

Curriculum Vitae

YANG ZHANG, Ph. D.

ADDRESS: Buffalo Center of Excellence in Bioinformatics
901 Washington St., Buffalo, NY 14203
Tel: 716-849-6716
Fax: 716-849-6747
Email: zhang6@buffalo.edu

DEGREES: Ph.D. in Physics, Institute of Physics,
Central China Normal University, Wuhan, China, 1996

EXPERIENCE:

- | | |
|------------------|--|
| 2002. 10 – now | Research Assistant Professor, Center of Excellence in Bioinformatics, University at Buffalo, Buffalo, NY |
| 2001.1 – 2002.9 | Postdoctoral research associate, Donald Danforth Plant Science Center, St. Louis, MO |
| 1999.1 – 2001.1 | Postdoctoral research associate, Institute of Theoretical Physics, Chinese Academy of Sciences, Beijing, China |
| 1996.8 – 1998.12 | Alexander von Humboldt research fellow, Physics Department, Free University Berlin, Berlin, Germany |

RESEARCH INTERESTS:

1. Structural bioinformatics (protein structure/function prediction and protein design)
2. Mechanical properties of biological macromolecules
3. Development of new Monte Carlo algorithms

REFEREED JOURNAL PUBLICATIONS:

1. H. Zhou and Y. Zhang. A hierarchical chain model of spider capture silk elasticity. *Phys. Rev. Lett.* 2004 (submitted).
2. Y. Zhang and J. Skolnick. Can protein structure prediction problem be solved using current PDB library? *Proc Natl Acad Sci USA* 2004 (in press).
3. Y. Zhang and J. Skolnick. A scoring function for the automated assessment of protein structure template quality. *Proteins* 2004 (in press).
4. Y. Zhang and J. Skolnick. Tertiary structure predictions on a comprehensive benchmark of medium to large size proteins. *Biophys. J* 2004; **87**:2647-2655.
5. W. Li, Y. Zhang, and J. Skolnick. Application of sparse NMR restraints to large-scale protein structure prediction. *Biophys J.* 2004; **87**: 1241-8.
6. Y. Zhang and J. Skolnick. Automated structure prediction of weakly homologous proteins on a genomic scale. *Proc Natl Acad Sci USA* 2004; **101**: 7594-9.
7. A. K. Arakaki, Y. Zhang, and J. Skolnick. Large-scale assessment of the utility of low resolution protein structures for biochemical assignment. *Bioinformatics* 2004; **20**:1087-96.
8. J. Skolnick, D. Kihara, and Y. Zhang. Development and testing of the PROSPECTOR 3.0 threading algorithm. *Proteins* 2004; **56**: 502-18.

9. Y. Zhang and J. Skolnick. SPICKER: A clustering approach to identify near-native protein folds. *J Comp Chem* 2004; **25**:865-71.
10. H. Zhou, Y. Zhang, and Z. Ouyang. On the elasticity of a single ssDNA/dsDNA molecule. *PRAMANA – J Phys* 2003; **61**:353-60.
11. Y. Zhang, A. Kolinski, and J. Skolnick. TOUCHSTONE II: A new approach to ab initio protein structure prediction. *Biophys J* 2003; **85**:1145-64.
12. W. Li, Y. Zhang, D. Kihara, Y. Huang, D. Zheng, G. Montelione, A. Kolinski, and J. Skolnick. TOUCHSTONEX: Protein structure prediction using sparse NMR data. *Proteins* 2003; **53**: 290-306.
13. Z. Ouyang, H. Zhou, and Y. Zhang. The elastic theory of a single DNA molecule. *Mod Phys Lett* 2003; **17**: 1-10.
14. Y. Zhang, D. Kihara, and J. Skolnick. Local energy landscape flattening: Parallel hyperbolic Monte Carlo sampling of protein folding. *Proteins* 2002; **48**: 192-201.
15. M. Dessinges, B. Maier, Y. Zhang, M. Peliti, D. Bensimon, and V. Croquette. Stretching single stranded DNA, a model polyelectrolyte. *Phys Rev Lett* 2002; **89**: 248102.
16. D. Kihara, Y. Zhang, H. Lu, A. Kolinski, and J. Skolnick. Ab initio protein structure prediction on a genomic scale: Application to the *Mycoplasma Genitalium* Genome. *Proc Natl Acad Sci USA* 2002; **99**: 5993-8.
17. H. Zhou, Y. Zhang, and Z. Ouyang. Elastic theories of single DNA molecules. *Physica* 2002; **A306**: 359-67.
18. Y. Zhang and J. Skolnick. Parallel-hat tempering: A Monte Carlo search scheme for the identification of low-energy structures. *J Chem Phys* 2001; **115**: 5027-32.
19. Y. Zhang, H. Zhou, and Z. Ouyang. Stretching single-stranded DNA: Interplay of electrostatic, base-pairing, and basepair stacking interactions. *Biophys J* 2001; **81**: 1133-43.
20. H. Zhou, and Y. Zhang. Pulling hairpinned polynucleotide chains: Does base-pair stacking interaction matter? *J Chem Phys* 2001; **114**: 8694-700.
21. H. Zhou, Y. Zhang, Z. Ouyang, X. Feng, S. Lindsay, P. Balagurumoorthy, and R. Harrington. Conformation and Rigidity of DNA Microcircles Containing wafI Response Element for p53 Regulatory Protein. *J Mol Biol* 2001; **306**: 225-36.
22. H. Zhou, Y. Zhang, and Z. Ouyang. Stretch-induced hairpin-coil transitions in designed polynucleotide chains. *Phys Rev Lett* 2001; **86**: 356-9.
23. Y. Zhang, H. Zhou, and Z. Ouyang. Monte Carlo implementation of supercoiled double-stranded DNA. *Biophys J* 2000; **78**: 1979-87.
24. H. Zhou, Y. Zhang, and Z. Ouyang. Elastic property of single double-stranded DNA molecules: Theoretical study and comparison with experiments. *Phys Rev* 2000; **E62**: 1045-58.
25. Y. Zhang. Approach to Monte Carlo calculation of the buckling of supercoiled DNA loops. *Phys Rev* 2000; **E62**: R5923-6.
26. C. Boros, T. Meng, R. Rittel, K. Tabelow, and Y. Zhang. Formation of color-singlet gluon cluster and inelastic diffractive scattering. *Phys Rev* 2000; **D61**: 094010.
27. H. Zhou, Y. Zhang, and Z. Ouyang. Bending and base-stacking interactions in double-stranded DNA. *Phys Rev Lett* 1999; **82**: 4560-3.
28. T. Meng, R. Rittel, and Y. Zhang. Inelastic diffraction and color-singlet gluon-clusters in high-energy hadron-hadron and lepton-hadron collisions. *Phys Rev Lett* 1999; **82**: 2044-7.
29. Y. Zhang. Characteristic plot of pomeron-exchange processes in diffractive DIS. *J Phys* 1999; **G25**: L63-9.

30. Y. Zhang. Factorial moment analysis in diffractive deep-inelastic ep scattering. Nucl Phys 1999; **B71**: 243-8.
31. Y. Zhang. Factorial moment analyses in diffractive lepton-nucleon scattering. Phys Rev 1998; **D57**: R1327-31.
32. Y. Zhang, Y. Deng, and L. Liu. On the restriction of transverse momentum conservation to the dynamic fluctuation in high energy collision. High Energy Phys Nucl Phys, 1997; **21**: 130-7.
33. L. Liu, Y. Zhang, and Y. Deng. On the influence of momentum conservation upon the scaling behaviour of factorial moments in high energy multiparticle productions. Z Phys 1997; **C73**: 535-9.
34. Y. Zhang and L. Liu. A quantitative criterion for anisotropic dynamic fluctuation in high energy collision. Science in China 1996; **A26**: 343-8.
35. Y. Zhang, Y. Wu, and L. Liu. The continuous scale behavior of random cascading model. High Energy Phys Nucl Phys 1996; **20**: 715-22.
36. H. Lin, Y. Zhang, and L. Liu. An analytical study of self-affine fractal in two-dimensional phase space of high energy collision. High Energy Phys Nucl Phys 1996; **20**: 65-75.
37. Y. Zhang, L. Liu, and Y. Wu. Levy stability for anisotropic dynamical fluctuation in high energy multiparticle production. Z Phys 1996; **C71**: 499-501.
38. L. Liu, Y. Zhang, and Y. Wu. On the random cascading model study of anomalous scaling in multiparticle production with continuously diminishing scale. Z Phys 1996; **C69**: 323-6.
39. Y. Zhang and L. Liu. On the bin-wise and strip integrals of density function in high energy multiparticle production. Z Phys 1995; **C68**: 463-5.
40. Y. Zhang, H. Lin, and L. Liu. Levy stability analysis of random cascade model. Comm Theo Phys 1995; **24**: 85-90.
41. Y. Wu, Y. Zhang, and L. Liu. Is there anomalous scaling in multiparticle final states of high energy collision?. Phys Rev 1995; **D51**: 6576-9.
42. H. Lin, Y. Zhang, and L. Liu. The refinement of Alpha-model and the analytical calculation of the Levy exponent. High Energy Phys Nucl Phys 1994; **18**: 858-64.
43. Y. Zhang, Y. Hu, Y. Wu, L. Liu, and Y. H. Zhang. On the intermittency and correlation integral of multiparticle final states in high energy collision. High Energy Phys Nucl Phys 1994; **18**: 621-9.
44. Y. Zhang and X. Cai. The cluster effect of the semi-inclusive single-particle rapidity distribution. High Energy Phys Nucl Phys 1994; **17**: 822-8.
45. Y. Zhang and L. Liu. The clustered production of final particles and forward-backward correlation in high energy p-p collision. High Energy Phys Nucl Phys 1994; **18**: 326-33.

BOOK CHAPTERS AND REVIEWS:

1. J. Skolnick, Y. Zhang, and A. Kolniski. Ab initio modeling. In: A. Edwards, M. Norin, and M. Sundstorm eds. Structural Proteomics. 2004, in press (Marcel Dekker Inc).
2. H. Zhou, Y. Zhang, and Z. Ouyang. In: M. Rieth and W. Schommers eds. Handbook of theoretical and computational nanotechnology. 2004, in press (American Scientific Publishers).
3. J. Skolnick, Y. Zhang. Protein structure prediction II. In: I. Rigoutsos and G. Stephanopoulos eds. System Biology. 2004, submitted (Springer-Verlag).

INVITED PRESENTATIONS:

1. J. Skolnick, Y. Zhang, A. K. Arakaki, A. Kolinski, M. Boniecki, A. Szilagyi, and D. Kihara. TOUCHSTONE: A unified approach to protein structure prediction. *Proteins* 2003; Suppl. **53**: 469-79.
2. Y. Zhang, H. Zhou, and Z. Ouyang. Theory of Stretching Individual Polynucleotide Molecule (Review). In: V. Sa-yakanit, L. Matsson, and H. Frauenfelder eds. *Proceeding of Biophysics 2000, Bangkok. 2000*; pp. 294-325 (World Scientific).
3. Y. Zhang. Fractality of pomeron-exchange processes in diffractive DIS. In: N. G. Antoniou et al eds. *Proceeding of 28th Int. Symp. on Multiparticle Dynamics, Delphi. 1998*; pp. 271-780 (World Scientific).
4. Y. Zhang. Intermittency phenomenon in diffractive deep-inelastic ep scattering. In: G. Pancheri et al eds. *Proceeding of 27th Int. Symp. on Multiparticle Dynamics, Rome 1997*; pp. 243-254 (World Scientific).

AWARDS:

1. Alexander von Humboldt Research Fellowship (1996-1998).
2. The First Prize of Excellent Doctoral Student in Center China Normal University (1996).

REFEREE FOR THE FOLLOWING JOURNALS:

1. Biopolymers
2. Polymer
3. Proteins
4. Biophysics Journal

REFERENCES:

1. Prof. Jeffrey Skolnick, Buffalo Center of Excellence in Bioinformatics
University at Buffalo
901 Washington St., Buffalo, NY 14203
Tel: 716-849-6711
Fax: 716-849-6747
Email: skolnick@buffalo.edu
2. Prof. Stuart Lindsay, Department of Physics and Astronomy
Arizona State University
Tempe, AZ 85287-1504
Tel: 480-965-4691
Fax: 480-965-7954
Email: stuart.Lindsay@asu.edu
3. Prof. Daniel Fischer, Buffalo Center of Excellence in Bioinformatics
University at Buffalo
901 Washington St., Buffalo, NY 14203
Tel: 716-849-6721
Fax: 716-849-6797
Email: dfischer@bioinformatics.buffalo.edu
4. Prof. Yaoqi Zhou, Department of Physiology & Biophysics
University at Buffalo
124 Sherman Hall, Buffalo, NY 14214
Tel: 716-829-2985
Fax: 716-829-2344
Email: yqzhou@buffalo.edu