Polly Fordyce

Associate Professor of Bioengineering and of Genetics

NIH Biosketch available Online   Resume available Online

CONTACT INFORMATION

- **Alternate Contact**

  Ana Morzan - Administrative Assistant

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Bio

BIO

Polly Fordyce is an Associate Professor of Genetics and Bioengineering and fellow of the ChEM-H Institute at Stanford, where her laboratory focuses on developing and applying new microfluidic platforms for quantitative, high-throughput biophysics and biochemistry and single-cell genomics. She graduated from the University of Colorado at Boulder with undergraduate degrees in physics and biology before moving to Stanford University, where she earned a Ph.D. in physics for work with Professor Steve Block developing instrumentation and assays for single-molecule studies of kinesin motor proteins. For her postdoctoral research, she worked with Professor Joe DeRisi to develop a new microfluidic platform for understanding how transcription factors recognize and bind their DNA targets as well as a new technology for bead-based multiplexing. She is the recipient of a number of awards, including the NIH New Innovator and Pioneer Awards, an NSF CAREER Award, the 2023 Eli Lilly Award in Biological Chemistry, the 2025 Schmidt Sciences Polymath Award, and is a Chan Zuckerberg Biohub Investigator.

ACADEMIC APPOINTMENTS

- Associate Professor, Bioengineering
- Associate Professor, Genetics
- Member, Bio-X
- Member, SPARK at Stanford
- Institute Scholar, Sarafan ChEM-H
- Member, Wu Tsai Neurosciences Institute

ADMINISTRATIVE APPOINTMENTS

- Director, Stanford Microfluidics Foundry, (2015- present)
- Investigator, Chan Zuckerberg Biohub, (2017- present)

HONORS AND AWARDS

- Alexander Cruikshank Lecturer, Gordon Research Conferences (2026)
- Polymath Award, Schmidt Sciences (2025-2030)
- Fellow, American Association for the Advancement of Science (AAAS) (2025)

- Fellow, American Institute for Medical and Biological Engineering (AIMBE) (2025)
- President's Award for Excellence Through Diversity, Stanford University (2024)
- Pioneer Award (DP1), NIH (2023-2028)
- Eli Lilly Award in Biological Chemistry, Eli Lilly Foundation (2023)
- Young Investigator Award, Protein Society (2023)
- Investigator, Chan Zuckerberg Biohub (2022-2017)
- Breakthrough Science Initiative Award, Ono Pharma Foundation (2019-2022)
- Investigator, Chan Zuckerberg Biohub (2017-2022)
- Alfred P. Sloan Foundation Research Fellow, Alfred P. Sloane Foundarion (2017-2019)
- New Innovator Award (DP2), NIH (2016-2021)
- Scialog Fellow, Gordon & Betty Moore Foundation (2016-2017)
- Pathway to Independence Award (K99), NIH (2012-2014)
- Helen Hay Whitney Postdoctoral Fellowship, Helen Hay Whitney Foundation (2008-2011)
- G. J. Lieberman Fellow, Stanford University (2003-2004)
- Graduate Research Fellow, National Science Foundation (2002-2005)

BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- Editorial Committee Member, Annual Reviews in Biophysics (2024 - present)
- Scientific Advisory Board, Evozyne (2023 - 2025)
- Advisory Board Member, Burroughs Wellcome CASI (2024 - present)
- Co-founder and Scientific Advisory Board, Velocity Bio (2023 - present)
- Advisory Board Member, Cell Systems (2020 - present)

PROFESSIONAL EDUCATION

- Postdoctoral Fellow, University of California San Francisco , Biophysics (2014)
- Ph.D., Stanford University , Physics (2007)
- B.A., University of Colorado at Boulder , Physics, Biology (2000)

PATENTS

- Polly Fordyce, Patrick Almhjell, Micah Olivas. "United States Patent 63/916,150 High-throughput production of protein variants", Leland Stanford Junior University, Chan Zuckerberg Biohub, Oct 16, 2025
- Polly Fordyce, Shawn Costello. "United States Patent 63/759,430 Systems and methods for high-throughput measurement of protein stability and druggable pockets", Leland Stanford Junior University, Feb 17, 2025
- Polly Fordyce, Shawn Costello. "United States Patent 63/759,430 Systems and methods for high-throughput measurement of protein stability and druggable pockets", Leland Stanford Junior University, Feb 12, 2025
- Polly Fordyce, Matt DeJong. "United States Patent 63/741,698 Library-scale single-molecule force spectroscopy on a chip", Leland Stanford Junior University, Jan 17, 2025
- Polly Fordyce, Daria Passow. "United States Patent 63/707,264 Systems and methods for high-throughput protein screening", Leland Stanford Junior University, Dec 15, 2024
- Fordyce, P.M., Hastings, R.L., Wilburn-Hayes, M.G., & Suzuki, P.H.. "United States Patent 63/611,965 Methods for ultra-high-throughput profiling of nucleic acid binding or modifying proteins", Leland Stanford Junior University, Chan Zuckerberg Biohub, Nov 1, 2023
- Polly Fordyce and Jamin Hein. "United States Patent 63/387,748 Microbeads with ratiometric lanthanide encoding for drug screening", Leland Stanford Junior University, Chan Zuckerberg Biohub, Dec 16, 2022
- Polly Fordyce and Jamin Hein. "United States Patent 63/387,757 Kinase/phosphatase substrate analysis and compositions using spectrally encoded microbeads", Leland Stanford Junior University, Chan Zuckerberg Biohub, Dec 16, 2022

- Polly Fordyce, Christina Curtis, Alex Sockell, and Wing Hing Wong. "United States Patent 63/378,229 Array platform for high-throughput organoid profiling", Leland Stanford Junior University, Chan Zuckerberg Biohub, Oct 3, 2022
- Yinnian Feng, Adam White, Polly Fordyce, Xiang Zhao, and K. Christopher Garcia. "United States Patent 63/108,162 High-throughput force-dependent cellular response assay using spectrally encoded smart beads", Leland Stanford Junior University, Chan Zuckerberg Biohub, Oct 30, 2020
- Yinnian Feng, Adam White, Jamin Hein, and Polly Fordyce. "United States Patent 63/037,804 Methods, devices, and compositions related to polymeric microbeads", Chan Zuckerberg Biohub, Jun 11, 2020
- Kara Brower, Sandy Klemm, William Greenleaf, Polly Fordyce. "United States Patent 62/693,800 Method to perform high-throughput single cell genomic and phenotypic analyses", Chan Zuckerberg Biohub, Jul 1, 2019
- Adam White, Huy Nguyen, Brian Yu, Tyler Shimko, Polly Fordyce, Nadya Andini, Sam Yang. "United States Patent 62/853,494 Method for multiplexed detection of nucleic acids using spectrally encoded beads", Chan Zuckerberg Biohub, May 28, 2019
- Kara Brower, Alex Sockell, Adam White, Polly Fordyce. "United States Patent 62/853,627 Multi-parameter single-cell analysis using spectrally encoded microbeads", Chan Zuckerberg Biohub, May 28, 2019
- Brian Baxter, Joe DeRisi, Polly Fordyce, Rachel Gerver, Rafael Gomez-Sjoberg, Kurt Thorn. "United States Patent 61/692,816. Spectrally encoded microbeads and methods and devices for making and using same", University of California San Francisco, Aug 23, 2013

LINKS

- My Lab Site: http://www.fordycelab.com

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

Cellular function and organismal homeostasis are governed by molecular interactions. Protein-DNA binding interactions are essential for regulating gene transcription and translation, dense networks of protein-protein and protein-peptide interactions further regulate cellular function, and enzymes make possible all of the chemical transformations essential to metabolism and signaling. Our goal is to understand, and eventually engineer, these complex processes by building and testing biophysical models of how the molecules that drive these processes work. To do so, an essential first step is to obtain the necessary quantitative measurements of the fundamental kinetic and thermodynamic constants of these molecular interactions and catalytic processes—the “universal language” needed to describe and ultimately predict function. In our lab, we use microfluidics and extensive hardware automation to perform these quantitative measurements at an unprecedented scale via 3 main platforms:

1. Array-based multiplexing experiments (MITOMI and HT-MEK) employ microfluidic devices containing 1,568 valved reaction chambers aligned to printed DNA arrays. We are currently using these devices to better understand how transcription factors find and bind their genomic targets to regulate gene expression, as well as to understand how enzymes achieve their extraordinary catalytic efficiency and substrate specificity.

2. MRBLEs (Microspheres with Ratiometric Barcode Lanthanide Encoding) rely on spectral multiplexing to track analytes throughout an experiment. We can create microspheres containing > 1,000 distinct ratios of lanthanide nanophosphors that can be uniquely identified via imaging alone, and are now using these MRBLEs in a variety of downstream assays.

3. Dropception is a microfluidic platform for creating double emulsion (water-in-oil-in-water) droplets that can be sorted in high-throughput using standard flow cytometers (FACS machines). We recently demonstrated the ability to generate and sort double emulsion droplets without breakage, isolate individual rare droplets of interest in wells of a multiwell plate, and recover all encapsulated nucleic acids, enabling a wide range of novel single-cell multi-omic techniques.

Teaching

COURSES

2025-26

- Microfluidic Device Laboratory: BIOE 301D, GENE 207 (Win)

2024-25

- Genetics and Developmental Biology Training Camp: DBIO 200, GENE 200 (Aut)
- Microfluidic Device Laboratory: BIOE 301D (Win)

2022-23

- Microfluidic Device Laboratory: BIOE 301D, GENE 207 (Win)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Christopher Choi, Ezekiel Delgado, Nicolai Dorka, Benjamin Doughty, Danilo Dubocanin, Owen Dunkley, Hajime Fujita, Gokul Kannan, Pranav Lalgudi, Felix Majewski, Omar Niagne, Carolina Rios-Martinez, Benjamin Rosenbluth, Kyle Zolkin

Postdoctoral Faculty Sponsor

Carlos Cortez, Shawn Costello, Chase Freschlin, Karl Krauth, Albert Lee, Byungjin Lee

Doctoral Dissertation Advisor (AC)

Eliel Akinbami, Matt DeJong, Michael Hayes, Jessica Karaguesian, Micah Lawrence, Lucas Melo, Micah Olivas, Daria Passow, Lillian Petersen

Doctoral Dissertation Co-Advisor (AC)

Yujia Bian, Maya Sheth, Alan Su

Doctoral (Program)

Hyejin Lee, Hope Leng, Carolina Rios-Martinez, Andrew Rodd, Sabra Sisler

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Bioengineering (Phd Program)
- Biophysics (Phd Program)
- Genetics (Phd Program)

Publications

PUBLICATIONS

- **uSort-M: Scalable isolation of user-defined sequences from diverse pooled libraries.** *bioRxiv : the preprint server for biology*
  Olivas, M. B., Almhjell, P. J., Shanahan, J. D., Fordyce, P. M.
  2026
- **Soft photonic skins with dynamic texture and colour control.** *Nature*
  Doshi, S., Güsken, N. A., Dijk, G., Carlström, J., Ortiz-Cárdenas, J. E., Suzuki, P., Li, B., Fordyce, P. M., Salleo, A., Melosh, N. A., Brongersma, M. L.
  2026; 649 (8096): 345-352
- **Functional Characterization of Glucokinase Variants to Aid Clinical Interpretation of Monogenic Diabetes** *INTERNATIONAL JOURNAL OF MOLECULAR SCIENCES*
  Rajesh, V., Ibarra, D., Yang, J., Zhang, H., Barrett, A., Kaplan, E. G., Kumthekar, A., Sunden, F., Sun, H., Addala, A., Misakian, A., Letourneau-Freiberg, L. R., Jodarski, et al
  2025; 27 (1)
- **Acoustic printing of conductive polymers.** *Proceedings of the National Academy of Sciences of the United States of America*
  Trepka, E., Cooper, L., Brinson, K., Thompson, S., Malinao, M. G., Rommelfanger, N. J., Fordyce, P., Hong, G.
  2025; 122 (48): e2509652122
- **ADAPT-M: A workflow for rapid, quantitative in vitro measurements of enriched protein libraries.** *bioRxiv : the preprint server for biology*

Perez, C. P., DelRosso, N. V., Noland, C. L., Parekh, U., Choe, C. A., Eguchi, R. R., Wen, Q., Fordyce, P. M., Huang, P. S.
2025

- **Large field of view fluorescence imaging of microfluidic devices with a tandem-lens macroscope†.** *bioRxiv : the preprint server for biology*
  Mokhtari, D. A., Lashkaripour, A., Fordyce, P. M.
  2025
- **Continuous FACS Sorting of Double Emulsion Picoreactors with a 3D-Printed Vertical Mixer.** *Analytical chemistry*
  Yang, Z., Thompson, S., Zhang, Y., Rutten, I., Van Duyse, J., Van Isterdael, G., Nichols, L., Lammertyn, J., Soh, H. T., Fordyce, P.
  2025
- **Discovery of FoTO1 and Taxol genes enables biosynthesis of baccatin III.** *Nature*
  McClune, C. J., Liu, J. C., Wick, C., De La Peña, R., Lange, B. M., Fordyce, P. M., Sattely, E. S.
  2025
- **Hydrophilic/Omniphobic Droplet Arrays for High-throughput and Quantitative Enzymology.** *Analytical chemistry*
  Lee, B., Sunden, F., Miller, M., Pak, B., Krebber, A., Lutz, S., Fordyce, P.
  2025
- **Continuous FACS sorting of double emulsion picoreactors with a 3D printed vertical mixer.** *bioRxiv : the preprint server for biology*
  Yang, Z., Thompson, S., Zhang, Y., Rutten, I., Van Duyse, J., Van Isterdael, G., Nichols, L., Lammertyn, J., Soh, H. T., Fordyce, P.
  2025
- **Library-scale single-molecule force spectroscopy on a chip**
  Dejong, M., Dunn, A. R., Fordyce, P.
  CELL PRESS.2025
- **Library-scale single-molecule force spectroscopy on a chip**
  Dejong, M., Dunn, A. R., Fordyce, P.
  CELL PRESS.2025
- **FACS-Sortable Triple Emulsion Picoreactors for Screening Reactions in Biphasic Environments.** *Advanced materials interfaces*
  Thompson, S., Zhang, Y., Yang, Z., Nichols, L., Fordyce, P. M.
  2025; 12 (3)
- **Quantifying protein unfolding kinetics with a high-throughput microfluidic platform.** *bioRxiv : the preprint server for biology*
  Atsavapranee, B., Sunden, F., Herschlag, D., Fordyce, P. M.
  2025
- **Mutations to transcription factor MAX allosterically increase DNA selectivity by altering folding and binding pathways.** *Nature communications*
  Hastings, R., Aditham, A. K., DelRosso, N., Suzuki, P. H., Fordyce, P. M.
  2025; 16 (1): 636
- **FACS-Sortable Triple Emulsion Picoreactors for Screening Reactions in Biphasic Environments** *ADVANCED MATERIALS INTERFACES*
  Thompson, S., Zhang, Y., Yang, Z., Nichols, L., Fordyce, P. M.
  2024
- **Multiplexed perturbation of yew reveals cryptic proteins that enable a total biosynthesis of baccatin III and Taxol precursors.** *bioRxiv : the preprint server for biology*
  McClune, C. J., Liu, J. C., Wick, C., De La Peña, R., Lange, B. M., Fordyce, P. M., Sattely, E. S.
  2024
- **High-throughput affinity measurements of direct interactions between activation domains and co-activators.** *bioRxiv : the preprint server for biology*
  DelRosso, N., Suzuki, P. H., Griffith, D., Lotthammer, J. M., Novak, B., Kocalar, S., Sheth, M. U., Holehouse, A. S., Bintu, L., Fordyce, P.
  2024
- **Design automation of microfluidic single and double emulsion droplets with machine learning.** *Nature communications*
  Lashkaripour, A., McIntyre, D. P., Calhoun, S. G., Krauth, K., Densmore, D. M., Fordyce, P. M.
  2024; 15 (1): 83

- **Phosphatase specificity principles uncovered by MRBLE:Dephos and global substrate identification.** *Molecular systems biology*
  Hein, J. B., Nguyen, H. T., Garvanska, D. H., Nasa, I., Kruse, T., Feng, Y., Lopez Mendez, B., Davey, N., Kettenbach, A. N., Fordyce, P. M., Nilsson, J.
  2023: e11782
- **Versatility and stability optimization of flow-focusing droplet generators via quality metric-driven design automation.** *Lab on a chip*
  McIntyre, D., Lashkaripour, A., Arguijo, D., Fordyce, P., Densmore, D.
  2023
- **Short tandem repeats bind transcription factors to tune eukaryotic gene expression.** *Science (New York, N.Y.)*
  Horton, C. A., Alexandari, A. M., Hayes, M. G., Marklund, E., Schaepe, J. M., Aditham, A. K., Shah, N., Suzuki, P. H., Shrikumar, A., Afek, A., Greenleaf, W. J., Gordân, R., Zeitlinger, et al
  2023; 381 (6664): eadd1250
- **A microwell platform for high-throughput longitudinal phenotyping and selective retrieval of organoids.** *Cell systems*
  Sockell, A., Wong, W., Longwell, S., Vu, T., Karlsson, K., Mokhtari, D., Schaepe, J., Lo, Y., Cornelius, V., Kuo, C., Van Valen, D., Curtis, C., Fordyce, et al
  2023; 14 (9): 764
- **Decoupling of catalysis and transition state analog binding from mutations throughout a phosphatase revealed by high-throughput enzymology.** *Proceedings of the National Academy of Sciences of the United States of America*
  Markin, C. J., Mokhtari, D. A., Du, S., Doukov, T., Sunden, F., Cook, J. A., Fordyce, P. M., Herschlag, D.
  2023; 120 (29): e2219074120
- **De novo distillation of thermodynamic affinity from deep learning regulatory sequence models of in vivo protein-DNA binding.** *bioRxiv : the preprint server for biology*
  Alexandari, A. M., Horton, C. A., Shrikumar, A., Shah, N., Li, E., Weilert, M., Pufall, M. A., Zeitlinger, J., Fordyce, P. M., Kundaje, A.
  2023
- **Double emulsions as a high-throughput enrichment and isolation platform for slower-growing microbes.** *ISME communications*
  McCully, A. L., Loop Yao, M., Brower, K. K., Fordyce, P. M., Spormann, A. M.
  2023; 3 (1): 47
- **Large-scale mapping and mutagenesis of human transcriptional effector domains.** *Nature*
  DelRosso, N., Tycko, J., Suzuki, P., Andrews, C., , Mukund, A., Liongson, I., Ludwig, C., Spees, K., Fordyce, P., Bassik, M. C., Bintu, L.
  2023
- **On the dependent recognition of some long zinc finger proteins.** *Nucleic acids research*
  Zuo, Z., Billings, T., Walker, M., Petkov, P. M., Fordyce, P. M., Stormo, G. D.
  2023
- **Microfluidic encapsulation of photosynthetic cyanobacteria in hydrogel microparticles augments oxygen delivery to rescue ischemic myocardium.** *Journal of bioscience and bioengineering*
  Stapleton, L. M., Farry, J. M., Zhu, Y., Lucian, H. J., Wang, H., Paulsen, M. J., Totherow, K. P., Roth, G. A., Brower, K. K., Fordyce, P. M., Appel, E. A., Woo, Y. J.
  2023
- **High-throughput, quantitative measurements reveal the biophysical mechanisms by which transcription factor mutations drive disease**
  Hastings, R., Aditham, A., Fordyce, P.
  CELL PRESS.2023: 171A
- **High throughput measurements of direct activation domain-coactivator interactions**
  DelRosso, N., Suzuki, P., Griffith, D., Holehouse, A. S., Bintu, L., Fordyce, P.
  CELL PRESS.2023: 68A
- **Alleviating Cell Lysate-Induced Inhibition to Enable RT-PCR from Single Cells in Picoliter-Volume Double Emulsion Droplets** *ANALYTICAL CHEMISTRY*
  Khariton, M., McClune, C. J., Brower, K. K., Klemm, S., Sattely, E. S., Fordyce, P. M., Wang, B.
  2023; 95 (2): 935-945
- **Metasurface optofluidics for dynamic control of light fields.** *Nature nanotechnology*

Li, Q., van de Groep, J., White, A. K., Song, J., Longwell, S. A., Fordyce, P. M., Quake, S. R., Kik, P. G., Brongersma, M. L.
2022

- **BATTLES: high-throughput screening of antigen recognition under force** *NATURE METHODS*
  Fordyce, P., Feng, Y.
  2022
- **A bead-based method for high-throughput mapping of the sequence- and force-dependence of T cell activation.** *Nature methods*
  Feng, Y., Zhao, X., White, A. K., Garcia, K. C., Fordyce, P. M.
  2022
- **Machine learning for microfluidic design and control.** *Lab on a chip*
  McIntyre, D., Lashkaripour, A., Fordyce, P., Densmore, D.
  2022
- **Systematic characterization of effect of flow rates and buffer compositions on double emulsion droplet volumes and stability.** *Lab on a chip*
  Calhoun, S. G., Brower, K. K., Suja, V. C., Kim, G., Wang, N., McCully, A. L., Kusumaatmaja, H., Fuller, G. G., Fordyce, P. M.
  2022
- **Tuning T cell receptor sensitivity through catch bond engineering.** *Science (New York, N.Y.)*
  Zhao, X., Kolawole, E. M., Chan, W., Feng, Y., Yang, X., Gee, M. H., Jude, K. M., Sibener, L. V., Fordyce, P. M., Germain, R. N., Evavold, B. D., Garcia, K. C.
  2022; 376 (6589): eabl5282
- **uPIC-M: Efficient and Scalable Preparation of Clonal Single Mutant Libraries for High-Throughput Protein Biochemistry.** *ACS omega*
  Appel, M. J., Longwell, S. A., Morri, M., Neff, N., Herschlag, D., Fordyce, P. M.
  2021; 6 (45): 30542-30554
- **MRBLE-pep Measurements Reveal Accurate Binding Affinities for B56, a PP2A Regulatory Subunit.** *ACS measurement science Au*
  Hein, J. B., Cyert, M. S., Fordyce, P. M.
  2021; 1 (2): 56-64
- **Revealing enzyme functional architecture via high-throughput microfluidic enzyme kinetics** *SCIENCE*
  Markin, C. J., Mokhtari, D. A., Sunden, F., Appel, M. J., Akiva, E., Longwell, S. A., Sabatti, C., Herschlag, D., Fordyce, P. M.
  2021; 373 (6553): 411-+
- **Fundamentals to function: Quantitative and scalable approaches for measuring protein stability.** *Cell systems*
  Atsavapranee, B., Stark, C. D., Sunden, F., Thompson, S., Fordyce, P. M.
  2021; 12 (6): 547-560
- **Double Emulsion Picoreactors for High-Throughput Single-Cell Encapsulation and Phenotyping via FACS.** *Analytical chemistry*
  Brower, K. K., Khariton, M., Suzuki, P. H., Still, C. 2., Kim, G., Calhoun, S. G., Qi, L. S., Wang, B., Fordyce, P. M.
  2020
- **Protocol for Peptide Synthesis on Spectrally Encoded Beads for MRBLE-pep Assays.** *Bio-protocol*
  Hein, J. B., Nguyen, H. Q., Cyert, M., Fordyce, P. M.
  2020; 10 (13): e3669
- **Protocol for Peptide Synthesis on Spectrally Encoded Beads for MRBLE-pep Assays** *BIO-PROTOCOL*
  Hein, J. B., Nguyen, H. Q., Cyert, M., Fordyce, P. M.
  2020; 10 (13)
- **Double emulsion flow cytometry with high-throughput single droplet isolation and nucleic acid recovery.** *Lab on a chip*
  Brower, K. K., Carswell-Crumpton, C., Klemm, S., Cruz, B., Kim, G., Calhoun, S. G., Nichols, L., Fordyce, P. M.
  2020
- **Leveraging Microfluidics for High-Throughput Studies of Transcription Factor/DNA Binding**
  Fordyce, P., Aditham, A., Horton, C., DelRosso, N., Mokhtari, D., Markin, C.
  WILEY.2020

- **A High-Throughput Assay Platform for Next-Generation Mechanistic Enzymology and Applications**
  Markin, C. J., Mokhtari, D. A., Sunden, F., Appel, M. J., Herschlag, D. M., Fordyce, P.
  CELL PRESS.2020: 535A
- **A High-Throughput Platform Characterizes Functional Effects of Transcription Factor Mutations**
  Aditham, A. K., DelRosso, N. V., Fordyce, P.
  CELL PRESS.2020: 74A–75A
- **MRBLES 2.0: High-throughput generation of chemically functionalized spectrally and magnetically encoded hydrogel beads using a simple single-layer microfluidic device.** *Microsystems & nanoengineering*
  Feng, Y., White, A. K., Hein, J. B., Appel, E. A., Fordyce, P. M.
  2020; 6: 109
- **DeCoDe: degenerate codon design for complete protein-coding DNA libraries.** *Bioinformatics (Oxford, England)*
  Shimko, T. C., Fordyce, P. M., Orenstein, Y. n.
  2020
- **High-Throughput Affinity Measurements of Transcription Factor and DNA Mutations Reveal Affinity and Specificity Determinants.** *Cell systems*
  Aditham, A. K., Markin, C. J., Mokhtari, D. A., DelRosso, N. n., Fordyce, P. M.
  2020
- **Quantitative mapping of protein-peptide affinity landscapes using spectrally encoded beads.** *eLife*
  Nguyen, H. Q., Roy, J., Harink, B., Damle, N. P., Latorraca, N. R., Baxter, B. C., Brower, K., Longwell, S. A., Kortemme, T., Thorn, K. S., Cyert, M. S., Fordyce, P. M.
  2019; 8
- **Live imaging of Aiptasia larvae, a model system for coral and anemone bleaching, using a simple microfluidic device.** *Scientific reports*
  Van Treuren, W., Brower, K. K., Labanieh, L., Hunt, D., Lensch, S., Cruz, B., Cartwright, H. N., Tran, C., Fordyce, P. M.
  2019; 9 (1): 9275
- **An open-source software analysis package for Microspheres with Ratiometric Barcode Lanthanide Encoding (MRBLEs)** *PLOS ONE*
  Harink, B., Huy Nguyen, Thorn, K., Fordyce, P.
  2019; 14 (3)
- **A Microfluidics-Based Assay for Mapping Connectivity in Highly Proficient Enzymes Reveals Functional Modularity**
  Markin, C. J., Mokhtari, D. A., Sunden, F., Herschlag, D., Fordyce, P. M.
  CELL PRESS.2019: 66A
- **A High-Throughput Platform for Probing Mechanisms of Transcription Factor-DNA Binding**
  Aditham, A., Fordyce, P. M.
  CELL PRESS.2019: 502A
- **Deep Learning Models Explore the Structural Effects of Transcription Factor-DNA Complexes on Binding Specificity**
  Shimko, T. C., Fordyce, P. M.
  CELL PRESS.2019: 503A
- **Bringing Enzymology into the Genomic Era: Developing and Deploying New Tools to Quantitatively Map Functional Connections Throughout an Enzyme**
  Markin, C., Mokhtari, D., Sunden, F., Herschlag, D., Fordyce, P. M.
  CELL PRESS.2019: 23A
- **Satb1 integrates DNA binding site geometry and torsional stress to differentially target nucleosome-dense regions.** *Nature communications*
  Ghosh, R. P., Shi, Q. n., Yang, L. n., Reddick, M. P., Nikitina, T. n., Zhurkin, V. B., Fordyce, P. n., Stasevich, T. J., Chang, H. Y., Greenleaf, W. J., Liphardt, J. T.
  2019; 10 (1): 3221
- **micrIO: an open-source autosampler and fraction collector for automated microfluidic input-output.** *Lab on a chip*
  Longwell, S. A., Fordyce, P. M.
  2019

- **An open-source software analysis package for Microspheres with Ratiometric Barcode Lanthanide Encoding (MRBLEs).** *PloS one*
  Harink, B., Nguyen, H., Thorn, K., Fordyce, P.
  2019; 14 (3): e0203725
- **Diversification of DNA binding specificities enabled SREBP transcription regulators to expand the repertoire of cellular functions that they govern in fungi.** *PLoS genetics*
  Del Olmo Toledo, V., Puccinelli, R., Fordyce, P. M., Perez, J. C.
  2018; 14 (12): e1007884
- **High-throughput chromatin accessibility profiling at single-cell resolution.** *Nature communications*
  Mezger, A., Klemm, S., Mann, I., Brower, K., Mir, A., Bostick, M., Farmer, A., Fordyce, P., Linnarsson, S., Greenleaf, W.
  2018; 9 (1): 3647
- **Discovering epistatic feature interactions from neural network models of regulatory DNA sequences.** *Bioinformatics (Oxford, England)*
  Greenside, P., Shimko, T., Fordyce, P., Kundaje, A.
  2018; 34 (17): i629-i637
- **Discovering epistatic feature interactions from neural network models of regulatory DNA sequences**
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