

Chase Clark

Postdoctoral Research Associate

Curriculum Vitae

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📍 VCRGE/BIOTECH/GENOMICS, School of Pharmacy, University of Wisconsin-Madison
🏠 chasemc.github.io
✉ chasingmicrobes@gmail.com
🐦 @ChasingMicrobes
🔗 chasemc
🌐 hirechase

Skills

- Bioinformatics
- Metabolomics
- Genomics/Metagenomics
- Natural product isolation and drug discovery

Current Bioinformatic Tools

- Advanced: R, Rmarkdown, Shiny, Neo4j, Nextflow
- Intermediate: Python, Flask, HTML
- Familiar: JavaScript

Education

2020	PhD Pharmacognosy Chicago, IL	University of Illinois at Chicago
2012	BS Biochemistry Mount Berry, GA	Berry College
2010	Principia Consortium Study Abroad Glasgow, Glasgow	University of Glasgow

Experience

2020-Current	Postdoctoral Research Associate School of Pharmacy, Pharmaceutical Sciences Division	University of Wisconsin-Madison
2021-Current	Computation and Informatics in Biology and Medicine (CIBM) Trainee	National Library of Medicine
2019-2020	F31 Fellow National Center for Complementary and Integrative Health	U.S. National Institutes of Health (NIH)
2015-2019	Ph.D. Student Medicinal Chemistry and Pharmacognosy	University of Illinois at Chicago
2013-2015	Research and Development Technician R&D, Method Development	Deerland Enzymes
2008-2012	Bonner Scholar	Bonner Foundation

Recent Solo Projects

2021	socialgene Repository-scale genome search platform	Python, Flask app, Nextflow, 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 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
2018	IDBac MALDI protein and small molecule bioinformatics platform	R, Shiny, Electron

Recent Team Projects

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

Awards

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

Talks

2020-06-01	IDBac: Bioinformatics Software for Microbial Drug Discovery Prioritization and Culturomics Characterization 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 May Institute 2020: Future developers meeting
2020-02-25	IDBac: Bioinformatics Software for Microbial Drug Discovery Prioritization and Culturomics Characterization 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

Poster Presentations

11/11/2016	Innovating Microbial Libraries for Drug Discovery Using MALDI-TOF-MS and the Cultivable Freshwater Sponge Microbiome. UIC College of Pharmacy Research Day	Chicago, IL
2/10/2017	MALDI-TOF MS to Innovate Microbial Library Generation in Drug Discovery UIC College of Pharmacy Research Day	Chicago, IL
1/1/2018	IDBac as a Tool to Evaluate Environmental Bacterial Collections in a Single Week American Society of Pharmacognosy	Lexington, KY

7/30/2017	Use of MALDI-TOF MS to Generate Low Redundancy Taxonomic and Specialized Metabolite Libraries from Freshwater Sponge Microbiomes American Society of Pharmacognosy	Portland, OR
7/14/2017	MALDI-TOF MS to Innovate Microbial Library Generation in Drug Discovery Chicago Mass Spec Day	Chicago, IL
5/24/2017	MALDI-TOF MS to Innovate Microbial Library Generation in Drug Discovery MBRB Research Day, UIC	Chicago, IL
07/30/2019	Using IDBac to Investigate the Microbial and Natural Product Potential of Freshwater Sponges WI American Society of Pharmacognosy	Madison,

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