Sihyun Ham Protein Symposium 2022

Program (Korean Standard Time, KST)

January 14 (Fri) - 15 (Sat), 2022
Offline venue: Sookmyung Women's University
Sihyun Ham Lecture Hall (Fri) and Room 104, Building Prime (Sat)
Online link: https://snu-ac-kr.zoom.us/j/3907204837

January 14 (Friday)

8:30 - 9:00	Registration	
Opening Remarks (Seokmin Shin)		
8:50 - 9:00	Jinho Lee, Dean of College of Science, Sookmyung Women's University	
9:00 - 9:10	Seokmin Shin, on behalf of the organizing committee	
9:10 - 9:20	Chang-Dae Ham, on behalf of Sihyun's family	
Chair (Yuji Sugita)		
9:20 - 9:45	Peter Rossky	Rice University
	Understanding the Message from a Sensing Fluorescent Protein	
9:45 - 10:10	Songi Han	UC Santa Barbara
	Water and proteins, an inseparable relationship	
10:10 - 10:35	Matthias Heyden	Arizona State University
	Solvation Free Energy Arithmetic and Solvent-Mediated Interactions	
10:35 - 10:50	Break	
Chair (Song-Ho Chong)		
10:50 - 11:15	Michael Feig	Michigan State University
	Protein diffusion in concentrated environments	
11:15 - 11:40	Yuji Sugita	RIKEN
	Reduced efficacy of a Src kinase inhibitor in crowded protein solution	
11:40 - 12:05	Yuko Okamoto	Nagoya University
	The early stage of secondary nucleation of Abeta fibril	
12:05 - 12:30	Wookyoung Yu	DGIST
	Exploring ensemble structures of Alzheimer's amyloid β (1-42) monomer using linear regression for the MD simulation and NMR chemical shift	
12:30 - 13:30	Lunch	
Chair (Yangmee Kim)		
13:30 - 13:55	Fumio Hirata	IMS (retired)
	Realization of the structural fluctuation of biomolecules in solution: Generalized Langevin Mode Analysis	
13:55 - 14:20	Song-Ho Chong	RIKEN

	Time-dependent communication between multiple amino acids during protein folding	
14:20 - 14:45	Changbong Hyeon	KIAS
	Generalized iterative annealing mechanism for the action of molecular chaperones	
14:45 - 15:10	Chaok Seok	SNU
	Computational protein research: hers and mine	
15:10 - 15:25	Break	
Chair (Wonpil Im)		
15:25 - 15:50	Juyong Lee	Kangwon U
	Finding reaction pathways using the Gaussian process	
15:50 - 16:15	Hyun-Suk Lim	POSTECH
	Development of alpha-helix mimetics based on the triazine-piperazine scaffold as protein-protein interaction modulators	
16:15 - 16:40	Yangmee Kim	Konkuk U
	Elucidation of mechanism underlying fatty acid and aryl polyene biosynthesis of *Acinetobacter baumannii*	

January 15 (Saturday)

Chair (Chaok Seok)		
9:00 - 9:25	Xuhui Huang	University of Wisconsin-Madison
	Memory Kernels of Protein Conformational Dynamics	
9:25 - 9:50	Bernie Brooks	NIH
	Using machine learning for predicting protonation states and understanding protein landscape	
9:50 - 10:15	Charles Brooks	University of Michigan
	Novel, high-throughput free-energy methods for drug design	
10:15 - 10:40	Sun Choi	Ewha WU
	Computational mechanistic studies of membrane proteins and drug discovery	
10:40 - 10:55	Break	
Chair (Hyun-Suk Lim)		
10:55 - 11:20	Ayyalusamy Ramamoorthy	University of Michigan
	Nanodiscs for Probing Protein-Protein Structural Interactions at the Membrane Interface	
11:20 - 11:45	John Straub	Boston University
	Curious orientational behavior of a modified cholesterol in lipid bilayers	
11:45 - 12:10	Guipeun Kang	UT Southwestern
	Probing structural determinants for partial agonism and allosteric modulation at human α4β2 nicotinic receptor	
12:10 - 12:35	Weontae Lee	Yonsei U

	Structure and Dynamics of Membrane Proteins by Cryo-EM and Serial Femtosecond X-ray Crystallography (SFX)	
12:35 - 13:30	Lunch	
Chair (Juyong Lee)		
13:30 - 13:55	Myung Keun Cho	SNU
	Site-Specific Backbone and Side-Chain Contributions to Thermodynamic Stabilizing Forces of the WW Domain	
13:55 - 14:20	Wonpil Im	Lehigh U
	What can CHARMM-GUI do for you?	
14:20 - 14:45	Myungjin Lee	NIH
	Extended antibody-framework-to-antigen distance observed exclusively with broad HIV-1-neutralizing antibodies recognizing glycan-dense surfaces	
14:45 - 15:00	Closing Remark (Fumio Hirata)	