

Wah Chiu

List of Publications by Year in descending order

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358
papers

27,539
citations

5558

82
h-index

8599

146
g-index

403
all docs

403
docs citations

403
times ranked

28536
citing authors

#	ARTICLE	IF	CITATIONS
1	Intrinsically disordered protein. <i>Journal of Molecular Graphics and Modelling</i> , 2001, 19, 26-59.	1.3	2,005
2	Cofilin Changes the Twist of F-Actin: Implications for Actin Filament Dynamics and Cellular Function. <i>Journal of Cell Biology</i> , 1997, 138, 771-781.	2.3	685
3	Paraneoplastic Thrombocytosis in Ovarian Cancer. <i>New England Journal of Medicine</i> , 2012, 366, 610-618.	13.9	651
4	Structure of the AcrAB-TolC multidrug efflux pump. <i>Nature</i> , 2014, 509, 512-515.	13.7	519
5	Designer nanoscale DNA assemblies programmed from the top down. <i>Science</i> , 2016, 352, 1534-1534.	6.0	500
6	Interbilayer-crosslinked multilamellar vesicles as synthetic vaccines for potent humoral and cellular immune responses. <i>Nature Materials</i> , 2011, 10, 243-251.	13.3	498
7	Remotely Triggered Liposome Release by Near-Infrared Light Absorption via Hollow Gold Nanoshells. <i>Journal of the American Chemical Society</i> , 2008, 130, 8175-8177.	6.6	471
8	The Structure of ClpB. <i>Cell</i> , 2003, 115, 229-240.	13.5	422
9	Three-dimensional structure of rotavirus. <i>Journal of Molecular Biology</i> , 1988, 199, 269-275.	2.0	363
10	Quantitative analysis of cryo-EM density map segmentation by watershed and scale-space filtering, and fitting of structures by alignment to regions. <i>Journal of Structural Biology</i> , 2010, 170, 427-438.	1.3	352
11	Protein Structure Fitting and Refinement Guided by Cryo-EM Density. <i>Structure</i> , 2008, 16, 295-307.	1.6	334
12	Superparamagnetic gadonanotubes are high-performance MRI contrast agents. <i>Chemical Communications</i> , 2005, , 3915.	2.2	310
13	Seeing the Herpesvirus Capsid at 8.5 Å . <i>Science</i> , 2000, 288, 877-880.	6.0	298
14	Convolutional neural networks for automated annotation of cellular cryo-electron tomograms. <i>Nature Methods</i> , 2017, 14, 983-985.	9.0	298
15	Bridging the information gap: computational tools for intermediate resolution structure interpretation. <i>Journal of Molecular Biology</i> , 2001, 308, 1033-1044.	2.0	282
16	Structure of epsilon15 bacteriophage reveals genome organization and DNA packaging/injection apparatus. <i>Nature</i> , 2006, 439, 612-616.	13.7	280
17	Refinement of Protein Structures into Low-Resolution Density Maps Using Rosetta. <i>Journal of Molecular Biology</i> , 2009, 392, 181-190.	2.0	272
18	The Molecular Architecture of the Eukaryotic Chaperonin TRiC/CCT. <i>Structure</i> , 2012, 20, 814-825.	1.6	261

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19	EMDataBank.org: unified data resource for CryoEM. <i>Nucleic Acids Research</i> , 2011, 39, D456-D464.	6.5	246
20	Common Ancestry of Herpesviruses and Tailed DNA Bacteriophages. <i>Journal of Virology</i> , 2005, 79, 14967-14970.	1.5	245
21	Close membrane-membrane proximity induced by Ca ²⁺ -dependent multivalent binding of synaptotagmin-1 to phospholipids. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 209-217.	3.6	235
22	EMDataBank unified data resource for 3DEM. <i>Nucleic Acids Research</i> , 2016, 44, D396-D403.	6.5	230
23	Measurement of atom resolvability in cryo-EM maps with Q-scores. <i>Nature Methods</i> , 2020, 17, 328-334.	9.0	230
24	Visualization of Tegument-Capsid Interactions and DNA in Intact Herpes Simplex Virus Type 1 Virions. <i>Journal of Virology</i> , 1999, 73, 3210-3218.	1.5	229
25	Backbone structure of the infectious μ 15 virus capsid revealed by electron cryomicroscopy. <i>Nature</i> , 2008, 451, 1130-1134.	13.7	204
26	Gating machinery of InsP3R channels revealed by electron cryomicroscopy. <i>Nature</i> , 2015, 527, 336-341.	13.7	199
27	Mechanism of folding chamber closure in a group II chaperonin. <i>Nature</i> , 2010, 463, 379-383.	13.7	196
28	Mitochondrial ATP Synthasome. <i>Journal of Biological Chemistry</i> , 2004, 279, 31761-31768.	1.6	193
29	Structural basis for scaffolding-mediated assembly and maturation of a dsDNA virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 1355-1360.	3.3	191
30	Coat protein fold and maturation transition of bacteriophage P22 seen at subnanometer resolutions. <i>Nature Structural Biology</i> , 2003, 10, 131-135.	9.7	190
31	An allosteric transport mechanism for the AcrAB-TolC multidrug efflux pump. <i>ELife</i> , 2017, 6, .	2.8	190
32	Identification of Secondary Structure Elements in Intermediate-Resolution Density Maps. <i>Structure</i> , 2007, 15, 7-19.	1.6	188
33	Protein Subunit Structures in the Herpes Simplex Virus A-capsid Determined from 400 kV Spot-scan Electron Cryomicroscopy. <i>Journal of Molecular Biology</i> , 1994, 242, 456-469.	2.0	187
34	Seeing GroEL at 6 Å... Resolution by Single Particle Electron Cryomicroscopy. <i>Structure</i> , 2004, 12, 1129-1136.	1.6	187
35	Electron cryomicroscopy and angular reconstitution used to visualize the skeletal muscle calcium release channel. <i>Nature Structural Biology</i> , 1995, 2, 18-24.	9.7	185
36	Capturing the swelling of solid-electrolyte interphase in lithium metal batteries. <i>Science</i> , 2022, 375, 66-70.	6.0	183

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37	Multifunctional RNA Nanoparticles. <i>Nano Letters</i> , 2014, 14, 5662-5671.	4.5	181
38	4.4 Å... cryo-EM structure of an enveloped alphavirus Venezuelan equine encephalitis virus. <i>EMBO Journal</i> , 2011, 30, 3854-3863.	3.5	176
39	Mitochondrial ATP Synthasome. <i>Journal of Biological Chemistry</i> , 2003, 278, 12305-12309.	1.6	171
40	Three-dimensional structure of the HSV1 nucleocapsid. <i>Cell</i> , 1989, 56, 651-660.	13.5	164
41	De Novo Backbone Trace of GroEL from Single Particle Electron Cryomicroscopy. <i>Structure</i> , 2008, 16, 441-448.	1.6	164
42	Three-dimensional Transformation of Capsids Associated with Genome Packaging in a Bacterial Virus. <i>Journal of Molecular Biology</i> , 1993, 231, 65-74.	2.0	163
43	Two structural configurations of the skeletal muscle calcium release channel. <i>Nature Structural and Molecular Biology</i> , 1996, 3, 547-552.	3.6	161
44	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015, 23, 1156-1167.	1.6	159
45	Assembly of VP26 in herpes simplex virus-1 inferred from structures of wild-type and recombinant capsids. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 1026-1030.	3.6	152
46	4.0-Å resolution cryo-EM structure of the mammalian chaperonin TRiC/CCT reveals its unique subunit arrangement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4967-4972.	3.3	152
47	Cryo-EM Asymmetric Reconstruction of Bacteriophage P22 Reveals Organization of its DNA Packaging and Infecting Machinery. <i>Structure</i> , 2006, 14, 1073-1082.	1.6	149
48	Interprotofilament interactions between Alzheimer's A β ₄₂ peptides in amyloid fibrils revealed by cryoEM. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 4653-4658.	3.3	147
49	The Pore Structure of the Closed RyR1 Channel. <i>Structure</i> , 2005, 13, 1203-1211.	1.6	142
50	Three-Dimensional Architecture of the Rod Sensory Cilium and Its Disruption in Retinal Neurodegeneration. <i>Cell</i> , 2012, 151, 1029-1041.	13.5	142
51	Structure of <i>Halothiobacillus neapolitanus</i> Carboxysomes by Cryo-electron Tomography. <i>Journal of Molecular Biology</i> , 2006, 364, 526-535.	2.0	139
52	Electron Cryomicroscopy of Biological Machines at Subnanometer Resolution. <i>Structure</i> , 2005, 13, 363-372.	1.6	138
53	Structure of a Biologically Active Estrogen Receptor-Coactivator Complex on DNA. <i>Molecular Cell</i> , 2015, 57, 1047-1058.	4.5	137
54	Structural changes in a marine podovirus associated with release of its genome into <i>Prochlorococcus</i> . <i>Nature Structural and Molecular Biology</i> , 2010, 17, 830-836.	3.6	136

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55	An Intrinsically Disordered Peptide from Ebola Virus VP35 Controls Viral RNA Synthesis by Modulating Nucleoprotein-RNA Interactions. <i>Cell Reports</i> , 2015, 11, 376-389.	2.9	136
56	A Single Immunization with Spike-Functionalized Ferritin Vaccines Elicits Neutralizing Antibody Responses against SARS-CoV-2 in Mice. <i>ACS Central Science</i> , 2021, 7, 183-199.	5.3	134
57	Cathode-Electrolyte Interphase in Lithium Batteries Revealed by Cryogenic Electron Microscopy. <i>Matter</i> , 2021, 4, 302-312.	5.0	127
58	Electron cryomicroscopy and bioinformatics suggest protein fold models for rice dwarf virus. <i>Nature Structural Biology</i> , 2001, 8, 868-873.	9.7	125
59	Visualizing virus assembly intermediates inside marine cyanobacteria. <i>Nature</i> , 2013, 502, 707-710.	13.7	123
60	Structural diversity of supercoiled DNA. <i>Nature Communications</i> , 2015, 6, 8440.	5.8	122
61	A 11.5 Å... single particle reconstruction of GroEL using EMAN. <i>Journal of Molecular Biology</i> , 2001, 314, 253-262.	2.0	119
62	Accelerated cryo-EM-guided determination of three-dimensional RNA-only structures. <i>Nature Methods</i> , 2020, 17, 699-707.	9.0	119
63	Zernike Phase Contrast Cryo-Electron Microscopy and Tomography for Structure Determination at Nanometer and Subnanometer Resolutions. <i>Structure</i> , 2010, 18, 903-912.	1.6	118
64	Bilamellar Cationic Liposomes Protect Adenovectors from Preexisting Humoral Immune Responses. <i>Molecular Therapy</i> , 2002, 5, 233-241.	3.7	117
65	An atomic model of the outer layer of the bluetongue virus core derived from X-ray crystallography and electron cryomicroscopy. <i>Structure</i> , 1997, 5, 885-893.	1.6	114
66	Accurate model annotation of a near-atomic resolution cryo-EM map. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 3103-3108.	3.3	111
67	Subnanometer-resolution electron cryomicroscopy-based domain models for the cytoplasmic region of skeletal muscle RyR channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 9610-9615.	3.3	106
68	An atomic model of brome mosaic virus using direct electron detection and real-space optimization. <i>Nature Communications</i> , 2014, 5, 4808.	5.8	105
69	A chikungunya fever vaccine utilizing an insect-specific virus platform. <i>Nature Medicine</i> , 2017, 23, 192-199.	15.2	105
70	Refinement of Protein Structures by Iterative Comparative Modeling and CryoEM Density Fitting. <i>Journal of Molecular Biology</i> , 2006, 357, 1655-1668.	2.0	104
71	The 3.5-Å... CryoEM Structure of Nanodisc-Reconstituted Yeast Vacuolar ATPase Vo Proton Channel. <i>Molecular Cell</i> , 2018, 69, 993-1004.e3.	4.5	103
72	Visualizing GroEL/ES in the Act of Encapsulating a Folding Protein. <i>Cell</i> , 2013, 153, 1354-1365.	13.5	102

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73	Cryo-EM Structures of Atomic Surfaces and Host-Guest Chemistry in Metal-Organic Frameworks. <i>Matter</i> , 2019, 1, 428-438.	5.0	102
74	Unravelling Degradation Mechanisms and Atomic Structure of Organic-Inorganic Halide Perovskites by Cryo-EM. <i>Joule</i> , 2019, 3, 2854-2866.	11.7	99
75	The Chaperonin TRiC/CCT Associates with Prefoldin through a Conserved Electrostatic Interface Essential for Cellular Proteostasis. <i>Cell</i> , 2019, 177, 751-765.e15.	13.5	98
76	Three-dimensional Structure of Scaffolding-containing Phage P22 Procapsids by Electron Cryo-microscopy. <i>Journal of Molecular Biology</i> , 1996, 260, 85-98.	2.0	97
77	Essential function of the built-in lid in the allosteric regulation of eukaryotic and archaeal chaperonins. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 432-440.	3.6	96
78	Dual Action of ATP Hydrolysis Couples Lid Closure to Substrate Release into the Group II Chaperonin Chamber. <i>Cell</i> , 2011, 144, 240-252.	13.5	94
79	Genome Sequence, Structural Proteins, and Capsid Organization of the Cyanophage Syn5: A "Horned" Bacteriophage of Marine <i>Synechococcus</i> . <i>Journal of Molecular Biology</i> , 2007, 368, 966-981.	2.0	92
80	Mechanism of lid closure in the eukaryotic chaperonin TRiC/CCT. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 746-753.	3.6	91
81	Cryo-EM and antisense targeting of the 28-kDa frameshift stimulation element from the SARS-CoV-2 RNA genome. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 747-754.	3.6	91
82	Role of the Scaffolding Protein in P22 Procapsid Size Determination Suggested by T=4 and T=7 Procapsid Structures. <i>Biophysical Journal</i> , 1998, 74, 559-568.	0.2	90
83	Cryo-EM structure of a 40 kDa SAM-IV riboswitch RNA at 3.7 Å resolution. <i>Nature Communications</i> , 2019, 10, 5511.	5.8	90
84	Altered Cardiac Energetics and Mitochondrial Dysfunction in Hypertrophic Cardiomyopathy. <i>Circulation</i> , 2021, 144, 1714-1731.	1.6	90
85	Structure of the herpesvirus major capsid protein. <i>EMBO Journal</i> , 2003, 22, 757-765.	3.5	88
86	Capsid expansion mechanism of bacteriophage T7 revealed by multistate atomic models derived from cryo-EM reconstructions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4606-14.	3.3	87
87	ADF/Cofilin weakens lateral contacts in the actin filament 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1999, 291, 513-519.	2.0	86
88	Subunit conformational variation within individual GroEL oligomers resolved by Cryo-EM. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8259-8264.	3.3	86
89	Ultra-thermostable RNA nanoparticles for solubilizing and high-yield loading of paclitaxel for breast cancer therapy. <i>Nature Communications</i> , 2020, 11, 972.	5.8	86
90	Structure of the Type 1 Inositol 1,4,5-Trisphosphate Receptor Revealed by Electron Cryomicroscopy. <i>Journal of Biological Chemistry</i> , 2003, 278, 21319-21322.	1.6	85

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91	Modulation of STAT3 Folding and Function by TRiC/CCT Chaperonin. <i>PLoS Biology</i> , 2014, 12, e1001844.	2.6	84
92	3D volume reconstruction of a mouse brain from histological sections using warp filtering. <i>Journal of Neuroscience Methods</i> , 2006, 156, 84-100.	1.3	83
93	An Examination of the Electrostatic Interactions between the N-Terminal Tail of the Brome Mosaic Virus Coat Protein and Encapsidated RNAs. <i>Journal of Molecular Biology</i> , 2012, 419, 284-300.	2.0	83
94	Structural Analysis of the Anaphase-Promoting Complex Reveals Multiple Active Sites and Insights into Polyubiquitylation. <i>Molecular Cell</i> , 2005, 20, 855-866.	4.5	81
95	Electron Cryotomography Reveals the Portal in the Herpesvirus Capsid. <i>Journal of Virology</i> , 2007, 81, 2065-2068.	1.5	81
96	Flexible Architecture of IP3R1 by Cryo-EM. <i>Structure</i> , 2011, 19, 1192-1199.	1.6	80
97	Symmetry-free cryo-EM structures of the chaperonin TRiC along its ATPase-driven conformational cycle. <i>EMBO Journal</i> , 2012, 31, 720-730.	3.5	80
98	Cryo-EM of macromolecular assemblies at near-atomic resolution. <i>Nature Protocols</i> , 2010, 5, 1697-1708.	5.5	79
99	Experimental Verification of Conformational Variation of Human Fatty Acid Synthase as Predicted by Normal Mode Analysis. <i>Structure</i> , 2004, 12, 185-191.	1.6	78
100	Automated Sequence Design of 3D Polyhedral Wireframe DNA Origami with Honeycomb Edges. <i>ACS Nano</i> , 2019, 13, 2083-2093.	7.3	77
101	Structure of Ca ²⁺ Release Channel at 14Å... Resolution. <i>Journal of Molecular Biology</i> , 2005, 345, 427-431.	2.0	76
102	Programmable Supraassembly of a DNA Surface Adapter for Tunable Chiral Directional Self-Assembly of Gold Nanorods. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 14632-14636.	7.2	76
103	Evaluation of charging on macromolecules in electron cryomicroscopy. <i>Ultramicroscopy</i> , 1998, 72, 41-52.	0.8	75
104	Structure of the acrosomal bundle. <i>Nature</i> , 2004, 431, 104-107.	13.7	75
105	Cryo-EM Structures of Human Drosha and DGCR8 in Complex with Primary MicroRNA. <i>Molecular Cell</i> , 2020, 78, 411-422.e4.	4.5	75
106	TRiC subunits enhance BDNF axonal transport and rescue striatal atrophy in Huntington's disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5655-64.	3.3	74
107	Cryogenic single-molecule fluorescence annotations for electron tomography reveal in situ organization of key proteins in <i>Caulobacter</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 13937-13944.	3.3	73
108	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDDataResource challenge. <i>Nature Methods</i> , 2021, 18, 156-164.	9.0	73

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109	TRiCâ€™s tricks inhibit huntingtin aggregation. <i>ELife</i> , 2013, 2, e00710.	2.8	73
110	Cryoâ€™EM model validation using independent map reconstructions. <i>Protein Science</i> , 2013, 22, 865-868.	3.1	72
111	SuRVoS: Super-Region Volume Segmentation workbench. <i>Journal of Structural Biology</i> , 2017, 198, 43-53.	1.3	72
112	GENFIRE: A generalized Fourier iterative reconstruction algorithm for high-resolution 3D imaging. <i>Scientific Reports</i> , 2017, 7, 10409.	1.6	71
113	Controllable Selfâ€™Assembly of RNA Tetrahedrons with Precise Shape and Size for Cancer Targeting. <i>Advanced Materials</i> , 2016, 28, 7501-7507.	11.1	70
114	Structural and Functional Impacts of ER Coactivator Sequential Recruitment. <i>Molecular Cell</i> , 2017, 67, 733-743.e4.	4.5	69
115	Machining protein microcrystals for structure determination by electron diffraction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 9569-9573.	3.3	69
116	Decontamination of SARS-CoV-2 and Other RNA Viruses from N95 Level Meltblown Polypropylene Fabric Using Heat under Different Humidities. <i>ACS Nano</i> , 2020, 14, 14017-14025.	7.3	69
117	Resolving individualâ€™atoms of protein complex by cryo-electron microscopy. <i>Cell Research</i> , 2020, 30, 1136-1139.	5.7	69
118	Three-dimensional structural analysis of tetanus toxin by electron crystallography. <i>Journal of Molecular Biology</i> , 1988, 200, 367-375.	2.0	68
119	Visualization of the maturation transition in bacteriophage P22 by electron cryomicroscopy. <i>Journal of Molecular Biology</i> , 2000, 297, 615-626.	2.0	68
120	Comparison of <i>Segger</i> and other methods for segmentation and rigidâ€™body docking of molecular components in Cryoâ€™EM density maps. <i>Biopolymers</i> , 2012, 97, 742-760.	1.2	68
121	Validated near-atomic resolution structure of bacteriophage epsilon15 derived from cryo-EM and modeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 12301-12306.	3.3	68
122	Structure of <i>Trypanosoma brucei</i> flagellum accounts for its bihelical motion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11105-11108.	3.3	66
123	Model of human low-density lipoprotein and bound receptor based on CryoEM. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 1059-1064.	3.3	65
124	Partially polymerized liposomes: stable against leakage yet capable of instantaneous release for remote controlled drug delivery. <i>Nanotechnology</i> , 2011, 22, 155605.	1.3	65
125	Contribution of the Type II Chaperonin, TRiC/CCT, to Oncogenesis. <i>International Journal of Molecular Sciences</i> , 2015, 16, 26706-26720.	1.8	65
126	Determination of the Gelsolin Binding Site on F-actin: Implications for Severing and Capping. <i>Biophysical Journal</i> , 1998, 74, 764-772.	0.2	64

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127	Structure of a Conserved Retroviral RNA Packaging Element by NMR Spectroscopy and Cryo-Electron Tomography. <i>Journal of Molecular Biology</i> , 2010, 404, 751-772.	2.0	63
128	Visualizing Individual RuBisCO and Its Assembly into Carboxysomes in Marine Cyanobacteria by Cryo-Electron Tomography. <i>Journal of Molecular Biology</i> , 2018, 430, 4156-4167.	2.0	63
129	REMBI: Recommended Metadata for Biological Images enabling reuse of microscopy data in biology. <i>Nature Methods</i> , 2021, 18, 1418-1422.	9.0	63
130	Control of the structural landscape and neuronal proteotoxicity of mutant Huntingtin by domains flanking the polyQ tract. <i>ELife</i> , 2016, 5, .	2.8	62
131	Structural Mechanism of SDS-Induced Enzyme Activity of Scorpion Hemocyanin Revealed by Electron Cryomicroscopy. <i>Structure</i> , 2009, 17, 749-758.	1.6	61
132	Electron cryotomography reveals ultrastructure alterations in platelets from patients with ovarian cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14266-14271.	3.3	61
133	The skeletal muscle Ca ²⁺ release channel has an oxidoreductase-like domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12155-12160.	3.3	60
134	Outcome of a Workshop on Archiving Structural Models of Biological Macromolecules. <i>Structure</i> , 2006, 14, 1211-1217.	1.6	60
135	Multi-scale 3D Cryo-Correlative Microscopy for Vitrified Cells. <i>Structure</i> , 2020, 28, 1231-1237.e3.	1.6	60
136	Mechanism of Scaffolding-Directed Virus Assembly Suggested by Comparison of Scaffolding-Containing and Scaffolding-Lacking P22 Procapsids. <i>Biophysical Journal</i> , 1999, 76, 3267-3277.	0.2	59
137	An Expanded Conformation of Single-Ring GroEL-GroES Complex Encapsulates an 86 kDa Substrate. <i>Structure</i> , 2006, 14, 1711-1722.	1.6	59
138	Visualizing the Structural Changes of Bacteriophage Epsilon15 and Its Salmonella Host during Infection. <i>Journal of Molecular Biology</i> , 2010, 402, 731-740.	2.0	59
139	Cryo-EM structures of full-length Tetrahymena ribozyme at 3.1Å... resolution. <i>Nature</i> , 2021, 596, 603-607.	13.7	59
140	Structure of Double-Shelled Rice Dwarf Virus. <i>Journal of Virology</i> , 1998, 72, 8541-8549.	1.5	59
141	Prospects for using an IVEM with a FEG for imaging macromolecules towards atomic resolution. <i>Ultramicroscopy</i> , 1993, 49, 407-416.	0.8	57
142	Quaternary structure of human fatty acid synthase by electron cryomicroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 138-143.	3.3	57
143	A Digital Atlas to Characterize the Mouse Brain Transcriptome. <i>PLoS Computational Biology</i> , 2005, 1, e41.	1.5	56
144	Neutralizing Antibodies Inhibit Chikungunya Virus Budding at the Plasma Membrane. <i>Cell Host and Microbe</i> , 2018, 24, 417-428.e5.	5.1	56

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145	Reprogramming an ATP-driven protein machine into a light-gated nanocage. <i>Nature Nanotechnology</i> , 2013, 8, 928-932.	15.6	55
146	Opportunities for Cryogenic Electron Microscopy in Materials Science and Nanoscience. <i>ACS Nano</i> , 2020, 14, 9263-9276.	7.3	55
147	Ab Initio Modeling of the Herpesvirus VP26 Core Domain Assessed by CryoEM Density. <i>PLoS Computational Biology</i> , 2006, 2, e146.	1.5	54
148	Human CCT4 and CCT5 Chaperonin Subunits Expressed in Escherichia coli Form Biologically Active Homo-oligomers. <i>Journal of Biological Chemistry</i> , 2013, 288, 17734-17744.	1.6	54
149	Fabrication of RNA 3D Nanoprisms for Loading and Protection of Small RNAs and Model Drugs. <i>Advanced Materials</i> , 2016, 28, 10079-10087.	11.1	54
150	The Structure of Barmah Forest Virus as Revealed by Cryo-Electron Microscopy at a 6-Angstrom Resolution Has Detailed Transmembrane Protein Architecture and Interactions. <i>Journal of Virology</i> , 2011, 85, 9327-9333.	1.5	53
151	Cryo-EM Structure of a Group II Chaperonin in the Prehydrolysis ATP-Bound State Leading to Lid Closure. <i>Structure</i> , 2011, 19, 633-639.	1.6	52
152	EMEN2: An Object Oriented Database and Electronic Lab Notebook. <i>Microscopy and Microanalysis</i> , 2013, 19, 1-10.	0.2	52
153	Structure of the 30ÅkDa HIV-1 RNA Dimerization Signal by a Hybrid Cryo-EM, NMR, and Molecular Dynamics Approach. <i>Structure</i> , 2018, 26, 490-498.e3.	1.6	52
154	Structural basis of amino acid surveillance by higher-order tRNA-mRNA interactions. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 1094-1105.	3.6	52
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156	Cryo-EM and MD infer water-mediated proton transport and autoinhibition mechanisms of V _o complex. <i>Science Advances</i> , 2020, 6, .	4.7	51
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