

Alex Crocker

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Professional Summary

Computational Biologist and Bioinformatician with 6+ years of experience translating large -omics and imaging datasets into mechanistic biological insights. Expert in building reproducible, version controlled pipelines and software for mathematical modelling of Biology. Proven track record of cross-functional scientific collaboration, technical leadership, and driving data-to-hypothesis translation for publications and discovery.

Experience

Postdoctoral Fellow | University of Minnesota - Biotechnology Institute | Nov. 2025 - Present

- Engineered and characterized synthetic microbial biofilms and living materials for environmental remediation.
- Led maintenance and user training for the department's microscopy equipment.

Visiting Scholar | Duke University School of Medicine | Mar. 2023 - Aug. 2025

- Developed and standardized bioinformatic software and workflows across our laboratory, reducing barriers for users and ensuring reproducibility.
- Coordinated research projects with domestic and international collaborators, leading to multiple publications.

Graduate Researcher | University of North Carolina at Chapel Hill | Aug. 2019 - June 2025

- Conceptualized, built, and benchmarked PDE mathematical models in Python and Julia to characterize intracellular signaling networks, translating raw experimental data into mechanistic hypotheses.
- Designed and taught a Python for Biologists curriculum, training more than 50 graduate students and faculty.

Teaching assistant | Woods Hole Marine Biological Laboratory | June 2024

- Instructed PhD and Postdoctoral researchers on integrating high-throughput imaging pipelines with computational modeling frameworks.
- Guided teams from hypothesis generation and experimental design through to final research presentations.

Laboratory Technician | Dartmouth College | Sep. 2016 - July 2019

- Collaborated with medical professionals to design and execute translational research projects.
- Contributed novel methods, data visualizations, and experimental data for publications in scholarly journals.

Education

PhD, Bioinformatics and Computational Biology | UNC Chapel Hill, Chapel Hill NC | Aug. 2019 - Aug. 2025

BA, Biology | Hendrix College, Conway AR | Aug. 2011 - May 2016

Skills

Computational Pipeline Tools: Python (NumPy, Pandas, scikit-learn, Biopython), R (R-Shiny, ggplot2), Julia, Matlab, Snakemake, Docker, Git/GitHub, Conda, Unix/Linux command line, Unix scripting

Data Science and Modeling: Statistical modeling, mathematical modeling (ODE & PDE), multi-omics data integration, metabolic modeling, data mining, exploratory data analysis (EDA), image analysis

Biological and Wet Lab: Metagenomics & Transcriptomics, microbiology (bacteria and fungi, biofilm mechanics), molecular biology, fluorescence microscopy (Confocal, FRAP, TIRF-M), flow cytometry

Hobbies: Homebrewing, rock climbing, insect photography, running

Publications

Sequence and structure of protein binding sites in RNA impact biomolecular condensates

Sierra J. Cole, Scott R. Allen, Bryan B. Guzmán, Yue Hu, Benjamin M. Stormo, Christine A. Roden, Joanne Ekena, Vita Zhang, Grace A. McLaughlin, [Alex W. Crocker](#), Alain Laederach, Daniel Dominguez, Amy S. Gladfelter (2026) Molecular Biology of the Cell

Mechanisms of nuclear segregation in a multinucleate multibudding yeast

Claudia A. Petrucco, [Alex W. Crocker](#), Alison C.E. Wirshing, Analeigha V. Colarusso, Maya Waarts, Amy S. Gladfelter, Daniel J. Lew (2025) Journal of Cell Biology

Negative feedback equalizes polarity sites in a multi-budding yeast

[Alex W. Crocker](#), Claudia A. Petrucco, Kaiyun Guan, Alison C.E. Wirshing, Joanne L. Ekena, Daniel J. Lew, Timothy C. Elston, Amy S. Gladfelter (2025) Current Biology

Assessing contributions of DNA sequences at the 3' end of a yeast gene on yFACT, RNA polymerase II, and nucleosome occupancy

Samuel E. Byrd, Brianna Hoyt, Sydney A. Ozersky, [Alex W. Crocker](#), Daniel Habenicht, Mattie R Nester, Heather Prowse, Claire E Turkal, Lauren Joseph, Andrea A Duina (2024) BMC Research Notes

Tools for live-cell imaging of cytoskeletal and nuclear behavior in the unconventional yeast, *Aureobasidium pullulans*

Claudia A. Petrucco, [Alex W. Crocker](#), Alec D'Alessandro, Edgar M. Medina, Olivia Gorman, Jessica McNeill, Amy S. Gladfelter, Daniel J. Lew (2024) Molecular Biology of the Cell

In host evolution of *Exophiala dermatitidis* in cystic fibrosis lung micro-environment.

Tania Kurbessoian, Daniel Murante, [Alex W. Crocker](#), Deborah A. Hogan, Jason E. Stajich (2023) G3 Genes|Genomes|Genetics

Calprotectin-mediated zinc chelation inhibits *Pseudomonas aeruginosa* protease activity in cystic fibrosis sputum.

Danielle M. Vermilyea, [Alex W. Crocker](#), Alex H. Gifford, Deborah A. Hogan (2021) Journal of Bacteriology

***Pseudomonas aeruginosa* ethanol oxidation by AdhA in low oxygen environments.**

[Alex W. Crocker](#), Colleen E. Harty, John H. Hammond, Sven D. Willger, Pedro Salazar, Nicholas J. Jacobs, Deborah A. Hogan (2019) Journal Bacteriology

The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens.

Naihui Zhou, Yuxiang Jiang, Timothy R Bergquist, Alexandra J Lee, Balint Z Kacsoh, [Alex W. Crocker](#), et al. (2019) Genome Biol

Evolution of drug resistance in an antifungal-naïve chronic *Candida lusitanae* infection.

Elora G. Demers, Amy Biermann, Sawyer Masonjones, [Alex W. Crocker](#), Alix Ashare, Jason Stajich, Deborah Hogan (2018) PNAS

Profiling of bacterial and fungal microbial communities in cystic fibrosis sputum using RNA.

Nora Grahl, Emily L. Dolben, Laura M. Filkins, [Alex W. Crocker](#), Sven D. Willger, Hillary G. Morrison, Mitchell L. Sogin, Alix Ashare, Alex H. Gifford, Nicholas J. Jacobs, Joseph D. Schwartzman, Deborah A. Hogan (2018) mSphere

Use of RNA-Protein Complexes for Genome Editing in Non-*albicans* *Candida* Species.

Nora Grahl, Elora G. Demers, [Alex W. Crocker](#) and Deborah A. Hogan (2017). mSphere