Wen Jiang

List of Publications by Year in descending order

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88	8,485	35	87
papers	citations	h-index	g-index
96	96	96	11179 citing authors
all docs	docs citations	times ranked	

#	Article	IF	CITATIONS
1	Helical Indexing in Real Space. Scientific Reports, 2022, 12, 8162.	3.3	3
2	Development of <i>CryoVR</i> , a virtual reality training system for hands-on cryoEM operations. Acta Crystallographica Section D: Structural Biology, 2022, 78, 903-910.	2.3	4
3	Cryo-EM structures of prion protein filaments from Gerstmann–Strässler–Scheinker disease. Acta Neuropathologica, 2022, 144, 509-520.	7.7	32
4	High resolution single particle Cryo-EM refinement using JSPR. Progress in Biophysics and Molecular Biology, 2021, 160, 37-42.	2.9	9
5	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. Cancer Cell, 2021, 39, 361-379.e16.	16.8	189
6	Affinity Capture of p97 with Small-Molecule Ligand Bait Reveals a 3.6 Ã Double-Hexamer Cryoelectron Microscopy Structure. ACS Nano, 2021, 15, 8376-8385.	14.6	14
7	Structure of Tau filaments in Prion protein amyloidoses. Acta Neuropathologica, 2021, 142, 227-241.	7.7	45
8	Proteogenomic characterization of pancreatic ductal adenocarcinoma. Cell, 2021, 184, 5031-5052.e26.	28.9	236
9	Chromatin hierarchical branching visualized at the nanoscale by electron microscopy. Nanoscale Advances, 2021, 3, 1019-1028.	4.6	5
10	Structural Studies of the Phage G Tail Demonstrate an Atypical Tail Contraction. Viruses, 2021, 13, 2094.	3.3	5
11	Ubiquitination and degradation of SUMO1 by small-molecule degraders extends survival of mice with patient-derived tumors. Science Translational Medicine, 2021, 13, eabh1486.	12.4	14
12	Cryo-electron microscopy structures of VCP/p97 reveal a new mechanism of oligomerization regulation. IScience, 2021, 24, 103310.	4.1	11
13	Deep-Learning-Derived Evaluation Metrics Enable Effective Benchmarking of Computational Tools for Phosphopeptide Identification. Molecular and Cellular Proteomics, 2021, 20, 100171.	3.8	9
14	Plasticity within the barrel domain of BamA mediates a hybrid-barrel mechanism by BAM. Nature Communications, 2021, 12, 7131.	12.8	34
15	Cryo-EM Structure of Heterologous Protein Complex Loaded Thermotoga Maritima Encapsulin Capsid. Biomolecules, 2020, 10, 1342.	4.0	8
16	Cryo-EM structures and functional characterization of homo- and heteropolymers of human ferritin variants. Scientific Reports, 2020, 10, 20666.	3.3	3
17	Simulations of Phage T7 Capsid Expansion Reveal the Role of Molecular Sterics on Dynamics. Viruses, 2020, 12, 1273.	3.3	13
18	Deep Learning in Proteomics. Proteomics, 2020, 20, e1900335.	2.2	91

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19	Arrangement of the Polymerase Complexes inside a Nine-Segmented dsRNA Virus. Structure, 2020, 28, 604-612.e3.	3.3	10
20	Phage G Structure at 6.1 à Resolution, Condensed DNA, and Host Identity Revision to a Lysinibacillus. Journal of Molecular Biology, 2020, 432, 4139-4153.	4.2	14
21	MBIR 3D Reconstruction Method Effectively Minimizes Missing Wedge Artifacts and Restores Missing Information in Cryo-electron Tomography. Microscopy and Microanalysis, 2020, 26, 3146-3149.	0.4	0
22	Coxsackievirus A10 atomic structure facilitating the discovery of a broad-spectrum inhibitor against human enteroviruses. Cell Discovery, 2019, 5, 4.	6.7	26
23	The transition structure of chromatin fibers at the nanoscale probed by cryogenic electron tomography. Nanoscale, 2019, 11, 13783-13789.	5.6	8
24	MBIR: A cryo-ET 3D reconstruction method that effectively minimizes missing wedge artifacts and restores missing information. Journal of Structural Biology, 2019, 206, 183-192.	2.8	33
25	Sub-3 Å apoferritin structure determined with full range of phase shifts using a single position of volta phase plate. Journal of Structural Biology, 2019, 206, 225-232.	2.8	14
26	Structure of the Marine Siphovirus TW1: Evolution of Capsid-Stabilizing Proteins and Tail Spikes. Structure, 2018, 26, 238-248.e3.	3.3	32
27	Defocus and magnification dependent variation of TEM image astigmatism. Scientific Reports, 2018, 8, 344.	3.3	4
28	States of phage T3/T7 capsids: buoyant density centrifugation and cryo-EM. Biophysical Reviews, 2018, 10, 583-596.	3.2	10
29	Cryo-EM structure of Escherichia coli If 70 RNA polymerase and promoter DNA complex revealed a role of If non-conserved region during the open complex formation. Journal of Biological Chemistry, 2018, 293, 7367-7375.	3.4	61
30	A 3.0-Angstrom Resolution Cryo-Electron Microscopy Structure and Antigenic Sites of Coxsackievirus A6-Like Particles. Journal of Virology, 2018, 92, .	3.4	14
31	Flaviviruses have imperfect icosahedral symmetry. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 11608-11612.	7.1	49
32	2.5 $\mbox{\ensuremath{\zeta}}^{\mbox{\tiny o}}$ Resolution Cryo-EM Structure of Human Apo-ferritin Using an Optimized Workflow for Volta Phase Plate. Microscopy and Microanalysis, 2018, 24, 900-901.	0.4	0
33	In vivo production of RNA nanostructures via programmed folding of single-stranded RNAs. Nature Communications, 2018, 9, 2196.	12.8	72
34	Real-time detection and single-pass minimization of TEM objective lens astigmatism. Journal of Structural Biology, 2017, 197, 210-219.	2.8	5
35	Structure of the immature Zika virus at 9 \tilde{A} resolution. Nature Structural and Molecular Biology, 2017, 24, 184-186.	8.2	149
36	A human antibody against Zika virus crosslinks the E protein to prevent infection. Nature Communications, 2017, 8, 14722.	12.8	122

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37	Structure of a headful DNA-packaging bacterial virus at 2.9 Ã resolution by electron cryo-microscopy. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3601-3606.	7.1	26
38	Cryo-EM structure of the bacteriophage T4 isometric head at 3.3-Ã resolution and its relevance to the assembly of icosahedral viruses. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E8184-E8193.	7.1	63
39	Adenoviral E4 34K protein interacts with virus packaging components and may serve as the putative portal. Scientific Reports, 2017, 7, 7582.	3.3	10
40	Stability of Cucumber Necrosis Virus at the Quasi-6-Fold Axis Affects Zoospore Transmission. Journal of Virology, 2017, 91, .	3.4	5
41	Atomic cryo-EM structures of viruses. Current Opinion in Structural Biology, 2017, 46, 122-129.	5.7	55
42	Antibody-induced uncoating of human rhinovirus B14. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 8017-8022.	7.1	49
43	A Digital Micrograph Script for Detection of Astigmatism in TEM Images. Microscopy and Microanalysis, 2016, 22, 2072-2073.	0.4	0
44	Structural Basis for Recognition of Human Enterovirus 71 by a Bivalent Broadly Neutralizing Monoclonal Antibody. PLoS Pathogens, 2016, 12, e1005454.	4.7	43
45	Atomic structure of a rhinovirus C, a virus species linked to severe childhood asthma. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 8997-9002.	7.1	62
46	Selective Capture of Histidine-tagged Proteins from Cell Lysates Using TEM grids Modified with NTA-Graphene Oxide. Scientific Reports, 2016, 6, 32500.	3.3	31
47	Antibody-based affinity cryo-EM grid. Methods, 2016, 100, 16-24.	3.8	60
48	Antibody-Based Affinity Cryoelectron Microscopy at 2.6-Ã Resolution. Structure, 2016, 24, 1984-1990.	3.3	34
49	An algorithm for estimation and correction of anisotropic magnification distortion of cryo-EM images without need of pre-calibration. Journal of Structural Biology, 2016, 195, 207-215.	2.8	37
50	2.9ÂÃ Resolution Cryo-EM 3D Reconstruction of Close-Packed Virus Particles. Structure, 2016, 24, 319-328.	3.3	74
51	Nonfouling NTA-PEG-Based TEM Grid Coatings for Selective Capture of Histidine-Tagged Protein Targets from Cell Lysates. Langmuir, 2016, 32, 551-559.	3.5	30
52	Affinity Cryo-Electron Microscopy Studies of Viral Particles Captured Directly From Cell Culture. Microscopy and Microanalysis, 2015, 21, 547-548.	0.4	4
53	Singleâ€Particle Cryoâ€EM and 3D Reconstruction of Hybrid Nanoparticles with Electronâ€Dense Components. Small, 2015, 11, 5157-5163.	10.0	6
54	Simultaneous determination of sample thickness, tilt, and electron mean free path using tomographic tilt images based on Beer–Lambert law. Journal of Structural Biology, 2015, 192, 287-296.	2.8	30

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55	De novo design of an RNA tile that self-assembles into a homo-octameric nanoprism. Nature Communications, 2015, 6, 5724.	12.8	64
56	CTF Challenge: Result summary. Journal of Structural Biology, 2015, 190, 348-359.	2.8	34
57	Self-Assembly of Molecule-like Nanoparticle Clusters Directed by DNA Nanocages. Journal of the American Chemical Society, 2015, 137, 4320-4323.	13.7	136
58	A fast cross-validation method for alignment of electron tomography images based on Beer–Lambert law. Journal of Structural Biology, 2015, 192, 297-306.	2.8	11
59	DNA Nanotubes: Self-Assembly of DNA Nanotubes with Defined Diameters and Lengths (Small 5/2014). Small, 2014, 10, 854-854.	10.0	1
60	Single-step antibody-based affinity cryo-electron microscopy for imaging and structural analysis of macromolecular assemblies. Journal of Structural Biology, 2014, 187, 1-9.	2.8	35
61	Length quantization of DNA partially expelled from heads of a bacteriophage T3 mutant. Virology, 2014, 456-457, 157-170.	2.4	19
62	DNA Nanocages Swallow Gold Nanoparticles (AuNPs) to Form AuNP@DNA Cage Core–Shell Structures. ACS Nano, 2014, 8, 1130-1135.	14.6	87
63	Capsid expansion mechanism of bacteriophage T7 revealed by multistate atomic models derived from cryo-EM reconstructions. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4606-14.	7.1	87
64	Construction of RNA nanocages by re-engineering the packaging RNA of Phi29 bacteriophage. Nature Communications, 2014, 5, 3890.	12.8	66
65	Single Particle Cryo-electron Microscopy and 3-D Reconstruction of Viruses. Methods in Molecular Biology, 2014, 1117, 401-443.	0.9	132
66	Visualization of uncorrelated, tandem symmetry mismatches in the internal genome packaging apparatus of bacteriophage T7. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6811-6816.	7.1	58
67	Cryo-EM Structure of a Novel Calicivirus, Tulane Virus. PLoS ONE, 2013, 8, e59817.	2.5	28
68	Dualities in the analysis of phage DNA packaging motors. Bacteriophage, 2012, 2, e23829.	1.9	19
69	A graph theory method for determination of cryo-EM image focuses. Journal of Structural Biology, 2012, 180, 343-351.	2.8	29
70	Structural basis for scaffolding-mediated assembly and maturation of a dsDNA virus. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1355-1360.	7.1	191
71	DNA Packaging-Associated Hyper-Capsid Expansion of Bacteriophage T3. Journal of Molecular Biology, 2010, 397, 361-374.	4.2	17
72	DNA self-assembly: from 2D to 3D. Faraday Discussions, 2009, 143, 221.	3.2	58

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73	Hierarchical self-assembly of DNA into symmetric supramolecular polyhedra. Nature, 2008, 452, 198-201.	27.8	1,138
74	Backbone structure of the infectious $\hat{l}\mu 15$ virus capsid revealed by electron cryomicroscopy. Nature, 2008, 451, 1130-1134.	27.8	204
75	Visualization of Bacteriophage T3 Capsids with DNA Incompletely Packaged In Vivo. Journal of Molecular Biology, 2008, 384, 1384-1399.	4.2	31
76	Conformational flexibility facilitates self-assembly of complex DNA nanostructures. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 10665-10669.	7.1	249
77	EMAN2: An extensible image processing suite for electron microscopy. Journal of Structural Biology, 2007, 157, 38-46.	2.8	2,798
78	Cryoelectron Microscopy of Icosahedral Virus Particles. Methods in Molecular Biology, 2007, 369, 345-363.	0.9	17
79	Structure of epsilon15 bacteriophage reveals genome organization and DNA packaging/injection apparatus. Nature, 2006, 439, 612-616.	27.8	280
80	Cryo-EM Asymmetric Reconstruction of Bacteriophage P22 Reveals Organization of its DNA Packaging and Infecting Machinery. Structure, 2006, 14, 1073-1082.	3.3	149
81	Electron cryomicroscopy of single particles at subnanometer resolution. Current Opinion in Structural Biology, 2005, 15, 571-577.	5.7	43
82	Cryo-EM and Mass Spectrometry Based Investigations of Viral Capsid Morphogenesis. Microscopy and Microanalysis, 2004, 10, 226-227.	0.4	0
83	Coat protein fold and maturation transition of bacteriophage P22 seen at subnanometer resolutions. Nature Structural Biology, 2003, 10, 131-135.	9.7	190
84	Applications of a bilateral denoising filter in biological electron microscopy. Journal of Structural Biology, 2003, 144, 114-122.	2.8	172
85	Electron cryomicroscopy and bioinformatics suggest protein fold models for rice dwarf virus. Nature Structural Biology, 2001, 8, 868-873.	9.7	125
86	Web-based Simulation for Contrast Transfer Function and Envelope Functions. Microscopy and Microanalysis, 2001, 7, 329-334.	0.4	2
87	Web-based Simulation for Contrast Transfer Function and Envelope Functions. Microscopy and Microanalysis, 2001, 7, 329-334.	0.4	5
88	Web-based Simulation for Contrast Transfer Function and Envelope Functions. Microscopy and Microanalysis, 2001, 7, 329-334.	0.4	2