

Steve Meisburger

Curriculum vitae

Cornell University
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Education

- Aug. 2014 **Doctor of Philosophy**, Applied Physics, Cornell University, Ithaca, NY.
Thesis: *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, MN, *Summa cum laude*.

Appointments

- 2020-present **Research Associate**, Chemistry & Chemical Biology, Cornell University.
Advisor: Nozomi Ando
- 2018-2020 **Postdoctoral Research Associate**, Chemistry & Chemical Biology, Cornell University.
Advisor: Nozomi Ando
- 2016-2018 **Postdoctoral Research Fellow**, Chemistry, Princeton University.
Support: NIH NRSA Postdoctoral Fellowship (F32)
Advisor: Nozomi Ando
- 2016-2018 **Postdoctoral Research Associate**, Chemistry, Princeton University.
Advisor: Nozomi Ando

Awards and Honors

- 2016-2018 **NIH NRSA Postdoctoral Fellowship**: “Allosteric motions of B₁₂ enzymes”, Princeton University, F32-GM117757. Sponsors: Nozomi Ando & Garnet Chan (Princeton Chemistry).
- May 2017 **Best Poster: Technical Achievement**, CHESS Users’ Meeting.
- May 2017 **Travel Award**, American Crystallographic Association, Meeting in New Orleans, LA.
- Apr. 2017 **Travel and Professional Development Award**, American Society for Biochemistry and Molecular Biology, Meeting in Chicago, IL.
- 2008-2011 **NIH Predoctoral Training Grant in Molecular Biophysics**, Cornell University, T32-GM008267.
- May 2007 **Distinction awarded for Senior Integrative Exercise (Thesis)**, Carleton College.

Teaching Experience

- Apr. 2021 **Instructor**, High Pressure Biology Workshop, Cornell High Energy Synchrotron Source, (Remote).
- (recurring) **Instructor**, Everything BioSAXS: Getting started in biological small-angle x-ray solution scattering, BioCAT beamline at Advanced Photon Source, (Remote).
Workshops in October 2020, March 2021
- Aug. 2020 **Instructor**, Applications of Small Angle Scattering to Structural Biology: An Introduction, Workshop at the ACA Annual Meeting, (Remote).
- (recurring) **Instructor**, BioSAXS Essentials: Getting Started in Biological Small-Angle X-ray Solution Scattering, Cornell High Energy Synchrotron Source, Ithaca, NY.
Workshops in Nov. 2014, May 2016, May 2017, and April 2018

Oct. 2018 **Lecturer**, *9th annual SIBYLS BioSAXS workshop*, Advanced Light Source, Berkeley, CA.
 Fall 2018 **Guest Lecturer**, *CHEM 2870: Introductory Physical Chemistry*, Cornell CCB.
 Fall 2015 **Guest Lecturer**, *CHM 515: Biophysical Chemistry I*, Princeton Chemistry.
 Spring 2014 **Guest Lecturer**, *CHM 516: Biophysical Chemistry II*, Princeton Chemistry.
 2007-2008 **Teaching Assistant**, *AEP 3630: Electronic Circuits*, Cornell Applied & Eng. Physics.

Research Experience

2020-present **Researcher Associate**, *Cornell Chemistry & Chemical Biology*.
 Lab of Nozomi Ando
New methods for dynamic structural biology.
 Developing algorithms and experimental methods for diffuse X-ray scattering, SAXS, and cryo-EM to reveal protein motions important for function.

2014-2020 **Postdoctoral Researcher**, *Princeton Chemistry, Cornell Chemistry & Chemical Biology*.
 Advisor: Nozomi Ando
Protein dynamics from diffuse X-ray scattering.
 Developed experimental and computational methods to utilize the diffuse scattering between the Bragg peaks to better understand protein motions within the crystal. Collaborators: David Case (Rutgers), Sol Gruner (Cornell), Eddie Arnold (Rutgers).
Allosteric motions of B₁₂ enzymes.
 Investigated domain motions involved in regulating catalytic cycle of B₁₂-dependent enzymes Methionine Synthase and Corrinoid FeS Protein / Methyltransferase using solution scattering and non-conventional X-ray crystallography. Collaborator: Stephen Ragsdale (U. Michigan).
Allosteric regulation of phenylalanine hydroxylase.
 Revealed role of domain motion in allosteric regulation by combining chromatography-coupled SAXS with mathematical deconvolution. Collaborator: Paul Fitzpatrick (UT Health San Antonio).

2008-2014 **Graduate Research Assistant**, *Cornell Applied & Engineering Physics*.
 Advisor: Lois Pollack
Instrumentation and methods for time-resolved SAXS and cryo-SAXS.
 Designed and fabricated a microfluidic mixer and adapted a commercial stopped-flow mixer for time-resolved SAXS experiments on RNA folding and nucleosome disassembly. Developed methods for cryo-cooling compatible with SAXS data collection. Collaborators: Ken Hampel (U. Vermont Medical Center), Rob Thorne (Cornell).
Characterizing the unfolded state of nucleic acids and proteins.
 Investigated electrostatic effects on single-stranded RNA and DNA homopolymers using SAXS. Applied polymer theory and atomistic modeling to reconcile SAXS and single-molecule FRET data from nucleic acids and protein L in the unfolded state. Collaborators: Gilad Haran (Weizmann Institute), Kevin Plaxco (UCSB), Tobin Sosnick (U. Chicago).
Measuring and modeling the ion atmosphere around RNA and DNA.
 Measured spatial distribution and number of positive ions surrounding DNA duplexes and RNA motifs using anomalous scattering from heavy atoms. Compared results with continuum electrostatic theory and atomistic simulations. Collaborators: Kurt Andresen (Gettysburg College), David Case (Rutgers), Ron Elber (U.T. Austin).

Summer 2006 **Undergraduate Researcher**, *REU at the Santa Fe Institute*, Santa Fe, New Mexico.
 Advisor: Alfred Hubler

Summer 2005 **Undergraduate Researcher**, *NNIN REU at Stanford University*, Palo Alto, California.
 Advisor: Fabian Pease

Publications

- [24] **Meisburger SP***, Xu D*, Ando N. *REGALS: a general method to deconvolve X-ray scattering data from evolving mixtures*. **IUCrJ** 8: 225-237 (2021). *equal contribution
- [23] **Meisburger SP**, Case DA, Ando N. *Diffuse X-ray Scattering from Correlated Motions in a Protein Crystal*. **Nat. Comm.** 11: 1271 (2020).

- [22] Khan CA, **Meisburger SP**, Ando N, Fitzpatrick PF. *The phenylketonuria-associated substitution R68S converts phenylalanine hydroxylase to a constitutively active enzyme but reduces its stability.* **J. Biol. Chem.** 294(12): 4359-67 (2019).
- [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

- [1] **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: Talks

- [13] Harvard-Hamburg Crystallographic Curiosities Seminar Series. (Remote) May 27, 2021. (Invited)
- [12] SBGrid Weekly Webinar Series. (Remote) April 6, 2021. (Invited)
- [11] ACA Annual Meeting, Session 2.1.4: Frontiers in SAS. (Remote) Aug. 13, 2020. (Invited)
- [10] CHESS Commons Meeting. (Remote) Mar. 20, 2020. (Invited)
- [9] ACS Northeast Regional Meeting. Saratoga Springs, NY. June 25, 2019. (Invited)
- [8] Center for Nonlinear Studies, Los Alamos National Laboratory. Oct. 16, 2018. (Invited)
- [7] ACA Annual Meeting, Session 1.1.1: Closing the R-Factor Gap in Protein Crystallography. Toronto, Ontario. July 21, 2018. (Contributed)
- [6] ACA Annual Meeting, Session 1.1.1: Hybrid Methods - BioSAXS Session. New Orleans, LA. May 27, 2017. (Contributed)
- [5] ASBMB Annual Meeting, Spotlight Session: Structural Dynamics of Enzymes. Chicago, IL. April 24, 2017. (Contributed)
- [4] CHESS-U Workshop: Biomolecules in Motion. Ithaca, NY. June 8, 2016. (Invited)
- [3] Biophysical Society Meeting, Platform: DNA Structure and Dynamics. San Francisco, CA. Feb. 18, 2014. (Contributed)
- [2] CHESS Users' Meeting. Ithaca, NY. June 2013. (Invited)
- [1] RNA-UNY. Rensselaerville, NY. Oct. 9, 2010. (Contributed)

Presentations: Posters (Selected)

- [6] Meisburger SP, Taylor AB, Khan CA, Zhang S, Fitzpatrick PF, Ando N. *Unmixing Enzyme Allostery*. *CHESS Users' Meeting. June 2017. **Best poster: technical achievement*
- [5] Meisburger SP, Warkentin M, Chen H, Hopkins JB, Katz AM, Gillilan RE, Thorne RE, Pollack L. *Introducing Cryo-SAXS for measuring low resolution macromolecular structure without radiation damage*. Biophysical Society Meeting. Feb. 2013.
- [4] Meisburger SP, Gillilan RE, Woll A, Pollack L. *A semi-transparent beamstop for accurate normalization of millisecond time-resolved SAXS profiles*. Chess Users' Meeting. June 2012.
- [3] Meisburger SP, Chen H, Pabit SA, Sutton JL, Webb WW, Pollack L. *Solution structures of flexible RNA molecules in mono- and divalent salt*. Biophysical Society Meeting. Feb 2012.
- [2] Meisburger SP, Pabit SA, Li L, Blose JM, Brooks K, Hampel K, Pollack L. *Measuring the dimensions of a compact kinetic intermediate in the folding pathway of the GlmS Ribozyme*. Biophysical Society Meeting. Feb 2011.
- [1] Meisburger SP, Pabit SA, Li L, Blose JM, Hampel K, Pollack L. *Visualizing the structure of the glmS riboswitch as it folds using time-resolved SAXS*. Biophysical Society Meeting. Feb 2010.

Professional Activities

- 2021 Chair, ACA Small Angle Scattering Scientific Interest Group
- Aug. 2020 Session chair, American Crystallographic Association (ACA) Meeting
- 2020 Chair-elect, ACA Small Angle Scattering Scientific Interest Group
- Aug. 2019 Session chair, ACA Meeting

2016-2019	Elected member, Cornell High Energy Synchrotron Source User Executive Committee
Feb. 2014	Platform session chair, Biophysical Society Meeting
2021	Reviewer for <i>Structural Dynamics</i>
2020-present	Reviewer for <i>Review of Scientific Instruments</i>
2017-present	Reviewer for <i>IUCrJ</i>
2015-present	Reviewer for <i>JACS</i>

Professional Memberships

2017-present	American Crystallographic Association
2009-2015	Biophysical Society

References

Available upon request.