

Bridget Carragher

List of Publications by Year in descending order

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Version: 2024-02-01

202
papers

17,494
citations

20817

60
h-index

17105

122
g-index

228
all docs

228
docs citations

228
times ranked

16642
citing authors

#	ARTICLE	IF	CITATIONS
1	Automated molecular microscopy: The new Legion system. <i>Journal of Structural Biology</i> , 2005, 151, 41-60.	2.8	1,608
2	Appion: An integrated, database-driven pipeline to facilitate EM image processing. <i>Journal of Structural Biology</i> , 2009, 166, 95-102.	2.8	848
3	A structural change in the kinesin motor protein that drives motility. <i>Nature</i> , 1999, 402, 778-784.	27.8	745
4	Addressing preferred specimen orientation in single-particle cryo-EM through tilting. <i>Nature Methods</i> , 2017, 14, 793-796.	19.0	708
5	Crystal structure of rhodopsin bound to arrestin by femtosecond X-ray laser. <i>Nature</i> , 2015, 523, 561-567.	27.8	683
6	Cryo-EM Structure of a Fully Glycosylated Soluble Cleaved HIV-1 Envelope Trimer. <i>Science</i> , 2013, 342, 1484-1490.	12.6	662
7	Myosin VI is an actin-based motor that moves backwards. <i>Nature</i> , 1999, 401, 505-508.	27.8	643
8	DoG Picker and TiltPicker: Software tools to facilitate particle selection in single particle electron microscopy. <i>Journal of Structural Biology</i> , 2009, 166, 205-213.	2.8	569
9	Architecture and design of the nuclear pore complex. <i>Cell</i> , 1992, 69, 1133-1141.	28.9	451
10	Beam-induced motion of vitrified specimen on holey carbon film. <i>Journal of Structural Biology</i> , 2012, 177, 630-637.	2.8	366
11	Legion: An Automated System for Acquisition of Images from Vitreous Ice Specimens. <i>Journal of Structural Biology</i> , 2000, 132, 33-45.	2.8	310
12	Structure of the Sec13/31 COPII coat cage. <i>Nature</i> , 2006, 439, 234-238.	27.8	286
13	Movies of Ice-Embedded Particles Enhance Resolution in Electron Cryo-Microscopy. <i>Structure</i> , 2012, 20, 1823-1828.	3.3	277
14	The Structure of an Infectious P22 Virion Shows the Signal for Headful DNA Packaging. <i>Science</i> , 2006, 312, 1791-1795.	12.6	276
15	Epitope-based vaccine design yields fusion peptide-directed antibodies that neutralize diverse strains of HIV-1. <i>Nature Medicine</i> , 2018, 24, 857-867.	30.7	256
16	Structural Basis for Cargo Regulation of COPII Coat Assembly. <i>Cell</i> , 2008, 134, 474-484.	28.9	242
17	Routine single particle CryoEM sample and grid characterization by tomography. <i>ELife</i> , 2018, 7, .	6.0	216
18	Organization of the Influenza Virus Replication Machinery. <i>Science</i> , 2012, 338, 1631-1634.	12.6	208

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19	Structure of the insulin receptorâ€“insulin complex by single-particle cryo-EM analysis. <i>Nature</i> , 2018, 556, 122-125.	27.8	184
20	Visualizing Ribosome Biogenesis: Parallel Assembly Pathways for the 30 S Subunit. <i>Science</i> , 2010, 330, 673-677.	12.6	181
21	Fully automated, sequential tilt-series acquisition with Legion. <i>Journal of Structural Biology</i> , 2009, 167, 11-18.	2.8	180
22	The molecular architecture of human Dicer. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 436-440.	8.2	175
23	Reducing effects of particle adsorption to the airâ€“water interface in cryo-EM. <i>Nature Methods</i> , 2018, 15, 793-795.	19.0	167
24	Unnatural Amino Acid Incorporation into Virus-Like Particles. <i>Bioconjugate Chemistry</i> , 2008, 19, 866-875.	3.6	164
25	Modular Assembly of the Bacterial Large Ribosomal Subunit. <i>Cell</i> , 2016, 167, 1610-1622.e15.	28.9	163
26	FACT caught in the act of manipulating the nucleosome. <i>Nature</i> , 2020, 577, 426-431.	27.8	160
27	2.8 Å... resolution reconstruction of the <i>Thermoplasma acidophilum</i> 20S proteasome using cryo-electron microscopy. <i>eLife</i> , 2015, 4, .	6.0	156
28	Legion: a system for fully automated acquisition of 1000 electron micrographs a day. <i>Ultramicroscopy</i> , 1999, 77, 153-161.	1.9	151
29	Bacteriophage Lambda Stabilization by Auxiliary Protein gpD: Timing, Location, and Mechanism of Attachment Determined by Cryo-EM. <i>Structure</i> , 2008, 16, 1399-1406.	3.3	150
30	Spotiton: New features and applications. <i>Journal of Structural Biology</i> , 2018, 202, 161-169.	2.8	140
31	Spotiton: A prototype for an integrated inkjet dispense and vitrification system for cryo-TEM. <i>Journal of Structural Biology</i> , 2012, 179, 68-75.	2.8	139
32	ACE: Automated CTF Estimation. <i>Ultramicroscopy</i> , 2005, 104, 8-29.	1.9	136
33	A new method for vitrifying samples for cryoEM. <i>Journal of Structural Biology</i> , 2016, 195, 190-198.	2.8	135
34	Automatic particle selection: results of a comparative study. <i>Journal of Structural Biology</i> , 2004, 145, 3-14.	2.8	129
35	Structure and drug resistance of the <i>Plasmodium falciparum</i> transporter PfCRT. <i>Nature</i> , 2019, 576, 315-320.	27.8	123
36	Serial Section Electron Tomography: A Method for Three-Dimensional Reconstruction of Large Structures. <i>NeuroImage</i> , 1994, 1, 230-243.	4.2	122

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37	High resolution single particle cryo-electron microscopy using beam-image shift. <i>Journal of Structural Biology</i> , 2018, 204, 270-275.	2.8	115
38	Routine determination of ice thickness for cryo-EM grids. <i>Journal of Structural Biology</i> , 2018, 204, 38-44.	2.8	114
39	Structural basis for translational surveillance by the large ribosomal subunit-associated protein quality control complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15981-15986.	7.1	111
40	Engineered nanostructured β -sheet peptides protect membrane proteins. <i>Nature Methods</i> , 2013, 10, 759-761.	19.0	110
41	Conformational states of the full-length glucagon receptor. <i>Nature Communications</i> , 2015, 6, 7859.	12.8	110
42	Antibody Lineages with Vaccine-Induced Antigen-Binding Hotspots Develop Broad HIV Neutralization. <i>Cell</i> , 2019, 178, 567-584.e19.	28.9	106
43	Time-resolved cryo-EM using Spotiton. <i>Nature Methods</i> , 2020, 17, 897-900.	19.0	96
44	Distinct Conformational Spectrum of Homologous Multidrug ABC Transporters. <i>Structure</i> , 2015, 23, 450-460.	3.3	94
45	Quaternary contact in the initial interaction of CD4 with the HIV-1 envelope trimer. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 370-378.	8.2	94
46	Initial evaluation of a direct detection device detector for single particle cryo-electron microscopy. <i>Journal of Structural Biology</i> , 2011, 176, 404-408.	2.8	91
47	Molecular architecture of mammalian nitric oxide synthases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3614-23.	7.1	91
48	Optimizing "self-wicking" nanowire grids. <i>Journal of Structural Biology</i> , 2018, 202, 170-174.	2.8	88
49	Visualization of clustered protocadherin neuronal self-recognition complexes. <i>Nature</i> , 2019, 569, 280-283.	27.8	86
50	Automated cryoEM data acquisition and analysis of 284742 particles of GroEL. <i>Journal of Structural Biology</i> , 2006, 155, 470-481.	2.8	84
51	Disassembly and reassembly of human papillomavirus virus-like particles produces more virion-like antibody reactivity. <i>Virology Journal</i> , 2012, 9, 52.	3.4	83
52	Uptake and transfection efficiency of PEGylated cationic liposome-DNA complexes with and without RGD-tagging. <i>Biomaterials</i> , 2014, 35, 4996-5005.	11.4	81
53	Distinct conformations of the kinesin Unc104 neck regulate a monomer to dimer motor transition. <i>Journal of Cell Biology</i> , 2003, 163, 743-753.	5.2	80
54	Characterization of Circulating Endothelial Cells in Acute Myocardial Infarction. <i>Science Translational Medicine</i> , 2012, 4, 126ra33.	12.4	77

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55	Leginon: New features and applications. <i>Protein Science</i> , 2021, 30, 136-150.	7.6	77
56	Automatic particle detection through efficient hough transforms. <i>IEEE Transactions on Medical Imaging</i> , 2003, 22, 1053-1062.	8.9	76
57	Engineered Mutations Change the Structure and Stability of a Virus-Like Particle. <i>Biomacromolecules</i> , 2012, 13, 2339-2348.	5.4	72
58	Structural analysis of polymers of sickle cell hemoglobin. <i>Journal of Molecular Biology</i> , 1988, 199, 315-331.	4.2	71
59	PHOELIX: a package for semi-automated helical reconstruction. <i>Ultramicroscopy</i> , 1995, 58, 245-259.	1.9	71
60	Structure-based design of a quadrivalent fusion glycoprotein vaccine for human parainfluenza virus types 1-4. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12265-12270.	7.1	70
61	Structure of the Human Dicer-TRBP Complex by Electron Microscopy. <i>Structure</i> , 2009, 17, 1326-1332.	3.3	69
62	A combined quantitative mass spectrometry and electron microscopy analysis of ribosomal 30S subunit assembly in <i>E. coli</i> . <i>ELife</i> , 2014, 3, .	6.0	65
63	The P22 Tail Machine at Subnanometer Resolution Reveals the Architecture of an Infection Conduit. <i>Structure</i> , 2009, 17, 789-799.	3.3	63
64	Cryo-EM for Small Molecules Discovery, Design, Understanding, and Application. <i>Cell Chemical Biology</i> , 2018, 25, 1318-1325.	5.2	63
65	Liquid Crystalline Phases of Dendritic Lipid-DNA Self-Assemblies: Lamellar, Hexagonal, and DNA Bundles. <i>Journal of Physical Chemistry B</i> , 2009, 113, 3694-3703.	2.6	62
66	Helical Processing Using PHOELIX. <i>Journal of Structural Biology</i> , 1996, 116, 107-112.	2.8	57
67	Single-particle EM reveals the higher-order domain architecture of soluble guanylate cyclase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2960-2965.	7.1	57
68	An Improved Holey Carbon Film for Cryo-Electron Microscopy. <i>Microscopy and Microanalysis</i> , 2007, 13, 365-371.	0.4	55
69	Characterization of virus-like particles in GARDASIL® by cryo transmission electron microscopy. <i>Human Vaccines and Immunotherapeutics</i> , 2014, 10, 734-739.	3.3	53
70	Data management challenges in three-dimensional EM. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1203-1207.	8.2	49
71	Automated Identification of Filaments in Cryoelectron Microscopy Images. <i>Journal of Structural Biology</i> , 2001, 135, 302-312.	2.8	48
72	Automated data collection in single particle electron microscopy. <i>Microscopy (Oxford, England)</i> , 2016, 65, 43-56.	1.5	48

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73	A Toolbox for ab initio 3-D reconstructions in single-particle electron microscopy. <i>Journal of Structural Biology</i> , 2010, 169, 389-398.	2.8	46
74	Toolbox for Non-Intrusive Structural and Functional Analysis of Recombinant VLP Based Vaccines: A Case Study with Hepatitis B Vaccine. <i>PLoS ONE</i> , 2012, 7, e33235.	2.5	46
75	Complete functional mapping of infection- and vaccine-elicited antibodies against the fusion peptide of HIV. <i>PLoS Pathogens</i> , 2018, 14, e1007159.	4.7	46
76	Cryomeshâ„¢: A New Substrate for Cryo-Electron Microscopy. <i>Microscopy and Microanalysis</i> , 2010, 16, 43-53.	0.4	45
77	Big data in cryoEM: automated collection, processing and accessibility of EM data. <i>Current Opinion in Microbiology</i> , 2018, 43, 1-8.	5.1	45
78	Ensemble cryoEM elucidates the mechanism of insulin capture and degradation by human insulin degrading enzyme. <i>ELife</i> , 2018, 7, .	6.0	45
79	PEGylation of Paclitaxel-Loaded Cationic Liposomes Drives Steric Stabilization of Bicelles and Vesicles thereby Enhancing Delivery and Cytotoxicity to Human Cancer Cells. <i>ACS Applied Materials & Interfaces</i> , 2020, 12, 151-162.	8.0	45
80	Better, Faster, Cheaper: Recent Advances in Cryoâ€“Electron Microscopy. <i>Annual Review of Biochemistry</i> , 2022, 91, 1-32.	11.1	45
81	Temperature Monitoring of an EM Environment. <i>Microscopy Today</i> , 2006, 14, 24-29.	0.3	43
82	Mechanotransduction by PCDH15 Relies on a Novel cis-Dimeric Architecture. <i>Neuron</i> , 2018, 99, 480-492.e5.	8.1	43
83	Waffle Method: A general and flexible approach for improving throughput in FIB-milling. <i>Nature Communications</i> , 2022, 13, 1857.	12.8	43
84	Genomic and functional analysis of <i>Vibrio</i> phage SIOâ€“2 reveals novel insights into ecology and evolution of marine siphoviruses. <i>Environmental Microbiology</i> , 2012, 14, 2071-2086.	3.8	42
85	Current outcomes when optimizing â€“standardâ€™ sample preparation for singleâ€“particle cryoâ€“EM. <i>Journal of Microscopy</i> , 2019, 276, 39-45.	1.8	41
86	Engineering the PP7 Virus Capsid as a Peptide Display Platform. <i>ACS Nano</i> , 2019, 13, 4443-4454.	14.6	40
87	Towards automated screening of two-dimensional crystals. <i>Journal of Structural Biology</i> , 2007, 160, 324-331.	2.8	39
88	Transmission Electron Microscopy as an Orthogonal Method to Characterize Protein Aggregates. <i>Journal of Pharmaceutical Sciences</i> , 2015, 104, 750-759.	3.3	39
89	Automation of random conical tilt and orthogonal tilt data collection using feature-based correlation. <i>Journal of Structural Biology</i> , 2007, 159, 335-346.	2.8	38
90	A new model for binding of kinesin 13 to curved microtubule protofilaments. <i>Journal of Cell Biology</i> , 2009, 185, 51-57.	5.2	38

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91	Single-particle EM reveals extensive conformational variability of the Ltn1 E3 ligase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1702-1707.	7.1	38
92	The structure of dual-variable-domain immunoglobulin molecules alone and bound to antigen. <i>MAbs</i> , 2013, 5, 364-372.	5.2	38
93	Family-wide Structural and Biophysical Analysis of Binding Interactions among Non-clustered β -Protocadherins. <i>Cell Reports</i> , 2020, 30, 2655-2671.e7.	6.4	35
94	CTF Challenge: Result summary. <i>Journal of Structural Biology</i> , 2015, 190, 348-359.	2.8	34
95	Benchmarking cryo-EM Single Particle Analysis Workflow. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 50.	3.5	34
96	The reconstruction of helical particles with variable pitch. <i>Ultramicroscopy</i> , 1988, 26, 255-270.	1.9	33
97	A test-bed for optimizing high-resolution single particle reconstructions. <i>Journal of Structural Biology</i> , 2008, 163, 29-39.	2.8	33
98	Block Liposomes from Curvature-Stabilizing Lipids: Connected Nanotubes, -rods, or -spheres. <i>Langmuir</i> , 2009, 25, 2979-2985.	3.5	32
99	Robotic grid loading system for a transmission electron microscope. <i>Journal of Structural Biology</i> , 2004, 146, 431-440.	2.8	30
100	Maximizing the potential of electron cryomicroscopy data collected using direct detectors. <i>Journal of Structural Biology</i> , 2013, 184, 193-202.	2.8	30
101	Cryo-EM Structures and Regulation of Arabinofuranosyltransferase AftD from <i>Mycobacteria</i> . <i>Molecular Cell</i> , 2020, 78, 683-699.e11.	9.7	27
102	Small Molecule Microcrystal Electron Diffraction for the Pharmaceutical Industry—Lessons Learned From Examining Over Fifty Samples. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 648603.	3.5	27
103	Capsomer Dynamics and Stabilization in the T ϕ 12 Marine Bacteriophage SIO-2 and Its Procapsid Studied by CryoEM. <i>Structure</i> , 2012, 20, 498-503.	3.3	26
104	DNA bending-induced phase transition of encapsidated genome in phage ϕ . <i>Nucleic Acids Research</i> , 2013, 41, 4518-4524.	14.5	25
105	emScope: A Tool Kit for Control and Automation of a Remote Electron Microscope. <i>Journal of Structural Biology</i> , 1997, 120, 309-319.	2.8	24
106	A relational database for cryoEM: experience at one year and 50 000 images. <i>Journal of Structural Biology</i> , 2002, 137, 273-282.	2.8	24
107	Automated three-dimensional reconstruction of keyhole limpet hemocyanin type 1. <i>Journal of Structural Biology</i> , 2003, 144, 301-312.	2.8	24
108	Polyvalent Display of Heme on Hepatitis B Virus Capsid Protein through Coordination to Hexahistidine Tags. <i>Chemistry and Biology</i> , 2008, 15, 513-519.	6.0	24

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109	Nucleotide dependent packing differences in helical crystals of the ABC transporter MsbA. <i>Journal of Structural Biology</i> , 2009, 165, 169-175.	2.8	24
110	Patterned Threadlike Micelles and DNA-Tethered Nanoparticles: A Structural Study of PEGylated Cationic Liposome-DNA Assemblies. <i>Langmuir</i> , 2015, 31, 7073-7083.	3.5	24
111	Allosteric Regulation of DNA Cleavage and Sequence-Specificity through Run-On Oligomerization. <i>Structure</i> , 2013, 21, 1848-1858.	3.3	23
112	Symmetric activation and modulation of the human calcium-sensing receptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	23
113	Improving the Positional Accuracy of the Goniometer on the Philips CM Series TEM. <i>Journal of Structural Biology</i> , 1999, 128, 250-256.	2.8	22
114	Rapid routine structure determination of macromolecular assemblies using electron microscopy: current progress and further challenges. <i>Journal of Synchrotron Radiation</i> , 2004, 11, 83-85.	2.4	22
115	Helical crystallization on lipid nanotubes: Streptavidin as a model protein. <i>Journal of Structural Biology</i> , 2005, 150, 90-99.	2.8	22
116	Automation in Single-Particle Electron Microscopy. <i>Methods in Enzymology</i> , 2010, 483, 291-338.	1.0	22
117	Optimod – An automated approach for constructing and optimizing initial models for single-particle electron microscopy. <i>Journal of Structural Biology</i> , 2013, 184, 417-426.	2.8	22
118	Label-free visual proteomics: Coupling MS- and EM-based approaches in structural biology. <i>Molecular Cell</i> , 2022, 82, 285-303.	9.7	21
119	Advances in Computational Image Processing for Microscopy. <i>Journal of Structural Biology</i> , 1996, 116, 2-8.	2.8	20
120	Maturation in Action: CryoEM Study of a Viral Capsid Caught during Expansion. <i>Structure</i> , 2012, 20, 1384-1390.	3.3	20
121	Nucleotide-dependent conformational changes in the N-Ethylmaleimide Sensitive Factor (NSF) and their potential role in SNARE complex disassembly. <i>Journal of Structural Biology</i> , 2012, 177, 335-343.	2.8	20
122	Nanoscale Assembly in Biological Systems: From Neuronal Cytoskeletal Proteins to Curvature Stabilizing Lipids. <i>Advanced Materials</i> , 2011, 23, 2260-2270.	21.0	19
123	DOLORS: Versatile Strategy for Internal Labeling and Domain Localization in Electron Microscopy. <i>Structure</i> , 2012, 20, 1995-2002.	3.3	19
124	Strategies for Automated CryoEM Data Collection Using Direct Detectors. <i>Methods in Enzymology</i> , 2016, 579, 87-102.	1.0	19
125	Does contamination buildup limit throughput for automated cryoEM?. <i>Journal of Structural Biology</i> , 2006, 154, 303-311.	2.8	17
126	Near-atomic resolution reconstructions using a mid-range electron microscope operated at 200kV. <i>Journal of Structural Biology</i> , 2014, 188, 183-187.	2.8	16

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127	The effect of salt and pH on block liposomes studied by cryogenic transmission electron microscopy. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2009, 1788, 1869-1876.	2.6	15
128	Block Liposomes. <i>Methods in Enzymology</i> , 2009, 465, 111-128.	1.0	15
129	Typhon: Multiplexed TEM Sample Preparation. <i>Microscopy and Microanalysis</i> , 2014, 20, 1158-1159.	0.4	14
130	Cryo-EM structure of arabinosyltransferase EmbB from <i>Mycobacterium smegmatis</i> . <i>Nature Communications</i> , 2020, 11, 3396.	12.8	14
131	EDITORIAL. <i>Journal of Structural Biology</i> , 1996, 116, 1.	2.8	12
132	EVAC: a virtual environment for control of remote imaging instrumentation. <i>IEEE Computer Graphics and Applications</i> , 1996, 16, 62-66.	1.2	12
133	Automated Image Acquisition for Single-Particle Reconstruction Using p97 as the Biological Sample. <i>Journal of Structural Biology</i> , 2001, 133, 102-107.	2.8	12
134	Laboratory Design for High-Performance Electron Microscopy. <i>Microscopy Today</i> , 2004, 12, 8-17.	0.3	12
135	JavaScope: A Web-Based TEM Control Interface. <i>Journal of Structural Biology</i> , 1999, 125, 229-234.	2.8	11
136	Windex: a toolset for indexing helices. <i>Journal of Structural Biology</i> , 2003, 144, 172-183.	2.8	11
137	Software tools for macromolecular microscopy. <i>Journal of Structural Biology</i> , 2007, 157, 1-2.	2.8	11
138	Software tools for molecular microscopy. <i>Journal of Structural Biology</i> , 2008, 163, 224-228.	2.8	11
139	Block liposome and nanotube formation is a general phenomenon of two-component membranes containing multivalent lipids. <i>Soft Matter</i> , 2011, 7, 8363.	2.7	11
140	Analytical Methods and Software Tools for Macromolecular Microscopy. <i>Journal of Structural Biology</i> , 2003, 144, 1-3.	2.8	10
141	Structure and View Estimation for Tomographic Reconstruction: A Bayesian Approach. , 0, , .		9
142	Software Tools for Molecular Microscopy. <i>Methods in Enzymology</i> , 2010, 482, 381-392.	1.0	9
143	Seeing Atoms: Single-Particle Cryo-EM Breaks the Atomic Barrier. <i>Molecular Cell</i> , 2020, 80, 938-939.	9.7	9
144	Broadening access to cryoEM through centralized facilities. <i>Trends in Biochemical Sciences</i> , 2022, 47, 106-116.	7.5	9

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145	Reducing cryoEM file storage using lossy image formats. <i>Journal of Structural Biology</i> , 2019, 207, 49-55.	2.8	8
146	Multiplexed TEM Specimen Preparation and Analysis of Plasmonic Nanoparticles. <i>Microscopy and Microanalysis</i> , 2015, 21, 1017-1025.	0.4	7
147	Automating Decision Making in the Cryo-EM Pre-processing Pipeline. <i>Structure</i> , 2020, 28, 727-729.	3.3	7
148	A helical processing pipeline for EM structure determination of membrane proteins. <i>Methods</i> , 2011, 55, 350-362.	3.8	5
149	Maskiton: Interactive, web-based classification of single-particle electron microscopy images. <i>Journal of Structural Biology</i> , 2013, 182, 155-163.	2.8	5
150	Spotiton and Chameleon Vitrification robots. <i>Microscopy and Microanalysis</i> , 2019, 25, 1010-1011.	0.4	5
151	Recombinant Virus-like Particle Protein Vaccines. , 2015, , 81-112.		4
152	Structural basis for the mechanisms of human presequence protease conformational switch and substrate recognition. <i>Nature Communications</i> , 2022, 13, 1833.	12.8	4
153	Automation for Cryo-TEM: from Specimen Grid to 3D Map. <i>Microscopy and Microanalysis</i> , 2001, 7, 970-971.	0.4	3
154	Self-Blotting Nanowire Grids for Cryo-EM Sample Preparation. <i>Microscopy and Microanalysis</i> , 2017, 23, 848-849.	0.4	3
155	Spotiton: a new method for vitrifying samples for cryo-EM. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C1295-C1295.	0.1	3
156	Assembly of Building Blocks by Double-End-Anchored Polymers in the Dilute Regime Mediated by Hydrophobic Interactions at Controlled Distances. <i>ACS Applied Materials & Interfaces</i> , 2020, 12, 45728-45743.	8.0	3
157	Cryo-Electron Microscopic Grid Preparation for Time-Resolved Studies using a Novel Robotic System, Spotiton. <i>Journal of Visualized Experiments</i> , 2021, , .	0.3	3
158	A Testbed for Automated Acquisition From a TEM. <i>Microscopy and Microanalysis</i> , 1998, 4, 8-9.	0.4	2
159	Automated Acquisition of Cryo Electron Micrographs Using Leginon. <i>Microscopy and Microanalysis</i> , 1999, 5, 376-377.	0.4	2
160	Bugscope: a Sustainable Web-Based Telemicroscopy Project for K-12 Classrooms. <i>Microscopy and Microanalysis</i> , 1999, 5, 514-515.	0.4	2
161	Adaptation of Leginon Software for Semi-Automated Recording of Electron Microscopic Images of Two-Dimensional Crystals. <i>Microscopy and Microanalysis</i> , 2003, 9, 1518-1519.	0.4	2
162	Improving Automation for Cryo-EM Specimen Preparation. <i>Microscopy and Microanalysis</i> , 2004, 10, 1508-1509.	0.4	2

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163	Implementing Best Practices at the National Center for Cryo-EM Access and Training. <i>Microscopy and Microanalysis</i> , 2020, 26, 324-325.	0.4	2
164	Webscope.TEM: A Modular System for Distributed TEM. <i>Proceedings Annual Meeting Electron Microscopy Society of America</i> , 1996, 54, 390-391.	0.0	2
165	Automated Filament Finding and Selection from Cryo Electron Micrographs. <i>Microscopy and Microanalysis</i> , 2001, 7, 986-987.	0.4	1
166	Application of a SQL Database for Automated Image Acquisition and Analysis for CRYOEM. <i>Microscopy and Microanalysis</i> , 2001, 7, 984-985.	0.4	1
167	Remote Scripting for Microscope Control Applications on the Tecnai TEM. <i>Microscopy and Microanalysis</i> , 2002, 8, 872-873.	0.4	1
168	Contaminant detection: improving template matching based particle selection for cryoelectron microscopy. , 0, , .		1
169	Applications of Automated Electron Microscopy: Using Leginon to Study the Structure of COPII Protein Complexes. <i>Microscopy and Microanalysis</i> , 2005, 11, .	0.4	1
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