

CURRICULUM VITAE

Zhong Ren

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PROFESSIONAL EXPERIENCES

- 2014-present Research Associate Professor, Department of Chemistry, University of Illinois at Chicago
- 2013-present CEO, Renz Research, Inc.
- 2006-2013 Research Beamline Scientist and Software Specialist, Center for Advanced Radiation Sources, The University of Chicago at the Advance Photon Source, Argonne National Laboratory
- 2001-2006 Founder and CEO, Renz Research, Inc.
- 1995-2001 Beamline Scientist, Center for Advanced Radiation Sources, The University of Chicago at Advance Photon Source, Argonne National Laboratory
- 1995-2001 Instructor, Department of Biochemistry and Molecular Biology, The University of Chicago

EDUCATION

- 1991-1995 Research Associate, Department of Biochemistry and Molecular Biology, The University of Chicago
- 1990-1991 Postdoctoral Research Associate, Department of Molecular Biology, The Scripps Research Institute
- 1987-1990 Department of Protein Crystallography, Institute of Biophysics, Beijing, China
- 1987-1988 Graduate School of Academia Sinica, Beijing, China
- 1983-1987 Department of Bioengineering, Huazhong University of Science and Technology, Wuhan, China. B.E.

PROFESSIONAL HIGHLIGHTS

- *Development of data processing algorithms for Laue diffraction and their software implementations* The Laue diffraction, based on polychromatic X-rays and stationary sample crystals, permits the briefest exposure at synchrotrons thus fast time resolution down to 100 ps (10^{-10} s). Processing of Laue diffraction data, however, is far more difficult than the conventional diffraction method using the monochromatic radiation. I have made the Laue diffraction a practical method for studying ultrafast chemical reactions in crystals via continuous R&D efforts over many years (1992-2006) with a suite of algorithms implemented in two software packages, *LaueView* and *Precognition*TM. These computer algorithms and programs have enabled many time-resolved projects and publications by other scientists around the world and it has also helped neutron crystallography. Here is an incomplete publication list by other scientists who have acknowledged the use of my software: Šrajer et al **Science** 274, 1726, 1996; Genick et al **Science** 275, 1471, 1997; Perman et al **Science** 279, 1946, 1998; Ravelli et al **Acta Cryst D**54,

- 1359, 1998; Šrajer et al **J Synchrotron Rad** 7, 236, 2000; Ihee et al **PNAS** 102, 7145, 2005; Schmidt et al **PNAS** 102, 11704, 2005; Knapp et al **PNAS** 103, 7649, 2006; Key et al **Biochemistry** 46, 4706, 2007; Knapp et al **Structure** 17, 1494, 2009; Kamiński et al **J Synchrotron Rad** 17, 479, 2010; Schmidt et al **Acta Cryst A** 66, 198, 2010; Wöhri et al **Science** 328, 630, 2010; Makal et al **Acta Cryst A** 67, 319, 2011; Yang et al **Nature** 479, 428, 2011; Tripathi et al **Biophys J** 102, 325, 2012; Schmidt et al **J Synchrotron Rad** 19, 264, 2012; Jung et al **Nat Chem** 5, 212, 2013; Munshi et al **Acta Cryst D** 70, 414, 2014; Perry et al **J Appl Cryst** 47, 1975, 2014; Pawate et al **Acta Cryst F** 71, 823, 2015; Hekstra et al **Nature** 540, 400, 2016; Sui et al **Lab Chip** 16, 3082, 2016; Kim et al **Science** 355, 262, 2017.
- *Extraction of structural dynamics from diffraction data of heterogeneous conformations* A dynamic process of a biological macromolecule often involves co-existence of heterogeneous structural species. It is often very difficult, if not impossible, to experimentally isolate each species for direct observation. Therefore, dynamic crystallography often has to deal with diffraction data from mixed conformations. I have formulated a general solution to isolate distinct structures via joint data analysis of structural heterogeneity in real space. The associated software implementation is now collected in the software package *dynamiX*. These methods have been exemplified in time-resolved crystallography and temperature-scan cryo-crystallography. The underlying principle for deconvolution of heterogeneous structures also applies to single particle scattering, where the crystal lattice is absent thus structural heterogeneity is expected to present extensively.
 - *Structural meta-analysis* Protein conformational changes during a biochemical reaction or a biological process are often depicted in a conceptual conformational space. I proposed a mathematically defined conformational space with limited dimensionality to facilitate large-scale joint structural analysis via a suite of computational tools. Functional-relevant structural dynamics can be extracted from a large collection of static structures archived in the Protein Data Bank, in which each static structure provides a snapshot of the protein structure in action. My recent work has addressed the historical debate on the mechanisms of hemoglobin cooperativity and extraordinary fidelity of DNA polymerases. The structural meta-analysis provides a comprehensive survey of experimental observations from multiple research groups that are often inconsistent or even conflicting. A sequence of molecular motions uncovered by meta-analysis enable reverse engineering of mechanical models that elucidate the inner workings of the macromolecular machinery. I am extending the method to jointly analyze even larger structural collections of phylogenetically related proteins. Both commonality and distinction found in structures and dynamics are insightful to reveal the functional mechanisms.
 - *Crystallization devices for large-scale in situ serial crystallography* I have invented a new type of crystallization devices, dubbed “crystal-on-crystal” chips that feature single crystal quartz as substrate material. Protein crystals grown on such chips can be directly transferred to a synchrotron or XFEL beamline for diffraction

- T. Graber, P. Anfinrud, H. Brewer, Y.-S. Chen, H.-S. Cho, N. Dashdorj, R.W. Henning, I. Kosheleva, G. Macha, M. Meron, R. Pahl, **Z. Ren**, S. Ruan, F. Schotte, V. Šrajer, P.J. Viccaro, F. Westferro & K. Moffat, BioCARS: a synchrotron resource for time-resolved X-ray science, *J. Synchrotron Rad.* 18, 658-670, 2011.
- Y.-L. Wu, X. Yang, **Z. Ren**, D.P. McDonnell, J.D. Norris, T.M. Willson & G.L. Greene, Structural basis for an unexpected mode of SERM-mediated ER antagonism, *Mol. Cell* 18, 413-424, 2005.
- M. Schmidt, R. Pahl, V. Šrajer, S. Anderson, **Z. Ren**, H. Ihee, S. Rajagopal & K. Moffat, Protein kinetics: Structures of intermediates and reaction mechanism from time-resolved x-ray data, *Proc. Natl. Acad. Sci. USA* 101, 4799-4804, 2004.
- M. Schmidt, S. Rajagopal, **Z. Ren** & K. Moffat, Application of singular value decomposition to the analysis of time-resolved macromolecular X-ray data, *Biophys. J.* 84, 2112-2129, 2003.
- J.S. Brunzelle, P. Shafae, X. Yang, S. Weigand, **Z. Ren** & W. F. Anderson, Automated crystallographic system for high-throughput protein structure determination, *Acta Cryst.* D59, 1138-1144, 2003.
- **Z. Ren**, B. Perman, V. Šrajer, T.-Y. Teng, C. Pradervand, D. Bourgeois, F. Schotte, T. Ursby, M. Wulff, R. Kort & K. Moffat, Molecular movie at 1.8 Å resolution displays the photocycle of photoactive yellow protein, a eubacterial blue-light receptor, from nanoseconds to seconds, *Biochemistry* 40, 13788-13801, 2001.
- V. Šrajer, **Z. Ren**, T.-Y. Teng, M. Schmidt, T. Ursby, D. Bourgeois, C. Pradervand, W. Schildkamp, M. Wulff & K. Moffat, Protein conformation relaxation and ligand migration in myoglobin: a nanosecond to millisecond molecular movie from time-resolved Laue X-ray diffraction, *Biochemistry* 40, 13802-13815, 2001.
- V. Šrajer, S. Crosson, M. Schmidt, J. Key, F. Schotte, S. Anderson, B. Perman, **Z. Ren**, T.-Y. Teng, D. Bourgeois, M. Wulff & K. Moffat, Extraction of accurate structure-factor amplitudes from Laue data: wavelength normalization with wiggler and undulator X-ray sources, *J. Synchrotron Rad.* 7, 236-244, 2000.
- **Z. Ren**, D. Bourgeois, J.R. Helliwell, K. Moffat, V. Šrajer & B.L. Stoddard, Laue crystallography: coming of age, *J. Synchrotron Rad.* 6, 891-917, 1999.
- C.C. Correll, A. Munishkin, Y.-L. Chan, **Z. Ren**, I. Wool & T.A. Steitz, Crystal structure of the ribosomal RNA domain essential for binding elongation factors, *Proc. Nat. Acad. Sci. U. S. A.* 95, 13436-13441, 1998.
- R.B.G. Ravelli, M.L. Raves, **Z. Ren**, D. Bourgeois, M. Roth, J. Kroon, I. Silman & J.L. Sussman, Static Laue diffraction studies on acetylcholinesterase, *Acta Cryst.* D54, 1359-1366, 1998.
- X. Yang, **Z. Ren** & K. Moffat, Structure refinement against synchrotron Laue data: strategies for data collection and reduction, *Acta Cryst.* D54, 367-377, 1998.
- J.J. Yue, T. Jiang, **Z. Ren**, Z.L. Wan, W.R. Chang & D.C. Liang, Crystal structure of deshexapeptide (B25-30) insulin at 0.15 nm resolution, *Progress Nat. Sci.* 8, 106-112, 1998.
- B. Perman, V. Šrajer, **Z. Ren**, T.-Y. Teng, C. Pradervand, T. Ursby, D. Bourgeois, F. Schotte, M. Wulff, R. Kort, K. Hellingwerf & K. Moffat, Energy transduction on

- the nanosecond time scale: early structural events in a xanthopsin photocycle, *Science* 279, 1946-1950, 1998.
- I.J. Clifton, E.M.H. Duke, S. Wakatsuki & **Z. Ren**, Evaluation of Laue diffraction patterns, *Meth. Enzymol.* 277, 448-467, 1997.
 - K. Moffat & **Z. Ren**, Synchrotron radiation applications to macromolecular crystallography, *Curr. Opin. Struct. Biol.* 7, 689-696, 1997.
 - U.K. Genick, G.E.O. Borgstahl, K. Ng, **Z. Ren**, C. Pradervand, P.M. Burke, V. Srajer, T.-Y. Teng, W. Schildkamp, D.E. McRee, K. Moffat & E.D. Getzoff, Millisecond time-resolved Laue crystallography: structure of a protein photocycle intermediate, *Science* 275, 1471-1475, 1997.
 - V. Srajer, T.-Y. Teng, T. Ursby, C. Pradervand, **Z. Ren**, S.-I. Adachi, W. Schildkamp, D. Bourgeois, M. Wulff & K. Moffat, Nanosecond time-resolved macromolecular crystallography: photolysis of carbonmonoxy myoglobin, *Science* 274, 1726-1729, 1996.
 - **Z. Ren**, K. Ng, G. Borgstahl, E. Getzoff & K. Moffat, Quantitative analysis of time-resolved Laue diffraction patterns, *J. Appl. Cryst.* 29, 246-260, 1996.
 - **Z. Ren** & K. Moffat, Quantitative analysis of synchrotron Laue diffraction pattern in macromolecular crystallography, *J. Appl. Cryst.* 28, 461-481, 1995.
 - **Z. Ren** & K. Moffat, Deconvolution of energy overlaps in Laue diffraction, *J. Appl. Cryst.* 28, 482-493, 1995.
 - W. Chang, T. Jiang, **Z. Ren**, Z. Wan, Y. Xu, D. Liang, S. Zhu & Y. Zhang, The crystal structure of deshexapeptide (B25-B30) insulin at 0.25 nm resolution, *Sci. China* B38, 1094-1100, 1995.
 - **Z. Ren** & K. Moffat, Laue crystallography for studying rapid reactions, *J. Synchrotron Rad.* 1, 78-82, 1994.
 - **Z. Ren**, T. Meyer & D.E. McRee, Atomic structure of a cytochrome c' with an unusual ligand-controlled dimer dissociation at 1.8 Å resolution, *J. Mol. Biol.* 234, 433-445, 1993.
 - **Z. Ren** & D.C. Liang, Molecular close-packing method and its application to crystal structure determination of deshexapeptide (B25-B30) insulin, *Sci. China* B35, 783-790, 1992.
 - **Z. Ren** & D.C. Liang, A molecular packing method in macromolecular crystallography, *Sci. China* B9, 931-936, 1991.

SYNERGISTIC ACTIVITIES

- I maintain and supply a Laue data processing software Precognition™ to the user community since 2002 to this date. The software manual and tutorial are online. Precognition user guide with reference and tutorials ([researchgate.net/publication/259441273_Precognition_User_Guide_with_Reference_and_Tutorials?ev=prf_pub](https://www.researchgate.net/publication/259441273_Precognition_User_Guide_with_Reference_and_Tutorials?ev=prf_pub))
How to process Laue data using Precognition ([researchgate.net/publication/259441538_How_to_Process_Laue_Data_Using_Precognition?ev=prf_pub](https://www.researchgate.net/publication/259441538_How_to_Process_Laue_Data_Using_Precognition?ev=prf_pub))
- Served as a reviewer for Phil. Trans. R. Soc. B, PLoS One, and Acta Cryst. D.

- I was invited by Y. Tao to visit the Institute of High Energy Physics, Academia Sinica, Beijing, China in 2013 to evaluate their plan for construction of a time-resolved beamline at the Beijing Advanced Photon Source.
- I was the organizer of Workshop on Dynamic X-ray Scattering in Structural Biology, November 2011 held at APS, Argonne National Laboratory (cars.uchicago.edu/biocars/pages/DXSworkshop11/index.shtml).
- P. Coppens graciously invited me in 2005 to spend a few days with his group in Department of Chemistry, The State University of New York at Buffalo to discuss SVD analysis of their time-resolved diffraction data.
- A figure illustration that I authored was collected in a middle school science textbook Nelson Science Perspectives 1, M. Di Giuseppe, B. LeDrew, J. Roberts, K. Walther & J. Young, Editors, Thomson Canada Limited, 2005.
- I spent the summer of 1995 at European Synchrotron Radiation Facility, Grenoble, France working with M. Wulff and D. Bourgeois to help them establish Laue data processing software on their beamline ID09.

INVITED TALKS

- Dynamic crystallography of bilin-based photoreceptors, 13th International Conference on Tetrapyrrole Photoreceptors of Photosynthetic Organisms (ICTPPO), Chicago, July 2017.
- Dynamic crystallography at synchrotrons and XFELs, Workshop on Diffraction Limited Applications at Advanced Photon Sources, Institute of High Energy Physics, Academia Sinica, Beijing, China, December 2016.
- Meta-analysis of DNA polymerase structures, plenary talk on Argentinian Association of Crystallography Meeting, San Luis, Argentina. November 2016.
- Structural events during translocation and proofreading in replicative DNA polymerase, Department of Physics, Ohio State University, Columbus, Ohio, December 2015.
- A reverse engineering approach to understand human hemoglobin, Department Mathematics, Statistics, and Computer Science, University of Illinois at Chicago, July 2012.
- Crystallographic observation of photodissociation at sub-X-ray-bunch time resolution, American Crystallographic Association Annual Meeting, Boston, July 2012.
- Observing structural dynamics by experimental and computational methods, Departmental Seminar, Department of Computer and Information Science, IUPUI, Indianapolis, IN, April 2012.
- Laue diffraction and its applications, Advanced Light Source User Meeting, Berkeley, CA, October 2011.
- A partially ligated state of dimeric hemoglobin observed at 100 ps, American Crystallographic Association Annual Meeting, New Orleans, May 2011.
- An introduction to Laue diffraction on the new 14-ID beamline of BioCARS, Physics Department Colloquium, University of Wisconsin at Milwaukee, December 2007.

- The Advantages and limitations of Laue microdiffraction, First European Workshop on High Brilliance Microcrystallography of Proteins, MRC Laboratory of Molecular Biology, Cambridge, October 2007.
- Recent advances in Laue data processing, Spallation Neutron Source, Oak Ridge National Lab, Oak Ridge, TN, June 2007.
- On-the-fly evaluation and in-depth analysis of Laue diffraction data, Workshop on Advanced Laue Diffraction in Frontier Science, ILL/ESRF, Grenoble, France, January 2007.
- Recent advances in Laue data processing, Department of Chemistry, The State University of New York, Buffalo, NY, November 2005.
- Molecular movie of the photocycle of a eubacterial blue-light receptor from nanoseconds to seconds, The 11th Users Meeting for the Advanced Photon Source, Argonne, IL, October 2001.
- The photocycle movie of photoactive yellow protein from nanoseconds to seconds, International Conference on Computational Nanoscience, Hilton Head Island, South Carolina, March 2001.
- The photocycle movie of photoactive yellow protein from nanoseconds to seconds, The Royal Netherlands Academy of Arts and Sciences Academy Colloquium: Photoreceptor proteins: structure, photochemistry and dynamics, Amsterdam, The Netherlands, November 2000.
- Synchrotron radiation transforms macromolecular crystallography, Structural Biology Symposium, Zhangjiajie, China, June 1999.