Monday, 13.09.2021		
9:00 - 9:30	REGISTRATION	
9:30 - 9:50	OPENING	
9:50 - 10:50	David Leigh	
	Making the Tiniest Machines	
10:50 - 11:10	COFFEE BREAK	
11:10 - 11:45	Rossen Apostolov	
	Driving European HPC for Biomolecular Research: Advanced Software Applications and Support Structures from BioExcel Centre of Excellence	
11:45 - 12:20	<u>Luca Tubiana</u> , Franco Ferrari, Enzo Orlandini	
	<i>Ring-o-rings: Joining the Ends of Poly[n]-Catenanes to Capture Supramolecular</i> <i>Torsion</i>	
12:20 - 14:00	LUNCH	
14:00 - 14:45	Noam Kaplan	
	Deciphering 3D Genome Organization with Probabilistic Models	
14:45 - 15:20	Svetozar Margenov	
	Iterative Solution of Large-Scale Biomedical Problems and Rational Approximation of Fractional Laplacian	
15:20 - 15:50	Andrey Brukhno	
	Interscale Simulation: a Novel Combined Methodology to Bridge Between Scales and Methods	
15:50 - 16:10	COFFEE BREAK	
16:10 - 16:40	Ivan Dimitrov, Mariyana Atanasova and Irini Doytchinova	
	AllerScreener: a Tool for Allergenicity and Cross-Reactivity Prediction of Proteins	
16:40 - 17:10	Meglena Lazarova, Svetoslav Markov, Andrey Vassilev	
	<i>The Reaction Network Approach in Mathematics of Life. Part I – Translation to ODE</i> <i>System</i>	
17:10 - 17:40	Meglena Lazarova, <u>Svetoslav Markov</u> , <u>Andrey Vassilev</u>	
	<i>The Reaction Network Approach in Mathematics of Life. Part II – Examples and Numerical Simulations</i>	
17:40 - 18:10	Nadezhda Bunzarova and Nina Pesheva	
	Numerical simulations and analytical studies of TASEP – a model of biological transport	
18:10 - 18:40	Diana Toneva, Silvia Nikolova, <u>Stanislav Harizanov</u> , Ivaylo Zhelev	
	Applied Mathematics for Forensic Medicine	
19:30	WELCOME	

Tuesday, 14.09.2021		
9:00 - 9:45	Antti J Niemi	
	Time Crystals and Rotary Molecular Motors	
9:45 - 10:30	Franco Ferrari	
	Modeling Polymer Systems in the Presence of Non-Trivial Topological Relations: a Combined Analytical-Numerical Approach	
10:30 - 10:50	COFFEE BREAK	
10:50 - 11:25	Ivan Coluzza	
	Heteropolymer Design: Learning Protein Evolution by Reverse	
	Engineering	
11:25 - 12:00	Raffaello Potestio	
	Optimal Reduced Representations and Multiple Resolution Models of Biomolecules	
12:00 - 14:00	LUNCH	
14:00 - 14:45	Adam Liwo	
	Theory and Practice of Coarse Graining	
14:45 - 15:15	<u>Vlad Sokhan</u> , Michael Seaton, Ilian Todorov	
	Phase Behaviour of Coarse-Grained Fluids	
15:15 - 15:45	Julyan Cartwright	
	Topological Aspects to How Life Uses Liquid Crystals	
15:45 - 16:15	Bogdan Rangelov and Andrey Milchev	
	Translocation Dynamics of Vesicles Through Narrow Pores	
16:15 - 16:35	COFFEE BREAK	
16:35 - 17:05	Mateusz Chwastyk	
	Nascent Folding of Proteins Across the Three Domains of Life	
17:05 - 17:35	Kristina Kapanova	
	Quantum Analog Computational Device in Life Sciences	
17:35 - 18:35	ROUND TABLE DISCUSSION	

Wednesday, 15.09.2021		
9:00 - 9:45	Pietro Faccioli	
	Pharmacological Protein Inactivation by Targeting Protein Folding Intermediates	
9:45 - 10:30	Sarah Harris	
	Understanding the Structure and Dynamics of the SARS-CoV2	
	Helicase (nsp13) from Molecular Dynamics Simulations	
10:30 - 10:50	COFFEE BREAK	
10:50 - 11:20	<u>Nevena Ilieva</u> , Peicho Petkov, Miroslav Rangelov, Elena Lilkova,	
	Nadezhda Todorova, and Leandar Litov	
	In silico Study of the Molecular Mechanism of LMWH Antiinflammatory Action Within the COVID-19 Context	
11:20 - 11:50	Vasilina Zayats, Agata P. Perlinska, Aleksandra I. Jarmolinska, Borys Jastrz ebski, Stanis law Dunin-Horkawicz, <u>Joanna I. Sulkowska</u>	
	Slipknotted and Unknotted Proteins Might Share a Common Ancestor	
11:50 - 12:20	SHORT TALKS – PART I	
12:20 - 14:00	LUNCH	
14:00 - 14:45	Marek Cieplak	
	D ynamics of Intrinsically Disordered Proteins and their Droplet-like Aggregates	
14:45 - 15:15	Piotr Su lkowski	
	Biomolecules and Random Matrices	
15:15 - 15:45	Petia Koprinkova-Hristova	
	Spike Timing Neural Network Model of Conscious Visual Perception	
15:45 - 16:15	SHORT TALKS – PART II	
16:30 - 19:30	CULTURAL PROGRAMME	
19:30	SOCIAL DINNER	

SHORT TALKS – PART I

- <u>Pawel Korzeb</u>, Bartosz Gren, Joanna Sulkowska Statistical properties of handcuffs in ideal polymers
- <u>Mateusz Fortunka</u>, Ya-Ming Hou, Adam Stasiulewicz, Agata Perlinska, Joanna Sulkowska Understanding the role of YARS2-tRNA complex in MLASA Disease
- Yadi Cheng, <u>Xubiao Peng</u>, Peicho Petkov, and Nevena Ilieva Grafting a <u>Parkinson Inhibitor Peptide on a Cyclotide: a Geometry and Dynamics Study</u>
- <u>Dessislava</u> Jereva, Maria Angelova, Ivanka Tsakovska, Petko Alov, Ilza Pajeva, Maria A. Miteva, Tania Pencheva InterCriteria Analysis Approach to Assess the AMMOS2 Software Platform Performance

SHORT TALKS – PART II

- <u>Wanda Niemyska</u>, Bartosz A. Gren, Pawel Dabrowski-Tumanski, Joanna I. Sulkowska Lasso Proteins – Is this Topology Functional?
- <u>Bartosz A. Gren</u>, Pawel Dabrowski-Tumanski, Joanna I. Sulkowska Statistical properties of lasso polymers and implications for lasso proteins
- <u>Adam Stasiulewicz</u>, Mai Lan Nguyen, Joanna Sulkowska Fighting Antimicrobial Resistance – In Silico Screening for Novel TrmD Inhibitors

SHORT TALKS – PART III

- <u>Elena Lilkova</u>, Peicho Petkov, Rositsa Marinova, Leandar Litov, Nevena Ilieva Enhanced Sampling Molecular Modeling of Peptide-Membrane Interactions: A Case Study
- **Pawel Rubach** Identification of Protein Topology Using Topoly and the KnotProt Database API

Thursday, 16.09.2021		
9:00 - 9:45	Roumen Anguelov	
	Mathematical Models and Analysis of the Impact of CTCE9908 and Kynurenine Metabolites on the Proliferation and Survival of Tumour Cells	
9:45 - 10:15	Rachid Ouifki	
	Mathematical Modeling of the Estrogen Paradox in the Treatment of Breast Cancer	
10:15 - 10:45	Anastas Pashov	
	Formal Representation of the Repertoire of IgM Antibody Specificities	
10:45 - 11:10	Anastas Pashov, <u>Peter Petrov</u>	
	Topological Approach for a Global Description of the Antibody	
	Repertoire	
11:10 - 11:30	SHORT TALKS – PART III	
11:30 - 11:40	CLOSING	
12:00 - 14:00	LUNCH	
14:00	DEPARTURE	