Chase M Clark

University of Wisconsin-Madison, School of Pharmacy

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Education

University of Illinois Chicago — *Chicago, IL*

PhD Pharmacognosy — *2015*

Berry College — *Mount Berry, GA*

BS Biochemistry — *2008*

University of Glasgow — *Glasgow, Glasgow*

Principia Consortium Study Abroad — *2010*

Employment

Remote, Chicago, IL

Computation and Informatics in Biology and Medicine (CIBM) Postdoctoral Fellow — *Jun 2021 - present*

- 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

University of Wisconsin-Madison — *Remote, Chicago, IL*

Postdoctoral Research Associate — *Sep 2020 - present*

University of Illinois at Chicago — *Chicago, IL, US*

NIH F31 Fellow — *May 2019 - Aug 2020*

University of Illinois at Chicago — *Chicago, IL, US*

Ph.D. Student — *Aug 2015 - Aug 2020*

- Natural product drug dicovery, 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 undergradaute and graduate students leading to publishable studies

Deerland Probiotics & Enzymes — *Kennesaw, GA, US*

Research and Development Technician — *Mar 2013 - Aug 2015*

- 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

Bonner Foundation — *Rome, GA, US*

Bonner Scholar — *Aug 2008 - May 2012*

- Four-year community service scholarship requiring weekly and summer commitments.

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.**.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

Rees, E. R., Uppal, S., **Clark, C. M.**.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

Waterworth, S. C., Rees, E. R., **Clark, C. M.**.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

Clark, C. M..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..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

Elfeki, M., Mantri, S., **Clark, C. M.**.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/acschembio.1c00653

Leao, T. F., **Clark, C. M.**.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

Clark, C. M..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

Braesel, J., **Clark, C. M.**.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 diazaquinomycins. *Microbiology Resource Announcements. Citations: 2*. 10.1128/mra.00165-19

Clark, C. M..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

Costa, M. S., **Clark, C. M.**.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

Clark, C. M..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

How to write reproducible code for data science — *Sep 2023*
- Chicago R User Group

Reproducibly building and analyzing knowledge graphs for drug discovery with Nextflow, Neo4j and Python — *Aug 2023*
- Chicago Python User Group

SocialGene: Large Scale Knowledge Graphs for Microbial Based Drug Discovery — *Mar 2023*
- Computation and Informatics in Biology and Medicine Seminars

Information-Rich Platforms for Natural Product Antibiotic Drug Discovery and Microbial Characterization — *Jan 2023*
- Northeastern University Department of Chemistry and Chemical Biology

SocialGene: A Large Scale Search Engine to Find Metagenomic BGCs in Free-Living Organisms — *Jan 2023*
- 2023 ASP Younger Members Symposium

Large Scale Analysis of Protein Homology for Microbial Drug Discovery — *Jun 2022*
- National Library of Medicine (NLM) T15 Training Conference

Towards near-instant, repository-scale searching for homologous BGCs with Socialgene (Selected alternate speaker, didn't present) — *Mar 2022*
- Gordon Research Conference on Marine Natural Products

New Computational Tools for Top-Down and Bottom-Up Natural Product Drug Discovery — *Nov 2021*
- Computation & Informatics in Biology & Medicine Seminars BMI 915

IDBac: Bioinformatics Software for Microbial Drug Discovery Prioritization and Culturomics Characterization — *Jun 2020*
- St. Jude National Graduate Student Symposium (cancelled due to Covid19)

Protein MS isn't the only MS… Programming in R for Metabolomics Mass Spectrometry — *May 2020*
- May Institute 2020: Future developers meeting

IDBac: Bioinformatics Software for Microbial Drug Discovery Prioritization and Culturomics Characterization — *Feb 2020*
- Gordon Research Conference on Marine Natural Products
- Gordon Research Seminar (GRS) on Marine Natural Products

Your Missing Step in Reproducible R Programming: Continuous Deployment — *Aug 2019*
- R/Pharma, Harvard University

Bioinformatics in R — *Apr 2019*
- satRdays Chicago

Single Function Lightning Talks: "lengths(), not length()" — *Jan 2019*
- Chicago R User Group

IDBac: A New Paradigm in Developing Microbial Libraries for Drug Discovery — *Aug 2018*
- R/Pharma, Harvard University

IDBac: A Shiny App to Analyze Bacterial Fingerprints and Aid in the Discovery of Potential New Antibiotics — *Jan 2018*
- Chicago R User Group

IDBac: A proteomic & chemometric pipeline for rapid bacterial characterization — *Mar 2017*
- Center for Biomolecular Sciences, UIC

Rational design of bacterial strain libraries for drug discovery — *Nov 2016*
- UIC Specialized Metabolite Community

Use of MALDI-MS to Create 'Smart' Libraries for Drug-Lead Discovery — *Jul 2016*
- Chicago Mass Spec Day

HPLC-DAD Method for Trace Detection of Benzoic and Sorbic Acids in High Protein Matrices — *Apr 2015*
- SSAOAC Annual Meeting

In-Progress

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

Select Individual Software Projects

Python, Django, Nextflow, Rust, High-throughput computing
SOCIALGENE — *Repository-scale genome pattern search platform* — *2021-2023*

R, Javascript, Node/Electron
ELECTRICSHINE — *Shiny packaging with Electron* — *2019*

R, Shiny
MZEASY — *Shiny app for converting and visualizing mass spectrometry data* — *2019*

R, Rmarkdown
MZPLOTTER — *Automated summary of of LC-MS/MS data with interactive Rmarkdown reports* — *2019*

R, Shiny
MZFROMIMAGE — *Predict a mass spectrum's values from a static image file* — *2019*

R
MGFPARSE — *Low-dependency R package for quickly and efficiently parsing mgf files into R* — *2019*

R, Shiny, Electron
IDBAC — *MALDI protein and small molecule bioinformatics platform* — *2018-2023*

Select Team Software Projects

Nextflow

Benchmark metagenomic profiling/binning software

metaBenchmarks

2021

Python, Nextflow

Automated binning pipeline for single metagenomes

Autometa

2020-2023

Workshops (host)

ASP Annual Meeting (Co-host) *Jul 2022*

- Hands-On training of IDBac, an informatics tool for strain prioritization

Department of Pharmacognosy *May 2019*

- IDBac tutorial

Workshops (participant)

Artificial Intelligence for Natural Product Drug Discovery (Invitation-Only; Lorentz Center) *Sep 2021*

Integration of Metabolomics and Genomics (University of Chicago) *Aug 2019*

PATRIC/RAST Workshop (Argonne National Laboratory) *Dec 2016*

Teaching

Invited Guest Lectures

University of Illinois at Chicago

PSCI 522 Advanced Pharmacognosy (two lectures) *Spring 2022*

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`