Alex Dickson

Contact Information

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Goals

To apply novel tools and techniques from molecular simulation to biological systems relevant to human disease.

Specific Areas of Interest

Kinetics-oriented drug discovery, molecular property prediction, algorithm development, biological systems modeling, network analysis, non-equilibrium systems, machine learning

Education and Experience

Michigan State University, East Lansing, MI

Associate Professor, Department of Biochemistry and Molecular Biology, July 2021–Present

Assistant Professor, Department of Biochemistry and Molecular Biology, September 2015–July 2021

- Joint appointment with the Department of Computational Mathematics, Science and Engineering

University of Michigan, Ann Arbor, MI

Postdoctoral Fellow, Department of Chemistry, September 2011–August 2015

Primary Mentor: Charles L. Brooks, III

- Studied relative path probabilities to elucidate mechanisms of chaperone activity in *E. coli*
- Developed analysis techniques ("hub scores") to elucidate high-level behaviors in complex networks
- Created and applied new custom enhanced sampling methods to explore new areas of configuration space in high-dimensional order parameter spaces ("WExplore")
- Elucidated mechanisms of interaction for the intrinsically disordered chaperone HdeA

University of Chicago, Chicago, IL

Ph.D., Department of Chemistry, July 2011

Dissertation Topic: *"Enhanced sampling methods for nonequilibrium systems"*

Advisor: Aaron R. Dinner

- Developed enhanced sampling methods to study systems driven out of equilibrium ("nonequilibrium umbrella sampling")
- Ran massively parallel simulations on supercomputing architectures
- Studied dynamical phase transitions using large deviation theory

M.S., Chemistry, May 2007

University of Toronto, Ontario, Canada

Hon. B. Sc., Chemical Physics (Minor: Mathematics), May 2006

Thesis: *"The effect of trajectory accuracy on statistical distributions in chaotic systems"*

Personal Information

I am a dual Canadian-American citizen.
I am an ACS member 30919152, and a member of ACS COMP since 2015.

Publications in submission

[*] = corresponding author

[1] Bose S, Kilinc C, **Dickson A*** (2024) Markov State Models with Weighted Ensemble Simulation: How to Eliminate the Trajectory Merging Bias *ChemRxiv* doi: 10.26434/chemrxiv-2024-z17mb .

Independent Publications

[*] = corresponding author

[1] Bose S, Lotz SD, Deb I, Shuck M, Lee KSS*, **Dickson A*** (2023) How Robust is the Ligand Binding Transition State? *J. Am. Chem. Soc.* 145(46), 25318-25331.

[2] Donyapour N, Fathi Niazi F, Roussey NM, Bose S, **Dickson A*** (2023) Flexible Topology: A Dynamic Model of a Continuous Chemical Space. *J. Chem. Theory Comput.* 19(15), 5088-5098.

[3] Babin KM, Karim JA, Gordon PH, Lennon J, **Dickson A***, Pioszak AA* (2023) Adrenomedullin 2/intermedin is a slow off-rate, long-acting endogenous agonist of the adrenomedullin2 G protein-coupled receptor. *J. Biol. Chem.* 299(6) doi: `https://doi.org/10.1016/j.jbc.2023.104785`.

[4] Soave C, Ducker C, Islam N, Kim S, Yurgelevic S, Nicely NI, Pardy L, Huang Y, Shaw P, Auner G, **Dickson A**, Ratnam M* (2023) The Small Molecule Antagonist KCI807 Disrupts Association of the Amino-terminal Domain of the Androgen Receptor with ELK1 by Modulating the Adjacent DNA Binding Domain. *Mol. Pharmacol.* 103(4), 211-220.

[5] Dixon T, MacPherson D, Mostofian B, Dauzhenka T, Lotz SD, McGee D, Shechter S, Shrestha UR, Wiewiora R, McDargh ZA, Pei F, Pal R, Ribiero JV, Wilkerson T, Sachdeva V, Gao N, Jain S, Sparks S, Li Y, Vinitsky A, Zhang X, Razavi AM, Kolossvary I, Imbriglio J, Evdokimov A, Bergeron L, Zhou W, Adhikari J, Ruprecht B, **Dickson A***, Xu H*, Sherman W*, Izaguirre JA* (2022) Atomic-Resolution Prediction of Degrader-mediated Ternary Complex Structures by Combining Molecular Simulations with Hydrogen Deuterium Exchange. *Nat. Commun.* 13(1), 5884. doi: `https://doi.org/10.1038/s41467-022-33575-4`.

[6] Raeburn CB, Ormsby AR, Cox D, Gerak CA, Makhoul C, Moily NS, Ebbinghaus S, **Dickson A**, McColl G, Hatters DM* (2022) A biosensor of protein foldedness identifies increased "holdase" activity of chaperones in the nucleus following increased cytosolic protein aggregation. *J. Biol. Chem.* 298(8), 102158 doi: `https://doi.org/10.1016/j.jbc.2022.102158`.

[7] Roussey NM and **Dickson A*** (2022) Quality over quantity: Sampling high probability rare events with the weighted ensemble algorithm. *J. Comp. Chem.* doi: `https://doi.org/10.1002/jcc.27054`.

[8] Roussey NM and **Dickson A*** (2022) Local Ion Densities can Influence Transition Paths of Molecular Binding. *Front. Mol Biosci.* 9, 858316. doi: `https://doi.org/10.3389/fmolb.2022.858316`.

[9] Dixon T, Lotz SD and **Dickson A*** (2022) Creating Maps of the Ligand Binding Landscape for Kinetics-Based Drug Discovery. *Computational Method for Estimating the Kinetic Parameters of Biological Systems*, Series: Methods in Molecular Biology, Publisher: Humana, New York, NY, 325-334.

[10] Jayaraman S, Kocot J, Esfahani SH, Wangler NJ, Uyar A, Mechref Y, Trippier PC, Abbruscato TJ, **Dickson A**, Aihara H, Ostrov DA, Karamyan VT* (2021) Identification and characterization of two structurally related dipeptides that enhance catalytic efficiency of neurolysin. *J. Pharmacol. Exp. Therapeut.* 379:191-202.

[11] Donyapour N and **Dickson A*** (2021) Predicting partition coecients for the SAMPL7 physical property challenge using the ClassicalGSG method. *J. Comp. Aided Drug Design* 35:819-830.

[12] Uyar A and **Dickson A*** (2021) Perturbation of ACE2 structural ensembles by SARS-CoV-2 spike protein binding. *J. Chem. Theory Comput.* 17:5896-5906.

[13] Donyapour N, Hirn, MJ, **Dickson A*** (2021) ClassicalGSG: Prediction of logP Using Classical Molecular Force Fields and Geometric Scattering for Graphs. *J. Comput. Chem.* 42:1006-1017.

[14] Dixon T, Uyar A, Ferguson-Miller S, **Dickson A*** (2021) Membrane-mediated ligand unbinding of the PK-11195 ligand from the translocator protein (TSPO). *Biophys. J.*, 120:158-167.

[15] Lotz SD and **Dickson A*** (2020) Wepy: A Flexible Software Framework for Simulating Rare Events with Weighted Ensemble Resampling. *ACS Omega*, 5:31608-31623.

[16] Roussey NM and **Dickson A*** (2020) Enhanced Jarzynski Free Energy Calculations using Weighted Ensemble. *J. Chem. Phys.* 153:134116.

[17] Hall R, Dixon T, **Dickson A*** (2020) On Calculating Free Energy Using Ensembles of Transition Paths. *Frontiers in Molecular Biosciences* 7:106.

[18] Rizzi A, Jensen T, Slochower DR, Aldeghi M, Gapsys V, Ntekoumes D, Bosisio S, Papadourakis M, Henriksen NM, de Groot BL, Cournia Z, **Dickson A**, Michel J, Gilson MK, Shirts MR, Mobley DM* and Chodera JD* (2020) The SAMPL6 SAMPLing challenge: assessing the reliability and efficiency of binding free energy calculations. *Journal of Computer Aided Molecular Design* 34:601-633.

[19] Bogetti AT, Mostofian B, **Dickson A**, Pratt AJ, Saglam AS, Harrison PO, Adelman JL, Dudek M, Torrillo PA, DeGrave AJ, Adhikari U, Zwier MC, Zuckerman DM* and Chong LT* (2019) A Suite of Tutorials for the WESTPA Rare-Events Sampling Software [Article v1.0]. *Living Journal of Computational Molecular Science* 1(2):10607.

[20] Donyapour N, Roussey NM and **Dickson A*** (2019) REVO: Resampling of Ensembles by Variation Optimization. *Journal of Chemical Physics* 150:244112.

[21] Liu Y, Hickey DP, Minteer SD, **Dickson A*** and Barton SC* (2019) Markov-State Transition Path Analysis of Electrostatic Channeling. *Journal of Physical Chemistry C* 123: 15284-15292. ****Cover article****

[22] Kirberger SE, Ycas PD, Johnson JA, Chen C, Ciccone M, Lu RWW, Urick AK, Zahid H, Shi K, Aihara H, McAllister SD, Kashani-Sabet M, Shi J, **Dickson A**, dos Santos CO* and Pomerantz WCK*

(2019) Selectivity, ligand deconstruction, and cellular activity analysis of a BPTF bromodomain inhibitor. *Organic & Biomolecular Chemistry* 17: 2020-2027.

[23] Bai N, Roder H, **Dickson A** and Karanicolas J* (2019) Isothermal Analysis of ThermoFluor Data can readily provide Quantitative Binding Affinities. *Scientific Reports* 9:2650.

[24] **Dickson A*** (2018) Mapping the Ligand Binding Landscape. *Biophysical Journal* 115:1707-1719.

[25] Dixon T, Lotz SD, **Dickson A*** (2018) Predicting Ligand Binding Affinity Using On- and Off-Rates for the SAMPL6 SAMPLing Challenge. *Journal of Computer-Aided Molecular Design* 32(10):1001-1012 ****Cover article****

[26] Zeng X, Uyar A, Sui D, Donyapour N, Wu D, **Dickson A***, Hu J* (2018) Structural Insights Into Lethal Contractural Syndrome Type 3 (LCCS3) Caused by a Missense Mutation of PIP5Ky. *Biochemical Journal* 475: 2257-2269.

[27] Lotz SD and **Dickson A*** (2018) Unbiased Molecular Dynamics of 11 min Timescale Drug Unbinding Reveals Transition State Stabilizing Interactions. *Journal of the American Chemical Society* 140: 618-628.

[28] Wood RJ, Ormsby AR, Radwan M, Cox D, Sharma A, Vopel T, Ebbinghaus S, Oliveberg M, Reid GE, **Dickson A**, Hatters DM* (2018) A Biosensor-Based Framework to Measure Latent Proteostasis Capacity. *Nature Communications* 9:287.

[29] Uyar A, Karamyan VT and **Dickson A*** (2018) Long-Range Changes in Neurolysin Dynamics Upon Inhibitor Binding. *Journal of Chemical Theory and Computation* 14: 444-452.

[30] **Dickson A***, Tiwary P and Vashisth H (2017) Kinetics of Ligand Binding Through Advanced Computational Approaches: A Review. *Current Topics in Medicinal Chemistry* 17: 2626-2641.

[31] **Dickson A***, Lotz SD (2017) Multiple Unbinding Pathways and Ligand-Induced Destabilization Revealed by WExplore and Conformation Space Networks. *Biophysical Journal* 112: 620-629.

[32] **Dickson A***, Bailey CT and Karanicolas J (2016) Optimal Allosteric Stabilization Sites Using Contact Stabilization Analysis. *Journal of Computational Chemistry* 38: 1138-1146.

[33] **Dickson A***, Lotz SD (2016) Ligand Release Pathways Obtained with WExplore: Residence Times and Mechanisms. *Journal of Physical Chemistry B* 120: 5377-5385.

Publications with Former Mentors

[*] = corresponding author

[1] Salmon L, Ahlstrom LS, Horowitz S, **Dickson A**, Brooks III CL*, Bardwell, JCA* (2016) Capturing a dynamic chaperone-substrate interaction using NMR-informed molecular modeling. *Journal of the American Chemical Society* 138: 9826-9839.

[2] **Dickson A**, Ahlstrom LS, Brooks III CL* (2015) Coupled Folding and Binding with 2D Window-Exchange Umbrella Sampling. *Journal of Computational Chemistry* 37: 587-594. ****Cover article****

[3] Ahlstrom LS, Law S, **Dickson A**, Brooks III CL* (2015) Multiscale Modeling of a Conditionally Disordered pH-Sensing Chaperone *Journal of Molecular Biology* 427: 1670-1680.

[4] Laricheva E, Goh G, **Dickson A**, Brooks III CL* (2015) pH-Dependent Transient Conformational States Control Optical Properties in Cyan Fluorescent Protein *Journal of the American Chemical Society* 137: 2892-2900.

[5] **Dickson A**, Mustoe AM, Salmon L, Brooks III CL* (2014) Efficient In-Silico Exploration of RNA Interhelical Conformations Using Euler Angles and WExplore. *Nucleic Acids Research* 42: 97-110.

[6] **Dickson A**, Brooks III CL* (2014) WExplore: Hierarchical exploration of high dimensional spaces using the weighted ensemble algorithm. *Journal of Physical Chemistry B* 118: 3532-3542. ****Cover article****

[7] **Dickson A**, Brooks III CL* (2013) Quantifying chaperone-mediated transitions in the proteostasis network of E. coli. *PLoS Computational Biology* 9: e1003324.

[8] **Dickson A**, Brooks III CL* (2013) Native states of fast-folding proteins are kinetic traps. *Journal of the American Chemical Society* 135: 4729–4734.

[9] Ahlstrom LS, **Dickson A**, Brooks III CL* (2013) Binding and Folding of the Small Bacterial Chaperone HdeA. *Journal of Physical Chemistry B* 117: 13219-13225.

[10] **Dickson A**, Brooks III CL* (2012) Quantifying hub-like behavior in protein folding networks. *Journal of Chemical Theory and Computation* 8: 3044–3052.

[11] **Dickson A**, Tabei SMA, Dinner AR* (2011) Entrainment of a driven oscillator as a dynamical phase transition. *Physical Review E* 84: 061134.

[12] **Dickson A**, Maienschein-Cline M, Tovo-Dwyer A, Hammond JR, Dinner AR* (2011) Flow-dependent unfolding and refolding of an RNA by nonequilibrium umbrella sampling. *Journal of Chemical Theory and Computation* 7: 2710–2720.

[13] **Dickson A**, Nasto A, Dinner AR* (2010) Incorporating friction and collective shear moves into a lattice gas. *Physical Review E* 81: 051111.

[14] **Dickson A**, Dinner AR* (2010) Enhanced sampling of nonequilibrium steady states. *Annual Reviews of Physical Chemistry* 61: 441–459.

[15] **Dickson A**, Warmflash A, Dinner AR* (2009) Separating forward and backward pathways in nonequilibrium umbrella sampling. *Journal of Chemical Physics* 131: 154104.

[16] **Dickson A**, Warmflash A, Dinner AR* (2009) Nonequilibrium umbrella sampling in spaces of many order parameters. *Journal of Chemical Physics* 130: 074104.

Active Funding

NSF CNS REU Grant **2024-2027** Total: $454,873 USD
REU Site: ACRES: Advanced Computational Research Experience for Students
PI: Alex Dickson (MSU)
Co-PI: Mahmoud Parvizi (MSU)

NIH NIGMS R01 Grant **2018-2026** Total: $2.6 M USD
Revealing pathways and kinetics of molecular recognition with advanced molecular simulation algorithms (2022-2026)
Mapping the ligand binding landscape with advanced molecular simulation methods (2018-2022)
PI: Alex Dickson (MSU)

NIH NIGMS R01 Grant **2023-2028** Total: $3.2 M USD
Development of soluble epoxide hydrolase inhibitors for the treatment of Alzheimer's disease
PI: Kin Sing Stephen Lee (MSU)
Co-I: Scott Counts, Theresa Krieger-Burke, Wenjuan Ma, Alex Dickson, Edmund Ellsworth, Anne Dorrance, Nicholas Kanaan (all at MSU).

NIH NIGMS R01 Grant (Sub-award) **2021-2025** Total: $99,256 USD
RAMP-altered Class B GPCR Hormone Binding and Signaling
PI: Augen Pioszak (University of Oklahoma Health Sciences Center)

Past Funding

NIH NIGMS R01 Administrative Supplement **2019** Total: $124,464 USD
Mapping the ligand binding landscape with advanced molecular simulation methods
PI: Alex Dickson (MSU)

DMS/NIGMS Research at the Interface of Bio. and Math. Sciences **2018-2022** Total: $1.1 M USD
Kinetics-driven drug discovery using persistent homology, rare event molecular dynamics and experimental data
Lead PI: Alex Dickson (MSU), **Co-PIs:** Guowei Wei (MSU), Kin Sing Stephen Lee (MSU)

Human Frontiers Science Program, Program Grant **2017-2021** Total: $1.2 M USD
Defining the Capacity of Cells to Keep the Proteome Folded Over Space and Time
Lead PI: Danny Hatters (U. Melbourne), **Co-PIs:** Alex Dickson (MSU), Hannah Nicholas (U. Sydney), Simon Ebbinghaus (Ruhr. Univ. Bochum)

Articles Reviewed

I serve as a referee (roughly 10-15 articles per year) for articles submitted to the journals *Proceedings of the National Academy of Sciences*, *Journal of the American Chemical Society*, *Nature Communications*, *Biophysical Journal*, *Journal of Chemical Information and Modeling*, *Journal of Molecular Graphics and Modelling*, *Journal of Computational Chemistry*, *Biopolymers*, *Computational Biology and Chemistry*, *Frontiers in Bioengineering and Biotechnology*, *PLoS Computational Biology*, *Scientific Reports*, *Journal of Physical Chemistry B* and *Proteins: Structure, Function and Bioinformatics*.

Proposals Reviewed

Panel Member, NSF 2022.
Ad hoc Reviewer, MSU-HFH Cancer grants, 2022.
Panel Member, NIH 2021/10 ZRG1 BCMB-G (02) M, 2021.
Ad hoc Reviewer, NSF 2020.

Panel Member, NSF 2019.
Ad hoc Reviewer, NSF 2019.
Ad hoc Reviewer, NSF 2018.

Teaching

CMSE201 **Spring 2024, Fall 2021 (Lead Instructor), Fall 2017-2019**
Introduction to Computational Modeling, 60 lecture hours, Lead Instructor manages 6 sections.
An introductory undergraduate course that teaches Python programming and computer modeling of real-world systems. Roughly 60-70 students per section.

PHM980 **Spring 2023, 2021, 2019**
Drug Discovery and Medicinal Chemistry, 1 lecture hour, Affiliate Instructor.
Present a lecture on docking, virtual screening and computational drug discovery.

BMB803/805 **Spring 2019-2024**
Protein Structure, Design and Mechanism, 11 lecture hours.
A series of lectures and computational laboratories on protein sequence, structure and function. Developed a final project component where students create molecular visualizations to present a molecular system to a broad audience.

BMB961 **Spring 2022**
Machine Learning for Molecular Dynamics, 21 lecture hours, Lead Instructor.
An innovative new course focusing on the intersection of machine learning and molecular dynamics. Content is hosted on a public-facing JupyterBook (`https://adicksonlab.github.io/ml4md-jb/intro.html`). Interactive lectures and labs conducted on Google Colab. Co-taught with Prof. Michael Feig.

BMB961/CMSE890 **Spring 2017**
Concepts in Protein Structure and Modeling, 12 lecture hours.
Lectures and laboratories concerning enhanced sampling methods, clustering and kinetic modeling, and binding free energy calculations. Co-taught with Prof. Michael Feig.

CMSE801 **Fall 2016**
Introduction to Computational Modeling, 24 lecture hours.
Co-taught with Prof. Alexei Bazavov. Graduate course with lectures and laboratories on creating physical and computational models; programming in Python; effective visualization of data; working in teams to computationally solve scientific problems.

NSC801 **Spring 2016**
Introduction to Computational Modeling, 24 lecture hours.
Graduate course co-taught with Prof. Mohsen Zayernouri. All course material was developed from scratch by myself and Prof. Zayernouri.

Mentees

Current group members
Dr. Samik Bose (Postdoctoral researcher)
Fatemeh Niazi (Ph.D.)
Ceren Kilinc (Ph.D.)
Seref Berk Atik (Ph. D.)

Past group members
Dr. Andre Wyzykowski (Postdoctoral researcher), now at SENAI-CIMATEC, Brazil.
Dr. Naeyma Islam (Postdoctoral researcher), now at Mayo Clinic.
Dr. Indrajit Deb (Postdoctoral researcher), now at University of Dundee.

Dr. Arzu Uyar (Postdoctoral researcher), now at Izmir Institute of Technology.
Nicole Roussey (Ph.D., 2022), now at Qubit Pharmaceuticals.
Nazanin Donyapour (Ph.D., 2022), now at Axle Informatics.
James Lennon (Ph.D. student, 2022)
Samuel D. Lotz (Ph.D. Biochemistry & Molecular Biology, 2021), now CTO at Examol.
Tom Dixon (Joint Ph.D. in Biochemistry & Molecular Biology and Computational Mathematics, Science and Engineering, 2021), now at Foghorn Therapeutics.
Thomas Diaz (M.Sc. Chemistry, 2019)
Robert Hall (Post baccalaureate student, now in graduate school at University of Pittsburgh)

Thesis committees
Annie Needs, Chemical Engineering & Materials Science (PI: Daniel Woldring) (2023-Present)
Majid Jafari, Chemistry (PI: Kenneth Merz) (2023-Present)
Antryg Benedict, Plant, Soil, and Microbial Sciences (PI: Wei Zhang) (2022-Present)
Duncan Boren, Biochemistry & Molecular Biology (PI: Josh Vermaas) (2022-Present)
Kuang-Wei Wang, Biochemistry & Molecular Biology (PI: Min-Hao Kuo) (2020-Present)
Melissa Meschkewitz, Pharmacology & Toxicology (PI: Rick Neubig) (2022-2024)
Sunanda Dey, Chemical Engineering and Materials Science (PI: David Hickey & Daniel Woldring) (2020-2024)
Yan Xie, Chemical Engineering and Materials Science (PI: Scott Barton) (2019-2023)
Keshav Prahalad, Chemistry (PI: Kin Sing Lee) (2020-2021)
Xavier Brumwell, CMSE (PI: Matt Hirn) (2018-2021)
Feng Gao, Plant Soil and Microbial Sciences and CMSE (PI: Matt Hirn & Stephen Boyd) (2018-2019)
Yuanchao Liu, Chemical Engineering and Materials Science (PI: Scott Barton) (2016-2018)

Faculty mentoring
Prof. Grace Smith Vidaurre, IBIO/CMSE, (2024-Present)

Invited Talks

Virtual Seminar, Odyssey Therapeutics, April 2024.
Modeling Molecular Recognition: The Present and Future, ACS Spring 2024.
School of Pharmacy Seminar, Temple University, October 2023.
FCCC Faculty Seminar, Fox Chase Cancer Center, September 2023.
Free Energy Methods in Drug Design, Novartis, May 2023.
Machine Learning in Chemistry, ACS Spring 2023.
ACS Award for Computers in Chemical & Pharmaceutical Research in honor of Charles L. Brooks III, ACS Spring 2022.
Sequence-Structure-Dynamics-Function Relationships of Proteins, ACS Fall 2021 (virtual).
MolSSI School on Open-Source Software for Rare-Event Sampling Strategies, June 2021 (virtual).
Biophysics Seminar, University of Maryland College Park, April 2021 (virtual).
The Future of AI in Drug Discovery, ACS Spring 2021 (virtual).
Biochemistry and Molecular Biology Seminar, University of Oklahoma Health Sciences Center, March 2021 (virtual).
Physical Chemistry Seminar, University of Florida, February 2021 (virtual).
Biophysics & Molecular Biology Seminar, Washington University in St. Louis, January 2021 (virtual).
Chemistry Colloquium, University of Chicago, January 2021 (virtual).
Workshop on Free Energy Methods in Drug Design, Novartis, Cambridge, November 2020 (virtual).
Integrated Applied Mathematics Seminar, University of New Hampshire, November 2020 (virtual).
Departmental Seminar, Biochemistry & Molecular Biology, Michigan State University, October 2020 (virtual).
Online Presentation, ACS Virtual Meeting, Fall 2020.
Departmental Seminar, Chemical and Biomolecular Engineering, University of California, Irvine, May

2020 (virtual)
Departmental Seminar, Biochemistry & Molecular Biology, University of Oklahoma, April 2020 (cancelled due to COVID-19)
From protein folding to ligand binding: adventures with free energies, ACS Meeting, March 2020 (cancelled due to COVID-19)
Biophysics Seminar, University of Michigan, September 2019.
Free energy calculations: Entering the fourth decade of adventure in chemistry and biophysics, Santa Fe, June 2019.
Sampling conformations and pathways in biomolecular systems, ACS Meeting, April 2019.
Bioinformatics Cluster Meeting, University of Rochester, April 2019.
Physics Seminar, Oakland University, December 2018.
Chemistry Seminar, William Paterson University, October 2018.
WExplore lecture @ WESTPA Workshop, University of Pittsburgh, August 2018.
WExplore plugin tutorial @ WESTPA Workshop, University of Pittsburgh, August 2018.
Mid-Atlantic Comp Chem Meeting (via web) with Merck, GlaxoSmithKline, Bristol-Myers Squibb, and Pfizer, March 2018.
Seminar, Department of Computational & Systems Biology, University of Pittsburgh, September 2017.
Modeling & Measuring Protein-Ligand Kinetics & Residence Times, ACS Meeting, August 2017.
Physical Chemistry Seminar, Michigan State University, September 2016.
Charlie Brooks 60th Birthday Celebration, ACS Meeting, March 2016.
Pharmacology & Toxicology Seminar, Michigan State University, February 2016.
Computer Science and Engineering Seminar, Michigan State University, October 2015.
WESTPA Workshop, University of Pittsburgh, July 2015.
University of British Columbia, Okanagan Campus, Department of Chemistry, February 2015.
Michigan State University, Department of Biochemistry and Molecular Biology, February 2015.
IUPUI, Department of Chemistry, February 2015.
University of Texas, El Paso, Department of Chemistry, December 2014.
University at Buffalo, Department of Chemistry, November 2014.
Protein Folding Consortium in Ann Arbor, MI, June 2014.
Washington University St. Louis, Department of Biochemistry and Molecular Biophysics, March 2014.
Protein Folding Consortium Workshop in Berkeley, June 2013.
After Mini Mini for path sampling methods in Berkeley, Jan 2010.
Multiscale Materials Modeling in Tallahassee, Oct 2008.

Contributed Talks and Poster Sessions

ACS Meeting (Poster), San Diego, August 2019.
Biophysical Society Meeting (Talk), Baltimore, March 2019.
Free Energy Methods, Kinetics and Markov State Models in Drug Design (Poster), Cambridge, May 2018.
Binding Kinetics: Time is of the Essence (Poster), Berlin, October 2017.
ACS Meeting (Talk), Washington DC, August 2017.
ACS Meeting (Talk), San Francisco, April 2017.
Biophysical Society Meeting (Talk), Los Angeles, February 2016.
q-bio Winter Meeting in Hawaii (Poster), February 2014.

Honors and Awards

Visiting Scholar, Fox Chase Cancer Center, 2023.
Roivant Discovery Open Science Fellowship, Roivant Discovery, 2021.
OpenEye Outstanding Junior Faculty Award, American Chemical Society, COMP Division, 2019.
Elizabeth R. Norton Prize for Excellence in Research in Chemistry, University of Chicago, 2010.
Postgraduate Scholarship, Natural Sciences and Engineering Research Council of Canada (NSERC), 2007-2011.
Freud Scholar Fellowship, University of Chicago, 2006.

Undergraduate Student Research Award, NSERC, 2005.
Undergraduate Student Research Award, NSERC, 2004.
Susan C. Gollop and William G. Gollop Scholarship in Chemistry, University of Toronto, 2002-2003.

Service

Program Director, Advanced Compuational Research Experience for Students, NSF REU program, 2023-Present.
Co-organizer, Machine Learning in Chemistry, ACS 2023-Present.
Chair, COMP Programming Committee, American Chemical Society, 2022-Present.
Co-chair, COMP Programming Committee, American Chemical Society, 2020-2022.
Co-organizer, Biophysical Society Virtual Networking Event: Biomolecular Modeling in the Age of Machine Learning, May 2021.
Organizer/presider, American Chemical Society Meeting: Kinetics of Macromolecular Systems, Virtual, Spring 2021.
Organizer/presider, American Chemical Society Meeting: The Future of AI in Chemistry and Drug Discovery, Virtual, Spring 2021.
Presider, American Chemical Society Meeting: Sampling Conformations & Pathways in Biomolecular Systems, Orlando, April 2019.
Session chair, Biophysical Society Meeting: Protein-Small Molecular Interactions, Baltimore, March 2019.
Organizer, Midwest Computational Chemistry Conference, East Lansing, MI, June 2017.
Organizer, BMB Departmental Retreat, East Lansing, MI, September 2016.
Organizer, Computational Biology Symposium, Ann Arbor, MI, September 2016.
Session chair, Biophysical Society Meeting: Protein-Small Molecule Interactions, Los Angeles, February 2016.
Session chair, Gordon Research Seminar: Computational Chemistry, July 2014.

Community Outreach

MSU Science Festival, Abrams Planetarium **2016-2019**
Small Molecules on the Big Screen (2019)
Small Molecules on the Big Screen (2018)
Small Molecules on the Big Screen (2017)
What Happens to Molecules When You Turn Up the Heat? (2016)
40-min talks with dome-formatted molecular visualizations designed to appeal to younger audiences. Topics include: phase transitions (ice → water → steam), DNA synthesis, destabilizing protein mutations, molecular definition of temperature.

MSU Grandparents' University **2016-2017**
How Do Molecules Find Their Perfect Fit?
Taught two 1.5 hr lectures for children and their grandparents, employing 3D printed models of proteins to demonstrate key principles of molecular interaction. Topics included: assembly of viral capsids, molecular recognition, protein conformational change.

Department, College and University-level Service

Annual Review Committee, CMSE, Michigan State University **2023-2024**

Billman Selection Committee, BMB, Michigan State University **2023**
Member

Graduate Studies Committee, BMB, Michigan State University **2022-2023**
Member

Search Committee for 1855 Professor in Data Science, CMSE, Michigan State University **2022-**

2023
Member

Organizing committee, Science at the Edge, Michigan State University **2019-2022**
Member

Faculty Expectations Committee, CMSE, Michigan State University **2022**
Member

Undergraduate Studies Committee, CMSE, Michigan State University **2017-2022**
Member

Faculty Annual Evaluation Committee, College of Natural Sciences, Michigan State University **2021-2022**
Member

Faculty Advisory Committee, BMB, Michigan State University **2019-2021**
Member

Computer committee, BMB, Michigan State University **2018-2020**
Chair

Ad-hoc Committee on Faculty Evaluations, College of Natural Sciences, Michigan State University **2019-2020**
Member

Faculty Advisory Committee, BMB, Michigan State University **2018**
Ad Hoc Member

Search Committee, Fixed Term Assistant Professor, Mathematics, Michigan State University **2018**
Member

Computer Committee, BMB, Michigan State University **2015-2017**
Member

Committee on Undergraduate Minor, CMSE, Michigan State University **2015-2017**
Member

Tiger Talks, Department of Chemistry, University of Chicago

Co-chair, Graphic Designer **2009-2010**
Ran a series of talks featuring senior graduate students presenting to an audience of their peers.

PSD Social Committee, Physical Sciences Division, University of Chicago

Beer Baron **2007-2009**
Helped organize many social events for graduate students in the PSD, including a weekly happy hour. Responsibilities included sampling and purchasing craft beers from local breweries.

Student Seminar Series, Department of Chemistry, University of Chicago

Co-creator, Student Interviewer **2007**
The goal of this seminar series was to provide junior graduate students with an intimate window into the lives of accomplished academics in chemistry. Two live, one-on-one interviews were conducted with Professors Harry Gray and Fraser Stoddart in front of an audience of graduate students.

Chemistry Students' Union, Department of Chemistry, University of Toronto

President **2005-2006**

Along with a small group of students from my cohort, I transformed the CSU from a defunct organization to a vibrant, active team of students that is still in operation today. The CSU organizes social and academic events for undergraduate students in the Department of Chemistry.

First-year Learning Communities, University of Toronto

Student Mentor **2005-2006**

Led a weekly course that helped integrate first-year students into undergraduate life. The course was designed to teach academic and personal skills that help students succeed in a University environment. Responsibilities included developing a curriculum, making lesson plans, and leading a class of 24 students.