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EDUCATION

Ph.D. Johns Hopkins University, Biophysics (2005-2010). Thesis: *Toward a protein fragment library from physical-chemical first principles*. Mentor: Dr. George Rose

B.S. University of Maryland, Baltimore County, Physics and Mathematics (2001-2005). *Summa cum laude*.

RESEARCH POSITIONS

- 12/9/19-Present Earl Stadtman Tenure-Track Investigator, NIH, National Library of Medicine
Project: Identification and prediction of fold-switching proteins
- 9/6/16-12/7/19 Research Scientist, HHMI, Janelia
Project: The identification and mechanisms of natural fold-switching proteins
Mentor: Dr. Loren Looger, Ashburn, VA
- 1/20/14-1/19/16 Postdoctoral fellow, University of Maryland,
Institute for Bioscience and Biotechnology Research
Project: Engineering proteins with high levels of sequence identity but different folds
Mentor: Dr. Philip Bryan, Rockville, MD
- 12/1/11-1/19/14 Research Scientist, Potomac Affinity Proteins
Project: Engineering proteins with high levels of sequence identity but different folds
Mentor: Dr. Philip Bryan, Rockville, MD
- 11/1/10-11/30/11 Postdoctoral fellow, T.C. Jenkins Department of Biophysics
Project: Computational identification of protein domains using thermodynamic principles
Mentor: Dr. George Rose, Baltimore, MD

HONORS AND AWARDS

- 2020 NIH Distinguished Scholar Award
- 2015 Outstanding Young Scientist Award, Academic Track, Maryland Academy of Sciences
- 2015 Best Poster Award, Proteins Gordon Research Conference, Holderness, NH
- 2005 Co-salutatorian, University of Maryland, Baltimore County (UMBC)
- 2005 Phi Beta Kappa
- 2005 Outstanding Senior in Mathematics Award (UMBC)
- 2005 Outstanding Senior in Physics Award (UMBC)
- 2005 Honors Certificate from the UMBC Honors College
- 2001 University Scholar (4-year full tuition, room and board scholarship at UMBC)

FUNDING AND FELLOWSHIPS

- 2020 National Institutes of Health Distinguished Scholar Award
- 2014 National Institutes of Health Ruth L. Kirschstein National Research Service Award F32
- 2010 Dean's Teaching Fellow at Johns Hopkins University (spring semester)

OTHER PROFESSIONAL ACTIVITIES

2022	Interviewed on NIH's Speaking of Science Podcast
2022	Discussion leader , Protein Folding Dynamics Gordon Conference, Oxnard, CA
2021-2022	Search committee member for Tenure-Track Investigator, Laboratory of Biochemistry and Genetics, NIDDK and for Staff Scientist, Laboratory of Protein Conformation and Dynamics, NHLBI
2021-2022	Judge for NIH Fellow Award for Research Excellence (FARE) competition
2021	Co-editor of a Biopolymers special issue on protein fold switching
2020	Reviewer of Discovery Grant for Natural Sciences and Engineering Council of Canada
2011-2021	Reviewer for <i>Nature Communications</i> , <i>eLife</i> , <i>PLOS Computational Biology</i> , <i>FEBS Letters</i> , <i>Biophysical Journal</i> , <i>Biochemistry</i> , <i>Protein Science</i> , and <i>Proteins</i>
July 2018	Interviewed by Tsh Oxenreider on Women's Work Podcast
March 2018	Judge for Loudoun County High School Science Fair, Ashburn, VA
Feb. 2018	Judge for Biophysical Society poster awards , San Francisco, CA
2017-2018	NSF Panelist , Life Sciences Division
2007-2011	Volunteer tutor for underprivileged children through Pen Lucy Youth Partnership
March 2008	Invited speaker at UMB: " <i>Why protein folding is still a problem</i> "
2008	Student co-organizer of the annual Institute for Biophysical Research Conference

PUBLICATIONS

1. Street, T.O., N.C. Fitzkee, **Perskie, L.L.**, and G.D. Rose. (2007) Physical-chemical determinants of turn conformations in globular proteins. *Protein Science*. 16:1720-1727.
2. **Perskie, L.L.**, T.O. Street and G.D. Rose (2008) Structures, basins and energies: A deconstruction of the Protein Coil Library. *Protein Science* 17:1151-1161.
3. **Perskie, L.L.**, Rose, G.D. (2010) Physical-chemical determinants of coil conformations in globular proteins. *Protein Science* 19:1127-1136 (*Commentary*)
4. **Porter, L.L.**, Rose, G.D. (2011) Redrawing the Ramachandran Plot after inclusion of hydrogen-bonding constraints. *Proc. Nat. Acad. Sci.* 1:109-113 (*Commentary*)
5. Gong, H., **Porter, L.L.** and G.D. Rose (2011) Counting peptide-water hydrogen bonds in unfolded proteins. *Protein Sci.* 2:417-427
6. **Porter, L.L.**, Rose, G.D. (2011) Comment on "Revising the Ramachandran plot from a new angle" *Protein Science* 11: 1171-1173
7. **Porter, L.L.**, Rose, G.D. (2012) A thermodynamic definition of protein domains. *Proc. Nat. Acad. Sci.* 24:9420-9425
8. **Porter, L.L.***, Y. He, Y. Chen, J. Orban and P.N. Bryan (2015) Subdomain interactions foster the design of two protein pairs with ~80% sequence identity but different folds. *Biophys. J.* 108:154-162 (**Corresponding author, Commentary*)
9. **Porter, L.L.***, Looger, L.L. (2018) Extant fold-switching proteins are widespread. *Proc. Nat. Acad. Sci.* 23:5968-5973 (**Corresponding author, Highlighted by two members of Faculty of 1000*)
10. Molineros, J.E., Looger, L.L., Kim, K., ... **Porter, L.L.**, ... Bae, S., and Nath, S.K. (2019) Amino acid signatures of HLA Class-I and II molecules are strongly associated with SLE susceptibility and autoantibody production. *PLOS Genetics* 15(4): e1008092
11. Mishra, S., Looger, L.L. and **Porter, L.L.*** (2019) Inaccurate secondary structure predictions often indicate protein fold switching *Protein Science* 28:1487-1493 (**Corresponding author, Highlighted in journal issue*)
12. Kim, A.K., **Porter L.L.*** (2021) Functional and regulatory roles of fold-switching proteins *Structure* 29:6-14
13. Kim, A.K., Looger, L.L., and **Porter, L.L.*** (2021) A high-throughput predictive method for sequence-similar fold switchers *Biopolymers*, e23416
14. Mishra, S., Looger, L.L., and **Porter L.L.*** (2021) A sequence-based method for predicting extant fold switchers that undergo α -helix \leftrightarrow β -strand transitions *Biopolymers*, e23471
15. **Porter L.L.*** (2021) Predictable fold switching by the SARS-CoV-2 protein ORF9b *Protein Science* 30:1723-1729
16. LiWang, A.*, **Porter L.L.***, Wang, L.P.* (2021) Fold-switching proteins *Biopolymers*, e23478
17. **Porter, L.L.***, Kim, A.K., Rimal, S., Looger, L.L., Majumdar, A., Mensh, B.D., Starich, M. (2022) Many

- sequence-diverse protein domains switch between α -helix and β -sheet folds *bioRxiv*
<https://www.biorxiv.org/content/10.1101/2021.06.10.447921>, in revision for *Nature Communications*
18. Chakravarty, D., Porter, L.L.* (2022) AlphaFold2 fails to predict protein fold switching *bioRxiv*
<https://www.biorxiv.org/content/10.1101/2022.03.08.483439>, under review in *Protein Science*
 (*Corresponding author)

CONFERENCES AND MEETINGS

- 2008 *Poster* “Structures, basins and energies in the Protein Coil Library” Gordon Conference on Biopolymers, Newport, RI.
- 2009 *Poster* “Structures, basins and energies in the Protein Coil Library” Gordon Conference on Protein Folding, Holderness, NH.
- 2009 *Speaker* “Constructing proteins from physics-based building blocks” Institute for Biophysical Research Conference Baltimore, MD
- 2010 *Speaker* “Physical-chemical determinants of coil conformations in globular proteins” Protein Society Annual Symposium San Diego, CA
- 2011 *Speaker* “Negative design in protein coils” Biophysical Society meeting, Baltimore, MD.
- 2011 *Poster* “Temperature dependence of transfer free energies for amino acid side chains and the peptide backbone” Gibbs Society for Biothermodynamics, Carbondale, IL.
- 2012 *Poster* “A thermodynamic definition of protein domains” Protein Society Annual Symposium, San Diego, CA.
- 2013 *Speaker* “Rational design of two proteins with 79% sequence identity but different folds” Gibbs Society for Biothermodynamics, Carbondale, IL.
- 2014 *Poster* “An intrinsically disordered protein bridges two proteins with 80% sequence identity but different folds” Gordon Conference on Intrinsically Disordered Proteins, Easton, MA.
- 2015 *Speaker* “Protein evolution across fold classes: a 3- α -helix bundle can switch folds to β , α/β , and $\alpha+\beta$ folds by stepwise mutation” Biophysical Society meeting, Baltimore, MD.
Session co-chair.
- 2015 *Poster* “The synergistic exon hypothesis: expanding the eukaryotic proteome through protein fold switching.” Gordon Conference on Proteins, Holderness, NH. **Best poster award.**
- 2017 *Speaker* “Protein fold switching is widespread.” Gordon Conference on Proteins, Holderness, NH.
- 2018 *Speaker* “Protein fold switching is widespread.” Biophysical Society meeting, San Francisco, CA.
Session co-chair
- 2018 *Poster* “Surveying the sequence space landscape of fold-switching proteins.” Biophysical Society’s Genome Biophysics meeting, Santa Cruz, CA.
- 2018 *Speaker* “Surveying the sequence space landscape of fold-switching proteins.” Gibbs Society for Biothermodynamics, Carbondale, IL.
- 2019 *Speaker* “Surveying the sequence space landscape of fold-switching proteins.” Biophysical Society meeting, Baltimore, MD. **Session co-chair**
- 2019 *Poster* “Surveying the sequence landscape of fold-switching proteins.” Gordon Research Conference on Proteins, Holderness, NH.
- 2020 *Speaker* “Surveying the sequence landscape of fold-switching proteins.” Gordon Research Conference on Protein Folding Dynamics, Galveston, TX.
- 2020 *Speaker* “Surveying the sequence space landscape of fold-switching proteins.” Biophysical Society meeting, San Diego, CA. **Invited symposium speaker.**
- 2020 *Speaker* “Surveying the sequence landscape of fold-switching proteins” Kansas University Medical Center
- 2021 *Speaker* “Surveying the sequence landscape of fold-switching proteins” University of Oregon
- 2021 *Speaker* “Many sequence-diverse protein domains switch between α -helix and β -sheet folds” A*STAR, Singapore
- 2022 *Speaker* “Many sequence-diverse protein domains switch between α -helix and β -sheet folds” American Physical Society meeting, Chicago, IL. **Invited symposium speaker**
- 2022 *Speaker* “Identification, prediction, and evolution of fold-switching proteins.” AEEB meeting Marseilles, France. **Invited speaker and session co-chair**
- 2022 *Speaker* “Many sequence-diverse protein domains switch between α -helix and β -sheet folds” Brown University
- 2022 *Speaker* “Many sequence-diverse protein domains switch between α -helix and β -sheet folds” Gibbs Society for Protein Thermodynamics, Carbondale, IL.

2022 *Discussion Leader and Panelist* Gordon Research Conference and Seminar on Protein Folding Dynamics, Ventura, CA

SELECTED MENTEES

- Summer 2018 **Soumya Mishra**, high school intern, HHMI, Janelia.
and 2019 Role: Primary mentor. Designed Soumya's project and guided her as she did the research.
Outcomes: Two first-author publications, successful end-of-summer oral presentation at Janelia; now a student in Carnegie Mellon's Computer Science undergraduate program.
- 2015-2016 **Dana Motabar**, master's student (Bioengineering), University of Maryland, College Park.
Role: Helped teach Dana how to purify proteins, design oligos, and run PCR reactions. Read and edited her master's thesis.
Outcomes: Successfully obtained master's degree; now works at MedImmune.
- 2011-2013 **Sofia Hu**, high school intern, University of Maryland, College Park.
Role: Helped teach Sofia how to purify proteins; assigned her tasks such as making buffers and doing minipreps. Outcomes: Harvard/M.I.T. M.D.-Ph.D. Program.