

Fei Sun

List of Publications by Year in descending order

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138
papers

7,009
citations

94433

37
h-index

66911

78
g-index

155
all docs

155
docs citations

155
times ranked

12600
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Inhibition of SARS-CoV-2 (previously 2019-nCoV) infection by a highly potent pan-coronavirus fusion inhibitor targeting its spike protein that harbors a high capacity to mediate membrane fusion. <i>Cell Research</i> , 2020, 30, 343-355. | 12.0 | 1,083 |
| 2 | Secreted Monocytic miR-150 Enhances Targeted Endothelial Cell Migration. <i>Molecular Cell</i> , 2010, 39, 133-144. | 9.7 | 1,059 |
| 3 | Crystal Structure of Mitochondrial Respiratory Membrane Protein Complex II. <i>Cell</i> , 2005, 121, 1043-1057. | 28.9 | 689 |
| 4 | Insights into SARS-CoV transcription and replication from the structure of the nsp7 and nsp8 hexadecamer. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 980-986. | 8.2 | 255 |
| 5 | The Intra-S Phase Checkpoint Targets Dna2 to Prevent Stalled Replication Forks from Reversing. <i>Cell</i> , 2012, 149, 1221-1232. | 28.9 | 149 |
| 6 | An electron transfer path connects subunits of a mycobacterial respiratory supercomplex. <i>Science</i> , 2018, 362, . | 12.6 | 117 |
| 7 | Structural basis of G _s and G _i recognition by the human glucagon receptor. <i>Science</i> , 2020, 367, 1346-1352. | 12.6 | 117 |
| 8 | Acyl-CoA Dehydrogenase Drives Heat Adaptation by Sequestering Fatty Acids. <i>Cell</i> , 2015, 161, 1152-1163. | 28.9 | 105 |
| 9 | Coexistence of ribbon and helical fibrils originating from hIAPP revealed by quantitative nanomechanical atomic force microscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2798-2803. | 7.1 | 104 |
| 10 | Molecular insights into the enzyme promiscuity of an aromatic prenyltransferase. <i>Nature Chemical Biology</i> , 2017, 13, 226-234. | 8.0 | 100 |
| 11 | Dodecamer Structure of Severe Acute Respiratory Syndrome Coronavirus Nonstructural Protein nsp10. <i>Journal of Virology</i> , 2006, 80, 7902-7908. | 3.4 | 95 |
| 12 | A single-cell transcriptomic landscape of primate arterial aging. <i>Nature Communications</i> , 2020, 11, 2202. | 12.8 | 95 |
| 13 | Atomic Model of Rabbit Hemorrhagic Disease Virus by Cryo-Electron Microscopy and Crystallography. <i>PLoS Pathogens</i> , 2013, 9, e1003132. | 4.7 | 94 |
| 14 | Three-dimensional super-resolution protein localization correlated with vitrified cellular context. <i>Scientific Reports</i> , 2015, 5, 13017. | 3.3 | 94 |
| 15 | New Antiviral Target Revealed by the Hexameric Structure of Mouse Hepatitis Virus Nonstructural Protein nsp15. <i>Journal of Virology</i> , 2006, 80, 7909-7917. | 3.4 | 85 |
| 16 | Structural insights into Ca ²⁺ -activated long-range allosteric channel gating of RyR1. <i>Cell Research</i> , 2016, 26, 977-994. | 12.0 | 84 |
| 17 | Crystal structure of <i>E. coli</i> lipoprotein diacylglycerol transferase. <i>Nature Communications</i> , 2016, 7, 10198. | 12.8 | 81 |
| 18 | Structural insights into the peroxidase activity and inactivation of human peroxiredoxin 4. <i>Biochemical Journal</i> , 2012, 441, 113-118. | 3.7 | 77 |

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|----|--|------|-----------|
| 19 | ICON: 3D reconstruction with "missing-information"™ restoration in biological electron tomography. <i>Journal of Structural Biology</i> , 2016, 195, 100-112. | 2.8 | 75 |
| 20 | The p53-induced Gene Ei24 Is an Essential Component of the Basal Autophagy Pathway. <i>Journal of Biological Chemistry</i> , 2012, 287, 42053-42063. | 3.4 | 68 |
| 21 | Crystal structure of human ERp44 shows a dynamic functional modulation by its carboxy-terminal tail. <i>EMBO Reports</i> , 2008, 9, 642-647. | 4.5 | 66 |
| 22 | Structures of human mGlu2 and mGlu7 homo- and heterodimers. <i>Nature</i> , 2021, 594, 589-593. | 27.8 | 66 |
| 23 | Atomic model of a cypovirus built from cryo-EM structure provides insight into the mechanism of mRNA capping. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 1373-1378. | 7.1 | 65 |
| 24 | Synthetic Multienzyme Complexes, Catalytic Nanomachineries for Cascade Biosynthesis <i>In Vivo</i> . <i>ACS Nano</i> , 2019, 13, 9895-9906. | 14.6 | 65 |
| 25 | Five mutations in N-terminus confer thermostability on mesophilic xylanase. <i>Biochemical and Biophysical Research Communications</i> , 2010, 395, 200-206. | 2.1 | 59 |
| 26 | Cryo-EM structure of the RC-LH core complex from an early branching photosynthetic prokaryote. <i>Nature Communications</i> , 2018, 9, 1568. | 12.8 | 59 |
| 27 | The Role and Structure of the Carboxyl-terminal Domain of the Human Voltage-gated Proton Channel Hv1. <i>Journal of Biological Chemistry</i> , 2010, 285, 12047-12054. | 3.4 | 56 |
| 28 | Cryo-EM structure of a transcribing cypovirus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 6118-6123. | 7.1 | 52 |
| 29 | Molecular insights into the membrane-associated phosphatidylinositol 4-kinase III β . <i>Nature Communications</i> , 2014, 5, 3552. | 12.8 | 52 |
| 30 | Crystal Structure of Tabtoxin Resistance Protein Complexed with Acetyl Coenzyme A Reveals the Mechanism for β -Lactam Acetylation. <i>Journal of Molecular Biology</i> , 2003, 325, 1019-1030. | 4.2 | 46 |
| 31 | Crystal structure and mutagenic analysis of GDOsp, a gentisate 1,2-dioxygenase from <i>Silicibacter Pomeroyi</i> . <i>Protein Science</i> , 2008, 17, 1362-1373. | 7.6 | 46 |
| 32 | Thiabendazole inhibits ubiquinone reduction activity of mitochondrial respiratory complex II via a water molecule mediated binding feature. <i>Protein and Cell</i> , 2011, 2, 531-542. | 11.0 | 45 |
| 33 | Three-dimensional reconstruction using an adaptive simultaneous algebraic reconstruction technique in electron tomography. <i>Journal of Structural Biology</i> , 2011, 175, 277-287. | 2.8 | 43 |
| 34 | Minireview of progress in the structural study of SARS-CoV-2 proteins. <i>Current Research in Microbial Sciences</i> , 2020, 1, 53-61. | 2.3 | 43 |
| 35 | An improved cryo-FIB method for fabrication of frozen hydrated lamella. <i>Journal of Structural Biology</i> , 2016, 194, 218-223. | 2.8 | 42 |
| 36 | Atlastin-1 regulates morphology and function of endoplasmic reticulum in dendrites. <i>Nature Communications</i> , 2019, 10, 568. | 12.8 | 41 |

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|----|--|------|-----------|
| 37 | Novel cleavage sites identified in SARS-CoV-2 spike protein reveal mechanism for cathepsin L-facilitated viral infection and treatment strategies. <i>Cell Discovery</i> , 2022, 8, . | 6.7 | 40 |
| 38 | Autotransporter passenger domain secretion requires a hydrophobic cavity at the extracellular entrance of the β^2 -domain pore. <i>Biochemical Journal</i> , 2011, 435, 577-587. | 3.7 | 39 |
| 39 | A novel fully automatic scheme for fiducial marker-based alignment in electron tomography. <i>Journal of Structural Biology</i> , 2015, 192, 403-417. | 2.8 | 39 |
| 40 | Crystal Structure of Group II Chaperonin in the Open State. <i>Structure</i> , 2010, 18, 1270-1279. | 3.3 | 38 |
| 41 | In situ protein micro-crystal fabrication by cryo-FIB for electron diffraction. <i>Biophysics Reports</i> , 2018, 4, 339-347. | 0.8 | 38 |
| 42 | Structural and functional basis for pan-CoV fusion inhibitors against SARS-CoV-2 and its variants with preclinical evaluation. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 288. | 17.1 | 38 |
| 43 | Cryo-EM structures of S-OPA1 reveal its interactions with membrane and changes upon nucleotide binding. <i>ELife</i> , 2020, 9, . | 6.0 | 38 |
| 44 | Design and Structure-Based Study of New Potential FKBP12 Inhibitors. <i>Biophysical Journal</i> , 2003, 85, 3194-3201. | 0.5 | 37 |
| 45 | Revealing various coupling of electron transfer and proton pumping in mitochondrial respiratory chain. <i>Current Opinion in Structural Biology</i> , 2013, 23, 526-538. | 5.7 | 35 |
| 46 | A marker-free automatic alignment method based on scale-invariant features. <i>Journal of Structural Biology</i> , 2014, 186, 167-180. | 2.8 | 35 |
| 47 | Structural Insights into the Intrinsic Self-Assembly of Par-3 N-Terminal Domain. <i>Structure</i> , 2013, 21, 997-1006. | 3.3 | 34 |
| 48 | Amorphous nickel titanium alloy film: A new choice for cryo electron microscopy sample preparation. <i>Progress in Biophysics and Molecular Biology</i> , 2020, 156, 3-13. | 2.9 | 33 |
| 49 | Structural Basis for the Specific Recognition of RET by the Dok1 Phosphotyrosine Binding Domain. <i>Journal of Biological Chemistry</i> , 2004, 279, 4962-4969. | 3.4 | 32 |
| 50 | A PH Domain in ACAP1 Possesses Key Features of the BAR Domain in Promoting Membrane Curvature. <i>Developmental Cell</i> , 2014, 31, 73-86. | 7.0 | 32 |
| 51 | Identification of SERPINB1 As a Physiological Inhibitor of Human Granzyme H. <i>Journal of Immunology</i> , 2013, 190, 1319-1330. | 0.8 | 31 |
| 52 | Cryo-EM structures of two bovine adenovirus type 3 intermediates. <i>Virology</i> , 2014, 450-451, 174-181. | 2.4 | 31 |
| 53 | Crystal structure of <i>E. coli</i> apolipoprotein N-acyl transferase. <i>Nature Communications</i> , 2017, 8, 15948. | 12.8 | 31 |
| 54 | Nanometer-resolution in situ structure of the SARS-CoV-2 postfusion spike protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, . | 7.1 | 30 |

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|----|---|------|-----------|
| 55 | The Crystal Structure of Human Isopentenyl Diphosphate Isomerase at 1.7Å... Resolution Reveals its Catalytic Mechanism in Isoprenoid Biosynthesis. <i>Journal of Molecular Biology</i> , 2007, 366, 1447-1458. | 4.2 | 29 |
| 56 | Large scale three-dimensional reconstruction of an entire <i>Caenorhabditis elegans</i> larva using AutoCUTS-SEM. <i>Journal of Structural Biology</i> , 2017, 200, 87-96. | 2.8 | 28 |
| 57 | Cryo-electron microscopy reconstructions of two types of wild rabbit hemorrhagic disease viruses characterized the structural features of Lagovirus. <i>Protein and Cell</i> , 2010, 1, 48-58. | 11.0 | 27 |
| 58 | High-vacuum optical platform for cryo-CLEM (HOPE): A new solution for non-integrated multiscale correlative light and electron microscopy. <i>Journal of Structural Biology</i> , 2018, 201, 63-75. | 2.8 | 27 |
| 59 | FIRT: Filtered iterative reconstruction technique with information restoration. <i>Journal of Structural Biology</i> , 2016, 195, 49-61. | 2.8 | 26 |
| 60 | Structural Basis for Proteolytic Specificity of the Human Apoptosis-Inducing Granzyme M. <i>Journal of Immunology</i> , 2009, 183, 421-429. | 0.8 | 25 |
| 61 | Mechanistic Insights into Regulated Cargo Binding by ACAP1 Protein. <i>Journal of Biological Chemistry</i> , 2012, 287, 28675-28685. | 3.4 | 25 |
| 62 | AuTom: A novel automatic platform for electron tomography reconstruction. <i>Journal of Structural Biology</i> , 2017, 199, 196-208. | 2.8 | 25 |
| 63 | NLRP6 self-assembles into a linear molecular platform following LPS binding and ATP stimulation. <i>Scientific Reports</i> , 2020, 10, 198. | 3.3 | 23 |
| 64 | 8 Å... structure of the outer rings of the <i>Xenopus laevis</i> nuclear pore complex obtained by cryo-EM and AI. <i>Protein and Cell</i> , 2022, 13, 760-777. | 11.0 | 23 |
| 65 | A cryo-electron microscopy support film formed by 2D crystals of hydrophobin HFBI. <i>Nature Communications</i> , 2021, 12, 7257. | 12.8 | 23 |
| 66 | Thermodynamics of voltage-gated ion channels. <i>Biophysics Reports</i> , 2018, 4, 300-319. | 0.8 | 22 |
| 67 | Three-dimensional reconstruction of <i>Picea wilsonii</i> Mast. pollen grains using automated electron microscopy. <i>Science China Life Sciences</i> , 2020, 63, 171-179. | 4.9 | 20 |
| 68 | Crystal Structure of a Novel Esterase Rv0045c from <i>Mycobacterium tuberculosis</i> . <i>PLoS ONE</i> , 2011, 6, e20506. | 2.5 | 20 |
| 69 | Structural Insights into the Substrate Specificity of Human Granzyme H: The Functional Roles of a Novel RKR Motif. <i>Journal of Immunology</i> , 2012, 188, 765-773. | 0.8 | 19 |
| 70 | A novel mitochondrial carrier protein Mme1 acts as a yeast mitochondrial magnesium exporter. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2015, 1853, 724-732. | 4.1 | 19 |
| 71 | Structure Based Hyperthermostability of Archaeal Histone HPhA from <i>Pyrococcus horikoshii</i> . <i>Journal of Molecular Biology</i> , 2003, 325, 1031-1037. | 4.2 | 18 |
| 72 | 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 α -crystallin domain. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120327. | 4.0 | 18 |

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|----|---|------|-----------|
| 73 | Cryo-EM Structure of Actin Filaments from <i>Zea mays</i> Pollen. <i>Plant Cell</i> , 2019, 31, 2855-2867. | 6.6 | 18 |
| 74 | MicroRNA-124 reduces caveolar density by targeting caveolin-1 in porcine kidney epithelial PK15 cells. <i>Molecular and Cellular Biochemistry</i> , 2013, 384, 213-219. | 3.1 | 17 |
| 75 | Molecular Details of the PH Domain of ACAP1 ^{BAR-PH} Protein Binding to PIP-Containing Membrane. <i>Journal of Physical Chemistry B</i> , 2017, 121, 3586-3596. | 2.6 | 17 |
| 76 | Accelerating electron tomography reconstruction algorithm ICON with GPU. <i>Biophysics Reports</i> , 2017, 3, 36-42. | 0.8 | 17 |
| 77 | Structure-based evidence for the enhanced transmissibility of the dominant SARS-CoV-2 B.1.1.7 variant (Alpha). <i>Cell Discovery</i> , 2021, 7, 109. | 6.7 | 17 |
| 78 | AuTom-dualx: a toolkit for fully automatic fiducial marker-based alignment of dual-axis tilt series with simultaneous reconstruction. <i>Bioinformatics</i> , 2019, 35, 319-328. | 4.1 | 15 |
| 79 | New interfaces on MiD51 for Drp1 recruitment and regulation. <i>PLoS ONE</i> , 2019, 14, e0211459. | 2.5 | 15 |
| 80 | VHUT-cryo-FIB, a method to fabricate frozen hydrated lamellae from tissue specimens for in situ cryo-electron tomography. <i>Journal of Structural Biology</i> , 2021, 213, 107763. | 2.8 | 15 |
| 81 | Single-particle reconstruction using L2-gradient flow. <i>Journal of Structural Biology</i> , 2011, 176, 259-267. | 2.8 | 14 |
| 82 | Determining the target protein localization in 3D using the combination of FIB-SEM and APEX2. <i>Biophysics Reports</i> , 2017, 3, 92-99. | 0.8 | 14 |
| 83 | Orienting the future of bio-macromolecular electron microscopy. <i>Chinese Physics B</i> , 2018, 27, 063601. | 1.4 | 14 |
| 84 | SmartBac, a new baculovirus system for large protein complex production. <i>Journal of Structural Biology: X</i> , 2019, 1, 100003. | 1.3 | 14 |
| 85 | Flexible interwoven termini determine the thermal stability of thermosomes. <i>Protein and Cell</i> , 2013, 4, 432-444. | 11.0 | 13 |
| 86 | A local-optimization refinement algorithm in single particle analysis for macromolecular complex with multiple rigid modules. <i>Protein and Cell</i> , 2016, 7, 46-62. | 11.0 | 13 |
| 87 | Imaging biological samples by integrated differential phase contrast (iDPC) STEM technique. <i>Journal of Structural Biology</i> , 2022, 214, 107837. | 2.8 | 13 |
| 88 | Cryo-EM structure and electrophysiological characterization of ALMT from <i>Glycine max</i> reveal a previously uncharacterized class of anion channels. <i>Science Advances</i> , 2022, 8, eabm3238. | 10.3 | 13 |
| 89 | Structural characterization of coatomer in its cytosolic state. <i>Protein and Cell</i> , 2016, 7, 586-600. | 11.0 | 12 |
| 90 | Using integrated correlative cryo-light and electron microscopy to directly observe syntaphilin-immobilized neuronal mitochondria in situ. <i>Biophysics Reports</i> , 2017, 3, 8-16. | 0.8 | 12 |

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|-----|--|------|-----------|
| 91 | The late stage of COPI vesicle fission requires shorter forms of phosphatidic acid and diacylglycerol. <i>Nature Communications</i> , 2019, 10, 3409. | 12.8 | 11 |
| 92 | A 3.3-Å Resolution Structure of Hyperthermophilic Respiratory Complex III Reveals the Mechanism of Its Thermal Stability. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 343-351. | 13.8 | 11 |
| 93 | Structural insights into membrane remodeling by SNX1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, . | 7.1 | 11 |
| 94 | Preliminary molecular characterization and crystallization of mitochondrial respiratory complex II from porcine heart. <i>FEBS Journal</i> , 2007, 274, 1524-1529. | 4.7 | 10 |
| 95 | Expression, purification and preliminary biochemical studies of the N-terminal domain of leucine-rich repeat kinase 2. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 1780-1784. | 2.3 | 10 |
| 96 | Dimerization Interface of 3-Hydroxyacyl-CoA Dehydrogenase Tunes the Formation of Its Catalytic Intermediate. <i>PLoS ONE</i> , 2014, 9, e95965. | 2.5 | 10 |
| 97 | Structural Insight into the Specific DNA Template Binding to DnaG primase in Bacteria. <i>Scientific Reports</i> , 2017, 7, 659. | 3.3 | 10 |
| 98 | Cryo-EM structures of the air-oxidized and dithionite-reduced photosynthetic alternative complex III from <i>Roseiflexus castenholzii</i> . <i>Science Advances</i> , 2020, 6, eaba2739. | 10.3 | 10 |
| 99 | Distinct symmetry and limited peptide refolding activity of the thermosomes from the acidothermophilic archaea <i>Acidianus tengchongensis</i> S5T. <i>Biochemical and Biophysical Research Communications</i> , 2010, 393, 228-234. | 2.1 | 9 |
| 100 | BrkAutoDisplay: functional display of multiple exogenous proteins on the surface of <i>Escherichia coli</i> by using BrkA autotransporter. <i>Microbial Cell Factories</i> , 2015, 14, 129. | 4.0 | 9 |
| 101 | Crystal structure of the N-terminal SH3 domain of mouse \hat{P}^{2} PIX, p21-activated kinase-interacting exchange factor. <i>Biochemical and Biophysical Research Communications</i> , 2006, 339, 407-414. | 2.1 | 8 |
| 102 | Purification, crystallization and preliminary crystallographic analysis of very-long-chain acyl-CoA dehydrogenase from <i>Caenorhabditis elegans</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 426-430. | 0.7 | 7 |
| 103 | Identification of neurons responsible for feeding behavior in the <i>Drosophila</i> brain. <i>Science China Life Sciences</i> , 2014, 57, 391-402. | 4.9 | 7 |
| 104 | Isolated Heme A Synthase from <i>Aquifex aeolicus</i> Is a Trimer. <i>MBio</i> , 2020, 11, . | 4.1 | 6 |
| 105 | Molecular mechanism of mitochondrial phosphatidate transfer by Ups1. <i>Communications Biology</i> , 2020, 3, 468. | 4.4 | 6 |
| 106 | Cellular 3D-reconstruction and analysis in the human cerebral cortex using automatic serial sections. <i>Communications Biology</i> , 2021, 4, 1030. | 4.4 | 6 |
| 107 | Expression, purification, crystallization and crystallographic study of the <i>Aspergillus terreus</i> aromatic prenyltransferase AtaPT. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 889-894. | 0.8 | 5 |
| 108 | The Unusual Homodimer of a Heme-Copper Terminal Oxidase Allows Itself to Utilize Two Electron Donors. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 13323-13330. | 13.8 | 5 |

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|-----|---|------|-----------|
| 109 | Crystallization and preliminary X-ray analysis of recombinant histone HPhA from the hyperthermophilic archaeon <i>Pyrococcus horikoshii</i> OT3. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 870-871. | 2.5 | 4 |
| 110 | A fast calculation strategy of density function in ISAF reconstruction algorithm. <i>Science China Information Sciences</i> , 2013, 56, 1-12. | 4.3 | 4 |
| 111 | Expression, purification and preliminary characterization of glucagon receptor extracellular domain. <i>Protein Expression and Purification</i> , 2013, 89, 232-240. | 1.3 | 4 |
| 112 | A 3.3 Å Resolution Structure of Hyperthermophilic Respiratory Complex III Reveals the Mechanism of Its Thermal Stability. <i>Angewandte Chemie</i> , 2020, 132, 351-359. | 2.0 | 4 |
| 113 | Prokaryotic Expression of Active Mitochondrial Uncoupling Protein 1*. <i>Progress in Biochemistry and Biophysics</i> , 2010, 37, 56-62. | 0.3 | 4 |
| 114 | Puzzle out the regulation mechanism of PI4KIII β activity. <i>Science China Life Sciences</i> , 2014, 57, 636-638. | 4.9 | 3 |
| 115 | ICON-MIC: Implementing a CPU/MIC Collaboration Parallel Framework for ICON on Tianhe-2 Supercomputer. <i>Journal of Computational Biology</i> , 2018, 25, 270-281. | 1.6 | 3 |
| 116 | Reprint of "Amorphous nickel titanium alloy film: A new choice for cryo electron microscopy sample preparation" <i>Progress in Biophysics and Molecular Biology</i> , 2021, 160, 5-15. | 2.9 | 3 |
| 117 | D Structural Investigation of Caveolae From Porcine Aorta Endothelial Cell by Electron Tomography*. <i>Progress in Biochemistry and Biophysics</i> , 2009, 2009, 729-735. | 0.3 | 3 |
| 118 | Developing Graphene Grids for Cryoelectron Microscopy. <i>Frontiers in Molecular Biosciences</i> , 0, 9, . | 3.5 | 3 |
| 119 | Expression, crystallization and preliminary X-ray studies of the recombinant PTB domain of mouse dok1 protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 334-336. | 2.5 | 2 |
| 120 | Three-dimensional visualization of arsenic stimulated mouse liver sinusoidal by FIB-SEM approach. <i>Protein and Cell</i> , 2016, 7, 227-232. | 11.0 | 2 |
| 121 | ACAP1 assembles into an unusual protein lattice for membrane deformation through multiple stages. <i>PLoS Computational Biology</i> , 2019, 15, e1007081. | 3.2 | 2 |
| 122 | Purification, crystallization and preliminary crystallographic analysis of 3-hydroxyacyl-CoA dehydrogenase from <i>Caenorhabditis elegans</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 515-519. | 0.7 | 1 |
| 123 | Expression, purification, crystallization and preliminary crystallographic study of the cytoplasmic domain of the mitochondrial dynamics protein MiD51. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 596-599. | 0.8 | 1 |
| 124 | C-terminal motif within Sec7 domain regulates guanine nucleotide exchange activity via tuning protein conformation. <i>Biochemical and Biophysical Research Communications</i> , 2014, 446, 380-386. | 2.1 | 1 |
| 125 | Autogdeterm: automatic geometry determination for electron tomography. <i>Tsinghua Science and Technology</i> , 2018, 23, 369-376. | 6.1 | 1 |
| 126 | A Fully Automatic Geometric Parameters Determining Method for Electron Tomography. <i>Lecture Notes in Computer Science</i> , 2017, , 385-389. | 1.3 | 1 |

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|-----|--|------|-----------|
| 127 | Site-Directed Mutagenesis and Preliminary X-Ray Crystallographic Studies of the Tabtoxin Resistance Protein. <i>Protein and Peptide Letters</i> , 2003, 10, 255-263. | 0.9 | 1 |
| 128 | Substrate Binding Properties of Thermosome ATPase from <i>Acidianus Tengchongensis</i> . <i>Progress in Biochemistry and Biophysics</i> , 2011, 38, 151-158. | 0.3 | 1 |
| 129 | Research of Mitochondrial Calcium Transportation. <i>Sheng Wu Wu Li Hsueh Bao</i> , 2013, 29, 167. | 0.1 | 1 |
| 130 | Accelerating Electron Tomography Reconstruction Algorithm ICON Using the Intel Xeon Phi Coprocessor on Tianhe-2 Supercomputer. <i>Lecture Notes in Computer Science</i> , 2017, , 258-269. | 1.3 | 1 |
| 131 | A fast mapping method in the ISAF reconstruction algorithm. , 2011, 2011, 3930-3. | | 0 |
| 132 | Interference microscopy volume illustration for biomedical data. , 2012, , . | | 0 |
| 133 | Fabrication of Frozen-Hydrated Sections by Focused Ion Beam (FIB) Method. <i>Microscopy and Microanalysis</i> , 2016, 22, 182-183. | 0.4 | 0 |
| 134 | Editorial overview: New insights into membrane protein machineries from technology revolution. <i>Current Opinion in Structural Biology</i> , 2020, 63, iii-v. | 5.7 | 0 |
| 135 | Frontispiz: A 3.3-Å Resolution Structure of Hyperthermophilic Respiratory Complex III Reveals the Mechanism of Its Thermal Stability. <i>Angewandte Chemie</i> , 2020, 132, . | 2.0 | 0 |
| 136 | Frontispiece: A 3.3-Å Resolution Structure of Hyperthermophilic Respiratory Complex III Reveals the Mechanism of Its Thermal Stability. <i>Angewandte Chemie - International Edition</i> , 2020, 59, . | 13.8 | 0 |
| 137 | The Unusual Homodimer of a Heme-Copper Terminal Oxidase Allows Itself to Utilize Two Electron Donors. <i>Angewandte Chemie</i> , 2021, 133, 13435-13442. | 2.0 | 0 |
| 138 | Electron Microscopy Reconstruction of Helical Assemblies. <i>Sheng Wu Wu Li Hsueh Bao</i> , 2013, 29, 879. | 0.1 | 0 |