Program

February 15 (Mon)

10:00-10:25	**Steven P. Gross (UC Irvine, and KIAS)** Single molecular motor heterogeneity and its implications for ensemble function
10:25-10:45	**Akihiko Nakamura (IMS)** Analysis of functional structure of cellulase by neutron crystallography
10:45-11:10	**Ryota Iino (IMS)** Direct observation of intermediate states during the stepping motion of kinesin-1
11:10-11:35	**Sota Sato (Tohoku Univ. & JST)** Biological functions implanted in artificial supramolecules
11:35-11:55	**Takayoshi Watanabe (Japan Adv. Inst. of Sci. & Tech.)** Novel method for site-specific protein pegylation using aromatic amine-containing non-natural amino acid
11:55-13:30	Lunch
13:30-13:55	**Keehyoung Joo (KIAS)** Contact Assisted Protein Structure Modeling by Global Optimization in CASP11
13:55-14:20	**Nam Ki Lee (POSTECH)** New single-molecule FRET method for observing fast dynamics and its application for dsDNA bending dynamics
14:20-14:45	**Masahide Terazima (Kyoto Univ.)** Time-resolved study on conformation change and inter-domain change during protein reactions
14:45-15:10	**Kunihiro Kuwajima (Tokyo Univ.)** The H/D-exchange kinetics of a fully unfolded protein studied by the DMSO-quenched and 2D NMR techniques
15:10-15:40	coffee break
15:40-16:00	**Balachandran Manavalan (KIAS)** StrRate: Structure-based protein folding type classification and folding rate prediction
16:00-16:20	**Seung Hwan Hong (KIAS)** Template based modeling by dynamic fragment assembly: revisited
16:20-16:45	**Ji-Joon Song (KAIST)** Understanding molecular Architecture of Huntington’s disease protein
17:30-	Banquet （事前申込必要、会費 5,000 円）

Februry 16 (Tue)

10:00-10:25	**Fumio Hirata (Ritsumeikan Univ.)** Multi-scale dynamics simulation of protein based on the generalized Langevin equation combined with 3D-RISM theory
10:25-10:45	**InSuk Joung (KIAS)** Efficient sampling of transition pathways using nudged elastic band and conformational space annealing
10:45-11:10	**Hisashi Okumura (IMS)** Pressure induced structural change of proteins by molecular dynamics simulations
11:10-11:35	**Seokmin Shin (Seoul National Univ.)** The two faces of self-assembly of peptides
11:35-12:00	**Jooyoung Lee (KIAS)** Atomistic mechanism of conformational transition of adenylate kinase investigated by Lorentzian structure-based potential
12:00-13:30	Lunch
13:30-13:55	**Chaok Seok (Seoul National Univ.)** Galaxy7TM: Modeling and docking of G-protein coupled receptors
13:55-14:15	**Takumi Yamaguchi (Japan Adv. Inst. of Sci. & Tech.)** Design and creation of Lewis X-expressing glycoclusters toward functional analyses of oligosaccharides in membrane systems
14:15-14:40	**Kazushi Kinbara (Tokyo Inst. of Tech.)** Development of Stimuli-Responsive Multiblock Amphiphilic Molecules Mimicking Multipass Transmembrane Proteins
14:40-15:05	**Weontae Lee (Yonsei Univ.)** NMR and X-ray crystallographic studies on syndecan, proteogylcan: Structure, function and diseases
15:05-15:35	coffee break
15:35-16:00	**Shinobu Itoh (Osaka Univ.)** Activation mechanism of fungal tyrosinase
16:00-16:25	**Masafumi Odaka (Akita Univ.)** Time-resolved crystallography of the reaction intermediate of nitrile hydratase: Revealing a role for the cysteinesulfenic acid ligand as a catalytic nucleophile
16:25-16:50	**Shuji Akiyama (IMS)** Atomic-scale origins of slowness in the cyanobacterial circadian clock
16:50-17:15	**Dong Hae Shin (Ewha Womans Univ.)** Structural properties of GmhA and GmhB from *Burkholderia thailandensis*
18:00-	Free Discussion

February 17 (Wed)

10:00-10:25	**Takeshi Uchida (Hokkaido Univ.)** Heme uptake proteins from *Vibrio cholerae*
10:25-10:50	**Hiroshi Sugimoto (RIKEN/SPring-8)** Structural mechanism of the heme transporter complex from pathogenic bacteria
10:50-11:10	**Norifumi Muraki (IMS)** Crystal structures of HtaA and HmuT, heme uptake proteins from *Corynebacterium glutamicum*
11:10-11:35	**Jeong-Yong Suh (Seoul National Univ.)** Structural basis for the preferential interaction of auxin-response transcriptional repressor with different transcription factors
11:35-11:55	**Saeko Yanaka (IMS)** Affinity improvement of antibody through mutational modification of the conformational dynamics
11:55-13:30	Lunch
13:30-13:55	**Susumu Uchiyama (Osaka Univ.)** Mass spectrometry of protein-ligand interactions
13:55-14:20	**Takafumi Ueno (Tokyo Inst. of Tech.)** Protein Crystals for Designing Biohybrid Solid Materials
14:20-14:45	**Tadashi Satoh (Nagoya City Univ.)** Structural insights into the working mechanisms of multi-domain enzymes involved in ER protein quality control
14:45-15:05	**Jaeyoung Byeon (Soongsil Univ.)** Protein contact prediction based on information theory
15:05-15:35	coffee break
15:35-16:00	**Julian Lee (Soongsil Univ.)** Prediction of protein rigid domains and hinge residues based on graph theory and elastic network model
16:00-16:25	**Takahiro Kosugi (IMS)** De novo design of protein function
16:25-16:50	**Changbong Hyeon (KIAS)** Mapping allosteric signaling of G protein-coupled receptors