CARLOS SIMMERLING, PH.D.

Laufer Center for Physical & Quantitative Biology Department of Chemistry Stony Brook University Stony Brook, NY 11794-3400

Phone: (631) 632-5424 E-mail: carlos.simmerling@stonybrook.edu Web: www.simmerlinglab.org

PROFESSIONAL EXPERIENCE

2018-present	Marsha Laufer Endowed Professor of Physical and Quantitative Biology
2015-present	Affiliated Faculty Member, SBU Institute for Advanced Computational
	Science
2010-present	Associate Director, Laufer Center for Physical and Quantitative Biology
2008-present	Professor, Department of Chemistry, Stony Brook University (SBU)
2006-present	Member, Graduate Program in Bioengineering, SBU
2005-present	Affiliated Faculty Member, Dept. of Applied Mathematics and Statistics, SBU
2005-present	Member, Brookhaven National Laboratory, Computational Science Center
2004-2008	Associate Professor, Department of Chemistry, SBU
2004-present	Member, Institute for Chemical Biology and Drug Discovery, SBU
2001-present	Member, Graduate Program in Pharmacological Sciences, SBU
2001-present	Member, Graduate Program in Biochemistry and Structural Biology, SBU
2000-present	Member, Graduate Program in Molecular and Cellular Biology, SBU
1998-2004	Assistant Professor, Department of Chemistry, SBU
1998-present	Member, Center for Structural Biology, SBU

EDUCATION

1994-1998	Postdoctoral Researcher, University of California, San Francisco, Dept. of
	Pharmaceutical Chemistry (with Peter Kollman)
1994	Ph.D., University of Illinois at Chicago, Dept. of Chemistry (with Ron Elber)
1991	B.A., University of Illinois at Chicago, Dept. of Chemistry

HONORS AND AWARDS

2021	Gordon Bell Special Prize for COVID-19
2021	SUNY Chancellor's Award for Excellence in Scholarship and Creative Activities
2016	Fellow, American Chemical Society
2007	"Humanitarian Impact Innovation Prize", Itanium Solutions Alliance (a coalition of
	Microsoft, Intel, HP, Oracle and other technology industry leaders)
2004/05/07/08/09	Outstanding Mentor, Siemens Foundation
2003	"Excellence in the Pursuit of Knowledge", SUNY Chancellor's Award
2001	Cottrell Scholar, Research Corporation for Science Advancement
2000	"Young Investigator in Women's Cancers", Academic Medicine Development Corp

POSITIONS HELD

2019-present	Academic Advisory Board member, Open Force Field Initiative
2019-present	MOLSSI Associate, The Molecular Sciences Software Institute
2014-present	Chair, Investigator Conflict of Interest Committee, SBU (member since 2006)
2011-present	Editorial board member, Reports in Theoretical Chemistry
2010-2014	NSF Scientific Advisory Board for Teragrid Supercomputing
2007-2012	Director of Computational Biology, Institute for Chemical Biology and Drug
	Discovery, SBU
2007-2014	Advisory Board Member, New York Center for Computational Science
2007-2012	Councilor, American Chemical Society, Division of Computers in Chemistry (COMP)

- 2006-present Executive Committee Member, American Chemical Society, Division of Computers in Chemistry (COMP)
- 2005-2011 Section Editor, American Chemical Society "Annual Report in Computational Chemistry"

RESEARCH SUMMARY

Professor Simmerling's research interests focus on the dynamic aspects of biomolecular function, and how conformational changes affect important processes such as protein folding, molecular recognition and enzymatic function. Specific applications of interest are the role of dynamics in drug resistance, recognition/repair of DNA damage, and the nature of the unfolded/disordered state of peptides and proteins. Most of his recent publications on biological systems have been co-authored with experimental collaborators, with a significant focus on integration of computation and experiment.

The biomolecular simulation field remains immature and thus improvement of methods and models is also a focus of the Simmerling lab. Prof. Simmerling has a long history of development and application of a variety of simulation methods, and is currently one of six members of the leadership team for the widely used Amber molecular simulation program (installed at over 12,000 sites, with over 10,000 site licenses; http://www.ambermd.org).

The accuracy of molecular simulations is crucially dependent on the physics model (the "force field") used to describe energies. Simmerling has been an international leader in protein force field development for over a decade. The Simmerling lab's ff99SB Amber force field set a new standard for protein model accuracy, with an impact extending well beyond Amber; it is available in every modern MD package and has been cited independently of Amber over 5,000 times. The force field served as a foundation for other groups' subsequent adaptation and adjustment, which have collectively received thousands of additional citations. Simmerling's follow up models ff12SB and ff14SB further improved accuracy, and have received over 2,000 citations, and the newest model, ff19SB, was recently released. The Simmerling lab also develops the primary implicit water models for Amber, with 5 articles each having >100 citations independent of Amber.

ENCOURAGING DIVERSITY AND EARLY ENGAGEMENT OF STEM STUDENTS IN RESEARCH

Prof. Simmerling is deeply committed to encouraging diversity in STEM, with 8 female of 25 total PhDs, and 3 female of 6 total postdocs. Four of 6 current PhD candidates in the lab are URM and/or female. Two URM graduate students have obtained NIH F31 NRSA fellowships. Undergraduates represent a significant part of Simmerling's research group (61 total; 58% female, 23% URM); 9 of 10 current lab undergrads are URM and/or female. Most go on to MD or PhD programs; our two 2021 graduates (both female/URM) went to PhD programs at Yale and U Chicago. Two undergraduate mentees received "Minority Access to Research Careers" (MARC) fellowships, one a 2014 HHMI EXROP award, and one captained the team that won the Student Cluster Challenge at the 2009 Supercomputing Conference. Simmerling also recruits and mentors local high school students (47 total; 38% female, 9% minority), including 8 Intel Science Talent Search (STS) and 9 Siemens Competition semi-finalists, 4 Intel STS national finalists, winner of the Best in Category Award (Biochemistry/Biology) at the 2010 International Science & Engineering Fair. a 2008 Davidson Fellow Laureate (\$50,000), and winner of the 2009 national first-prize award in the Siemens Competition (\$100,000). In the past 5 years, 6 high school and undergraduate students were co-authors on 6 peer-reviewed publications, and 4 more are co-authors on manuscripts under review. Simmerling has received the Siemens Foundation "Outstanding Mentor" award 5 times, and his efforts were described in the 2012 Newsday article "The Mentor Experiment", and the 2013 New York Times article "A Laboratory Grows Young Scientists".

POSTDOCTORAL FELLOWS MENTORED AND CURRENT POSITIONS (6 TOTAL)

Name	Program	Торіс	Date
Hornak, Viktor	Chemistry	New Methods for Biomolecular Simulations	1999-2000

	Investigator III,	Novartis Institutes for Biomedical Research		
Song, Kun	Chemistry	Recognition of DNA Damage	2007-2008	
	Computational	Chemist, AstraZeneca		
Fu, Lin	Pharmacology	Recognition of DNA Damage	2009-2011	
	Wenzhou Medi	cal University		
Pias, Sally	Chemistry	Simulation Methods for Drug Resistance	2009-2011	
	Associate Profe	essor, New Mexico Tech Department of Chemis	try	
Carvalho, Alexandra	Chemistry	DNA Scanning by Repair Enzymes	2010-2013	
	Assistant Investigator, University of Coimbra, CNC-Center for Neuroscience			
	and Cell Biolog	у		
Miguez, Angela	Chemistry	Proofreading Mechanism of DNA Polymerase	2015-2017	
	Assistant Profe	ssor, SUNY Oneonta		

GRADUATE STUDENTS MENTORED AND CURRENT POSITIONS (29 TOTAL)

Name	Program	Торіс	Degree/Date
Cui, Guanglei	Chemistry	New methods for biomolecular simulations	PhD, 2003
	Computationa	al Chemist, GlaxoSmithKline Pharmaceuticals	
Cheng, Xiaolin	Chemistry	Simulations of modified DNA	PhD, 2004
0,	Associate Pro	fessor, College of Pharmacy, The Ohio State L	Iniversity
Strockbine, Bentley		ySimulating folding of small proteins	PhD, 2006
· · ·	Forensic Psyc		
Geney, Raphael	Chemistry	Structure-based drug design of paclitaxel	PhD, 2005
	Patent Associ	iate, Galapagos	
Okur, Asim	Chemistry	New methods for biomolecular simulations	PhD, 2006
,		rmation Officer, National Institute of Mental Hea	,
Song, Kun	Chemistry	Enzyme ecognition of DNA damage	PhD, 2007
0,		al Chemist, AstraZeneca	,
Roe, Daniel	Chemistry	Improved solvation models for simulations	PhD, 2007
,		t, National Institutes of Health	,
Rafi, Salma	Chemistry	Structure and inhibition of enoyl reductase	PhD, 2008
,		ntist at Schrödinger	,
Wickstrom, Lauren	Chemistry	Comparison of simulation and NMR data	PhD, 2009
,		ofessor, Borough of Manhattan Community Colle	
Ding, Fangyu		Simulations of HIV-1 protease mutants	PhD, 2010
5, 5,	unknown	·	,
Campbell, Arthur	Chemistry	Structure and dynamics of crosslinked DNA	PhD, 2011
- ,	,	r, Senior Computational Chemist I at Broad Inst	,
Bergonzo, Christina	Chemistry	Enzyme recognition of DNA damage	PhD, 2012
9		emist, National Institutes of Standards & Technol	,
Shang, Yi	Chemistry	Dynamics of drug resistant HIV-1 protease	PhD, 2013
0,		n School of Medicine at Mt. Sinai	,
Carr, Amber	Chemistry	Self-guided MD simulation methods	PhD, 2013
-)		ow, Duke University	,
Martinez, Carmenza	Chemistry	Improving protein force fields	PhD, 2013
,	unknown		,
Lai, Cheng-Tsung		Rational design of slow-binding inhibitors	PhD, 2014
,		Fellow, Northwestern University	· ··-, -• · ·
Li, Haoquan	Chemistry	Enzyme recognition of DNA damage	PhD, 2014
		elopment Engineer II at Amazon Drive	,
Nguyen, Hai	Chemistry	Improved implicit solvent for biopolymers	PhD, 2015
JJ,		ist II, Schrödinger	,
Maier, James		Improved protein side chain force field	PhD, 2015

Data Scientist,	, Viasat Inc.	
Chemistry	Recognition of DNA by transcription factors	PhD, 2016
Senior Scienti	st, Vir Biotechnology Inc	
Chemistry	New methods for nonpolar solvation	PhD, 2018
Postdoctoral S	Scholar at Tufts University	
Chemistry	Application of alchemical free energy methods	PhD, 2019
Senior Scientia	st, Xtalpi Inc.	
Chemistry	Improved protein backbone force field	PhD, 2019
Research Scie	entist, Eli Lilly	
Chemistry	Using structure reservoirs to speed sampling	PhD, 2020
Principal Scier	ntist at Schrödinger	
Chemistry	Conformational studies of retroviral proteases	PhD, 2021
Project Modeli	ing Investigator, Roivant Sciences	
Mol Cell Bio	Improved methods for simulations of RNA	PhD, 2020
Chemistry	Simulations of phosphorylated proteins	PhD, 2022 (est)
Chemistry	•	PhD, 2022 (est)
Chemistry	More accurate protein implicit solvent models	PhD, 2024 (est)
Applied Mathe	matics Modeling the SARS-CoV-2 Spike	PhD, 2025 (est)
	Chemistry Senior Scienti Chemistry Postdoctoral S Chemistry Senior Scienti Chemistry Research Scien Chemistry Principal Scien Chemistry Project Modeli Mol Cell Bio Chemistry Chemistry Chemistry	Senior Scientist, Vir Biotechnology IncChemistryNew methods for nonpolar solvationPostdoctoral Scholar at Tufts UniversityChemistryApplication of alchemical free energy methodsSenior Scientist, Xtalpi Inc.ChemistryImproved protein backbone force fieldResearch Scientist, Eli LillyChemistryUsing structure reservoirs to speed samplingPrincipal Scientist at SchrödingerChemistryConformational studies of retroviral proteasesProject Modeling Investigator, Roivant SciencesMol Cell BioImproved methods for simulations of RNAChemistrySimulations of phosphorylated proteinsChemistryProofreading mechanism of DNA polymerase

UNDERGRADUATE STUDENTS MENTORED IN RESEARCH (60 TOTAL)

Padma Kandadai (1999), Thomas Canseco (1999-2000), Ruth Li (1999), William Olivo (1999), Hitomi Oda (1999), My Tu (2001-2002), Brock Adams (2002), Mfon Akpan (2001), Kinning Poon (2002), Patrice Leahy (2003), Kerri Goldgraben (2003), Jing Moy (2003), Noel Carascal (2003 - 2004), Isaac Pflaum (2004), Eric Absgarten (2006-2007), Lester Leong (2006-2007), Marie Majkut (2007), Richard Yao (2007-2008), Dan Talmasov (2007-2008), Aaron Pellman-Isaacs (2008-2009), Dan Martingano (2008-2011), Catherine Kelso (2008), Michael Sperandeo (2008), Henry Lederer (2008), James Maier (2008-2009), Yinglin Gao (2008-2009), Nora Asamoah (2008-2010), Paraskevas Xenophontos (2009-2010), Esther Shin (2009-2010), Jon McGinn (2009), Ben Sherman (2010), Lukas Klees (2010), Neville Bethel (2009-2013), Sherry Bermeo (2012-2015), James Alrassi (2014), Victoria Perrone (2014-2017), Emily Liu (2014-2015), Bernard Essuman (2014, 2019-presen), Dillon Higginson (2015), Gabriela Witek (2015-2017), Rebecca Chang (2017), Grace Manalo (2017), Jorge Pincay (2017-2020), Kelley Chiu (2018-present), Jackelyne Garcia Cruz (2018-2019), Christian Arty (2018), Jose Guerra (2019-2021), Abbigayle Cuomo (2019-2021), Juliana Pham (2019-2021), Stephanie Helbock (2020-present), Isabel Yang (2020-2021), Stephanie Budhan (2020-present), Sarah Varghese (2020-present), Sarah Jacobson (2020-2021), Michelle Twan (2020-2021), Samer Mahmoud (2021-present), Sarah Gunasekera (2021-present), Isra Ahmed (2021-present), Sharena Brown (2021-present), Kezia Kelley (2021)

HIGH SCHOOL STUDENTS MENTORED IN RESEARCH (46 TOTAL)

Michael Lee (1999), Kristen Regan (2000), Asad Sheth (2000), Dan Noe (2000-2001), Max Bernstein (2001), Jason Barell (2002), Kevin Wang (2003, 2004), Zack Goldberg (2003), Jillian Cypser (2003), David Rosenman (2004), Catherine Kelso (2004-2007), Julian Hershowitz (2004,2005), Oleksandr Dagayev (2005-2006), Rachel Orifici (2005), Alex Iyer (2005), Stephanie Clemente (2006), Karthik Kasaraneni (2006), Tom Petracca (2006), Zuha Qazi (2006), Jaime Campos (2007), Christine Shrock (2007-2009), Viraj Shah (2007), Ruoyi Jiang (2008-2009), Brian Miranda (2008-2010), Evan Tilley (2009), Prashant Kota (2009-2010), Kevin Zhao (2009), Dianna Hu (2009-2010), Hannah Kenagy (2010-2011), Anvit Kalra-Lall (2011), Carlos Pena-Lobel (2011), Daniel Wang (2011-2012), John Gee (2012), Anna Whitney (2011), Mayuri Sridhar (2012), Elissa (Yiqing) He (2014), Brandon Gong (2015), Ben Schiffer (2015), Ziheng (Tony) Wang (2015), Rinni Bhansali (2015), Anna Lou (2016-2017), Annie Chang (2016-2017), Merrick Cai (2017-2018), Shobhita Sundaram (2017-2018), Keene Lu (2018), Kyra Ramonetti (2019-present)

AWARDS AND FELLOWSHIPS RECEIVED BY MENTORED GRADUATE STUDENTS

Kellon Belfon: 2018 NIH/NIGMS NRSA F31 Fellowship, 2017 ACM SIGHPC/Intel Computational & Data Science Fellowship, 2017 AGEP Travel Award, 2014-2019, the Dr. W. Burghardt Turner Fellowship, 2014-2016 IMSD-MERGE Graduate Fellowship

Lauren Raguette: 2018 Chemistry Award for First-Year Graduate Student Teaching Assistant

Zachary Fallon: 2017 Graduate Assistance in Areas of National Need Fellowship

Chuan Tian: 2019 IACS Travel Scholarship, 2018 Sigma Xi Travel Award, Image Challenge Winner at the 2016 7th Annual Center for Functional Nanomaterials (CFN) retreat

James Maier: 2013 Sigma Xi Travel Award

Kevin Hauser: 2014 AGEP-T FRAME Conference Travel Award, 2014 American Chemical Society NVIDIA GPU Research Award, 2012-2016 NIH/NIGMS NRSA F31 Fellowship, Invited participant for the 2013 Lindau Meeting of Nobel Laureates, 2011-2012 NIH CBTP T32 Fellowship, 2009-2011 NSF LSAMP-BD Fellowship, 2011 NSF GRFP Honorable Mention, 2011 NSF AGEP Travel Award

Cheng-Tsung (Eric) Lai: Fall 2014 American Chemical Society CCG Graduate Research Excellence Award, 2013 New York Structural Biology Discussion Group 8th Winter Meeting Poster Award, 2011 Institute for Chemical Biology & Drug Discovery Best Poster Award

Hai Nguyen: 2012 Sigma Xi Award

- *Miranda Yi Shang*: Fall 2011 American Chemical Society CCG Graduate Research Excellence Award
- *Christina Bergonzo*: Spring 2011 American Chemical Society CCG Graduate Research Excellence Award
- Amber Carr: 2013 Chemistry Award for Outstanding Service, 2011-2012, 2012-2103 IBM Research Fellowship, 2010 American Chemical Society Peter Kollman Graduate Award in Supercomputing
- *Ding Fangyu*: Fall 2009 American Chemical Society CCG Graduate Research Excellence Award, Sigma Xi Excellence in Research Award
- *Lauren Wickstrom*: 2007 Sigma Xi Excellence in Research award, Fall 2007 American Chemical Society CCG Research Excellence Award
- Salma Rafi: Spring 2007 American Chemical Society CCG Graduate Research Excellence Award
- *Kun Song*: 2007 Merck Achievement Award by the Chemical Toxicology Division of the American Chemical Society, 2005 American Chemical Society CCG Graduate Research Excellence Award

Raphaël Geney: Fall 2004 American Chemical Society CCG Graduate Research Excellence Award *Melinda Layten*: 2004 Kevin King and John Miller Scholarship

Asim Okur: Spring 2004 American Chemical Society CCG Graduate Research Excellence Award

Xiaolin Cheng: Spring 2004 American Chemical Society CCG Graduate Research Excellence Award

Guanglei Cui: 2003 ACS American Chemical Society CCG Graduate Research Excellence Award

Ben Strockbine: 2003 American Chemical Society CCG Graduate Research Excellence Award

TEACHING EXPERIENCE

General Chemistry (1200+ students per semester), 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, Modern

Drug Discovery, Introductory Synthetic and Spectroscopic Laboratory Techniques, Tools of Chemistry

CURRENT SUPPORT

NIH R01GM107104 (Simmerling, PI) 08/01/2013 - 6/30/2022 New solvent models, sampling methods and maintenance of Amber software The goal of this program is to support the continued development, maintenance, testing and evaluation of existing software.

NIH RM1 GM135136 (Dill, PI; Simmerling- co-PI) Solvation modeling for next-gen biomolecule simulations

To understand biological processes in health and disease, and to develop drugs and other therapies, we need computational models for proteins and how they interact with each other in the wet environments inside and around our cells. Here we develop models based on physical principles and geometrical descriptions of the interactions that determine how proteins behave.

NSF CTMC-1665159 (Simmerling, PI, Wu co-investigator) 07/01/2017 - 06/30/2021 Chemical Theory, Models and Computational Methods

Improving the Accuracy of the Amber Force Field for Biomolecular Simulation

This project is centered on developing more accurate physics models (force fields) that will facilitate a much broader and more reliable application of simulation tools to biophysics problems.

R43 GM134756 (Tsai, Simmerling, Shen MPI)

07/01/2019 - 06 /30/2021

A Cloud-Based Web Application To Accelerate Targeted Covalent Drug Discovery

This project seeks to develop a cloud-based on-demand web application that offers rapid and accurate predictions of covalently targetable hotspots in proteins and more broadly the protonation states of any titratable sites in macromolecules to accelerate drug discovery.

NIH R01 GM102864 (Tonge PI; Simmerling co-investigator) 09/15/2012 - 03/31/2022 Mechanism of Slow Onset Enzyme Inhibition and Drug Target Residence Time

The goal is to determine the mechanism by which some enzyme inhibitors exhibit slow-onset kinetics. Further studies include the rational design of inhibitors with longer residence times.

Research Corporation for Scientific Advancement (Simmerling, PI) 06/15/2020 - 06/14/2021 Pan-Covid-19 MultiValent Binders (MVBs) to Block Virus Entry

This project aims to determine the mechanism of membrane fusion induced by coronavirus spike proteins, and work with experimental collaborators to identify inhibitors.

Research Corporation for Scientific Advancement (Simmerling, PI) 06/15/2020 - 06/14/2021 Modulating Ribosomal Frameshifts to Interfere with Viral Protein Translation

This project aims to model the structure and interactions of the coronavirus RNA pseudoknot, and develop ligands to interfere with the pseudoknot role in transcript of viral RNA

Software license fees, "Amber"

Period: ongoing

Principal Investigators: David Case, Tom Cheatham, Ken Merz, Adrian Roitberg, Carlos Simmerling

This project involves the development and distribution of the Amber suite of programs for molecular simulation. The core developers listed above equally share the proceeds from license fees to support algorithm and code development in their labs.

COMPLETED SUPPORT

AMDeC Foundation 07/1/2000 - 06/30/2003 Computer Simulations: A New Tool in the Detection and Treatment of Cancer

NIH R01 GM061678 (Simmerling, PI)

06/01/2000 - 03/31/2011

04/1/2020 - 03/31/2025

Computational Studies of Model Systems for Protein Unfolded States

Research Corporation for Science Advancement (Simmerling, PI)	07/01/2000 - 06/30/2002
Using Large Clusters of Personal Computers to Improve Simulations	in the Condensed Phase

NIH S10 RR017855 (Smith, PI; Simmerling, Co-investigator) Computational Facility for Structural Biology	03/01/2004 - 02/28/2007
Academy of Applied Science (Simmerling, PI) Research Engineering and Apprenticeship Program	06/01/2005 - 05/30/2006
Academy of Applied Science (Simmerling, PI) Research Engineering and Apprenticeship Program NIH R37 CA017395 (Grollman, PI, Simmerling, co-Investigator) Molecular Pharmacology of Oxidative DNA Damage: Structure and B	06/01/2006 - 05/30/2007 04/01/2007 - 03/31/2012 Energetics
Academy of Applied Science (Simmerling, PI) Research Engineering and Apprenticeship Program	06/01/2007 - 05/30/2008
SBU/BNL SEED grant (Simmerling, PI) Simulations of Biomolecular Systems on Massively Parallel Superco	06/01/2007 - 05/30/2008 mputers
NIH R01 GM079383 (Duan, PI; Simmerling MPI) AMBER force field consortium: a coherent biomolecular simulation p	07/01/2007 - 06/30/2011 latform
NSF/Computing Research Association CIF-A-231 (Simmerling, PI) Computing Innovation Fellow	09/15/2009 - 10/14/2011
Academy of Applied Science (Simmerling, PI) Research Engineering and Apprenticeship Program	06/01/2011 - 05/30/2012
NIH R01 GM098102 (Hall, PI; Simmerling, Cheatham MPI) <i>RNA-ligand interactions: simulation and experiment</i>	09/30/2011 - 08/31/2016
AstraZeneca Pharmaceuticals LP 2000281000 (Simmerling, PI) Developing Computational Chemistry Tools for Modeling Time Depe	11/07/2011 - 06/05/2012 Indent Inhibition
NSF 1137097 (Dongarra, PI; Simmerling co-PI) Beacon: A Strategic Path to Scientific Discovery Enabled by the Inte	04/15/2012 - 03/31/2014 el MIC Architecture
Academy of Applied Science (Simmerling, PI) Research Engineering and Apprenticeship Program	06/01/2012 - 05/30/2013
NIH/NCI R01 CA165911(Schärer, PI; Simmerling, co-investigator) Synthesis, structure and repair of DNA interstrand crosslinks	07/01/2012 - 04/30/2017
NIH F31 GM101946 NIH Fellowship (Kevin Hauser) NRSA: Modeling the mechanism of MTERF1-DNA binding and recog	08/01/2012 - 07/31/2016 gnition
NIH F31 GM123767 NIH Fellowship (Kellon Belfon) NRSA: Characterization of a Potential Allosteric Target in the Dimer Proteases	03/10/2018 - 03/11/2020 Interface of Retroviral

	Carlos Simmerling
IBM PhD Fellowship Award Fellowship for Amber Carr	08/01/2012 - 07/31/2014
Academy of Applied Science Research Engineering and Apprenticeship Program	06/01/2013 - 05/30/2014
SUPERCOMPUTER TIME SUPPORT	
National Cancer Institute, Advanced Biomedical Computing Center Refinement of Cancer-Related Biomolecular Structures	04/01/2000 - 03/31/2001
NSF NRAC MCA02N028 Improving Biomolecular Simulations: Energy Functions and Conform	10/01/2002 – 09/30/2003 national Sampling
NSF NRAC MCA02N028 Computer Simulations of Biomolecular Structure and Dynamics	04/01/2004 - 03/31/2005
NSF NRAC MCA02N028 Computer Simulations of Biomolecular Structure and Dynamics	04/01/2005 - 03/31/2006
NSF LRAC MCA02N028 Computer Simulations of Biomolecular Structure and Dynamics	04/01/2006 - 03/31/2007
NSF LRAC MCA02N028 Computer Simulations of Biomolecular Structure and Dynamics	04/01/2007 - 03/31/2008
NSF TRAC MCA02N028 Computer Simulations of Biomolecular Structure and Dynamics	04/01/2009 - 03/31/2010
NSF XSEDE MCA02N028 Computer Simulations of Biomolecular Structure and Dynamics	04/01/2010 - 03/31/2011

NSF OCI-1036208 (PI: Cheatham; co-PIs Simmerling, York, Walker, Roitberg) 12/01/10 - 4/30/14 *PRAC- Hierarchical molecular dynamics sampling for assessing pathways and free energies of RNA catalysis, ligand binding, and conformational change*

NSF ACI-1515572 (PI: Cheatham; co-PIs Simmerling, York, Walker, Roitberg) 08/01/15 -07/31/18 *PRAC- Ensembles of molecular dynamics engines for assessing force fields, conformational change, and free energies of proteins and nucleic acids*

The COVID-19 High Performance Computing Consortium MCB200069 (PI Ramanathan) Artificial intelligence driven integrative biology for accelerating therapeutic discovery against SARS-CoV-2

COMPLETE LISTS OF PUBLISHED WORK

http://www.ncbi.nlm.nih.gov/sites/myncbi/11q01Ng9li-Qk/bibliography/48048182/public/

https://scholar.google.com/citations?user=KFOBbygAAAAJ

PUBLICATIONS (reverse chronological order)

Citation statistics as of October 2021: Total citations = 43,140; H-Index = 56; I-10 = 114)

- 1. Zou, J., Li, Z., Liu, S., Peng, C., Fang, D., Wan, X., Lin, Z., Lee, T., Raleigh, D., Yang, M., and Simmerling, C.*, *Scaffold Hopping Transformations Using Auxiliary Restraints for Calculating Accurate Relative Binding Free Energies.* J. Chem. Theory Comput. 2021, 17, 6, 3710–3726
- 2. Zou, J., Xiao, S., Simmerling, C., and Raleigh, D., *Quantitative Analysis of Protein Unfolded* State Energetics: Experimental and Computational Studies Demonstrate That Non-Native Side-

Chain Interactions Stabilize Local Native Backbone Structure., J. Phys. Chem. B, 2021, 125, 13, 3269–3277

- Casalino, L., Dommer, A., Gaieb, Z., Barros, E., Sztain, T., Ahn, S., Trifan, A., Brace, A., Bogetti, A., Ma, H., Lee, H., Turilli, M., Khalid, S., Chong, L., Simmerling, C., Hardy, D., Maia, J., Phillips, J., Kurth, T., Stern, A., Huang, L., McCalpin, J., Tatineni, M., Gibbs, T., Stone, J., Jha, S., Ramanathan, A., Amaro, R., *AI-Driven Multiscale Simulations Illuminate Mechanisms of SARS-CoV-2 Spike Dynamics.* International Journal of High Performance Computing Applications, in press 2021
- Fallon, L., Raguette, L., Wang, Y., Corbo, C., Stepanenko, D., Cuomo, A., Guerra, J., Budhan, S., Varghese, S., Rizzo, R., Simmerling, C., *Free Energy Landscapes for RBD Opening in SARS-CoV-2 Spike Glycoprotein Simulations Suggest Key Interactions and a Potentially Druggable Allosteric Pocket.* J. Am. Chem. Soc., 2021, 143, 30, 11349–11360
- 5. Brini, E., Simmerling, C., Dill, K. Protein Storytelling through Physics, Science 370:6520 (2020)
- Barros, E. P., Casalino, L., Gaieb, Z., Dommer, A. C., Wang, Y., Fallon, L., Raguette, L., Belfon, K., Simmerling, C., Amaro, R. E. *The Flexibility of ACE2 in the Context of SARS-CoV-2 Infection*. Biophysical Journal Special Issue on COVID-19, in press 2020
- Kasavajhala, Koushik; Lam, Kenneth; Simmerling, Carlos. *Exploring Protocols to Build* Reservoirs to Accelerate Temperature Replica Exchange MD Simulations. Journal of Chemical Theory & Computation, 16 (12), 7776-7799 (2020)
- Iuliano, J., Jinnette Tolentino Collado, Agnieszka A. Gil, Pavithran T. Ravindran, Andras Lukacs, SeungYoun Shin, Helena A. Woroniecka, Katrin Adamczyk, James M. Aramini, Uthama R. Edupuganti, Christopher R. Hall, Gregory M. Greetham, Igor V. Sazanovich, Ian P. Clark, Taraneh Daryaee, Jared E. Toettcher, Jarrod B. French, Kevin H. Gardner, Carlos L. Simmerling*, Stephen R. Meech*, and Peter J. Tonge, *Unraveling the Mechanism of a LOV Domain Optogenetic Sensor: A Glutamine Lever Induces Unfolding of the Jα Helix*, ACS Chem. Biol. 2020, 15, 10, 2752–2765 DOI: 10.1021/acschembio.0c00543
- Crooks, E., B. Irizarry, M. Ziliox, T. Kawakam, T. Victor, F. Xu, H. Hojo, K. Chiu, C. Simmerling, W. Van Nostrand, S. Smith and L. Miller, "*Copper stabilizes antiparallel β-sheet fibrils of the amyloid β40 (Aβ40)-lowa variant*", J. Biol. Chem., 295:8914-8927, (2020) DOI: 10.1074/jbc.RA119.011955
- 10. Tian, C., Kasavajhala, K., Belfon, K., Raguette, L., Huang, H., Miguez, A., Bickel, J., Wang, Y., Pincay, J., Wu, Q., Simmerling, C. *"ff19SB: Amino-Acid Specific Protein Backbone Parameters Trained Against Quantum Mechanics Energy Surfaces in Solution"*, Journal of Chemical Theory and Computation, 2020, 16, 1, 528-552, DOI:10.1021/acs.jctc.9b00591
- Zou, J., Simmerling, C.*, Raleigh, D.*, "Dissecting the Energetics of Intrinsically Disordered Proteins via a Hybrid Experimental and Computational Approach", J. Phys. Chem. B 123 (49), 10394-10402, 2019, DOI:10.1021/acs.jpcb.9b08323
- Ghoreishi, D., Cerutti, D., Fallon, Z., Simmerling, C., Roitberg, A., "A Fast Implementation of the Nudged Elastic Band Method in AMBER", Journal of Chemical Theory and Computation, 2019, DOI: 10.1021/acs.jctc.9b00329
- 13. Zou, J., Tian, C., Simmerling, C., "Blinded Prediction of Protein-Ligand Binding Affinity Using Amber Thermodynamic Integration for the 2018 D3R Grand Challenge 4", Journal of Computer Aided Molecular Design (2019), DOI:10.1007/s10822-019-00223-x
- 14. Huang, H. and Simmerling, C., *"Fast Pairwise Approximation of Solvent Accessible Surface Area for Implicit Solvent Simulations of Proteins on CPUs and GPUs"*, Journal of Chemical Theory and Computation, 2018, DOI: 10.1021/acs.jctc.8b00413

- 15. Hummel, M. H., Yu, B., Simmerling, C., Coutsias, E., "*Laguerre-Intersection Method for Implicit Solvation*", Int J Comput Geom Appl. 2018 Mar; 28(1): 1–38.
- 16. Hauser, K.; He Y.; Garcia-Diaz M.; Simmerling C.; Coutsias E.; "*Characterization of Biomolecular Helices and Their Complementarity Using Geometric Analysis*", Journal of Chemical Information and Modeling, 2017, DOI: 10.1021/acs.jcim.6b00721
- Li, H., Endutkin, A., Bergonzo, C., Fu, L., Grollman, A., Zharkov, D. and Simmerling, C.; "DNA Deformation-Coupled Recognition of 8-Oxoguanine: Conformational Kinetic Gating in Human DNA Glycosylase", Journal of the American Chemical Society, 2017, 139 (7), 2682-2692 DOI: 10.1021/jacs.6b11433 PMCID: PMC5321822
- Zou, Junjie; Song, Benben; Simmerling, Carlos; Raleigh, Daniel, "Experimental and Computational Analysis of Protein Stabilization by Gly-to-D-Ala Substitution: A Convolution of Native State and Unfolded State Effects", Journal of the American Chemical Society, 2016, 138 (48), 15682–15689 DOI: 10.1021/jacs.6b09511
- Neckles,, C. Pschibul, A., Lai, C.-T, Hirschbeck, M., Kuper, J. Davoodi, S., Zou, J., Liu, N., Pan P., Shah, S., Daryaee, F., Bommineni, G., Lai, C., Simmerling, C., Kisker, C. Tonge, P., "Selectivity of Pyridone-and Diphenyl Ether-Based Inhibitors for the Yersinia pestis FabV Enoyl-ACP Reductase FabV", Biochemistry, 55 (21), 2992–3006 (2016) DOI: 10.1021
- 20. Perez, A.; Morrone, JA; Simmerling, C.; Dill, KA; *"Advances in free-energy-based simulations of protein folding and ligand binding"*, Current Opinion in Structural Biology 36, 25-31 (2016)
- Hauser, K.; Essuman, B.; He, Y.; Coutsias, E.; Garcia-Diaz, M.; Simmerling, C., "A human transcription factor in search mode", Nucleic Acids Research, 44 (1), 63-74 (2016) doi: 10.1093/nar/gkv1091
- 22. Li, H.; Endutkin, AV; Bergonzo, C.; Campbell, AJ; de los Santos, C.; Grollman, AP; Simmerling, C.; "A dynamic checkpoint in oxidative lesion discrimination by formamidopyrimidine–DNA glycosylase", Nucleic Acids Research, 44 (2): 683-694 (2016). doi: 10.1093/nar/gkv1092
- 23. Byrnes, J.; Hauser, K.; Mejia, E.,; Norona, L.; Simmerling, C.; Garcia-Diaz, M.; "Base flipping by MTERF1 can accommodate multiple conformations and occurs in a stepwise fashion.", J. Mol. Biol., in press. doi:10.1016/j.jmb.2015.10.021
- Perez, A.; MacCallum, JL; Brini, E., Simmerling, C.; Dill, KA; "A grid-based backbone correction to the ff12SB protein force field for implicit-solvent simulations", J. Chem. Theor. Comput., 11 (10), 4770-4779 (2015) DOI: 10.1021/acs.jctc.5b00662
- 25. Lai, C-T; Li, H; Yu, W; Shah, S; Bommineni, G; Perrone, V; Garcia-Diaz, M; Tonge, P; Simmerling, C, "Rational modulation of the induced-fit conformational change for slow-onset inhibition in M. tuberculosis InhA", Biochemistry, 54 (30), 4683-4691 (2015) DOI: 10.1021/acs.biochem.5b00284
- 26. Maier, J.A.; Martinez, C.; Kasavajhala, K.; Wickstrom, L.; Hauser, K.E.; Simmerling, C.; *ff14SB: Improving the accuracy of protein side chain and backbone parameters from ff99SB,* Journal of Chemical Theory and Computation 11 (8), 3696-3713 (2015) DOI: 10.1021/acs.jctc.5b00255
- Nguyen, H.; Pérez, A.; Bermeo, S.; Simmerling, C., "*Refinement of Generalized Born Implicit Solvation Parameters for Nucleic Acids and Their Complexes with Proteins*", Journal of Chemical Theory and Computation 11 (8), 3714-3728 (2015) DOI: 10.1021/acs.jctc.5b00271
- 28. Kuznetsov, N.; Bergonzo, C.; Campbell, A.; Li, H; Mechetin, G.; de los Santos, C.; Grollman, A.; Fedorova, O.; Zharkov, D.; Simmerling, C.; "Active destabilization of base pairs by a DNA glycosylase wedge initiates damage recognition", Nucleic Acids Research, 43 (1): 272-281 (2015) DOI: 10.1093/nar/gku1300.

- Nguyen, H., Maier, J., Huang, H., Perrone, V., and Simmerling, C., "Folding simulations for proteins with diverse topologies are accessible in days with a single physics-based force field and implicit solvent", J. Am. Chem. Soc., 136 (40), pp 13959–13962 (2014) DOI: 10.1021/ja5032776
- Huang, X., Britto, M., Kear, J., Boone, C., Rocca, J., Simmerling, C., McKenna, R., Bieri, M., Gooley, P., Dunn, B. and Fanucci, G., "*The Role of Select Subtype Polymorphisms on HIV-1 Protease Conformational Sampling and Dynamics*", J. Biol. Chem., 289, pp17203-17214 (2014). DOI: 10.1074/jbc.M114.571836
- 31. Li, Huei-Jiun; Lai, Cheng-Tsung; Pan, Pan; Yu, Weixuan; Liu, Nina; Bommineni, Gopal; Garcia-Diaz, Miguel; Simmerling, Carlos; Tonge, Peter, "A structural and energetic model for the slowonset inhibition of the Mycobacterium tuberculosis enoyl-ACP reductase InhA", ACS Chemical Biology, 2014, 9 (4), pp 986–993 DOI: 10.1021/cb400896g
- 32. Pan, P., Knudson, SE, Bommineni, GR, Li, H., Lai, C., Liu, N., Garcia-Diaz, M., Simmerling, C., Patil, SS, Slayden, RA, Tonge, PJ, "*Time-Dependent Diaryl Ether Inhibitors of InhA: Structure– Activity Relationship Studies of Enzyme Inhibition, Antibacterial Activity, and in vivo Efficacy*", ChemMedChem 9 (4), pp 776–791, 2014 DOI: 10.1002/cmdc.201300429
- Brust, R., Haigney, A., Lukacs, A., Gil., A., Hossain, S., Addison, K., Lai, CT, Towrie, M., Greetham, GM, Clark, IP, Illarionov, B., Bacher, A., Kim, RR, Fischer, M., Simmerling, C., Meech, SR and Tonge, PJ, "Ultrafast Structural Dynamics of BlsA, a Photoreceptor from the Pathogenic Bacterium Acinetobacter baumannii", J. Phys. Chem. Lett., 5, 220-224, 2014 DOI: 10.1021/jz4023738
- Nguyen, H., Roe, D. and Simmerling, C., "Improved Generalized Born Solvent Model Parameters for Protein Simulations", J. Chem. Theory & Comput., 9, 2020–2034 (2013) DOI: 10.1021/ct3010485
- 35. Gee, J., Weaver, E., Shang, Y., Simmerling, C., "*Development of an Automated Event Detection Algorithm for HIV-1 Protease's Flap Backbone Dihedral Change*", J. Expt. Sec. Sci., 2 (4), 2013
- 36. Kapilashrami, K; Bommineni, G; Machutta, C; Kim, P; Lai, C; Simmerling, C; Picart, F; Tonge, P., "Thiolactomycin-based beta-Ketoacyl-AcpM Synthase A (KasA) Inhibitors: Fragment-Based Inhibitor Discovery Using Transient One-Dimensional Nuclear Overhauser Effect NMR Spectroscopy", J. Biol. Chem., 288, 6045-6052, (2013)
- Huang, X., Veloro, A., De Vera, I., Rocca, J., Simmerling, C., Dunn, B. and Fanucci, G., "Backbone 1H, 13C, and 15N Chemical Shift Assignment for HIV-1 Protease Subtypes and Multi-Drug Resistant Variant MDR 769", Biomolecular NMR Assignments, Volume 7, Issue 2, pp 199-202 (2013)
- Huang, X; de Vera, IMS; Veloro, AM; Blackburn, ME; Kear, JL; Carter, JD; Rocca, JR; Simmerling, C; Dunn, BM; Fanucci, GE, "Inhibitor-Induced Conformational Shifts and Ligand-Exchange Dynamics for HIV-1 Protease Measured by Pulsed EPR and NMR Spectroscopy", J. Phys. Chem. B, 116, 14235-14244 (2012)
- Eilers M, Goncalves J, Ahuja S, Kirkup C, Hirshfeld A, Simmerling C, Reeves P, Sheves M, Smith S. "Structural Transitions of Transmembrane Helix 6 in the Formation of Metarhodopsin I", J. Phys. Chem. B, 116, 10477-10489 (2012)
- 40. Shang, Y. and Simmerling, C., "*Molecular dynamics applied in drug discovery: the case of HIV-1 protease*", Computational Drug Discovery and Design, 819:527-549 (2012)
- Li, x., Liu, N., Zhang, H., Knudson, S., Li, H., Lai, C., Simmerling, C., Slayden, R and Tonge, P., "CoA Adducts of 4-Oxo-4-phenylbut-2-enoates: Inhibitors of MenB from the M. tuberculosis Menaquinone Biosynthesis Pathway", Med. Chem. Letters, 2, 818-823 (2011)

- 42. Bergonzo, C., Campbell, A., de los Santos, C., Grollman, A and Simmerling, C. "*Energetic Preference of 8-oxoG Eversion Pathways in a DNA Glycosylase*", J. Am. Chem. Soc., 133, 14504–14506 (2011) DOI: 10.1021/ja205142d
- 43. Bergonzo, C. and Simmerling, C., "*An Overview of String-Based Path Sampling Methods*", Annual Report in Computational Chemistry, **7**:89-97 (2011)
- Shang, Y., Nguyen, H., Wickstrom, L., Okur, A. and Simmerling, C., "Improving the description of salt bridge strength and geometry in a Generalized Born model", J. Mol. Graphics & Model., 29, 676-684 (2011)
- 45. Guainazzi, A., Campbell, A., Angelov, T., Simmerling, C. and Schärer, O., *"Synthesis and Molecular Modeling of a Nitrogen Mustard DNA Interstrand Crosslink"*, Chemistry: A European Journal, 16, 12100-12103 (2010).
- 46. Luchko, T., Gusarov, S., Roe, D., Simmerling, C., Case, D., Tuszynski, J. and Kovalenko, A., *"Three-dimensional molecular theory of solvation coupled with molecular dynamics in Amber"*, J. Chem. Theory & Comput, 6, 607-624 (2010).
- 47. Machutta, C., Gopal, B., Luckner, S., Kapilashrami, K., Ruzsicska, B., Simmerling, C., Kisker, C., and Tonge, P., *"Slow onset inhibition of bacterial & β-ketoacyl-ACP synthases by thiolactomycin"*, J. Biol. Chem., 285, 6161-6169 (2010)
- Song, K., Campbell, A., Bergonzo, C., de los Santos, C., Grollman, A., Simmerling, C., "An Improved Reaction Coordinate for Nucleic Acid Base Flipping Studies", J. Chem. Theory & Comput., 5, 3105-3113 (2009)
- Bergonzo, C., Campbell, A., Walker, R.,; Simmerling, C. "A Partial Nudged Elastic Band Implementation for Use with Large or Explicitly Solvated Systems", Intl. J. Quantum Chem., 109, 3781-3790 (2009)
- 50. Sun, L., Simmerling, C. and Ojima, I., "*Recent Advances in the Study of the Bioactive Conformation of Taxol*", ChemMedChem, 4, 719-731 (2009)
- 51. Wickstrom, L., Okur, A. and Simmerling, C., "*Evaluating the Performance of the FF99SB Force Field Based on NMR Scalar Coupling Data*", Biophys. J., 97, 853-856 (2009)
- 52. Ding, F. and Simmerling, C., "Studies of Drug Resistance and the Dynamic Behavior of HIV-1 Protease through Molecular Dynamics Simulations", in Drug Design: Structure- and Ligand-Based Approaches, D. Ringe, C. Reynolds and K. Merz, editors, Cambridge Press, 2010.
- 53. Gallia, G., Dunning, T., Head-Gordon, M., Kotliar, G., Grossman, J., Ho, K., Chou, M., Dupois, M., Asta, M. and Simmerling, C., "*Discovery In Basic Energy Sciences: The Role Of Computing At The Extreme Scale*", DOE Workshop Report, 2010.
- 54. Galiano, L., Ding, F., Veloro, A., Blackburn, M., Simmerling, C.* and Fanucci, G.*, "Drug Pressure Selected Mutations in HIV-1 Protease Alter Flap Conformations", J. Am. Chem. Soc., 131, 430-431 (2009) PMID: 19140783
- 55. Song, K., Stewart, J., Fesinmeyer, M. Andersen, N., Simmerling, C., "*Structural Insights for Designed Alanine-rich Helices: Comparing NMR Helicity Measures and Conformational Ensembles from Molecular Dynamics Simulation*", Biopolymers, 89:747-760 (2008)
- 56. Ding, F.; Layten, M.; Simmerling, C., "Solution Structure of HIV-1 Protease Flaps Probed by Comparison of Molecular Dynamics Simulation Ensembles and EPR Experiments", J. Am. Chem. Soc., 130: 7184-7185 (2008)
- 57. Okur, A., Wickstrom, L. and Simmerling, C., "*Evaluation of salt bridge structure and energetics in peptides using explicit, implicit and hybrid solvation models*", J. Chem. Theory Comput., 4:288-298 (2008)

- 58. Song, K., Kelso, C., de los Santos, C., Grollman, A. and Simmerling, C., "*Molecular simulations reveal a common binding mode for glycosylase binding of oxidatively damaged DNA lesions*". J. Am. Chem. Soc., 129:14536 (2007)
- 59. Song, K., Hornak, V., de los Santos, C., Grollman, A. and Simmerling, C., "*Molecular Mechanics Parameters for the FapydG DNA lesion*", J. Comput. Chem., 9:17 (2007)
- 60. 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)
- 61. 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)
- 63. Hornak, V. and Simmerling, C., "*Targeting structural flexibility in HIV-1 protease inhibitor binding*", Drug Discovery Today, 12:132-138 (2007)
- 64. 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., 3:557-568 (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)
- 66. 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).
- 67. 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).
- 68. Simmerling, C. and Gomperts, R., "Simulating HIV-1 Protease at its Most Vulnerable Instant", Scientific Computing, 7:32-34, 2006.
- 69. 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)
- 70. Rafi, S., Novichenok, P., Kolappan, S., Zhang, X., Strattor, C., Rawat, R., Kisker, C., Simmerling, C. and Tonge, P., "Structure of Acyl Carrier Protein Bound to Fabl, the FASII Enoyl Reductase from Escherichia Coli", J. Biol. Chem., 281: 39285-39293 (2006)
- 71. 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).c
- 72. 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)
- 73. 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).

- 74. 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 Bionformatics, 3:712-725 (2006). (Most highly cited article in history of this journal)
- 75. Geney, R., Layten, M., Gomperts, R., Hornak, V. and Simmerling, C., "*Investigation of salt bridge stability in a Generalized Born solvent model*", J. Chem. Theory Comput., 2:115, 2006.
- 76. Okur, A., Wickstrom, L., Layten, M., Geney, R., Song, K., Hornak, V. and Simmerling, C., "Improved Efficiency of Replica Exchange Simulations through Use of a Hybrid Explicit/Implicit Solvation Model", J. Chem. Theory Comput., 2:420, 2006.
- 77. 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).
- 78. Okur, A. and Simmerling, C., "*Hybrid Explicit/Implicit Solvation Methods*", Annual Reports in Computational Chemistry, 2:97-109 (2006).
- 79. Case, D. A.; Cheatham, T. E.; Darden, T.; Gohlke, H.; Luo, R.; Merz, K. M.; Onufriev, A.; Simmerling, C.; Wang, B.; Woods, R. J., *"The Amber biomolecular simulation program"*, J. Comput. Chem. 26:1668, 2005
- Kubatzky, K., Liu, W., Goldgraben, K., Simmerling, C., Steven O. Smith, S., and Constantinescu, S., "Structural Requirements of the Extracellular To Transmembrane Domain Junction for Erythropoietin Receptor Function", J. Biol. Chem., 280, 14844-14854 (2005)
- Geney, R., Sun, L., Pera, P., Bernacki, R., Xia, R., Horwitz, S., Simmerling, C., and Ojima, I. "Use of the tubulin-bound paclitaxel conformation for structure-based rational drug design", Chemistry & Biology, 12, 339-348 (2005)
- 82. Roe, D., Hornak, V. and Simmerling, C., *"Folding Cooperativity in a Three-stranded β-sheet Model"*, J. Mol. Biol., 352, 370-281 (2005)
- 83. Cheng, X., Kelso, C., Hornak, V., de los Santos, C., Grollman, A. and Simmerling, C., "*Dynamic Behavior of DNA Base Pairs Containing 8-oxoguanine*", J. Am. Chem. Soc., 127:13906, 2005.
- 84. 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
- 85. 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
- 86. Hornak, V. and Simmerling, C., *"Development of Softcore Potential Functions for Overcoming Steric Barriers in MD"*, J. Mol. Graphics & Modeling, 22: 403, 2004
- 87. Sivaraman, S., Sullivan, T., Johnson, F., Novichenok, P., Cui, G., Simmerling, C., Johnson, F. and Tonge, P. "Inhibition of the Bacterial Enoyl Reductase Fabl by Triclosan: A Structure-Reactivity Analysis of Fabl Inhibition by Triclosan Analogs", J. Med. Chem., 47:509, 2004
- 88. Roitberg, A. and Simmerling, C., "Foreword", J. Mol. Graphics & Modeling, 22:317, 2004
- 89. 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.
- 90. Hornak, V. and Simmerling, C., *"Generation of Accurate Protein Loop Conformations through Low-barrier Molecular Dynamics"*, Proteins: Struct. Func. Genet., 51:577,2003
- 91. Simmerling, C., Strockbine, B and Roitberg, A., *All-Atom Structure Prediction and Folding Simulations of a Stable Protein*, J. Am. Chem. Soc, 124:11258, 2002.

- 92. Cui, G and Simmerling, C., 'Conformational Heterogeneity Observed in Simulations of a Pyrene-Substituted DNA', J. Am. Chem. Soc., 124:12154, 2002.
- 93. Shewmaker, F., Maskos, K., Simmerling, C. and Landry, S. J. *'The Disordered Mobile Loop of GroES Folds into a Defined β Hairpin upon Binding GroEL'* J. Biol. Chem., 276:33, 2001
- 94. Simmerling, C., Lee, M.R, Ortiz, AR., Kolinski, A., Skolnick, J., Kollman, P.A., 'Combining MONSSTER and LES/PME to Predict Protein Structure from Amino Acid Sequence: Application to the Small Protein CMTI-I', J. Am. Chem. Soc., 122:8392 (2000)
- 95. Simmerling, C., Miller, J. L., and Kollman, P., 'Combined Locally Enhanced Sampling and Particle Mesh Ewald as a Strategy to Locate the Experimental Structure of a Non-helical Nucleic Acid', J. Am. Chem. Soc, 120:7149 (1998)
- 96. Simmerling, C., Fox, T. and Kollman, P., 'The Use of Locally Enhanced Sampling in Free Energy Calculations: Testing and Application to the $\alpha \rightarrow \beta$ Anomerization of Glucose', J. Am. Chem. Soc, 120:5771 (1998)
- 97. Case, D.A., Pearlman, D.A., Caldwell, J.A., Cheatham, T.E., Ross, W.S., Simmerling, C.L., Darden, T.A., Merz, K.M., Stanton, R.V., Cheng, A.L., Vincent, J.J., Crowley, M., Ferguson, D.M., Radmer, R.J., Seibel, G.L., Singh, U.C., Weiner, P.K. and Kollman, P.A., *AMBER 5*, University of California, San Francisco (1997)
- 98. Elber, R., Mohanty, D. and Simmerling, C. "Dynamics of Peptide Folding" in <u>Classical and</u> <u>Quantum Dynamics in Condensed Phase Simulations</u>, B. Berne et. al. (eds.) World Scientific, Singapore (1998)
- 99. Elber, R., Roitberg, A., Simmerling, C., Goldstein, R., Verkhivker, G., Li, H. and Ulitsky, A., '*MOIL- A Program for Simulation of Macromolecules*', Comp. Phys. Comm., 91:159 (1995)
- 100. 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 <u>Modeling of Biomolecular Structures and Mechanisms</u>, A. Pullman et al. (eds.) Kluwer Acad. Publishers, Netherlands (1995)
- 101. Simmerling, C. and Elber, R., 'Computer Determination of Peptide Conformations in Water: Different Roads to Structure', Proc. Nat. Acad. Sci. USA, 92:3190 (1995)
- 102. 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)
- 103. Elber, R., Roitberg, A., Simmerling, C., Goldstein, R., Verkhivker, G. and Li, H., 'MOIL- A Molecular Dynamics Program with Emphasis on Conformational Searches and Reaction Path Calculations in Large Biological Molecules' in <u>Statistical Mechanics, Protein Structure and</u> <u>Protein-Substrate Interactions</u>, S Doniach (ed.), Plenum Press, NY (1994)