

Marc G Chevrette

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🎓 Education & Training

University of Wisconsin-Madison

Madison, WI

DOCTOR OF PHILOSOPHY (PHD) – GENETICS

04/2019

MASTER OF SCIENCE (MS) – GENETICS

10/2017

- **Advisor:** Cameron R Currie, PhD
- **Research Focus:** Evolution of Microbial Metabolic Diversity, Chemically-mediated Microbiome Interactions, & Antibiotic Discovery
- **Thesis:** Evolution of Antibiotic Biosynthesis in Actinobacteria: A Framework for Drug Discovery
- Ira L Baldwin Distinguished Predoctoral Fellow (2018-2019)
- NIH Chemistry-Biology Interface Predoctoral Fellow (2016-2018)

Institut Pasteur

Annecy, France

DIPLOMA – INTERNATIONAL COURSE ON ANTIBIOTICS AND RESISTANCE

11/2017

Harvard University Extension

Cambridge, MA

MASTER OF LIBERAL ARTS (ALM) – BIOTECHNOLOGY (BIOENGINEERING & NANOTECHNOLOGY)

03/2015

- **Advisor:** Tomás Maira-Litrán, PharmD, PhD
- **Research Focus:** Genome-wide Experimental & Computational Characterization of *In Vivo* Fitness Factors in Bacterial Infections
- **Thesis:** Transposon-Directed Insertion Site Sequencing for Determination of Fitness Factors in Pulmonary Infection by *A. baumannii*.

Rensselaer Polytechnic Institute

Troy, NY

BACHELOR OF SCIENCE (BSc) – MOLECULAR BIOLOGY & BIOINFORMATICS

12/2010

🏢 Experience

Handelsman Lab, Wisconsin Institute for Discovery

Madison, WI

POSTDOCTORAL ASSOCIATE

06/2016–present

- Genomics and metabolomics of antibiotic discovery through the Tiny Earth initiative.

WiSolve Consulting

Madison, WI

CO-FOUNDER, DIRECTOR OF TECHNOLOGY, SENIOR CONSULTANT

03/2016–present

- Provided business services (including market research analysis, business plan development, competitive landscape analysis, SBIR grant writing, and others) to early-stage companies in the biotech and pharmaceutical industries.

Currie Lab, University of Wisconsin-Madison

Madison, WI

POSTDOCTORAL ASSOCIATE

04/2019–05/2019

PHD CANDIDATE

08/2015–04/2019

- Built genomics-driven computational and analytic pipelines to uncover novel therapeutics and study the evolution of biosynthesis in free-living and host-associated microbes.
- Systems investigated include insects (leaf-cutting ants, honey bees, & insects broadly), marine invertebrates, soil communities, & the human microbiome.
- Led computational arm of Wisconsin Antimicrobial Drug Discovery & Development Center (NIH CETR).

Johnson Biosignatures Lab, Harvard & Georgetown Universities

Cambridge, MA

LEAD COMPUTATIONAL BIOLOGIST

10/2013–10/2015

- Performed whole genome sequencing and metagenomic analysis of environmental samples from sulfur-rich, extreme environments with implications in microbial ecology, biogeochemistry, and exobiology.
- Characterized biosynthetic potential of metagenomic data.

Warp Drive Bio

Cambridge, MA

HEAD OF EXPERIMENTAL GENOMICS

04/2013–08/2015

- Executed genomic-directed natural products drug discovery, high throughput Next Generation Sequencing (htNGS), computational biology, and molecular biology of actinomycetes and fungi.
- Designed and implemented genomic natural products searches over various scaffolds of business development and internal interest.
- Developed and curated computational pipelines and databases for assembly, annotation, and custom analysis of public and internal htNGS data (160,000 bacterial genomes, >150 closed and complete genomes) for analysis of novel polyketide, non-ribosomal peptide, and other natural product classes.
- Handled processing and management of sequence data, predictions, and analyses supporting multiple projects across discovery, molecular biology, engineering, and synthetic biology.
- Executed elucidation and prediction of novel chemical products of bacterial biosynthetic gene clusters and metabolic pathways (e.g. beta-lactams, aminoglycosides, rapamycin analogues, etc.).

- Developed internal pipelines for applied phylogenomic annotations and prioritizations of multiple data types to inform discovery and engineering efforts.
- Oversaw all lab and experimental support of actinomycete and fungal sequencing efforts for Illumina, Pacific Biosciences, and Oxford-Nanopore platforms.
- Bioinformatics software development to support molecular and synthetic biology efforts.
- Direct written and verbal communication of findings to senior leadership and business partners.
- Database management and delivery of sequence information to molecular biology, microbiology, and chemistry groups to aid drug discovery, strain engineering, and generation of expression constructs.

Maira-Litrán Infectious Disease Lab, Brigham & Women's Hospital

Boston, MA

RESEARCH ASSISTANT, MICROBIOLOGY & COMPUTATIONAL BIOLOGY

03/2013–08/2015

- Investigated *in vivo* fitness, horizontal gene transmission, and pathogenesis of *Acinetobacter baumannii*, *Staphylococcus aureus*, *Salmonella typhi*, and other virulent pathogens through microbiology, computational, and genomic techniques.
- Developed and optimized genetic tools to enable novel examinations of pathogen fitness, invasion, and virulence using high-throughput transposon-directed insertion site sequencing of infections in murine models.

Broad Institute of MIT & Harvard

Cambridge, MA

RESEARCH ASSOCIATE II, MOLECULAR BIOLOGY PROCESS DEVELOPMENT

01/2011–03/2013

- Independently designed development initiatives including supporting htNGS, microfluidics, and automation goals.
- Oversaw production and up-scaling of microbial mate-pair library construction (LC), integrated internal development with vendor technologies, and managed sample-tracking via real-time messaging to internal LIMS.
- Increased throughput of microbial LC Platform 4-fold by automation and protocol development.
- Worked extensively with mate-pair NGS LC, sequence analysis tools, genomic databases, statistical software, and programming/operating lab robotics.

Rutledge Molecular Genetics Lab, Rensselaer Polytechnic Institute

Troy, NY

RESEARCH ASSOCIATE, MOLECULAR GENETICS

05/2010–12/2010

- Designed and developed protocols and operating procedures for transgenic *Caenorhabditis elegans* cultures to model stress-induced neural degeneration and Parkinson's Disease.

BCR Biotech

Jamestown, RI

RESEARCH ASSISTANT, MICROBIOLOGY

09/2009–12/2009

- Wrote and optimized protocols and methods for engineering synthetic biosensing functions in *Bacillus* spores.

Publications, Talks, & Abstracts

PEER-REVIEWED PUBLICATIONS

*contributed equally

- P16 EJ Caldera*, **MG. Chevette***, BR McDonald, CR Currie. "Local adaptation of bacterial symbionts within a geographic mosaic of antibiotic coevolution." *In prep, available upon request.*
- P15 **MG. Chevette***, RM Stubbendieck*, JR Bratburd*, CR Currie. "Experimental microbiomes: Models not to scale." *In prep, available upon request.*
- P14 BR McDonald, **MG Chevette**, JL Klassen, HA Horn, EJ Caldera, E Wendt-Pienkowski, MJ Cafaro, AC Ruzzini, EB Van Arnam, GM Weinstock, NM Gerardo, M Poulsen, G Suen, J Clardy, CR Currie. "Biogeography and microscale diversity shape the biosynthetic potential of fungus-growing ant-associated *Pseudonocardia*." *Submitted. Preprint available. [Link](#)*
- P13 HA Horn*, E Gemperline*, **MG. Chevette**, BR McDonald, JR Bratburd, L Li, CR Currie. "Specialized chemical responses to pathogens in the defensive symbionts of fungus-growing ants." *Under review.*
- P12 GR Lewin, NM Davis, BR McDonald, AJ Book, **MG Chevette**, S Suh, A Boll, CR Currie. "Long-term cellulose enrichment selects for highly cellulolytic consortia and competition for public goods." *In revision.*
- P11 **MG Chevette**, CM Carlson, HE Ortega, C Thomas, GE Ananiev, KJ Barns, AJ Book, J Cagnazzo, C Carlos, W Flanigan, KJ Grubbs, HA Horn, FM Hoffmann, JL Klassen, JJ Knack, GR Lewin, BR McDonald, L Muller, WGP Melo, AA Pinto-Tomás, A Schmitz, E Wendt-Pienkowski, S Wildman, M Zhao, F Zhang, TS Bugni, DR Andes, MT Pupo, CR Currie. (2019). "The antimicrobial potential of *Streptomyces* from insect microbiomes." *Nature Communications*, 10(1), 516. [Link](#)
- P10 RM Stubbendieck, DS May, **MG Chevette**, MI Temkin, E Wendt-Pienkowski, J Cagnazzo, CM Carlson, JE Gern, CR Currie. "Competition among nasal bacteria suggests a role for siderophore-mediated interactions in shaping the human nasal microbiota." *Applied & Environmental Microbiology*, *In press.* [Link](#)
- P9 N Liu*, H Li*, **MG Chevette**, L Zhang, L Cao, H Zhou, X Zhou, Z Zhou, PB Pope, CR Currie, Y Huang, Q Wang. (2019). "Functional metagenomics reveals polysaccharide-degrading gene clusters and cellobiose utilization pathways in gut microbiota of a wood-feeding termite." *ISME Journal*, 13(1), 104-117. [Link](#)
- P8 **MG Chevette**, CR Currie. (2018). "Emerging evolutionary paradigms in antibiotic discovery." *Journal of Industrial Microbiology & Biotechnology*, *In press.* [Link](#)

- N Adnani, **MG Chevette**, SN Adibhatla, F Zhang, Q Yu, D Braun, J Nelson, SW Simpkins, BR McDonald, CL Myers, J Piotrowski, C Thompson, CR Currie, L Li, SR Rajske, TS Bugni. (2017). "Co-culture of marine invertebrate-associated bacteria and interdisciplinary technologies enable biosynthesis and discovery of a new antibiotic, keyicin." *ACS Chemical Biology*, 12(12), 3093. [Link](#)
- P7 [Highlighted by Nature, [Link](#)]
- AF Sanchez-Larrayoz, NM Elshamy, **MG Chevette**, Y Fu, P Giunta, RG Spallanzani, K Ravi, GB Pier, S Lory, T Maira-Litrán. (2017). "Complexity of complement-resistance factors expressed by *Acinetobacter baumannii* needed for survival in human serum." *Journal of Immunology*, 199: ji1700877. [Link](#)
- P6 **MG Chevette**, F Aicheler, O Kohlbacher, CR Currie, MH Medema. (2017). "SANDPUMA: Ensemble predictions of nonribosomal peptide chemistry reveals biosynthetic diversity across Actinobacteria." *Bioinformatics*, 2017, 1–9. [Link](#)
- P5 IJ Miller, **MG Chevette**, JC Kwan. (2017). "Interpreting microbial biosynthesis in the genomic age: Biological and practical considerations." *Marine Drugs*, 15(6), 165. [Link](#)
- P4 [Cover Image for Issue 6, Volume 15 in June 2017]
- K Blin, T Wolf, **MG Chevette**, X Lu, CJ Schwalen, SA Kautsar, HG Suarez Duran, ELC de los Santos, HUK Kim, M Nave, JS Dickschat, DA Mitchell, E Shelest, R Breitling, E Takano, SY Lee, T Weber, MH Medema. (2017). "antiSMASH 4.0 - Improvements in chemistry prediction and gene cluster boundary identification." *Nucleic Acids Research*, 45(1), 1019–1037. [Link](#)
- P3 GR Lewin, C Carlos, **MG Chevette**, HA Horn, BR McDonald, RJ Stankey, BG Fox, CR Currie. (2016). "Ecology and evolution of Actinobacteria and their bioenergy applications." *Annual Review of Microbiology*. 70: 235–254. [Link](#)
- P2 SS Johnson, **MG Chevette**, BL Ehlmann, KC Benison. (2015). "Insights from the metagenome of an acid salt lake: The role of biology in an extreme depositional environment." *PLOS ONE*. 2015 Apr; 10(4):e0122869. [Link](#)
- P1

INVITED TALKS

- T6 "Drugs from bugs of bugs: a novel source for antimicrobials." American Society for Microbiology Microbe. San Francisco, CA. Jun 21, 2019.
- T5 "Mining microbiomes for antimicrobials." Synthetic Biology for Natural Products Conference. Puerto Vallarta, Mexico. Jun 02, 2019.
- T4 "Host-associated microbes as a source of new antimicrobials." Natural Product Discovery & Development in the Genomic Era, Society for Industrial Microbiology & Biotechnology. Clearwater Beach, FL. Jan 22, 2018.
- T3 "Natural natural products: Leveraging chemical ecology in the search for new drugs." Evolution Seminar Series, JF Crow Institute for the Study of Evolution. Madison, WI. Oct 26, 2017.
- T2 "Computational insights into the diverse nonribosomal peptide chemistry of Actinobacteria." Synthetic Biology for Natural Products Conference. Cancun, Mexico. Mar 6, 2017.
- [Highlighted in *ACS Synthetic Biology*, [Link](#)]
- T1 "Darwinian drug discovery: Chemical ecology at fine and coarse evolutionary scales." International Chemical Biology Society Annual Conference. Madison, WI. Oct 24, 2016.
- [Highlighted in *ACS Chemical Biology*, [Link](#)]

PATENTS

- Q1 DC Gray, E Li, BR Bowman, GL Verdine, K Robison, **MG Chevette**, D Udway, PS Wang, A Li, JP Morgenstern. Compositions and methods for the production of compounds. Publication Number WO/2018/081590. Patent Application PCT/US2017/058800, filed Oct 27, 2017. [Link](#)

PUBLICATIONS, EDITORIAL REVIEW ONLY

- E5 **MG Chevette**. (2018). "Natural products reawakened: New trends in discovery and development." *SIMB News Magazine, Society for Industrial Microbiology and Biotechnology*, In press.
- E4 DR Braun, **MG Chevette**, D Acharya, CR Currie, SR Rajske, TS Bugni. (2018). "Draft genome of *Micromonospora* sp. WMMA1996, a marine sponge-associated bacterium." *Genome Announcements*, 6(8), e00077-18. [Link](#)
- E3 DR Braun, **MG Chevette**, D Acharya, CR Currie, SR Rajske, K Ritchie, TS Bugni. (2018). "Complete genome of *Dietzia* sp. WMMA184, a marine coral-associated bacterium." *Genome Announcements*, 6(5), e01582-17. [Link](#)
- E2 N Adnani, DR Braun, BR McDonald, **MG Chevette**, CR Currie, TS Bugni. (2017). "Draft genome of *Micromonospora* sp. WMMB-235, a marine ascidian-associated bacterium." *Genome Announcements*, 5(2), 1–2. [Link](#)
- E1 N Adnani, DR Braun, BR McDonald, **MG Chevette**, CR Currie, TS Bugni. (2016). "Complete genome sequence of *Rhodococcus* sp. strain WMMA185, a marine sponge-associated bacterium." *Genome Announcements*, 4(6), 1–2. [Link](#)

INTERNAL SEMINARS

- I4 "Drugs & bugs of bugs: Insect microbiomes as a source of new antibiotics." Genetics Colloquium, UW-Madison. Aug 8, 2018.
- I3 "Host-microbe interactions as a source of new antimicrobials." Highlights at the Chemistry-Biology Interface Colloquium, UW-Madison. Dec 12, 2017.

- I2 “Genome-based natural product discovery, modular biosynthesis, & applications.” Highlights at the Chemistry-Biology Interface Colloquium, UW-Madison. Feb 2, 2017.
- I1 “Genome assembly: Tools & analysis.” Computational Biology, Ecology, & Evolution (ComBEE), UW-Madison. Apr 27, 2016.

ABSTRACTS

- A28 K Throckmorton, V Vinnik, TB Cook, R Chowdhury, **MG Chevette**, CD Maranas, BF Pflieger, MG Thomas. “Directed evolution of an adenylation domain specificity code.” Presented at: Synthetic Biology for Natural Products Conference; Puerto Vallarta, Mexico; Jun 2, 2019.
- A27 CL Hansen, **MG Chevette**, M Selvaraj, A Vasquez Echeverri, D Maldonado Perez, C Eno, J Hernandez-Ortiz, F Pelegri. “Helical supramolecular assembly of a germline specific membraneless organelle.” Presented at: Phase Separation in Biology & Disease; New York, NY; Feb 20, 2019.
- A26 **MG Chevette**, CM Carlson, H Ortega, F Zhang, KJ Grubbs, MT Pupo, TS Bugni, DR Andes, CR Currie. “Insect-associated *Streptomyces* are a rich source of new antimicrobials.” Presented at: Beneficial Microbes; Madison, WI; Jul 9, 2018.
- A25 HA Horn, E Gemperline, K Delaney, **MG Chevette**, L Li, CR Currie. “Host specificity influences chemical response in *in vivo* symbiotic interactions.” Presented at: Beneficial Microbes; Madison, WI; Jul 9, 2018.
- A24 BR McDonald, **MG Chevette**, J Klassen, HA Horn, EJ Caldera, E Wendt-Pienkowski, MJ Cafaro, AC Ruzzini, EB Van Arnem, GM Weinstock, NM Gerardo, MG Poulsen, G Suen, J Clardy, CR Currie. “Biogeography and microscale diversity shapes the biosynthetic potential of fungus-growing ant associated *Pseudonocardia*.” Presented at: Beneficial Microbes; Madison, WI; Jul 9, 2018.
- A23 **MG Chevette**, CM Carlson, H Ortega, F Zhang, KJ Grubbs, MT Pupo, TS Bugni, DR Andes, CR Currie. “Insect-associated *Streptomyces* are a rich source of new antimicrobials with activity against resistant human pathogens.” Presented at: Perlman Antibiotic Discovery and Development Symposium; Madison, WI; Apr 27, 2018.
- A22 DD Acharya, IJ Miller, Y Cui, DR Braun, **MG Chevette**, M Berres, L Li, J Kwan, CR Currie, TS Bugni. “Chemical cross-talk in bacterial co-cultures affects differential gene expression and antibiotic production.” Presented at: Perlman Antibiotic Discovery and Development Symposium; Madison, WI; Apr 27, 2018.
- A21 R Zarnowski, **MG Chevette**, E Dominguez, DR Andes. “Modeling high-throughput proteomics into predictive metabolomics - A novel tool for studies of medical device-associated *Candida spp.* biofilm infections.” Presented at: Metabolomics Circle 2017 - Bioanalytical & Omics Science, Wrocław, Poland; Nov 18, 2017.
- A20 D Acharya, N Adnani, D Braun, IJ Miller, Q Yu, **MG Chevette**, M Berres, CR Currie, L Li, JC Kwan, TS Bugni. “Chemical cross-talk in bacterial co-cultures affects differential gene expression and antibiotic production.” Presented at: American Society for Pharmacognosy Annual Meeting, Portland, OR; Jul 30, 2017.
- A19 AF Sanchez-Larrayoz, NM Elhosseiny, **MG Chevette**, Y Fu, P Giunta, G Spallanzani, GB Pier, S Lory, T Maira-Litrán. “The membrane lipid asymmetry transport system plays a key role in protecting *Acinetobacter baumannii* against killing by human complement via the alternative pathway.” Presented at: American Society for Microbiology Microbe, New Orleans, LA; Jun 2, 2017.
- A18 **MG Chevette**, CM Carlson, C Thomas, TS Bugni, DR Andes, CR Currie. “Evolutionary trends in secondary metabolism reveal insect-associated *Streptomyces* as an underexploited antibiotic resource.” Presented at: Perlman Antibiotic Discovery and Development Symposium; Madison, WI; Mar 31, 2017.
- A17 EJ Caldera, **MG Chevette**, CR Currie. “The geographic mosaic of antibiotic coevolution in a bacterial symbiont of the fungus-farming ant *Apterostigma dentigerum*.” Presented at: Perlman Antibiotic Discovery and Development Symposium; Madison, WI; Mar 31, 2017.
- A16 J Bratburd, C Keller, E Vivas, **MG Chevette**, F Rey, L Li, CR Currie. “The human gut microbiota metabolomic response to infection.” Presented at: Perlman Antibiotic Discovery and Development Symposium; Madison, WI; Mar 31, 2017.
- A15 **MG Chevette**, CR Currie, MH Medema. “prediCAT: An accurate predictive method for substrate specificity of nonribosomal peptide synthetase adenylation domains.” Presented at: 30th Annual Kenneth B. Raper Symposium on Microbial Research; Madison, WI; Sep 2, 2016.
- A14 J Bratburd, BR McDonald, **MG Chevette**, JL Klassen, HA Horn, CR Currie. “Comparative genomics of fungus-growing ant-associated *Pseudonocardia*.” Presented at: 30th Annual Kenneth B. Raper Symposium on Microbial Research; Madison, WI; Sep 2, 2016.
- A13 HA Horn, E Gemperline, **MG Chevette**, BR McDonald, J Bratburd, E Mevers, J Clardy, L Li, CR Currie. “Mass spectrometry imaging reveals differential chemical response to pathogens in an ancient ant-microbe symbiosis.” Presented at: ISME International Symposium on Microbial Ecology; Montreal, QC, Canada; Aug 21-26, 2016.
- A12 **MG Chevette**, CR Currie, MH Medema. “Computational predictions of substrate specificity in nonribosomal peptide synthetases through comparative adenylation domain trees.” Presented at: American Society for Microbiology Microbe; Boston, MA; Jun 16-20, 2016.
- A11 SS Johnson, ML Soni, DJ Collins, KC Benison, MR Mormile, **MG Chevette**, BL Ehlmann. “Biosignatures in mars analog acid salt lakes.” Presented at: USRA Biosignature, Preservation and Detection in Mars Analog Environments; Lake Tahoe, Nevada; May 16-19, 2016.

- A10 **MG Chevette**, C Carlson, C Thomas, TS Bugni, CR Currie. “Multifaceted antibiotic profiling across Actinomycete chemical ecology.” Presented at: Perlman Antibiotic Discovery and Development Symposium; Madison, WI; Apr 29, 2016.
- A9 N Adnani, S Adibhatla, E Vazquez-Rivera, GA Ellis, D Braun, **MG Chevette**, BR McDonald, C Thompson, JS Piotrowski, Q Yu, L Li, CR Currie, TS Bugni. “Driving production of novel natural products through marine microbial interspecies interactions.” Presented at: Gordon Marine Natural Products; Ventura, CA; Mar 6-11, 2016.
- A8 **MG Chevette**, DW Udway, CR Currie, SS Johnson. “Functional classification and secondary metabolism of an extreme metagenome.” Presented at: 29th Annual Kenneth B. Raper Symposium on Microbial Research; Madison, WI; Sep 1, 2015.
- A7 **MG Chevette**, BL Ehlmann, KC Benison, SS Johnson. “Microbial diversity and biosynthetic potential of an extreme sediment metagenome.” Presented at: Gordon Applied and Environmental Microbiology; South Hadley, MA; Jul 12-17, 2015.
- A6 **MG Chevette**, M Vinacur, T Maira-Litrán. “Transposon-directed insertion site sequencing reveals *in vivo* fitness factors in *Acinetobacter baumannii* lung infections.” Presented at: Boston Bacterial Meeting; Cambridge, MA; Jun 18-19, 2015.
- A5 DW Udway, K Robison, **MG Chevette**, GL Verdine. “Lessons from long read assembly of 100+ Actinomycete genomes.” Presented at: Gordon Marine Natural Products; Ventura, CA; Mar 2-7, 2014.
- A4 K Robison, DW Udway, **MG Chevette**, GL Verdine. “Long read assembly of >100 Actinomycete genomes.” Presented at: Advances in Genome Biology & Technology; Marco Island, FL; Feb 12-15, 2014.
- A3 S Young, S Steelman, R Daza, **MG Chevette**, R Lintner, S Gnerre, A Berlin, B Walker, C Nusbaum, R Nicol. “Generation of high-quality draft assemblies with a single sequencing library.” Presented at: Sequencing, Finishing, Analysis in the Future; Santa Fe, NM; May 29-31, 2013.
- A2 S Steelman, R Daza, **MG Chevette**, P Kompella, P Trang, T Surabian, R Lintner, CZ Zhang, J Jung, M Meyerson, C Nusbaum, R Nicol. “Automated low input mate-pair library construction for Illumina sequencing.” Presented at: Advances in Genome Biology & Technology; Marco Island, FL; Feb 15-18, 2012.
- A1 S Steelman, R Daza, **MG Chevette**, P Kompella, P Trang, T Surabian, R Lintner, R Nicol. “Microbial mate-pair library construction for de novo detection of structural rearrangements.” Presented at: Broad Institute Symposium; Boston, MA; Nov 7-8, 2011.

Honors & Awards

Ira L Baldwin Distinguished Predoc. Fellowship for Excellence in Research	Bacteriology – UW-Madison	05/2018–04/2019
Chemistry-Biology Interface Predoctoral Fellowship	National Institutes of Health, NIGMS – UW-Madison	06/2016–03/2018
Passed with Distinction	Preliminary Examination A - Dept. of Genetics - UW-Madison	07/2017
Issue Cover	Marine Drugs 15(6): Connecting Marine Microbial Natural Products to Biosynthetic Pathways	06/2017
Bacteriology Departmental Travel Grant	University of Wisconsin-Madison	2016
Vilas Travel Grant	University of Wisconsin-Madison	2016
Dean's Academic Achievement Award	Harvard University Extension	03/2015
Finalist, Core Value Award: "Courageous: Uncompromising Science"	Warp Drive Bio	2014
Finalist, Core Value Award: "Unbounded: Reimagining the Possible"	Warp Drive Bio	2014
Featured Scientific Researcher – "Who is Broad?"	Broad Institute of MIT & Harvard	01/2012
Rensselaer Alumni Scholarship	Rensselaer Polytechnic Institute	2004–2008
Sal H. Alfiero Scholarship	Rensselaer Polytechnic Institute	2004–2008
Rhode Island State Scholarship	Rensselaer Polytechnic Institute	2004–2008

Service & Outreach

Ad hoc Reviewer	World Journal of Microbiology & Biotechnology, Microbial Genetics, Frontiers in Microbiology, FEMS Microbiology Letters, Microbial Cell Factories	
Evolution Coordinating Committee	JF Crow Institute for the Study of Evolution – UW-Madison	01/2017–present
Mentor	Google Summer of Code – antiSMASH – Open Bioinformatics Foundation	03/2016–09/2017
Co-chair	Computational Biology, Ecology, & Evolution (ComBEE) – UW-Madison	01/2016–08/2018
Co-organizer	Discovery Niche – Wisconsin Institutes for Discovery	10/2015–11/2015
Volunteer	Wisconsin Science Festival	10/2015
Open Genomics Adviser	Revive & Restore – Long Now Foundation	04/2014–10/2015
Environmental, Health, and Safety Representative	Broad Institute of MIT & Harvard	01/2011–03/2013

Teaching Experience ---

Microbiology 450: Diversity, Ecology, & Evolution of Microorganisms, UW-Madison	Lecturer	Fa 2018
Programming in R, ComBEE, UW-Madison	Group Leader, Lecturer	Sp 2016
Genetics 468: General Genetics II, UW-Madison	Lecturer, Teaching Assistant	Sp 2016
Microbiology 450: Diversity, Ecology, & Evolution of Microorganisms, UW-Madison	Lecturer, Teaching Assistant	Fa 2016

Professional Societies & Groups ---

International Chemical Biology Society	2016–present
Natural Products Discovery and Bioengineering Network	2016–present
American Society for Microbiology	2015–present
Computational Biology, Ecology, & Evolution (ComBEE) – UW-Madison	2015–present
JF Crow Institute for the Study of Evolution	2015–present
Society for Industrial Microbiology and Biotechnology	2014–present
Laboratory Robotics Interest Group – New England Chapter	2011–2015