

**BIOGRAPHICAL SKETCH**

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| NAME<br>SUN, FEI  |                           | POSITION TITLE<br>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<br>(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<br>Microscopy                        |
| National University of Singapore, Singapore   | Visitor                   | 03/07   | Biological Electron<br>Microscopy (EMBO<br>Course) |
| The Scripps Research Institute, CA, USA   | Visitor                   | 08/08   | Cryo-Electron<br>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 combine various structural research approaches including crystallography and cryo-electron microscopy (cryoEM) as well as developing new methodologies to determine 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 methodology development orientating to biological imaging.

In addition, 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 nano-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 imaging approaches.

In recent years, together with my teams and collaborators, I have got great achievements in both scientific researches and methodology developments. I authored 44 peer-review papers with 35 in my supervision. The representatives of those work include high resolution cryoEM structure of rabbit hemorrhagic disease virus, structural studies of protein assemblies, molecular mechanism of membrane remodeling by BAR-PH containing protein, crystal structure of membrane-associated phosphatidylinositol 4-kinase and molecular mechanism of its activity regulation, high resolution cryoEM structure of calcium activated RyR1, molecular mechanism of the promiscuity of an aromatic prenyltransferase, and technology developments orientating to high resolution cryoEM from sample preparation (D-cryoFIB, in situ cryoFIB-MicroED), imaging technology to image processing algorithm (MarkerAuto, LO-refinement, FIRT and ICON).

The construction and operation of our CBI was also proved quite successful in the past four years and there were dozens of good papers published each year based on our professional technical services (<http://cbi.ibp.ac.cn/cbiweb/cgzs/>). The representative works of our users include the cryoEM structure of 30-nm chromatin fiber and near-atomic structure of spinach photosystem II-LHCII supercomplex. More importantly, we have successfully built up complete 3D electron microscopy techniques from molecular scale to tissue scale, which endows our CBI an international leading role in biological electron microscopy.

In the future, I will lead my teams to 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, opening a new window of structure biology that is called in situ structure biology. Using the latest technologies, I will continue to investigate the membrane dynamics and its regulation in the cell as well as various 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

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

### Selected Invited presentations

April 2016  
2<sup>nd</sup> Cryo-EM 3D Image Analysis Symposium, Lake Tahoe, California  
Title: *Electron Tomography Reconstruction with restoration of missing information*

September 2016  
Advanced Bio-Electron Microscopy Symposium at Korea Basic Science Institute (KBSI)  
Title: *3DEM Technique from nano-scale to meso-scale*

June 2017  
Gordon Research Conference of Three Dimensional Electron Microscopy  
Title: *eHEC, an Algorithm to Process the Raw Frames from Falcon III Camera for Landau Noise Reduction*

## C. Representative Peer-reviewed Publications (\*co-corresponds author, #first author)

### (Methodology development)

1. 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.
2. **Sun F.\*** (2018) Orienting the future of bio-macromolecular electron microscopy. *Chinese Physics B*, 27 (6): 060503. doi: 10.1088/1674-1056/27/6/06360.
3. 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.
4. 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.
5. 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.
6. 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.
7. 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.
8. 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.
9. Sun F. (Sun Fang), Pang X., Xie T., Zhai Y., Wang G.G.\* and **Sun F.\*** (2015), BrkAutoDisplay: functional display of multiple exogenous proteins on the surface of *Escherichia coli* by using BrkA autotransporter. *Microbial Cell Factories*. 14: 129.

#### (Biological question study)

10. 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.
11. 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.
12. Lu G., Xu Y., Zhang K., Xiong Y., Li H., Cui L., Wang X., Lou J., Zhai Y.\*, **Sun F.\*** and Zhang X.C.\* (2017), Crystal structure of *E. coli* apolipoprotein N-acyltransferase. *Nature Communications*, 8:15948.
13. Chen R., Gao B., Liu, X., Ruan F., Zhang Y., Lou J., Feng K., Wunsch C., Li S.M., Dai J.\* and **Sun F.\*** (2017), Molecular insights into the enzyme promiscuity of an aromatic prenyltransferase. *Nature Chemical Biology* 13(2): 226-234.
14. 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 Ca<sup>2+</sup>-activated long-range allosteric channel gating of RyR1. *Cell Research* 26: 977-994 (Cover story).
15. 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.
16. 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 IIa. *Nature Communications*, 5:3552. doi:10.1038/ncomms4552.
17. Wang X., Xu F., Liu J., Gao B., Liu Y., Zhai Y., Ma J., Zhang K., Baker T.S., Schulten K., Zheng D.\*, Pang H.\* and **Sun F.\*** (2013), Atomic model of rabbit hemorrhagic disease virus by cryo-electron microscopy and crystallography. *PLoS Pathogens*, 9(1): e1003132.
18. Zhai Y., Zhang K., Huo Y., Zhu Y., Zhou Q., Lu J., Black I., Pang X., Roszk A.W., Zhang X., Isaacs N.W., **Sun F.\*** (2011), Autotransporter passenger domain secretion requires a hydrophobic cavity at the extracellular entrance of the beta-domain pore. *Biochem. J.*, 435:577-587.

19. Hu YW, Hu ZJ, Zhang K, Wang L, Zhai Y, Zhou QJ, Lander G, Zhu J, He YZ, Pang XY, Xu W, Bartlam M, Dong ZY, **Sun F.\***. (2010). Crystal structure of group II chaperonin in the open state. **Structure**, 18(10): 1270-1279. (Cover story)
20. Hu Z., Tian X., Zhai Y., Xu W., Zheng D., **Sun F.\*** (2010), Cryo-Electron Microscopy Reconstructions of Two Types of Wild Rabbit Hemorrhagic Disease Viruses Characterized the Structural Features of Lagovirus. **Protein & Cell**, 1(1):48-58. (Cover story)
21. **Sun F#**, Huo X, Zhai Y, Wang A, Xu J, Su D, Bartlam M& Rao Z. (2005). Crystal structure of mitochondrial respiratory membrane protein complex II. **Cell**, 121: 1043-1057.

### **All publications (2013-2017)**

1. Lu, J., Zhai, Y., and Sun, F. (2013) Research of Mitochondrial Calcium Transportation. *ACTA BIOPHYSICA SINICA* **29**, 167-180
2. Quinlan, R. A., Zhang, Y., Lansbury, A., Williamson, I., Pohl, E., and Sun, F. (2013) Changes in the quaternary structure and function of MjHSP16.5 attributable to deletion of the IXI motif and introduction of the substitution, R107G, in the alpha-crystallin domain. *Philosophical transactions of the Royal Society of London. Series B, Biological sciences* **368**, 20120327
3. Sun, F., Zhou, Q., Pang, X., Xu, Y., and Rao, Z. (2013) Revealing various coupling of electron transfer and proton pumping in mitochondrial respiratory chain. *Current opinion in structural biology* **23**, 526-538
4. Wang, G., Zhang, F., Fan, L., Sun, F., and Liu, Z. (2013) Contrast Transfer Function Correction Model Based on Sine and Gaussian Modulation and Spline Interpolation. *Journal of Computer Research and Development* **50**, 808-814
5. Wang, G., Zhang, F., Fan, L., Sun, F., and Liu, Z. (2013) A fast calculation strategy of density function in ISAF reconstruction algorithm. *Scientia Sinica Informationis* **43**, 584-598
6. Wang, L., Li, Q., Wu, L., Liu, S., Zhang, Y., Yang, X., Zhu, P., Zhang, H., Zhang, K., Lou, J., Liu, P., Tong, L., Sun, F., and Fan, Z. (2013) Identification of SERPINB1 as a physiological inhibitor of human granzyme H. *J Immunol* **190**, 1319-1330
7. Wang, X., Xu, F., Liu, J., Gao, B., Liu, Y., Zhai, Y., Ma, J., Zhang, K., Baker, T. S., Schulten, K., Zheng, D., Pang, H., and Sun, F. (2013) Atomic model of rabbit hemorrhagic disease virus by cryo-electron microscopy and crystallography. *PLoS Pathog* **9**, e1003132
8. Wu, L., Zhai, Y., Lu, J., Wang, Q., and Sun, F. (2013) Expression, purification and preliminary characterization of glucagon receptor extracellular domain. *Protein expression and purification* **89**, 232-240
9. Xu, Y., and Sun, F. (2013) Purification, crystallization and preliminary crystallographic analysis of 3-hydroxyacyl-CoA dehydrogenase from *Caenorhabditis elegans*. *Acta Crystallogr Sect F Struct Biol Cryst Commun* **69**, 515-519
10. Yang, S., Liu, X., Li, X., Sun, S., Sun, F., Fan, B., and Zhao, S. (2013) MicroRNA-124 reduces caveolar density by targeting caveolin-1 in porcine kidney epithelial PK15 cells. *Molecular and cellular biochemistry* **384**, 213-219
11. Zhang, K., Wang, L., Liu, Y., Chan, K. Y., Pang, X., Schulten, K., Dong, Z., and Sun, F. (2013) Flexible interwoven termini determine the thermal stability of thermosomes. *Protein Cell* **4**, 432-444
12. Zhang, S., Andreasen, M., Nielsen, J. T., Liu, L., Nielsen, E. H., Song, J., Ji, G., Sun, F., Skrydstrup, T., Besenbacher, F., Nielsen, N. C., Otzen, D. E., and Dong, M. (2013) Coexistence of ribbon and helical fibrils originating from hIAPP20-29 revealed by quantitative nanomechanical atomic force microscopy. *Proc Natl Acad Sci U S A* **110**, 2798-2803
13. Zhang, Y., and Sun, F. (2013) Electron Microscopy Reconstruction of Helical Assemblies. *Acta Biophys Sin* **29**, 879-898

14. Zhang, Y., Wang, W., Chen, J., Zhang, K., Gao, F., Gao, B., Zhang, S., Dong, M., Besenbacher, F., Gong, W., Zhang, M., Sun, F., and Feng, W. (2013) Structural insights into the intrinsic self-assembly of Par-3 N-terminal domain. *Structure* **21**, 997-1006
15. Cheng, L., Huang, X., Li, X., Xiong, W., Sun, W., Yang, C., Zhang, K., Wang, Y., Liu, H., Huang, X., Ji, G., Sun, F., Zheng, C., and Zhu, P. (2014) Cryo-EM structures of two bovine adenovirus type 3 intermediates. *Virology* **450-451**, 174-181
16. Han, R., Zhang, F., Wan, X., Fernandez, J. J., Sun, F., and Liu, Z. (2014) A marker-free automatic alignment method based on scale-invariant features. *J Struct Biol*
17. Ma, J., and Sun, F. (2014) Expression, purification, crystallization and preliminary crystallographic study of the cytoplasmic domain of the mitochondrial dynamics protein MiD51. *Acta crystallographica. Section F, Structural biology communications* **70**, 596-599
18. 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**, 73-86
19. Qiu, B., Zhang, K., Wang, S., and Sun, F. (2014) C-terminal motif within Sec7 domain regulates guanine nucleotide exchange activity via tuning protein conformation. *Biochem Biophys Res Commun*
20. Sun, F., Li, J., and Chen, C. (2014) Puzzle out the regulation mechanism of PI4KIIalpha activity. *Science China. Life sciences*
21. Xu, Y., Li, H., Jin, Y. H., Fan, J., and Sun, F. (2014) Dimerization Interface of 3-Hydroxyacyl-CoA Dehydrogenase Tunes the Formation of Its Catalytic Intermediate. *PLoS One* **9**, e95965
22. 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 IIalpha. *Nature communications* **5**, 3552
23. Cui, Y., Zhao, S., Wang, J., Wang, X., Gao, B., Fan, Q., Sun, F., and Zhou, B. (2015) A novel mitochondrial carrier protein Mme1 acts as a yeast mitochondrial magnesium exporter. *Biochim Biophys Acta* **1854**, 724-732
24. Gao, B., Chen, R., Liu, X., Dai, J., and Sun, F. (2015) Expression, purification, crystallization and crystallographic study of the *Aspergillus terreus* aromatic prenyltransferase AtaPT. *Acta crystallographica. Section F, Structural biology communications* **71**, 889-894
25. 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. *J Struct Biol* **192**, 403-417
26. Liu, B., Xue, Y., Zhao, W., Chen, Y., Fan, C., Gu, L., Zhang, Y., Zhang, X., Sun, L., Huang, X., Ding, W., Sun, F., Ji, W., and Xu, T. (2015) Three-dimensional super-resolution protein localization correlated with vitrified cellular context. *Sci Rep* **5**, 13017
27. Ma, D. K., Li, Z., Lu, A. Y., Sun, F., Chen, S., Rothe, M., Menzel, R., Sun, F., and Horvitz, H. R. (2015) Acyl-CoA Dehydrogenase Drives Heat Adaptation by Sequestering Fatty Acids. *Cell* **161**, 1152-1163
28. Sun, F., Pang, X., Xie, T., Zhai, Y., Wang, G., and Sun, F. (2015) BrkAutoDisplay: functional display of multiple exogenous proteins on the surface of *Escherichia coli* by using BrkA autotransporter. *Microb Cell Fact* **14**, 129
29. Chen, Y., Zhang, Y., Zhang, K., Deng, Y., Wang, S., Zhang, F., and Sun, F. (2016) FIRT: filtered iterative reconstruction technique with information restoration. *J Struct Biol*
30. 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. *J Struct Biol*
31. Li, W., Ding, W., Ji, G., Wang, L., Zhang, J., and Sun, F. (2016) Three-dimensional visualization of arsenic stimulated mouse liver sinusoidal by FIB-SEM approach. *Protein Cell* **7**, 227-232

32. Mao, G., Zhao, Y., Kang, X., Li, Z., Zhang, Y., Wang, X., Sun, F., Sankaran, K., and Zhang, X. C. (2016) Crystal structure of *E. coli* lipoprotein diacylglyceryl transferase. *Nature communications* **7**, 10198
33. Shan, H., Wang, Z., Zhang, F., Xiong, Y., Yin, C. C., and Sun, F. (2016) A local-optimization refinement algorithm in single particle analysis for macromolecular complex with multiple rigid modules. *Protein Cell* **7**, 46-62
34. Wang, S., Zhai, Y., Pang, X., Niu, T., Ding, Y. H., Dong, M. Q., Hsu, V. W., Sun, Z., and Sun, F. (2016) Structural characterization of coatomer in its cytosolic state. *Protein Cell* **7**, 586-600
35. 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. J., Sun, F., and Yin, C. C. (2016) Structural insights into Ca<sup>2+</sup>-activated long-range allosteric channel gating of RyR1. *Cell Res* **26**, 977-994
36. Zhang, J., Ji, G., Huang, X., Xu, W., and Sun, F. (2016) An improved cryo-FIB method for fabrication of frozen hydrated lamella. *J Struct Biol* **194**, 218-223
37. Shi Y., Wang L., Zhang J., Zhai Y., and Sun, F. (2017), Determining the target protein localization in 3D using the combination of FIB-SEM and APEX2. *Biophysics Reports*, 3: 92-99. doi: 10.1007/s41048-017-0043-x
38. 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. doi: 10.1016/j.jsb.2017.09.010.
39. Han R., Wan X., Wang Z., Hao Y., Zhang J., Chen Y., Gao X., Liu Z., Ren F., Su, F., and Zhang F. (2017), AuTom: a novel automatic platform for electron tomography reconstruction. *Journal of Structural Biology*, 199(3): 196-208.
40. Wang S., Li S., Ji G., Huang X. and Sun F. (2017), Using integrated correlative cryo-light and electron microscopy to directly observe syntaphilin-immobilized neuronal mitochondria *in situ*. *Biophysics Reports*, 3: 8-16. doi: 10.1007/s41048-017-0035-x
41. Chen Y., Wang Z., Zhang J., Li L., Wan X., Sun F., and Zhang F. (2017), Accelerating electron tomography reconstruction algorithm ICON with GPU. *Biophysics Reports*, 3: 36-42. doi: 10.1007/s41048-017-0041-z
42. Lu G., Xu Y., Zhang K., Xiong Y., Li H., Cui L., Wang X., Lou J., Zhai Y., Sun F. and Zhang X.C. (2017), Crystal structure of *E. coli* apolipoprotein N-acyltransferase. *Nature Communications*, 8:15948. doi: 10.1038/ncomms15948.
43. Zhou Y., Lou H., Liu Z., Yang M., Pang X., Sun F. and Wang G.\* (2017), Structural insight into the specific DNA template binding to DnaG primase in Bacteria. *Scientific Report*, 7(1): 659. doi: 10.1038/s41598-017-00767-8.
44. Chan K.C., Lu L., Sun F., Fan J. (2017), Molecular details of the PH domain of ACAP1 protein binding to PIP-containing membrane. *J Phys Chem B*, 121(15): 3586-3596.
45. Chen R., Gao B., Liu, X., Ruan F., Zhang Y., Lou J., Feng K., Wunsch C., Li S.M., Dai J. and Sun F. (2017), Molecular insights into the enzyme promiscuity of an aromatic prenyltransferase. *Nature Chemical Biology*, 13(2): 226-234.
46. 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.

#### **All publications (before 2013)**

1. Li, T., Ji, X., Sun, F., Gao, R., Cao, S., Feng, Y., and Rao, Z. (2002) Crystallization and preliminary X-ray analysis of recombinant histone HPhA from the hyperthermophilic archaeon *Pyrococcus horikoshii* OT3. *Acta Crystallogr D Biol Crystallogr* **58**, 870-871

2. Lin, W., Sun, F., and Rao, Z. (2002) Tri-residue contact potential: a new knowledge-based energetic method. *Progress in Natural Science* **12**, 826-840
3. Ding, Y., Li, S., Li, X., Sun, F., Liu, J., Zhao, N., and Rao, Z. (2003) Site-directed mutagenesis and preliminary x-ray crystallographic studies of the tabtoxin resistance protein. *Protein Pept Lett* **10**, 255-263
4. He, H., Ding, Y., Bartlam, M., Sun, F., Le, Y., Qin, X., Tang, H., Zhang, R., Joachimiak, A., Liu, J., Zhao, N., and Rao, Z. (2003) Crystal structure of tabtoxin resistance protein complexed with acetyl coenzyme A reveals the mechanism for beta-lactam acetylation. *J Mol Biol* **325**, 1019-1030
5. Li, T., Sun, F., Ji, X., Feng, Y., and Rao, Z. (2003) Structure based hyperthermostability of archaeal histone HPhA from *Pyrococcus horikoshii*. *J Mol Biol* **325**, 1031-1037
6. Lin, W., Sun, F., and Rao, Z. (2003) A statistical analysis of protein-protein interaction with knowledge-based potential at residue level. *Tsinghua Science and Technology* **8**, 402-406
7. Sun, F., Li, P., Ding, Y., Wang, L., Bartlam, M., Shu, C., Shen, B., Jiang, H., Li, S., and Rao, Z. (2003) Design and structure-based study of new potential FKBP12 inhibitors. *Biophys J* **85**, 3194-3201
8. Shi, N., Liu, Y., Ni, M., Yang, M., Wu, J., Peng, Y., Gao, F., Sun, F., Peng, X., Qiang, B., Rao, Z., and Yuan, J. (2004) Expression, crystallization and preliminary X-ray studies of the recombinant PTB domain of mouse dok1 protein. *Acta Crystallogr D Biol Crystallogr* **60**, 334-336
9. Shi, N., Ye, S., Bartlam, M., Yang, M., Wu, J., Liu, Y., Sun, F., Han, X., Peng, X., Qiang, B., Yuan, J., and Rao, Z. (2004) Structural basis for the specific recognition of RET by the Dok1 phosphotyrosine binding domain. *J Biol Chem* **279**, 4962-4969
10. Sun, F., Huo, X., Zhai, Y., Wang, A., Xu, J., Su, D., Bartlam, M., and Rao, Z. (2005) Crystal structure of mitochondrial respiratory membrane protein complex II. *Cell* **121**, 1043-1057
11. Zhai, Y., Sun, F., Li, X., Pang, H., Xu, X., Bartlam, M., and Rao, Z. (2005) Insights into SARS-CoV transcription and replication from the structure of the nsp7-nsp8 hexadecamer. *Nat Struct Mol Biol* **12**, 980-986
12. Li, X., Liu, X., Sun, F., Gao, J., Zhou, H., Gao, G. F., Bartlam, M., and Rao, Z. (2006) Crystal structure of the N-terminal SH3 domain of mouse betaPIX, p21-activated kinase-interacting exchange factor. *Biochem Biophys Res Commun* **339**, 407-414
13. Su, D., Lou, Z., Sun, F., Zhai, Y., Yang, H., Zhang, R., Joachimiak, A., Zhang, X. C., Bartlam, M., and Rao, Z. (2006) Dodecamer structure of severe acute respiratory syndrome coronavirus nonstructural protein nsp10. *J Virol* **80**, 7902-7908
14. Xu, X., Zhai, Y., Sun, F., Lou, Z., Su, D., Xu, Y., Zhang, R., Joachimiak, A., Zhang, X. C., Bartlam, M., and Rao, Z. (2006) New antiviral target revealed by the hexameric structure of mouse hepatitis virus nonstructural protein nsp15. *J Virol* **80**, 7909-7917
15. Huo, X., Su, D., Wang, A., Zhai, Y., Xu, J., Li, X., Bartlam, M., Sun, F., and Rao, Z. (2007) Preliminary molecular characterization and crystallization of mitochondrial respiratory complex II from porcine heart. *Febs J* **274**, 1524-1529
16. Zheng, W., Sun, F., Bartlam, M., Li, X., Li, R., and Rao, Z. (2007) The crystal structure of human isopentenyl diphosphate isomerase at 1.7 Å resolution reveals its catalytic mechanism in isoprenoid biosynthesis. *J Mol Biol* **366**, 1447-1458
17. Chen, J., Li, W., Wang, M., Zhu, G., Liu, D., Sun, F., Hao, N., Li, X., Rao, Z., and Zhang, X. C. (2008) Crystal structure and mutagenic analysis of GDOsp, a gentisate 1,2-dioxygenase from *Silicibacter pomeroyi*. *Protein Sci* **17**, 1362-1373
18. Sun, F., Zhou, Q., Sun, J., Zhai, Y., and Rao, Z. (2008) Structure of mitochondrial respiratory membrane protein complexes. *Chinese Bulletin of Life Sciences* **20**, 566-578

19. Wang, L., Vavassori, S., Li, S., Ke, H., Anelli, T., Degano, M., Ronzoni, R., Sitia, R., Sun, F., and Wang, C. C. (2008) Crystal structure of human ERp44 shows a dynamic functional modulation by its carboxy-terminal tail. *EMBO Rep* **9**, 642-647
20. Sun, S., Zhang, K., Xu, W., Wang, G., Chen, J., and Sun, F. (2009) 3D structural investigation of caveolae from porcine aorta endothelial cell by electron tomography. *Progress in Biochemistry and Biophysics* **36**, 729-735
21. Wu, L., Wang, L., Hua, G., Liu, K., Yang, X., Zhai, Y., Bartlam, M., Sun, F., and Fan, Z. (2009) Structural basis for proteolytic specificity of the human apoptosis-inducing granzyme M. *J Immunol* **183**, 421-429
22. Zhang, K., Zhang, C., and Sun, F. (2009) Disclosing the Structure and Function of Translation Machine - Introduction of the Noble Prize in Chemistry 2009. *ACTA BIOPHYSICA SINICA* **25**, 325-334
23. Hu, Z., Tian, X., Zhai, Y., Xu, W., Zheng, D., and Sun, F. (2010) Cryo-electron microscopy reconstructions of two types of wild rabbit hemorrhagic disease viruses characterized the structural features of Lagovirus. *Protein Cell* **1**, 48-58
24. Huo, Y., Hu, Z., Zhang, K., Wang, L., Zhai, Y., Zhou, Q., Lander, G., Zhu, J., He, Y., Pang, X., Xu, W., Bartlam, M., Dong, Z., and Sun, F. (2010) Crystal structure of group II chaperonin in the open state. *Structure* **18**, 1270-1279
25. Li, S. J., Zhao, Q., Zhou, Q., Unno, H., Zhai, Y., and Sun, F. (2010) The role and structure of the carboxyl-terminal domain of the human voltage-gated proton channel Hv1. *J Biol Chem* **285**, 12047-12054
26. Li, Z., Zhai, Y., Fang, J., Zhou, Q., Geng, Y., and Sun, F. (2010) Purification, crystallization and preliminary crystallographic analysis of very-long-chain acyl-CoA dehydrogenase from *Caenorhabditis elegans*. *Acta Crystallogr Sect F Struct Biol Cryst Commun* **66**, 426-430
27. Li, Z., Zhang, K., Zhai, Y., Zhou, Q., Geng, Y., and Sun, F. (2010) Cloning, Expression, Purification and Preliminary Crystallographic Analysis of *Caenorhabditis elegans* Enoyl-CoA Hydratase. *ACTA BIOPHYSICA SINICA* **26**, 37-48
28. Lu, B., Zhai, Y., Wu, C., Pang, X., Xu, Z., and Sun, F. (2010) Expression, purification and preliminary biochemical studies of the N-terminal domain of leucine-rich repeat kinase 2. *Biochim Biophys Acta* **1804**, 1780-1784
29. Ma, J., and Sun, F. (2010) Translocation of mitochondrial proteins. *ACTA BIOPHYSICA SINICA* **26**, 880-893
30. Wang, L., Hu, Z. J., Luo, Y. M., Huo, Y. W., Ma, Q., He, Y. Z., Zhang, Y. Y., Sun, F., and Dong, Z. Y. (2010) Distinct symmetry and limited peptide refolding activity of the thermosomes from the acidothermophilic archaea *Acidianus tengchongensis* S5(T). *Biochem Biophys Res Commun* **393**, 228-234
31. Xu, L., Guo, J., Zheng, X., Wen, T., Sun, F., Liu, S., and Pang, H. (2010) Crystallization and preliminary X-ray analysis of a novel esterase Rv0045c from *Mycobacterium tuberculosis*. *Acta Crystallogr Sect F Struct Biol Cryst Commun* **66**, 1579-1582
32. Zhang, K., Zhang, Y., Hu, Z., Ji, G., and Sun, F. (2010) Development and frontier of electron microscopy 3D reconstruction. *ACTA BIOPHYSICA SINICA* **26**, 209-215
33. Zhang, S., Zhang, K., Chen, X., Chu, X., Sun, F., and Dong, Z. (2010) Five mutations in N-terminus confer thermostability on mesophilic xylanase. *Biochem Biophys Res Commun* **395**, 200-206
34. Zhang, Y., Liu, D., Chen, X., Li, J., Li, L., Bian, Z., Sun, F., Lu, J., Yin, Y., Cai, X., Sun, Q., Wang, K., Ba, Y., Wang, Q., Wang, D., Yang, J., Liu, P., Xu, T., Yan, Q., Zhang, J., Zen, K., and Zhang, C. Y. (2010) Secreted monocytic miR-150 enhances targeted endothelial cell migration. *Mol Cell* **39**, 133-144
35. Zhou, Q., Sun, J., Zhai, Y., and Sun, F. (2010) Prokaryotic Expression of Active Mitochondrial Uncoupling Protein 1. *Progress in Biochemistry and Biophysics* **37**, 56-62
36. Chen, S., Pang, X., and Sun, F. (2011) Mitochondrial movement and its related cytoskeletons and proteins. *ACTA BIOPHYSICA SINICA* **27**, 1019-1029



37. Cheng, L., Sun, J., Zhang, K., Mou, Z., Huang, X., Ji, G., Sun, F., Zhang, J., and Zhu, P. (2011) Atomic model of a cypovirus built from cryo-EM structure provides insight into the mechanism of mRNA capping. *Proc Natl Acad Sci U S A* **108**, 1373-1378
38. Chu, Q., Zhang, K., Wan, X., Zhang, C., Zhang, Y., Zhang, G., Shen, B., Lu, X., Zhao, K., Chu, X., Zhang, F., and Sun, F. (2011) A GPU powered package for electron tomography reconstruction. *ACTA BIOPHYSICA SINICA* **27**, 231-241
39. Li, M., Xu, G., Sorzano, C. O., Sun, F., and Bajaj, C. L. (2011) Single-particle reconstruction using L(2)-gradient flow. *J Struct Biol* **176**, 259-267
40. Sun, F., and Wang, X. (2011) Application and aspect of cryo-electron microscopy for the structural study of membrane protein. *Chinese Bulletin of Life Sciences* **23**, 1130-1139
41. Wan, X., Zhang, F., Chu, Q., Zhang, K., Sun, F., Yuan, B., and Liu, Z. (2011) Three-dimensional reconstruction using an adaptive simultaneous algebraic reconstruction technique in electron tomography. *J Struct Biol* **175**, 277-287
42. Wang, G., Zhang, F., Fan, L., Sun, F., and Liu, Y. (2011) Analysis and solution of complexity of basis function in ISAF reconstruction algorithm. *Journal of Computer-Aided Design & Computer Graphics* **23**, 1148-1158
43. Wang, L., Zhang, K., Fan, Z., Dong, Z., and Sun, F. (2011) Substrate binding properties of thermosome ATcpn-beta from *Acidianus Tengchongensis*. *Progress in Biochemistry and Biophysics* **38**, 151-158
44. Zhai, Y., Zhang, K., Huo, Y., Zhu, Y., Zhou, Q., Lu, J., Black, I., Pang, X., Roszak, A. W., Zhang, X., Isaacs, N. W., and Sun, F. (2011) Autotransporter passenger domain secretion requires a hydrophobic cavity at the extracellular entrance of the beta-domain pore. *Biochem J* **435**, 577-587
45. Zheng, X., Guo, J., Xu, L., Li, H., Zhang, D., Zhang, K., Sun, F., Wen, T., Liu, S., and Pang, H. (2011) Crystal structure of a novel esterase Rv0045c from *Mycobacterium tuberculosis*. *PLoS One* **6**, e20506
46. Zhou, Q., Zhai, Y., Lou, J., Liu, M., Pang, X., and Sun, F. (2011) Thiabendazole inhibits ubiquinone reduction activity of mitochondrial respiratory complex II via a water molecule mediated binding feature. *Protein Cell* **2**, 531-542
47. Bai, M., Pang, X., Lou, J., Zhou, Q., Zhang, K., Ma, J., Li, J., Sun, F., and Hsu, V. W. (2012) Mechanistic Insights into Regulated Cargo Binding by ACAP1 Protein. *J Biol Chem* **287**, 28675-28685
48. Guo, H., Yuan, X., Liu, J., Shan, G., Chi, X., and Sun, F. (2012) Interference microscopy volume illustration for biomedical data. *Pacific Visualization Symposium (PacificVis) 2012 IEEE*, 177-184
49. Hu, J., Sun, L., Shen, F., Chen, Y., Hua, Y., Liu, Y., Zhang, M., Hu, Y., Wang, Q., Xu, W., Sun, F., Ji, J., Murray, J. M., Carr, A. M., and Kong, D. (2012) The intra-S phase checkpoint targets Dna2 to prevent stalled replication forks from reversing. *Cell* **149**, 1221-1232
50. Wang, G., Zhang, F., Sun, F., and Liu, Z. (2012) An accelerated ISAF algorithm with the fast mapping strategy. *Journal of Computers* **7**, 528-533
51. Wang, L., Zhang, K., Wu, L., Liu, S., Zhang, H., Zhou, Q., Tong, L., Sun, F., and Fan, Z. (2012) Structural insights into the substrate specificity of human granzyme H: the functional roles of a novel RKR motif. *J Immunol* **188**, 765-773
52. Wang, S., and Sun, F. (2012) Dynactin is an indispensable helper for dynein's function in intracellular motility. *ACTA BIOPHYSICA SINICA* **28**, 785-793
53. Wang, X., Wang, L., Sun, F., and Wang, C. C. (2012) Structural insights into the peroxidase activity and inactivation of human peroxiredoxin 4. *Biochem J* **441**, 113-118
54. Yang, C., Ji, G., Liu, H., Zhang, K., Liu, G., Sun, F., Zhu, P., and Cheng, L. (2012) Cryo-EM structure of a transcribing cypovirus. *Proc Natl Acad Sci U S A* **109**, 6118-6123
55. Zhao, Y. G., Zhao, H., Miao, L., Wang, L., Sun, F., and Zhang, H. (2012) The p53-induced gene Ei24 is an essential component of the basal autophagy pathway. *J Biol Chem* **287**, 42053-42063

## D. Research Support

### Ongoing Research Support

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

### Completed Research Support

Strategic Priority Research Program of CAS XDB08030202 Sun(PI) 01/01/2014 – 12/31/2018  
New methods and new technologies for structural studies of supra bio-macromolecular complexes  
Role: PI

“973” project 2014CB910700 Sun (PI) 01/01/2014-08/31/2018  
Structure and function of supra bio-macromolecular complexes by high-resolution cryo-electron microscopic reconstruction  
Role: PI

“973” project 2011CB910301 Zhang (PI) 01/01/11-08/31/15  
Structural and functional studies on key membrane proteins and protein complexes in essential life activities  
Role: Co-Investigator

“973” project 2011CB910901 Li (PI) 01/01/11-08/31/15  
Lipid metabolic regulation and functional domain of plasma membrane  
Role: Co-Investigator

NSFC 31170700 Sun (PI) 01/01/12-12/31/15  
Dynamic structure and cooperativity of Group II chaperonin  
Role: PI

“973” project 2006CB806506 NIU (PI) 09/01/06-08/31/10  
Structural and functional studies on molecular mechanism of mitochondrial respiratory chain  
Role: Co-Investigator

“973” project 2006CB911001 Chen (PI) 12/01/06-12/31/10  
Structures and regulatory mechanism of energy transfer related membrane proteins  
Role: Co-Investigator

NSFC 30770496 Sun (PI) 01/01/08-12/31/10  
Structure determination of Archaea Group II chaperonin by Cryo-EM and crystallography  
Role: PI

NSFC 30721003 Chang (PI) 01/01/08-12/31/10  
Structural studies on membrane proteins and protein complexes  
Role: Co-Investigator

CAS KSCX2-YW-R-126 Sun (PI) 06/01/07-12/31/10

Program Director/Principal Investigator (Last, First, Middle):

Foundation and application of Cryo-electron tomography imaging techniques

Role: PI

CAS                    KG CX1-YW-13                    Sun (PI)                    06/01/07-08/31/11

High-performance computational research on protein science--raw data set of Cryo-EM 3D reconstruction

Role: PI

NSFC                    31021062                    Jiang (PI)                    01/01/11-12/31/13

Structural studies on membrane proteins and protein complexes

Role: Co-Investigator

CAS                    XXXXX-XX-X-###                    Sun (PI)                    01/01/12-12/31/13

Phase plate system for Cryo-electron microscopy image contrast enhancement

Role: PI