BIOGRAPHICAL SKETCH

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NAME: Sui, Haixin

eRA COMMONS USER NAME (credential, e.g., agency login): WADS138

POSITION TITLE: Principal Investigator

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
Dalian University of Technology, Dalian, China	B.S.	07/1989	Materials Sci. & Eng.
Dalian Univ. Tech. & Beijing Lab. of Electron Microscopy, Chinese Academy of Sciences	M.S.	07/1992	Material Physics & Chemistry
Same as above	Ph.D.	05/1996	Same as above
Lawrence Berkeley National Lab., Berkeley, CA	Postdoctoral Fellow & Postdoctoral Scientist	03/2003	Cryo-EM & x-ray crystallography of Membrane Proteins & Cytoskeleton

A. Personal Statement

I have extensive experience in several aspects of structural biology. My relevant experience and unique expertise make me an ideal investigator to successfully carry out the structural studies of CabP filaments in this proposal. My post-graduate Master's and Doctoral works were in the areas of electron microscopy (EM) under Prof. K.H. Kuo who is internationally renowned in EM. This training provided me with a solid background in electron optics and high-resolution EM image processing. As a postdoctoral fellow in Bing K. Jap's group at Berkeley Lab, I purified and crystallized the aquaporin-1 water channel and determined its structure at 2.2Å resolution by x-ray crystallography. I also expressed, purified, and successfully obtained 2D crystals in the membrane for KcsA potassium channels before the work was predominated by Dr. Rod MacKinnon's great success in potassium channel structure determination. In Ken Downing's group at the Berkeley Lab, I successfully obtained a structural map of motile-cilium microtubule doublets using cryo-electron tomography and a self-developed algorithm of sub-tomogram averaging. After establishing my lab at Wadsworth Center, I developed a set of programs for image data processing and successfully corrected artifacts in cryo-tomograms obtained using Zernike phase-plate imaging. I also obtained structural maps at resolutions beyond 9Å for multiple types of microtubules, despite structural heterogeneity among these microtubules. This was achieved using self-developed sets of comprehensive image-processing programs that combined both single particle and helical reconstruction methods. This experience enhanced my capability in computational imaging processing. With these experiences in protein biochemistry, x-ray crystallography, a strong background in cryo-EM method development, application, and computational image processing. I am currently leading a research group utilizing structural imaging methods for a broad range of projects that are disease relevant.

Ongoing projects:

R01 GM143223
Sui (PI)
09/01/21-06/30/25
Intraflagellar transport process in primary cilium maintenance

1R56AI168356
McDonough (PI) & Sui (PI)
08/01/23-07/31/24
RNA regulation associated with mcr11-abmR locus in M. tuberculosis

Citations:

1. Sun, S.H., Fisher, R.L., Bowser, S.S, Pentecost, B.T., and **Sui, H.***, (2019) Three-dimensional architecture of epithelial primary cilia, Proc Natl Acad Sci U S A,116(19):9370-9379. PMID: 31004057
2. **Sui, H.***, and Downing, K.H. (2010). Structural basis of inter-protofilament interaction and lateral deformation of microtubules, Structure, 18, 1022-1031 [PMID: 20696402]
3. **Sui, H.** and Downing, K.H.* (2006) Molecular architecture of axonemal microtubule doublets revealed by cryo-electron tomography. Nature *442*, 475-478. PMID: 16738547
4. **Sui, H.**, Han, B.G., Lee, J.K., Walian, P., and Jap, B.K.* (2001). Structural basis of water-specific transport through the AQP1 water channel. Nature *414*, 872-878. PMID: 11780053

B. Positions, Scientific Appointments, and Honors

Positions and Scientific Appointments

2023 – present	NIH Peer Review Committee: Cell structure and function study section 1 - CSF1
2023 – present	Editorial Board Member, Journal of Biological Chemistry
2023 – present	Editorial Board Member, Biology
2022 – present	Proposal Review Board for the DOE Molecular Foundry Imaging Facility at Lawrence Berkeley National Laboratory
2022	NIH Peer Review Committee: Special Emphasis Panel, ZRG1 CDB-L (30)
2022	NIH Peer Review Committee: Special Emphasis Panel, ZGM1 TWD-8 (KR)
2020 – present	User proposal review committee, NIH National Center for Cryo-EM Access and Training at NYSBC
2020 – present	Proposal Review Board for the Imaging Facility of Biophysics Institute, Chinese Academy of Sciences
2019 – 2020	NIH Peer Review Committee: Study Section, ZRG1 IMST-B (12) B
2017	International Committee for Human Frontier Science Program: a*d hoc* reviewer
2017	Review panel member, Tan Kah Kee Scientific Award Foundation
2016	NIH Peer Review Committee: Biological Chemistry and Macromolecular Biophysics Special Emphasis Panel, ZRG1 BCMB-S (40)
2015 – present	Research Scientist V, Laboratory of Molecular and Cell basis of Diseases, Division of Translational Medicine, Wadsworth Center, NYS Department of Health, Albany, NY
2015 – 2019	Member, Review Committee for the Imaging Facility of Biophysics Institute, Chinese Academy of Sciences
2014 – 2017	Member, Proposal Review Board for the Molecular Foundry Imaging Facility at Lawrence Berkeley National Laboratory
2011	Stanford Synchrotron Beamline grant: User Proposal Review Panel
2008	Bank of America Virginia Research Fellowship, *ad hoc* reviewer
2008 – 2015	Research Scientist IV, Laboratory of Molecular and Cell basis of Diseases, Division of Translational Medicine, Wadsworth Center, NYS Department of Health, Albany, NY
2008 – present	Assistant Professor, Department of Biomedical Sciences, School of Public Health, University at Albany, State University of New York, Albany, NY
2008 – present	Member, American Society for Cell Biology
2003 – 2008	Biochemist Scientist (career), Mentor: Dr. Kenneth H. Downing, Life Sciences Division, Lawrence Berkeley National Laboratory, Berkeley, CA
2001 – 2003	Postdoctoral Scientist (term), Mentor: Dr. Kenneth H. Downing, Life Sciences Division, Lawrence Berkeley National Laboratory, Berkeley, CA
1998 – 2019	Member, Biophysics Society
1997 – 2001	Member, Microscopy Society of America

1996 – 2001 Postdoctoral Fellow/Scientist, Mentor: Dr. Bing K. Jap, Life Sciences Division, Lawrence Berkeley National Laboratory, Berkeley, CA

1994 - 1994 Visiting Scientist, Arrhenius Lab, Structural Chemistry Div., Stockholm University, Sweden

Honors

06/1995 Takashi Mukaibo Award (1st place), Dalian University of Technology, by Dr. Takashi Mukaibo, the former President of Tokyo University, Japan.

C. Contributions to Science (* indicates corresponding author)

1. *Structure and function of microtubules and axonemal complexes in cilia/flagella*: In a surprising and noteworthy discovery, my lab determined the 3D structure of full-length primary cilia and demonstrated that it differs significantly from the commonly accepted 9+0 model. This updated structural knowledge generated new and fundamental questions about the process and functional roles of intraflagellar transport (IFT) in primary cilium structure maintenance. We also found that the 3D molecular architectures of transition fibers at primary cilium base are not "alar sheet" as previously suggested. We discovered that motile cilium tips are subject to structural development and modification during growth. In addition, we obtained structural maps at resolutions beyond 9 Å for multiple types of microtubules, which have provided new structural understanding about microtubule bending and lateral deformation. This work has been included in the textbook *Cell and Molecular Biology: Concepts and Experiments* by Gerald Karp, Janet Iwasa, and Wallace Marshall (8th Edition, 2016). Using cryo-electron cryo-tomography and 3D image averaging, we determined the 3D molecular architecture of microtubule doublets from motile cilia, which not only revealed the structural features of the doublets that define their function in flagella axonemes, but also provided novel insights into locations and roles of particular proteins within the doublets. We also reported a new type of microtubule-associated proteins that bind to the intraluminal side of the microtubules (also see the comment by Linda Amos, *Structure*, 2010, 18:894-895).
   a. Sun, S.H., Fisher, R.L., Bowser, S.S, Pentecost, B.T., and **Sui, H.*** (2019) Three-dimensional architecture of epithelial primary cilia, Proc Natl Acad Sci U S A,116(19):9370-9379. PMID: 31004057
   b. Bowler M, Kong D, Sun S, Nanjundappa R, Evans L, Farmer V, Holland A, Mahjoub MR, **Sui H**, Loncarek J. (2019) High-resolution characterization of centriole distal appendage morphology and dynamics by correlative STORM and electron microscopy, Nat Commun. 10(1):993. PMID: 30824690
   c. Reynolds, M.J., Phetruen, T., Fisher, R.L., Chen, K., Pentecost, B.T., Gomez, G., Ounjai, P., and **Sui, H.***, (2018) Scientific Reports, 8(1):7977. PMID: 29789632
   d. **Sui, H.***, and Downing, K.H. (2010). Structural basis of inter-protofilament interaction and lateral deformation of microtubules, Structure, 18, 1022-1031 PMID: 20696402
   e. **Sui, H.**, and Downing, K.H.* (2006). Molecular architecture of axonemal microtubule doublets revealed by cryo-electron tomography. Nature *442*, 475-478. PMID: 16738547

2. *Structure and function of the kinetochore in mitosis*: By correlative LM/EM, super-resolution LM, and 3D LM image analysis, we demonstrated that there is a high degree of variability in kinetochore architecture during mitosis. This work overturned the traditional structural understanding about the functional mechanism of kinetochores, and challenged the widely accepted concept of intrakinetochore tension and its role in the control of mitotic progression. Owing to the importance of the result, the *Journal of Cell Biology* published an "In Focus" editorial on our work.
   a. Magidson, V., He J., Ault, J.G., O'Connell, C.B., Yang, N.C., McEwen, B.F., **Sui, H.***, and Khodjakov, A*. (2016) Radial expansion and compaction of the outer kinetochore during mitosis: Changes in the kinetochore shape during mitosis, Journal of Cell Biology 212(3):307-19. PMID: 26833787
   b. Sikirzhytski, V, Magidson, V, Steinman, J.B., He, J, Le Berre, M., Tikhonenko, I., Ault, J.G., McEwen, B.F., Chen, J.K., **Sui, H.**, Piel, M., Kapoor, T.M., Khodjakov, A.* (2014) Direct kinetochore-spindle pole connections are not required for chromosome segregation, The Journal of cell biology. 206(2):231-43. PMID: 25023516

3. *Cryo-EM method development for cellular structural imaging*: Driven by our project needs, we invested effort in developing and optimizing methods for studying vitreously frozen cells by cryo-electron tomography. We designed and re-engineered the Leica transferring block and successfully eliminated the lamella breakage problem. This enabled us to routinely obtain and study vitreously frozen cell specimens prepared using a cryo-focused ion beam (cryo-FIB) milling technique. In addition, we proved that the

fringes of Zernike phase-plate imaging can lead to incorrect representation of structures, and developed a set of programs for image de-fringing, which can remove the artifacts. Phase-plate imaging is a cutting-edge imaging method to obtain high-contrast micrographs in cryo-EM. This technique is particularly useful for cellular structural imaging by cryo-electron tomography.

a. He, J., Hsieh, C., Wu, Y., Schmelzer, T., Wang, P., Lin, Y., Marko, M., **Sui, H*.** (2017) Cryo-FIB specimen preparation for use in a cartridge-type cryo-TEM. Journal of Structural Biology. May 27. pii: S1047-8477(17)30091-6. doi: 10.1016/j.jsb.2017.05.011. PubMed PMID: 28559166
b. Kishchenko, G.P., Danev, R., Fisher, R., He, J., Hsieh, C., Marko, M., **Sui, H.*** (2015). Effect of fringe-artifact correction on sub-tomogram averaging from Zernike phase-plate cryo-TEM. Journal of Structural Biology, 191(3):299-305. PMID: 26210582

4. *Functional mechanisms of membrane channel proteins*: Using electron and x-ray crystallography, we studied membrane channel proteins, including water cancel aquaporin 1, and potassium channels KcsA and Kch. I determined the first high-resolution x-ray structure of water-specific channel Aquaporin 1, which contributed to the understanding of how membrane channel proteins facilitate the specific transport of water molecules or ions across cell membranes. This work was acknowledged in the Advanced Information of the 2003 Nobel Prize in Chemistry, which was shared by Dr. Peter Agre for the discovery of water channels and Dr. Roderick MacKinnon for structural and mechanistic studies of ion channels. This work has also been included in the popular college textbook “Molecular Cell Biology” (Lodish et al.) since 2003.
   a. **Sui, H.**, Han, B.G., Lee, J.K., Walian, P., and Jap, B.K.* (2001). Structural basis of water-specific transport through the AQP1 water channel. Nature *414*, 872-878. PMID: 11780053
   b. Li, H.L., **Sui, H.X.**, Ghanshani, S., Lee, S., Walian, P.J., Wu, C.L., Chandy, K.G., and Jap, B.K.* (1998). Two-dimensional crystallization and projection structure of KcsA potassium channel. Journal of Molecular Biology *282*, 211-216. PMID: 9735281

Complete List of Published Work in MyBibliography:
https://www.ncbi.nlm.nih.gov/sites/myncbi/haixin.sui.1/bibliography/43643469/public/?sort=date&direction=descending