Chase Clark

Postdoctoral Research Associate

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Curriculum Vitae
September 2021

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 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** Python, Nextflow
Automated binning pipeline for single metagenomes

2021 **metaBenchmarks** Nextflow
Benchmark metagenomic profiling/binning software

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.** Chicago, IL
UIC College of Pharmacy Research Day

2/10/2017 **MALDI-TOF MS to Innovate Microbial Library Generation in Drug Discovery** Chicago, IL
UIC College of Pharmacy Research Day

1/1/2018 **IDBac as a Tool to Evaluate Environmental Bacterial Collections in a Single Week** Lexington, KY
American Society of Pharmacognosy

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** American Society of Pharmacognosy	Madison, WI

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