

Wah Chiu

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

348
papers

21,480
citations

75
h-index

134
g-index

403
ext. papers

24,836
ext. citations

10.1
avg, IF

6.65
L-index

#	Paper	IF	Citations
348	Intrinsically disordered protein. <i>Journal of Molecular Graphics and Modelling</i> , 2001 , 19, 26-59	2.8	1747
347	Cofilin changes the twist of F-actin: implications for actin filament dynamics and cellular function. <i>Journal of Cell Biology</i> , 1997 , 138, 771-81	7.3	601
346	Paraneoplastic thrombocytosis in ovarian cancer. <i>New England Journal of Medicine</i> , 2012 , 366, 610-8	59.2	505
345	Remotely triggered liposome release by near-infrared light absorption via hollow gold nanoshells. <i>Journal of the American Chemical Society</i> , 2008 , 130, 8175-7	16.4	429
344	Interbilayer-crosslinked multilamellar vesicles as synthetic vaccines for potent humoral and cellular immune responses. <i>Nature Materials</i> , 2011 , 10, 243-51	27	426
343	Structure of the AcrAB-TolC multidrug efflux pump. <i>Nature</i> , 2014 , 509, 512-5	50.4	401
342	Designer nanoscale DNA assemblies programmed from the top down. <i>Science</i> , 2016 , 352, 1534	33.3	370
341	The structure of ClpB: a molecular chaperone that rescues proteins from an aggregated state. <i>Cell</i> , 2003 , 115, 229-40	56.2	366
340	Three-dimensional structure of rotavirus. <i>Journal of Molecular Biology</i> , 1988 , 199, 269-75	6.5	292
339	Superparamagnetic gadonanotubes are high-performance MRI contrast agents. <i>Chemical Communications</i> , 2005 , 3915-7	5.8	279
338	Seeing the herpesvirus capsid at 8.5 Å. <i>Science</i> , 2000 , 288, 877-80	33.3	269
337	Protein structure fitting and refinement guided by cryo-EM density. <i>Structure</i> , 2008 , 16, 295-307	5.2	266
336	Structure of epsilon15 bacteriophage reveals genome organization and DNA packaging/injection apparatus. <i>Nature</i> , 2006 , 439, 612-6	50.4	258
335	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, 427-38	3.4	250
334	Bridging the information gap: computational tools for intermediate resolution structure interpretation. <i>Journal of Molecular Biology</i> , 2001 , 308, 1033-44	6.5	250
333	Refinement of protein structures into low-resolution density maps using rosetta. <i>Journal of Molecular Biology</i> , 2009 , 392, 181-90	6.5	230
332	Common ancestry of herpesviruses and tailed DNA bacteriophages. <i>Journal of Virology</i> , 2005 , 79, 14967-70		229

331	The molecular architecture of the eukaryotic chaperonin TRiC/CCT. <i>Structure</i> , 2012 , 20, 814-25	5.2	216
330	EMDataBank.org: unified data resource for CryoEM. <i>Nucleic Acids Research</i> , 2011 , 39, D456-64	20.1	209
329	Visualization of tegument-capsid interactions and DNA in intact herpes simplex virus type 1 virions. <i>Journal of Virology</i> , 1999 , 73, 3210-8	6.6	208
328	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, 209-17	17.6	205
327	Backbone structure of the infectious epsilon15 virus capsid revealed by electron cryomicroscopy. <i>Nature</i> , 2008 , 451, 1130-4	50.4	188
326	Mechanism of folding chamber closure in a group II chaperonin. <i>Nature</i> , 2010 , 463, 379-83	50.4	180
325	Coat protein fold and maturation transition of bacteriophage P22 seen at subnanometer resolutions. <i>Nature Structural Biology</i> , 2003 , 10, 131-5		176
324	Mitochondrial ATP synthasome: three-dimensional structure by electron microscopy of the ATP synthase in complex formation with carriers for Pi and ADP/ATP. <i>Journal of Biological Chemistry</i> , 2004 , 279, 31761-8	5.4	172
323	Seeing GroEL at 6 Å resolution by single particle electron cryomicroscopy. <i>Structure</i> , 2004 , 12, 1129-36	5.2	169
322	Electron cryomicroscopy and angular reconstitution used to visualize the skeletal muscle calcium release channel. <i>Nature Structural Biology</i> , 1995 , 2, 18-24		165
321	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, 1355-60	11.5	162
320	Gating machinery of InsP3R channels revealed by electron cryomicroscopy. <i>Nature</i> , 2015 , 527, 336-41	50.4	159
319	Convolutional neural networks for automated annotation of cellular cryo-electron tomograms. <i>Nature Methods</i> , 2017 , 14, 983-985	21.6	155
318	De novo backbone trace of GroEL from single particle electron cryomicroscopy. <i>Structure</i> , 2008 , 16, 441-8	5.2	153
317	Mitochondrial ATP synthasome. Cristae-enriched membranes and a multiwell detergent screening assay yield dispersed single complexes containing the ATP synthase and carriers for Pi and ADP/ATP. <i>Journal of Biological Chemistry</i> , 2003 , 278, 12305-9	5.4	153
316	Identification of secondary structure elements in intermediate-resolution density maps. <i>Structure</i> , 2007 , 15, 7-19	5.2	152
315	Three-dimensional transformation of capsids associated with genome packaging in a bacterial virus. <i>Journal of Molecular Biology</i> , 1993 , 231, 65-74	6.5	151
314	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, 456-69	6.5	151

313	Multifunctional RNA nanoparticles. <i>Nano Letters</i> , 2014 , 14, 5662-71	11.5	136
312	Cryo-EM asymmetric reconstruction of bacteriophage P22 reveals organization of its DNA packaging and infecting machinery. <i>Structure</i> , 2006 , 14, 1073-82	5.2	136
311	Two structural configurations of the skeletal muscle calcium release channel. <i>Nature Structural and Molecular Biology</i> , 1996 , 3, 547-52	17.6	136
310	4.4 Å cryo-EM structure of an enveloped alphavirus Venezuelan equine encephalitis virus. <i>EMBO Journal</i> , 2011 , 30, 3854-63	13	133
309	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015 , 23, 1156-67	5.2	131
308	Electron cryomicroscopy of biological machines at subnanometer resolution. <i>Structure</i> , 2005 , 13, 363-72	5.2	129
307	The pore structure of the closed RyR1 channel. <i>Structure</i> , 2005 , 13, 1203-11	5.2	129
306	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, 1026-30	17.6	129
305	Interprotofilament interactions between Alzheimer's Aβ1-42 peptides in amyloid fibrils revealed by cryoEM. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 4653-8	11.5	127
304	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, 4967-72	11.5	125
303	Three-dimensional structure of the HSV1 nucleocapsid. <i>Cell</i> , 1989 , 56, 651-60	56.2	124
302	Three-dimensional architecture of the rod sensory cilium and its disruption in retinal neurodegeneration. <i>Cell</i> , 2012 , 151, 1029-41	56.2	122
301	An allosteric transport mechanism for the AcrAB-TolC multidrug efflux pump. <i>ELife</i> , 2017 , 6,	8.9	121
300	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, 830-6	17.6	121
299	Structure of <i>Halothiobacillus neapolitanus</i> carboxysomes by cryo-electron tomography. <i>Journal of Molecular Biology</i> , 2006 , 364, 526-35	6.5	121
298	A 11.5 Å single particle reconstruction of GroEL using EMAN. <i>Journal of Molecular Biology</i> , 2001 , 314, 253-62	6.5	114
297	EMDataBank unified data resource for 3DEM. <i>Nucleic Acids Research</i> , 2016 , 44, D396-403	20.1	113
296	Electron cryomicroscopy and bioinformatics suggest protein fold models for rice dwarf virus. <i>Nature Structural Biology</i> , 2001 , 8, 868-73		113

295	Zernike phase contrast cryo-electron microscopy and tomography for structure determination at nanometer and subnanometer resolutions. <i>Structure</i> , 2010 , 18, 903-12	5.2	110
294	An Intrinsically Disordered Peptide from Ebola Virus VP35 Controls Viral RNA Synthesis by Modulating Nucleoprotein-RNA Interactions. <i>Cell Reports</i> , 2015 , 11, 376-89	10.6	106
293	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, 885-93	5.2	105
292	Structure of a biologically active estrogen receptor-coactivator complex on DNA. <i>Molecular Cell</i> , 2015 , 57, 1047-1058	17.6	103
291	Bilamellar cationic liposomes protect adenovectors from preexisting humoral immune responses. <i>Molecular Therapy</i> , 2002 , 5, 233-41	11.7	102
290	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, 9610-5	11.5	98
289	Visualizing virus assembly intermediates inside marine cyanobacteria. <i>Nature</i> , 2013 , 502, 707-10	50.4	96
288	An atomic model of bromo mosaic virus using direct electron detection and real-space optimization. <i>Nature Communications</i> , 2014 , 5, 4808	17.4	95
287	Refinement of protein structures by iterative comparative modeling and CryoEM density fitting. <i>Journal of Molecular Biology</i> , 2006 , 357, 1655-68	6.5	93
286	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	11.5	92
285	Structural diversity of supercoiled DNA. <i>Nature Communications</i> , 2015 , 6, 8440	17.4	89
284	Three-dimensional structure of scaffolding-containing phage p22 procapsids by electron cryo-microscopy. <i>Journal of Molecular Biology</i> , 1996 , 260, 85-98	6.5	88
283	Dual action of ATP hydrolysis couples lid closure to substrate release into the group II chaperonin chamber. <i>Cell</i> , 2011 , 144, 240-52	56.2	81
282	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, 432-40	17.6	81
281	Structure of the type 1 inositol 1,4,5-trisphosphate receptor revealed by electron cryomicroscopy. <i>Journal of Biological Chemistry</i> , 2003 , 278, 21319-22	5.4	81
280	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, 559-68	2.9	81
279	ADF/cofilin weakens lateral contacts in the actin filament. <i>Journal of Molecular Biology</i> , 1999 , 291, 513-96.5		79
278	Genome sequence, structural proteins, and capsid organization of the cyanophage Syn5: a "horned" bacteriophage of marine synechococcus. <i>Journal of Molecular Biology</i> , 2007 , 368, 966-81	6.5	78

277	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	6.5	76
276	Visualizing GroEL/ES in the act of encapsulating a folding protein. <i>Cell</i> , 2013 , 153, 1354-65	56.2	76
275	Mechanism of lid closure in the eukaryotic chaperonin TRiC/CCT. <i>Nature Structural and Molecular Biology</i> , 2008 , 15, 746-53	17.6	75
274	Electron cryotomography reveals the portal in the herpesvirus capsid. <i>Journal of Virology</i> , 2007 , 81, 2065-68	5.8	75
273	Structural analysis of the anaphase-promoting complex reveals multiple active sites and insights into polyubiquitylation. <i>Molecular Cell</i> , 2005 , 20, 855-66	17.6	75
272	Structure of the herpesvirus major capsid protein. <i>EMBO Journal</i> , 2003 , 22, 757-65	13	75
271	Cryo-EM of macromolecular assemblies at near-atomic resolution. <i>Nature Protocols</i> , 2010 , 5, 1697-708	18.8	74
270	Structure of the acrosomal bundle. <i>Nature</i> , 2004 , 431, 104-7	50.4	72
269	A chikungunya fever vaccine utilizing an insect-specific virus platform. <i>Nature Medicine</i> , 2017 , 23, 192-199	9.5	71
268	Experimental verification of conformational variation of human fatty acid synthase as predicted by normal mode analysis. <i>Structure</i> , 2004 , 12, 185-91	5.2	71
267	Measurement of atom resolvability in cryo-EM maps with Q-scores. <i>Nature Methods</i> , 2020 , 17, 328-334	21.6	70
266	Flexible architecture of IP3R1 by Cryo-EM. <i>Structure</i> , 2011 , 19, 1192-9	5.2	70
265	Unravelling Atomic Structure and Degradation Mechanisms of Organic-Inorganic Halide Perovskites by Cryo-EM. <i>Joule</i> , 2019 , 3, 2854-2866	27.8	69
264	The 3.5-Å CryoEM Structure of Nanodisc-Reconstituted Yeast Vacuolar ATPase V Proton Channel. <i>Molecular Cell</i> , 2018 , 69, 993-1004.e3	17.6	68
263	3D volume reconstruction of a mouse brain from histological sections using warp filtering. <i>Journal of Neuroscience Methods</i> , 2006 , 156, 84-100	3	68
262	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	11.5	66
261	Structure of Ca ²⁺ release channel at 14 Å resolution. <i>Journal of Molecular Biology</i> , 2005 , 345, 427-31	6.5	65
260	Cryo-EM model validation using independent map reconstructions. <i>Protein Science</i> , 2013 , 22, 865-8	6.3	64

259	Visualization of the maturation transition in bacteriophage P22 by electron cryomicroscopy. <i>Journal of Molecular Biology</i> , 2000 , 297, 615-26	6.5	62
258	Evaluation of charging on macromolecules in electron cryomicroscopy. <i>Ultramicroscopy</i> , 1998 , 72, 41-52	3.1	61
257	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	16.8	60
256	Cryo-EM structures of atomic surfaces and host-guest chemistry in metal-organic frameworks. <i>Matter</i> , 2019 , 1, 428-438	12.7	59
255	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, 1059-64	11.5	59
254	Determination of the gelsolin binding site on F-actin: implications for severing and capping. <i>Biophysical Journal</i> , 1998 , 74, 764-72	2.9	59
253	Three-dimensional structural analysis of tetanus toxin by electron crystallography. <i>Journal of Molecular Biology</i> , 1988 , 200, 367-75	6.5	59
252	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, 12301-6	11.5	58
251	Symmetry-free cryo-EM structures of the chaperonin TRiC along its ATPase-driven conformational cycle. <i>EMBO Journal</i> , 2012 , 31, 720-30	13	58
250	TRiCB tricks inhibit huntingtin aggregation. <i>ELife</i> , 2013 , 2, e00710	8.9	58
249	Partially polymerized liposomes: stable against leakage yet capable of instantaneous release for remote controlled drug delivery. <i>Nanotechnology</i> , 2011 , 22, 155605	3.4	57
248	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, 12155-60	11.5	57
247	Mechanism of scaffolding-directed virus assembly suggested by comparison of scaffolding-containing and scaffolding-lacking P22 procapsids. <i>Biophysical Journal</i> , 1999 , 76, 3267-77	2.9	57
246	Cathode-Electrolyte Interphase in Lithium Batteries Revealed by Cryogenic Electron Microscopy. <i>Matter</i> , 2021 , 4, 302-312	12.7	57
245	Structural mechanism of SDS-induced enzyme activity of scorpion hemocyanin revealed by electron cryomicroscopy. <i>Structure</i> , 2009 , 17, 749-58	5.2	56
244	Structure of Trypanosoma brucei flagellum accounts for its bihelical motion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 11105-8	11.5	56
243	An expanded conformation of single-ring GroEL-GroES complex encapsulates an 86 kDa substrate. <i>Structure</i> , 2006 , 14, 1711-22	5.2	56
242	Modulation of STAT3 folding and function by TRiC/CCT chaperonin. <i>PLoS Biology</i> , 2014 , 12, e1001844	9.7	55

241	Visualizing the structural changes of bacteriophage Epsilon15 and its Salmonella host during infection. <i>Journal of Molecular Biology</i> , 2010 , 402, 731-40	6.5	55
240	Programmable Supra-Assembly of a DNA Surface Adapter for Tunable Chiral Directional Self-Assembly of Gold Nanorods. <i>Angewandte Chemie - International Edition</i> , 2017 , 56, 14632-14636	16.4	53
239	Structure of a conserved retroviral RNA packaging element by NMR spectroscopy and cryo-electron tomography. <i>Journal of Molecular Biology</i> , 2010 , 404, 751-72	6.5	53
238	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	11.5	53
237	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, 138-43	11.5	51
236	Controllable Self-Assembly of RNA Tetrahedrons with Precise Shape and Size for Cancer Targeting. <i>Advanced Materials</i> , 2016 , 28, 7501-7	24	51
235	Ultra-thermostable RNA nanoparticles for solubilizing and high-yield loading of paclitaxel for breast cancer therapy. <i>Nature Communications</i> , 2020 , 11, 972	17.4	49
234	GENFIRE: A generalized Fourier iterative reconstruction algorithm for high-resolution 3D imaging. <i>Scientific Reports</i> , 2017 , 7, 10409	4.9	49
233	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	11.5	49
232	Outcome of a workshop on archiving structural models of biological macromolecules. <i>Structure</i> , 2006 , 14, 1211-7	5.2	49
231	A digital atlas to characterize the mouse brain transcriptome. <i>PLoS Computational Biology</i> , 2005 , 1, e41	5	49
230	Prospects for using an IVEM with a FEG for imaging macromolecules towards atomic resolution. <i>Ultramicroscopy</i> , 1993 , 49, 407-16	3.1	49
229	Structure of double-shelled rice dwarf virus. <i>Journal of Virology</i> , 1998 , 72, 8541-9	6.6	48
228	Cryo-EM structure of a 40kDa SAM-IV riboswitch RNA at 3.7 Å resolution. <i>Nature Communications</i> , 2019 , 10, 5511	17.4	48
227	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	11.5	48
226	SuRVoS: Super-Region Volume Segmentation workbench. <i>Journal of Structural Biology</i> , 2017 , 198, 43-53	3.4	47
225	Automated Sequence Design of 3D Polyhedral Wireframe DNA Origami with Honeycomb Edges. <i>ACS Nano</i> , 2019 , 13, 2083-2093	16.7	47
224	Accelerated cryo-EM-guided determination of three-dimensional RNA-only structures. <i>Nature Methods</i> , 2020 , 17, 699-707	21.6	46

223	Contribution of the Type II Chaperonin, TRiC/CCT, to Oncogenesis. <i>International Journal of Molecular Sciences</i> , 2015 , 16, 26706-20	6.3	46
222	Comparison of Segger and other methods for segmentation and rigid-body docking of molecular components in cryo-EM density maps. <i>Biopolymers</i> , 2012 , 97, 742-60	2.2	46
221	Ab initio modeling of the herpesvirus VP26 core domain assessed by CryoEM density. <i>PLoS Computational Biology</i> , 2006 , 2, e146	5	46
220	Improved Peak Detection and Deconvolution of Native Electrospray Mass Spectra from Large Protein Complexes. <i>Journal of the American Society for Mass Spectrometry</i> , 2015 , 26, 2141-51	3.5	45
219	Structural and Functional Impacts of ER Coactivator Sequential Recruitment. <i>Molecular Cell</i> , 2017 , 67, 733-743.e4	17.6	45
218	Cryo-EM structure of a group II chaperonin in the prehydrolysis ATP-bound state leading to lid closure. <i>Structure</i> , 2011 , 19, 633-9	5.2	45
217	Reprogramming an ATP-driven protein machine into a light-gated nanocage. <i>Nature Nanotechnology</i> , 2013 , 8, 928-32	28.7	44
216	Low dose electron microscopy of the crotoxin complex thin crystal. <i>Journal of Molecular Biology</i> , 1983 , 164, 329-46	6.5	44
215	Roles of triplex and scaffolding proteins in herpes simplex virus type 1 capsid formation suggested by structures of recombinant particles. <i>Journal of Virology</i> , 1999 , 73, 6821-30	6.6	44
214	Structure of the 30kDa HIV-1 RNA Dimerization Signal by a Hybrid Cryo-EM, NMR, and Molecular Dynamics Approach. <i>Structure</i> , 2018 , 26, 490-498.e3	5.2	43
213	Fabrication of RNA 3D Nanoprisms for Loading and Protection of Small RNAs and Model Drugs. <i>Advanced Materials</i> , 2016 , 28, 10079-10087	24	43
212	EMEN2: an object oriented database and electronic lab notebook. <i>Microscopy and Microanalysis</i> , 2013 , 19, 1-10	0.5	43
211	A newly isolated reovirus has the simplest genomic and structural organization of any reovirus. <i>Journal of Virology</i> , 2015 , 89, 676-87	6.6	42
210	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, 9327-33	6.6	42
209	Structural biology of cellular machines. <i>Trends in Cell Biology</i> , 2006 , 16, 144-50	18.3	42
208	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	16.7	42
207	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, 14266-71	11.5	41
206	Filamentous, mixed micelles of triblock copolymers enhance tumor localization of indocyanine green in a murine xenograft model. <i>Molecular Pharmaceutics</i> , 2012 , 9, 135-43	5.6	41

205	Deriving folds of macromolecular complexes through electron cryomicroscopy and bioinformatics approaches. <i>Current Opinion in Structural Biology</i> , 2002 , 12, 263-9	8.1	41
204	Control of the structural landscape and neuronal proteotoxicity of mutant Huntingtin by domains flanking the polyQ tract. <i>ELife</i> , 2016 , 5,	8.9	41
203	Validation of cryo-EM structure of IPB1 channel. <i>Structure</i> , 2013 , 21, 900-9	5.2	40
202	Near-atomic-resolution cryo-EM for molecular virology. <i>Current Opinion in Virology</i> , 2011 , 1, 110-7	7.5	40
201	Electron imaging of crotoxin complex thin crystal at 3.5 Å. <i>Journal of Molecular Biology</i> , 1984 , 175, 93-7	6.5	40
200	Capturing the swelling of solid-electrolyte interphase in lithium metal batteries.. <i>Science</i> , 2022 , 375, 66-70	7.3	40
199	Electron Cryo-microscopy Structure of Ebola Virus Nucleoprotein Reveals a Mechanism for Nucleocapsid-like Assembly. <i>Cell</i> , 2018 , 172, 966-978.e12	56.2	39
198	Gorgon and pathwalking: macromolecular modeling tools for subnanometer resolution density maps. <i>Biopolymers</i> , 2012 , 97, 655-68	2.2	38
197	Human CCT4 and CCT5 chaperonin subunits expressed in Escherichia coli form biologically active homo-oligomers. <i>Journal of Biological Chemistry</i> , 2013 , 288, 17734-44	5.4	38
196	Cryogenic single-molecule fluorescence annotations for electron tomography reveal in situ organization of key proteins in. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 13937-13944	11.5	37
195	A tail-like assembly at the portal vertex in intact herpes simplex type-1 virions. <i>PLoS Pathogens</i> , 2012 , 8, e1002961	7.6	37
194	Estimates of validity of projection approximation for three-dimensional reconstructions at high resolution. <i>Ultramicroscopy</i> , 1984 , 14, 219-26	3.1	36
193	The Chaperonin TRiC/CCT Associates with Prefoldin through a Conserved Electrostatic Interface Essential for Cellular Proteostasis. <i>Cell</i> , 2019 , 177, 751-765.e15	56.2	35
192	Multiple functional roles of the accessory I-domain of bacteriophage P22 coat protein revealed by NMR structure and CryoEM modeling. <i>Structure</i> , 2014 , 22, 830-41	5.2	35
191	Determination of icosahedral virus structures by electron cryomicroscopy at subnanometer resolution. <i>Advances in Protein Chemistry</i> , 2003 , 64, 93-124		35
190	Alignment algorithms and per-particle CTF correction for single particle cryo-electron tomography. <i>Journal of Structural Biology</i> , 2016 , 194, 383-94	3.4	35
189	Neutralizing Antibodies Inhibit Chikungunya Virus Budding at the Plasma Membrane. <i>Cell Host and Microbe</i> , 2018 , 24, 417-428.e5	23.4	33
188	A 3D cellular context for the macromolecular world. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 841-5	17.6	33

187	The pattern of tegument-capsid interaction in the herpes simplex virus type 1 virion is not influenced by the small hexon-associated protein VP26. <i>Journal of Virology</i> , 2001 , 75, 11863-7	6.6	33
186	Lemon-shaped halo archaeal virus His1 with uniform tail but variable capsid structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 2449-54	11.5	32
185	Cryo-EM Structures of Human Drosha and DGCR8 in Complex with Primary MicroRNA. <i>Molecular Cell</i> , 2020 , 78, 411-422.e4	17.6	32
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