

Bridget Carragher

List of Publications by Year in descending order

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Version: 2024-02-01

202
papers

17,494
citations

20759

60
h-index

17055

122
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228
all docs

228
docs citations

228
times ranked

16642
citing authors

#	ARTICLE	IF	CITATIONS
1	Broadening access to cryoEM through centralized facilities. Trends in Biochemical Sciences, 2022, 47, 106-116.	3.7	9
2	Label-free visual proteomics: Coupling MS- and EM-based approaches in structural biology. Molecular Cell, 2022, 82, 285-303.	4.5	21
3	Better, Faster, Cheaper: Recent Advances in Cryo-EM Electron Microscopy. Annual Review of Biochemistry, 2022, 91, 1-32.	5.0	45
4	Waffle Method: A general and flexible approach for improving throughput in FIB-milling. Nature Communications, 2022, 13, 1857.	5.8	43
5	Structural basis for the mechanisms of human presequence protease conformational switch and substrate recognition. Nature Communications, 2022, 13, 1833.	5.8	4
6	Leginon: New features and applications. Protein Science, 2021, 30, 136-150.	3.1	77
7	Cryo-Electron Microscopic Grid Preparation for Time-Resolved Studies using a Novel Robotic System, Spotiton. Journal of Visualized Experiments, 2021, , .	0.2	3
8	A resolution record for cryoEM. Faculty Reviews, 2021, 10, 64.	1.7	1
9	Testing and implementing a live processing workflow at the New York Structural Biology Center. Microscopy and Microanalysis, 2021, 27, 2296-2297.	0.2	0
10	Small Molecule Microcrystal Electron Diffraction for the Pharmaceutical Industry- Lessons Learned From Examining Over Fifty Samples. Frontiers in Molecular Biosciences, 2021, 8, 648603.	1.6	27
11	The National Center for Cryoem Access and Training: Nationwide Access to Cryoem Technology and Curricula. Microscopy and Microanalysis, 2021, 27, 2294-2294.	0.2	0
12	Symmetric activation and modulation of the human calcium-sensing receptor. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	23
13	FACT caught in the act of manipulating the nucleosome. Nature, 2020, 577, 426-431.	13.7	160
14	PEGylation of Paclitaxel-Loaded Cationic Liposomes Drives Steric Stabilization of Bicelles and Vesicles thereby Enhancing Delivery and Cytotoxicity to Human Cancer Cells. ACS Applied Materials & Interfaces, 2020, 12, 151-162.	4.0	45
15	Better, faster, and even cheap. Science, 2020, 370, 171-171.	6.0	0
16	Seeing Atoms: Single-Particle Cryo-EM Breaks the Atomic Barrier. Molecular Cell, 2020, 80, 938-939.	4.5	9
17	Time-resolved cryo-EM using Spotiton. Nature Methods, 2020, 17, 897-900.	9.0	96
18	Assembly of Building Blocks by Double-End-Anchored Polymers in the Dilute Regime Mediated by Hydrophobic Interactions at Controlled Distances. ACS Applied Materials & Interfaces, 2020, 12, 45728-45743.	4.0	3

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19	Implementing Best Practices at the National Center for Cryo-EM Access and Training. <i>Microscopy and Microanalysis</i> , 2020, 26, 324-325.	0.2	2
20	Time-resolved CryoEM Using Spotiton. <i>Microscopy and Microanalysis</i> , 2020, 26, 326-327.	0.2	0
21	Optimizing Self-wicking Grids for Chameleon. <i>Microscopy and Microanalysis</i> , 2020, 26, 334-335.	0.2	0
22	What's Going On with My CryoEM/CryoFIB-SEM Sample, and How Might I Improve It?. <i>Microscopy and Microanalysis</i> , 2020, 26, 1894-1895.	0.2	0
23	Cryo-EM Structures and Regulation of Arabinofuranosyltransferase AftD from Mycobacteria. <i>Molecular Cell</i> , 2020, 78, 683-699.e11.	4.5	27
24	Cryo-EM structure of arabinosyltransferase EmbB from <i>Mycobacterium smegmatis</i> . <i>Nature Communications</i> , 2020, 11, 3396.	5.8	14
25	Automating Decision Making in the Cryo-EM Pre-processing Pipeline. <i>Structure</i> , 2020, 28, 727-729.	1.6	7
26	Family-wide Structural and Biophysical Analysis of Binding Interactions among Non-clustered Γ -Protocadherins. <i>Cell Reports</i> , 2020, 30, 2655-2671.e7.	2.9	35
27	Antibody Lineages with Vaccine-Induced Antigen-Binding Hotspots Develop Broad HIV Neutralization. <i>Cell</i> , 2019, 178, 567-584.e19.	13.5	106
28	Spotiton and Chameleon Vitrification robots. <i>Microscopy and Microanalysis</i> , 2019, 25, 1010-1011.	0.2	5
29	Best Practices at the National Center for CryoEM Access and Training. <i>Microscopy and Microanalysis</i> , 2019, 25, 2662-2663.	0.2	1
30	Current outcomes when optimizing "standard" sample preparation for single-particle cryo-EM. <i>Journal of Microscopy</i> , 2019, 276, 39-45.	0.8	41
31	Scorpion: Facilitating High Throughput Electron Microscopy. <i>Microscopy and Microanalysis</i> , 2019, 25, 1002-1003.	0.2	1
32	Strategies for Data Flow and Storage for High Throughput, High Resolution Cryo-EM Data Collection. <i>Microscopy and Microanalysis</i> , 2019, 25, 1394-1395.	0.2	0
33	Reducing cryoEM file storage using lossy image formats. <i>Journal of Structural Biology</i> , 2019, 207, 49-55.	1.3	8
34	Engineering the PP7 Virus Capsid as a Peptide Display Platform. <i>ACS Nano</i> , 2019, 13, 4443-4454.	7.3	40
35	Visualization of clustered protocadherin neuronal self-recognition complexes. <i>Nature</i> , 2019, 569, 280-283.	13.7	86
36	Structure and drug resistance of the <i>Plasmodium falciparum</i> transporter PfCRT. <i>Nature</i> , 2019, 576, 315-320.	13.7	123

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37	Structure of the insulin receptorâ€“insulin complex by single-particle cryo-EM analysis. <i>Nature</i> , 2018, 556, 122-125.	13.7	184
38	Optimizing â€œself-wickingâ€•nanowire grids. <i>Journal of Structural Biology</i> , 2018, 202, 170-174.	1.3	88
39	Spotiton: New features and applications. <i>Journal of Structural Biology</i> , 2018, 202, 161-169.	1.3	140
40	Big data in cryoEM: automated collection, processing and accessibility of EM data. <i>Current Opinion in Microbiology</i> , 2018, 43, 1-8.	2.3	45
41	Self-Wicking Nanowire Grids. <i>Microscopy and Microanalysis</i> , 2018, 24, 906-907.	0.2	0
42	Structure-based design of a quadrivalent fusion glycoprotein vaccine for human parainfluenza virus types 1â€“4. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12265-12270.	3.3	70
43	Reducing effects of particle adsorption to the airâ€“water interface in cryo-EM. <i>Nature Methods</i> , 2018, 15, 793-795.	9.0	167
44	High Resolution Cryo-TEM Single-Particle Averaging Reconstruction with Beam-Image Shift. <i>Microscopy and Microanalysis</i> , 2018, 24, 902-903.	0.2	0
45	Routine Determination of Ice Thickness by Energy Filtration. <i>Microscopy and Microanalysis</i> , 2018, 24, 898-899.	0.2	0
46	Ensemble cryoEM elucidates the mechanism of insulin capture and degradation by human insulin degrading enzyme. <i>ELife</i> , 2018, 7, .	2.8	45
47	High resolution single particle cryo-electron microscopy using beam-image shift. <i>Journal of Structural Biology</i> , 2018, 204, 270-275.	1.3	115
48	Mechanotransduction by PCDH15 Relies on a Novel cis-Dimeric Architecture. <i>Neuron</i> , 2018, 99, 480-492.e5.	3.8	43
49	Benchmarking cryo-EM Single Particle Analysis Workflow. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 50.	1.6	34
50	Routine determination of ice thickness for cryo-EM grids. <i>Journal of Structural Biology</i> , 2018, 204, 38-44.	1.3	114
51	Complete functional mapping of infection- and vaccine-elicited antibodies against the fusion peptide of HIV. <i>PLoS Pathogens</i> , 2018, 14, e1007159.	2.1	46
52	Cryo-EM for Small Molecules Discovery, Design, Understanding, and Application. <i>Cell Chemical Biology</i> , 2018, 25, 1318-1325.	2.5	63
53	Epitope-based vaccine design yields fusion peptide-directed antibodies that neutralize diverse strains of HIV-1. <i>Nature Medicine</i> , 2018, 24, 857-867.	15.2	256
54	Routine single particle CryoEM sample and grid characterization by tomography. <i>ELife</i> , 2018, 7, .	2.8	216

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55	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.	3.6	94
56	Self-Blotting Nanowire Grids for Cryo-EM Sample Preparation. <i>Microscopy and Microanalysis</i> , 2017, 23, 848-849.	0.2	3
57	Addressing preferred specimen orientation in single-particle cryo-EM through tilting. <i>Nature Methods</i> , 2017, 14, 793-796.	9.0	708
58	Lessons Learned from using a Cs-Corrected, Energy-Filtered, Phase-Plate TEM for Single-Particle CryoEM. <i>Microscopy and Microanalysis</i> , 2017, 23, 824-825.	0.2	0
59	Spotiton: a new method for vitrifying samples for cryo-EM. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C1295-C1295.	0.0	3
60	Structural Characterization of Monoclonal Antibody Therapeutics by Transmission Electron Microscopy and 2D Classification Analysis. <i>Microscopy and Microanalysis</i> , 2016, 22, 1082-1083.	0.2	0
61	Modular Assembly of the Bacterial Large Ribosomal Subunit. <i>Cell</i> , 2016, 167, 1610-1622.e15.	13.5	163
62	Strategies for Automated CryoEM Data Collection Using Direct Detectors. <i>Methods in Enzymology</i> , 2016, 579, 87-102.	0.4	19
63	A new method for vitrifying samples for cryoEM. <i>Journal of Structural Biology</i> , 2016, 195, 190-198.	1.3	135
64	Automated data collection in single particle electron microscopy. <i>Microscopy (Oxford, England)</i> , 2016, 65, 43-56.	0.7	48
65	Electron Microscopy as an Emerging Analytical Tool for Characterizing Biopharmaceuticals. <i>Microscopy and Microanalysis</i> , 2015, 21, 65-66.	0.2	1
66	Multiplexed TEM Specimen Preparation and Analysis of Plasmonic Nanoparticles. <i>Microscopy and Microanalysis</i> , 2015, 21, 1017-1025.	0.2	7
67	Patterned Threadlike Micelles and DNA-Tethered Nanoparticles: A Structural Study of PEGylated Cationic Liposome-DNA Assemblies. <i>Langmuir</i> , 2015, 31, 7073-7083.	1.6	24
68	Distinct Conformational Spectrum of Homologous Multidrug ABC Transporters. <i>Structure</i> , 2015, 23, 450-460.	1.6	94
69	Transmission Electron Microscopy as an Orthogonal Method to Characterize Protein Aggregates. <i>Journal of Pharmaceutical Sciences</i> , 2015, 104, 750-759.	1.6	39
70	Recombinant Virus-like Particle Protein Vaccines. , 2015, , 81-112.		4
71	Conformational states of the full-length glucagon receptor. <i>Nature Communications</i> , 2015, 6, 7859.	5.8	110
72	Crystal structure of rhodopsin bound to arrestin by femtosecond X-ray laser. <i>Nature</i> , 2015, 523, 561-567.	13.7	683

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73	CTF Challenge: Result summary. <i>Journal of Structural Biology</i> , 2015, 190, 348-359.	1.3	34
74	Recent advances in new technologies and applications for molecular TEM. <i>Journal of Structural Biology</i> , 2015, 192, 145.	1.3	0
75	2.8 Å... resolution reconstruction of the <i>Thermoplasma acidophilum</i> 20S proteasome using cryo-electron microscopy. <i>ELife</i> , 2015, 4, .	2.8	156
76	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.	3.3	57
77	Uptake and transfection efficiency of PEGylated cationic liposome-DNA complexes with and without RGD-tagging. <i>Biomaterials</i> , 2014, 35, 4996-5005.	5.7	81
78	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.	3.3	111
79	Near-atomic resolution reconstructions using a mid-range electron microscope operated at 200kV. <i>Journal of Structural Biology</i> , 2014, 188, 183-187.	1.3	16
80	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.	3.3	91
81	Characterization of virus-like particles in GARDASIL® by cryo transmission electron microscopy. <i>Human Vaccines and Immunotherapeutics</i> , 2014, 10, 734-739.	1.4	53
82	Typhon: Multiplexed TEM Sample Preparation. <i>Microscopy and Microanalysis</i> , 2014, 20, 1158-1159.	0.2	14
83	Getting the Most out of Direct Detection Cameras for Low-Dose Transmission Electron Microscopy. <i>Microscopy and Microanalysis</i> , 2014, 20, 2140-2141.	0.2	0
84	A combined quantitative mass spectrometry and electron microscopy analysis of ribosomal 30S subunit assembly in <i>E. coli</i> . <i>ELife</i> , 2014, 3, .	2.8	65
85	Maskiton: Interactive, web-based classification of single-particle electron microscopy images. <i>Journal of Structural Biology</i> , 2013, 182, 155-163.	1.3	5
86	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.	1.3	22
87	Cryo-EM Structure of a Fully Glycosylated Soluble Cleaved HIV-1 Envelope Trimer. <i>Science</i> , 2013, 342, 1484-1490.	6.0	662
88	Allosteric Regulation of DNA Cleavage and Sequence-Specificity through Run-On Oligomerization. <i>Structure</i> , 2013, 21, 1848-1858.	1.6	23
89	Maximizing the potential of electron cryomicroscopy data collected using direct detectors. <i>Journal of Structural Biology</i> , 2013, 184, 193-202.	1.3	30
90	Engineered nanostructured β -sheet peptides protect membrane proteins. <i>Nature Methods</i> , 2013, 10, 759-761.	9.0	110

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91	DNA bending-induced phase transition of encapsidated genome in phage λ . <i>Nucleic Acids Research</i> , 2013, 41, 4518-4524.	6.5	25
92	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.	3.3	38
93	The structure of dual-variable-domain immunoglobulin molecules alone and bound to antigen. <i>MAbs</i> , 2013, 5, 364-372.	2.6	38
94	The molecular architecture of human Dicer. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 436-440.	3.6	175
95	Data management challenges in three-dimensional EM. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1203-1207.	3.6	49
96	Organization of the Influenza Virus Replication Machinery. <i>Science</i> , 2012, 338, 1631-1634.	6.0	208
97	Maturation in Action: CryoEM Study of a Viral Capsid Caught during Expansion. <i>Structure</i> , 2012, 20, 1384-1390.	1.6	20
98	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.	1.3	20
99	Beam-induced motion of vitrified specimen on holey carbon film. <i>Journal of Structural Biology</i> , 2012, 177, 630-637.	1.3	366
100	Spotiton: A prototype for an integrated inkjet dispense and vitrification system for cryo-TEM. <i>Journal of Structural Biology</i> , 2012, 179, 68-75.	1.3	139
101	Movies of Ice-Embedded Particles Enhance Resolution in Electron Cryo-Microscopy. <i>Structure</i> , 2012, 20, 1823-1828.	1.6	277
102	DOLORS: Versatile Strategy for Internal Labeling and Domain Localization in Electron Microscopy. <i>Structure</i> , 2012, 20, 1995-2002.	1.6	19
103	Characterization of Circulating Endothelial Cells in Acute Myocardial Infarction. <i>Science Translational Medicine</i> , 2012, 4, 126ra33.	5.8	77
104	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.	1.1	46
105	Engineered Mutations Change the Structure and Stability of a Virus-Like Particle. <i>Biomacromolecules</i> , 2012, 13, 2339-2348.	2.6	72
106	Capsomer Dynamics and Stabilization in the T _A = 12 Marine Bacteriophage SIO-2 and Its Procapsid Studied by CryoEM. <i>Structure</i> , 2012, 20, 498-503.	1.6	26
107	Genomic and functional analysis of <i>Vibrio</i> phage SIO-2 reveals novel insights into ecology and evolution of marine siphoviruses. <i>Environmental Microbiology</i> , 2012, 14, 2071-2086.	1.8	42
108	Disassembly and reassembly of human papillomavirus virus-like particles produces more virion-like antibody reactivity. <i>Virology Journal</i> , 2012, 9, 52.	1.4	83

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109	Block liposome and nanotube formation is a general phenomenon of two-component membranes containing multivalent lipids. <i>Soft Matter</i> , 2011, 7, 8363.	1.2	11
110	Initial evaluation of a direct detection device detector for single particle cryo-electron microscopy. <i>Journal of Structural Biology</i> , 2011, 176, 404-408.	1.3	91
111	A helical processing pipeline for EM structure determination of membrane proteins. <i>Methods</i> , 2011, 55, 350-362.	1.9	5
112	Nanoscale Assembly in Biological Systems: From Neuronal Cytoskeletal Proteins to Curvature Stabilizing Lipids. <i>Advanced Materials</i> , 2011, 23, 2260-2270.	11.1	19
113	Cryomeshâ,,ç: A New Substrate for Cryo-Electron Microscopy. <i>Microscopy and Microanalysis</i> , 2010, 16, 43-53.	0.2	45
114	Introducing Students to Research: Electron Microscopy of Bacteriophages. <i>Microscopy Today</i> , 2010, 18, 30-33.	0.2	0
115	Automation in Single-Particle Electron Microscopy. <i>Methods in Enzymology</i> , 2010, 483, 291-338.	0.4	22
116	Software Tools for Molecular Microscopy. <i>Methods in Enzymology</i> , 2010, 482, 381-392.	0.4	9
117	Visualizing Ribosome Biogenesis: Parallel Assembly Pathways for the 30 S Subunit. <i>Science</i> , 2010, 330, 673-677.	6.0	181
118	A Toolbox for ab initio 3-D reconstructions in single-particle electron microscopy. <i>Journal of Structural Biology</i> , 2010, 169, 389-398.	1.3	46
119	A new model for binding of kinesin 13 to curved microtubule protofilaments. <i>Journal of Cell Biology</i> , 2009, 185, 51-57.	2.3	38
120	The P22 Tail Machine at Subnanometer Resolution Reveals the Architecture of an Infection Conduit. <i>Structure</i> , 2009, 17, 789-799.	1.6	63
121	Structure of the Human Dicer-TRBP Complex by Electron Microscopy. <i>Structure</i> , 2009, 17, 1326-1332.	1.6	69
122	Block Liposomes from Curvature-Stabilizing Lipids: Connected Nanotubes, -rods, or -spheres. <i>Langmuir</i> , 2009, 25, 2979-2985.	1.6	32
123	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.	1.4	15
124	Nucleotide dependent packing differences in helical crystals of the ABC transporter MsbA. <i>Journal of Structural Biology</i> , 2009, 165, 169-175.	1.3	24
125	Appion: An integrated, database-driven pipeline to facilitate EM image processing. <i>Journal of Structural Biology</i> , 2009, 166, 95-102.	1.3	848
126	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.	1.3	569

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127	Fully automated, sequential tilt-series acquisition with Legimon. <i>Journal of Structural Biology</i> , 2009, 167, 11-18.	1.3	180
128	Block Liposomes. <i>Methods in Enzymology</i> , 2009, 465, 111-128.	0.4	15
129	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.	1.2	62
130	Polyvalent Display of Heme on Hepatitis B Virus Capsid Protein through Coordination to Hexahistidine Tags. <i>Chemistry and Biology</i> , 2008, 15, 513-519.	6.2	24
131	Unnatural Amino Acid Incorporation into Virus-Like Particles. <i>Bioconjugate Chemistry</i> , 2008, 19, 866-875.	1.8	164
132	Bacteriophage Lambda Stabilization by Auxiliary Protein gpD: Timing, Location, and Mechanism of Attachment Determined by Cryo-EM. <i>Structure</i> , 2008, 16, 1399-1406.	1.6	150
133	Software tools for molecular microscopy. <i>Journal of Structural Biology</i> , 2008, 163, 224-228.	1.3	11
134	A test-bed for optimizing high-resolution single particle reconstructions. <i>Journal of Structural Biology</i> , 2008, 163, 29-39.	1.3	33
135	Structural Basis for Cargo Regulation of COPII Coat Assembly. <i>Cell</i> , 2008, 134, 474-484.	13.5	242
136	Automated Large Scale Tilt Pair Data Collection for TEM. <i>Microscopy and Microanalysis</i> , 2008, 14, 798-799.	0.2	0
137	Software tools for macromolecular microscopy. <i>Journal of Structural Biology</i> , 2007, 157, 1-2.	1.3	11
138	Automation of random conical tilt and orthogonal tilt data collection using feature-based correlation. <i>Journal of Structural Biology</i> , 2007, 159, 335-346.	1.3	38
139	Towards automated screening of two-dimensional crystals. <i>Journal of Structural Biology</i> , 2007, 160, 324-331.	1.3	39
140	An Improved Holey Carbon Film for Cryo-Electron Microscopy. <i>Microscopy and Microanalysis</i> , 2007, 13, 365-371.	0.2	55
141	TEM of Bacteriophages Found in Marine Sources. <i>Microscopy Today</i> , 2007, 15, 28-31.	0.2	1
142	Does contamination buildup limit throughput for automated cryoEM?. <i>Journal of Structural Biology</i> , 2006, 154, 303-311.	1.3	17
143	Automated cryoEM data acquisition and analysis of 284742 particles of GroEL. <i>Journal of Structural Biology</i> , 2006, 155, 470-481.	1.3	84
144	Temperature Monitoring of an EM Environment. <i>Microscopy Today</i> , 2006, 14, 24-29.	0.2	43

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145	A Case Study in Automated Molecular Microscopy. <i>Microscopy and Microanalysis</i> , 2006, 12, 1096-1097.	0.2	0
146	Automated Data Collection for Serial Section TEM. <i>Microscopy and Microanalysis</i> , 2006, 12, 1106-1107.	0.2	0
147	Structure of the Sec13/31 COPII coat cage. <i>Nature</i> , 2006, 439, 234-238.	13.7	286
148	The Structure of an Infectious P22 Virion Shows the Signal for Headful DNA Packaging. <i>Science</i> , 2006, 312, 1791-1795.	6.0	276
149	Characterizing Ice Contamination Using Legion. <i>Microscopy and Microanalysis</i> , 2005, 11, .	0.2	0
150	Applications of Automated Electron Microscopy: Using Legion to Study the Structure of COPII Protein Complexes. <i>Microscopy and Microanalysis</i> , 2005, 11, .	0.2	1
151	ACE: Automated CTF Estimation. <i>Ultramicroscopy</i> , 2005, 104, 8-29.	0.8	136
152	Helical crystallization on lipid nanotubes: Streptavidin as a model protein. <i>Journal of Structural Biology</i> , 2005, 150, 90-99.	1.3	22
153	Automated molecular microscopy: The new Legion system. <i>Journal of Structural Biology</i> , 2005, 151, 41-60.	1.3	1,608
154	Laboratory Design for High-Performance Electron Microscopy. <i>Microscopy Today</i> , 2004, 12, 8-17.	0.2	12
155	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.	1.0	22
156	Automatic particle selection: results of a comparative study. <i>Journal of Structural Biology</i> , 2004, 145, 3-14.	1.3	129
157	Robotic grid loading system for a transmission electron microscope. <i>Journal of Structural Biology</i> , 2004, 146, 431-440.	1.3	30
158	Improving Automation for Cryo-EM Specimen Preparation. <i>Microscopy and Microanalysis</i> , 2004, 10, 1508-1509.	0.2	2
159	A Project Database Management System for Microscopy. <i>Microscopy and Microanalysis</i> , 2004, 10, 1276-1277.	0.2	0
160	Update on a Robotic Grid Loading System for TEM. <i>Microscopy and Microanalysis</i> , 2004, 10, 1376-1377.	0.2	0
161	Automated EM Data Acquisition using Legion II. <i>Microscopy and Microanalysis</i> , 2004, 10, 1510-1511.	0.2	0
162	Automated three-dimensional reconstruction of keyhole limpet hemocyanin type 1. <i>Journal of Structural Biology</i> , 2003, 144, 301-312.	1.3	24

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163	Windex: a toolset for indexing helices. <i>Journal of Structural Biology</i> , 2003, 144, 172-183.	1.3	11
164	Analytical Methods and Software Tools for Macromolecular Microscopy. <i>Journal of Structural Biology</i> , 2003, 144, 1-3.	1.3	10
165	Automatic particle detection through efficient hough transforms. <i>IEEE Transactions on Medical Imaging</i> , 2003, 22, 1053-1062.	5.4	76
166	Distinct conformations of the kinesin Unc104 neck regulate a monomer to dimer motor transition. <i>Journal of Cell Biology</i> , 2003, 163, 743-753.	2.3	80
167	An Automated Grid Handling System for TEM. <i>Microscopy and Microanalysis</i> , 2003, 9, 1214-1215.	0.2	0
168	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.	0.2	2
169	A relational database for cryoEM: experience at one year and 50 000 images. <i>Journal of Structural Biology</i> , 2002, 137, 273-282.	1.3	24
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