Stanford

Polly Fordyce

Associate Professor of Bioengineering and of Genetics

NIH Biosketch available Online Curriculum Vitae available Online

CONTACT INFORMATION

- **Alternate Contact**

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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 an NIH New Innovator Award, an NSF CAREER Award, the 2023 Eli Lilly Award in Biological Chemistry, 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

- Investigator, Chan Zuckerberg Biohub, (2017-2022)

HONORS AND AWARDS

- 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

- 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

- 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

2022-23

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

2021-22

- Microfluidic Device Laboratory: BIOE 301D (Win)

2020-21

- Bioengineering Departmental Research Colloquium: BIOE 393 (Aut)

2019-20

- Microfluidic Device Laboratory: BIOE 301D (Win)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Katie Antilla, Rebecca Culver, Benjamin Doughty, Michaela Hinks, Ethan Li, Elisabeth Meyer, Michael Montgomery, Carla Perez

Postdoctoral Faculty Sponsor

Karl Krauth, Ali Lashkaripour, Byungjin Lee, Jennifer Ortiz Cardenas, Samuel Thompson

Doctoral Dissertation Advisor (AC)

Eliel Akinbami, Beatriz Atsavapranee, Suzanne Calhoun, Min Sung Cho, Matt DeJong, Nicole DelRosso, Renee Hastings, Michael Hayes, Scott Longwell, Micah Olivas, Lexy Strom, Peter Suzuki, Daria Wonderlick

Orals Evaluator

Amr Mohamed

Master's Program Advisor

Karsten Householder

Doctoral Dissertation Co-Advisor (AC)

Amr Mohamed, Daniel Mokhtari, Alexandra Sockell

Undergraduate Major Advisor

Emilie Kono

Doctoral (Program)

Beatriz Atsavapranee, Manish Ayushman, Hope Leng, Carolina Rios-Martinez, Avin Veerakumar, Cassandra Villicana

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

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

Publications

PUBLICATIONS

- **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**
  Greenside, P., Shimko, T., Fordyce, P., Kundaje, A.
  OXFORD UNIV PRESS.2018: 629–37

- **Comprehensive, high-resolution binding energy landscapes reveal context dependencies of transcription factor binding** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Le, D. D., Shimko, T. C., Aditham, A. K., Keys, A. M., Longwell, S. A., Orenstein, Y., Fordyce, P. M.
  2018; 115 (16): E3702–E3711

- **An Open-Source, Programmable Pneumatic Setup for Operation and Automated Control of Single- and Multi-Layer Microfluidic Devices.** *HardwareX*
  Brower, K., Puccinelli, R., Markin, C. J., Shimko, T. C., Longwell, S. A., Cruz, B., Gomez-Sjoberg, R., Fordyce, P. M.
  2018; 3: 117–34

- **BET-seq: Binding energy topographies revealed by microfluidics and high-throughput sequencing.** *Methods in cell biology*
  Aditham, A. K., Shimko, T. C., Fordyce, P. M.
  2018; 148: 229–50

- **Optimized Sequence Library Design for Efficient In Vitro Interaction Mapping.** *Cell systems*
  Orenstein, Y., Puccinelli, R., Kim, R., Fordyce, P., Berger, B.
  2017; 5 (3): 230-236.e5

- **Programmable Microfluidic Synthesis of Over One Thousand Uniquely Identifiable Spectral Codes** *ADVANCED OPTICAL MATERIALS*
  Nguyen, H. Q., Baxter, B. C., Brower, K., Diaz-Botia, C. A., DeRisi, J. L., Fordyce, P. M., Thorn, K. S.
  2017; 5 (3)

- **Multi-step Variable Height Photolithography for Valved Multilayer Microfluidic Devices.** *Journal of visualized experiments : JoVE*
  Brower, K., White, A. K., Fordyce, P. M.
  2017

- **Joker de Bruijn: Sequence Libraries to Cover All k-mers Using Joker Characters**
  Orenstein, Y., Kim, R., Fordyce, P., Berger, B., Sahinalp, S. C.
  SPRINGER-VERLAG BERLIN.2017: 389–90

- **How duplicated transcription regulators can diversify to govern the expression of nonoverlapping sets of genes** *GENES & DEVELOPMENT*
  Perez, J. C., Fordyce, P. M., Lohse, M. B., Hanson-Smith, V., DeRisi, J. L., Johnson, A. D.
  2014; 28 (12): 1272-1277

- **Structure of the transcriptional network controlling white-opaque switching in Candida albicans** *MOLECULAR MICROBIOLOGY*
  Hernday, A. D., Lohse, M. B., Fordyce, P. M., Nobile, C. J., DeRisi, J. L., Johnson, A. D.
  2013; 90 (1): 22-35

- **Microfluidic affinity and ChIP-seq analyses converge on a conserved FOXP2-binding motif in chimp and human, which enables the detection of evolutionarily novel targets** *NUCLEIC ACIDS RESEARCH*
  Nelson, C. S., Fuller, C. K., Fordyce, P. M., Greninger, A. L., Li, H., DeRisi, J. L.
  2013; 41 (12): 5991-6004

- **Identification and characterization of a previously undescribed family of sequence-specific DNA-binding domains** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Lohse, M. B., Hernday, A. D., Fordyce, P. M., Noiman, L., Sorrells, T. R., Hanson-Smith, V., Nobile, C. J., DeRisi, J. L., Johnson, A. D.
  2013; 110 (19): 7660-7665

- **Programmable microfluidic synthesis of spectrally encoded microspheres** *LAB ON A CHIP*
  Gerver, R. E., Gomez-Sjoeberg, R., Baxter, B. C., Thorn, K. S., Fordyce, P. M., Diaz-Botia, C. A., Helms, B. A., DeRisi, J. L.
  2012; 12 (22): 4716-4723

- **Basic leucine zipper transcription factor Hac1 binds DNA in two distinct modes as revealed by microfluidic analyses** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Fordyce, P. M., Pincus, D., Kimmig, P., Nelson, C. S., El-Samad, H., Walter, P., DeRisi, J. L.
  2012; 109 (45): E3084-E3093

- **Systematic characterization of feature dimensions and closing pressures for microfluidic valves produced via photoresist reflow** *LAB ON A CHIP*
  Fordyce, P. M., Diaz-Botia, C. A., DeRisi, J. L., Gomez-Sjoberg, R.
  2012; 12 (21): 4287-4295
- **De novo identification and biophysical characterization of transcription-factor binding sites with microfluidic affinity analysis** *NATURE BIOTECHNOLOGY*
  Fordyce, P. M., Gerber, D., Tran, D., Zheng, J., Li, H., DeRisi, J. L., Quake, S. R.
  2010; 28 (9): 970-976
- **Individual dimers of the mitotic kinesin motor Eg5 step processively and support substantial loads in vitro** *NATURE CELL BIOLOGY*
  Valentine, M. T., Fordyce, P. M., Krzysiak, T. C., Gilbert, S. P., Block, S. M.
  2006; 8 (5): 470-U89
- **Eg5 steps it up!** *CELL DIVISION*
  Valentine, M. T., Fordyce, P. M., Block, S. M.
  2006; 1
- **Simultaneous, coincident optical trapping and single-molecule fluorescence** *NATURE METHODS*
  Lang, M. J., Fordyce, P. M., Engh, A. M., Neuman, K. C., Block, S. M.
  2004; 1 (2): 133-139
- **Stepping and stretching - How kinesin uses internal strain to walk processively** *JOURNAL OF BIOLOGICAL CHEMISTRY*
  Rosenfeld, S. S., Fordyce, P. M., Jefferson, G. M., King, P. H., Block, S. M.
  2003; 278 (20): 18550-18556
- **Combined optical trapping and single-molecule fluorescence.** *Journal of biology*
  Lang, M. J., Fordyce, P. M., Block, S. M.
  2003; 2 (1): 6-?