

	26 August, Wednesday	27 August, Thursday	28 August, Friday	29 August, Saturday
Morning session I.		10:00-10:50 <u>Zsuzsanna Dosztányi:</u> <i>Prediction of disordered proteins and disordered binding regions based on estimated pairwise energies</i>	10:00-10:50 <u>László Patthy:</u> <i>Protein structure prediction as a tool for the identification of mispredicted, abnormal and incomplete sequences in public databases.</i>	Informal discussions
COFFEE		10:50-11:20 COFFEE	10:50-11:20 COFFEE	10:40-11:20 COFFEE
Morning session II.	Registration Informal discussions	11:20-12:10 <u>Nir Ben-Tal:</u> <i>Modeling and validation of transmembrane protein structures</i> 12:10-13:00 <u>Rita Casadio:</u> <i>Predicting protein structure and function from sequence with BAR, the Bologna Annotation Resource</i>	11:20-12:10 <u>Arne Elofsson:</u> <i>Improved topology prediction of membrane proteins using improved computational methods or first principles experimental data</i> 12:10-13:00 <u>Charlotte Deane:</u> <i>TBA</i>	11:20-12:10 <u>Jennifer Gady:</u> <i>Perspectives on subcellular localization prediction: lessons from PSORTb and friends</i> 12:10 – 13:00 <u>István Simon:</u> <i>Shedding light on transmembrane topology prediction</i>
LUNCH	13:00-14:30 LUNCH	13:00-14:30 LUNCH	13:00-14:30 LUNCH	13:00-14:30 LUNCH
Afternoon session I.	14:30-15:20 <u>David Jones:</u> <i>TBA</i>	14:30-14:55 <u>Ilona Kifer:</u> <i>Protein Structure Prediction method based on the hierarchical folding model</i> 14:55-15:20 <u>Sean Ward:</u> <i>GPGPU Acceleration of Energy Models</i>	14:30-14:55 <u>Aron Hennerdal:</u> <i>Half of all large TM proteins are duplicated</i>	Informal discussions
COFFEE	15:20-16:00 COFFEE	15:20-16:00 COFFEE	15:30-16:00 COFFEE	
Afternoon session II.	16:00-16:50 <u>András Fiser:</u> <i>Comparative Protein Structure Modeling</i>	Informal discussions	Informal discussions	
	17:30- <i>Wine & cheese party</i>		18:00- <i>Boat tour</i>	