

Dr. Giovanni Settanni

Centre for Protein Engineering, room 308
MRC Centre
Hills Road, Cambridge CB2 0QH, UK

Phone: +44 1223 402133 Fax: +44 1223 402140
email: gs@mrc-lmb.cam.ac.uk
Nationality: Italian

Theoretical and computational studies of protein folding and dynamics

Education

1997 - 2001 **Condensed Matter Theory Sector, SISSA, Trieste, Italy**

PhD, Thesis: "The role of native state topology in protein folding and dynamics". supervisors Prof. Amos Maritan and Prof. Paolo Carloni. Approved *cum laude*.

1997 - 1998 **Condensed Matter Theory Sector, SISSA, Trieste, Italy**

Master, Thesis: "Potential extraction by threading", supervisor Prof. Amos Maritan. Full marks.

1992 - 1997 **University of Turin, Italy**

Degree in Physics (Laurea in Fisica), Thesis: "Aspects of learning in realistic neural networks", supervisor Dr. Alessandro Treves (SISSA, Trieste). Full marks *cum laude* and *menzione d'onore* (i.e. average score on all examination higher than 99%).

Academic Appointments

2005 - present **MRC Centre for Protein Engineering, Cambridge, UK**

Postdoctoral scientist in Prof. Fersht's Lab, Research activity: Theoretical Biophysics and Molecular Dynamics Simulations for the Characterization of the Folding Process of Proteins and Peptides.

2001 - 2004 **Biochemisches Institut, University of Zurich, Switzerland**

Postdoctoral research assistant in Prof. Caflisch's Group, Research activity: Folding Transition State of Proteins and Peptides investigated by Molecular Dynamics Simulations.

1997 **Cognitive Neuroscience Sector, SISSA, Trieste, Italy**

Research contract on the project "Aspects of learning in realistic neural networks".

Grants & Awards

2009 MRC-Centre for Protein Engineering Additional Salary Reward.

2008 Poster presentation award at Gordon Research Conference on Protein Folding Dynamics, Ventura, CA, USA

2006 Swiss National Science Foundation Young Scientist Fellowship (~12'000 GBP).

2005 Stiefel-Zangger Stiftung fellowship (~24'000 GBP).
Novartis Foundation research support (~6'000 GBP).
EMBO Short term fellowship (~4'500 GBP).

2002 IUPAB Travel Fellow Award to attend the IUPAB meeting, Buenos Aires, Argentina.

2001 Grant for the FEBS Meeting, Lisbon, Portugal.

2000 Grant for the Varenna School of Physics, Varenna, Italy.

1998 Grant for the NATO ASI Soft Condensed Matter Conference, Geilo, Norway.

1997 - PhD fellowship at SISSA, Trieste, Italy, Condensed Matter Theory Sector
- PhD fellowship at SISSA, Trieste, Italy, Neuroscience Sector (declined)
- Grant for the School on Vectorial and Parallel Computing, CINECA, Bologna, Italy.

1993 Academic excellence award, University of Turin, Turin, Italy.

1992 Selected for the final stage of the Italian Mathematics Olympic Games, Cesena, Italy.

1991 1st rank (regional), 3rd rank (national) at the Italian Chemistry Games (*Lyceum* category), Turin and Frascati, Italy.

Invited Talks

- 2010** - Title: “Kinetic analysis of molecular dynamics simulations of reversible folding”, D.E. Shaw Research, New York, USA
- 2008** - Title: “Theoretical Bio-/Soft-Matter Physics: My contribution and future plans.”, Department of Physics, University of Surrey, Guildford, UK
- Department of Chemical Engineering, University of Strathclyde, Glasgow, UK
- 2007** - Department of Physics, University College, Dublin, IR
- 2006** - Title: “The folding properties of a beta hairpin investigated by MD simulations”, Department of Chemistry, Cambridge University, Cambridge, UK
- Title: “Theoretical characterization of the folding free energy landscape of proteins”, SISSA, Trieste, Italy
- 2005** - Title: “Phi-value analysis by molecular dynamics simulations of reversible folding”, Department of Medical Biochemistry, Biology and Physics, University of Bari, Italy
- Title: “Phi-value analysis by molecular dynamics simulations of reversible folding”, BIOPH05, Department of Physics, University of Bari, Italy
- Title: “A modular model of the Ankyrin Repeat proteins”, Faudo Retreat, Faudo, Switzerland
- Title: “Phi-value analysis by molecular dynamics simulations of reversible folding”, Department of Chemistry, Cambridge University, Cambridge, UK
- 2004** - Title: “Phi-value analysis by molecular dynamics simulations of reversible folding”, International School for Advanced Studies (SISSA), Trieste, Italy
- 2003** - Title: “Formation of the folding nucleus of an SH3 domain investigated by Loosely Coupled Molecular Dynamics simulations“, Max Planck Institut for Polymer Research, Mainz, Germany
- 2002** - Title: “Folding of SH3 domain from denatured conformations investigated through biased molecular dynamics simulations”; NCCR seminar, Zurich, Switzerland
- 2001** - Title: “The Role Of Topology In Immunoglobulin Variable Domain Investigated by MD Simulations”, International workshop on protein folding, structure and design, ICTP, Trieste, Italy
- Title: “The Role Of Topology In Immunoglobulin Variable Domain Investigated By MD Simulations”, Department of Biochemistry, University of Zurich, Switzerland

Editorial and Reviewing work:

Reviewing grant proposals submitted to The American Chemical Society Petroleum Research Fund, Engineering and Physical Sciences Research Council (EPSRC) UK, British Council BIRAX.

Reviewing manuscripts submitted to “PLOS Computational Biology”, “Journal of Physical Chemistry”, “Journal of Chemical Theory and Computation”, “Biophysical Chemistry”, “Proteins: Structure, Function, and Bioinformatics”, and “BMC Structural Biology”.

Languages and technical skills:

Italian	Mother tongue
English	Fluent
German	Basic
UNIX operating systems, tools, scripting languages (bash, csh, tcsh, awk, perl, tcl) and Linux cluster management	Extensive experience
Windows operating system and tools	Extensive experience
C and Fortran programming	Extensive experience
Molecular dynamics and visualization packages: CHARMM, NAMD, GROMACS, AMBER, VMD, Pymol	Extensive experience
Parallel programming with MPI on Cray, sgi, alpha and linux cluster machines	Extensive experience

Teaching Activity

- 2005 – present** **MRC-Centre of Protein Engineering, Cambridge, UK**
Co-Supervision of a graduate student on the research project: “Protein folding transition state investigated by Molecular Dynamics simulations”
- 2002 – 2004** **University of Zurich, Biochemistry Department**
Co-supervision of graduate students on projects related to Molecular Dynamics Simulations of biological systems
- 1998 – 2000** **SISSA Trieste, Italy**
Tutor of undergraduate students of the University of Trieste on Mathematics

Administrative Experience

Administrative duties : IT management of the computer cluster used for research by Dr. Settanni and co-supervised student, since 2005, at the MRC-Centre for protein engineering, Cambridge.
IT management of Linux workstations and sector web-pages, 1998-2001, SISSA, Trieste, Italy.

People management or supervision : co-supervision of a graduate student working on Molecular Dynamics simulations, since 2005, at the MRC, Centre for protein engineering, Cambridge.

Budget or resource management : management of the budget devoted to the purchase of the computer facilities (computer cluster, data storage, backup systems etc. ~15'000GBP) needed for computational research at the Centre for protein engineering.

Project management. management of the project “Combining Molecular Dynamics Simulations and Experiments to Accurately Characterize the Denatured and Folding Transition State of Structured Peptides”, since 2005, at the Centre for protein engineering.

Referees

Prof. Amos Maritan,

PhD supervisor, Dipartimento di Fisica G. Galilei, Universita' di Padova, via Marzolo 8, 35131 Padova, Italy, Phone: +39 049 8277175, Fax +39 049 8277102, e-mail: maritan@pd.infn.it

Prof. Sir Alan R. Fersht,

postdoc supervisor, Director of the MRC Centre for Protein Engineering, Cambridge CB2 2QH, UK, Phone: +44 1223 402137, Fax: +44 1223 402140 e-mail: arf25@cam.ac.uk

Prof. Amedeo Caflisch,

postdoc supervisor, University of Zurich, Winterthurerstrasse 190, 8057 Zurich, Switzerland, Phone: +41 1 63 55521, Fax: +41 1 63 56862 e-mail: caflisch@bioc.uzh.ch, cc: Mrs. Christiane Gujan e-mail: gujan@bioc.unizh.ch

List of Publications

Book Chapters

Rao F., **Settanni G.**, Caflisch A.

Estimation of folding probabilities and phi values from molecular dynamics simulations of reversible Peptide folding.

Methods Mol Biol. **2007**; 350:225-49.

Articles in peer reviewed journals

Wetzel S.K., Ewald C., Jurt S., **Settanni G.**, Plückthun A. And Zerbe O.

Residue-resolved stability of full-consensus ankyrin repeat proteins probed by NMR

J. Mol. Biol. **2010** *in press*

Serquera D., Lee W., **Settanni G.**, Paci E., Marszalek P.E. and Itzhaki L.S.

Mechanical unfolding of an ankyrin repeat protein

Biophys. J. **2010** 98(7):1294-301

Basse N., Kaar J. L., **Settanni G.**, Joerger A. C., Rutherford T. J., Fersht A. R.

Towards the Rational Design of p53 Stabilizing Drugs: Probing the Surface of the Oncogenic Y220C Mutant

Chemistry & Biology, **2010** 17(1):46-56

Huang F., Rajagopalan S., **Settanni G.**, Marsh R., Armoogum D., Nicolaou N., Bain A., Lener E., Haas E., Ying L., Fersht A. R.

Multiple conformations of full-length p53 detected with single-molecule fluorescence resonance energy transfer.

Proc. Natl. Acad. Sci. USA. **2009** 106(49):20758-20763

Settanni G., Fersht A. R.

Downhill versus barrier-limited folding of BBL 3. Heterogeneity of the native state of the BBL peripheral subunit binding domain and its implications for folding mechanisms.

J. Mol. Biol. **2009** 387(4):993-1001

Yu G.W., Vaysburd M., Allen M.D., **Settanni G.** and Fersht A.R.

The structure of human MDM4 N-terminal domain bound to a single domain antibody

J. Mol. Biol. **2009** 385(5):1578-89

Settanni G., Fersht A. R.

High Temperature Unfolding Simulations of the TRPZ1 peptide

Biophys. J. **2008** 94(11):4444-53

Huang F., **Settanni G.**, Fersht A. R.

Fluorescence resonance energy transfer analysis of the folding pathway of Engrailed

Homeodomain. *Protein Eng. Des. Sel.* **2008** 21(3):131-46

Wetzel S.K., **Settanni G.**, Kenig M., Binz K., Plückthun A.

Folding and Unfolding Mechanism of Highly Stable Full Consensus Ankyrin Repeat Proteins

J. Mol. Biol. **2008** 376(1):241-57

Interlandi G., Wetzel S.K., **Settanni G.**, Plückthun A., Caflisch A.

Unfolding of designed ankyrin repeat proteins characterized by molecular dynamics simulations and chemical denaturation experiments

J. Mol. Biol. **2008** 375(3):837-54

Seeber M., Cecchini M., Rao F., **Settanni G.**, Caflisch A.

Wordom: a program for efficient analysis of molecular dynamics simulations

Bioinformatics. **2007** 23(19):2625-7

Interlandi G., **Settanni G.**, Caflisch A.

Unfolding transition state and intermediates of the tumor suppressor p16INK4a investigated by

molecular dynamics simulations.
Proteins. **2006** Jul 1;64(1):178-92.

Rao F., **Settanni G.**, Guarnera E., Caflisch A.
Estimation of protein folding probability from equilibrium simulations.
J. Chem. Phys., **2005**, 122:184901

Settanni G., Rao F., Caflisch A.
Phi-value analysis by molecular dynamics simulations of reversible folding
Proc. Natl. Acad. Sci. USA, **2005**, 102:628-33.

Settanni G., Gsponer J., Caflisch A.
Formation of the folding nucleus of an SH3 domain investigated by loosely coupled molecular dynamics simulations
Biophys J., **2004**; 86:1691-1701

Settanni G., Cattaneo, A., Carloni P.
Molecular Dynamics Simulations of the NGF / TrkA domain 5 Complex and Comparison with Biological Data
Biophys J. **2003** Apr;84(4):2282-92.

Settanni, G., Hoang, T.X., Micheletti, C., Maritan, A.
Folding Pathways of Prion and Doppel
Biophys J. **2002** Dec;83(6):3533-41.

Visintin, M., **Settanni, G.**, Graziosi, S., Maritan, A., Marks, J.D., Cattaneo, A.
The intracellular antibody capture technology (IACT): towards an optimal consensus sequence for intracellular antibodies.
J. Mol. Biol. **2002** 317 (1): 73-83

Settanni G, Cattaneo A, Maritan A
The role of native-state topology in the stabilization of intracellular antibodies
Biophys. J. **2001** 81: 2935-2945

Dima⁺ RI, **Settanni⁺ G**, Micheletti C, Banavar JR, Maritan A
Extraction of interaction potentials between amino acids from native protein structures
J Chem Phys 112: (20) 9151-9166 May 22 **2000**
⁺These two authors equally contributed to the work

Settanni G, Treves A
Analytical model for the effects of learning on spike count distributions
Neural Comput 12: (8) 1773-1787 Aug **2000**

Refereed Conference papers

Uk B., M. Taufer, T. Stricker, **G. Settanni**, A. Cavalli, A. Caflisch
Combining Task- and Data Parallelism to Speed up Protein Folding on a Desktop Grid Platform
Proc. of the CCGRID 2003, IEEE International Symposium on Cluster Computing and the Grid, May **2003**, Tokyo, Japan.

Uk B., M. Taufer, T. Stricker, **G. Settanni**, A. Cavalli
Implementation and Characterization of Protein Folding on a Desktop Computational Grid
Proc. of IPDPS 2003, IEEE/ACM International, Parallel and Distributed Processing Symposium, April **2003**, Nice, France.

Other Publications

Patents

Rabbits T.H., **Settanni G.**, Maritan A., Cattaneo A., Visintin M.
Intracellular Antibodies. **2003**. Patent number WO03014960.