ICTP - The Abdus Salam International Centre for Theoretical Physics, Trieste, Italy

# smr1316/Programme

Speakers and dates in alphabetic order.

Amzel 13 Evaluation of Entropy Changes in Binding and Folding Bastolla 21 Connectivity of neutral networks and the substitution process in protein evolution (15 min talk) Broglia 12 Reading the three--dimensional structure of lattice model designed proteins from their amino acid sequence Bruscolini 21 Nonpolar compounds and polymers hydration: a simple hydration model, a lattice mean field technique, and experimental result (15 min talk) Butt 15 Protein Composition of Spring Wheats Grown in Pakistan (15 min talk) Carloni 20 Ab Initio Approach to Drug-Target Interactions Cassia-Moura 13 Memory Effect on Biomembrane-Protein (15 min talk) Cecconi 14 Molecular Dynamics Studies on HIV-1 Protease: Drug Resistance and Folding Pathways Chan 11, 12 1. Polymer Principles of Protein Calorimetric Two-State Cooperativity 2. Towards a Consistent Modelling of Protein Thermodynamics and Kinetic Cooperativity Chang 20 A Route to a Solution of the Protein Threading Problem by Learning Chen 21 Stochastic Dynamics Simulation of Proteins with Full Poisson-Boltzmann Electrostatics (15 min talk) Clementi 11 Topology and energetics in protein folding: beyond the Go-like approach Dadlez 12 Folding initiation sites as detected by disulfide formation kinetics I De Los Rios 12 Protein Design with Explicit Solvent (15 min talk) DesJarlais 12, 15 1. Protein Design: Predicting Sequence from Structure 2. Determinants of Conformational Change

Dill 14, 18 1. A Simple Model of Water, the Hydrophobic Effect 2. Ion Solvation Dokholyan 14, 15 1.Understanding hierarchical protein evolution from the first principles 2.Direct observation of folding transition state ensemble of C-Src SH3 domain in molecular dynamics simulations Doniach 18, 21 1. Protein folding and misfolding 2. Protein folding and misfolding Domany 14 Part A. Automated Protein Structure Classification Part B. Do Contact Vectors Determine a Protein's Structure? Eaton 15, 19 1. Fast processes in protein folding 2. Simple models for protein folding Simple models for protein folding Ejtehadi 14 The ground states in HP lattice models Garcia 14, 21 1. Atomic Simulations of Helix-Coil Transition in Peptides 2. Water Penetration in Proteins Godzik 19 \*\*\*\*\*\* Goldstein 18, 21, 22 1. Evolutionary Perspectives on Protein Folding, Stability, and Function 2. Evolutionary Perspectives on Protein Folding, Stability, and Function 3. Evolutionary Perspectives on Protein Folding, Stability, and Function Hackl 21 \*\*\*\*\*\* Trback 18 Folding Thermodynamics of Small Helical Proteins: A Model Study Jernigan 15, 18 1. Extracting Functional Motions from Protein Structures 2. Strong Packing Regularities in Proteins L Kuhn 18, 20 1. Protein Unfolding Pathways and Folding Nucleation Sites Predicted by Graph Theory 2. Modeling Protein and Small Molecule Flexibility in Ligand Screening and Docking Lesk 19, 22 1. Prediction of Protein Function from Structure. 2. Conformational Changes in Proteins. Maddocks 13 Modelling of the Folding Twisting and Bending of DNA

Matthews: 11, 13, 14 1. (Introductory Talk): Challenges and Opportunities in Experimental Protein Folding 2. Rough Energy Landscapes: Early Commitments Can Have Long-lasting Consequences 3. Conserved Folding Mechanisms in Homologous Proteins: Are Mechanisms better Conserved than Sequences? Mai 13 Side Chain Effect on Protein Folding Micheletti 14 Protein-like structures emerging from general variational principles Mirny 19 What Evolution Can Tell us about Protein-DNA Interactions. Molinari 15 Folding and interaction studies of beta-lactoglobulins Mozzarelli 15 Unfolding of PLP-Dependent Enzymes Oliveberg 19, 20 Plaxco 20 The convergence of theory and experiment in the folding of the simplest proteins Privalov 12, 15 1. Climbing the Hierarchy of Protein Structure 2. Climbing the Hierarchy of Protein Structure Settanni 14 The Role of Topology in the Stabilization of Intracellular Ig Domains Shifman 11 Redisign of Calmodulin Receptor Directed Towards Improving its Binding Specificity (15 min talk) Simon 13, 19 1. Topology of Transmembrane Proteins 2. Stabilization Centers and Protein Stability Srivastava 21 Orthogonalization of vectors Thorpe 18, 20 1. Ligand and Protein Flexibility using Constraint Theory 2. Protein Unfolding: Rigidity Lost Tiana 12 Statistical analysis of contact formation in model proteins Tramontano 20 Advancements and pitfalls in protein comparative modelling Trinh 14 Sequencing of folding events in model proteins (15 min talk) Vaiana 12

Protein Conformation vs Aggregation: Interaction Between Processes in Two Cases of Different Complexity

Vendruscolo 19 Structural Determination of Partially Folded States of Proteins from Residue-Specific Experimental Data

Vishveshwara 13 Insights on Structure and Topology of Proteins from Graph Spectral Method

White 11, 13 1. Energetics of Folding Proteins into Membranes 2. Global Statistics of Protein Sequences

\_\_\_\_\_ \_\_\_\_\_ PROGRAM OF THE WORKSHOP " PROTEIN FOLDING, STRUCTURE AND DESIGN" 8:30 REGISTRATION 9:45 C R Matthews Introductory Talk: Challenges and Opportunities in Experimental Protein Folding I 10:30 COFFEE BREAK 11:00 H S Chan Polymer Principles of Protein Calorimetric Two-State Cooperativity 11:45 S White Global Statistics of Protein Sequences I 12:30 LUNCH 14:00 C Clementi Topology and energetics in protein folding: beyond the Go-like approach 14:45 M R Ejtehadi The ground states in HP lattice models 15:30 COFFEE BREAK 16:00 J M Shifman Redisign of Calmodulin Receptor Directed Towards Improving its Binding Specificity

16:15 End 9:00 P Privalov Climbing the Hierarchy of Protein Structure I 9:45 J DesJarlais Protein Design: Predicting Sequence from Structure I 10:30 COFFEE BREAK 11:00 M Dadlez Protein Folding Initiation Structures as Detected by the Disulphide Formation Kinetics Studies. 11:45 H S Chan Towards a Consistent Modelling of Protein Thermodynamics and Kinetic Cooperativity 12:30 LUNCH 14:00 G Tiana Statistical analysis of contact formation in model proteins 14:45 R Broglia Reading the three--dimensional structure of lattice model designed proteins from their amino acid sequence 15:30 COFFEE BREAK 16:00 S Vaiana Protein Conformation vs Aggregation: Interaction Between Processes in Two Cases of Different Complexity 16:15 P De Los Rios Protein Design with Explicit Solvent 16:30 End 9:00 C R Matthews Rough Energy Landscapes: Early Commitments Can Have Long-lasting Consequences II 9:45 M Amzel Evaluation of Entropy Changes in Binding and Folding 10:30 COFFEE BREAK 11:00 S Vishveshwara Insights on Structure and Topology of Proteins from Graph Spectral Method. 11:45 J Maddocks Modelling of the Folding Twisting and Bending of DNA 12:30 LUNCH

14:00 I Simon Topology of Transmembrane Proteins I 14:45 S H White Energetics of Folding Proteins into Membranes II 15:30 COFFEE BREAK 16:00 R Cassia-Moura Memory Effect on Biomembrane Protein 16:15 S L Mai Side Chain Effect on Protein Folding 16:30 End 9:00 C R Matthews: Conserved Folding Mechanisms in Homologous Proteins: Are Mechanisms Better Conserved than Sequences? III 9:45 E Domany Part A. Automated Protein Structure Classification Part B. Do Contact Vectors Determine a Protein's Structure? 10:30 COFFEE BREAK 11:00 K Dill A Simple Model of Water, the Hydrophobic Effect I 11:45 N V Dokholyan Understanding hierarchical protein evolution from the first principles I 12:30 LUNCH 14:00 A Garcia Atomic Simulations of Helix-Coil Transition in Peptides 14:45 C Micheletti Geometrical Aspects of Protein Folding 15:30 COFFEE BREAK 16:00 G Settanni The Role of Topology in the Stabilization of Intracellular Ig Domains 16:15 F Cecconi Molecular Dynamics Studies on HIV-1 Protease: Drug Resistance and Folding Pathways 16:30 H X Trinh Sequencing of folding events in model proteins

16:45 POSTER SECTION I

9:00 W A Eaton Fast processes in protein folding I 9:45 J DesJarlais Determinants of Conformational Change II 10:30 COFFEE BREAK 11:00 P Privalov Climbing the Hierarchy of Protein Structure II 11:45 R. Jernigan Extracting Functional Motions from Protein Structures I 12:30 LUNCH 14:00 H Molinari Folding and interaction studies of beta-lactoglobulins 14:45 N Dokholyan Direct observation of folding transition state ensemble of C-Src SH3 domain in molecular dynamics simulations II 15:30 COFFEE BREAK 16:00 A Mozzarelli Unfolding of PLP-Dependent Enzymes 16:45 End 9:00 M F Thorpe Ligand and Protein Flexibility using Constraint Theory I 9:45 L Kuhn Protein Unfolding Pathways and Folding Nucleation Sites Predicted by Graph Theory I 10:30 COFFEE BREAK 11:00 Doniach Protein Folding and Misfolding I 11:45 K Dill Ion Solvation II 12:30 LUNCH 14:00 R. Goldstein Evolutionary Perspectives on Protein Folding, Stability and Function I 14:45 R Jernigan Strong Packing Regularities in Proteins II

15:30 COFFEE BREAK 16:00 A Irback Folding Thermodynamics of Small Helical Proteins: A Model Study 16:45 End 9:00 W A Eaton Simple models for protein folding II 9:45 I Simon Stabilization Centers and Protein Stability II 10:30 COFFEE BREAK 11:00 A M Lesk Prediction of Protein Function from Structure I 11:45 M Oliveberg Protein engineering analysis of two-state folding I 12:30 LUNCH 14:00 L Mirny What Evolution Can Tell us about Protein-DNA Interactions 14:45 M Vendruscolo Structural Determination of Partially Folded States of Proteins from Residue-Specific Experimental Data 15:30 COFFEE BREAK 16:00 Godzik ????????(to be communicated) 16:45 M S Butt Protein Composition of Spring Wheats Grown in Pakistan 17:00 End 9:00 A Tramontano Advancements and pitfalls in protein comparative modelling 9:45 M Oliveberg Folding gate keepers: experimental evidence for anti-design II 10:30 COFFEE BREAK 11:00 Plaxco The convergence of theory and experiment in the folding of the

simplest proteins 11:45 M F Thorpe Protein Unfolding: Rigidity Lost II 12:30 LUNCH 14:00 L Kuhn Modeling Protein and Small Molecule Flexibility in Ligand Screening and Docking II 14:45 I Chang A Route to a Solution of the Protein Threading Problem by Learning 15:30 COFFEE BREAK 16:00 P Carloni Ab Initio Approach to Drug-Target Interactions 16:45 POSTER SECTION II 9:00 S Doniach Protein folding and misfolding II 9:45 A Garcia Water Penetration in Proteins II 10:30 COFFEE BREAK 11:00 11:45 R Goldstein Evolutionary Perspectives on Protein Folding, Stability and Function II 12:30 LUNCH 14:00 V Srivastava Orthogonalization of vectors 14:45 E Hackl ??????? (to be communicated) 15:30 COFFEE BREAK 16:00 P Bruscolini Nonpolar compounds and polymers hydration: a simple hydration model, a lattice mean field technique, and experimental results 16:15 W Chen Stochastic Dynamics Simulation of Proteins with Full Poisson-Boltzmann Electrostatics

16:30 U. Bastolla Connectivity of neutral networks and the substitution process in BACK to <u>ICTP smr1316</u>