Micah Olivas

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Education

Ph.D., Genetics — 2020–2026 *(expected)*
Stanford University, Stanford, CA
Advisor: Polly Fordyce
Thesis: *Function-informed sequence modeling through high-throughput enzymology*

B.S. with Honors (*summa cum laude*), Biochemistry — 2016–2020
California State University, Fresno, Fresno, CA
Advisor: Laurent Dejean
Thesis: *Particulate matter-induced oxidative stress in alveolar macrophages*

Visiting Student, Chemistry and Cell Biology — 2019
University of Oxford, Oxford, UK
Host Advisor: Aziz Aboobaker

Grants

F31HG013267, National Human Genome Research Institute — 09/2023–08/2026
High-throughput thermodynamic and kinetic measurements for variant effects prediction in a major protein superfamily
Role: PI; Funding: $143,908

Awards and honors

Selected graduate speaker (only graduate student), *Gordon Research Conference on Enzymes*	2025
American Chemical Society Poster Award, *Gordon Research Conference on Enzymes*	2024
Ruth L. Kirschstein National Research Service Award, *National Institutes of Health*	2023
Stanford ADVANCE Scholar	2020–2021
Graduate Fellowship, *Phi Kappa Phi*	2020
Marshall Scholarship Finalist	2020
Amgen Scholar, *Stanford University*	2019
Barry M. Goldwater Scholar	2019
Chemistry Department Honors, *Fresno State*	2019
Presidents Scholar, *Fresno State*	2016
Smittcamp Family Honors Scholar (full-tuition undergraduate scholarship)	2016

Publications

[†]denotes equal contributions

Manuscripts in preparation

1. P. Almhjell[†], M. Olivas[†], F. Zepezauer, D. Herschlag, and P. Fordyce. "Expansive and systematic perturbation of enzyme function via microfluidic variant assays with suppressor tRNAs." Manuscript in preparation.

2. M. Olivas†, P. Almhjell†, F. Zepezauer, D. Herschlag, and P. Fordyce. "uSort-M: scalable isolation of user-defined clones from pooled gene libraries." Manuscript in preparation for ***ACS Synthetic Biology***.

3. M. Olivas, C. Fannjiang, N. Naik, and P. Fordyce. "[Experimental validation of protein language models for enzyme design and characterization]." Manuscript in preparation.

Peer-reviewed publications

1. K. Han, S. E. Pierce, A. Li, K. Spees, G. R. Anderson, J. A. Seoane, Y. H. Lo, M. Dubreuil, M. Olivas, *et al*. "CRISPR screens in cancer spheroids identify 3D growth-specific vulnerabilities." ***Nature*** 580 (2020), 136–141. DOI: gg2bv3

Conference papers

1. C. Fannjiang†, M. Olivas†, *et al*. "Designing active and thermostable enzymes with sequence-only predictive models." *NeurIPS Learning Meaningful Representations of Life workshop* (2022). OpenReview: Nc7EsfpZ7C

Patents

Pending

P. Almhjell, M. Olivas, & P. Fordyce. High-throughput production of protein variants.
U.S. Provisional Patent Application No. 63/916,150.

Contributed talks

Jul 2025	Using high-throughput microfluidic enzymology to investigate machine learning for function prediction *Gordon Research Conference on Enzymes. Waterville Valley, NH*
Apr 2025	Reimagining mutational scanning through microfluidic variant assays with suppressor tRNAs *Chan-Zuckerberg Biohub Interlab Meeting. San Francisco, CA*
Feb 2025	Reimagining mutational scanning through variant assays with suppressor tRNAs *Current Issues in Genetics. Stanford, CA*
May 2024	Insights from high-throughput enzymology in a small enzyme *Current Issues in Genetics. Stanford, CA*
Aug 2023	Beyond Structure: Exploring the Language of Enzyme Function with HT-MEK *Current Issues in Genetics. Stanford, CA*
Mar 2018	Sewn in Your Genes: Reimagining Disease in the Age of Genetic Editing *18th annual Smittcamp Family Honors College Colloquium. Fresno, CA*

Contributed posters

Sep 2025	Reimagining mutational scanning through microfluidic variant assays with suppressor tRNAs *Genetics Department Retreat. Stanford, CA*
Jul 2025	Using high-throughput microfluidic enzymology to investigate machine learning for function prediction *Gordon Research Conference (GRC) on Enzymes. Waterville Valley, NH*
Jun 2025	Reimagining mutational scanning through microfluidic variant assays with suppressor tRNAs *Mutational Scanning Symposium. Barcelona, Spain*
Apr 2025	Reimagining mutational scanning through microfluidic variant assays with suppressor tRNAs *NHGRI Trainee Meeting. Philadelphia, PA*
Jul 2024	Using high-throughput microfluidic enzymology to investigate machine learning for functional prediction *Gordon Research Conference (GRC) on Enzymes. Waterville Valley, NH*
Sep 2023	Leveraging novel protein language models to understand constraints on enzyme function and design *Genetics Department Annual Retreat. Monterey, CA*

2022	Leveraging novel protein language models to understand constraints on enzyme function and design *Chan Zuckerberg Biohub Interlab Confabulation. San Francisco, CA*
Sep 2022	Leveraging novel protein language models to understand constraints on enzyme function and design *Quantitative Biology Institute Bay Area Chemical Biology Symposium. San Francisco, CA*
Sep 2021	Developing predictive models of enzyme function from physics and phylogeny *Genetics Department Annual Retreat. Stanford, CA*
Aug 2019	Genome-wide CRISPR screens in 3D tumor spheroids reveal growth dependencies in lung adenocarcinoma *Stanford Summer Research Program Symposium. Stanford, CA*
July 2018	Development of an inducible Cas9 for temporally controlled gene editing *BioCoRE symposium. Durham, NC*
Apr 2018	PM2.5 Exposure and ROS Production in NR8383 Alveolar Macrophages *CSU Honors Research Conference. Northridge, CA*
Jan 2018	PM2.5 Exposure and ROS Production in NR8383 Alveolar Macrophages *CSU Program for Education and Research in Biotechnology (CSUPERB). Santa Clara, CA*
Apr 2017	Effects of particulate matter aerosols on ROS production in alveolar macrophage cells *Central California Research Symposium. Fresno, CA*

Academic service

Scientific mentorship

Winter 2025	Diego Pomales-Matos	Stanford Genetics Graduate Student
Summer 2024	Forrest Zepezauer	Summer Undergraduate Student