List of Publications by Year in descending order

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1EMAI 20072Hiera 198-23Struct appa4Confi the N	N2: An extensible image processing suite for electron microscopy. Journal of Structural Biology, 7, 157, 38-46. archical self-assembly of DNA into symmetric supramolecular polyhedra. Nature, 2008, 452, 201. cture of epsilon15 bacteriophage reveals genome organization and DNA packaging/injection ratus. Nature, 2006, 439, 612-616. Formational flexibility facilitates self-assembly of complex DNA nanostructures. Proceedings of National Academy of Sciences of the United States of America, 2008, 105, 10665-10669. eogenomic characterization of pancreatic ductal adenocarcinoma. Cell, 2021, 184, 5031-5052.e26.	 2.8 27.8 27.8 7.1 28.0 	2,798 1,138 280 249
 2 Hiera 198-2 3 Structor 4 Confidence 5 Protocomposition 	archical self-assembly of DNA into symmetric supramolecular polyhedra. Nature, 2008, 452, 201. cture of epsilon15 bacteriophage reveals genome organization and DNA packaging/injection aratus. Nature, 2006, 439, 612-616. Formational flexibility facilitates self-assembly of complex DNA nanostructures. Proceedings of National Academy of Sciences of the United States of America, 2008, 105, 10665-10669. eogenomic characterization of pancreatic ductal adenocarcinoma. Cell, 2021, 184, 5031-5052.e26.	27.8 27.8 7.1	1,138 280 249
 3 Structappa 4 Confidence 4 the N 	cture of epsilon15 bacteriophage reveals genome organization and DNA packaging/injection matus. Nature, 2006, 439, 612-616. Formational flexibility facilitates self-assembly of complex DNA nanostructures. Proceedings of National Academy of Sciences of the United States of America, 2008, 105, 10665-10669. eogenomic characterization of pancreatic ductal adenocarcinoma. Cell, 2021, 184, 5031-5052.e26.	27.8 7.1	280 249
4 Conf 4 the N	Formational flexibility facilitates self-assembly of complex DNA nanostructures. Proceedings of National Academy of Sciences of the United States of America, 2008, 105, 10665-10669. Reogenomic characterization of pancreatic ductal adenocarcinoma. Cell, 2021, 184, 5031-5052.e26.	7.1	249
5 Droto	eogenomic characterization of pancreatic ductal adenocarcinoma. Cell, 2021, 184, 5031-5052.e26.	28.0	
5 FIUL		20.9	236
6 Back 2008	bone structure of the infectious lµ15 virus capsid revealed by electron cryomicroscopy. Nature, 3, 451, 1130-1134.	27.8	204
7 Struc 7 the N	ctural basis for scaffolding-mediated assembly and maturation of a dsDNA virus. Proceedings of National Academy of Sciences of the United States of America, 2011, 108, 1355-1360.	7.1	191
8 Coat Natu	protein fold and maturation transition of bacteriophage P22 seen at subnanometer resolutions. Ire Structural Biology, 2003, 10, 131-135.	9.7	190
9 Prote carcii	eogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell noma. Cancer Cell, 2021, 39, 361-379.e16.	16.8	189
10 Appli Biolo	ications of a bilateral denoising filter in biological electron microscopy. Journal of Structural ygy, 2003, 144, 114-122.	2.8	172
11 Cryo- and I	-EM Asymmetric Reconstruction of Bacteriophage P22 Reveals Organization of its DNA Packaging Infecting Machinery. Structure, 2006, 14, 1073-1082.	3.3	149
12 Struc 2017	cture of the immature Zika virus at 9 Ã resolution. Nature Structural and Molecular Biology, 7, 24, 184-186.	8.2	149
13 Self-A Amer	Assembly of Molecule-like Nanoparticle Clusters Directed by DNA Nanocages. Journal of the rican Chemical Society, 2015, 137, 4320-4323.	13.7	136
14 Singl Biolo	le Particle Cryo-electron Microscopy and 3-D Reconstruction of Viruses. Methods in Molecular ygy, 2014, 1117, 401-443.	0.9	132
15 Elect Natu	rron cryomicroscopy and bioinformatics suggest protein fold models for rice dwarf virus. ire Structural Biology, 2001, 8, 868-873.	9.7	125
16 A hur Com	man antibody against Zika virus crosslinks the E protein to prevent infection. Nature munications, 2017, 8, 14722.	12.8	122
17 Deep	D Learning in Proteomics. Proteomics, 2020, 20, e1900335.	2.2	91
18 DNA Struc	Nanocages Swallow Gold Nanoparticles (AuNPs) to Form AuNP@DNA Cage Core–Shell	14.6	87

#	Article	IF	CITATIONS
19	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
20	2.9ÂÃ Resolution Cryo-EM 3D Reconstruction of Close-Packed Virus Particles. Structure, 2016, 24, 319-328.	3.3	74
21	In vivo production of RNA nanostructures via programmed folding of single-stranded RNAs. Nature Communications, 2018, 9, 2196.	12.8	72
22	Construction of RNA nanocages by re-engineering the packaging RNA of Phi29 bacteriophage. Nature Communications, 2014, 5, 3890.	12.8	66
23	De novo design of an RNA tile that self-assembles into a homo-octameric nanoprism. Nature Communications, 2015, 6, 5724.	12.8	64
24	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
25	Atomic structure of a rhinovirus C, a virus species linked to severe childhood asthma. Proceedings of the United States of America, 2016, 113, 8997-9002.	7.1	62
26	Cryo-EM structure of Escherichia coli σ70 RNA polymerase and promoter DNA complex revealed a role of ΃ non-conserved region during the open complex formation. Journal of Biological Chemistry, 2018, 293, 7367-7375.	3.4	61
27	Antibody-based affinity cryo-EM grid. Methods, 2016, 100, 16-24.	3.8	60
28	DNA self-assembly: from 2D to 3D. Faraday Discussions, 2009, 143, 221.	3.2	58
29	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
30	Atomic cryo-EM structures of viruses. Current Opinion in Structural Biology, 2017, 46, 122-129.	5.7	55
31	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
32	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
33	Structure of Tau filaments in Prion protein amyloidoses. Acta Neuropathologica, 2021, 142, 227-241.	7.7	45
34	Electron cryomicroscopy of single particles at subnanometer resolution. Current Opinion in Structural Biology, 2005, 15, 571-577.	5.7	43
35	Structural Basis for Recognition of Human Enterovirus 71 by a Bivalent Broadly Neutralizing Monoclonal Antibody. PLoS Pathogens, 2016, 12, e1005454.	4.7	43
36	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

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37	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
38	CTF Challenge: Result summary. Journal of Structural Biology, 2015, 190, 348-359.	2.8	34
39	Antibody-Based Affinity Cryoelectron Microscopy at 2.6-Ã Resolution. Structure, 2016, 24, 1984-1990.	3.3	34
40	Plasticity within the barrel domain of BamA mediates a hybrid-barrel mechanism by BAM. Nature Communications, 2021, 12, 7131.	12.8	34
41	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
42	Structure of the Marine Siphovirus TW1: Evolution of Capsid-Stabilizing Proteins and Tail Spikes. Structure, 2018, 26, 238-248.e3.	3.3	32
43	Cryo-EM structures of prion protein filaments from Gerstmann–StrÃ ¤ ssler–Scheinker disease. Acta Neuropathologica, 2022, 144, 509-520.	7.7	32
44	Visualization of Bacteriophage T3 Capsids with DNA Incompletely Packaged In Vivo. Journal of Molecular Biology, 2008, 384, 1384-1399.	4.2	31
45	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
46	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
47	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
48	A graph theory method for determination of cryo-EM image focuses. Journal of Structural Biology, 2012, 180, 343-351.	2.8	29
49	Cryo-EM Structure of a Novel Calicivirus, Tulane Virus. PLoS ONE, 2013, 8, e59817.	2.5	28
50	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
51	Coxsackievirus A10 atomic structure facilitating the discovery of a broad-spectrum inhibitor against human enteroviruses. Cell Discovery, 2019, 5, 4.	6.7	26
52	Dualities in the analysis of phage DNA packaging motors. Bacteriophage, 2012, 2, e23829.	1.9	19
53	Length quantization of DNA partially expelled from heads of a bacteriophage T3 mutant. Virology, 2014, 456-457, 157-170.	2.4	19
54	Cryoelectron Microscopy of Icosahedral Virus Particles. Methods in Molecular Biology, 2007, 369, 345-363.	0.9	17

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55	DNA Packaging-Associated Hyper-Capsid Expansion of Bacteriophage T3. Journal of Molecular Biology, 2010, 397, 361-374.	4.2	17
56	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
57	Sub-3â€ [−] à 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
58	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
59	Phage G Structure at 6.1â€ [−] à Resolution, Condensed DNA, and Host Identity Revision to a Lysinibacillus. Journal of Molecular Biology, 2020, 432, 4139-4153.	4.2	14
60	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
61	Simulations of Phage T7 Capsid Expansion Reveal the Role of Molecular Sterics on Dynamics. Viruses, 2020, 12, 1273.	3.3	13
62	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
63	Cryo-electron microscopy structures of VCP/p97 reveal a new mechanism of oligomerization regulation. IScience, 2021, 24, 103310.	4.1	11
64	Adenoviral E4 34K protein interacts with virus packaging components and may serve as the putative portal. Scientific Reports, 2017, 7, 7582.	3.3	10
65	States of phage T3/T7 capsids: buoyant density centrifugation and cryo-EM. Biophysical Reviews, 2018, 10, 583-596.	3.2	10
66	Arrangement of the Polymerase Complexes inside a Nine-Segmented dsRNA Virus. Structure, 2020, 28, 604-612.e3.	3.3	10
67	High resolution single particle Cryo-EM refinement using JSPR. Progress in Biophysics and Molecular Biology, 2021, 160, 37-42.	2.9	9
68	Deep-Learning-Derived Evaluation Metrics Enable Effective Benchmarking of Computational Tools for Phosphopeptide Identification. Molecular and Cellular Proteomics, 2021, 20, 100171.	3.8	9
69	The transition structure of chromatin fibers at the nanoscale probed by cryogenic electron tomography. Nanoscale, 2019, 11, 13783-13789.	5.6	8
70	Cryo-EM Structure of Heterologous Protein Complex Loaded Thermotoga Maritima Encapsulin Capsid. Biomolecules, 2020, 10, 1342.	4.0	8
71	Singleâ€Particle Cryoâ€EM and 3D Reconstruction of Hybrid Nanoparticles with Electronâ€Đense Components. Small, 2015, 11, 5157-5163.	10.0	6
72	Web-based Simulation for Contrast Transfer Function and Envelope Functions. Microscopy and Microanalysis, 2001, 7, 329-334.	0.4	5

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73	Real-time detection and single-pass minimization of TEM objective lens astigmatism. Journal of Structural Biology, 2017, 197, 210-219.	2.8	5
74	Stability of Cucumber Necrosis Virus at the Quasi-6-Fold Axis Affects Zoospore Transmission. Journal of Virology, 2017, 91, .	3.4	5
75	Chromatin hierarchical branching visualized at the nanoscale by electron microscopy. Nanoscale Advances, 2021, 3, 1019-1028.	4.6	5
76	Structural Studies of the Phage G Tail Demonstrate an Atypical Tail Contraction. Viruses, 2021, 13, 2094.	3.3	5
77	Affinity Cryo-Electron Microscopy Studies of Viral Particles Captured Directly From Cell Culture. Microscopy and Microanalysis, 2015, 21, 547-548.	0.4	4
78	Defocus and magnification dependent variation of TEM image astigmatism. Scientific Reports, 2018, 8, 344.	3.3	4
79	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
80	Cryo-EM structures and functional characterization of homo- and heteropolymers of human ferritin variants. Scientific Reports, 2020, 10, 20666.	3.3	3
81	Helical Indexing in Real Space. Scientific Reports, 2022, 12, 8162.	3.3	3
82	Web-based Simulation for Contrast Transfer Function and Envelope Functions. Microscopy and Microanalysis, 2001, 7, 329-334.	0.4	2
83	Web-based Simulation for Contrast Transfer Function and Envelope Functions. Microscopy and Microanalysis, 2001, 7, 329-334.	0.4	2
84	DNA Nanotubes: Self-Assembly of DNA Nanotubes with Defined Diameters and Lengths (Small 5/2014). Small, 2014, 10, 854-854.	10.0	1
85	Cryo-EM and Mass Spectrometry Based Investigations of Viral Capsid Morphogenesis. Microscopy and Microanalysis, 2004, 10, 226-227.	0.4	0
86	A Digital Micrograph Script for Detection of Astigmatism in TEM Images. Microscopy and Microanalysis, 2016, 22, 2072-2073.	0.4	0
87	2.5 Ǻ 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
88	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