PROGRAMME

Wednesday, 14 June 2023

15:00 – 20:00 REGISTRATION

18:00 – 19:00 WELCOME RECEPTION — GARDEN PARTY

OPENING — chairperson: Mateusz Chwastyk

19:00 – 19:10 Mateusz Chwastyk
Institute of Physics, Polish Academy of Sciences, Warsaw, Poland
Welcome address

19:10 – 19:50 George Rose
Department of Biophysics, Johns Hopkins University, USA
Have we been thinking about protein folding "upside down"?

20:00 – 22:00 DINNER AT BONFIRE

Thursday, 15 June 2023

THE INNER LIFE OF THE CELL — chairperson: Anna Niedźwiecka

9:00 – 9:30 Gary Pielak
University of North Carolina, USA
Protein stability in living cells & under crowded conditions in vitro

9:30 – 10:00 Sebastian Glatt
Malopolska Centre of Biotechnology, Jagiellonian University, Poland
tRNAslational Control of Eukaryotic Gene Expression

10:00 – 10:30 Yuji Sugita
Laboratory for Biomolecular Function Simulation, RIKEN
Center for Biosystems Dynamics Research, Japan
How cellular environments are regulated by non-specific molecular interaction

10:30 – 11:00 COFFEE BREAK

MOLECULAR ENGINEERING — chairperson: Mateusz Chwastyk

11:00 – 11:30 Damien Thompson
Department of Physics, University of Limerick, Ireland
Molecular engineering of bio-assemblies: prospects and design rules for sustainable materials for therapeutics and sensing

11:30 – 12:00 Joanna Trylska
Centre of New Technologies, University of Warsaw, Poland
Stapled peptides and peptide nucleic acids as antibacterials

12:00 – 12:30	David J. Wales *University of Cambridge, United Kingdom* **Energy landscapes: from molecules and nanodevices to machine learning**
12:30 – 13:00	Piotr Garstecki *Institute of Physical Chemistry, Polish Academy of Sciences, Poland* **From idea to a product for medical diagnostics**
13:00 – 14:30	LUNCH

COVID-19 — chairperson: Damien Thompson

14:30 – 15:00	Peter Hinterdorfer *Institute of Biophysics, Johannes Kepler University Linz, Austria* **Avidity amplification of SARS-Cov-2 spike variants viewed on the single molecule level**
15:00 – 15:30	Mateusz Sikora *Max Planck Institute of Biophysics, Germany* **Protein flexibility and glycan dynamics of the SARS-CoV-2 spike**
15:30 – 16:00	Mai Suan Li *Institute of Physics, Polish Academy of Sciences, Poland* **In silico study of Covid-19**
16:00 – 16:15	Adolfo Poma *Institute of Fundamental Technological Research, Polish Academy of Sciences, Poland* **Nanomechanical investigation of the binding interface stability of SARS-CoV-2 variants with ACE2 receptor**
16:15 – 16:30	Yoo Jin Oh *Institute of Biophysics, Johannes Kepler University Linz, Austria* **Investigation of lectin binding to SARS-CoV-2 spike glycans using single molecule force spectroscopy**
16:30 – 17:00	COFFEE BREAK

IN MEMORY OF PROF. MAREK CIEPLAK — chairperson: Mariano Carrión-Vázquez

17:00 – 17:15	Marta Cieplak, Maja Cieplak-Rotowska, Mateusz Chwastyk
17:15 – 17:30	Jayanth Banavar (online)
17:30 – 17:45	George Rose
17:45 – 18:00	Władek Minor
18:00 – 18:15	Anna Niedźwiecka
18:15 – 20:00	DINNER
20:00 – 22:00	POSTER SESSION I (odd numbers presenting authors)

Friday, 16 June 2023

STRUCTURAL BIOLOGY — chaiperson: Andrzej Kłoczkowski

9:00 – 9:30 Andrzej Joachimiak
Department of Biochemistry and Molecular Biology, University of Chicago, USA
Dynamic X-ray Crystallography: Time-Resolved β-lactam Cleavage by L1 Metallo-β-Lactamase

9:30 – 9:45 Przemyslaw Nogly
Faculty of Biochemistry, Biophysics and Biotechnology, Jagiellonian University, Poland
Time-resolved X-ray crystallography on membrane proteins: watching ions moving in time and space

9:45 – 10:15 Mariusz Jaskólski
Faculty of Chemistry, A. Mickiewicz University and Institute of Bioorganic Chemistry, Polish Academy of Sciences, Poland
Stereochemical restraints for nucleic acids revisited

10:15 – 10:50 Władek Minor
Department of Molecular Physiology and Biological Physics, University of Virginia, USA
Structural biology response to biomedical threats

10:50 – 11:10 COFFEE BREAK

THE WORLD OF PROTEINS WITH STRUCTURE — chairperson: Mateusz Sikora

11:10 – 11:40 Edward O'Brien
Department of Chemistry, Pennsylvania State University, USA
A newly discovered class of protein misfolding explains decades-old biochemical and molecular biology observations

11:40 – 11:55 Elisa Rioual
IBS, Université Grenoble Alpes and iLM, Université Claude Bernard Lyon 1, France
Visualizing a Functional Rare State of Human HSP90 ATP Binding Domain

11:55 – 12:10 Peter Røgen
Department of Applied Mathematics and Computer Science, Technical University of Denmark, Denmark
Sequence-Similar, Structure- and Topologically-Dissimilar Protein Domain Pairs

12:10 – 12:25 Antonio Trovato
Department of Physics and Astronomy, University of Padova and INFN, Italy
Entangled motifs in protein structures

12:25 – 12:40 Tomasz Włodarski
University College London, UK
A computational microscope to study co-translational protein folding

12:40 – 14:30 LUNCH

14:30 – 18:30 FREE TIME (EXCURSION)

18:30 – 20:00 DINNER

20:00 – 22:00 POSTER SESSION II (even numbers presenting authors)

Saturday, 17 June 2023

MANAGING BIOLOGICAL PROCESSES — chairperson: Joanna Trylska

9:00 – 9:30 Michael Feig
Department of Biochemistry and Molecular Biology, Michigan State University, USA
Enzyme Function in Crowded Environments

9:30 – 10:00 Dariusz Plewczynski
Laboratory of Bioinformatics and Computational Genomics, Warsaw University of Technology, Poland
LEM: loop extrusion model of the Human Genome Topology

10:00 – 10:15 Maja Cieplak-Rotowska
IMol Polish Academy of Sciences, Poland
Cwc25's role in choosing the right adenosine as the branch site during the first step of splicing

10:15 – 10:40 COFFEE BREAK

BETWEEN ORDER AND DISORDER — chairperson: Adam Liwo

10:40 – 11:10 Yaakov (Koby) Levy
Department of Chemical and Structural Biology, Weizmann Institute of Science, Israel
Optimized protein function via disordered regions

11:10 – 11:40 Mariano Carrión-Vázquez
Instituto Cajal, IC-CSIC, Spain
Exploring early amyloidogenesis in search for novel pharmacological targets

11:40 – 12:10 Hisashi Okumura
Institute for Molecular Science, The Graduate University for Advanced Studies, Japan
Replica-permutation and nonequilibrium molecular dynamics simulations for protein aggregates

12:10 – 12:40 Artem Badasyan
University of Nova Gorica, Slovenia
Potts spins, protein conformations, and implicit water model

12:40 – 14:30 LUNCH

14:30 – 15:00 Nevena Ilieva
Institute of Information and Communication Technologies & Institute of Mathematics and Informatics at the Bulgarian Academy of Sciences, Bulgaria
A new concept of the mechanism of action of antimicrobial peptides

15:00 – 15:15 Peter Košovan
Department of Physical and Macromolecular Chemistry, Charles University, Czechia
Exploiting the liquid-liquid phase separation in polyelectrolyte complexes for sequestration of small ions, weak acids and bases

15:15 – 15:30 Michał Białobrzewski
Institute of Physics, Polish Academy of Sciences, Poland
Liquid-liquid phase separation of GW182 silencing domain

15:30 – 16:15 COFFEE BREAK

SPOTLIGHT ON THE WORLD OF PROTEINS chairperson: Michael Feig

16:15 – 16:45 Christian Kaiser
Department of Biology, Johns Hopkins University, USA
Co-translational stabilization drives folding of a kinetically stable protein

16:45 – 17:20 Jayanth Banavar (online)
University of Oregon, USA
A framework for understanding proteins

17:20 – 17:50 COFFEE BREAK

CLOSING LECTURE chairperson: George Rose

17:50 – 18:30 Gerhard Hummer
Max Planck Institute of Biophysics, Germany
Molecular simulations in the era of AI and exascale computing

19:00 CONFERENCE BANQUET

Sunday, 18 June 2023

Breakfast