Chase Clark

University of Wisconsin-Madison, School of Pharmacy

chasemc ChasingMicrobes chasingmicrobes@gmail.com hirechase chasemc.github.io

Employment

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

Experience

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.

Data Science Skills

Bioinformatics: metabomics () • 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

2022	**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	**IDBac** MALDI protein and small molecule bioinformatics platform	R, Shiny, Electron

Select Team Software Projects

2021	**metaBenchmarks** Benchmark metagenomic profiling/binning software	Nextflow
2020-2022	**Autometa** Automated binning pipeline for single metagenomes	Python, Nextflow

Talks

2023-08-10 **ChiPy**
- Reproducibly building and analyzing knowledge graphs for drug discovery with Nextflow, Neo4j and Python

2023-03-07 **Computation and Informatics in Biology and Medicine Seminars**
- SocialGene: Large Scale Knowledge Graphs for Microbial Based Drug Discovery

2023-01-30 **Northeastern University Department of Chemistry and Chemical Biology**
- Information-Rich Platforms for Natural Product Antibiotic Drug Discovery and Microbial Characterization

2023-01-30 **2023 ASP Younger Members Symposium**
- SocialGene: A Large Scale Search Engine to Find Metagenomic BGCs in Free-Living Organisms

2022-06-23 **National Library of Medicine (NLM) T15 Training Conference**
- Large Scale Analysis of Protein Homology for Microbial Drug Discovery

2022-03-09 **Gordon Research Conference on Marine Natural Products**
- Towards near-instant, repository-scale searching for homologous BGCs with Social-gene (Selected alternate speaker, didn't present)

2021-11-02 **Computation & Informatics in Biology & Medicine Seminars BMI 915**
- New Computational Tools for Top-Down and Bottom-Up Natural Product Drug Discovery

2020-06-01 **St. Jude National Graduate Student Symposium (cancelled due to Covid19)**
- IDBac: Bioinformatics Software for Microbial Drug Discovery Prioritization and Culturomics Characterization

2020-05-08 **May Institute 2020: Future developers meeting**
- Protein MS isn't the only MS… Programming in R for Metabolomics Mass Spectrometry

2020-02-25 **Gordon Research Conference on Marine Natural Products**
- IDBac: Bioinformatics Software for Microbial Drug Discovery Prioritization and Culturomics Characterization

2020-02-23 **Gordon Research Seminar (GRS) on Marine Natural Products**
- IDBac: Bioinformatics Software for Microbial Drug Discovery Prioritization and Culturomics Characterization

2019-08-23 **R/Pharma, Harvard University**
- Your Missing Step in Reproducible R Programming: Continuous Deployment

2019-04-27 **satRdays Chicago**
- Bioinformatics in R

2019-01-23 **Chicago R User Group**
- Single Function Lightning Talks: "lengths(), not length()"

2018-08-15 **R/Pharma, Harvard University**
- IDBac: A New Paradigm in Developing Microbial Libraries for Drug Discovery

2018-01-27 **Chicago R User Group**
- IDBac: A Shiny App to Analyze Bacterial Fingerprints and Aid in the Discovery of Potential New Antibiotics

2017-03-09 **Center for Biomolecular Sciences, UIC**
- IDBac: A proteomic & chemometric pipeline for rapid bacterial characterization

2016-11-03 **UIC Specialized Metabolite Community**
- Rational design of bacterial strain libraries for drug discovery

2016-07-22 **Chicago Mass Spec Day**
- Use of MALDI-MS to Create 'Smart' Libraries for Drug-Lead Discovery

2015-04-15 **SSAOAC Annual Meeting**
- HPLC-DAD Method for Trace Detection of Benzoic and Sorbic Acids in High Protein Matrices

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** Four-year community service scholarship for students with need of financial assistance and a commitment to service
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. 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
2. 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
3. Mullowney, M. W., Duncan, K. R., Elsayed, S. S., Garg, N., van der Hooft, J. J. J., Martin, N. I., Meijer, D., Terlouw, B. R., Biermann, F., Blin, K., Durairaj, J., González, M. G., Helfrich, E. J. N., Huber, F., Leopold-Messer, S., Rajan, K., de Rond, T., van Santen, J. A., Sorokina, M., … Medema, M. H. (2023). Artificial intelligence for natural product drug discovery. *Nature Reviews Drug Discovery. Citations: 0.* 10.1038/s41573-023-00774-7
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