

# Curriculum Vitae

## Ying Yin

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### EDUCATION

- **Ph.D Student** in Physics, August 2004 – present (expected graduation time: 2009),  
University of Illinois at Urbana-Champaign (UIUC), Urbana, Illinois, USA
- **M.S.** in Physics, January 2008,  
UIUC, Urbana, Illinois, USA
- **B.S.** in Physics, July 2003,  
Lanzhou University, Lanzhou, Gansu, China

### RESEARCH INTERESTS

Biological membranes; Membrane Proteins; Computational Modeling; Structural Biology; Cell Morphology; Diet and Nutrition; Application of nanotubes to medicine.

### ACADEMIC EXPERIENCE

- **Research Assistant**, Theoretical and Computational Biophysics Group, UIUC, May, 2005 – present  
Includes current Ph.D. research, Ph.D. and Masters level coursework and research projects.
- **Teaching Assistant**, Department of Physics, UIUC, Spring, 2007  
Assisted in a graduate level course Biomolecular Physics in the Physics Department. Shared responsibility for lectures, exams, homework assignments, and grades.
- **Research Assistant**, High Energy Physics, UIUC, August 2004 – May 2005  
Analyzed data for Upsilon particle production under Professor Jen-Chieh Peng.
- Author of VMD Tutorial, Myoglobin Case Study for the NIH Resource for Macromolecular Modeling and Bioinformatics.

PROFESSIONAL  
EXPERIENCE

- **Electrical Engineer and Project Manager**, SiemensVDO, Anhui, China, August 2003 – July 2004  
Responsible for transferring the production line of Electrical Exhaust Gas Regulator (EEGR) from Germany to China.

MEMBERSHIPS  
AND AWARDS

- Biophysical Society, Student member
- Honors Society of Phi Kappa Phi
- Excellent Graduate from Lanzhou University, 2003
- Chun-Tsung Scholar sponsored by the Nobel Prize winner Dr. T. D. Lee, 2002
- Baogang Scholar, 2002
- Lucent Global Science Scholar funded by the Lucent Technologies Foundation and managed by the Institute of International Education (IIE), 2001

PUBLICATIONS  
\* – denotes  
equal  
contributions.

1. **Y. Yin\***, A. Arkhipov\*, and K. Schulten. 2008. Membrane tubulation by lattices of amphiphysin BAR domains. Submitted.
2. P. L. Freddolino, A. Arkhipov, A. Y. Shih, **Y. Yin**, Z. Chen, and K. Schulten. 2008. Application of residue-based and shape-based coarse graining to biomolecular simulations. In G. A. Voth, editor, *Coarse-Graining of Condensed Phase and Biomolecular Systems*. Chapman and Hall/CRC Press, Taylor and Francis Group. In press.
3. J. Hsin, A. Arkhipov, **Y. Yin**, J. E. Stone, and K. Schulten. 2008. Using VMD - an introductory tutorial. *Current Protocols - Bioinformatics*. In press.
4. A. Arkhipov\*, **Y. Yin\***, and K. Schulten. 2008. Four-scale description of membrane sculpting by BAR domains. *Biophysical Journal*. 95:2806–2821.
5. A. Aksimentiev, R. Brunner, J. Cohen, J. Comer, E. Cruz-Chu, D. Hardy, A. Rajan, A. Shih, G. Sigalov, **Y. Yin**, and K. Schulten. 2008. Computer modeling in biotechnology, a partner in development. In *Protocols in Nanos-structure Design*, Methods in Molecular Biology. Humana Press, pages 181–234.
6. L. Y. Zhu, P. E. Reimer, B. A. Mueller, T. C. Awes, M. L. Brooks, C. N. Brown, J. D. Bush, T. A. Carey, T. H. Chang, W. E. Cooper, C. A. Gagliardi, G. T. Garvey, D. F. Geesaman, E. A. Hawker, X. C. He, D. E. Howell, L. D. Isenhower, D. M. Kaplan, S. B. Kaufman, S. A. Klinksiek, D. D. Koetke, D. M. Lee, W. M. Lee, M. J. Leitch, N. Makins, P. L. McGaughey, J. M. Moss, P. M. Nord, V. Papavassiliou, B. K. Park, G. Petitt, J. C. Peng, M. E. Sadler, W. E. Sondheim, P. W. Stankus, T. N. Thompson, R. S. Towell, R. E. Tribble, M. A. Vasiliev, J. C. Webb, J. L. Willis, P. Winter, D. K. Wise, **Y. Yin** and G. R.

Yong. 2008 Measurement of upsilon production for p+p and p+d interactions at 800 gev/c. *Physical Review Letters*. 100:062301.

7. M. Ø. Jensen, **Y. Yin**, E. Tajkhorshid, and K. Schulten. 2007. Sugar transport across lactose permease probed by steered molecular dynamics. *Biophysical Journal*. 93:92–102.
8. **Y. Yin**, M. Ø. Jensen, E. Tajkhorshid, and K. Schulten. 2006. Sugar binding and protein conformational changes in lactose permease. *Biophysical Journal*. 91:3972–3985.

CONFERENCE  
PRESENTATIONS

1. Membrane Tubulation by BAR domains,  
6th Annual Biophysics and Computational Biology Symposium, 2008, Beckman Institute, Urbana, IL
2. Multiscale Simulations of Membrane Tubulation by BAR domains,  
Biophysical Society Annual Meeting, 2008, Long Beach
3. Sugar Transport Across Lactose Permease Probed by Molecular Dynamics Simulations,  
Biophysical Society Annual Meeting, 2007, Baltimore, MD
4. Accurate and Efficient Modeling for Carbon Nanotube in Biological Applications,  
First Annual Frontier of Theoretical Chemistry Symposium, 2006, Urbana, IL
5. The Mechanism of Sugar Transport Across *E. coli* Lactose Permease,  
Biophysical Society Annual Meeting, 2006, Salt Lake City, UT
6. Coupling of Proton Translocation and Protein Conformational Changes in Lactose Permease,  
Biophysical Society Annual Meeting, 2006, Salt Lake City, UT

RESEARCH AC-  
COMPLISHMENTS

- **BAR Domain Proteins Sculpting Cellular Membranes** with Anton Arkhipov and Klaus Schulten. Living cells are characterized by intricately curved internal membranes forming organelles. The membrane curvature is sculpted by proteins that act through concerted action. A key sculpting mechanism is furnished by proteins, so-called BAR domains, that form lattice-like scaffolds adhering to membrane surfaces. We have investigated the membrane sculpting by BAR domains at different levels of resolutions (from an atomic to a continuum level). These studies have resulted in a coarse-graining (CG) model, which allowed us to reach time scales of 100  $\mu$ s-1 ms. Using this CG model, we have sampled various lattices of BAR domains and observed complete membrane tubulation.

- **Coarse-Graining Methods for Biomolecular simulations** with Anton Arkhipov and Klaus Schulten. One of the main unresolved problems in biological science is the time-scale and length-scale gap between computational and experimental methods of studying biological systems. This project is aimed to bridge computational studies with experimental techniques by developing coarse-graining (CG) method, which represents a system by a reduced (in comparison with an all-atom description) number of degrees of freedom. We have developed such a CG method that leads to an increase of orders of magnitude in the simulated time and length scales. This method has been applied successfully to a variety of systems including BAR domain-membrane system.
- **Conformational Changes in Lactose Permease** with Morten Jensen, Emad Tajkhorshid and Klaus Schulten. Lactose permease (LacY) is a membrane protein that translocates the sugar, lactose, across cell's membrane utilizing an electrical potential maintained in the form of a trans-membrane proton gradient. We have investigated one step of the proton-sugar translocation, namely, how binding and unbinding of the proton activates a spring-like bond, a so-called salt bridge, that closes and opens the inner channel exit of the protein. We have also probed the molecular and energetic details of lactose translocation across LacY. During translocation, lactose was found to undergo a rotation and to induce a widening of the narrowest part of the protein's channel.
- **Modeling Carbon Nanotube-Biomolecular Assemblies** with Klaus Schulten *et al.* Carbon nanotubes (CNTs) are hexagonal lattices of carbon atoms rolled up into seamless cylinders. Due to their unique electronic, thermal, chemical, and mechanical properties, they are of great interest for many nanotechnological applications such as biosensors to detect various biomolecules. We have been developing computational methodologies for simulating CNT in complex with biomolecules.
- **Measurement of Upsilon Particle Production** with Jen-Chieh Peng *et al.* The Upsilon particle is a meson formed by a bottom quark and its antiparticle. Here, we measured the Upsilon production for proton+proton and proton+deuterium interactions at 800 GeV/c. The results indicate that the gluon distributions in proton and neutron are very similar.

COMPUTER  
SKILLS

- Molecular Dynamics Simulations packages: VMD, NAMD.
- Computer Languages: C/C++, Tcl, HTML, Microsoft Office; some use of Unix shell scripts.
- Operating Systems: Unix/Linux, MacOSX, Windows.

## REFERENCES

- Dr. Klaus Schulten (Ph.D advisor)  
Swanlund Professor of Physics  
Director, NIH Resource for Biomolecular Modeling and Bioinformatics  
University of Illinois at Urbana-Champaign  
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- Dr. Jen-Chieh Peng  
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- Dr. Emad Tajkhorshid  
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