VIJAY S. PANDE

EDUCATION

1988-1992	BA, Physics, Princeton University, Princeton, NJ (Thesis advisor: P. W. Anderson, Nobel Laureate)
1992-1995	PhD, Physics, Massachusetts Institute of Technology, Cambridge, MA (Thesis advisors: T. Tanaka, and A. Grosberg)

PROFESSIONAL EXPERIENCE

1986	Undergraduate research, Princeton University, (R. Austin)
1987	Undergraduate research, Princeton University, (R. Goldstein)
1987	Undergraduate research, Princeton University, (J. Taylor, Nobel Laureate)
1995-1996	Postdoctoral fellow, CMSE, MIT, Cambridge, MA (T. Tanaka, M. Kardar)
1996-1998	Miller Fellow, U. C. Berkeley, Berkeley, CA (D. Rokhsar)
1998-1999	LBNL fellow in physical biosciences (D. Rokhsar)
1999-	Assistant Professor of Chemistry, Stanford University, Stanford, CA
2000-	Assistant Professor of SSRL (by courtesy), Stanford University, Stanford, CA
2000-	Assistant Professor of Structural Biology (by courtesy), Stanford University, Stanford, CA

HONORS AND AWARDS

2003	Dreyfus Teacher-Scholar Award
2002-2005	Frederick E. Terman Fellow, Stanford University
2002	Named to the TR100 (MIT *Tech Review* top 100 young innovators of 2002)
2002	Keynote speaker, OpenEye conference
2001	Keynote speaker, workshop on Evolvable Hardware JPL
1996-1998	Miller Fellow, Miller Institute for Basic Research, UC Berkeley
1992-1995	National Science Foundation Graduate Fellow (Physics Dept, MIT)
1992	Kawasaki Prize in experimental physics, Princeton University
1988-1992	ONR Science Fellowship
1988-1992	Westinghouse Science Talent Search Scholarship (4th place)
1988-1992	TRW Science Scholarship

TEACHING

1999-	Chemistry 171: Chemical Thermodynamics (undergraduate)
1999-2003	Chemistry 275: *Statistical Mechanics* (graduate)
2002	Nominated for university teaching award
2003	Dreyfus Teacher-Scholar Award

COMMITTEE DUTIES

1999-	Computational infrastructure (Chemistry Department, chair)
2000-	Admissions (Biophysics Program)
2001-	Executive committee (Biophysics Program)
2001-	Supercomputer (BioX, co-chair)
2002-	Curriculum (Chemistry Department)
2002-	Graduate student awards (Chemistry Department)
2002-	Admissions (Chemistry Department)
2002-	Admissions (Structural Biology Department)
2002-	Interdisciplinary Initiatives Program (BioX)
2002-	Computational infrastructure (BioX)

FORMER GRADUATE STUDENTS AND POSTDOCTORAL FELLOWS

2000-2002	Siraj Khaliq, Masters in Computer Science. *Folding@Home: Worldwide distributed computing for biomedical research.* Presently at Google Corporation.
1999-2003	Bradley J. Nakatani, Masters in Chemistry. *Coarse grained simulations of RNA folding.*
2000-2003	Bojan Zagrovic, PhD in Biophysics. *Simulations of protein folding.* Presently a postdoctoral fellow at ETH, with Prof. Wilfred van Gunsteren.
2000-2004	Stefan Larson, PhD in Biophysics. *Simulations of protein design and folding.* Presently a consultant at McKinsey.
1999-2004	Sidney Elmer, PhD in Chemistry. *Simulations of the folding of non-biological foldamers.*
2000-2004	Michael Shirts, PhD in Chemistry. *Novel methods for free energy calculation.* Will be a postdoc with Richard Freisner, Columbia University

PUBLICATIONS

Publications of work performed at MIT (1992-1996):

1. V. S. Pande, A. Yu. Grosberg, and T. Tanaka. Non-Randomness in Protein Sequences: Evidence for a Physically Driven Stage of Evolution? *Proceeding of the National Academy of Science, U.S.A.*, **91**, 12972 (1994)
2. V. S. Pande, A. Yu. Grosberg, and T. Tanaka. Thermodynamic Procedure to Synthesize Heteropolymers that can Renature to Recognize a Given Target Molecule. *Proceeding of the National Academy of Science, U.S.A.*, **91**, 12976 (1994)
3. V. S. Pande, C. Joerg, A. Yu. Grosberg, and T. Tanaka. Enumeration of the Hamiltonian Walks on a Cubic Sublattice. *Journal of Physics*, **A27**, 6231 (1994)
4. V. S. Pande, A. Yu. Grosberg, and T. Tanaka. Phase Diagram of Imprinted Copolymers, *Journal of Physics (Paris)*, **4**, 1771 (1994)
5. V. S. Pande, A. Yu. Grosberg, and T. Tanaka. Folding Thermodynamics and Kinetics of Imprinted Renaturable Heteropolymers, *Journal of Chemical Physics*, **101**, 8246 (1994)
6. V. S. Pande and C. Joerg, Enumeration of the Hamiltonian Walks on a Sublattice, *Student Workshop on Scalable Computing*, MIT/LCS/TR-622, **53** (1994)
7. V. S. Pande, A. Yu. Grosberg, and T. Tanaka. Freezing Transition of Random Heteropolymers Consisting of an Arbitrary Set of Monomers. *Physical Review*, **E51**, 3381 (1995)
8. V. S. Pande, A. Yu. Grosberg, and T. Tanaka, Phase Diagram of Heteropolymers with an Imprinted Conformation. *Macromolecules*, **28**, 2218 (1995)
9. V. S. Pande, A. Yu. Grosberg, and T. Tanaka. Freezing Transition of an Imprinted Copolymer in a Random External Field. *Journal of Physics* **A28**, 3657 (1995)
10. V. S. Pande, A. Yu. Grosberg, and T. Tanaka. How Accurate Must Potentials Be for Successful Modeling of Protein Folding? *Journal of Chemical Physics* **103,** 9482 (1995)
11. T. Tanaka, C-n Wang, A. English, S. Masamune, H. Gold, R. Levy, K. King, V. S. Pande, and A. Yu. Grosberg. Polymer Gels that can Recognize and Recover Molecules. *Faraday Discussions*, **101**, 201-206 (1995)
12. V. S. Pande, A. Yu. Grosberg, C. Joerg, and T. Tanaka. How Well is Heteropolymer Freezing Described by the Random Energy Model? *Physical Review Letters,* **76**, 3987-3990 (1995)
13. V. S. Pande, A. Yu. Grosberg, M. Kardar, C. Joerg, and T. Tanaka. Polyampholyte Freezing Transition. *Physical Review Letters,* **77**, 3565-3568 (1996)
14. V. S. Pande, A. Yu. Grosberg, and T. Tanaka. On the Theory of Folding Kinetics for Short Proteins. *Folding and Design* **2,** 109 (1997)
15. V. S. Pande and J. Onuchic. Electron Transport in Disordered Polymeric Systems. *Physical Review Letters* **78,** 146 (1997)
16. V. S. Pande, A. Yu. Grosberg, and T. Tanaka. How to make Heteropolymers which can Renature to Recognize a Given Target Molecule, **107** 316 *Physica D* (1997)

17. V. S. Pande, A. Yu. Grosberg, and T. Tanaka. Statistical Mechanics of Simple Models of Protein Folding. *Biophysical Journal* **73,** 3192-3210 (1997)
18. V. S. Pande, A. Yu. Grosberg, and T. Tanaka. Thermodynamics of the coil to frozen globule transition in heteropolymers. *Journal of Chemical Physics* **107**, 5118-5124 (1997)
19. M. Tanaka, A. Yu. Grosberg, V. S. Pande, and T. Tanaka. Molecular Dynamics Study of the Structural Organization of a Strongly-Coupled Chain of Charged Particles. *Physical Review E* **56** 5798-5808 (1997)

Publications of work performed at UC Berkeley (1996-1999):

20. A. Chakraborty, E. I. Shakhnovich, and V. S. Pande. Broken Ergodicity in Compact Random Heteropolymers with Correlated Sequence Fluctuations. *Journal of Chemical Physics* . **108**, 1683-1687 (1997)
21. R. Du, V. S. Pande, A. Yu. Grosberg, T. Tanaka, and E. I. Shakhnovich. On the Transition Coordinate for Protein Folding. *Journal of Chemical Physics* **108,** 334-350 (1998)
22. V. S. Pande and D. S. Rokhsar. Is the Molten Globule a third Phase of Proteins? *Proceedings of the National Academy of Science, USA* **95** 1490-1494 (1998)
23. V. S. Pande, A. Yu. Grosberg, and T. Tanaka, D. S. Rokhsar. Protein Folding Pathways: Is a "new view" needed? *Current Opinion in Structural Biology* **8** 68-79 (1998)
24. V. S. Pande and D. S. Rokhsar. Folding Pathway of a Lattice Model for Protein Folding. *Proceedings of the National Academy of Science, USA* **96,** 1273-1278 (1999)
25. R. Du, V. S. Pande, A. Yu. Grosberg, T. Tanaka, and E. I. Shakhnovich. On the Role of Conformational Geometry in Protein Folding. **111,** 10375-10380 *Journal of Chemical Physics* (1999)
26. A. Golumbfskie, V. S. Pande, and A. Chakraborty. Simulation of biomimetic recognition between polymers and surfaces. *Proceedings of the National Academy of Science, USA,* **96,** 11707-11712 (1999)
27. V. S. Pande and D. S. Rokhsar. Molecular dynamics simulation of unfolding and refolding of a β-hairpin. *Proceedings of the National Academy of Science, USA* **96** 9062-9067 (1999)
28. Z. Bryant, V. S. Pande, and D. S. Rokhsar. Mechanical unfolding of a beta hairpin using molecular dynamics. *Biophysical Journal,* **78**, 584-589 (2000)
29. V. S. Pande, A. Yu. Grosberg, and T. Tanaka. Heteropolymer Freezing and Design: Towards Physical Models of Protein Folding. *Reviews of Modern Physics* **72**, 259-286 (2000)
30. R. Anderson, V. S. Pande, and C. Radke. Dynamic lattice Monte Carlo simulation of a model protein at an oil-water interface. *Journal of Chemical Physics*, **112**, 9167-9185 (2000)

Publications of work performed at Stanford University (1999-present):

31. M. R. Shirts and V. S. Pande. Screen Savers of the World, Unite! *Science*, **290**, 1903-1904 (2000)
32. S. Elmer and V. S. Pande. A new twist on the helix-coil transition: a non-biological polymer with protein-like intermediates. *Journal of Physical Chemistry B,* **105**, 482-485 (2001)
33. M. R. Shirts and V. S. Pande. Mathematical Foundations of Ensemble Dynamics. *Physical Review Letters*, **86**, 4983-4987 (2001)
34. B. Zagrovic, E. Sorin, and V. S. Pande. Atomistic folding simulations of a beta hairpin. *Journal of Molecular Biology* **313**, 151-169 (2001)
35. V. S. Pande, I. Baker, J. Chapman, S. P. Elmer, S. Khaliq, S. M. Larson, Y. M. Rhee, M. R. Shirts, C. Snow, E. Sorin, B. Zagrovic. Atomistic protein folding simulations on the submillisecond time scale using worldwide distributed computing. *Kollman Memorial Issue, Biopolymers,* **68**(1), 91-109 (2003)
36. E. Sorin, M. Engelhardt, D. Herschlag, and V. S. Pande. Unfolding simulations of a GNRA tetraloop. *Journal of Molecular Biology*, **317**, 493-506 (2002)
37. R. Russell, I. S. Millet, M. W. Tate, L. W. Kwok, B. Nakatani, S. M. Gruner, S. G. J. Mochrie, V. S. Pande, S. Doniach, D. Herschlag, and L. Pollack. Rapid Compaction During RNA Folding. *Proceedings of the National Academy of Science, USA,* **99**, 4266-4271 (2002)
38. B. Zagrovic, C. Snow, S. Khaliq, M. Shirts, and V. S. Pande. Native-like mean structure in the unfolded ensemble of small proteins. *Journal of Molecular Biology* **323**, 153-164 (2002)
39. C. Snow, H. Nguyen, V. S. Pande, and M. Gruebele. Folding of a ββα protein: simulation and theory. *Nature*, **420***,* 102-106 (2002)
40. B. Zagrovic, C. D. Snow, M. R. Shirts and V. S. Pande. Simulation of Folding of a small alpha-helical protein in atomistic detail using worldwide-distributed computing. *Journal of Molecular Biology*, **323**, 927-937 (2002)
41. S. M. Larson, J. England, J. DesJarlais, and V. S. Pande. Thoroughly sampling sequence space: large-scale protein design of structural ensembles. *Protein Science* **11** 2804-2813 (2002)
42. Y. M. Rhee and V. S. Pande. Multiplexed Replica Exchange Molecular Dynamics Method for Protein Folding Simulation. *Biophysical Journal,* **84,** 775–786 (2003)
43. C. Snow, B. Zagrovic, and V. S. Pande. The Trp Cage: Folding Kinetics and Unfolded State Topology via Molecular Dynamics Simulations. *Journal American Chemical Society,* **124**, 14548-14549 (2002)
44. A. I. Jewett, V. S. Pande, and K. W. Plaxco. Cooperativity, smooth energy landscapes and the origins of topology-dependent protein folding rates. *Journal of Molecular Biology,* **326** 247-253 (2003)

45. S. M. Larson, A. Garg, J. DesJarlais, and V. S. Pande. Increased detection of structural templates using alignments of designed sequences. *Proteins: Structure, Function, and Genetics* **51** 390-396 (2003)

46. B. Zagrovic and V. S. Pande. Solvent Viscosity Dependence of the Folding Rate of a Small Protein: a Distributed Computing Study. *Journal of Computational Chemistry,* **24** 1432–1436 (2003)

47. E. Sorin, Y. M. Rhee, B. Nakatani, and V. S. Pande. Insights into nucleic acid hairpin conformational dynamics from massively parallel stochastic simulations. *Biophysical Journal,* **85** 790-803 (2003)

48. M. R. Shirts, J. W. Pitera, W. C. Swope, and V. S. Pande. Extremely Precise Free Energy Calculations of Amino Acid Side Chain Analogs: Comparison of Common Molecular Mechanics Force Fields for Proteins. *Journal of Chemical Physics,* **119** 5740-5761 (2003)

49. S. M. Larson and V. S. Pande. Sequence optimization for native state stability determines the evolution and folding kinetics of a small protein. *Journal of Molecular Biology,* **332** 275-286 (2003)

50. S. M. Larson, C. Snow, V. S. Pande. Folding@Home and Genome@Home: Using distributed computing to tackle previously intractable problems in computational biology. *Modern Methods in Computational Biology,* R. Grant, *ed,* Horizon Press*,* (2003)

51. M. R. Shirts, E. Bair, G. Hooker, and V. S. Pande. Equilibrium free energies from nonequilibrium measurements using maximum likelihood methods. *Physical Review Letters,* **91** (2003)

52. B. Zagrovic and V. S. Pande. How Can Proteins be Unfolded and yet Have Native-like Properties: Structural Correspondence between the Alpha Helix and the Random-Flight Chain. *Nature Structural Biology,* **10** 955-961 (2003)

53. V. S. Pande. Meeting half way on the bridge between protein folding theory and experiment. *Proceedings of the National Academy of Sciences, USA,* **100** 3555-3556 (2003)

54. P. Lenz, B. Zagrovic, J. Shapiro, and V. S. Pande. Folding probabilities: a novel approach to folding transitions. *Journal of Chemical Physics,* **120** 6769-6778 (2003)

55. E. Sorin, B. Nakatani, Y. M. Rhee, G. Jayachandran, V. Vishal, and V. S. Pande. Does Native State Topology Determine the RNA Folding Mechanism? *Journal of Molecular Biology* **337** 789-797 (2003)

56. Y. M. Rhee, E. J. Sorin, G. Jayachandran, E. Lindahl, V. S. Pande. Does water play a structural role in protein folding. *Proceedings of the National Academy of Science, USA* **101** 6456-6461 (2003)

57. C. D. Snow, L. Qiu, D. Du, F. Gai, S. J. Hagen, and V. S. Pande. Tryptophan Zipper Folding Kinetics via Molecular Dynamics and Temperature Jump Spectroscopy. *Proceedings of the National Academy of Sciences, USA,* **101** 4077-4082 (2004)

58. P. Kasson and V. S. Pande. Molecular Dynamics Simulation of Lipid Reorientation at Bilayer Edges. *Biophysical Journal,* **86** 3744-3749 (2004)

59. N. Singhal, C. Snow, and V. S. Pande. Path sampling to build better roadmaps: predicting the folding rate and mechanism of a Trp Zipper beta hairpin. *Journal of Chemical Physics* **121** 415-425 (2004)

60. V. S. Pande. Atomistic models of protein folding. *Encyclopedia of Materials Research* (2004)

61. B. Zagrovic and V. S. Pande. How Does Averaging Affect Protein Structure Comparison on the Ensemble Level? *Biophysical Journal, in press* (2004)

62. J. E. Kohn, I. S. Millett, J. Jacob, B. Zagrovic, T. M. Dillon, N. Cingel, R. S. Dothager, S. Seifert, P. Thiyagarajan, T. R. Sosnick, M. Z. Hasan, V. S. Pande, I. Ruczinski, S. Doniach and K. W. Plaxco. Do the dimensions of chemically unfolded proteins differ significantly from the expectations of a random-coil model? *Proceedings of the National Academy of Sciences, USA, in press* (2004)

63. S. Elmer and V. S. Pande. Simulations of Self-Assembling Nanopolymers: Novel Computational Methods and Applications to poly-Phenylacetylene Oligomers. *Journal of Chemical Physics, in press* (2004)

64. V. S. Pande. Protein Aggregation and Disease: A universal TANGO? *Nature Biotechnology* **22**, 1240-1241 (2004)

65. C. D. Snow, E. J. Sorin, Y. M. Rhee, and V. S. Pande. How well can simulation predict protein folding kinetics and thermodynamics? *Annual Reviews of Biophysics*, *in press* (2004)

66. Y. M. Rhee and V. S. Pande. One-dimensional reaction coordinate and the corresponding potential of mean force from commitment probability distribution. *Journal of Chemical Physics, submitted* (2004)

67. E. Sorin and V. S. Pande. Absolute Assessment of Protein Folding Potentials from Equilibrium Simulations. *Journal of the American Chemical Society, submitted* (2003)

68. E. Sorin, Y. M. Rhee, and V. S. Pande. Does water play a structural role in the folding of small nucleic acids? *Biophysical Journal, submitted* (2003)

69. L. T. Chong, C. D. Snow, Y. M. Rhee, and V. S. Pande. Dimerization of the p53 oligomerization domain: Identification of a folding nucleus by molecular dynamics simulations. *Journal of Molecular Biology, in press* (2004)

70. S. Elmer and V. S. Pande. Length Dependent Folding Kinetics of poly-Phenylacetylene Oligomers: Structural Characterization of a Kinetic Trap, *to be submitted* (2004)

71. G. Jayachandran, V. Vishal, and V. S. Pande. Folding Simulations of the Villin Headpiece in All-Atom Detail, *to be submitted* (2004)

INVITED TALKS

1. Boston University, *Polymer Physics Seminar*, October 1995
2. University of California, Berkeley, *Condensed Matter Physics Seminar*, November 1995
3. University of California, San Diego, *Condensed Matter Theory Seminar*, November 1995
4. Harvard University, *Polymer Chemistry Seminar*, December 1995
5. Lawrence Berkeley National Laboratory, *LBNL Biophysics Meeting*, September 1996
6. Rutgers University, *Statistical Mechanics Meeting*, December 1996
7. University of California, Berkeley, *Condensed Matter Physics Seminar*, October 1997
8. Stanford University, *Physical Chemistry Seminar*, January 25, 1998
9. University of California, Berkeley, *Chemical Engineering Seminar*, February 12, 1998
10. Lawrence Berkeley National Laboratory, *NERSC Seminar*, February 20, 1998
11. Massachusetts Institute of Technology, *Chemical Engineering Seminar*, March 9, 1998
12. University of California, Berkeley, *Molecular and Cell Biology Seminar*, March 30, 1998
13. Los Alamos National Laboratory, *Third International Symposium on Biological Physics*, September 20, 1998
14. National Institutes of Health, *Laboratory of Chemical Physics*, March 17, 1999
15. National Centre for Biological Sciences (NCBS), Banglore, India; *Frontiers in Structural Biology*, August 25-27, 1999
16. UC Berkeley, *Statistical Mechanics Meeting*, January 2000
17. La Jolla Interfaces in Science (LJIS), *Quantitative Challenges in the Post Genomic Sequence Era*, January 11-12, 2000
18. International School of Physics, Enrico Fermi, Varenna, Lake Como Italy, July 11, 2000
19. Columbia University, *Chemistry Dept Seminar*, December 2000
20. IBM Watson Research center, *Blue Gene seminar,* December 2000
21. Jet Propulsion Lab, Pasadena, CA, Seminar, February 2001
22. UCSD, *Blue Gene Conference*, March 2001
23. ACS meeting, *symposium on folding and energy landscapes,* March 2001
24. National Museum of Natural History, *Supercomputing Symposium,* 2001
25. Rockefeller University, *Chemistry Dept Seminar*, 2001
26. Kyoto University, *Fourth International Symposium on Biological Physics*, July 2001
27. Chicago ACS meeting, September 2001
28. IBM Almaden research center, San Jose, October 2001
29. Polarizable Forcefields Workshop, University of Utah, December 2001

30. ICAM/LANL conference on self organizing systems, Santa Fe, January 2002
31. *Protein Folding Gordon Conference*, January 2002
32. UCSF, *Kollman Memorial Symposium*, February 2002
33. UCSD, Chemistry Dept *Student Invited Seminar*, February 2002
34. OpenEye conference, keynote speaker, February 2002
35. Stanford University, *Materials Science Departmental Seminar*, February 2002
36. Stanford University, *Mechanical Engineering Departmental Seminar*, April 2002
37. UIUC, *Theoretical Biophysics Seminar*, April 15, 2002
38. Stanford University, *CPIMA Forum*, August 9, 2002
39. Caltech, *Biophysics Seminar,* October 24, 2002
40. Aspen Meeting on Single Molecule Experiments, January 2003
41. UC Davis, *Physics Colloquium*, January 27, 2003
42. University of Pennsylvania, *Chemistry Department Seminar*, February 20, 2003
43. Princeton University, *Chemical Engineering Department Seminar*, February 21, 2003
44. Association for Lab Automation (ALA), *Session on bioinformatic applications to proteomics,* Palm Springs, February 2003
45. International Symposium on Simulation Science, March 6, 2003
46. American Physical Society Meeting, March 3, 2003
47. Chemistry Symposium, Seoul National University, March 13, 2003
48. Cambridge Health Tech Conference, *Strategic Biocomputing: Implementations, Applications and Results*. March 18, 2003
49. Johns Hopkins, *"Coolfont" Protein Folding Meeting*, March 22-25, 2003
50. University of Maryland, *Statistical Physics/Biophysics Seminar*, March 26, 2003
51. Biomedical Engineering Society (BMES). *Understanding the Role of Protein Unfolded States in Folding, Function, Evolution and Disease,* April 11, 2003
52. SD Forum, Sun Microcomputers, "Build A Bioinformatics Supercomputer Using Grid Technology," June 17, 2003
53. Telluride 2003 workshop on "Energy Landscapes and Dynamics," July 2003
54. ACS Meeting, Session on Protein Folding Kinetics, September 2003
55. ACS Meeting, Session on Protein Design, September 2003
56. Keynote address, 16th annual workshop on Languages and Compilers for Parallel Computing (LCPC). (declined), October 2-4, 2003
57. CECAM Meeting, October 2003, declined
58. Biophysics seminary, Cornell University, October 29, 2003

59. NIH BISTI conference, declined, November 2003
60. *Science at the Interface Seminar*, Michigan State University, November 14, 2003
61. DGRIDS 2003, Phoenix, November 17, 2003
62. ALA meeting, February 2004
63. U. Minnesota, February 10, 2004
64. Biophysical society, February 2004
65. Xerox PARC, February 19, 2004
66. Isaac Newton Workshop, March 15-19 2004, declined
67. Keystone Meeting on Structural Biology. April, 2004
68. NSF Workshop on Cyber infrastructure. April 20, 2004
69. CECAM Meeting on Free Energy Methods. May, 2004
70. Protein Society. August, 2004
71. "Algorithms for Macromolecular Modeling" Leicester, UK, August 19-21, 2004
72. ACS Meeting. Session on High Performance Supercomputing in Drug Design. August, 2004
73. Washington University, St Louis. December, 2004
74. Chemistry Department, New York University, January, 2005
75. Chemistry Department, Northwestern University, February, 2005
76. Chemistry Department, University of Wisconsin, February, 2005
77. Chemistry Department, MIT, February, 2005
78. American Physical Society, March 2005
79. Asilomar Meeting on Protein Folding, May 2005
80. Proteins Gordon Conference, June 2005
81. ACT, July 2006