

# Steve Meisburger

## Curriculum vitae

Cornell University  
Department of Chemistry & Chemical Biology  
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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– **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
- 2014-2016 **Postdoctoral Research Associate**, *Chemistry*, Princeton University.  
Advisor: Nozomi Ando

### Awards and Honors

- 2016-2018 **NIH NRSA Postdoctoral Fellowship: “Allosteric motions of B<sub>12</sub> 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.

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## Research Experience

- 2020– **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 for measuring correlated protein motions within the crystal. Collaborators: David Case (Rutgers), Sol Gruner (Cornell), Eddie Arnold (Rutgers).  
**Allosteric motions of B<sub>12</sub> enzymes.**  
Investigated domain motions involved in regulating catalytic cycle of B<sub>12</sub>-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).
- 2006 **Undergraduate Researcher**, *REU at the Santa Fe Institute*, Santa Fe, New Mexico.  
Mentor: Alfred Hubler. Project: *Chaos in Wall Following Robots*.
- 2005 **Undergraduate Researcher**, *NNIN REU at Stanford University*, Palo Alto, California.  
Mentors: Fabian Pease, Dan Pickard. Project: *Characterization of Beam Aberrations due to Magnetic Field Tilt in DIVA for Massively Parallel Electron Beam Lithography*.

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## Publications

- [26] **Meisburger SP**, Ando N. *Separating internal and external correlated protein motions in the crystalline state by total X-ray scattering analysis and vibrational dynamics simulation*. Submission scheduled for Feb. 2022.
- [25] Xu D\*, **Meisburger SP\***, Ando N. *Correlated motions in structural biology*. **Biochemistry** 60: 2331-40 (2021). \*equal contribution

- [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. Commun.** 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.** 45(9): e66 (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).

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## 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).

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## Presentations: Talks

- [15] U. at Buffalo, Protein Science Group Seminar. (Remote) Oct. 6, 2021. (Invited)
- [14] SSRL/LCLS Users' meeting. (Remote) Sep. 21, 2021. (Invited)
- [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. 3, 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. 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)

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## 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.

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## Professional Memberships

- 2020– American Association for the Advancement of Science (AAAS)
- 2017– American Crystallographic Association (ACA)
- 2009-2015 Biophysical Society

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## Professional Activities

- Aug. 2021 Session chair, ACA Meeting, *BioWAXS: Experiment and Interpretation*.
- 2021 Chair, Small Angle Scattering Scientific Interest Group (SAS SIG) of the ACA
- Aug. 2020 Session chair, ACA Meeting, *Structural Dynamics I: Protein collective motions studied by X-ray scattering and diffraction*.
- 2020 Chair-elect, SAS SIG of the ACA
- Aug. 2019 Session chair, ACA Meeting, *Diffuse scattering for biological structure and dynamics*.
- 2016-2019 Elected member, CHESS User Executive Committee
- Feb. 2014 Platform session chair, Biophysical Society Meeting
- 2021– Reviewer for *Structural Dynamics Journal*
- 2020– Reviewer for *Review of Scientific Instruments*
- 2017– Reviewer for *IUCrJ*
- 2015– Reviewer for *JACS*

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## References

Available upon request.