Curriculum Vitae

Marcos Rubén Betancourt

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Education

Ph.D. in Physics, University of California, San Diego, September 1995.
M.S. in Physics, University of California, San Diego, December 1988.
B.S. in Physics, University of Puerto Rico, Mayagüez, May 1986.

Experience

2002-date **Research Assistant Professor**
UB Buffalo Center of Excellence in Bioinformatics
Buffalo, New York
Topic: *protein modeling.*

2001-2002 **Domain Assistant Member**
Laboratory of Computational Genomics
Donald Danforth Plant Science Center
St. Louis, Missouri
Topic: *protein modeling.*

1999-2000 **Postdoctoral Fellow**
Laboratory of Computational Genomics
Donald Danforth Plant Science Center
Creve Coeur, Missouri
Topic: *protein structure prediction* problem.

1996-1999 **National Science Foundation Postdoctoral Fellow**
Institute for Physical Science and Technology
University of Maryland, College Park
Topics: *protein design and assisted folding modeling.*

1996	**Research associate** Institute for physical Science and Technology University of Maryland, College Park Topic: simulations of *protein folding kinetics.*
1992–95	**Teaching assistant** Department of Physics, University of California, San Diego Topic: simulations of *protein folding kinetics.*
1992	**NDSEG fellow summer program** NRaD, San Diego, California Topics: *stochastic resonance* and *chaos.*
1989–92	**NDSEG fellow** Department of Physics, University of California, San Diego Topics: nonlinear dynamics including *spatio-temporal chaos* and *time series analysis.*
1988–89	**Research assistant** Department of Physics, University of California, San Diego Topics: *fluid dynamics* and *liquid cavitation.*
1986–88	**San Diego Fellowship** Department of Physics, University of California, San Diego
1986	**LLNL summer student internship program** Lawrence Livermore National Laboratories , Livermore, California Participated in computer analysis of electron-pair production experiments.
1985	**LLNL summer student internship program** Lawrence Livermore National Laboratories , Livermore, California Participated in the setup of an experiment for developing a γ-ray laser.
1981	Participant in the NSF Workshop on *Solar Energy and Engineering* University of Colorado, Boulder.

Teaching Experience

2003-summer	Invited speaker at the UB, Center for Computational Research, High School Summer Program in Computational Science
1992–1995	Assistant Instructor for several physics coursers, such as a graduate level course in statistical physics.

Awards

National Science Foundation Postdoctoral Fellowship (Maryland, 1996, 1998).
National Defense Science and Engineering Graduate (NDSEG) **Fellow** (San Diego, 1989).
San Diego and Graduate Opportunity Research Fellowship (San Diego, 1986, 1987).
Enrico Fermi Award, physics department top honor student (Mayagüez, 1986).

Affiliations

American Physical Society

Miscellaneous

Army National Guard Officer (1991-2003).
Programming experience in Assembler, Pascal, Fortran, C, and C++, Objective C, & Perl.

Pending Grants

Studies of protein folding by reduced models. Submitted to NIH & NSF. (2003)

Publications

1. Betancourt, M. B. and Onuchic, J. N., Kinetics of protein-like models: The energy landscape factors that determine folding. *J. Chem. Phys.* **103**, 773–787 (1995).
2. Betancourt, M. B, Protein Folding Dynamics: Studies on Simple Lattice Models. Ph.D. Dissertation, University of California, San Diego, 1995.
3. Thirumalai, D. Klimov, D. K. and Betancourt, M. B., Exploring the folding mechanisms of proteins using lattice models. in *Monte Carlo approach to biopolymers and protein folding*, Grassberger, P., Barkema, G. T., and Nadler, W. (eds.), workshop at HLRZ, Forschungszentrum Jülich, Germany (World Scientific, Singapore 1997).
4. Betancourt, M. B., Smoothing the landscapes of protein folding: Insights from a minimal model. *J. Chem. Phys.* **109**, 1545–1554 (1998).
5. Klimov, D. K., Betancourt, M. B. and Thirumalai, D., Virtual atom representation of hydrogen bonds in minimal off-lattice models of α-helices: Effects on stability, cooperativity and kinetics. *Folding & Design* **3**, 481–496 (1998).
6. Betancourt, M. B. and Thirumalai, D., Pair potentials for protein folding: Choice of reference states and sensitivity of predicted native states to variations in the interaction schemes. *Prot. Sci.* **8**, 361–369 (1999).

7. Betancourt, M. B. and Thirumalai, D., Exploring the kinetic requirements for enhancement of protein folding rates in the GroEL cavity. *J. Mol. Biol.* **287**, 627–644 (1999).

8. Betancourt, M. B. and Skolnick, J., Finding the needle in a haystack: Educing native folds from ambiguous *ab initio* protein structure predictions. *J. Comput. Chem.* **22**, 339–353 (2001).

9. Kolinski, A., Betancourt, M. R., Kihara, D., Rotkiewicz, P., and Skolnick, J., Generalized Comparative Modeling (GENECOMP): a combination of Sequence comparison, threading, lattice and off-lattice modeling for protein structure prediction and refinement. *Proteins* **44**, 133–149 (2001)

10. Betancourt, M. B. and Skolnick, J., Universal similarity measure for comparing protein structures. *Biopolymers* **59**, 305–309 (2001).

11. Skolnick, J., Kolinski, A., Kihara, D., Betancourt, M., Rotkiewicz, P., and Boniecki, M., *Ab initio* protein structure prediction via a combination of threading, lattice folding, clustering, and structure refinement. *Proteins* **Suppl 5**, 149–156 (2001).

12. Betancourt, M. B. and Thirumalai, D., Protein sequence design by energy landscaping. *J. Phys. Chem. B* **106**, 599–609 (2002).

13. Betancourt, M. B. and Thirumalai, D., Designing fast-folding protein sequences by tuning the energy landscape. in *Recent Research Developments in Protein Folding, Stability and Design*, Michalel Gromiha, M., and Selvaraj, S., (eds.), (Research Signpost, Kerala, India 2002).

14. Betancourt, M. B., Reduced protein model with accurate native-structure identification ability. *Proteins*, **53**, – (2003).

15. Betancourt, M. B. and Skolnick, J., Higher correlations of backbone dihedral angles in proteins and related knowledge based potentials. (in preparation, 2003).

16. Betancourt, M. B., An efficient Monte Carlo method for off-lattice polypeptide folding simulations. (in preparation, 2003).

17. Betancourt, M. B. and Skolnick, J., A new Monte Carlo based gapped threading method. (in preparation, 2003).

18. Betancourt, M. B. and Skolnick, J., Extracting protein native structure information from unrelated structures by threading. (in preparation, 2003).

Letters of Reference Provided by:

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