

**TRACK 1: COMPUTATIONAL BIOPHYSICS AND MEDICINE****Date 1: July 25<sup>th</sup>, 2019****Venue: Ballroom #2**

<b>Time</b>	<b>Agenda</b>	<b>Code</b>
14:00 14:30	<b>Cluster formation and phase separation in crowded biomolecular solutions</b> <i>Michael Feig</i>	BC-01
14:30 15:00	<b>Protein folding in the presence of interacting macromolecular crowders</b> <i>Anders Irbäck</i>	BC-02
15:30 16:00	<b>Critical phenomena in the temperature -pressure-crowding phase diagram of a protein</b> <i>Margaret S. Cheung</i>	BC-03
16:00 16:15	Coffee break	
16:15 16:45	<b>Computational modeling of protein RNA interactions</b> <i>Ralf Bundschuh</i>	BC-04
16:45 17:00	<b>Application of machine learning methods in computational biophysics: from learning to reinforcement learning</b> <i>Duy Phuoc Tran</i>	BC-05
17:00 17:30	<b>A Transiently Populated Intermediate in Prion Folding Leads to Early Precursors in Prion Dimerization</b> <i>Govardhan Reddy</i>	BC-06

**Date 2: July 26<sup>th</sup>, 2019****Venue: Ballroom #2**

<b>Time</b>	<b>Agenda</b>	<b>Code</b>
9:00 9:30	<b>Computer simulations of amyloid proteins in various environments and folded proteins in a cell-like environment</b> <i>Philippe Derreumaux</i>	BC-07
9:30 10:00	<b>Challenges, advances and perspectives of protein aggregation simulations</b> <i>Birgit Strodel</i>	BC-08
10:00 10:15	Coffee break	
10:15 10:45	<b>Simulating amyloid formation, conversion and propagation</b> <i>Ulrich H.E. Hansmann</i>	BC-09
10:45 11:00	<b>Aggregation rate of amyloid beta peptide is controlled by beta-content in monomeric state</b> <i>Tran Thi Minh Thu</i>	BC-10
11:00 12:00	<b>Poster session</b> <i>Venue: Ballroom #1</i>	
12:00 13:30	Lunch	
13:30 14:00	<b>Modeling structure, stability and dynamics of proteins and protein aggregates</b> <i>Andrzej Kloczkowski</i>	BC-11
14:00 14:30	<b>Multi-protein complexes: membrane-mediated binding cooperativity, ESCRT-induced membrane budding, and regulation mechanisms of lipid kinases</b> <i>Bartosz Różycki</i>	BC-12
14:30 15:00	<b>Predicting protein transmembrane regions by using LSTM model</b> <i>Pham The Bao</i>	BC-13

15:00 15:15	Coffee break	
15:15 15:45	<b>Binding free energy calculation methods based on the implicit ligand theory</b> <i>Nguyen Trung Hai</i>	BC-14
15:45 16:00	<b>Protein translocation in the ribosome: Steered molecular dynamics approach</b> <i>Mai Suan Li</i>	BC-15
16:00 16:30	<b>Truss-like arrangement of cadherins is responsible for desmosome strength</b> <i>Mateusz Sikora</i>	BC-16
16:30 17:00	<b>Introduction to convergence research at Key Laboratory for Multiscale Simulation of Complex Systems, Vietnam National University</b> <i>Toan T Nguyen</i>	BC-17
17:30 18:00	<b>Poster Award and Closing Ceremony</b> <i>Venue: Grand Ballroom</i>	