

Chase M Clark

📍 University of Wisconsin-Madison, School of Pharmacy

🌐 chasemc 🐦 ChasingMicrobes ✉ chasingmicrobes@gmail.com 💼 hirechase 🏠 chasemc.github.io

Education

2015	PhD Pharmacognosy Chicago, IL	University of Illinois Chicago
2008	BS Biochemistry Mount Berry, GA	Berry College
2010	Principia Consortium Study Abroad Glasgow, Glasgow	University of Glasgow

Employment

Jun 2021 - present	Computation and Informatics in Biology and Medicine (CIBM) Postdoctoral Fellow Remote, Chicago, IL <ul style="list-style-type: none">• Appointment to UW-Madison/National Library of Medicine T15 training grant• Developing genomic and metagenomic bioinformatics software• Currently developing a repository-scale analysis platform for comparative genomics	
Sep 2020 - present	Postdoctoral Research Associate Remote, Chicago, IL	University of Wisconsin-Madison
May 2019 - Aug 2020	NIH F31 Fellow Chicago, IL, US	University of Illinois at Chicago
Aug 2015 - Aug 2020	Ph.D. Student Chicago, IL, US <ul style="list-style-type: none">• Natural product drug discovery, specifically bacterial-derived antibiotics• Conceived, learned to code, and built a bioinformatics program (R Shiny app) for rapid bacterial metabolomics analyses• Isolated and cultured 1000's of bacterial isolates and performed natural product isolation and structure elucidation• First or co-first author on four studies/manuscripts• Mentored undergraduate and graduate students leading to publishable studies	University of Illinois at Chicago
Mar 2013 - Aug 2015	Research and Development Technician Kennesaw, GA, US <ul style="list-style-type: none">• Assisted in the design and results analysis of three clinical studies• Presented monthly projects to CEO, VP Sales and VP Science & Technology• Head of method development and identification of raw materials to meet CFR 21, FDA requirements.• Developed identifications for over 140 materials, from enzymes and botanicals to minerals and additives.• Overhauled the Method Development Department establishing inter-departmental responsibilities, improving and creating new SOPs, streamlining identification requests by establishing a formal request process and interactive database• Strengthened and created new relationships with third-party vendors, labs, and universities.• Controlled budget of method development for purchase of standards, consumables, equipment and third-party testing.• Mentored interns from Kennesaw Mountain High School magnet program	Deerland Probiotics & Enzymes
Aug 2008 - May 2012	Bonner Scholar Rome, GA, US <ul style="list-style-type: none">• Four-year community service scholarship requiring weekly and summer commitments.	Bonner Foundation

Select Funding/Awards

2021-present	Computation and Informatics in Biology and Medicine (CIBM) Training Program (T32) \$100,000.00
2020	St. Jude National Graduate Student Symposium (cancelled due to Covid19) One of 40 participants selected from 1,000 invite-only applications
2019-2020	NIH Predoctoral Individual National Research Service Award (F31) \$90,000.00
2018	R/Pharma, Travel Award \$500
2017	W.E. van Doren Scholar \$1,000
2017	American Society of Pharmacognosy Student Travel Award \$600
2017	University of Illinois at Chicago Provost/Deiss Award \$2,500
2008-2012	Bonner Scholar Scholarship for students with financial need "in exchange for weekly commitment to intensive and meaningful service with a local community organization over the four years"
2008-2012	Academic Scholarship
2011	McCaleb, Hubert Scholarship
2011	Frank Plummer Scholarship
2010	Griggs Academic Scholarship
2009	John R. Bertrand Scholarship
2008	Sierra Club College Scholarship
2008	Cherokee Area Eagle Scout of the Year Scholarship

Publications

- Mullowney, M. W., ..., Clark, C. M., ..., & Medema, M. H. (2023). Artificial intelligence for natural product drug discovery. *Nature Reviews Drug Discovery*. Citations: 0. 10.1038/s41573-023-00774-7
- Waterworth, S. C., Rees, E. R., Clark, C. M., Carlson, S., Miller, I. J., Puglisi, M., & Kwan, J. C. (2023). Elevated expression of srp RiPPs across bacterial phyla in marine sponges. *Citations: 0*. 10.1101/2023.06.09.544420
- Rees, E. R., Uppal, S., Clark, C. M., Lail, A. J., Waterworth, S. C., Roesemann, S. D., Wolf, K. A., & Kwan, J. C. (2023). Autometa 2: A versatile tool for recovering genomes from highly-complex metagenomic communities. *Citations: 0*. 10.1101/2023.09.01.555939
- Clark, C. M., Hernandez, A., Mullowney, M. W., Fitz-Henley, J., Li, E., Romanowski, S. B., Pronzato, R., Manconi, R., Sanchez, L. M., & Murphy, B. T. (2022). Relationship between bacterial phylotype and specialized metabolite production in the culturable microbiome of two freshwater sponges. *ISME Communications*. Citations: 2. 10.1038/s43705-022-00105-8
- Clark, C. M., Nguyen, L., Pham, V. C., Sanchez, L. M., & Murphy, B. T. (2022). Automated microbial library generation using the bioinformatics platform IDBac. *Molecules*. Citations: 2. 10.3390/molecules27072038
- Leao, T. F., Clark, C. M., Bauermeister, A., Elijah, E. O., Gentry, E. C., Husband, M., Oliveira, M. F., Bandeira, N., Wang, M., & Dorrestein, P. C. (2021). Quick-start infrastructure for untargeted metabolomics analysis in GNPS. *Nature Metabolism*. Citations: 8. 10.1038/s42255-021-00429-0
- Elfeki, M., Mantri, S., Clark, C. M., Green, S. J., Ziemert, N., & Murphy, B. T. (2021). Evaluating the distribution of bacterial natural product biosynthetic genes across lake huron sediment. *ACS Chemical Biology*. Citations: 4. 10.1021/acscchembio.1c00653
- Clark, C. M., Murphy, B. T., & Sanchez, L. M. (2020). A call to action: The need for standardization in developing open-source mass spectrometry-based methods for microbial subspecies discrimination. *mSystems*. Citations: 2. 10.1128/msystems.00813-19
- Clark, C. M., Costa, M. S., Conley, E., Li, E., Sanchez, L. M., & Murphy, B. T. (2019). Using the open-source MALDI TOF-MS IDBac pipeline for analysis of microbial protein and specialized metabolite data. *Journal of Visualized Experiments*. Citations: 9. 10.3791/59219

10. Braesel, J., Clark, C. M., Kunstman, K. J., Green, S. J., Maienschein-Cline, M., Murphy, B. T., & Eustáquio, A. S. (2019). Genome sequence of marine-derived streptomyces sp. Strain F001, a producer of akashin a and diaza-quinomycins. *Microbiology Resource Announcements*. Citations: 2. 10.1128/mra.00165-19
11. Costa, M. S., Clark, C. M., Ómarsdóttir, S., Sanchez, L. M., & Murphy, B. T. (2019). Minimizing taxonomic and natural product redundancy in microbial libraries using MALDI-TOF MS and the bioinformatics pipeline IDBac. *Journal of Natural Products*. Citations: 16. 10.1021/acs.jnatprod.9b00168
12. Clark, C. M., Costa, M. S., Sanchez, L. M., & Murphy, B. T. (2018). Coupling MALDI-TOF mass spectrometry protein and specialized metabolite analyses to rapidly discriminate bacterial function. *Proceedings of the National Academy of Sciences*. Citations: 66. 10.1073/pnas.1801247115

Talks

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| Sep 2023 | How to write reproducible code for data science <ul style="list-style-type: none">• Chicago R User Group |
| Aug 2023 | Reproducibly building and analyzing knowledge graphs for drug discovery with Nextflow, Neo4j and Python <ul style="list-style-type: none">• Chicago Python User Group |
| Mar 2023 | SocialGene: Large Scale Knowledge Graphs for Microbial Based Drug Discovery <ul style="list-style-type: none">• Computation and Informatics in Biology and Medicine Seminars |
| Jan 2023 | Information-Rich Platforms for Natural Product Antibiotic Drug Discovery and Microbial Characterization <ul style="list-style-type: none">• Northeastern University Department of Chemistry and Chemical Biology |
| Jan 2023 | SocialGene: A Large Scale Search Engine to Find Metagenomic BGCs in Free-Living Organisms <ul style="list-style-type: none">• 2023 ASP Younger Members Symposium |
| Jun 2022 | Large Scale Analysis of Protein Homology for Microbial Drug Discovery <ul style="list-style-type: none">• National Library of Medicine (NLM) T15 Training Conference |
| Mar 2022 | Towards near-instant, repository-scale searching for homologous BGCs with Socialgene (Selected alternate speaker, didn't present) <ul style="list-style-type: none">• Gordon Research Conference on Marine Natural Products |
| Nov 2021 | New Computational Tools for Top-Down and Bottom-Up Natural Product Drug Discovery <ul style="list-style-type: none">• Computation & Informatics in Biology & Medicine Seminars BMI 915 |
| Jun 2020 | IDBac: Bioinformatics Software for Microbial Drug Discovery Prioritization and Culturomics Characterization <ul style="list-style-type: none">• St. Jude National Graduate Student Symposium (cancelled due to Covid19) |
| May 2020 | Protein MS isn't the only MS... Programming in R for Metabolomics Mass Spectrometry <ul style="list-style-type: none">• May Institute 2020: Future developers meeting |
| Feb 2020 | IDBac: Bioinformatics Software for Microbial Drug Discovery Prioritization and Culturomics Characterization <ul style="list-style-type: none">• Gordon Research Conference on Marine Natural Products• Gordon Research Seminar (GRS) on Marine Natural Products |
| Aug 2019 | Your Missing Step in Reproducible R Programming: Continuous Deployment <ul style="list-style-type: none">• R/Pharma, Harvard University |
| Apr 2019 | Bioinformatics in R <ul style="list-style-type: none">• satRdays Chicago |
| Jan 2019 | Single Function Lightning Talks: "lengths()", not length()" <ul style="list-style-type: none">• Chicago R User Group |

Aug 2018	IDBac: A New Paradigm in Developing Microbial Libraries for Drug Discovery • R/Pharma, Harvard University
Jan 2018	IDBac: A Shiny App to Analyze Bacterial Fingerprints and Aid in the Discovery of Potential New Antibiotics • Chicago R User Group
Mar 2017	IDBac: A proteomic & chemometric pipeline for rapid bacterial characterization • Center for Biomolecular Sciences, UIC
Nov 2016	Rational design of bacterial strain libraries for drug discovery • UIC Specialized Metabolite Community
Jul 2016	Use of MALDI-MS to Create 'Smart' Libraries for Drug-Lead Discovery • Chicago Mass Spec Day
Apr 2015	HPLC-DAD Method for Trace Detection of Benzoic and Sorbic Acids in High Protein Matrices • SSAOAC Annual Meeting

In-Progress

IDBacDB Manuscript	Web resource for sharing and searching FAIR MALDI-MS microbial spectra
SocialGene Manuscript	Repository-scale analyses of protein similarity
clusterrule Manuscript	Multinational collaboration to create a standardized collection of NP HMM models
Autometa 2.0 Manuscript	Code standardization and enhancements including addition of a Nextflow pipeline
Metagenomics Review Manuscript	Co-writing a review on genome resolved metagenomics and natural product discovery
Transcriptomics	Mapping transcriptional regulation in Actinobacteria
Metagenomics	Improving multisample genome resolved metagenomics

Select Individual Software Projects

2021-2023	socialgene Repository-scale genome pattern search platform	Python, Django, Nextflow, Rust, High-throughput computing
2019	electricShine Shiny packaging with Electron	R, Javascript, Node/Electron
2019	mzEasy Shiny app for converting and visualizing mass spectrometry data	R, Shiny
2019	mzPlotter Automated summary of LC-MS/MS data with interactive Rmarkdown reports	R, Rmarkdown
2019	mzFromImage Predict a mass spectrum's values from a static image file	R, Shiny
2019	mgfparse Low-dependency R package for quickly and efficiently parsing mgf files into R	R
2018-2023	IDBac MALDI protein and small molecule bioinformatics platform	R, Shiny, Electron

Select Team Software Projects

2021	metaBenchmarks Benchmark metagenomic profiling/binning software	Nextflow
2020-2023	Autometa Automated binning pipeline for single metagenomes	Python, Nextflow

Workshops (host)

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| Jul 2022 | ASP Annual Meeting (Co-host) <ul style="list-style-type: none">• Hands-On training of IDBac, an informatics tool for strain prioritization |
| May 2019 | Department of Pharmacognosy <ul style="list-style-type: none">• IDBac tutorial |

Workshops (participant)

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| Sep 2021 | Artificial Intelligence for Natural Product Drug Discovery (Invitation-Only; Lorentz Center) |
| Aug 2019 | Integration of Metabolomics and Genomics (University of Chicago) |
| Dec 2016 | PATRIC/RAST Workshop (Argonne National Laboratory) |

Teaching

Invited Guest Lectures

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| Spring 2022 | PSCI 522 Advanced Pharmacognosy (two lectures)
University of Illinois at Chicago |
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Peer Review

- Journal of Natural Products
- CRC press
- rOpenSci
- Microbiology Spectrum

Memberships/Professional Affiliations

- American Society of Pharmacognosy
- Chicago R User Group
- Chicago Python User group

The code for building this CV is available at: <https://github.com/chasemc/resume>