

Marielle Russo

Microbiology PhD candidate, MIT · DJ

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FIG. 01

Summary

PhD candidate in Microbiology at MIT developing next-generation directed evolution methodologies to engineer proteins with enhanced and novel functions. Expertise spans computational protein design (ProteinMPNN, ESMFold), machine learning, molecular biology, high-throughput screening, and lab automation (PyLabRobot, Praxis development). Research focuses on overcoming fitness barriers by integrating structure-guided design, computational optimization techniques, and experimental validation using PRANCE, with the ultimate goal of creating a generalizable framework for navigating complex fitness landscapes.

FIG. 02

Education

Microbiology, BSc

Texas A&M University · College Station, TX · 2019 · GPA: 3.7

FIG. 03

Research experience

Graduate Student, Microbiology PhD Program

Ovchinnikov Lab, Biology, Massachusetts Institute of Technology ·
Cambridge, MA · 2024 – Present

- Developed an enzyme engineering pipeline integrating multiple sequence alignments (MSA) using the UniRef database with ProteinMPNN and ESM to predict thermostable protease variants to seed evolutions with. An initial pool of over 500 ProteinMPNN designs was further filtered using inverse folding and protein language model likelihood metrics to ~120 candidate sequences for each protease.
- Developing Praxis, an open-source, PyLabRobot-based lab automation framework with an intuitive, tiered-access user interface promoting robust documentation, standardized data management, version control, and cross-platform hardware compatibility.

Graduate Researcher

Sculpting Evolution, Media Lab, Massachusetts Institute of Technology ·
Cambridge, MA · 2023 – 2024

Rotation November 2022; full appointment June 2023 – January 2024.

- Characterized a library of TEV protease variants using PRANCE, evaluating their activity and specificity across a panel of four diverse peptide substrates, presenting findings at the Molecular Mechanisms of Evolution Gordon Research Conference.
- Debugged and improved a PyHamilton PRANCE experimental script, incorporating continuous well-mixing for enhanced culture homogeneity.
- Contributed to the PyLabRobot open-source project by developing a new pump module and designing and testing a 3D-printed pipette tip washer, increasing hardware compatibility.
- Developed and optimized a high-throughput assay (growth curves and DNS) to screen over 100 environmental isolates, collected from over 50 locations, for L-glucose catabolism. The assay processed over 1000 data samples per time point, including biological and technical triplicates, to robustly characterize sugar consumption.
- Developed a fully automated, low-volume, high-throughput split luciferase assay pipeline for characterizing protein-protein interactions, enabling efficient evaluation of over 1500 designs.

Research Assistant I

Reynolds Lab, Department of Bioinformatics, UT Southwestern Medical
Center · Dallas, TX · 2020 – 2022

- Developed strategies, outlined assays, and deployed proposed schema to refine the purification of a unique putatively light-dependent recombinant protein, eliminating contamination that disrupted crystallization efforts.
- Performed the initial hardware configuration, proposed and conducted assessments, and elaborated SOPs for the eVOLVER, an open-source continuous culture framework incorporating Python and Arduino scripting.
- Independently managed and pursued additional research projects, efficiently executing collaboratively formulated experimentation.

Research Technician II

Danhuser/Schmid Lab, Department of Cell Biology, UT Southwestern Medical
Center · Dallas, TX · 2019 – 2020

- Developed and executed experiments examining quiescence entry and cell cycle in *S. cerevisiae* via genetic manipulation and fluorescence microscopy imaging coupled with computational analysis.
- Independently managed lab databases and stock, including solutions and media, and coordinated planning for ongoing and frequently shifting research projects.

Lab Assistant

Department of Entomology, Texas A&M University · College Station, TX ·
2018 – 2019

- Reared and supervised discrete *A. aegypti* lines through all stages of development.

Undergraduate Research Assistant

SACLabs, Texas A&M University · College Station, TX · 2016 – 2017

Primarily summer work.

- Executed and analyzed experiments studying structure-function relationships of Acetyl-CoA Carboxylase in *M. tuberculosis*.
- Production, purification, and crystallization of proteins, and high-throughput screening of compounds for drug discovery.

FIG. 04

Publications

1. James W. McCormick, Jerry C. Dinan, Marielle AX Russo, Kimberly A. Reynolds. Local disorder is associated with enhanced catalysis in an engineered photoswitch (<https://doi.org/10.1101/2024.11.26.625553>). *bioRxiv* Preprint (2024).
2. James W. McCormick, Jerry C. Dinan, Marielle AX Russo, Kimberly A. Reynolds. Determining the mechanisms of the allosteric architecture of DHFR. *Biophysical Journal* 122(3), 49a (2023).
3. Orlando Argüello-Miranda, Ashley J. Marchand, Taylor Kennedy, Marielle A.X. Russo, Jungsik Noh. Cell cycle-independent integration of stress signals by Xbp1 promotes Non-G1/G0 quiescence entry (<https://doi.org/10.1083/jcb.202103171>). *Journal of Cell Biology* 221(1), e202103171 (2022).
4. James W. McCormick, Marielle AX Russo, Samuel Thompson, Aubrie Blevins, Kimberly A. Reynolds. Structurally distributed surface sites tune allosteric regulation (<https://elifesciences.org/articles/68346v1>). *eLife* 10, e68346 (2021).
5. Marielle Russo, Tram Le, Russell Moreland, Carlos F. Gonzalez, Mei Liu, Jolene Ramsey. Complete Genome Sequence of Xanthomonas Phage Pagan (<https://journals.asm.org/doi/full/10.1128/MRA.01031-19>). *Microbiology Resource Announcements* 8(39), e01031-19 (2019).

FIG. 05

Posters

- TEvolution: Exploring Directed Evolution of TEV Protease – *Molecular Mechanisms of Evolution Gordon Research Conference* (2023)

- Crystallization of a Synthetic Light-Dependent Allosteric Switch – *UT Southwestern Biophysics Department Retreat* (2020)
- Temporal coordination of stress responses and cell cycle controls defines a quiescence entry program in *S. cerevisiae* – *UT Southwestern Cell Biology Department Retreat* (2019)
- A structure-guided fragment-based approach for the discovery of inhibitors targeting Indole-3-glycerol phosphate synthase from *Mycobacterium tuberculosis* – *Texas A&M Undergraduate Research Symposium* (2016)

FIG. 06

Conferences

- Winter Rosetta Conference (2025)
- Society for Lab Automation and Screening (SLAS) (2024)
- Molecular Mechanisms of Evolution Gordon Research Conference (2023)
- American Association of Immunology (2016)

FIG. 07

Funding

Quantifying the Prevalence and Phenotypic Consequences of Transcriptional Irreversibility in Bacteria

National Science Foundation · UT Southwestern – Reynolds Lab · 2022–2026
 · Award No. 2206974 · \$1,093,791

Contributed data and writing; left the lab in September 2022.

Open Philanthropy · MIT – Esvelt Lab · 2023–2025

MIT Microbiology Program Lab Transition Funding

MIT – Ovchinnikov Lab · 2025

FIG. 08

Academic service and leadership

Microbial Engineering and Sciences Seminar (MESS) Series

Co-organizer · 2024 – Present

Co-organize and manage a trainee-led seminar series focused on microbial engineering and sciences: identifying and inviting speakers, managing event logistics, and promoting the series to trainees across Boston-area institutions.

MIT Integrative Microbiology Initiative (MIMI) Seminar Series

Organizer • 2023 – 2024

Managed all aspects of a student-run seminar series fostering interdisciplinary collaboration: speaker selection and invitation, travel arrangements, coordination of meetings with MIT faculty, and logistics.

UT Southwestern Bioinformatics Diversity, Equity, and Inclusion Committee

Committee member • 2022

Collaborated on strategies to increase recruitment and retention of scientists from a wider range of backgrounds.

FIG. 09

Awards and honors

- National Merit Scholar Finalist (2016)

FIG. 10

Skills

Machine Learning

Developing and applying machine learning models for protein design, including de novo models, protein language models (pLMs), and computational filtering metrics. Supervised, unsupervised, and deep learning methods. Scikit-learn, TensorFlow, Jax, PyTorch.

Lab Automation

Programming and optimizing liquid-handling robots using PyHamilton and PyLabRobot. Developed novel automation solutions including liquid pumping array and plate reader support, requiring reverse engineering of firmware commands and extensive testing.

Data Science

Extracting biological and chemical insights from complex datasets, including statistical analysis of biological assays. Data visualization (matplotlib, seaborn, plotly), data wrangling (numpy, pandas, polars), and coevolution analysis using SCA, DCA, and MirrorTrees. SQL and NoSQL.

Full Stack Software Development

Front-end frameworks (React, Flutter), back-end (Python/FastAPI), and databases (PostgreSQL, MongoDB). Lead developer of Praxis. Deployment using AWS and Docker.

Molecular Biology

PCR, qPCR, molecular cloning (Gibson Assembly, Golden Gate) for library construction, DNA sequencing (Sanger, NGS), protein expression in *E. coli*, protein purification (affinity and size exclusion chromatography), and crystallization.

FIG. 11

References

Available on request.