JÃ¹/₄rgen M Plitzko

List of Publications by Year in descending order

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147 papers 12,378 citations

25014 57 h-index 30894 102 g-index

169 all docs

169 docs citations

169 times ranked 11776 citing authors

#	Article	IF	CITATIONS
1	Disclosure of the mycobacterial outer membrane: Cryo-electron tomography and vitreous sections reveal the lipid bilayer structure. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 3963-3967.	3.3	511
2	Visualizing the molecular sociology at the HeLa cell nuclear periphery. Science, 2016, 351, 969-972.	6.0	493
3	An acidic protein aligns magnetosomes along a filamentous structure in magnetotactic bacteria. Nature, 2006, 440, 110-114.	13.7	486
4	Nuclear Pore Complex Structure and Dynamics Revealed by Cryoelectron Tomography. Science, 2004, 306, 1387-1390.	6.0	451
5	Volta potential phase plate for in-focus phase contrast transmission electron microscopy. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15635-15640.	3.3	448
6	TOM software toolbox: acquisition and analysis for electron tomography. Journal of Structural Biology, 2005, 149, 227-234.	1.3	424
7	Correlative microscopy: Bridging the gap between fluorescence light microscopy and cryo-electron tomography. Journal of Structural Biology, 2007, 160, 135-145.	1.3	356
8	Focused ion beam micromachining of eukaryotic cells for cryoelectron tomography. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 4449-4454.	3.3	356
9	The Eukaryotic CO2-Concentrating Organelle Is Liquid-like and Exhibits Dynamic Reorganization. Cell, 2017, 171, 148-162.e19.	13.5	298
10	Structure of the adenosine-bound human adenosine A1 receptor–Gi complex. Nature, 2018, 558, 559-563.	13.7	274
		10.7	
11	Transcription initiation complex structures elucidate DNA opening. Nature, 2016, 533, 353-358.	13.7	250
11	Transcription initiation complex structures elucidate DNA opening. Nature, 2016, 533, 353-358. Near-atomic resolution structural model of the yeast 26S proteasome. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 14870-14875.		250
	Near-atomic resolution structural model of the yeast 26S proteasome. Proceedings of the National	13.7	
12	Near-atomic resolution structural model of the yeast 26S proteasome. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 14870-14875. Micromachining tools and correlative approaches for cellular cryo-electron tomography. Journal of	13.7	242
12 13	Near-atomic resolution structural model of the yeast 26S proteasome. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 14870-14875. Micromachining tools and correlative approaches for cellular cryo-electron tomography. Journal of Structural Biology, 2010, 172, 169-179. Native architecture of the Chlamydomonas chloroplast revealed by in situ cryo-electron tomography.	13.7 3.3 1.3	242
12 13	Near-atomic resolution structural model of the yeast 26S proteasome. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 14870-14875. Micromachining tools and correlative approaches for cellular cryo-electron tomography. Journal of Structural Biology, 2010, 172, 169-179. Native architecture of the Chlamydomonas chloroplast revealed by in situ cryo-electron tomography. ELife, 2015, 4, . Optimized cryo-focused ion beam sample preparation aimed at in situ structural studies of membrane	13.7 3.3 1.3 2.8	242 230 224
12 13 14	Near-atomic resolution structural model of the yeast 26S proteasome. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 14870-14875. Micromachining tools and correlative approaches for cellular cryo-electron tomography. Journal of Structural Biology, 2010, 172, 169-179. Native architecture of the Chlamydomonas chloroplast revealed by in situ cryo-electron tomography. ELife, 2015, 4, . Optimized cryo-focused ion beam sample preparation aimed at in situ structural studies of membrane proteins. Journal of Structural Biology, 2017, 197, 73-82. Cryo-EM structure of the active, Gs-protein complexed, human CGRP receptor. Nature, 2018, 561,	13.7 3.3 1.3 2.8	242 230 224 216

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19	Opening windows into the cell: focused-ion-beam milling for cryo-electron tomography. Current Opinion in Structural Biology, 2013, 23, 771-777.	2.6	179
20	Deep classification of a large cryo-EM dataset defines the conformational landscape of the 26S proteasome. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5544-5549.	3.3	177
21	Structure of the human 26S proteasome at a resolution of 3.9 \tilde{A} Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7816-7821.	3.3	174
22	Structure of transcribing mammalian RNA polymerase II. Nature, 2016, 529, 551-554.	13.7	174
23	Site-Specific Cryo-focused Ion Beam Sample Preparation Guided by 3D Correlative Microscopy. Biophysical Journal, 2016, 110, 860-869.	0.2	172
24	A cryo-FIB lift-out technique enables molecular-resolution cryo-ET within native Caenorhabditis elegans tissue. Nature Methods, 2019, 16, 757-762.	9.0	165
25	Graphene oxide: A substrate for optimizing preparations of frozen-hydrated samples. Journal of Structural Biology, 2010, 170, 152-156.	1.3	155
26	The structure of the COPI coat determined within the cell. ELife, 2017, 6, .	2.8	152
27	Structural insights into the functional cycle of the ATPase module of the 26S proteasome. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1305-1310.	3.3	151
28	Loss of the actinâ€like protein MamK has pleiotropic effects on magnetosome formation and chain assembly in <i>Magnetospirillum gryphiswaldense</i>). Molecular Microbiology, 2010, 77, 208-224.	1.2	143
29	Dissecting the molecular organization of the translocon-associated protein complex. Nature Communications, 2017, 8, 14516.	5.8	131
30	Structure of a transcribing RNA polymerase II–DSIF complex reveals a multidentate DNA–RNA clamp. Nature Structural and Molecular Biology, 2017, 24, 809-815.	3.6	130
31	The cation diffusion facilitator proteins MamB and MamM of Magnetospirillum gryphiswaldense have distinct and complex functions, and are involved in magnetite biomineralization and magnetosome membrane assembly. Molecular Microbiology, 2011, 82, 818-835.	1.2	125
32	A focused ion beam milling and lift-out approach for site-specific preparation of frozen-hydrated lamellas from multicellular organisms. Journal of Structural Biology, 2015, 192, 262-269.	1.3	125
33	Proteasomes tether to two distinct sites at the nuclear pore complex. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 13726-13731.	3.3	123
34	Insights into the molecular architecture of the 26S proteasome. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11943-11947.	3.3	116
35	Biogenic regions of cyanobacterial thylakoids form contact sites with the plasma membrane. Nature Plants, 2019, 5, 436-446.	4.7	114
36	Preparing samples from whole cells using focused-ion-beam milling for cryo-electron tomography. Nature Protocols, 2020, 15, 2041-2070.	5.5	114

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37	Electron Microscopy of Biological Materials at the Nanometer Scale. Annual Review of Materials Research, 2012, 42, 33-58.	4.3	108
38	Expanded Coverage of the 26S Proteasome Conformational Landscape Reveals Mechanisms of Peptidase Gating. Cell Reports, 2018, 24, 1301-1315.e5.	2.9	108
39	In situ architecture of the algal nuclear pore complex. Nature Communications, 2018, 9, 2361.	5.8	107
40	Structures of the cyanobacterial circadian oscillator frozen in a fully assembled state. Science, 2017, 355, 1181-1184.	6.0	106
41	Cryo-focused Ion Beam Sample Preparation for Imaging Vitreous Cells by Cryo-electron Tomography. Bio-protocol, 2015, 5, .	0.2	105
42	Investigating the reaction path and growth kinetics in CuOx/Al multilayer foils. Journal of Applied Physics, 2003, 94, 2923-2929.	1.1	104
43	Cryo-focused-ion-beam applications in structural biology. Archives of Biochemistry and Biophysics, 2015, 581, 122-130.	1.4	102
44	Correlative cryo-light microscopy and cryo-electron tomography: from cellular territories to molecular landscapes. Current Opinion in Biotechnology, 2009, 20, 83-89.	3.3	100
45	In situ structural analysis of Golgi intracisternal protein arrays. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11264-11269.	3.3	94
46	Structure of a hibernating 100S ribosome reveals an inactive conformation of the ribosomal protein S1. Nature Microbiology, 2018, 3, 1115-1121.	5.9	92
47	Structures of Lysenin Reveal a Shared Evolutionary Origin for Pore-Forming Proteins And Its Mode of Sphingomyelin Recognition. Structure, 2012, 20, 1498-1507.	1.6	90
48	Bacterial encapsulins as orthogonal compartments for mammalian cell engineering. Nature Communications, 2018, 9, 1990.	5.8	88
49	Three-dimensional architecture of actin filaments in <i>Listeria monocytogenes</i> comet tails. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20521-20526.	3.3	81
50	Incomplete pneumolysin oligomers form membrane pores. Open Biology, 2014, 4, 140044.	1.5	81
51	Magnetosome chains are recruited to cellular division sites and split by asymmetric septation. Molecular Microbiology, 2011, 82, 1316-1329.	1.2	80
52	Architecture of the RNA polymerase II-Paf1C-TFIIS transcription elongation complex. Nature Communications, 2017, 8, 15741.	5.8	80
53	Charting the native architecture of Chlamydomonas thylakoid membranes with single-molecule precision. ELife, 2020, 9, .	2.8	80
54	The magnetosome proteins <scp>MamX</scp> , <scp>MamZ</scp> and <scp>MamH</scp> are involved in redox control of magnetite biomineralization in <i><scp>M</scp>agnetospirillum gryphiswaldense</i> Molecular Microbiology, 2013, 89, 872-886.	1.2	79

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55	3.9 Ã structure of the nucleosome core particle determined by phase-plate cryo-EM. Nucleic Acids Research, 2016, 44, 8013-8019.	6.5	78
56	Structural basis for VIPP1 oligomerization and maintenance of thylakoid membrane integrity. Cell, 2021, 184, 3643-3659.e23.	13.5	76
57	Correlated Light and Electron Cryo-Microscopy. Methods in Enzymology, 2010, 481, 317-341.	0.4	72
58	Structural Biology outside the box — inside the cell. Current Opinion in Structural Biology, 2017, 46, 110-121.	2.6	72
59	Direct visualization of degradation microcompartments at the ER membrane. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1069-1080.	3.3	68
60	A modular platform for automated cryo-FIB workflows. ELife, 2021, 10, .	2.8	65
61	Volta phase plate cryo-EM of the small protein complex Prx3. Nature Communications, 2016, 7, 10534.	5.8	64
62	Cryo-EM structure of the native rhodopsin dimer in nanodiscs. Journal of Biological Chemistry, 2019, 294, 14215-14230.	1.6	64
63	Liquid-crystalline phase transitions in lipid droplets are related to cellular states and specific organelle association. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 16866-16871.	3.3	64
64	A streamlined workflow for automated cryo focused ion beam milling. Journal of Structural Biology, 2021, 213, 107743.	1.3	60
65	Integrative Approaches for Cellular Cryo-electron Tomography. Methods in Cell Biology, 2012, 111, 259-281.	0.5	59
66	RNA polymerase I–Rrn3 complex at 4.8 à resolution. Nature Communications, 2016, 7, 12129.	5.8	58
67	MamY is a membrane-bound protein that aligns magnetosomes and the motility axis of helical magnetotactic bacteria. Nature Microbiology, 2019, 4, 1978-1989.	5.9	58
68	Quantitative analysis of electron spectroscopic imaging series. Micron, 1997, 28, 361-370.	1.1	55
69	Unraveling the structure of membrane proteins in situ by transfer function corrected cryo-electron tomography. Journal of Structural Biology, 2012, 180, 488-496.	1.3	53
70	Overproduction of Magnetosomes by Genomic Amplification of Biosynthesis-Related Gene Clusters in a Magnetotactic Bacterium. Applied and Environmental Microbiology, 2016, 82, 3032-3041.	1.4	53
71	Genetic and Ultrastructural Analysis Reveals the Key Players and Initial Steps of Bacterial Magnetosome Membrane Biogenesis. PLoS Genetics, 2016, 12, e1006101.	1.5	51
72	Structural Basis for Subunit Assembly in UDP-glucose Pyrophosphorylase from Saccharomyces cerevisiae. Journal of Molecular Biology, 2006, 364, 551-560.	2.0	49

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73	Computer controlled cryo-electron microscopy – TOM2 a software package for high-throughput applications. Journal of Structural Biology, 2011, 175, 394-405.	1.3	49
74	Segregation of prokaryotic magnetosomes organelles is driven by treadmilling of a dynamic actin-like MamK filament. BMC Biology, 2016, 14, 88.	1.7	48
75	In situ cryo-electron tomography reveals gradient organization of ribosome biogenesis in intact nucleoli. Nature Communications, 2021, 12, 5364.	5.8	46
76	Quantitative thin film analysis by energy filtering transmission electron microscopy. Ultramicroscopy, 1999, 78, 207-219.	0.8	43
77	Automated screening of 2D crystallization trials using transmission electron microscopy: A high-throughput tool-chain for sample preparation and microscopic analysis. Journal of Structural Biology, 2011, 173, 365-374.	1.3	38
78	A Tailored <i>galK</i> Counterselection System for Efficient Markerless Gene Deletion and Chromosomal Tagging in Magnetospirillum gryphiswaldense. Applied and Environmental Microbiology, 2014, 80, 4323-4330.	1.4	38
79	In vivo veritas: electron cryotomography of cells. Trends in Biotechnology, 2002, 20, S40-S44.	4.9	35
80	The dual role of MamB in magnetosome membrane assembly and magnetite biomineralization. Molecular Microbiology, 2018, 107, 542-557.	1.2	35
81	Analysis of Magnetosome Chains in Magnetotactic Bacteria by Magnetic Measurements and Automated Image Analysis of Electron Micrographs. Applied and Environmental Microbiology, 2013, 79, 7755-7762.	1.4	34
82	Automated cryoelectron microscopy of "single particles―applied to the 26S proteasome. FEBS Letters, 2007, 581, 2751-2756.	1.3	33
83	Molecular-scale visualization of sarcomere contraction within native cardiomyocytes. Nature Communications, 2021, 12, 4086.	5.8	33
84	The FtsZ-Like Protein FtsZm of Magnetospirillum gryphiswaldense Likely Interacts with Its Generic Homolog and Is Required for Biomineralization under Nitrate Deprivation. Journal of Bacteriology, 2014, 196, 650-659.	1.0	32
85	Quantitative electron spectroscopic imaging studies of microelectronic metallization layers. Journal of Microscopy, 1999, 194, 71-78.	0.8	29
86	Structural studies of <i>Acidianus</i> tailed spindle virus reveal a structural paradigm used in the assembly of spindle-shaped viruses. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 2120-2125.	3.3	29
87	In situ structural studies of tripeptidyl peptidase II (TPPII) reveal spatial association with proteasomes. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 4412-4417.	3.3	27
88	Tripartite phase separation of two signal effectors with vesicles priming B cell responsiveness. Nature Communications, 2020, $11,848$.	5.8	27
89	Integrated Cryo-Correlative Microscopy for Targeted Structural Investigation <i>In Situ</i> Microscopy Today, 2021, 29, 20-25.	0.2	27
90	<i>In Vivo</i> Coating of Bacterial Magnetic Nanoparticles by Magnetosome Expression of Spider Silk-Inspired Peptides. Biomacromolecules, 2018, 19, 962-972.	2.6	26

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91	Determinants shaping the nanoscale architecture of the mouse rod outer segment. ELife, 2021, 10, .	2.8	25
92	Connectivity of centermost chromatophores in <i>Rhodobacter sphaeroides</i> bacteria. Molecular Microbiology, 2018, 109, 812-825.	1.2	24
93	Evidence for cubic phase in deposited germanium nanocrystals. Journal of Physics Condensed Matter, 2003, 15, 1017-1028.	0.7	22
94	Revisiting the Structure of Hemoglobin and Myoglobin with Cryo-Electron Microscopy. Journal of Molecular Biology, 2017, 429, 2611-2618.	2.0	22
95	Copper Segregation to the $\hat{A}5$ (310)/[001] Symmetric Tilt Grain Boundary in Aluminum. Journal of Materials Science, 2004, 12, 165-174.	1.2	19
96	Contrast and scattering efficiency of scattering-type near-field optical probes. Applied Physics Letters, 2004, 85, 4466.	1.5	18
97	In situ Microfluidic Cryofixation for Cryo Focused Ion Beam Milling and Cryo Electron Tomography. Scientific Reports, 2019, 9, 19133.	1.6	18
98	Expamers: a new technology to control T cell activation. Scientific Reports, 2020, 10, 17832.	1.6	17
99	The Polar Organizing Protein PopZ Is Fundamental for Proper Cell Division and Segregation of Cellular Content in <i>Magnetospirillum gryphiswaldense</i>). MBio, 2019, 10, .	1.8	16
100	A bacterial cytolinker couples positioning of magnetic organelles to cell shape control. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 32086-32097.	3.3	16
101	Electron tomography of structures in the wall of hazel pollen grains. Journal of Structural Biology, 2009, 166, 263-271.	1.3	15
102	Recent Advances in Gas Injection System-Free Cryo-FIB Lift-Out Transfer for Cryo-Electron Tomography of Multicellular Organisms and Tissues. Microscopy Today, 2022, 30, 42-47.	0.2	15
103	A gradientâ€forming MipZ protein mediating the control of cell division in the magnetotactic bacterium <i>MagnetospirillumÂgryphiswaldense</i> . Molecular Microbiology, 2019, 112, 1423-1439.	1.2	12
104	Molecular architecture of the SYCP3 fibre and its interaction with DNA. Open Biology, 2019, 9, 190094.	1.5	12
105	Highâ€Yield Production, Characterization, and Functionalization of Recombinant Magnetosomes in the Synthetic Bacterium <i>Rhodospirillum rubrum "magneticumâ€</i> . Advanced Biology, 2021, 5, e2101017.	1.4	12
106	Cryo-EM structure of the cetacean morbillivirus nucleoprotein-RNA complex. Journal of Structural Biology, 2021, 213, 107750.	1.3	12
107	Microstructural dependence of giant-magnetoresistance in electrodeposited Cu-Co alloys. Journal of Materials Science, 2004, 39, 5701-5709.	1.7	10
108	Cryoelectron Tomography (CET). , 2007, , 535-604.		10

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109	Correlation Microscopy: Bridging the Gap between Light- and Cryo-Electron Microscopy. Microscopy and Microanalysis, 2005, 11, .	0.2	9
110	Addressing cellular compartmentalization by in situ cryo-electron tomography. Current Opinion in Colloid and Interface Science, 2018, 34, 89-99.	3.4	9
111	Low-dose (S)TEM elemental analysis of water and oxygen uptake in beam sensitive materials. Ultramicroscopy, 2020, 208, 112855.	0.8	9
112	Sample Preparation by 3D-Correlative Focused Ion Beam Milling for High-Resolution Cryo-Electron Tomography. Journal of Visualized Experiments, 2021, , .	0.2	9
113	Cryo-Electron Tomography. Springer Handbooks, 2019, , 189-228.	0.3	7
114	A transformation clustering algorithm and its application in polyribosomes structural profiling. Nucleic Acids Research, 2022, 50, 9001-9011.	6.5	7
115	Automated Cryo-tomography and Single Particle Analysis with a New Type of Phase Plate. Microscopy and Microanalysis, 2014, 20, 206-207.	0.2	5
116	Cryo-FIB Lamella Milling: A Comprehensive Technique to Prepare Samples of Both Plunge- and High-pressure Frozen-hydrated Specimens for in situ Studies Microscopy and Microanalysis, 2018, 24, 820-821.	0.2	5
117	Aberrationâ€corrected microscopy for structural biology applications. Journal of Microscopy, 2009, 233, 170-177.	0.8	3
118	Focal issue on hybrid imaging. Journal of Structural Biology, 2010, 172, 159.	1.3	3
119	Opening Windows into the Cell: Focused-Ion-Beam Milling for Cryo-Electron Tomography. Biophysical Journal, 2014, 106, 600a.	0.2	3
120	Precise 3D-correlative FIB-milling of biological samples using METEOR, an integrated cryo-CLEM imaging system. Microscopy and Microanalysis, 2021, 27, 3230-3232.	0.2	3
121	Diffusion of oxygen in CdSe-photosensor arrays. Materials Science and Engineering B: Solid-State Materials for Advanced Technology, 2002, 94, 123-130.	1.7	2
122	In Situ Tomography of Membrane Proteins Enabled by Advanced Cryo-FIB Sample Preparation and Phase Plate Imaging. Microscopy and Microanalysis, 2015, 21, 1119-1120.	0.2	2
123	Cryo-FIB Lift-out Sample Preparation Using a Novel Cryo-gripper Tool. Microscopy and Microanalysis, 2017, 23, 844-845.	0.2	2
124	ENZEL - A cryogenic, retrofittable, coincident fluorescence, electron, and ion beam solution for the cryo-electron tomography workflow Microscopy and Microanalysis, 2021, 27, 3228-3229.	0.2	2
125	STOPGAP_refine: Tilt series refinement for high-resolution subtomogram averaging. Microscopy and Microanalysis, 2021, 27, 3240-3240.	0.2	2
126	In vivo Architecture of the Polar Organizing Protein Z (PopZ) Meshwork in the Alphaproteobacteria Magnetospirillum gryphiswaldense and Caulobacter crescentus. Journal of Molecular Biology, 2022, 434, 167423.	2.0	2

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127	Investigation of Copper Segregation to the Σ5(310)/[001] Symmetric Tilt Grain Boundary in Aluminum. Materials Research Society Symposia Proceedings, 1999, 589, 301.	0.1	1
128	Experimental Assessment of Strain Gradient Plasticity. Materials Research Society Symposia Proceedings, 2000, 653, .	0.1	1
129	Initiation identification in fused-silica 35-nm optics. , 2002, 4679, 17.		1
130	Exploring the Inner Space of Cells by Cryoelectron-Tomography. Microscopy and Microanalysis, 2004, 10, 152-153.	0.2	1
131	Opening Windows into the Cell: Focused Ion Beam Micromachining of Eukaryotic Cells for Cryo-Electron Tomography. Biophysical Journal, 2013, 104, 353a-354a.	0.2	1
132	Phase Contrast Cryo-Electron Tomography and Single Particle Analysis with a New Phase Plate. Microscopy and Microanalysis, 2014, 20, 232-233.	0.2	1
133	Fluorescence-guided lamella fabrication with ENZEL, an integrated cryogenic CLEM solution for the cryo-electron tomography workflow. Microscopy and Microanalysis, 2021, 27, 3234-3235.	0.2	1
134	Deposition-free Cryo-FIB Lift-out Transfer for Cryo-Electron Tomography Specimen Preparation. Microscopy and Microanalysis, 2021, 27, 3032-3034.	0.2	1
135	The State of the Art in Cryo-Electron Tomography. Microscopy and Microanalysis, 2003, 9, 174-175.	0.2	0
136	Grain Boundary Structure and Its Effect on Plasticity. Microscopy and Microanalysis, 2004, 10, 12-13.	0.2	0
137	Accessing Subcellular Structural Information with Advanced Targeting and Sectioning Techniques. Microscopy and Microanalysis, 2009, 15, 570-571.	0.2	0
138	Structural Cell Biology: Preparing Specimens for Cryo-Electron Tomography Using Focused-Ion-Beam Milling. Microscopy and Microanalysis, 2014, 20, 1222-1223.	0.2	0
139	Cryo-FIB Sample Preparation for Cryo-ET With the Volta Phase Plate. Microscopy and Microanalysis, 2016, 22, 72-73.	0.2	0
140	High-resolution Imaging of Reconstituted Protein-DNA Complexes Using Phase Plate Electron Cryo Microscopy. Microscopy and Microanalysis, 2016, 22, 68-69.	0.2	0
141	Charting Cellular Landscapes in Molecular Detail by in Situ Cryo-Electron Tomography. Biophysical Journal, 2016, 110, 2a.	0.2	0
142	Charting Molecular Landscapes Using Cryo-Electron Tomography. Microscopy Today, 2017, 25, 26-31.	0.2	0
143	Site Specific Cryo-FIB Preparations Aimed at in situ Cryo-Electron Tomography. Microscopy and Microanalysis, 2017, 23, 250-251.	0.2	0
144	3.9â€Ã phase plate cryo-EM reconstruction of the nucleosome core particle. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C1293-C1293.	0.0	0

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145	Experimental Assessment of Strain Gradient Plasticity. Materials Research Society Symposia Proceedings, 2000, 653, 1.	0.1	0
146	Expanded Coverage of the 26S Proteasome Conformational Landscape Reveals Mechanisms of Peptidase Gating. FASEB Journal, 2019, 33, .	0.2	0
147	Recent advances in cryo-electron tomography for in situ structural biology. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, e81-e81.	0.0	0