BIOGRAPHICAL SKETCH

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NAME	POSITION TITLE
SUN, FEI	Professor of Structural Biology
eRA COMMONS USER NAME (credential, e.g., agency login)	

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)*	MM/YY	FIELD OF STUDY
Nanjing University, China	B.S.	07/01	Biophysics
Tsinghua University, China	Ph.D.	07/06	Structural Biology
Oxford University, UK	Visitor	05/06	Cryo-Electron Microscopy
National University of Singapore, Singapore	Visitor	03/07	Biological Electron Microscopy (EMBO Course)
The Scripps Research Institute, CA, USA	Visitor	08/08	Cryo-Electron Microscopy

A. Personal Statement

The research interests of my team (http://feilab.ibp.ac.cn) are mainly related with the structures and functions of biological macromolecules including membrane proteins and supra macromolecular assemblies. The aim of our group is to utilize and develop advanced biological imaging approaches, especially cryo-electron microscopy, to study the architecture of the biological system, in vitro and in vivo, from nano-scale to meso-scale. Currently we are focusing on molecular mechanism of bio-membrane dynamics, structure and function of supra macromolecular assembly and bio-imaging methodology development. In recent years, together with my colleagues and collaborators, I have got great achievements in both scientific researches and methodology developments. I authored 130 peer-review papers with xxx in my supervision.

Besides, I am also leading another team to manage a biological imaging center (Centre for Biological Imaging, CBI, see http://cbi.ibp.ac.cn), which provides biologists in the nation with our state-of-art imaging services from structure biology, cell biology to architecture biology. The overall goal of our center is to combine different imaging tools (majorly electron microscopy and fluorescence microscopy) to achieve 3D imaging of biological system from nao-scale to meso-scale in nanometer resolution. Besides facility operation and services offer, we are also performing various technology developments to expand the efficiency, capacity and resolution of our facility. Based on our technology support, our users got great scientific achievements (http://cbi.ibp.ac.cn/cbiweb/cgzs/) including cryoEM structure of 30-nm chromatin fiber and near-atomic structure of spinach photosystem II-LHCII supercomplex.

In the future, I will continue technology developments by focusing on high resolution cryo-electron tomography and realize the possibility of resolving high resolution structure of macromolecular assemblies in their intact states. Based on the latest technologies, I will continue to investigate important supra macromolecular assemblies in the cell.

B. Positions and Honors

Positions and Employment

Jul. 2006 – present **Professor, Principal Investigator**
Laboratory of Biological Electron Microscopy and Structural Biology (Fei Sun's lab), Institute of Biophysics, Chinese Academy of Sciences

Jul. 2006 – present **Director and Chief Scientist**
Center for Biological Imaging, Core Facilities for Protein Sciences, Institute of Biophysics, Chinese Academy of Sciences

Other Experience and Professional Memberships

2018 – present	Co-editor, CryoEM Section of IUCrJ
2018 – present	Executive member of the council of the Biophysical Society of China (BSC)
2018 – present	Vice president of Chinese CryoEM sub-society of BSC
2018 – present	Executive member of the council of Chinese Electron Microscopy Society
2018– present	Vice president of Beijing Electron Microscopy Society
2012 – present	Council member of Chinese Crystallographic Society
2014 – present	Associate Editor, Biophysics Reports

Honors

China National Funds for Distinguished Young Scientists, 2020
National Middle-&-Youth Talent of Science and Technology Innovation, 2019
Youth professor, Chang Jiang Scholars Program of China, 2018
Outstanding contribution of Chinese cryo-electron microscopy society, 2017
National Youth Top-notch Talent, 2012
Beishi Zhang Prize for Young Scientist in Biophysics, 2009
Top 100, Excellent Ph.D thesis of China, 2008

C. Contributions to Science

1. Cellular internal membrane system (mitochondrion, ER, Golgi complex, endosome) play the very important role in cellular physiological process, e.g. cargo traffic, energy transformation and signal transduction. The dynamics of these membrane, fusion/fission, remodeling and biogenesis, are highly relevant to regulation of cellular physiological process. We studied how protein factors (MiD51, OPA1, ACAP1, Ups1/Mdm35, Coatomer and PI4KIIa) interact with membrane and how they regulate the dynamics of membrane.

a. Lu J., Chan C., Yu L., Fan J.*, **Sun F.*** and Zhai Y.* (2020) Molecular mechanism of mitochondrial phosphatidate transfer by Ups1. ***Communications Biology***. doi: 10.1038/s42003-020-01121-x (in press)
b. Zhang D., Zhang Y., Ma J., Zhu C., Niu T., Chen W., Pang X., Zhai Y., and **Sun F.*** (2020) Cryo-EM structures of S-OPA1 reveal its interactions with membrane and changes upon nucleotide binding. ***eLife*** 9: e50294. doi: 10.7554/eLife.50294
c. Ma J., Zhai Y., Chen M., Zhang K., Chen Q., Pang X.*, and **Sun F.*** (2019), New interfaces on MiD51 for Drp1 recruitment and regulation. ***PLoS One 14***, e0211459.
d. Chan C. Pang X., Zhang Y., Niu T., Yang S., Zhao D., Li J., Lu L., Hsu, V.W., Zhou J.*, **Sun F.*** and Fan J.* (2019), ACAP1 assembles into an unusual protein lattice for membrane deformation through multiple stages. ***PLOS Computational Biology***,15 (7): e1007081. doi: 10.1371/journal.pcbi.1007081.
e. Wang S., Zhai Y., Pang X., Niu T., Ding Y.H., Dong, M.Q., Hsu W.V. Sun Z.* and **Sun F.*** (2016), Structural characterization of coatomer in its cytosolic state. ***Protein Cell*** 7(8): 586-600.
f. Pang, X., Fan, J., Zhang, Y., Zhang, K., Gao, B., Ma, J., Li, J., Deng, Y., Zhou, Q., Egelman, E.H., Hsu, V.W.* and **Sun, F.*** (2014), A PH Domain in ACAP1 Possesses Key Features of the BAR Domain in Promoting Membrane Curvature. ***Developmental Cell***, 31(1): 3-4.
g. Zhou, Q., Li, J., Yu, H., Zhai, Y., Gao Z., Liu, Y., Pang, X., Zhang, L., Schulten K., **Sun, F.*** and Chen, C.* (2014), Molecular insights into the membrane-associated phosphatidylinositol 4-kinase IIα. ***Nature Communications***, 5:3552. doi:10.1038/ncomms4552.

2. Most supra macromolecular complexes have large molecular weight, comprises multi-subunits and are highly structural dynamic, which have become a huge barrier to cope with to study their structures and functions. In

recent years, with the advantages of direct electron detectors and sophisticated image processing algorithm, cryo-electron microscopy (cryo-EM) has gone into its evolution phase and become the most important and unique approach to study the 3D structures of supra macromolecular complex. We utilized our expertise in high-resolution electron cryo-microscopy to study structures of various supra macromolecular complexes, especially membrane complexes, respiratory complex, light harvesting complex and calcium channel.

a. Shi Y.#, Xin Y.#, Wang C.#, Blankenship R.E., **Sun F.*** and Xu XL.* (2020) Cryo-EM structure of the air-oxidized and dithionite-reduced photosynthetic alternative complex III from *Roseiflexus castenholzii*. ***Science Advances***, 6 (31): eaba2739. doi: 10.1126/sciadv.aba2739.
b. Qiao A., Han S., Li X., Li Z., Zhao P., Dai A., Chang R., Tai L., Tan Q., Chu X., Ma L., Thorsen T.S., Reedtz-Runge S., Yang D., Wang M., Sexton P.M., Wootten D., **Sun F.***, Zhao Q.*, and Wu B.* (2020) Structural basis of Gs and Gi recognition by the human glucagon receptor. ***Science***, 367: 1346-1352. doi: 10.1126/science.aaz5346.
c. Zhu G., Zeng H., Zhang S., Juli J., Pang X., Hoffmann J., Zhang Y., Morgner N., Zhu Y.*, Peng G.*, Michel H.* and **Sun F.*** (2020) A 3.3 A-resolution structure of hyperthermophilic respiratory complex III reveals the mechanism of its thermal stability. ***Angew Chem Int Ed Engl.*** 59 (1): 343-351. doi: 10.1002/anie.201911554.
d. Ren Z., Zhang Y., Zhang Y., He Y., Du P., Wang Z., **Sun F.*** and Ren H.* (2019) Cryo-EM structure of actin filaments from Zea mays pollen. ***Plant Cell***. pii: tpc.00973.2018. doi: 10.1105/tpc.18.00973.
e. Gong H., LI L., Xu A., Tang Y., Ji W., Gao R., Wang S., Yu L., Tian C., Li J., Yen H.Y., Lam S.M., Shui G., Yang X., Sun Y., Li X., Jia M., Yang C., Jiang B., Lou Z., Robinson C., Wong L.L., Guddat L.W., **Sun F.***, Wang Q.* and Rao Z.* (2018), A electron transfer path connects subunits of a mycobacterial respiratory supercomplex. ***Science*** 362 (6418), eaat8923.
f. Xin Y., Shi Y., Niu T., Wang Q., Niu W., Huang X., Ding W., Yang L., Blankenship R. E., Xu X.* and **Sun F.*** (2018) Cryo-EM structure of the RC-LH core complex from an early branching photosynthetic prokaryote. ***Nature communications,*** **9**: 1568.
g. Wei R., Wang X., Zhang Y., Mukherjee S., Zhang L., Chen Q., Huang X., Jing S., Liu C., Li S., Wang G., Xu Y., Zhu S., Williams A., **Sun F.*** and Yin C.C.* (2016), Structural insights into Ca2+ -activated long-range allosteric channel gating of RyR1. ***Cell Research*** 26: 977-994 (Cover story).

3. In the past ten years, cryoEM has been developed very fast not only on the hardware but also on the image processing software as well as sample preparation methods. According to different sample characteristics, cryoEM contains three different technologies, which are single particle analysis, electron tomography and electron crystallography. Cryo-electron tomography (cryo-ET) will be the next phase of technology to study macromolecular structures *in situ*. To achieve high resolution cryo-ET, lots of technology developments from sample preparation, imaging technology to image processing are demanded. We developed D-cryoFIB and VHUT-cryoFIB techniques to enable preparation of cryo-lamella of both cellular and tissue sample. We developed a novel cryo-correlative fluorescence and electron microscopy system called HOPE to enable cryo-ET of target region. We developed a software package AuTom (including many new algorithms, MarkerAuto, FIRT and ICON) to enable high throughput processing of cryo-ET dataset with high resolution and quality.

a. Huang X.#, Zhang L.#, Wen Z., Chen H., Li S., Ji G., Yin C.C. and **Sun F.*** (2020) Amorphous nickel titanium alloy film: a new choice for cryo electron microscopy sample preparation. ***Progress in Biophysics and Molecular Biology***. doi: 10.1016/j.pbiomolbio.2020.07.009 [Epub ahead of print]
b. Li S., Ji G.*, Shi Y., Klausen L.H., Niu T., Wang S., Huang X., Ding W., Zhang X., Dong M., Xu W., and **Sun F.*** (2018), High-vacuum optical platform for cryo-CLEM(HOPE): a new solution for non-integrated multiscale correlative light and electron microscopy. ***Journal of Structural Biology*** 201(1): 63-75.
c. Han R., Wan X., Wang Z., Hao Y., Zhang J., Chen Y., Gao X., Liu Z., Ren F., **Sun F.*,** and Zhang F.* (2017), AuTom: a novel automatic platform for electron tomography reconstruction. ***Journal of Structural Biology*** 199(3): 196-208. doi: 10.1016/j.jsb.2017.07.008.
d. Zhang J., Ji G., Huang X., Xu W.*, and **Sun F.***, (2016) An improved cryo-FIB method for fabrication of frozen hydrated lamella. ***Journal of Structural Biology*** 194(2): 218-223.

e. Deng Y., Chen Y., Zhang Y., Wang S., Zhang F.* and **Sun F.*** (2016), ICON: 3D reconstruction with 'missing-information' restoration in biological electron tomography. ***Journal of Structural Biology*** 195(1): 100-112.
f. Chen Y., Zhang Y., Zhang K.*, Deng Y., Zhang F.* and **Sun F.*** (2016), FIRT: filtered iterative reconstruction technique with information restoration. ***Journal of Structural Biology*** 195(1): 49-61.
g. Han R., Wang L., Liu Z., **Sun F.*** and Zhang F.* (2015), A novel fully automatic scheme for fiducial marker-based alignment in electron tomography. ***Journal of Structural Biology*** 192: 403-17.

4. Orientating the future of biological electron microscopy, we also developed various new techniques including cryoFIB-MicroED and AutoCUTS-SEM. CryoFIB-MicroED expands the capability of MicroED and enables us to utilize MicroED to study large protein crystals. AutoCUTS-SEM is an important technique of volume electron microcopy and has wide application in developmental and neuron biology.

a. Li X., Zhang S., Zhang J. and **Sun F.*** (2018), In situ protein micro-crystal fabrication by cryo-FIB for electron diffraction. ***Biophysics Reports*** 4(6): 339-347. doi: 10.1007/s41048-018-0075-x.
b. Li X., Ji G.*, Chen X., Ding W., Sun L., Xu W., Han H., and **Sun F.*** (2017), Large scale three-dimensional reconstruction of an entire Caenorhabditis elegans larva using AutoCUTS-SEM. ***Journal of Structural Biology***, 200(2): 87-96.

Complete List of Published Work in MyBibliography:

https://www.ncbi.nlm.nih.gov/myncbi/1HSFexzW8i5Q_/bibliography/public/

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

Ongoing Research Support

CAS XDB37040102 Sun(PI) 01/01/2020 – 12/31/2024
High resolution cryo-electron tomography for in situ structural analysis
Role: PI

CAS ZDKYYQ20170002 Sun(PI) 10/01/2017 – 09/30/2020
Developing ultrafast biological electron cryo-microscope
Role: PI

NSFC 31830020 Sun (PI) 01/01/2019-12/31/2023
In situ structural biology by electron cryo-microscope
Role: PI