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PROFESSIONAL EXPERIENCE

2005-present Member, Brookhaven National Laboratory, Computational Science Center
2005-present Adjunct Associate Professor, Dept. of Applied Mathematics and Statistics, SUNY Stony Brook
2004-present Associate Professor, Dept. of Chemistry, SUNY Stony Brook
2004-present Member, Institute for Chemical Biology and Drug Discovery, SUNY Stony Brook
2001-present Member, Graduate Program in Pharmacological Sciences, SUNY Stony Brook
2001-present Member, Graduate Program in Biochemistry and Structural Biology, SUNY Stony Brook
2000-present Member, Graduate Program in Molecular and Cellular Biology, SUNY Stony Brook
1998-2004 Assistant Professor, Dept. of Chemistry, SUNY Stony Brook
1998-present Member, Center for Structural Biology, SUNY Stony Brook

EDUCATION

1994-1998 Postdoctoral Researcher, University of California, San Francisco, Dept. of Pharmaceutical Chemistry
1994 Ph.D., University of Illinois at Chicago, Dept. of Chemistry
1991 B.A., University of Illinois at Chicago, Dept. of Chemistry

AWARDS

2007 Itanium Solutions Alliance, top award in "Humanitarian Impact Innovation"
2003 SUNY Chancellor's Award "Excellence in the Pursuit of Knowledge"
2001 Research Corporation Cottrell Scholar
2000 AMDeC Tartikoff/Perelman/EIF Young Investigator in Women's Cancers

POSITIONS HELD

2007-present Director of Computational Biology, Institute for Chemical Biology and Drug Discovery, Stony Brook University
2006-present Councilor, American Chemical Society, Division of Computers in Chemistry (COMP)
2006-present Member, NIH study section Macromolecular Structure and Function (MSF-D)
2005-present Section Editor, American Chemical Society "Annual Report in Computational Chemistry"
2001-2005 Member, NSF "National Resource Allocations Committee"

RESEARCH INTERESTS

Application of computational tools to the study of the structure and dynamics of molecules involved in biological processes. Specific areas include 1) the development of new algorithms, programs and parameters to carry out and analyze efficient simulations, with emphasis on conformational sampling; 2) application of these tools to the prediction of structure and dynamics when experimental data is limited or unavailable; and 3) determination of factors (at an atomic level) that result in these structures, and use of that information to gain new insights into function and guide the design of novel molecules.

TEACHING EXPERIENCE

General Chemistry, Introductory General Chemistry, General Chemistry Lab, Honors General Chemistry Lab, Physical Chemistry, Physical Chemistry for Life Sciences, Theoretical Chemistry, Computational Structural Biology, Advanced Structural Biology, Principles of Pharmacology

SOFTWARE DEVELOPMENT

Author of molecular visualization program "MOIL-View", with over 200 registered research installation sites; see <http://morita.chem.sunysb.edu/mlv.html>.

One of five core development team members for the Amber molecular simulation program. Amber9 was released in April 2006 and has over 500 licensed users. See <http://amber.scripps.edu>

Development team member for the MOIL molecular simulation program, see <http://www.tc.cornell.edu/reports/NIH/resource/CompBiologyTools/moil/>

RECENT PUBLICATIONS

Song, K., Hornak, V., de los Santos, C., Grollman, A. and Simmerling, C., "Molecular Mechanics Parameters for the FapydG DNA lesion", *J. Comput. Chem.*, in press

Wickstrom, L., Bi, Y., Hornak, V., Raleigh, D. and Simmerling, C., "Reconciling the Solution and X-ray Structures of the Villin Headpiece Helical Subdomain: Molecular Dynamics Simulations and Double Mutant Cycles Reveal a Stabilizing Cation-Pi Interaction", *Biochemistry*, 46:3624-3634 (2007) (listed as "Hot Article" by *Biochemistry*)

Roitberg, A., Okur, A. and Simmerling, C., "Coupling of Replica Exchange Simulations to a non-Boltzmann structure reservoir", *J. Phys. Chem. B*, 111:2415-2418 (2007)

Roe, D., Okur, A., Wickstrom, L., Hornak, V. and Simmerling, C., "Secondary Structure Bias in Generalized Born Solvent Models: Comparison of Conformational Ensembles and Free Energy of Solvent Polarization from Explicit and Implicit Solvation", *J. Phys. Chem. B*, 111:1846-1857 (2007)

Hornak, V. and Simmerling, C., "Targeting structural flexibility in HIV-1 protease inhibitor binding", *Drug Discovery Today*, 12:132-138 (2007)

Okur, A., Roe, D., Cui, G., Hornak, V. and Simmerling, C., "Improving Convergence of Replica Exchange Simulations through Coupling to a High Temperature Structure Reservoir", *J. Chem. Theory & Comput.*, 111:1846-1857 (2007)

Mongan, J., Simmerling, C., McCammon, J. A., Case, D. and Onufriev, A., Generalized Born model with a simple, robust molecular volume correction, *J. Chem. Theory & Comput.*, 3:156-169 (2007)

Hornak, V.; Okur, A., Rizzo, R. and Simmerling, C., "HIV-1 protease flaps spontaneously open and reclose in molecular dynamics simulations", *Proc. Nat. Acad. Sci. USA*, 103:915-920 (2006).

Hornak, V.; Okur, A., Rizzo, R. and Simmerling, C., "HIV-1 Protease Flaps Spontaneously Close to the Correct Structure in Simulations Following Manual Placement of an Inhibitor into the Open State", *J. Am. Chem. Soc.*, 128: 2812 (2006).

Simmerling, C. and Gomperts, R., "Simulating HIV-1 Protease at its Most Vulnerable Instant", *Scientific Computing*, 7:32-34, 2006.

- Layten, M., Hornak, V. and Simmerling, C., The open structure of a multi drug resistant HIV-1 protease is stabilized by crystal packing contacts, *J. Am. Chem. Soc.*, 128: 13360-13361 (2006)
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- Wickstrom, L., Okur, A., Song, K., Hornak, V., Raleigh, D. and Simmerling, C., "The Unfolded State of the Villin Headpiece Helical Subdomain: Computational Studies of the Role of Locally Stabilized Structure", *J. Mol. Biol.*, 360:1094-1107 (2006).
- Song, K., Hornak, V., de los Santos, C., Grollman, A. and Simmerling, C., Computational analysis of the binding mode of 8-oxo-guanine to formamidopyrimidine-DNA glycosylase, *Biochemistry*, 45:10886-10894 (2006)
- Rafi, S., Cui, G., Song, K., Cheng, X., Tonge, P. and Simmerling, C., "Insight through MM-PBSA Calculations into the Binding Affinity of Triclosan and Three Analogs for FabI, the E. Coli Enoyl Reductase", *J. Med. Chem.*, 49:4574-4580 (2006).
- Hornak, V., Abel, R., Okur, A., Strockbine, B., Roitberg, A. and Simmerling, C., "Comparison of multiple Amber force fields and development of improved protein backbone parameters", *Proteins: Structure, Function and Genetics*, 3:712-725 (2006).
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- Kelso, C. and Simmerling, C., "Enhanced Sampling Methods for Simulation of Nucleic Acids", in *Computational Studies of DNA and RNA*, J. Sponer and F. Lankas (Editors), Springer Publishers, 147-168 (2006).
- Okur, A. and Simmerling, C., "Hybrid Explicit/Implicit Solvation Methods", *Annual Reports in Computational Chemistry*, 2:97-109 (2006).
- Roe, D., Hornak, V. and Simmerling, C., "Folding Cooperativity in a Three-stranded β -sheet Model", *J. Mol. Biol.*, 352, 370-281 (2005)
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- Cheng, X., Cui, G., Hornak, V. and Simmerling, C., "*Modified Replica Exchange Simulation Methods for Local Structure Refinement*". *J. Phys. Chem. B*, 109, 8220-8230 2005
- Cheng, X., Hornak, V. and Simmerling, C., "*Improved Conformational Sampling through an Efficient Combination of Mean-Field Simulation Approaches*". *J. Phys. Chem.*, 108:426, 2004
- Hornak, V. and Simmerling, C., "*Development of Softcore Potential Functions for Overcoming Steric Barriers in MD*", *J. Mol. Graphics & Modeling*, 22: 403, 2004

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- Roitberg, A. and Simmerling, C., “*Foreword*”, *J. Mol. Graphics & Modeling*, 22:317, 2004
- Okur, A., Strockbine, B., Hornak, V. and Simmerling, C., ‘*Using PC Clusters to Evaluate the Transferability of Molecular Mechanics Force Fields for Proteins*’, *J. Comput. Chem.*, 24:21, 2003.
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- Simmerling, C., Elber, R. and Zhang, J., ‘*MOIL-View: A Program for Visualization of Structure and Dynamics of Biomolecules and STO: a Program for Computing Stochastic Paths*’, in Modeling of Biomolecular Structures and Mechanisms, A. Pullman et al. (eds.) Kluwer Acad. Publishers, Netherlands (1995)
- Simmerling, C. and Elber, R., ‘*Computer Determination of Peptide Conformations in Water: Different Roads to Structure*’, *Proc. Nat. Acad. Sci. USA*, 92:3190 (1995)
- Simmerling, C. and Elber, R., ‘*Hydrophobic “Collapse” in a Cyclic Hexapeptide: Computer Simulations of CHDLFC and CAAAAC in Water*’, *J. Am. Chem. Soc.*, 16:2534 (1994)
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Calculations in Large Biological Molecules' in Statistical Mechanics, Protein Structure and Protein-Substrate Interactions, S Doniach (ed.), Plenum Press, NY (1994)

RESEARCH SUPPORT

Current

“Computational studies of model systems for protein unfolded states”

Principal Investigator: Carlos L Simmerling

Agency: NIH R01 GM61678

Period: 4/1/06-3/31/10

This project involves the ongoing development and validation of protein force field parameters, development of a new conformational sampling simulation methodology, and generation of conformational ensembles for several small model peptides and protein fragments. Mutational studies will be used to investigate the factors that drive folding and the role of residual structure in the unfolded state.

“Molecular Pharmacology of Oxidative DNA Damage: Structure and Energetics”

Principal Investigator: Arthur P Grollman (CS co-investigator, 50% budget)

Agency: NIH R01 CA017395

Period: 4/1/07-3/31/11

This project involves a collaborative computational/experimental effort to gain new insight into how glycosylases recognize and repair oxidatively damaged DNA.

“Computer Simulations of Biomolecular Structure and Dynamics”

Principal Investigator: Carlos L Simmerling

Agency: NSF PACI-MCA02N028 (supercomputer resources, 6 million Itanium CPU hours)

Period: 4/1/2007-3/31/2008

This provides supercomputer time in support of all projects in the Simmerling lab. The allocation is renewed each year. In 2006, our group was the 11th largest user of cycles at the NSF-funded national supercomputer centers.

“Research and Engineering Apprenticeship Program”

Principal Investigator: Carlos L Simmerling

Agency: Academy of Applied Sciences

Period: 7/1/06-6/31/07

This project provides summer support for 3 high school students.

Pending

“AMBER force field consortium: a coherent biomolecular simulation platform”

Principal Investigator: Yong Duan, UC Davis (CS co-investigator, 20% budget)

Agency: NIH

Period: 4/1/07-3/31/11

This project involves a collaborative effort to improve the energy functions that are used for biomolecular simulation.

“Efficient Methods for Generation of Equilibrium Ensembles in the Condensed Phase”

Principal Investigator: Carlos Simmerling

Agency: NSF

Period: 6/15/07-6/14/10

This project involves the development of new algorithms for simulations of biomolecular structure.

“Multiprocessor SGI Altix Computer”

Principal Investigator: Carlos L Simmerling

Agency: NIH

Period: 4/1/2008-3/31/2009

This is a proposal to the NIH shared instrumentation program for a large multiprocessor computer.

Completed

“Enhanced Mean-Field Simulations of Antibody CDR Loops”

Principal Investigator: Carlos L Simmerling

Agency: NIH GM61678

Period: 4/1/06-3/31/10

“Research and Engineering Apprenticeship Program”

Principal Investigator: Carlos L Simmerling

Agency: Academy of Applied Sciences

Period: 7/1/05-6/31/06 (*also multiple previous years, this is an annual grant*)

This project involves summer research programs for high school students and typically supports 3 students and their expenses.

“Computer Simulations of Biomolecular Structure and Dynamics”

Principal Investigator: Carlos L Simmerling

Agency: NSF PACI-MCA02N028 (supercomputer resources)

Period: *each of the past 5 years, this is an annual grant*

This project involves the development of biomolecular simulation methods and the application of simulations to study protein folding and formation of complexes between proteins, small molecules and nucleic acids.

“*Computer Simulations of Biomolecular Structure and Dynamics*”

Principal Investigator: Carlos L Simmerling

Agency: Research Corporation

Period: 4/1/2006-3/31/2007

This project involves the development of *biomolecular simulation methods and the application of simulations to study protein folding and formation of complexes between proteins, small molecules and nucleic acids.*

“*Young Investigator in Women’s Cancer*”

Principal Investigator: Carlos L Simmerling

Agency: AMDeC Foundation

Period: 4/1/2006-3/31/2007

This project involves the development of *biomolecular simulation methods and the application of simulations to study protein folding and formation of complexes between proteins, small molecules and nucleic acids.*