

# Chase Clark

📍 University of Wisconsin-Madison, School of Pharmacy

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## Employment

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

## Experience

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

## Data Science Skills

**Bioinformatics:** metabonomics () • genomics () • metagenomics ()

**Cloud Computing:** remote server computing (ssh, etc) • high-performance and high-throughput computing (Open science grid, HTCondor)

**Communication:** presentations (public speaking, technical writing, peer-reviewed publications, SOPs) • writing (customer-facing documents, peer-reviewed publications, SOPs) • full-stack design (Shiny, Flask, Django) • reports (Rmarkdown, Jupyter) • visualization (Base R, ggplot2, plotly, leaflet, cytoscape, networkx, gephi, etc)

**Programming:** general (R, Python) • database (Neo4j, SQL) • automation (Nextflow, Make) • containers (Docker) • pipeline (Nextflow, Make)

**Software Development:** source control (Git) • CI/CD (Github, Travis, Azure, DevOps, etc.) • automated testing (testthat, pytest, etc)

**Statistics:** machine learning () • experimental design ()

## Select Individual Software Projects

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

## Select Team Software Projects

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

## Talks

2023-09-21	<b>Chicago R User Group</b> • How to write reproducible code for data science
2023-08-10	<b>Chicago Python User Group</b> • Reproducibly building and analyzing knowledge graphs for drug discovery with Nextflow, Neo4j and Python
2023-03-07	<b>Computation and Informatics in Biology and Medicine Seminars</b> • SocialGene: Large Scale Knowledge Graphs for Microbial Based Drug Discovery
2023-01-30	<b>Northeastern University Department of Chemistry and Chemical Biology</b> • Information-Rich Platforms for Natural Product Antibiotic Drug Discovery and Microbial Characterization
2023-01-30	<b>2023 ASP Younger Members Symposium</b> • SocialGene: A Large Scale Search Engine to Find Metagenomic BGCs in Free-Living Organisms

2022-06-23	<b>National Library of Medicine (NLM) T15 Training Conference</b> <ul style="list-style-type: none"> <li>Large Scale Analysis of Protein Homology for Microbial Drug Discovery</li> </ul>
2022-03-09	<b>Gordon Research Conference on Marine Natural Products</b> <ul style="list-style-type: none"> <li>Towards near-instant, repository-scale searching for homologous BGCs with Social-gene (Selected alternate speaker, didn't present)</li> </ul>
2021-11-02	<b>Computation &amp; Informatics in Biology &amp; Medicine Seminars BMI 915</b> <ul style="list-style-type: none"> <li>New Computational Tools for Top-Down and Bottom-Up Natural Product Drug Discovery</li> </ul>
2020-06-01	<b>St. Jude National Graduate Student Symposium (cancelled due to Covid19)</b> <ul style="list-style-type: none"> <li>IDBac: Bioinformatics Software for Microbial Drug Discovery Prioritization and Culturomics Characterization</li> </ul>
2020-05-08	<b>May Institute 2020: Future developers meeting</b> <ul style="list-style-type: none"> <li>Protein MS isn't the only MS... Programming in R for Metabolomics Mass Spectrometry</li> </ul>
2020-02-25	<b>Gordon Research Conference on Marine Natural Products</b> <ul style="list-style-type: none"> <li>IDBac: Bioinformatics Software for Microbial Drug Discovery Prioritization and Culturomics Characterization</li> </ul>
2020-02-23	<b>Gordon Research Seminar (GRS) on Marine Natural Products</b> <ul style="list-style-type: none"> <li>IDBac: Bioinformatics Software for Microbial Drug Discovery Prioritization and Culturomics Characterization</li> </ul>
2019-08-23	<b>R/Pharma, Harvard University</b> <ul style="list-style-type: none"> <li>Your Missing Step in Reproducible R Programming: Continuous Deployment</li> </ul>
2019-04-27	<b>satRdays Chicago</b> <ul style="list-style-type: none"> <li>Bioinformatics in R</li> </ul>
2019-01-23	<b>Chicago R User Group</b> <ul style="list-style-type: none"> <li>Single Function Lightning Talks: "lengths()", not length()"</li> </ul>
2018-08-15	<b>R/Pharma, Harvard University</b> <ul style="list-style-type: none"> <li>IDBac: A New Paradigm in Developing Microbial Libraries for Drug Discovery</li> </ul>
2018-01-27	<b>Chicago R User Group</b> <ul style="list-style-type: none"> <li>IDBac: A Shiny App to Analyze Bacterial Fingerprints and Aid in the Discovery of Potential New Antibiotics</li> </ul>
2017-03-09	<b>Center for Biomolecular Sciences, UIC</b> <ul style="list-style-type: none"> <li>IDBac: A proteomic &amp; chemometric pipeline for rapid bacterial characterization</li> </ul>
2016-11-03	<b>UIC Specialized Metabolite Community</b> <ul style="list-style-type: none"> <li>Rational design of bacterial strain libraries for drug discovery</li> </ul>
2016-07-22	<b>Chicago Mass Spec Day</b> <ul style="list-style-type: none"> <li>Use of MALDI-MS to Create 'Smart' Libraries for Drug-Lead Discovery</li> </ul>
2015-04-15	<b>SSAOAC Annual Meeting</b> <ul style="list-style-type: none"> <li>HPLC-DAD Method for Trace Detection of Benzoic and Sorbic Acids in High Protein Matrices</li> </ul>

## Awards

2021-present	<b>Computation and Informatics in Biology and Medicine (CIBM) Training Program (T32)</b> \$100,000.00
2020	<b>St. Jude National Graduate Student Symposium (cancelled due to Covid19)</b> One of 40 participants selected from 1,000 invite-only applications
2019-2020	<b>NIH Predoctoral Individual National Research Service Award (F31)</b> \$90,000.00

2018	<b>R/Pharma, Travel Award</b> \$500
2017	<b>W.E. van Doren Scholar</b> \$1,000
2017	<b>American Society of Pharmacognosy Student Travel Award</b> \$600
2017	<b>University of Illinois at Chicago Provost/Deiss Award</b> \$2,500
2008-2012	<b>Bonner Scholar</b> 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	<b>Academic Scholarship</b>
2011	<b>McCaleb, Hubert Scholarship</b>
2011	<b>Frank Plummer Scholarship</b>
2010	<b>Griggs Academic Scholarship</b>
2009	<b>John R. Bertrand Scholarship</b>
2008	<b>Sierra Club College Scholarship</b>
2008	<b>Cherokee Area Eagle Scout of the Year Scholarship</b>

## Publications

1. 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
2. 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
3. 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
4. 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
5. 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
6. 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
7. 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
8. 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
9. 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
10. 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