Stanford

Polly Fordyce

Assistant Professor of Genetics and of Bioengineering

Curriculum Vitae available Online

Bio

BIO

Polly Fordyce is an Assistant 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. 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 Alfred P. Sloan Foundation Research Fellowship, a McCormick and Gabilan Fellowship, an NIH Pathway to Independence Award (K99/R00), and a Helen Hay Whitney Postdoctoral Fellowship, and was recently named a Chan Zuckerberg Biohub Investigator.

ACADEMIC APPOINTMENTS

- Assistant Professor, Genetics
- Assistant Professor, Bioengineering
- Member, Bio-X
- Faculty Fellow, Stanford ChEM-H

HONORS AND AWARDS

- 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)

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)

LINKS

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

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

The Fordyce Lab is focused on developing new instrumentation and assays for making quantitative, systems-scale biophysical measurements of molecular interactions. Current research in the lab is focused on two main areas: using microfluidic tools we have developed to build ground-up quantitative models of how gene expression is regulated, and developing new tools to transform how scientists explore protein-protein interactions.

Microfluidic studies of transcription factor specificity:

Cutting-edge technologies have identified genomic DNA regulatory elements and revealed the binding preferences for many transcription factors. However, our ability to predict in vivo patterns of transcription factor binding from DNA sequence alone remains poor, and measured in vivo binding often cannot explain gene expression patterns, even for well-studied eukaryotic promoters. Improving our understanding of these processes could have far-reaching impacts for revealing how mutations in regulatory elements cause disease and for designing transcriptional circuits for use in synthetic biology. Using a microfluidic technique we have recently developed for making high-throughput, quantitative measurements of transcription factor binding interactions (MITOMI 2.0), we propose to use a "ground-up" approach to reverse engineer transcriptional regulation by systematically adding in components and observing how they influence steady-state occupancies and binding kinetics.

Spectral encoding for biological multiplexing:

Biological multiplexing allows using very small amounts of samples to test for many different things in parallel. Bead-based multiplexing has many advantages, but poses a central challenge: beads must be encoded in some way. We have recently developed new microfluidic methods to produce beads that are spectrally encoded via the ratiometric incorporation of different lanthanide nanonanophosphors. These materials have unique spectral signatures, meaning that beads can later be imaged to "read" the embedded codes. We have previously demonstrated the ability to make up to 82 distinct codes using three lanthanide species (Europium, Samarium, and Dysprosium). We are currently working on expanding our code space to include up to 1,000 distinct spectral codes by using additional lanthanide species, as well as on functionalizing beads for downstream assays.

Teaching

COURSES

2018-19

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

2017-18

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

2016-17

- Microfluidic Device Laboratory: BIOE 301D (Win)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Kalli Kappel

Postdoctoral Faculty Sponsor

Yinnian Feng, Adam White, Zheng Zuo

Doctoral Dissertation Advisor (AC)

Arjun Aditham

Doctoral (Program)

Beatriz Atsavapranee, Caitlyn Miller

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

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

Publications

PUBLICATIONS

- **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
- **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

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