Wah Chiu

List of Publications by Year in Descending Order

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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	21,480 citations	75	134
papers		h-index	g-index
403	24,836 ext. citations	10.1	6.65
ext. papers		avg, IF	L-index

#	Paper	IF	Citations
348	Capturing the swelling of solid-electrolyte interphase in lithium metal batteries <i>Science</i> , 2022 , 375, 66	-739 .3	40
347	Cryo-EM, Protein Engineering, and Simulation Enable the Development of Peptide Therapeutics against Acute Myeloid Leukemia ACS Central Science, 2022, 8, 214-222	16.8	1
346	Cryo-EM analysis of Ebola virus nucleocapsid-like assembly STAR Protocols, 2022, 3, 101030	1.4	
345	Electron crystallography of chiral and non-chiral small molecules. <i>Ultramicroscopy</i> , 2022 , 232, 113417	3.1	
344	Methods and Applications of Campenot Trichamber Neuronal Cultures for the Study of Neuroinvasive Viruses <i>Methods in Molecular Biology</i> , 2022 , 2431, 181-206	1.4	1
343	Mapping the catalytic conformations of an assembly-line polyketide synthase module. <i>Science</i> , 2021 , 374, 729-734	33.3	8
342	Altered Cardiac Energetics and Mitochondrial Dysfunction in Hypertrophic Cardiomyopathy. <i>Circulation</i> , 2021 , 144, 1714-1731	16.7	11
341	Structural analyses of an RNA stability element interacting with poly(A). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	6
340	Structural and functional dissection of reovirus capsid folding and assembly by the prefoldin-TRiC/CCT chaperone network. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	4
339	RNA nanotechnology to build a dodecahedral genome of single-stranded RNA virus. <i>RNA Biology</i> , 2021 , 18, 2390-2400	4.8	4
338	REMBI: Recommended Metadata for Biological Images-enabling reuse of microscopy data in biology. <i>Nature Methods</i> , 2021 , 18, 1418-1422	21.6	16
337	Regulation of reversible conformational change, size switching, and immunomodulation of RNA nanocubes. <i>Rna</i> , 2021 , 27, 971-980	5.8	1
336	Explore the complexity of proteins with an expanded CryoET data processing pipeline. <i>Microscopy and Microanalysis</i> , 2021 , 27, 2816-2817	0.5	
335	CryoEM Map-Model Scores: From Average Density to Q-scores. <i>Microscopy and Microanalysis</i> , 2021 , 27, 1382-1384	0.5	
334	Cathode-Electrolyte Interphase in Lithium Batteries Revealed by Cryogenic Electron Microscopy. <i>Matter</i> , 2021 , 4, 302-312	12.7	57
333	Three-Dimensional Analysis of Particle Distribution on Filter Layers inside N95 Respirators by Deep Learning. <i>Nano Letters</i> , 2021 , 21, 651-657	11.5	23
332	The N-terminus of varicella-zoster virus glycoprotein B has a functional role in fusion. <i>PLoS Pathogens</i> , 2021 , 17, e1008961	7.6	4

331	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
330	Cryo-Electron Microscopy (CEM) Structures of Viruses 2021 , 233-241		
329	Evolution of standardization and dissemination of cryo-EM structures and data jointly by the community, PDB, and EMDB. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100560	5.4	4
328	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. <i>Nature Methods</i> , 2021 , 18, 156-164	21.6	22
327	Cryogenic Electron Microscopy for Energy Materials. <i>Accounts of Chemical Research</i> , 2021 , 54, 3505-351	724.3	9
326	Cryo-electron tomography provides topological insights into mutant huntingtin exon 1 and polyQ aggregates. <i>Communications Biology</i> , 2021 , 4, 849	6.7	1
325	Resolve cathode electrolyte interphase in lithium batteries with cryo-EM. <i>Microscopy and Microanalysis</i> , 2021 , 27, 2188-2190	0.5	
324	High Resolution Data Collection at S2C2, a National CryoEM Center. <i>Microscopy and Microanalysis</i> , 2021 , 27, 1152-1154	0.5	
323	Validation, analysis and annotation of cryo-EM structures. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021 , 77, 1142-1152	5.5	O
322	CryoEM reveals the stochastic nature of individual ATP binding events in a group II chaperonin. <i>Nature Communications</i> , 2021 , 12, 4754	17.4	1
321	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	17.6	23
320	Cryo-EM structures of full-length Tetrahymena ribozyme at 3.1 resolution. <i>Nature</i> , 2021 , 596, 603-607	50.4	16
319	Rapid prototyping of arbitrary 2D and 3D wireframe DNA origami. <i>Nucleic Acids Research</i> , 2021 , 49, 1020	65⊚1₁02	?7g 1
318	Target highlights in CASP14: Analysis of models by structure providers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021 , 89, 1647-1672	4.2	7
317	The N-terminus of varicella-zoster virus glycoprotein B has a functional role in fusion 2021 , 17, e100896	51	
316	The N-terminus of varicella-zoster virus glycoprotein B has a functional role in fusion 2021 , 17, e100896	51	
315	The N-terminus of varicella-zoster virus glycoprotein B has a functional role in fusion 2021 , 17, e100896	1	
314	The N-terminus of varicella-zoster virus glycoprotein B has a functional role in fusion 2021 , 17, e100896	1	

313	Sub-figstrfh-resolution MicroED Using a Direct Detection Camera. <i>Microscopy and Microanalysis</i> , 2020 , 26, 1524-1526	0.5	
312	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
311	Cryo-EM structures of NPC1L1 reveal mechanisms of cholesterol transport and ezetimibe inhibition. <i>Science Advances</i> , 2020 , 6, eabb1989	14.3	18
310	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
309	Accelerated cryo-EM-guided determination of three-dimensional RNA-only structures. <i>Nature Methods</i> , 2020 , 17, 699-707	21.6	46
308	Structure of the G protein chaperone and guanine nucleotide exchange factor Ric-8A bound to GIII. <i>Nature Communications</i> , 2020 , 11, 1077	17.4	5
307	Arrangement of the Polymerase Complexes inside a Nine-Segmented dsRNA Virus. <i>Structure</i> , 2020 , 28, 604-612.e3	5.2	4
306	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
305	Measurement of atom resolvability in cryo-EM maps with Q-scores. <i>Nature Methods</i> , 2020 , 17, 328-334	21.6	70
304	TrkA undergoes a tetramer-to-dimer conversion to open TrkH which enables changes in membrane potential. <i>Nature Communications</i> , 2020 , 11, 547	17.4	5
303	Cryogenic Correlative Single-Particle Photoluminescence Spectroscopy and Electron Tomography for Investigation of Nanomaterials. <i>Angewandte Chemie - International Edition</i> , 2020 , 59, 15642-15648	16.4	5
302	Evolving data standards for cryo-EM structures. Structural Dynamics, 2020, 7, 014701	3.2	16
301	Cryo-electron Microscopy and Exploratory Antisense Targeting of the 28-kDa Frameshift Stimulation Element from the SARS-CoV-2 RNA Genome 2020 ,		26
300	A single immunization with spike-functionalized ferritin vaccines elicits neutralizing antibody responses against SARS-CoV-2 in mice 2020 ,		14
299	Cryo-EM and MD infer water-mediated proton transport and autoinhibition mechanisms of V complex. <i>Science Advances</i> , 2020 , 6,	14.3	22
298	Full-length three-dimensional structure of the influenza A virus M1 protein and its organization into a matrix layer. <i>PLoS Biology</i> , 2020 , 18, e3000827	9.7	7
297	Cryogenic Correlative Single-Particle Photoluminescence Spectroscopy and Electron Tomography for Investigation of Nanomaterials. <i>Angewandte Chemie</i> , 2020 , 132, 15772-15778	3.6	O
296	Opportunities for Cryogenic Electron Microscopy in Materials Science and Nanoscience. <i>ACS Nano</i> , 2020 , 14, 9263-9276	16.7	26

295	Multi-scale 3D Cryo-Correlative Microscopy for Vitrified Cells. <i>Structure</i> , 2020 , 28, 1231-1237.e3	5.2	25
294	3D RNA nanocage for encapsulation and shielding of hydrophobic biomolecules to improve the biodistribution. <i>Nano Research</i> , 2020 , 13, 3241-3247	10	1
293	Unique cellular protrusions mediate breast cancer cell migration by tethering to osteogenic cells. <i>Npj Breast Cancer</i> , 2020 , 6, 42	7.8	6
292	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
291	A glycoprotein B-neutralizing antibody structure at 2.8 luncovers a critical domain for herpesvirus fusion initiation. <i>Nature Communications</i> , 2020 , 11, 4141	17.4	11
2 90	A 3.4-Eryo-electron microscopy structure of the human coronavirus spike trimer computationally derived from vitrified NL63 virus particles. <i>QRB Discovery</i> , 2020 , 1, e11	2.7	2
289	Resolving individual atoms of protein complex by cryo-electron microscopy. Cell Research, 2020, 30, 11	3 6 -41. 1 13	924
288	Inhibition mechanisms of AcrF9, AcrF8, and AcrF6 against type I-F CRISPR-Cas complex revealed by cryo-EM. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 71	76-758	2 ¹⁷
287	Full-length three-dimensional structure of the influenza A virus M1 protein and its organization into a matrix layer 2020 , 18, e3000827		
286	Full-length three-dimensional structure of the influenza A virus M1 protein and its organization into a matrix layer 2020 , 18, e3000827		
285	Full-length three-dimensional structure of the influenza A virus M1 protein and its organization into a matrix layer 2020 , 18, e3000827		
284	Full-length three-dimensional structure of the influenza A virus M1 protein and its organization into a matrix layer 2020 , 18, e3000827		
283	Cryo-EM Study of Chaperonin Mm-CpnB Conformational Heterogeneity under Different ATP Conditions. <i>Microscopy and Microanalysis</i> , 2019 , 25, 1006-1007	0.5	1
282	Unravelling Atomic Structure and Degradation Mechanisms of Organic-Inorganic Halide Perovskites by Cryo-EM. <i>Joule</i> , 2019 , 3, 2854-2866	27.8	69
281	Segmentation and Comparative Modeling in an 8.6-ICryo-EM Map of the Singapore Grouper Iridovirus. <i>Structure</i> , 2019 , 27, 1561-1569.e4	5.2	6
280	Cryo-EM structures of atomic surfaces and host-guest chemistry in metal-organic frameworks. <i>Matter</i> , 2019 , 1, 428-438	12.7	59
279	Cryo-EM structures of vacuolating cytotoxin A oligomeric assemblies at near-atomic resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 6800-6805	11.5	20
278	Coupling of ssRNA cleavage with DNase activity in type III-A CRISPR-Csm revealed by cryo-EM and biochemistry. <i>Cell Research</i> , 2019 , 29, 305-312	24.7	18

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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
Redox Engineering of Cytochrome c using DNA Nanostructure-Based Charged Encapsulation and Spatial Control. <i>ACS Applied Materials & Spatial Control (Nature of Action and Spatial Control of Action and Spatial Control of C</i>	9.5	17
Stanford-SLAC Cryo-EM Center (S2C2). Microscopy and Microanalysis, 2019, 25, 2658-2659	0.5	
Cryo-electron microscopy targets in CASP13: Overview and evaluation of results. <i>Proteins:</i> Structure, Function and Bioinformatics, 2019 , 87, 1128-1140	4.2	13
Structural basis of amino acid surveillance by higher-order tRNA-mRNA interactions. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 1094-1105	17.6	29
Cryo-EM structure of a 40lkDa SAM-IV riboswitch RNA at 3.7 lresolution. <i>Nature Communications</i> , 2019 , 10, 5511	17.4	48
Photo-controlled release of paclitaxel and model drugs from RNA pyramids. <i>Nano Research</i> , 2019 , 12, 41-48	10	24
Structure of Calcarisporiella thermophila Hsp104 Disaggregase that Antagonizes Diverse Proteotoxic Misfolding Events. <i>Structure</i> , 2019 , 27, 449-463.e7	5.2	22
Structures of TRPV2 in distinct conformations provide insight into role of the pore turret. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 40-49	17.6	30
Automated Sequence Design of 3D Polyhedral Wireframe DNA Origami with Honeycomb Edges. <i>ACS Nano</i> , 2019 , 13, 2083-2093	16.7	47
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
The 3.5-ICryoEM Structure of Nanodisc-Reconstituted Yeast Vacuolar ATPase V Proton Channel. <i>Molecular Cell</i> , 2018 , 69, 993-1004.e3	17.6	68
Structure of the 30lkDa 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
Evaluation system and web infrastructure for the second cryo-EM model challenge. <i>Journal of Structural Biology</i> , 2018 , 204, 96-108	3.4	9
The first single particle analysis Map Challenge: A summary of the assessments. <i>Journal of Structural Biology</i> , 2018 , 204, 291-300	3.4	11
Neutralizing Antibodies Inhibit Chikungunya Virus Budding at the Plasma Membrane. <i>Cell Host and Microbe</i> , 2018 , 24, 417-428.e5	23.4	33
	Essential for Cellular Proteostasis. <i>Cell</i> , 2019 , 177, 751-765.e15 Redox Engineering of Cytochrome c using DNA Nanostructure-Based Charged Encapsulation and Spatial Control. <i>ACS Applied Materials & amp; Interfaces</i> , 2019 , 11, 13874-13880 Stanford-SLAC Cryo-EM Center (S2C2). <i>Microscopy and Microanalysis</i> , 2019 , 25, 2658-2659 Cryo-electron microscopy targets in CASP13: Overview and evaluation of results. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 1128-1140 Structural basis of amino acid surveillance by higher-order tRNA-mRNA interactions. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 1094-1105 Cryo-EM structure of a 40lkDa SAM-IV riboswitch RNA at 3.7 (Fesolution. <i>Nature Communications</i> , 2019 , 10, 5511 Photo-controlled release of paclitaxel and model drugs from RNA pyramids. <i>Nano Research</i> , 2019 , 12, 41-48 Structure of Calcarisporiella thermophila Hsp104 Disaggregase that Antagonizes Diverse Proteotoxic Misfolding Events. <i>Structure</i> , 2019 , 27, 449-463.e7 Structures of TRPV2 in distinct conformations provide insight into role of the pore turret. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 40-49 Automated Sequence Design of 3D Polyhedral Wireframe DNA Origami with Honeycomb Edges. <i>ACS Nano</i> , 2019 , 13, 2083-2093 Electron Cryo-microscopy Structure of Ebola Virus Nucleoprotein Reveals a Mechanism for Nucleocapsid-like Assembly. <i>Cell</i> , 2018 , 172, 966-978.e12 The 3.5-ICryoEM Structure of Nanodisc-Reconstituted Yeast Vacuolar ATPase V Proton Channel. <i>Molecular Cell</i> , 2018 , 69, 993-1004.e3 Structure of the 30lkDa HIV-1 RNA Dimerization Signal by a Hybrid Cryo-EM, NMR, and Molecular Dynamics Approach. <i>Structure</i> , 2018 , 26, 490-498.e3 Evaluation system and web infrastructure for the second cryo-EM model challenge. <i>Journal of Structural Biology</i> , 2018 , 204, 96-108 The first single particle analysis Map Challenge: A summary of the assessments. <i>Journal of Structural Biology</i> , 2018 , 204, 99-300	Essential For Cellular Proteostasis. Cell, 2019, 177, 751-765.e15 Redox Engineering of Cytochrome c using DNA Nanostructure-Based Charged Encapsulation and Spatial Control. ACS Applied Materials & Amp; Interfaces, 2019, 11, 13874-13880 9.5 Stanford-SLAC Cryo-EM Center (S2C2). Microscopy and Microanalysis, 2019, 25, 2658-2659 0.5 Cryo-electron microscopy targets in CASP13: Overview and evaluation of results. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1128-1140 Structural basis of amino acid surveillance by higher-order tRNA-mRNA interactions. Nature Structural and Molecular Biology, 2019, 26, 1094-1105 Cryo-EM structure of a 40 kDa SAM-IV riboswitch RNA at 3.7 (Jesolution. Nature Communications, 2019, 10, 5511 7.4 Photo-controlled release of paclitaxel and model drugs from RNA pyramids. Nano Research, 2019, 12, 41-48 Structure of Calcarisporiella thermophila Hsp104 Disaggregase that Antagonizes Diverse Proteotoxic Misfolding Events. Structure, 2019, 27, 449-463.e7 5.2 Structures of TRPV2 in distinct conformations provide insight into role of the pore turret. Nature Structural and Molecular Biology, 2019, 26, 40-49 Automated Sequence Design of 31D Polyhedral Wireframe DNA Origami with Honeycomb Edges. ACS Nano, 2019, 13, 2083-2093 Electron Cryo-microscopy Structure of Ebola Virus Nucleoprotein Reveals a Mechanism for Nucleocapsid-like Assembly. Cell, 2018, 172, 966-978.e12 The 3.5-(CryoEM Structure of Nanodisc-Reconstituted Yeast Vacuolar ATPase V Proton Channel. Molecular Cell, 2018, 69, 993-1004.e3 Structure of the 30/kDa HIV-1 RNA Dimerization Signal by a Hybrid Cryo-EM, NMR, and Molecular Dynamics Approach. Structure, 2018, 26, 490-498.e3 Evaluation system and web infrastructure for the second cryo-EM model challenge. Journal of Structural Biology, 2018, 204, 96-108 The first single particle analysis Map Challenge: A summary of the assessments. Journal of Structural Biology, 2018, 204, 291-300 Neutralizing Antibodies Inhibit Chikungunya Virus Budding at the Plasma Membrane.

Visualizing Individual RuBisCO and Its Assembly into Carboxysomes in Marine Cyanobacteria by

Flagellum couples cell shape to motility in. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E5916-E5925

Cryo-Electron Tomography. Journal of Molecular Biology, 2018, 430, 4156-4167

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259	Purification of AcrAB-TolC Multidrug Efflux Pump for Cryo-EM Analysis. <i>Methods in Molecular Biology</i> , 2018 , 1700, 71-81	1.4	
258	Novel Insect-Specific Eilat Virus-Based Chimeric Vaccine Candidates Provide Durable, Mono- and Multivalent, Single-Dose Protection against Lethal Alphavirus Challenge. <i>Journal of Virology</i> , 2018 , 92,	6.6	25
257	Distribution of evaluation scores for the models submitted to the second cryo-EM model challenge. <i>Data in Brief</i> , 2018 , 20, 1629-1638	1.2	4
256	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
255	GENFIRE: from Precisely Localizing Single Atoms in Materials to High Resolution 3D Imaging of Cellular Structures. <i>Microscopy and Microanalysis</i> , 2018 , 24, 1446-1447	0.5	
254	Programming molecular topologies from single-stranded nucleic acids. <i>Nature Communications</i> , 2018 , 9, 4579	17.4	29
253	Assessment of structural features in Cryo-EM density maps using SSE and side chain Z-scores. Journal of Structural Biology, 2018 , 204, 564-571	3.4	17
252	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
251	Visualizing Adsorption of Cyanophage P-SSP7 onto Marine Prochlorococcus. <i>Scientific Reports</i> , 2017 , 7, 44176	4.9	15
250	SuRVoS: Super-Region Volume Segmentation workbench. <i>Journal of Structural Biology</i> , 2017 , 198, 43-53	33.4	47
249	A chikungunya fever vaccine utilizing an insect-specific virus platform. <i>Nature Medicine</i> , 2017 , 23, 192-19	99 0.5	71
248	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
247	Programmable Supra-Assembly of a DNA Surface Adapter for Tunable Chiral Directional Self-Assembly of Gold Nanorods. <i>Angewandte Chemie</i> , 2017 , 129, 14824-14828	3.6	12
246	Responses to Atomic resolutionPa badly abused term in structural biology. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017 , 73, 381-383	5.5	5
245	Structural and Functional Impacts of ER Coactivator Sequential Recruitment. <i>Molecular Cell</i> , 2017 , 67, 733-743.e4	17.6	45
244	Convolutional neural networks for automated annotation of cellular cryo-electron tomograms. <i>Nature Methods</i> , 2017 , 14, 983-985	21.6	155
243	GENFIRE: A generalized Fourier iterative reconstruction algorithm for high-resolution 3D imaging. <i>Scientific Reports</i> , 2017 , 7, 10409	4.9	49
242	Subunit conformational variation within individual GroEL oligomers resolved by Cryo-EM. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 8259-8264	11.5	49

241	Electron Cryomicroscopy of Viruses at Near-Atomic Resolutions. <i>Annual Review of Virology</i> , 2017 , 4, 28	7-340.8	14
240	Influence of DNA sequence on the structure of minicircles under torsional stress. <i>Nucleic Acids Research</i> , 2017 , 45, 7633-7642	20.1	23
239	Going Deeper in Cryo Electron Tomography with Neural Networks. <i>Microscopy and Microanalysis</i> , 2017 , 23, 814-815	0.5	
238	An allosteric transport mechanism for the AcrAB-TolC multidrug efflux pump. <i>ELife</i> , 2017 , 6,	8.9	121
237	Organelle changes in a Huntington® disease model using cryogenic soft x-ray tomography 2016 , 284-28	85	
236	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
235	Chaperonin TRiC/CCT Recognizes Fusion Oncoprotein AML1-ETO through Subunit-Specific Interactions. <i>Biophysical Journal</i> , 2016 , 110, 2377-2385	2.9	8
234	Resolution and Probabilistic Models of Components in CryoEM Maps of Mature P22 Bacteriophage. <i>Biophysical Journal</i> , 2016 , 110, 827-39	2.9	28
233	EMDataBank unified data resource for 3DEM. <i>Nucleic Acids Research</i> , 2016 , 44, D396-403	20.1	113
232	The Electron Microscopy eXchange (EMX) initiative. <i>Journal of Structural Biology</i> , 2016 , 194, 156-63	3.4	11
231	Computational Tools to Improve Visualization by Cryo-Electron Tomography. <i>Biophysical Journal</i> , 2016 , 110, 159a	2.9	2
230	Chaperonin TRiC/CCT Modulates the Folding and Activity of Leukemogenic Fusion Oncoprotein AML1-ETO. <i>Journal of Biological Chemistry</i> , 2016 , 291, 4732-41	5.4	19
229	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
228	Controllable Self-Assembly of RNA Tetrahedrons with Precise Shape and Size for Cancer Targeting. <i>Advanced Materials</i> , 2016 , 28, 7501-7	24	51
227	Quantifying Variability of Manual Annotation in Cryo-Electron Tomograms. <i>Microscopy and Microanalysis</i> , 2016 , 22, 487-96	0.5	14
226	Designer nanoscale DNA assemblies programmed from the top down. <i>Science</i> , 2016 , 352, 1534	33.3	370
225	Alignment algorithms and per-particle CTF correction for single particle cryo-electron tomography. Journal of Structural Biology, 2016 , 194, 383-94	3.4	35
224	TRiC subunits enhance BDNF axonal transport and rescue striatal atrophy in Huntingtonß disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E5655-64	11.5	53

(2015-2016)

223	Visualizing red blood cell sickling and the effects of inhibition of sphingosine kinase 1 using soft X-ray tomography. <i>Journal of Cell Science</i> , 2016 , 129, 3511-7	5.3	16
222	Structure of a biologically active estrogen receptor-coactivator complex on DNA. <i>Molecular Cell</i> , 2015 , 57, 1047-1058	17.6	103
221	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
220	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
219	Structural Mechanisms of Mutant Huntingtin Aggregation Suppression by the Synthetic Chaperonin-like CCT5 Complex Explained by Cryoelectron Tomography. <i>Journal of Biological Chemistry</i> , 2015 , 290, 17451-61	5.4	25
218	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015 , 23, 1156-67	5.2	131
217	CTF Challenge: Result summary. Journal of Structural Biology, 2015, 190, 348-59	3.4	29
216	Gating machinery of InsP3R channels revealed by electron cryomicroscopy. <i>Nature</i> , 2015 , 527, 336-41	50.4	159
215	Structural diversity of supercoiled DNA. <i>Nature Communications</i> , 2015 , 6, 8440	17.4	89
214	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
213	The pseudo-atomic structure of an RND-type tripartite multidrug efflux pump. <i>Biological Chemistry</i> , 2015 , 396, 1073-82	4.5	7
212	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
211	Contribution of the Type II Chaperonin, TRiC/CCT, to Oncogenesis. <i>International Journal of Molecular Sciences</i> , 2015 , 16, 26706-20	6.3	46
210	Modeling Protein Structure in Macromolecular Assemblies at Near Atomic Resolutions. <i>Microscopy and Microanalysis</i> , 2015 , 21, 541-542	0.5	
209	IP3R1 - Assessing Map Interpretability at Near Atomic Resolution. <i>Microscopy and Microanalysis</i> , 2015 , 21, 543-544	0.5	
208	Zernike Phase Plate Configuration at Intermediate Lens Position on JEM2200FS. <i>Microscopy and Microanalysis</i> , 2015 , 21, 2143-2144	0.5	O
207	Optimization of JEM2200FS for Zernike Phase Contrast Cryo-EM. <i>Microscopy and Microanalysis</i> , 2015 , 21, 1577-1578	0.5	0
206	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, 1426	56 ⁻ 7 ⁻ 7	41

205	Structure of the AcrAB-TolC multidrug efflux pump. <i>Nature</i> , 2014 , 509, 512-5	50.4	401
204	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
203	Crystal structure of a nematode-infecting virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 12781-6	11.5	21
202	Multifunctional RNA nanoparticles. <i>Nano Letters</i> , 2014 , 14, 5662-71	11.5	136
201	Chaperonin-containing TCP-1 complex directly binds to the cytoplasmic domain of the LOX-1 receptor. <i>FEBS Letters</i> , 2014 , 588, 2133-40	3.8	11
200	Visualizing Virus Assembly Intermediates Inside Marine Cyanobacteria by Zernike Phase Contrast Electron Cryo-Tomography. <i>Microscopy and Microanalysis</i> , 2014 , 20, 202-203	0.5	1
199	Seeing the Portal in Membrane-containing Bacteriophage PRD1 by Cryo-EM. <i>Microscopy and Microanalysis</i> , 2014 , 20, 1250-1251	0.5	
198	Modulation of STAT3 folding and function by TRiC/CCT chaperonin. <i>PLoS Biology</i> , 2014 , 12, e1001844	9.7	55
197	A structural model of the genome packaging process in a membrane-containing double stranded DNA virus. <i>PLoS Biology</i> , 2014 , 12, e1002024	9.7	31
196	An atomic model of brome mosaic virus using direct electron detection and real-space optimization. <i>Nature Communications</i> , 2014 , 5, 4808	17.4	95
195	A 3D cellular context for the macromolecular world. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 841-5	17.6	33
194	Protruding knob-like proteins violate local symmetries in an icosahedral marine virus. <i>Nature Communications</i> , 2014 , 5, 4278	17.4	12
193	Zernike phase-contrast electron cryotomography applied to marine cyanobacteria infected with cyanophages. <i>Nature Protocols</i> , 2014 , 9, 2630-42	18.8	20
192	Preparation of primary neurons for visualizing neurites in a frozen-hydrated state using cryo-electron tomography. <i>Journal of Visualized Experiments</i> , 2014 , e50783	1.6	5
191	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
190	Identifying the assembly pathway of cyanophage inside the marine bacterium using electron cryo-tomography. <i>Microbial Cell</i> , 2014 , 1, 45-47	3.9	5
189	Cryo-EM structure of a molluscan hemocyanin suggests its allosteric mechanism. <i>Structure</i> , 2013 , 21, 604-13	5.2	27
188	Visualizing virus assembly intermediates inside marine cyanobacteria. <i>Nature</i> , 2013 , 502, 707-10	50.4	96

(2012-2013)

187	Reprogramming an ATP-driven protein machine into a light-gated nanocage. <i>Nature Nanotechnology</i> , 2013 , 8, 928-32	28.7	44
186	Validation of cryo-EM structure of IP R 1 channel. <i>Structure</i> , 2013 , 21, 900-9	5.2	40
185	Cryo-EM model validation using independent map reconstructions. <i>Protein Science</i> , 2013 , 22, 865-8	6.3	64
184	Visualizing GroEL/ES in the act of encapsulating a folding protein. <i>Cell</i> , 2013 , 153, 1354-65	56.2	76
183	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
182	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
181	EMEN2: an object oriented database and electronic lab notebook. <i>Microscopy and Microanalysis</i> , 2013 , 19, 1-10	0.5	43
180	TRiCB tricks inhibit huntingtin aggregation. <i>ELife</i> , 2013 , 2, e00710	8.9	58
179	Constructing and validating initial Clmodels from subnanometer resolution density maps with pathwalking. <i>Structure</i> , 2012 , 20, 450-63	5.2	28
178	The molecular architecture of the eukaryotic chaperonin TRiC/CCT. Structure, 2012, 20, 814-25	5.2	216
177	Three-dimensional architecture of the rod sensory cilium and its disruption in retinal neurodegeneration. <i>Cell</i> , 2012 , 151, 1029-41	56.2	122
176	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
175	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
174	Supramolecular non-amyloid intermediates in the early stages of Esynuclein aggregation. <i>Biophysical Journal</i> , 2012 , 102, 1127-36	2.9	27
173	Gorgon and pathwalking: macromolecular modeling tools for subnanometer resolution density maps. <i>Biopolymers</i> , 2012 , 97, 655-68	2.2	38
172	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
171	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
170	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

169	Paraneoplastic thrombocytosis in ovarian cancer. New England Journal of Medicine, 2012, 366, 610-8	59.2	505
168	Near-atomic-resolution cryo-EM for molecular virology. Current Opinion in Virology, 2011, 1, 110-7	7.5	40
167	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
166	Interbilayer-crosslinked multilamellar vesicles as synthetic vaccines for potent humoral and cellular immune responses. <i>Nature Materials</i> , 2011 , 10, 243-51	27	426
165	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
164	Flexible architecture of IP3R1 by Cryo-EM. <i>Structure</i> , 2011 , 19, 1192-9	5.2	70
163	The group II chaperonin Mm-Cpn binds and refolds human D crystallin. <i>Protein Science</i> , 2011 , 20, 30-41	6.3	11
162	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
161	EMDataBank.org: unified data resource for CryoEM. <i>Nucleic Acids Research</i> , 2011 , 39, D456-64	20.1	209
160	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
159	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
158	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
157	4.4 ©ryo-EM structure of an enveloped alphavirus Venezuelan equine encephalitis virus. <i>EMBO Journal</i> , 2011 , 30, 3854-63	13	133
156	Structural changes in a marine podovirus associated with release of its genome into Prochlorococcus. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 830-6	17.6	121
155	Mechanism of folding chamber closure in a group II chaperonin. <i>Nature</i> , 2010 , 463, 379-83	50.4	180
154	Cryo-EM of macromolecular assemblies at near-atomic resolution. <i>Nature Protocols</i> , 2010 , 5, 1697-708	18.8	74
153	4.0-A 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
152	Automated specimen search in cryo-TEM observation with DIFF-defocus imaging. <i>Journal of Electron Microscopy</i> , 2010 , 59, 299-310		10

(2008-2010)

151	Discrete structure of an RNA folding intermediate revealed by cryo-electron microscopy. <i>Journal of the American Chemical Society</i> , 2010 , 132, 16352-3	16.4	26
150	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
149	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
148	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
147	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
146	A Unique BSL-3 Cryo-Electron Microscopy Laboratory at UTMB. <i>Applied Biosafety</i> , 2010 , 15, 130-136	1.3	3
145	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
144	4.0 [Resolution Cryo-EM Structure of the Mammalian Chaperonin TRiC/CCT Reveals its Unique Subunit Arrangement. <i>FASEB Journal</i> , 2010 , 24, 684.5	0.9	
143	Interprotofilament interactions between Alzheimerß Abeta1-42 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
142	Structural mechanism of SDS-induced enzyme activity of scorpion hemocyanin revealed by electron cryomicroscopy. <i>Structure</i> , 2009 , 17, 749-58	5.2	56
141	Refinement of protein structures into low-resolution density maps using rosetta. <i>Journal of Molecular Biology</i> , 2009 , 392, 181-90	6.5	230
140	Effects of bilayer phases on phospholipid-poloxamer interactions. Soft Matter, 2009, 5, 1496	3.6	30
139	Conformational Changes of Eukaryotic Chaperonin TRiC/CCT in the Nucleotide Cycle Revealed by CryoEM. <i>FASEB Journal</i> , 2009 , 23, 850.12	0.9	
138	Rocking Motion of the Equatorial Domains of a Group II Chaperonin between Two Biochemical States Revealed by Single-Particle Cryo-EM at Near-atomic and Subnanometer Resolutions. <i>FASEB Journal</i> , 2009 , 23, 673.12	0.9	
137	Backbone structure of the infectious epsilon15 virus capsid revealed by electron cryomicroscopy. <i>Nature</i> , 2008 , 451, 1130-4	50.4	188
136	Mechanism of lid closure in the eukaryotic chaperonin TRiC/CCT. <i>Nature Structural and Molecular Biology</i> , 2008 , 15, 746-53	17.6	75
135	Protein structure fitting and refinement guided by cryo-EM density. <i>Structure</i> , 2008 , 16, 295-307	5.2	266
134	De novo backbone trace of GroEL from single particle electron cryomicroscopy. <i>Structure</i> , 2008 , 16, 44	1-8.2	153

133	Crystallographic conformers of actin in a biologically active bundle of filaments. <i>Journal of Molecular Biology</i> , 2008 , 375, 331-6	6.5	32
132	Location and flexibility of the unique C-terminal tail of Aquifex aeolicus co-chaperonin protein 10 as derived by cryo-electron microscopy and biophysical techniques. <i>Journal of Molecular Biology</i> , 2008 , 381, 707-17	6.5	13
131	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
130	Segmentation-free skeletonization of grayscale volumes for shape understanding 2008,		21
129	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
128	Learning-based segmentation framework for tissue images containing gene expression data. <i>IEEE Transactions on Medical Imaging</i> , 2007 , 26, 728-44	11.7	19
127	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
126	Modular software platform for low-dose electron microscopy and tomography. <i>Journal of Microscopy</i> , 2007 , 228, 384-9	1.9	10
125	Identification of secondary structure elements in intermediate-resolution density maps. <i>Structure</i> , 2007 , 15, 7-19	5.2	152
124	Electron cryotomography reveals the portal in the herpesvirus capsid. <i>Journal of Virology</i> , 2007 , 81, 200	55 6 86	75
123	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
122	Single-particle electron cryomicroscopy of the ion channels in the excitation-contraction coupling junction. <i>Methods in Cell Biology</i> , 2007 , 79, 407-35	1.8	10
121	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
120	Outcome of a workshop on archiving structural models of biological macromolecules. <i>Structure</i> , 2006 , 14, 1211-7	5.2	49
119	An expanded conformation of single-ring GroEL-GroES complex encapsulates an 86 kDa substrate. <i>Structure</i> , 2006 , 14, 1711-22	5.2	56
118	Structural biology of cellular machines. <i>Trends in Cell Biology</i> , 2006 , 16, 144-50	18.3	42
117	Ab initio modeling of the herpesvirus VP26 core domain assessed by CryoEM density. <i>PLoS Computational Biology</i> , 2006 , 2, e146	5	46
116	Cryoelectron microscopy of protein IX-modified adenoviruses suggests a new position for the C terminus of protein IX. <i>Journal of Virology</i> , 2006 , 80, 11881-6	6.6	30

(2004-2006)

115	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
114	Structure of Halothiobacillus neapolitanus carboxysomes by cryo-electron tomography. <i>Journal of Molecular Biology</i> , 2006 , 364, 526-35	6.5	121
113	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
112	Structure of epsilon15 bacteriophage reveals genome organization and DNA packaging/injection apparatus. <i>Nature</i> , 2006 , 439, 612-6	50.4	258
111	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
110	Common ancestry of herpesviruses and tailed DNA bacteriophages. <i>Journal of Virology</i> , 2005 , 79, 14967	'-B.G	229
109	Structure of Ca2+ release channel at 14 A resolution. <i>Journal of Molecular Biology</i> , 2005 , 345, 427-31	6.5	65
108	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
107	Superparamagnetic gadonanotubes are high-performance MRI contrast agents. <i>Chemical Communications</i> , 2005 , 3915-7	5.8	279
106	Electron cryomicroscopy of biological machines at subnanometer resolution. Structure, 2005, 13, 363-77	25.2	129
105	Macromolecular Assemblies Highlighted. <i>Structure</i> , 2005 , 13, 339-341	5.2	5
104	The pore structure of the closed RyR1 channel. <i>Structure</i> , 2005 , 13, 1203-11	5.2	129
103	Building 3D surface networks from 2D curve networks with application to anatomical modeling. <i>Visual Computer</i> , 2005 , 21, 764-773	2.3	22
102	A digital atlas to characterize the mouse brain transcriptome. <i>PLoS Computational Biology</i> , 2005 , 1, e41	5	49
101	The 3-Dimensional Architecture of Platelets in the Native State by Electron Cryotomography <i>Blood</i> , 2005 , 106, 1658-1658	2.2	1
100	A Digital Atlas to Characterize the Mouse Brain Transcriptome. <i>PLoS Computational Biology</i> , 2005 , preprint, e41	5	
99	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
98	Structure of the bifunctional and Golgi-associated formiminotransferase cyclodeaminase octamer. <i>EMBO Journal</i> , 2004 , 23, 2963-71	13	22

97	Structure of the acrosomal bundle. <i>Nature</i> , 2004 , 431, 104-7	50.4	72
96	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
95	Seeing GroEL at 6 A resolution by single particle electron cryomicroscopy. Structure, 2004 , 12, 1129-36	5.2	169
94	Cryo-EM and Mass Spectrometry Based Investigations of Viral Capsid Morphogenesis. <i>Microscopy and Microanalysis</i> , 2004 , 10, 226-227	0.5	
93	GroEL Structure at 6 IResolution Using Electron Cryomicroscopy and EMAN. <i>Microscopy and Microanalysis</i> , 2004 , 10, 1494-1495	0.5	
92	Subnanometer Imaging of Spherical Viruses in a JEOL3000 SFF Liquid Helium Electron Cryomicroscope. <i>Microscopy and Microanalysis</i> , 2004 , 10, 1504-1505	0.5	
91	Structure of the type 1 inositol 1,4,5-trisphosphate receptor revealed by electron cryomicroscopy. Journal of Biological Chemistry, 2003 , 278, 21319-22	5.4	81
90	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
89	Determination of icosahedral virus structures by electron cryomicroscopy at subnanometer resolution. <i>Advances in Protein Chemistry</i> , 2003 , 64, 93-124		35
88	Studying large viruses. Advances in Protein Chemistry, 2003 , 64, 379-408		9
87	Imaging Ice Embedded Single Particles With A 16 Megapixel CCD Camera. <i>Microscopy and Microanalysis</i> , 2003 , 9, 962-963	0.5	
86	High-Resolution 3D Reconstruction of Cytoplasmic Polyhedrosis Virus. <i>Microscopy and Microanalysis</i> , 2003 , 9, 1366-1367	0.5	
85	Structure of the herpesvirus major capsid protein. EMBO Journal, 2003, 22, 757-65	13	75
84	Coat protein fold and maturation transition of bacteriophage P22 seen at subnanometer resolutions. <i>Nature Structural Biology</i> , 2003 , 10, 131-5		176
83	Architecture of the herpes simplex virus major capsid protein derived from structural bioinformatics. <i>Journal of Molecular Biology</i> , 2003 , 331, 447-56	6.5	27
82	The structure of ClpB: a molecular chaperone that rescues proteins from an aggregated state. <i>Cell</i> , 2003 , 115, 229-40	56.2	366
81	Structure of isolated nucleocapsids from venezuelan equine encephalitis virus and implications for assembly and disassembly of enveloped virus. <i>Journal of Virology</i> , 2003 , 77, 659-64	6.6	26
80	Merging Focal Pairs for Improved Particle Selection and Orientation Determination. <i>Microscopy and Microanalysis</i> , 2002 , 8, 216-217	0.5	

(2000-2002)

79	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
78	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
77	The skeletal muscle Ca2+ 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
76	Bilamellar cationic liposomes protect adenovectors from preexisting humoral immune responses. <i>Molecular Therapy</i> , 2002 , 5, 233-41	11.7	102
75	Electron cryo-microscopy of VAT, the archaeal p97/CDC48 homologue from Thermoplasma acidophilum. <i>Journal of Molecular Biology</i> , 2002 , 317, 673-81	6.5	31
74	High resolution structural studies of complex icosahedral viruses: a brief overview. <i>Virus Research</i> , 2002 , 82, 9-17	6.4	13
73	Electron Cryomicroscopy and Three-dimensional Computer Reconstruction of Biological Molecules 2001 ,		1
72	Web-based Simulation for Contrast Transfer Function and Envelope Functions. <i>Microscopy and Microanalysis</i> , 2001 , 7, 329-334	0.5	2
71	Intrinsically disordered protein. Journal of Molecular Graphics and Modelling, 2001, 19, 26-59	2.8	1747
70	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
69	Venezuelan equine encephalomyelitis virus structure and its divergence from old world alphaviruses. <i>Journal of Virology</i> , 2001 , 75, 9532-7	6.6	30
68	Web-based Simulation for Contrast Transfer Function and Envelope Functions. <i>Microscopy and Microanalysis</i> , 2001 , 7, 329-334	0.5	5
67	Bridging the information gap: computational tools for intermediate resolution structure interpretation. <i>Journal of Molecular Biology</i> , 2001 , 308, 1033-44	6.5	250
66	Finding and using local symmetry in identifying lower domain movements in hexon subunits of the herpes simplex virus type 1 B capsid. <i>Journal of Molecular Biology</i> , 2001 , 309, 903-14	6.5	17
65	A 11.5 A single particle reconstruction of GroEL using EMAN. <i>Journal of Molecular Biology</i> , 2001 , 314, 253-62	6.5	114
64	Electron cryomicroscopy and bioinformatics suggest protein fold models for rice dwarf virus. Nature Structural Biology, 2001 , 8, 868-73		113
63	Web-based Simulation for Contrast Transfer Function and Envelope Functions. <i>Microscopy and Microanalysis</i> , 2001 , 7, 329-334	0.5	2
62	Electron Crystallographic Structure of the Limulus Acrosomal Bundle at 20 「Resolution. <i>Microscopy and Microanalysis</i> , 2000 , 6, 242-243	0.5	_

61	Macromolecular Structure Visualization Tools at NCMI. <i>Microscopy and Microanalysis</i> , 2000 , 6, 282-283	0.5	7
60	Estimates of the Fourier Amplitude Decay of Electron Micrographs of Single Particles. <i>Microscopy and Microanalysis</i> , 2000 , 6, 256-257	0.5	
59	Identification of additional coat-scaffolding interactions in a bacteriophage P22 mutant defective in maturation. <i>Journal of Virology</i> , 2000 , 74, 3871-3	6.6	23
58	Visualization of the maturation transition in bacteriophage P22 by electron cryomicroscopy. Journal of Molecular Biology, 2000 , 297, 615-26	6.5	62
57	Seeing the herpesvirus capsid at 8.5 A. <i>Science</i> , 2000 , 288, 877-80	33.3	269
56	400 Kv Electron Cryo-Microscopic Imaging Of Large Icosahedral Viruses Towards Atomic Resolution. <i>Microscopy and Microanalysis</i> , 1999 , 5, 186-187	0.5	
55	Solution x-ray scattering-based estimation of electron cryomicroscopy imaging parameters for reconstruction of virus particles. <i>Biophysical Journal</i> , 1999 , 76, 2249-61	2.9	32
54	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
53	ADF/cofilin weakens lateral contacts in the actin filament. Journal of Molecular Biology, 1999, 291, 513-	96.5	79
52	The three-dimensional structure of the Limulus acrosomal process: a dynamic actin bundle. <i>Journal of Molecular Biology</i> , 1999 , 294, 139-49	6.5	27
51	Visualization of tegument-capsid interactions and DNA in intact herpes simplex virus type 1 virions. Journal of Virology, 1999 , 73, 3210-8	6.6	208
50	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
49	Evaluation of charging on macromolecules in electron cryomicroscopy. <i>Ultramicroscopy</i> , 1998 , 72, 41-52	2 3.1	61
48	Multivariate analysis of single unit cells in electron crystallography. <i>Ultramicroscopy</i> , 1998 , 74, 179-99	3.1	21
47	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
46	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
45	Electron crystallographic analysis of two-dimensional streptavidin crystals coordinated to metal-chelated lipid monolayers. <i>Biophysical Journal</i> , 1998 , 74, 2674-9	2.9	17
44	Structure of double-shelled rice dwarf virus. <i>Journal of Virology</i> , 1998 , 72, 8541-9	6.6	48

43	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
42	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
41	Electron crystallography of macromolecular periodic arrays on phospholipid monolayers. <i>Advances in Biophysics</i> , 1997 , 34, 161-72		29
40	Improved common line-based icosahedral particle image orientation estimation algorithms. <i>Ultramicroscopy</i> , 1997 , 68, 231-55	3.1	32
39	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
38	Two structural configurations of the skeletal muscle calcium release channel. <i>Nature Structural and Molecular Biology</i> , 1996 , 3, 547-52	17.6	136
37	Electron cryomicroscopy and angular reconstitution used to visualize the skeletal muscle calcium release channel. <i>Nature Structural Biology</i> , 1995 , 2, 18-24		165
36	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
35	Electron cryomicroscopy of Bacillus stearothermophilus 50 S ribosomal subunits crystallized on phospholipid monolayers. <i>Journal of Molecular Biology</i> , 1994 , 239, 689-97	6.5	31
34	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
33	Imaging frozen, hydrated acrosomal bundle from Limulus sperm at 7 A resolution with a 400 kV electron cryomicroscope. <i>Journal of Molecular Biology</i> , 1993 , 230, 384-6	6.5	17
32	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
31	Low-dose thickness measurement of glucose-embedded protein crystals by electron energy loss spectroscopy and STEM dark-field imaging. <i>Ultramicroscopy</i> , 1993 , 52, 157-66	3.1	3
30	Flopping polypeptide chains and Suleikaß subtle imperfections: analysis of variations in the electron micrograph of a purple membrane crystal. <i>Ultramicroscopy</i> , 1993 , 49, 387-96	3.1	12
29	Prospects for using an IVEM with a FEG for imaging macromolecules towards atomic resolution. <i>Ultramicroscopy</i> , 1993 , 49, 407-16	3.1	49
28	Electron crystallography of macromolecules. Current Opinion in Biotechnology, 1993, 4, 397-402	11.4	4
27	Computer-controlled spot-scan imaging of crotoxin complex crystals with 400 keV electrons at near-atomic resolution. <i>Ultramicroscopy</i> , 1992 , 46, 229-40	3.1	27
26	The thickness determination of organic crystals under low dose conditions using electron energy loss spectroscopy. <i>Microscopy Research and Technique</i> , 1992 , 21, 166-70	2.8	8

25	Analysis of symmetry and three-dimensional reconstruction of thin gp32*I crystals. <i>Journal of Molecular Biology</i> , 1991 , 217, 551-62	6.5	12
24	Three-dimensional structure of the HSV1 nucleocapsid. <i>Cell</i> , 1989 , 56, 651-60	56.2	124
23	Containment system for the preparation of vitrified-hydrated virus specimens. <i>Journal of Electron Microscopy Technique</i> , 1988 , 8, 343-8		15
22	The characterization of structural variations within a crystal field. <i>Ultramicroscopy</i> , 1988 , 26, 345-60	3.1	31
21	Cryo electron microscopy of unstained, unfixed RecA-cssDNA complexes. <i>Journal of Structural Biology</i> , 1988 , 100, 166-72		21
20	Three-dimensional structural analysis of tetanus toxin by electron crystallography. <i>Journal of Molecular Biology</i> , 1988 , 200, 367-75	6.5	59
19	Three-dimensional structure of rotavirus. <i>Journal of Molecular Biology</i> , 1988 , 199, 269-75	6.5	292
18	High resolution cryo system designed for JEM 100CX electron microscope. <i>Ultramicroscopy</i> , 1987 , 23, 61-6	3.1	10
17	Potential for high-resolution electron crystallography at intermediate high voltage. <i>Annals of the New York Academy of Sciences</i> , 1986 , 483, 149-56	6.5	7
16	Specimen preparative methods for electron crystallography of soluble proteins. <i>Ultramicroscopy</i> , 1984 , 13, 19-25	3.1	8
15	Experimental strategy in three-dimensional structure determination of crotoxin complex thin crystal. <i>Ultramicroscopy</i> , 1984 , 13, 27-34	3.1	5
14	Estimates of validity of projection approximation for three-dimensional reconstructions at high resolution. <i>Ultramicroscopy</i> , 1984 , 14, 219-26	3.1	36
13	Electron imaging of crotoxin complex thin crystal at 3.5 A. Journal of Molecular Biology, 1984, 175, 93-7	6.5	40
12	Quantitative assessment of radiation damage in a thin protein crystal. <i>Journal of Microscopy</i> , 1984 , 136, 35-44	1.9	30
11	Low dose electron microscopy of the crotoxin complex thin crystal. <i>Journal of Molecular Biology</i> , 1983 , 164, 329-46	6.5	44
10	Perspectives and outlook for electron microscopy in biology in general. <i>Ultramicroscopy</i> , 1982 , 10, 165-	73.1	5
9	Effect of stray magnetic field on image resolution in transmission electron microscopy. <i>Ultramicroscopy</i> , 1980 , 5, 351-356	3.1	10
8	Structure of the surface layer protein of the outer membrane of Spirillum serpens. <i>Journal of Ultrastructure Research</i> , 1979 , 66, 235-42		31

LIST OF PUBLICATIONS

7	Crystallization of preliminary electron diffraction study to 3.7 A of DNA helix-destabilizing protein gp32*I. <i>Journal of Molecular Biology</i> , 1978 , 122, 103-7	24	
6	Single atom image contrast: conventional dark-field and bright-field electron microscopy. <i>Journal of Microscopy</i> , 1975 , 103, 33-54	15	
5	The N-terminus of varicella-zoster virus glycoprotein B has a functional role in fusion	1	
4	Multi-Scale 3D Cryo-Correlative Microscopy for Vitrified Cells	2	
3	Resolving Individual-Atom of Protein Complex using Commonly Available 300-kV Cryo-electron Microscopes	2	
2	Topological Insights into Mutant Huntingtin Exon 1 and PolyQ Aggregates by Cryo-Electron Tomography	1	
1	Electron Cryomicroscopy of Molecular Nanomachines and Cells89	1	