

Wolfgang Baumeister

List of Publications by Year in descending order

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137
papers

16,765
citations

16411

64
h-index

18075

120
g-index

156
all docs

156
docs citations

156
times ranked

13419
citing authors

#	ARTICLE	IF	CITATIONS
1	STRUCTURAL STUDIES BY ELECTRON TOMOGRAPHY: From Cells to Molecules. Annual Review of Biochemistry, 2005, 74, 833-865.	5.0	614
2	Phase separation of a yeast prion protein promotes cellular fitness. Science, 2018, 359, .	6.0	534
3	Three-Dimensional Structure of Herpes Simplex Virus from Cryo-Electron Tomography. Science, 2003, 302, 1396-1398.	6.0	507
4	Visualizing the molecular sociology at the HeLa cell nuclear periphery. Science, 2016, 351, 969-972.	6.0	493
5	From words to literature in structural proteomics. Nature, 2003, 422, 216-225.	13.7	473
6	Nuclear Pore Complex Structure and Dynamics Revealed by Cryoelectron Tomography. Science, 2004, 306, 1387-1390.	6.0	451
7	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
8	TOM software toolbox: acquisition and analysis for electron tomography. Journal of Structural Biology, 2005, 149, 227-234.	1.3	424
9	Phase-plate cryo-EM structure of a class B GPCRâ€“G-protein complex. Nature, 2017, 546, 118-123.	13.7	424
10	Molecular architecture of the 26S proteasome holocomplex determined by an integrative approach. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 1380-1387.	3.3	422
11	Perspectives of Molecular and Cellular Electron Tomography. Journal of Structural Biology, 1997, 120, 276-308.	1.3	393
12	Correlative microscopy: Bridging the gap between fluorescence light microscopy and cryo-electron tomography. Journal of Structural Biology, 2007, 160, 135-145.	1.3	356
13	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
14	Cryo-electron tomography: The challenge of doing structural biology in situ. Journal of Cell Biology, 2013, 202, 407-419.	2.3	337
15	In Situ Structure of Neuronal C9orf72 Poly-GA Aggregates Reveals Proteasome Recruitment. Cell, 2018, 172, 696-705.e12.	13.5	311
16	Retrovirus envelope protein complex structure in situ studied by cryo-electron tomography. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4729-4734.	3.3	299
17	A molecular census of 26 <i>S</i> proteasomes in intact neurons. Science, 2015, 347, 439-442.	6.0	287
18	Structure of the adenosine-bound human adenosine A1 receptorâ€“Gi complex. Nature, 2018, 558, 559-563.	13.7	274

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19	In Situ Architecture and Cellular Interactions of PolyQ Inclusions. <i>Cell</i> , 2017, 171, 179-187.e10.	13.5	271
20	Phase-plate cryo-EM structure of a biased agonist-bound human GLP-1 receptor-Gs complex. <i>Nature</i> , 2018, 555, 121-125.	13.7	263
21	Cryo-Electron Tomography: Can it Reveal the Molecular Sociology of Cells in Atomic Detail?. <i>Trends in Cell Biology</i> , 2016, 26, 825-837.	3.6	261
22	Identification of macromolecular complexes in cryoelectron tomograms of phantom cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 14153-14158.	3.3	246
23	Micromachining tools and correlative approaches for cellular cryo-electron tomography. <i>Journal of Structural Biology</i> , 2010, 172, 169-179.	1.3	230
24	Native architecture of the <i>Chlamydomonas</i> chloroplast revealed by in situ cryo-electron tomography. <i>ELife</i> , 2015, 4, .	2.8	224
25	Electron tomography: towards visualizing the molecular organization of the cytoplasm. <i>Current Opinion in Structural Biology</i> , 2002, 12, 679-684.	2.6	217
26	Optimized cryo-focused ion beam sample preparation aimed at in situ structural studies of membrane proteins. <i>Journal of Structural Biology</i> , 2017, 197, 73-82.	1.3	216
27	A visual approach to proteomics. <i>Nature Reviews Molecular Cell Biology</i> , 2006, 7, 225-230.	16.1	212
28	Cryo-EM structure of haemoglobin at 3.2 Å... determined with the Volta phase plate. <i>Nature Communications</i> , 2017, 8, 16099.	5.8	211
29	Cryo-EM structure of the active, Gs-protein complexed, human CGRP receptor. <i>Nature</i> , 2018, 561, 492-497.	13.7	210
30	Stress- and ubiquitylation-dependent phase separation of the proteasome. <i>Nature</i> , 2020, 578, 296-300.	13.7	204
31	Three-dimensional architecture of murine rod outer segments determined by cryoelectron tomography. <i>Journal of Cell Biology</i> , 2007, 177, 917-925.	2.3	192
32	Automated segmentation of electron tomograms for a quantitative description of actin filament networks. <i>Journal of Structural Biology</i> , 2012, 177, 135-144.	1.3	186
33	Cryo-electron Tomography of <i>Neurospora</i> Mitochondria. <i>Journal of Structural Biology</i> , 2000, 129, 48-56.	1.3	179
34	Opening windows into the cell: focused-ion-beam milling for cryo-electron tomography. <i>Current Opinion in Structural Biology</i> , 2013, 23, 771-777.	2.6	179
35	Structure of the human 26S proteasome at a resolution of 3.9 Å.... <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 7816-7821.	3.3	174
36	Structure of transcribing mammalian RNA polymerase II. <i>Nature</i> , 2016, 529, 551-554.	13.7	174

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37	Site-Specific Cryo-focused Ion Beam Sample Preparation Guided by 3D Correlative Microscopy. <i>Biophysical Journal</i> , 2016, 110, 860-869.	0.2	172
38	Regulated assembly of a supramolecular centrosome scaffold in vitro. <i>Science</i> , 2015, 348, 808-812.	6.0	170
39	The promise and the challenges of cryo-electron tomography. <i>FEBS Letters</i> , 2020, 594, 3243-3261.	1.3	170
40	A cryo-FIB lift-out technique enables molecular-resolution cryo-ET within native <i>Caenorhabditis elegans</i> tissue. <i>Nature Methods</i> , 2019, 16, 757-762.	9.0	165
41	In Situ Cryo-Electron Tomography: A Post-Reductionist Approach to Structural Biology. <i>Journal of Molecular Biology</i> , 2016, 428, 332-343.	2.0	160
42	The structure of the COPI coat determined within the cell. <i>ELife</i> , 2017, 6, .	2.8	152
43	Organization of Actin Networks in Intact Filopodia. <i>Current Biology</i> , 2007, 17, 79-84.	1.8	151
44	Structural insights into the functional cycle of the ATPase module of the 26S proteasome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1305-1310.	3.3	151
45	Cryo-EM single particle analysis with the Volta phase plate. <i>ELife</i> , 2016, 5, .	2.8	141
46	Electron cryotomography of vitrified cells with a Volta phase plate. <i>Journal of Structural Biology</i> , 2015, 190, 143-154.	1.3	140
47	The Regulatory Complex of <i>Drosophila melanogaster</i> 26s Proteasomes. <i>Journal of Cell Biology</i> , 2000, 150, 119-130.	2.3	138
48	Dissecting the molecular organization of the translocon-associated protein complex. <i>Nature Communications</i> , 2017, 8, 14516.	5.8	131
49	A focused ion beam milling and lift-out approach for site-specific preparation of frozen-hydrated lamellas from multicellular organisms. <i>Journal of Structural Biology</i> , 2015, 192, 262-269.	1.3	125
50	The cryo-electron microscopy structure of huntingtin. <i>Nature</i> , 2018, 555, 117-120.	13.7	125
51	Proteasomes tether to two distinct sites at the nuclear pore complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 13726-13731.	3.3	123
52	An integrated workflow for crosslinking mass spectrometry. <i>Molecular Systems Biology</i> , 2019, 15, e8994.	3.2	120
53	Quantitative live-cell imaging reveals spatio-temporal dynamics and cytoplasmic assembly of the 26S proteasome. <i>Nature Communications</i> , 2014, 5, 3396.	5.8	111
54	Using the Volta phase plate with defocus for cryo-EM single particle analysis. <i>ELife</i> , 2017, 6, .	2.8	109

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55	Electron Microscopy of Biological Materials at the Nanometer Scale. Annual Review of Materials Research, 2012, 42, 33-58.	4.3	108
56	Expanded Coverage of the 26S Proteasome Conformational Landscape Reveals Mechanisms of Peptidase Gating. Cell Reports, 2018, 24, 1301-1315.e5.	2.9	108
57	In situ architecture of the algal nuclear pore complex. Nature Communications, 2018, 9, 2361.	5.8	107
58	Cryo-focused Ion Beam Sample Preparation for Imaging Vitreous Cells by Cryo-electron Tomography. Bio-protocol, 2015, 5, .	0.2	105
59	Structural characterization of the interaction of Ubp6 with the 26S proteasome. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 8626-8631.	3.3	98
60	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
61	Molecular Details Underlying Dynamic Structures and Regulation of the Human 26S Proteasome. Molecular and Cellular Proteomics, 2017, 16, 840-854.	2.5	93
62	Expanding the boundaries of cryo-EM with phase plates. Current Opinion in Structural Biology, 2017, 46, 87-94.	2.6	87
63	Tricalbin-Mediated Contact Sites Control ER Curvature to Maintain Plasma Membrane Integrity. Developmental Cell, 2019, 51, 476-487.e7.	3.1	87
64	Deep learning improves macromolecule identification in 3D cellular cryo-electron tomograms. Nature Methods, 2021, 18, 1386-1394.	9.0	84
65	A Selective Autophagy Pathway for Phase-Separated Endocytic Protein Deposits. Molecular Cell, 2020, 80, 764-778.e7.	4.5	82
66	Charting the native architecture of Chlamydomonas thylakoid membranes with single-molecule precision. ELife, 2020, 9, .	2.8	80
67	From proteomic inventory to architecture. FEBS Letters, 2005, 579, 933-937.	1.3	77
68	Structural basis for VIPP1 oligomerization and maintenance of thylakoid membrane integrity. Cell, 2021, 184, 3643-3659.e23.	13.5	76
69	Molecular and structural architecture of polyQ aggregates in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3446-E3453.	3.3	68
70	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
71	In situ architecture of neuronal α -Synuclein inclusions. Nature Communications, 2021, 12, 2110.	5.8	66
72	Cryo-EM structures of the archaeal PAN-proteasome reveal an around-the-ring ATPase cycle. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 534-539.	3.3	65

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73	Volta phase plate cryo-EM of the small protein complex Prx3. Nature Communications, 2016, 7, 10534.	5.8	64
74	Cryo-EM structure of the native rhodopsin dimer in nanodiscs. Journal of Biological Chemistry, 2019, 294, 14215-14230.	1.6	64
75	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
76	Template-free detection and classification of membrane-bound complexes in cryo-electron tomograms. Nature Methods, 2020, 17, 209-216.	9.0	60
77	Maximum likelihood based classification of electron tomographic data. Journal of Structural Biology, 2011, 173, 77-85.	1.3	56
78	The Architecture of Traveling Actin Waves Revealed by Cryo-Electron Tomography. Structure, 2019, 27, 1211-1223.e5.	1.6	53
79	Morphologies of synaptic protein membrane fusion interfaces. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 9110-9115.	3.3	51
80	Mass Spectrometry Reveals the Missing Links in the Assembly Pathway of the Bacterial 20 S Proteasome. Journal of Biological Chemistry, 2007, 282, 18448-18457.	1.6	50
81	Actin Organization in Cells Responding to a Perforated Surface, Revealed by Live Imaging and Cryo-Electron Tomography. Structure, 2016, 24, 1031-1043.	1.6	50
82	Mapping molecular landscapes inside cells. Biological Chemistry, 2004, 385, 865-872.	1.2	49
83	Towards Visual Proteomics at High Resolution. Journal of Molecular Biology, 2021, 433, 167187.	2.0	49
84	In situ cryo-electron tomography reveals gradient organization of ribosome biogenesis in intact nucleoli. Nature Communications, 2021, 12, 5364.	5.8	46
85	Pleomorphic linkers as ubiquitous structural organizers of vesicles in axons. PLoS ONE, 2018, 13, e0197886.	1.1	34
86	Coordinate transformation based cryo-correlative methods for electron tomography and focused ion beam milling. Ultramicroscopy, 2014, 143, 15-23.	0.8	33
87	Molecular and cellular dynamics of the 26S proteasome. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2021, 1869, 140583.	1.1	33
88	Molecular-scale visualization of sarcomere contraction within native cardiomyocytes. Nature Communications, 2021, 12, 4086.	5.8	33
89	Cryoelectron Tomography Reveals Nanoscale Organization of the Cytoskeleton and Its Relation to Microtubule Curvature Inside Cells. Structure, 2020, 28, 991-1003.e4.	1.6	32
90	Molecular Biology of Assemblies and Machines. , 0, , .		32

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91	A voyage to the inner space of cells. <i>Protein Science</i> , 2009, 14, 257-269.	3.1	31
92	Proteasomes: unfoldase-assisted protein degradation machines. <i>Biological Chemistry</i> , 2019, 401, 183-199.	1.2	29
93	STOPGAP: A Software Package for Subtomogram Averaging and Refinement. <i>Microscopy and Microanalysis</i> , 2020, 26, 2516-2516.	0.2	29
94	Gelâ€like inclusions of C-terminal fragments of TDPâ€43 sequester stalled proteasomes in neurons. <i>EMBO Reports</i> , 2022, 23, e53890.	2.0	28
95	Localization of Protein Complexes by Pattern Recognition. <i>Methods in Cell Biology</i> , 2007, 79, 615-638.	0.5	27
96	In situ structural studies of tripeptidyl peptidase II (TPPII) reveal spatial association with proteasomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4412-4417.	3.3	27
97	Hierarchical detection and analysis of macromolecular complexes in cryo-electron tomograms using Pyto software. <i>Journal of Structural Biology</i> , 2016, 196, 503-514.	1.3	26
98	Determinants shaping the nanoscale architecture of the mouse rod outer segment. <i>ELife</i> , 2021, 10, .	2.8	25
99	Connectivity of centermost chromatophores in <i>Rhodobacter sphaeroides</i> bacteria. <i>Molecular Microbiology</i> , 2018, 109, 812-825.	1.2	24
100	Investigating the Structure of Neurotoxic Protein Aggregates Inside Cells. <i>Trends in Cell Biology</i> , 2020, 30, 951-966.	3.6	24
101	Three-dimensional organization of the cytoskeleton: A cryo-electron tomography perspective. <i>Protein Science</i> , 2020, 29, 1302-1320.	3.1	24
102	Structure-Driven Developments of 26S Proteasome Inhibitors. <i>Annual Review of Pharmacology and Toxicology</i> , 2016, 56, 191-209.	4.2	23
103	Reliable estimation of membrane curvature for cryo-electron tomography. <i>PLoS Computational Biology</i> , 2020, 16, e1007962.	1.5	23
104	Trans-synaptic assemblies link synaptic vesicles and neuroreceptors. <i>Science Advances</i> , 2021, 7, .	4.7	23
105	Revisiting the Structure of Hemoglobin and Myoglobin with Cryo-Electron Microscopy. <i>Journal of Molecular Biology</i> , 2017, 429, 2611-2618.	2.0	22
106	Removing Contamination-Induced Reconstruction Artifacts from Cryo-electron Tomograms. <i>Biophysical Journal</i> , 2016, 110, 850-859.	0.2	21
107	Challenges of Integrating Stochastic Dynamics and Cryo-Electron Tomograms in Whole-Cell Simulations. <i>Journal of Physical Chemistry B</i> , 2017, 121, 3871-3881.	1.2	14
108	Elasticity of podosome actin networks produces nanonewton protrusive forces. <i>Nature Communications</i> , 2022, 13, .	5.8	14

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109	Amyloid-like aggregating proteins cause lysosomal defects in neurons via gain-of-function toxicity. <i>Life Science Alliance</i> , 2022, 5, e202101185.	1.3	13
110	The evolution of the huntingtin-associated protein 40 (HAP40) in conjunction with huntingtin. <i>BMC Evolutionary Biology</i> , 2020, 20, 162.	3.2	11
111	Pathological polyQ expansion does not alter the conformation of the Huntingtin-HAP40 complex. <i>Structure</i> , 2021, 29, 804-809.e5.	1.6	8
112	Statistical spatial analysis for cryo-electron tomography. <i>Computer Methods and Programs in Biomedicine</i> , 2022, 218, 106693.	2.6	8
113	Interphase epichromatin: last refuge for the 30-nm chromatin fiber?. <i>Chromosoma</i> , 2021, 130, 91-102.	1.0	7
114	A transformation clustering algorithm and its application in polyribosomes structural profiling. <i>Nucleic Acids Research</i> , 2022, 50, 9001-9011.	6.5	7
115	Automated Cryo-tomography and Single Particle Analysis with a New Type of Phase Plate. <i>Microscopy and Microanalysis</i> , 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.. <i>Microscopy and Microanalysis</i> , 2018, 24, 820-821.	0.2	5
117	Lipoprotein-like particles in a prokaryote: quinone droplets of <i>Thermoplasma acidophilum</i> . <i>FEMS Microbiology Letters</i> , 2016, 363, fnw169.	0.7	4
118	A feature-guided, focused 3D signal permutation method for subtomogram averaging. <i>Journal of Structural Biology</i> , 2022, 214, 107851.	1.3	4
119	In Situ Tomography of Membrane Proteins Enabled by Advanced Cryo-FIB Sample Preparation and Phase Plate Imaging. <i>Microscopy and Microanalysis</i> , 2015, 21, 1119-1120.	0.2	2
120	Cryo-FIB Lift-out Sample Preparation Using a Novel Cryo-gripper Tool. <i>Microscopy and Microanalysis</i> , 2017, 23, 844-845.	0.2	2
121	Exploring the Inner Space of Cells by Cryoelectron-Tomography. <i>Microscopy and Microanalysis</i> , 2004, 10, 152-153.	0.2	1
122	Phase Contrast Cryo-Electron Tomography and Single Particle Analysis with a New Phase Plate. <i>Microscopy and Microanalysis</i> , 2014, 20, 232-233.	0.2	1
123	Practical Aspects and Usage Tips for the Volta Phase Plate. <i>Microscopy and Microanalysis</i> , 2015, 21, 1391-1392.	0.2	1
124	In situ studies of cellular architecture by Electron Cryo-Tomography with Volta Phase Plate. <i>Microscopy and Microanalysis</i> , 2015, 21, 1835-1836.	0.2	1
125	Single Particle Analysis with the Volta Phase Plate. <i>Microscopy and Microanalysis</i> , 2016, 22, 82-83.	0.2	1
126	Single Particle Imaging with the Volta Phase Plate. <i>Microscopy and Microanalysis</i> , 2019, 25, 7-8.	0.2	1

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127	Autophagy ENDing unproductive phase-separated endocytic protein deposits. <i>Autophagy</i> , 2021, 17, 3264-3265.	4.3	1
128	1S-B2-2In Situ Structural Studies of Macro Molecular Complexes in Cells by Cryo-electron Tomography with Volta Phase Plate. <i>Microscopy (Oxford, England)</i> , 2017, 66, i9-i9.	0.7	1
129	1S-B2-1Single Particle Analysis Applications of the Volta Phase Plate. <i>Microscopy (Oxford, England)</i> , 2017, 66, i9-i9.	0.7	1
130	Structural Cell Biology: Preparing Specimens for Cryo-Electron Tomography Using Focused-Ion-Beam Milling. <i>Microscopy and Microanalysis</i> , 2014, 20, 1222-1223.	0.2	0
131	Phase-Contrast Cryo-Electron Tomography of Primary Cultured Neuronal Cells. <i>Microscopy and Microanalysis</i> , 2014, 20, 208-209.	0.2	0
132	Cryo-FIB Sample Preparation for Cryo-ET With the Volta Phase Plate. <i>Microscopy and Microanalysis</i> , 2016, 22, 72-73.	0.2	0
133	Charting Molecular Landscapes Using Cryo-Electron Tomography. <i>Microscopy Today</i> , 2017, 25, 26-31.	0.2	0
134	The persuasive power of Ernesto Carafoli. <i>Biochemical and Biophysical Research Communications</i> , 2019, 520, 657-658.	1.0	0
135	Structural Genomics and Structural Proteomics: A Global Perspective. , 2008, , 505-537.		0
136	A12â€¦The cryo-electron microscopy structure of huntingtin. , 2018, , .		0
137	Expanded Coverage of the 26S Proteasome Conformational Landscape Reveals Mechanisms of Peptidase Gating. <i>FASEB Journal</i> , 2019, 33, .	0.2	0