Sunday 9.09	Monday 10.09	Tuesday 11.09	Wednesday 12.09
19:00 – 21:00 Welcome reception	8:00 – 8:50 – Breakfast	8:00 – 8:50 – Breakfast	8:00 – 8:50 – Breakfast
18:30 – 21:00 Registration desk	CHAIR: Andrzej Kłoczkowski	CHAIR: Weontae Lee	CHAIR: Jooyoung Lee
	9:00 – 9:35 – IL1: Changbong Hyeon	9:00 – 9:35 – IL9: Sylvie Ricard-Blum	9:00 – 9:35 – L15: Weontae Lee
conference bus	Energetic costs, precision, and transport	Intrinsic disorder in the extracellular matrix:	Structure and Dynamics of Membrane
16:00 - Faculty of Chemistry, U Gdansk	efficiency of molecular motors.	does binding promote folding?	Proteins by NMR, X-RAY Crystallography and Femtosecond Laser.
19:00 - Port110 Ilawa	9:35 – 10:10 – IL2: Marek Cieplak	9:35 – 10:10 – IL10: Sergey Samsonov	9:35 – 10:10 – L16: Joanna Sułkowska
Thursday 13.09	Empirical elements in coarse-grained models	Computational Insights into the	Proteins' knotty problems.
8:00 – 9:00 – Breakfest	of proteins: protein films at fluid-fluid	Glycosaminoglycan-mediated Molecular	The state of the s
The end of the conference.	interfaces & dual binding in cellulosomes	mechanisms Underlying Cell Signaling.	
	10:10 - 10:45 - IL3: Andrzej Koliński	10:10 – 10:45 – IL11: Fabien Lecaille	
conference bus	Multipools and delines of another and another	Court and an area area and area of the control of t	
10:00 - Port110 Ilawa 13:00 - Faculty of Chemistry, U Gdansk	Multiscale modeling of proteins and protein	Sweet spots on cysteine cathepsin S:	10:10 – 10:30 - coffee break
	complexes	how glycosaminoglycans and derivatives modulate its proteolytic activity.	
	10:45 – 11:15 – coffee break	10:45 – 11:15 – coffee break	10:30 – 11:05 – L17: Martin Zacharias
	CHAIR: Changbong Hyeon	CHAIR: Joanna Sułkowska	Efficient refinement of predicted protein-
	CHAIR: Changbong Hyeon	CHAIR: Joanna Suikowska	protein and peptide-protein complexes.
	11:15 – 11:50 – IL4: Juyong Lee	11:15 – 11:50 – L12: Igor Konieczny	11:05 – 11:40 – L18: Bernard Brooks
	Finding multiple reaction pathways via global	Bacterial DNA replication initiation	Recent Advances in Protonation State
	optimization of action.	proteins – structure, stability and replication	Modeling and Constant pH simulations.
		control.	S a s a s a s a s a s a s a s a s a s a
	11:50 – 12:25 – IL5: Mai Suan Li	11:50 – 12:25 – L13: Victor Munoz	12:00 - 13:00 - Lunch
	Pulling for understanding biomolecular	Eukaryotic transcription factors can track and	CHAIR: Adam Liwo
	processes.	control their target genes using DNA antennas	
	12:25 – 13:00 – IL6: Hirokazu Yagi	12:25 - 13:00 - L14: Ji-Joon Song	13:00 – 13:35 – L19: Xiao-Dong Su
	Assembly and disassembly mechanisms of	Toward Understanding Architectures and	Deltabodies - Application of <i>E. coli</i> inclusion
	proteasome revealed by multilateral	Molecular Sociology of Life.	body expression and refolded dimeric Fv
	biophysical approaches.		based antibodies.
	13:00 – 14:00 – Lunch	13:00 – 14:00 – Lunch	13:35 – 14:10 – L20: Maciej Kozak
	15:00 – 18:00 – excursion	15:00 – 18:00 – excursion	From disordered chain to fibrils – SAXS and
	(kayak cruise)	(City Sightseeing)	spectroscopic studies of protein fibrillation.
	19:00 – 20:00 – Dinner		14:10 – 14:45 – L21: Jejoong Yoo
	CHAIR: Cezary Czaplewski	19:00 – 20:00 – Dinner	Champaign-Urbana nbFIX (CUFIX): improved
			AMBER and CHARMM parameters for accurate calculations of charge–charge and hydrophobic
			interactions.
	20:00 – 20:35 – IL7: Chaok Seok	20:00 – 21:00 – POSTER SESSION	14:45 – 15:20 – L22: Jooyoung Lee
	Prediction of protein and protein complex		Global Optimization by Conformational Space
	structure by GALAXY.		Annealing and its Applications to Protein Structure
			Prediction/Determination and Machine Learning.
	20:35 – 21:10 – IL8: Andrzej Kloczkowski		15:40 – 21:00 – Conference Banquet
	Modeling Structure, Stability and Dynamics		(take warm clothes)
	of Proteins and Protein Aggregates.		