BIOGRAPHICAL SKETCH

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NAME: Bo Hu

eRA COMMONS USER NAME (credential, e.g., agency login): BOHU123

POSITION TITLE: Assistant Professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Nankai University	B.S.	06/2003	Biological science
Nankai University	Ph.D.	06/2010	Microbiology
University of Texas Medical School at Houston (now McGovern Medical School)	Postdoctoral	04/2016	Cryo electron microscopy

A. Personal Statement

With seven years of training in microbiology/biochemistry and another seven years experience in cryo electron tomography (Cryo-ET), I have acquired the necessary expertise to successfully carry out the proposed research projects. I developed and now employ a high-throughput Cryo-ET pipeline, our pipeline effectively integrates dose-fractionation in a direct detector device with specific software, allowing massive data collection, drift correction, fiducial model generation, alignment, contrast transfer function (CTF) correction, and reconstruction of several thousands of tomograms at high magnification. This pipeline has been successfully applied to address a broad range of biological question, resulting in several high-profile peer-reviewed publications. During and since my postdoctoral training with Dr. Jun Liu, my research has focused on understanding the structure and function of bacterial nanomachines *in situ*. In 2017, I joined McGovern Medical School as an Assistant Professor. In collaboration with Dr. Christie, a professor in our Dept and an expert in bacterial type IV secretion systems (T4SSs), I solved *in situ* structures of the *Legionella pneumophila* Dot/Icm system, the *Escherichia coli* F plasmid-encoded T4SS, and the *Helicobacter pylori* Cag T4SS. These structures have revealed the architectures of the T4SSs in the native bacterial cell envelope in unprecedented resolution. For the first time, we have visualized the arrangements of the three ATPases that assemble at the entrance to the translocation channel, and we have determined the physical interaction of the translocation channel with the extracellular conjugative pilus. I also have invested considerable effort in developing novel methodologies to handle 4K x 4K tomographic data with three-dimensional contrast transfer function, with a goal of improving the resolution of Cryo-ET cellular imaging to the sub-nanometer range. As evidence of my success in this area, we now have solved the structure of the *H. pylori* Cag T4SS at a resolution of ~15 Å. Very recently, in collaboration with Dr. Richard J. Lamont, we determined the *in situ* architecture of the type IX secretion systems (T9SS) machinery in its native context in *Porphorymonas gingivalis*. Our work has revealed the T9SS is the largest of the known bacterial secretion systems and evidently arranges as multiple, independently functioning translocation motors.

Since 2017, my lab has published 17 primary research papers and 2 reviews. I have demonstrated that within my area of expertise, I am able to identify critical deficiencies in our knowledge of bacterial nanomachine structures, and then exploit innovative methods to solve structures in the context of the native membrane environment. The knowledge gained from these structures supplies fundamental new insights into their

mechanism of assembly and action, and paves the way for development of intervention strategies aimed at blocking machine assembly or function for disease mitigation. In addition to my research and deep commitment to education/training, I have acquired the necessary administrative skills, first as Assistant Research Professor and now as Assistant Professor on the scientist/educator tenure track, to successfully direct my research program. I am also keenly aware of the importance of collaboration with other experts in the bacterial secretion/pathogenesis fields, and of the value of frequent communication among project members. The current application builds logically on a strong foundation of technical knowledge and broader training I have acquired since joining the faculty of the MMG Department at McGovern Medical School.

1. Morado, D. R., **Hu, B.**, Liu, J. (2016) Using Tomoauto: A Protocol for high-throughput automated cryo-electron tomography. *J. Vis. Exp*. e53608, doi:10.3791/53608. PMCID: PMC4781705
2. Farley M., **Hu B.**, Margolin W., Liu J. (2016) Minicells, Back in Fashion. *J. Bacteriol.* 198 (8), 1186-1195. PMCID: PMC4859596
3. **Hu, B.**, Lara-Tejero M, Kong Q, Galán JE, Liu J. (2017) In situ molecular architecture of the *Salmonella* type III secretion machine. *Cell* 168(6):1065-1074. PMCID: PMC5393631
4. Liu X, Khara P, Baker ML, Christie PJ, **Hu B**. (2022) Structure of a type IV secretion system core complex encoded by multi-drug resistance F plasmids. *Nat Commun.* 13(1):379. doi: 10.1038/s41467-022-28058-5. PMCID: PMC8770708.

B. Positions, Scientific Appointments, and Honors

2010-2016 Postdoctoral Fellow, University of Texas Medical School at Houston, Houston, TX
2016-2017 Research Assistant Professor, McGovern Medical School (newly renamed), Houston, TX
09/2017- Assistant Professor, McGovern Medical School, Houston, TX

C. Contributions to Science

1. My early publications directly addressed the biosynthesis and regulation of bacterial surface antigen: O polysaccharide and flagellin, also known respectively as the O and H antigens. My research is primarily concerned with the functions of these glycosyltransferases which have the potential to be applied in the targeted synthesis of specific glycoconjugates. Another project is about the flagellar phase variation in *E. coli* strains. Although the flagellar phase variation in *Salmonella* has been well studied, the mechanism involved in unilateral flagellar phase variation in *E. coli* remains unclear. Using *E. coli* H3 and H17 serotype strains as models, our results demonstrate that the flagellin gene is within a genomic island (GI), and an integrase mediates the excision of the GI from the chromosome, which causes the occurrence of unilateral flagellar phase variation.

a. Brockhausen, I., **Hu, B.**, Liu, B., Lau, K., Szarek, W. A., Wang, L., and Feng, L. (2008) Characterization of two beta-1,3-glucosyltransferases from *Escherichia coli* serotypes O56 and O152, *J. Bacteriol.* 190, 4922-4932. PMCID: PMC2446995
b. **Hu, B.**, Perepelov, A. V., Liu, B., Shevelev, S. D., Guo, D., Senchenkova, S. N., Shashkov, A. S., Feng, L., Knirel, Y. A., and Wang, L. (2010) Structural and genetic evidence for the close relationship between *Escherichia coli* O71 and *Salmonella enterica* O28 O-antigens, *FEMS Imm. Med. Microbiol.* 59, 161-169. PMID: 20482625
c. Liu, B., **Hu, B.**, Zhou, Z., Guo, D., Guo, X., Ding, P., Feng, L., and Wang, L. (2012) A novel non-homologous recombination-mediated mechanism for *Escherichia coli* unilateral flagellar phase variation, *Nucleic Acids Res.* 40, 4530-4538. PMCID: PMC3378880

2. In addition to the contributions described above, I have focused on visualizing the virus-host interaction by Cryo-ET. With collaboration Dr. William Margolin, we developed methods to genetically modify Gram-negative bacteria to produce minicells, which has proven to be a very powerful subject for structural research by Cryo-ET. I also developed methods to purify minicells from different species. Together with high throughput Cryo-ET and sub-volume averaging, we generated high-resolution reconstructions of cell-virus complexes and were able to capture T7 virions at successive stages of infection. Our structures revealed the first complete pathway of infection initiation by any phage. In addition to virus T7, I also conducted a research project on T4 Bacteriophage, which is a genetically

and biochemically well-studied member of the Myoviridae family. What are less well understood, and what my studies have focused on, are the mechanism by which the phage absorbs to the bacterial membrane and the interaction of the phage DNA injection tube with the inner membrane of *E. coli*.

a. **Hu, B.**, Margolin, W., Molineux, I. J., and Liu, J. (2013). The bacteriophage t7 virion undergoes extensive structural remodeling during infection. *Science* 339, 576-579. PMCID: PMC3873743
b. **Hu, B.**, Margolin, W., Molineux, I. J., and Liu, J. (2015) Structural remodeling of bacteriophage T4 and host membranes during infection initiation, *Proc. Natl. Acad. Sci. USA* 112, E4919-E4928. PMCID: PMC4568249

3. Understanding of the mechanisms underlying bacterial pathogenesis in humans is a major focus of microbiological research and the elucidation of the infectious process yields practical applications of new antibiotics and improved vaccines. One example is the bacterial type III secretion system (T3SS). Many infectious bacteria such as *Shigella* and *Salmonella* use type III secretion machines, to transfer virulence proteins into eukaryotic host cells, cause diarrheal disease. In my more recent studies, I conducted a comprehensive study on the structure and function of the bacterial T3SSs from *Shigella* and *Salmonella*. In these projects, I combined advanced imaging and genetic techniques to visualize the frozen-hydrated diarrheal pathogen *Shigella flexneri* and revealed the intact type III secretion machine and its interaction with a host cell for the first time. In addition, we reported a high-resolution *in situ* structure of the *Salmonella Typhimurium* type III secretion machine. Through molecular modeling and comparative analysis of machines assembled with protein-tagged components or from different deletion mutants, we determined the molecular architecture of the secretion machine in situ and localized its structural components.

a. **Hu B**., Dustin R. Morado, William Margolin, John R. Rohde, Olivia Arizmendi, Wendy L. Picking, William D. Picking, and Jun Liu (2015) Visualization of the type III secretion sorting platform of *Shigella flexneri*. *Proc. Natl. Acad. Sci.* USA 112, 1047-1052. PMCID: PMC4313800
b. **Hu B**., Lara-Tejero M, Kong Q, Galán JE, Liu J. (2017) In situ molecular architecture of the *Salmonella* type III secretion machine. *Cell* 168, 1065-1074. PMCID: PMC5393631
c. Park D, Lara-Tejero M, Waxham MN, Li W, **Hu B**, Galán JE, Liu J (2018) Visualization of the type III secretion mediated *Salmonella*-host cell interface using cryo-electron tomography. *Elife*. 2018 Oct 3;7. doi: 10.7554/eLife.39514. PMCID: PMC6175578
d. Lara-Tejero M, Qin Z, **Hu B**, Butan C, Liu J, Galán JE (2019) Role of SpaO in the assembly of the sorting platform of a *Salmonella* type III secretion system. *PLoS Pathog*. Jan;15(1):e1007565. doi: 10.1371/journal.ppat.1007565. PMCID: PMC6358110

4. Structural definition of bacterial type IV secretion systems (T4SSs). T4SSs are complex nanomachines used by bacteria to deliver protein and DNA complexes into target host cells. Recently, I collaborated with Dr. Christie at McGovern and Drs. J. Liu, C. Roy, and D. Chetrit at Yale to solve the structure of the *Legionella pneumophila* Dot/Icm T4SS. The Dot/Icm T4SS is phylogenetically unrelated to the IVA systems, and representative of a second large type IVB subfamily. It is, however, composed of the three signature ATPases of T4SSs, VirB4-like DotO, DotB, and DotL. Using Cryo-ET, we generated a 3D map of the Dot/Icm system at ~3 nm resolution. The new Dot/Icm structure spans both bacterial membranes, and most strikingly is composed of a highly symmetrical inner membrane subassembly, which distinguishes it from previously solved T4SS substructures. Structural analyses of mutant machines lacking one of the three ATPases, coupled with the use of GFP as a traceable tag, established that DotO and DotB assemble as stacked hexamers at the entrance to the T4SS channel. Very recently, I collaborated with Drs. Christie and Tim Cover to solve the structures of F plasmid-encoded T4SS substructures alone and in association with the F pilus and *Helicobacter pylori* Cag T4SS. These data change the existing paradigm for how T4SSs are architecturally configured at the cytoplasmic entrance, offer a view of how substrates dock and are translocated across the inner membrane and, for the first time, begin to define the nature of the physical relationship of the envelope-spanning T4SS and the conjugative pilus.

a. Chetrit D*, **Hu B***, Christie PJ, Roy CR, Liu J. (2018) A unique cytoplasmic ATPase complex defines the

Legionella pneumophila type IV secretion channel. *Nat. Microbiol*. Jun;3(6):678-686. PMCID: PMC5970066

b. **Hu B**, Khara P, Song L, Lin AS, Frick-Cheng AE, Harvey ML, Cover TL, Christie PJ. (2019) In Situ Molecular Architecture of the *Helicobacter pylori* Cag Type IV Secretion System. *MBio*. May 14;10(3). doi: 10.1128/mBio.00849-19. PMCID: PMC6520456.

c. **Hu B**, Khara P, Christie PJ. (2019) Structural bases for F plasmid conjugation and F pilus biogenesis in *Escherichia coli*. *Proc Natl Acad Sci* U S A. Jul 9;116(28):14222-14227. doi: 10.1073/pnas.1904428116. PMCID: PMC6628675

5. Structural definition of bacterial type IX secretion systems. The newly described T9SSs translocate virulence factors and can mediate specialized gliding motility among bacterial pathogens of the *Fibrobacteres–Chlorobi–Bacterioidetes* superphylum. We visualized the spatial organization of the T9SS in its native context in the *Porphorymonas gingivalis* cell by Cryo-ET. The T9SS exhibits distinct symmetries across the bacterial cell envelope: a cytoplasmic complex requiring PorL and PorM for assembly exhibits 12-fold symmetry; a periplasmic complex composed of PorM exhibits 18-fold symmetry and attaches to a PorKN ring near the outer membrane; and eight Sov translocons are arranged with 8-fold symmetry at the cell surface. The T9SS is the largest of the known bacterial secretion systems and evidently arranges as multiple, independently functioning translocation motors.

a. Song, L., D. J. Perpich, C. Wu, T. Doan, J. Potempa, J. P. Christie, E. Cascales, J. R. Lamont and **B. Hu**. (2022) A Unique Bacterial Secretion Machinery with Multiple Secretion Centers. *Proc Natl Acad Sci* U S A. doi: 10.1073/pnas.2119907119. PMCID: PMC9170169.

Complete List of Published Work in MyBibliography:
https://www.ncbi.nlm.nih.gov/myncbi/bo.hu.4/bibliography/public/

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

Departmental Start-Up Grant, McGovern Medical School.
Research Start-Up Funds PI: Bo Hu
The purpose of these funds is to set up the PI's laboratory and fund preliminary studies needed for successful grant submissions for extramural research support.

National Science Foundation
(subcontract from Texas AgriLife Research Service) 08/01/2019-07/31/2022
Molecular Mechanism for Genomic RNA Delivery in ssRNA Phages
The major goal of this project is to reveal the mechanisms of how single stranded RNA bacteriophages deliver their genomic RNA into a specific host by combing genetics, single particle cryo-EM, high-throughput cryo-ET, and high resolution fluorescence microscopy.

National Institute of General Medical Sciences
1 R35 GM138301-01 PI: Bo Hu 09/01/2020-08/31/2025
In Situ Architecture of Specialized Bacterial Secretion Systems
This application seeks to define the structures and subunit compositions of three bacterial secretion systems (E. coli F plasmid Tra, H. pylori Cag T4SSs and P. gingivalis T9SS) using in situ cryo-electron tomography techniques.

BIOGRAPHICAL SKETCH

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NAME: Liu, Xiangan

eRA COMMONS USER NAME (agency login): xianganl

POSITION TITLE: Research Scientist

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable.)*

INSTITUTION AND LOCATION	DEGREE (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
Jilin University, Changchun, Jilin, China	BS	07/1992	Nuclear Physics
China Institute of Atomic Energy, Beijing, China	MS	07/1995	Nuclear Physics
University of Houston, Houston, TX	MEE	05/2001	Electrical & Computer Engineering
University of Houston, Houston, TX	PHD	05/2003	Computational Physics
University of Houston, Houston, TX	Postdoc	01/2004	X-ray Crystallography
Baylor College of Medicine, Houston, TX	Postdoc	05/2007	Electron Microscopy

A. Personal Statement

My research has mainly focused on virus structural biology. I have determined a wide range of virus structures (spanning from human, animal, and plant viruses to bacteriophages) to atomic or near atomic resolution using single particle cryo-electron microscopy (cryoEM). I have studied structures ranging in size from simple chemical compounds, small peptides, small proteins to macromolecular complexes including large viruses and cellular machines. I have been mainly focusing on a novel cryoEM method MPSA (Multi-Path Simulated Annealing) and its applications for over 12 years with Dr. Wah Chiu at Baylor College of Medicine. I was able to apply the method to determine bacteriophage P22 structure at 3.5Å. The package has been disseminated in the cryoEM community and has been widely used to determine asymmetric structure of viruses and large macromolecular complexes.

I moved to the McGovern Medical School since 2015. In addition to virus structures, I am particularly interested in small protein (complex) structures and how viral and bacterial pathogens interact with their host cells. My goal is to study structures of small proteins (complexes) at (near) atomic resolution and macromolecular machines at subnanometer resolution *in situ*. For achieving the high-resolution goals, I have developed a triple-tilt single-particle-imaging scheme for small proteins and a hybrid cellular-imaging scheme combing cryoEM and cryoET together. The corresponding image processing tools are being integrated into ETEEM (cryoET Enhanced cryoEM) software, which can resolve some challenge issues in cryoEM, such as particle defocus variations due to either tilting or sample thickness, particle overlapping, and model bias, etc.

1. Dai W, Fu C, Raytcheva D, Flanagan J, Khant HA, Liu X, Rochat RH, Haase-Pettingell C, Piret J, Ludtke SJ, Nagayama K, Schmid MF, King JA, Chiu W. Visualizing virus assembly intermediates inside marine cyanobacteria. Nature. 2013 Oct 31;502(7473):707-10. PubMed PMID: 24107993; PubMed Central PMCID: PMC3984937.
2. Murata K, Liu X, Danev R, Jakana J, Schmid MF, King J, Nagayama K, Chiu W. Zernike phase contrast cryo-electron microscopy and tomography for structure determination at nanometer and subnanometer resolutions. Structure. 2010 Aug 11;18(8):903-12. PubMed PMID: 20696391; PubMed Central PMCID: PMC2925294.
3. Liu X, Zhang Q, Murata K, Baker ML, Sullivan MB, Fu C, Dougherty MT, Schmid MF, Osburne MS, Chisholm SW, Chiu W. Structural changes in a marine podovirus associated with release of its genome into Prochlorococcus. Nat Struct Mol Biol. 2010 Jul;17(7):830-6. PubMed PMID: 20543830; PubMed Central PMCID: PMC2924429.

4. Liu X, Jiang W, Jakana J, Chiu W. Averaging tens to hundreds of icosahedral particle images to resolve protein secondary structure elements using a Multi-Path Simulated Annealing optimization algorithm. J Struct Biol. 2007 Oct;160(1):11-27. PubMed PMID: 17698370; PubMed Central PMCID: PMC2039893.

B. Positions and Honors

Positions and Employment

2003 - 2004 Postdoc, University of Houston, Houston, TX

2004 - 2007 Postdoc, National Center for Macromolecular Imaging, Baylor College of Medicine, TX

2007 - 2010 Research Associate, National Center for Macromolecular Imaging, Baylor College of Medicine, Houston, TX

2010 - 2015 Instructor, Department of Biochemistry and Molecular Biology, Baylor College of Medicine, Houston, TX

2015 - 2017 Research Assistant Professor, Department of Pathology and Laboratory Medicine, McGovern Medical School, The University of Texas Health Science Center at Houston, Houston, TX

2017 - Research Scientist, Department of Microbiology and Molecular Genetics, McGovern Medical School, The University of Texas Health Science Center at Houston, Houston, TX

Other Experience and Professional Memberships

2008 - 2012 Member, Biophysics Society

2009 - 2011 Elected member, Sigma Xi, The Scientific Research Society

C. Contribution to Science

1. **Method development for X-ray crystallography.** Phase problem has been a challenge for protein crystallographer. In general, it requires an initial model to refine the crystal structure, however it is not always easy to construct a model. I developed dual space method to solve X-ray structure *ab initio*, which can solve small protein molecule crystal structures without providing an initial model.
   a. Liu X, Su WP. Multiresolution phase extension of a trypsin inhibitor structure from 5 A to 2 A based on diffraction amplitudes alone. Phys Rev E Stat Nonlin Soft Matter Phys. 2009 Oct;80(4 Pt 2):047701. PubMed PMID: 19905490.
   b. Liu X, Su WP. Improved Monte Carlo sampling in a real space approach to the crystallographic phase problem. Phys Rev E Stat Nonlin Soft Matter Phys. 2002 Dec;66(6 Pt 2):066703. PubMed PMID: 12513440.
   c. Liu X, Su WP. A hybrid minimal principle for the crystallographic phase problem. Acta Crystallogr A. 2000 Nov;56(Pt 6):525-8. PubMed PMID: 11058837.

2. **Method and algorithm development for cryoEM. I** developed MPSA (Multi-Path Simulated Annealing) software for high resolution cryoEM 3D reconstructions. More than 60 cryoEM maps in EMDB have been solved using MPSA. The highest resolution is 3.5Å. The software is powered by an innovative global optimization algorithm, multi-path simulated annealing. This was the first optimization algorithm used in cryoEM field to globally align the center and orientation simultaneously. Proposed a consistency criterion to check if a cryoEM particle image is good or bad. Pointed out how low resolution information plays a critical role in determining the alignment parameters of a cryoEM particle image. Proposed the best-particle-image concept: for a high-resolution reconstruction, a few high-quality single particle images are just as informative as a vast number of regular quality particle images.
   a. Wang Z, Hryc CF, Bammes B, Afonine PV, Jakana J, Chen DH, Liu X, Baker ML, Kao C, Ludtke SJ, Schmid MF, Adams PD, Chiu W. An atomic model of brome mosaic virus using direct electron detection and real-space optimization. Nat Commun. 2014 Sep 4;5:4808. PubMed PMID: 25185801; PubMed Central PMCID: PMC4155512.
   b. Kostyuchenko VA, Jakana J, Liu X, Haddow AD, Aung M, Weaver SC, Chiu W, Lok SM. The structure of barmah forest virus as revealed by cryo-electron microscopy at a 6-angstrom resolution has detailed transmembrane protein architecture and interactions. J Virol. 2011 Sep;85(18):9327-33. PubMed PMID: 21752915; PubMed Central PMCID: PMC3165765.
   c. Zhang R, Hryc CF, Cong Y, Liu X, Jakana J, Gorchakov R, Baker ML, Weaver SC, Chiu W. 4.4 Å cryo-EM structure of an enveloped alphavirus Venezuelan equine encephalitis virus. EMBO J. 2011 Aug 9;30(18):3854-63. PubMed PMID: 21829169; PubMed Central PMCID: PMC3173789.

d. Liu X, Jiang W, Jakana J, Chiu W. Averaging tens to hundreds of icosahedral particle images to resolve protein secondary structure elements using a Multi-Path Simulated Annealing optimization algorithm. J Struct Biol. 2007 Oct;160(1):11-27. PubMed PMID: 17698370; PubMed Central PMCID: PMC2039893.

3. **2/3 Nyquist frequency resolution from CCD images.** The maximum attainable resolution from CCD images was long thought to be 2/5 Nyquist frequency. With the power of MPSA, I was the first to obtain cryoEM structures that reached 2/3 Nyquist frequency resolution using CCD images.
   a. Zhang J, Nakamura N, Shimizu Y, Liang N, Liu X, Jakana J, Marsh MP, Booth CR, Shinkawa T, Nakata M, Chiu W. JADAS: a customizable automated data acquisition system and its application to ice-embedded single particles. J Struct Biol. 2009 Jan;165(1):1-9. PubMed PMID: 18926912; PubMed Central PMCID: PMC2634810.
   b. Chen DH, Jakana J, Liu X, Schmid MF, Chiu W. Achievable resolution from images of biological specimens acquired from a 4k x 4k CCD camera in a 300-kV electron cryomicroscope. J Struct Biol. 2008 Jul;163(1):45-52. PubMed PMID: 18514542; PubMed Central PMCID: PMC2504495.

4. **Practicality demonstration of phase plate cryoEM.** Phase plate imaging had been pursued by a handful of scientists, but most did not believe it would be useful in solving high resolution cryoEM structures. Using MPSA, I was the first to reconstruct a virus structure to subnanometer resolution using Zernike phase plate images. This demonstration aroused a broad interest in the cryoEM field, and phase plates are now commercialized by FEI; all kinds of phase plates are now under development.
   a. Dai W, Fu C, Raytcheva D, Flanagan J, Khant HA, Liu X, Rochat RH, Haase-Pettingell C, Piret J, Ludtke SJ, Nagayama K, Schmid MF, King JA, Chiu W. Visualizing virus assembly intermediates inside marine cyanobacteria. Nature. 2013 Oct 31;502(7473):707-10. PubMed PMID: 24107993; PubMed Central PMCID: PMC3984937.
   b. Murata K, Liu X, Danev R, Jakana J, Schmid MF, King J, Nagayama K, Chiu W. Zernike phase contrast cryo-electron microscopy and tomography for structure determination at nanometer and subnanometer resolutions. Structure. 2010 Aug 11;18(8):903-12. PubMed PMID: 20696391; PubMed Central PMCID: PMC2925294.

5. **Catching a glimpse of infection's opening act.** This is the Cell journal Editor's Leading Edge report on my high-resolution viral DNA ejection machine reconstruction. MPSA software was further developed for asymmetrically reconstructing virus structure in order to obtain the special infection apparatus. MPSA virus asymmetric reconstruction protocol is available online from 'Nature Protocol Exchange', and the whole MPSA is freely downloadable.
   a. Hong C, Oksanen HM, Liu X, Jakana J, Bamford DH, Chiu W. A structural model of the genome packaging process in a membrane-containing double stranded DNA virus. PLoS Biol. 2014 Dec;12(12):e1002024. PubMed PMID: 25514469; PubMed Central PMCID: PMC4267777.
   b. Rochat RH, Liu X, Murata K, Nagayama K, Rixon FJ, Chiu W. Seeing the portal in herpes simplex virus type 1 B capsids. J Virol. 2011 Feb;85(4):1871-4. PubMed PMID: 21106752; PubMed Central PMCID: PMC3028901.
   c. Liu X, Zhang Q, Murata K, Baker ML, Sullivan MB, Fu C, Dougherty MT, Schmid MF, Osburne MS, Chisholm SW, Chiu W. Structural changes in a marine podovirus associated with release of its genome into Prochlorococcus. Nat Struct Mol Biol. 2010 Jul;17(7):830-6. PubMed PMID: 20543830; PubMed Central PMCID: PMC2924429.

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http://www.ncbi.nlm.nih.gov/sites/myncbi/xiangan.liu.1/bibliography/47255671/public/?sort=date&direction=ascending

D. Research Support

Departmental Start-Up Grant, McGovern Medical School.
Research Start-Up Funds PI: Bo Hu 09/01/17-09/30/20
The purpose of these funds is to set up the PI's laboratory and fund preliminary studies needed for successful grant submissions for extramural research support.