# Steve Meisburger

Curriculum Vitae

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#### Education

Aug. 2014 **Doctor of Philosophy**, Applied Physics, Cornell University, Ithaca, New York.

Ion interactions with single- and double-stranded DNA measured using solution X-ray scattering. Advisor - Lois Pollack

May 2007 Bachelor of Arts, Physics, Carleton College, Northfield, Minnesota.

Summa cum laude

#### Grants and Awards

2016-2018 NIH NRSA Postdoctoral Fellowship: "Allosteric motions of B<sub>12</sub> enzymes",

Princeton University, Princeton, New Jersey.

Advisor - Nozomi Ando (Chemistry). F32-GM117757.

May 2017 Best Poster: Technical Achievement, CHESS Users' Meeting.

For "Unmixing Enzyme Allostery".

May 2017 Travel Award, American Crystallographic Association.

To attend annual meeting in New Orleans, LA.

Apr. 2017 Travel and Professional Development Award, American Society for Biochemistry

and Molecular Biology.

To attend annual meeting in Chicago, IL.

2008-2011 NIH Predoctoral Training Grant in Molecular Biophysics, Cornell University,

Ithaca, New York.

Advisor - Lois Pollack (Applied & Engineering Physics). T32-GM008267.

May 2007 Distinction awarded for Senior Integrative Exercise (Thesis), Carleton College,

Northfield, Minnesota.

### Research Experience

2018-present **Postdoctoral Research Associate**, Cornell University, Ithaca, New York.

Advisor - Nozomi Ando (Chemistry and Chemical Biology).

2016-2018 **Postdoctoral Research Fellow**, Princeton University, Princeton, New Jersey.

Advisor - Nozomi Ando (Chemistry).

 $\circ$  Investigated the dynamics of highly flexible multi-dommain metalloenzymes using solution

• Trained in biophysical chemistry of metalloproteins, including anaerobic technique,

small-angle X-ray scattering (SAXS) and X-ray diffuse scattering from crystals.

expression, purification, and crystallization.

2014-2016 **Postdoctoral Research Associate**, Princeton University, Princeton, New Jersey.

Advisor - Nozomi Ando (Chemistry).

 $\circ$ Established equilibrium model for allosteric regulation of liver Phenylalanine Hydroxylase

by combining chromatography-coupled SAXS with mathematical deconvolution.

2008-2014 Graduate Research Assistant, Cornell University, Ithaca, New York.

Advisor - Lois Pollack (Applied & Engineering Physics)

• Microfabricated rapid mixers at the Cornell NanoScale Science & Technology Facility.

• Performed time-resolved and anomalous SAXS experiments at Cornell High Energy Synchrotron Source (CHESS) and the Advanced Photon Source (APS).

- Transcribed, purified, and characterized RNA using biophysical techniques including fluorescence, UV melting, and atomic emission spectroscopy.
- Thesis combined theory and experiment to understand the interplay of electrostatics and flexibility in the processes of RNA folding and DNA compaction.
- Summer 2006 **Undergraduate Researcher**, Santa Fe Institute (REU), Santa Fe, New Mexico. Advisor Alfred Hubler
- Summer 2005 **Undergraduate Researcher**, Stanford University, NNIN (REU), Palo Alto, California. Advisor Fabian Pease

#### **Publications**

- [21] Parker MJ, Maggiolo AO, Thomas WC, Kim A, **Meisburger SP**, Ando N, Boal AK, Stubbe J. An endogenous dAMP ligand in Bacillus subtilis class Ib RNR promotes assembly of a noncanonical dimer for regulation by dATP. **PNAS** 115: E4594–E4603 (2018).
- [20] Meisburger SP\*, Thomas WC\*, Watkins MB\*, and Ando N. X-ray scattering studies of protein structural dynamics. Chem. Rev. 117(12): 7615–72 (2017).
   \*equal contribution
- [19] Meisburger SP & Ando N. Correlated motions from crystallography beyond diffraction. Acc. Chem. Res 50: 580–583 (2017).
- [18] Plumridge A, Meisburger SP, Andresen K, and Pollack L. The impact of base stacking on the conformations and electrostatics of single-stranded DNA. Nucl. Acids Res. 45: 3932-3943 (2017).
- [17] Plumridge A\*, Meisburger SP\*, Pollack L. Visualizing single-stranded nucleic acids in solution. Nucl. Acids Res. gkw1297 (2017).
   \*equal contribution
- [16] Meisburger SP, Taylor AB, Khan CA, Zhang S, Fitzpatrick PF, Ando N. Domain movements upon activation of phenylalanine hydroxylase characterized by crystallography and chromatography-coupled small-angle X-ray scattering. JACS 138(20): 6506–16 (2016).
- [15] Chen Y, Tokuda JM, Topping T, **Meisburger SP**, Pabit SA, Gloss LM, Pollack L. Asymmetric unwrapping of nucleosomal DNA propagates asymmetric opening and dissociation of the histone core. **PNAS** 114: 334-339 (2016).
- [14] Rustiguel JK, Soares ROS, **Meisburger SP**, Davis KM, Malzbender KL, Ando N, Dias-Baruffi M, Nonato MC. Full-length model of the human galectin-4 and insights into dynamics of inter-domain communication. **Sci. Rep.** 6: 33633 (2016).
- [13] Meisburger SP, Pabit SA, Pollack L. Determining the locations of ions and water around DNA from X-ray scattering measurements. Biophys. J. 108: 2886-95 (2015).
- [12] Hopkins JB, Katz AM, **Meisburger SP**, Warkentin MA, Thorne RE, Pollack L. A microfabricated fixed path length silicon sample holder enables robust background subtraction for cryoSAXS. **J. Appl. Cryst.** 48: 227-37 (2015).
- [11] Chen Y, Tokuda JM, Topping T, Sutton JL, **Meisburger SP**, Pabit SA, Gloss LM, Pollack L. Revealing transient structures of nucleosomes as DNA unwinds. **Nucl. Acids Res.** 42: 8767-76 (2014).
- [10] Nguyen HT, Pabit SA, **Meisburger SP**, Pollack L, Case DA. Accurate small and wide angle x-ray scattering profiles from atomic models of proteins and nucleic acids. **J. Chem. Phys.** 141: 22D508 (2014).
- [9] **Meisburger SP**, Sutton JL, Chen H, Pabit SA, Kirmizialtin S, Elber R, Pollack L. Polyelectrolyte properties of single stranded DNA measured using SAXS and single-molecule FRET: beyond the wormlike chain model. **Biopolymers** 99: 1032-45 (2013).
- [8] **Meisburger SP**, Warkentin M, Chen H, Hopkins JB, Gillilan RE, Pollack L, Thorne RE. Breaking the radiation damage limit with Cryo-SAXS. **Biophys. J.** 104(1): 227-36 (2013).

- [7] Chen H\*, **Meisburger SP**\*, Pabit SA, Sutton JL, Webb WW, Pollack L. *Ionic strength-dependent persistence lengths of single-stranded RNA and DNA*. **PNAS** 109(3): 799-804 (2012).
  - \*equal contribution
- [6] Yoo TY\*, **Meisburger SP**\*, Hinshaw J\*, Pollack L, Haran G, Sosnick TR, Plaxco K. Small-angle X-ray scattering and single-molecule FRET spectroscopy produce highly divergent views of the low-denaturant unfolded state. **J. Mol. Biol.** 418(3-4): 226-36 (2012).
  - \*equal contribution
- [5] Kirmizialtin S, Pabit SA, **Meisburger SP**, Pollack L, Elber R. RNA and its ionic cloud: solution scattering experiments and atomically detailed simulations. **Biophys. J.** 102(4): 819-28 (2012).
- [4] Blose JM, Pabit SA, **Meisburger SP**, Li L, Jones CD, Pollack L. Effects of a protecting osmolyte on the ion atmosphere surrounding DNA duplexes. **Biochemistry** 50(40): 8540-7 (2011).
- [3] Li L, Pabit SA, Meisburger SP, Pollack L. Double-stranded RNA resists condensation. Phys. Rev. Lett. 106: 108101 (2011).
- [2] Pabit SA, **Meisburger SP**, Li L, Blose JM, Jones CD, Pollack L. Counting ions around DNA with anomalous small-angle X-ray scattering. **JACS** 132(46): 16334-6 (2010).
- [1] Pabit SA, Qiu X, Lamb JS, Li L, **Meisburger SP**, Pollack L. Both helix topology and counterion distribution contribute to the more effective charge screening in dsRNA compared with dsDNA. **Nucl. Acids Res.** 37: 3887-96 (2009).

#### Patents

Meisburger SP, Warkentin MA, Hopkins JB, Katz AM, Pollack L, and Thorne RE. (2018). Apparatus and methods for low temperature small angle x-ray scattering. US 9,927,336 (June 4, 2012).

#### Presentations

#### Invited Talks

Unmixing Enzyme Allostery. Meisburger SP, Taylor AB, Khan CA, Zhang S, Fitzpatrick PF, Ando N. **ASBMB Annual Meeting**: Structural Dynamics of Enzymes Spotlight Session. April 24, 2017. *Invited*.

X-ray imaging of enzymes in motion. Meisburger SP. CHESS-U Workshops: Biomolecules in Motion. June 8, 2016.

Introducing Cryo-SAXS: Solution structures from nanoliter volumes. Meisburger SP, Warkentin M, Chen H, Hopkins JB, Katz AM, Gillilan RE, Pollack L. CHESS Users' Meeting. June 2013.

#### Contributed Talks

Correlated Motions from Protein Crystallography. Meisburger SP, Case DA, Ando N. ACA Annual Meeting: Session 1.1.1 Closing the R-Factor Gap in Protein Crystallography. July 21, 2018.

A new method for computational purification of complex mixtures by chromatography-coupled SAXS. Meisburger SP, Taylor AB, Khan CA, Zhang S, Fitzpatrick PF, Ando N. ACA Annual Meeting: Hybrid Methods - BioSAXS Session. May 27, 2017.

Sorting out the structure of single-stranded DNA. Meisburger SP, Sutton JL, Chen H, Andresen K, Pollack L. **58th Annual Biophysical Society Meeting.** Feb. 2014.

Time-Resolved SAXS Reconstructions Reveal a Kinetic Intermediate in RNA Folding. Meisburger SP, Pabit SA, Li L, Blose JM, Brooks K, Hampel K, Pollack L. RNA-UNY Conference. Oct. 2010.

#### Posters (selected)

Unmixing Enzyme Allostery.\* Meisburger SP, Taylor AB, Khan CA, Zhang S, Fitzpatrick PF, Ando N. CHESS Users' Meeting. June 2017.

\*Awarded best poster: technical achievement

Introducing Cryo-SAXS for measuring low resolution macromolecular structure without radiation damage. Meisburger SP, Warkentin M, Chen H, Hopkins JB, Katz AM, Gillilan RE, Thorne RE, Pollack L. 57th Annual Biophysical Society Meeting. Feb. 2013.

A semi-transparent beamstop for accurate normalization of millisecond time-resolved SAXS profiles. Meisburger SP, Gillilan RE, Woll A, Pollack L. Chess Users' Meeting. June 2012.

Solution structures of flexible RNA molecules in mono- and divalent salt. Meisburger SP, Chen H, Pabit SA, Sutton JL, Webb WW, Pollack L. **56th Annual Biophysical Society Meeting.** Feb 2012.

Measuring the dimensions of a compact kinetic intermediate in the folding pathway of the GlmS Ribozyme. Meisburger SP, Pabit SA, Li L, Blose JM, Brooks K, Hampel K, Pollack L. **55th Annual Biophysical Society Meeting.** Feb 2011.

Visualizing the structure of the glmS riboswitch as it folds using time-resolved SAXS. Meisburger SP, Pabit SA, Li L, Blose JM, Hampel K, Pollack L. **54th Annual Biophysical Society Meeting.** Feb 2010.

## Teaching & Mentoring

- April 2018 Lecturer, Cornell High Energy Synchrotron Source, Ithaca, New York.

  BioSAXS Essentials 8: Getting Started in Biological Small-Angle X-ray Solution Scattering
- May 2017 Lecturer, Cornell High Energy Synchrotron Source, Ithaca, New York.

  BioSAXS Essentials 7: Getting Started in Biological Small-Angle X-ray Solution Scattering
- May 2016 Lecturer, Cornell High Energy Synchrotron Source, Ithaca, New York.

  BioSAXS Essentials 6: Getting Started in Biological Small-Angle X-ray Solution Scattering
- Fall 2015 **Teaching Assistant**, Princeton University, Princeton, New Jersey. CHM 515: Biophysical Chemistry I
- Spring 2014 **Guest Lecturer**, Princeton University, Princeton, New Jersey. CHM 516: Biophysical Chemistry II
  - Nov. 2014 Lecturer, Cornell High Energy Synchrotron Source, Ithaca, New York.

    BioSAXS Essentials 5: Getting Started in Biological Small-Angle X-ray Solution Scattering
  - Fall 2013 Guest Lecturer, Cornell University, Ithaca, New York. ENGRD 2520: Physics of Life
  - 2012-2013 **Mentor**, Cornell University, Ithaca, New York. Supervised two undergraduate honors thesis projects in Applied Physics
  - 2012-2013 **Teaching Assistant**, Cornell University, Ithaca, New York. AEP 3630: Electronic Circuits

#### Professional Societies

#### 2017-present American Crystallographic Association.

- o Active member of Small-Angle Scattering Special Interest Group
- Speaker at 2018 Annual Meeting: Correlated Motions from Protein Crystallography
- Co-chair for session on diffuse scattering in 2019

#### 2009-2015 Biophysical Society.

- Co-chair of *Platform AR: DNA Structure & Dynamics* at the 58th Annual Meeting (Feb 2014), San Francisco, CA
- $\circ$  Platform speaker at the 58th Annual Meeting (Feb 2014): Sorting out the structure of single-stranded DNA
- o Poster presenter at the 2010, 2011, 2012, and 2013 Annual Meetings

# Committees and Service

 $2016\text{--}2018 \quad \textbf{User Executive Committee}, \ \textit{Cornell High Energy Synchrotron Source}, \ \textbf{Ithaca}, \ \textbf{New}$ 

York

 $2015\text{-present}\quad \textbf{Reviewer}, \textit{JACS}.$ 

2017-present Reviewer, *IUCR*.