# Chase Clark

University of Wisconsin-Madison, School of Pharmacy, VCRGE/BIOTECH/GENOMICS

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## Employment

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|---|---|---|
| 2020 | **PhD Pharmacognosy**<br>Chicago, IL | University of Illinois at Chicago |
| 2012 | **BS Biochemistry**<br>Mount Berry, GA | Berry College |
| 2010 | **Principia Consortium Study Abroad**<br>Glasgow, Glasgow | University of Glasgow |

## Experience

Jun 2021 - present **Computation and Informatics in Biology and Medicine (CIBM) Postdoctoral Trainee**
Remote, Chicago, IL

- Training grant funded through the National Library of Medicine
- Developing genomic and metagenomic bioinformatics software
- Currently developing a repository scale analysis platform (synthesizing tens of billions of data points)

Sep 2020 - present **Postdoctoral Research Associate** University of Wisconsin-Madison
Remote, Chicago, IL

May 2019 - Aug 2020 **F31 Fellow** U.S. National Institutes of Health (NIH)
Chicago, IL, US

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

- 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 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

**Cloud Computing**: Remote server computing (ssh, etc) ● high-performance and high-throughput computing (Open science grid, HTCondor)
**Communication**: presentations () ● full-stack design (Shiny, Flask) ● reports (Rmarkdown, Jupyter) ● visualization (Base R, ggplot2, plotly, leaflet, cytoscape, networkx, gephi, etc) ● technical writing (peer-reviewed publications)
**Pipeline**: Nextflow, Make ()
**Programming Languages**: R () ● Python () ● Neo4j () ● SQL ()
**Software Development**: source control (Git) ● CI/CD (Github, Travis, Azure, DevOps, etc.) ● automated testing ()
**Statistics**: machine learning () ● data analysis () ● cluster analysis () ● factor analysis () ● principal components analysis () ● cross-validation () ● experimental design ()

## Select Individual Software Projects

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

## Select Team Software Projects

| | | |
|---|---|---|
| 2021 | **Autometa**<br>Automated binning pipeline for single metagenomes | Python, Nextflow |
| 2021 | **metaBenchmarks**<br>Benchmark metagenomic profiling/binning software | Nextflow |

## Awards

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|---|---|
| 2017 | **American Society of Pharmacognosy Student Travel Award**<br>$600 |
| 2017 | **University of Illinois at Chicago Provost Deiss Award**<br>$2,500 |
| 2019-2020 | **NIH Predoctoral Individual National Research Service Award (F31)**<br>$90,000.00 |
| 2021-2023 | **Computation and Informatics in Biology and Medicine (CIBM) training**<br>$100,000.00 |

## Talks

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|---|---|
| 2020-06-01 | **IDBac: Bioinformatics Software for Microbial Drug Discovery Prioritization and Culturomics Characterization**<br>St. Jude National Graduate Student Symposium (cancelled due to Covid19) |
| 2020-05-08 | **Protein MS isn't the only MS… Programming in R for Metabolomics Mass Spectrometry**<br>May Institute 2020: Future developers meeting |
| 2020-02-25 | **IDBac: Bioinformatics Software for Microbial Drug Discovery Prioritization and Culturomics Characterization**<br>Gordon Research Conference on Marine Natural Products |

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

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

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

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

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

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

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

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

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

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

## Publications


1. 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. *Citations: 0*. 10.1038/s42255-021-00429-0
2. 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. *Citations: 2*. 10.1128/msystems.00813-19
3. 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. *Citations: 7*. 10.3791/59219
4. 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. *Citations: 0*. 10.1128/mra.00165-19
5. 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. *Citations: 7*. 10.1021/acs.jnatprod.9b00168
6. 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. *Citations: 34*. 10.1073/pnas.1801247115