray Crystallographic Screening	Takeshi Yokoyama	Univ. Toyama, Japan	
14:50	15:05	Coffee Break				
Session 9 Drug Discovery 2 (Chair: Satoshi Sogabe, Rod Hubbard)						
15:05	15:35	O-30	Data integration and computational systems approaches to drug discovery	Kenji Mizuguchi	Osaka Univ. / NIBIOHN, Japan	
15:35	15:50	O-31	Drug design for malaria: fosmidomycin analogues	Sanjeewani Sooriyaarachchi	Uppsala Univ., Sweden	
15:50	16:05	O-32	Inactive dimer structure of the protease domain of stomatin operon partner protein	Hideshi Yokoyama	Tokyo Univ. Sci., Japan	
16:05	16:35	O-33	A protein crystallization strategy for structure-based drug design	Terese Bergfors	Uppsala Univ., Sweden	
16:35	16:40	Closing Remarks		Tsuyoshi Inoue	Osaka Univ., Japan	