Chase M Clark

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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

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

May 2019 - Aug 2020 **NIH F31 Fellow** University of Illinois at Chicago
Chicago, IL, US

Aug 2015 - Aug 2020 **Ph.D. Student** University of Illinois at Chicago
Chicago, IL, US

- 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

Mar 2013 - Aug 2015 **Research and Development Technician** Deerland Probiotics & Enzymes
Kennesaw, GA, US

- 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

Aug 2008 - May 2012 **Bonner Scholar** Bonner Foundation
Rome, GA, US

- 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

1. 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
2. Waterworth, S. C., Rees, E. R., Clark, C. M., Carlson, S., Miller, I. J., Puglisi, M., & Kwan, J. C. (2023). Elevated expression ofsrpRiPPs across bacterial phyla in marine sponges. *Citations: 0.* 10.1101/2023.06.09.544420
3. 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
4. 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
5. 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
6. 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
7. 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/acschembio.1c00653
8. 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
9. 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 diazaquinomycins. *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

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

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

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

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

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

Jun 2022 **Large Scale Analysis of Protein Homology for Microbial Drug Discovery**
- 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)**
- Gordon Research Conference on Marine Natural Products

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

Jun 2020 **IDBac: Bioinformatics Software for Microbial Drug Discovery Prioritization and Culturomics Characterization**
- 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**
- May Institute 2020: Future developers meeting

Feb 2020 **IDBac: Bioinformatics Software for Microbial Drug Discovery Prioritization and Culturomics Characterization**
- 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**
- R/Pharma, Harvard University

Apr 2019 **Bioinformatics in R**
- satRdays Chicago

Jan 2019 **Single Function Lightning Talks: "lengths(), not length()"**
- 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 pipleine**
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 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)

Jul 2022 **ASP Annual Meeting (Co-host)**
- Hands-On training of IDBac, an informatics tool for strain prioritization

May 2019 **Department of Pharmacognosy**
- IDBac tutorial

Workshops (participant)

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

Spring 2022 **PSCI 522 Advanced Pharmacognosy (two lectures)**
University of Illinois at Chicago

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