LILLIAN T. CHONG

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APPOINTMENTS

University of Pittsburgh **Pittsburgh, PA**

Associate Professor of Chemistry (with Tenure)	2012-present
University of Pittsburgh Honors College Faculty Fellow	2018-present
Assistant Professor of Chemistry	2006-2011
Assistant Professor of Computational Biology (Secondary Appointment)	2006-2011
Affiliated Faculty, Joint CMU-Pitt Computational Biology Program	2006-present
Affiliated Faculty, Joint CMU-Pitt Molecular Biophysics/Structural Biology Program	2006-present

EDUCATION

Stanford University/IBM Almaden Research Center **Stanford, CA and San Jose, CA**
Postdoctoral fellow with Vijay Pande/William Swope 2005-2006

Stanford University **Stanford, CA**
Postdoctoral fellow with Vijay Pande 2002-2005

University of California at San Francisco **San Francisco, CA**
Ph.D. in Biophysics with Peter Kollman (deceased in 2001)/Irwin Kuntz 1997-2002
Thesis Title: "Computational Studies of Antibody and Enzyme Catalysis"

Massachusetts Institute of Technology **Cambridge, MA**
B.S. in Chemistry with Bruce Tidor 1993-1997

HONORS

ACM Gordon Bell Special Prize for HPC-Based COVID-19 Research	2020
Silicon Therapeutics Open Science Fellowship	2020
University of Pittsburgh Arts & Sciences Bellet Teaching Excellence Award	2017
National Science Foundation CAREER Award	2009-2014
Carnegie Science Emerging Female Scientist Award	2012
Hewlett-Packard Outstanding Junior Faculty Award	2008

TEACHING

Graduate course in quantum mechanics (2006-2008); undergraduate courses in quantum mechanics (2009, 2011, 2013, 2016-2020), statistical thermodynamics (2014, 2015, 2017-2021), computational drug discovery (2008-2012, 2014), and summer workshop in creative science writing (2017-2019).

SERVICE

Co-organizer of TSRC Workshop on Designing Biomolecular Switches (2014, 2017)
Co-organizer of WESTPA workshop, University of Pittsburgh (2015, 2018)
National Science Foundation XSEDE Allocations Resource Committee (2011-2014)

LILLIAN T. CHONG

INVITED REVIEWS

DM Zuckerman and LT Chong. "Weighted ensemble simulation: Review of methodology, applications and software." *Ann. Rev. Biophys.*, 46: 43-57 (2017).

LT Chong, AS Saglam, and DM Zuckerman. "Path-sampling strategies for simulating rare events in biomolecular systems." *Curr. Opin. Struct. Biol.*, 43: 88-94 (2017).

MC Zwier and LT Chong. "Reaching biological timescales with all-atom molecular dynamics simulations." *Curr. Opin. Pharmacol.*, 10: 745-752 (2010).

PEER-REVIEWED PUBLICATIONS

‡ Undergraduate researcher

PA Torrillo, AT Bogetti, and LT Chong. "A minimal, adaptive binning scheme for weighted ensemble simulations." *J. Phys. Chem. A* Article ASAP DOI: 10.1021/acs.jpca.0c10724.

AT Bogetti, HE Piston, JMG Leung, CC Cabalteja, DT Yang, AJ DeGrave, KT Debiec, DS Cerutti, DA Case, WS Horne, and LT Chong, L. T. "A twist in the road less traveled: The AMBER ff15ipq-m force field for protein mimetics." *J. Chem. Phys.*, 153: 6, 064101 (2020).

AT Bogetti, B Mostofian, A Dickson, AJ Pratt, AS Saglam, PO Harrison, JL Adelman, M Dudek, PA Torrillo, AJ DeGrave, U Adhikari, MC Zwier, DM Zuckerman, and LT Chong. "A suite of tutorials for the WESTPA rare-event sampling software." *LiveCoMS Journal*, 1: 10607 (2019).

AS Saglam and LT Chong. "Protein-protein binding pathways and calculations of rate constants using fully-continuous, explicit-solvent simulations." *Chemical Sciences*, 10: 2360 (2019).

AJ DeGrave‡, J-H Ha, SN Loh, and LT Chong. "Large enhancement of response times of a protein conformational switch by computational design." *Nature Comm.*, 9: 1013 (2018).

KT Debiec, MJ Whitley, LMI Koharudin, AM Gronenborn, and LT Chong. "Integrating NMR, SAXS, and atomistic simulations: Structure and dynamics of a two-domain protein." *Biophys. J.*, 114: 839-855 (2018).

AS Saglam, DW Wang‡, MC Zwier, and LT Chong. "Flexibility vs preorganization: Direct comparison of binding kinetics for a disordered peptide and its exact preorganized analogues." *J. Phys. Chem. B*, 121: 10046-10054 (2017).

DS Cerutti, KT Debiec, DA Case, and LT Chong. "Links between the charge model and bonded parameter force constants in biomolecular force fields." *J. Chem. Phys.*, 147: 161730 (2017).

KT Debiec, DS Cerutti, LR Baker‡, AM Gronenborn, DA Case, and LT Chong. "Further along the road less traveled: AMBER ff15ipq, an original protein force field built on a self-consistent physical model." *J. Chem. Theory Comput.*, 12: 3926-3947 (2016).

MC Zwier, AJ Pratt, JL Adelman, JW Kaus‡, DM Zuckerman, and LT Chong. "Efficient atomistic simulation of pathways and calculation of rate constants for a protein-peptide binding process: Application to the MDM2 protein and an intrinsically disordered p53 peptide." *J. Phys. Chem. Lett.*, 7: 3440-3445 (2016).

AS Saglam and LT Chong. "Highly efficient computation of the basal k_{on} using direct simulation of protein-protein association with flexible molecular models." *J. Phys. Chem. B*, 120: 117-122 (2016).

E Suarez, AJ Pratt, LT Chong, and DM Zuckerman. "Estimating first passage time distributions from weighted ensemble simulations and non-Markovian analyses." *Protein Sci.*, 25: 67-78 (2016).

MC Zwier, JL Adelman, JW Kaus‡, AJ Pratt, KF Wong, NB Rego‡, E Suarez, S Lettieri, DW Wang‡, M Grabe, DM Zuckerman, and LT Chong. "WESTPA: An interoperable, highly scalable software package for weighted ensemble simulation and analysis". *J. Chem. Theory Comput.* 11: 800-809 (2015).

PEER-REVIEWED PUBLICATIONS (continued)

KT Debiec, AM Gronenborn, and LT Chong. "Evaluating the strength of salt bridges – a comparison of current biomolecular force fields." *J. Phys. Chem. B*, 118: 6561-6569 (2014).

E Suarez, S Lettieri, MC Zwier, CA Stringer, SR Subramanian, LT Chong, and DM Zuckerman. "Simultaneous computation of dynamical and equilibrium information using a weighted ensemble of trajectories." *J. Chem. Theory Comput.*, 10: 2658-2667 (2014).

KM Oshaben, R Salari, DM Caslin, LT Chong, and WS Horne. "The native GCN4 leucine-zipper domain does not uniquely specify a dimeric oligomerization state." *Biochemistry*, 51: 9581-9591 (2012).

R Salari and LT Chong. "Effects of high temperature on desolvation costs of salt bridges across protein binding interfaces: Similarities and differences between implicit and explicit solvent models." *J. Phys. Chem. B,* 116: 2561-2567 (2012).

MT Panteva‡, R Salari, M Bhattacharjee‡, and LT Chong. "Direct observations of shifts in the β-sheet register of a protein-peptide complex using explicit solvent simulations." *Biophys. J.,* 100: L50-L52 (2011).

K Xiong, MC Zwier, NS Myshakina, VM Burger, SA Asher, and LT Chong. "Direct observations of conformational distributions of intrinsically disordered p53 peptides using UV Raman and explicit solvent simulations." *J. Phys. Chem. A*, 115: 9520-9527 (2011).

BM Mills‡ and LT Chong. "Molecular simulations of mutually exclusive folding in a two-domain protein switch." *Biophys. J.*, 100: 756-764 (2011).

MC Zwier, JW Kaus‡, and LT Chong. "Efficient explicit-solvent molecular dynamics simulations of molecular associations: Methane/methane, Na+/Cl-, methane/benzene, and K+/18-crown-6 ether." *J. Chem. Theory Comput.*, 7: 1189-1197 (2011).

JL Adelman, A Scarbrough, MC Zwier, D Bhatt, LT Chong, DM Zuckerman, and M Grabe. "Simulations of the alternating access mechanism of the sodium symporter Mhp1." *Biophys. J.*, 101: 2399-2407 (2011).

R Salari and LT Chong. "Desolvation costs of salt bridges across protein binding interfaces: Similarities and differences between implicit and explicit solvent models." *J. Phys. Chem. Lett.*, 1: 2844-2848 (2010).

TA Cutler, BM Mills‡, DJ Lubin, LT Chong, and SN Loh. "Effect of interdomain linker length on an antagonistic folding-unfolding equilibrium between two protein domains." *J. Mol. Biol.*, 386: 854-868 (2009).

LT Chong, JW Pitera, WC Swope, and VS Pande. "Comparison of computational approaches for predicting the effects of missense mutations on p53 function." *J. Mol. Graph. Model.,* 27: 978-982 (2009).

PEER-REVIEWED PUBLICATIONS (continued)

Before 2006

LT Chong, WC Swope, JW Pitera, and VS Pande. "Kinetic computational alanine scanning: application to p53 oligomerization." *J. Mol. Biol.*, 357: 1039-1049 (2006).

LT Chong, CD Snow, YM Rhee, and VS Pande. "Dimerization of the p53 oligomerization domain: identification of a folding nucleus by molecular dynamics simulations." *J. Mol. Biol.*, 345: 869-78 (2005).

LT Chong, P Bandyopadhyay, TS Scanlan, ID Kuntz, and PA Kollman. "Direct hydroxide attack is a plausible mechanism for amidase antibody 43C9." *J. Comp. Chem.*, 24: 1371-77 (2003).

TS Lee*, LT Chong*, JD Chodera, and PA Kollman. "An alternative explanation for the catalytic proficiency of orotidine 5'-phosphate decarboxylase." *J. Am. Chem. Soc.*, 123: 12837-48 (2001). *equal authorship

PA Kollman, I Massova, C Reyes, B Kuhn, S Huo, LT Chong, MR Lee, TS Lee, Y Duan, W Wang, O Donini, P Cieplak, J Srinivasan, D Case, and TE Cheatham 3rd. "Calculating structures and free energies of complex molecules: combining molecular mechanics and continuum models." *Accounts of Chemical Research* 33:889-97 (2000).

LT Chong, Y Duan, L Wang, I Massova, PA Kollman. "Molecular dynamics simulation and free energy calculations applied to affinity maturation in antibody 48G7." *Proc. Natl. Acad. Sci. USA* 96: 14330-5 (1999).

K Lin, HS Ateeq, SH Hsiung, LT Chong, CN Zimmerman, A Castro, WC Lee, CE Hammond, S Kalkunte, LL Chen, RB Pepinsky RB, DR Leone, AG Sprague, WM Abraham, A Gill, RR Lobb, and SP Adams. "Selective, tight-binding inhibitors of integrin alpha-4-beta-1 that inhibit allergic airway responses." *J. Med. Chem.*, 42: 920-34 (1999).

LT Chong, SE Dempster, ZS Hendsch, L-P Lee, and B Tidor. "Computation of electrostatic complements to proteins: a case of charge stabilized binding." *Protein Sci.* 7: 206-10 (1998).