

Wolfgang Baumeister

List of Publications by Year in Descending Order

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Version: 2024-04-26

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

139
papers

12,351
citations

61
h-index

111
g-index

156
ext. papers

15,057
ext. citations

12.4
avg, IF

6.68
L-index

#	Paper	IF	Citations
139	Statistical spatial analysis for cryo-electron tomography.. <i>Computer Methods and Programs in Biomedicine</i> , 2022 , 218, 106693	6.9	1
138	A feature-guided, focused 3D signal permutation method for subtomogram averaging.. <i>Journal of Structural Biology</i> , 2022 , 107851	3.4	0
137	Amyloid-like aggregating proteins cause lysosomal defects in neurons via gain-of-function toxicity.. <i>Life Science Alliance</i> , 2022 , 5,	5.8	4
136	Gel-like inclusions of C-terminal fragments of TDP-43 sequester stalled proteasomes in neurons.. <i>EMBO Reports</i> , 2022 , e53890	6.5	1
135	Deep learning improves macromolecule identification in 3D cellular cryo-electron tomograms. <i>Nature Methods</i> , 2021 , 18, 1386-1394	21.6	9
134	Trans-synaptic assemblies link synaptic vesicles and neuroreceptors. <i>Science Advances</i> , 2021 , 7,	14.3	4
133	In situ architecture of neuronal β synuclein inclusions. <i>Nature Communications</i> , 2021 , 12, 2110	17.4	24
132	Interphase epichromatin: last refuge for the 30-nm chromatin fiber?. <i>Chromosoma</i> , 2021 , 130, 91-102	2.8	2
131	Molecular-scale visualization of sarcomere contraction within native cardiomyocytes. <i>Nature Communications</i> , 2021 , 12, 4086	17.4	9
130	Molecular and cellular dynamics of the 26S proteasome. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2021 , 1869, 140583	4	15
129	Structural basis for VIPP1 oligomerization and maintenance of thylakoid membrane integrity. <i>Cell</i> , 2021 , 184, 3643-3659.e23	56.2	17
128	Towards Visual Proteomics at High Resolution. <i>Journal of Molecular Biology</i> , 2021 , 433, 167187	6.5	12
127	Pathological polyQ expansion does not alter the conformation of the Huntingtin-HAP40 complex. <i>Structure</i> , 2021 , 29, 804-809.e5	5.2	3
126	Autophagy ENDing unproductive phase-separated endocytic protein deposits. <i>Autophagy</i> , 2021 , 17, 3264-3265	17.4	6
125	In situ cryo-electron tomography reveals gradient organization of ribosome biogenesis in intact nucleoli. <i>Nature Communications</i> , 2021 , 12, 5364	17.4	6
124	Determinants shaping the nanoscale architecture of the mouse rod outer segment.. <i>ELife</i> , 2021 , 10,	8.9	3
123	The evolution of the huntingtin-associated protein 40 (HAP40) in conjunction with huntingtin. <i>BMC Evolutionary Biology</i> , 2020 , 20, 162	3	4

122	STOPGAP: A Software Package for Subtomogram Averaging and Refinement. <i>Microscopy and Microanalysis</i> , 2020 , 26, 2516-2516	0.5	8
121	Stress- and ubiquitylation-dependent phase separation of the proteasome. <i>Nature</i> , 2020 , 578, 296-300	50.4	92
120	Three-dimensional organization of the cytoskeleton: A cryo-electron tomography perspective. <i>Protein Science</i> , 2020 , 29, 1302-1320	6.3	13
119	Charting the native architecture of thylakoid membranes with single-molecule precision. <i>ELife</i> , 2020 , 9,	8.9	41
118	Direct visualization of degradation microcompartments at the ER membrane. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 1069-1080	11.5	37
117	Template-free detection and classification of membrane-bound complexes in cryo-electron tomograms. <i>Nature Methods</i> , 2020 , 17, 209-216	21.6	25
116	Cryoelectron Tomography Reveals Nanoscale Organization of the Cytoskeleton and Its Relation to Microtubule Curvature Inside Cells. <i>Structure</i> , 2020 , 28, 991-1003.e4	5.2	12
115	Investigating the Structure of Neurotoxic Protein Aggregates Inside Cells. <i>Trends in Cell Biology</i> , 2020 , 30, 951-966	18.3	8
114	The promise and the challenges of cryo-electron tomography. <i>FEBS Letters</i> , 2020 , 594, 3243-3261	3.8	51
113	A Selective Autophagy Pathway for Phase-Separated Endocytic Protein Deposits. <i>Molecular Cell</i> , 2020 , 80, 764-778.e7	17.6	33
112	Reliable estimation of membrane curvature for cryo-electron tomography. <i>PLoS Computational Biology</i> , 2020 , 16, e1007962	5	6
111	Cryo-EM structure of the native rhodopsin dimer in nanodiscs. <i>Journal of Biological Chemistry</i> , 2019 , 294, 14215-14230	5.4	34
110	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	21.6	90
109	Liquid-crystalline phase transitions in lipid droplets are related to cellular states and specific organelle association. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 16866-16871	11.5	28
108	The Architecture of Traveling Actin Waves Revealed by Cryo-Electron Tomography. <i>Structure</i> , 2019 , 27, 1211-1223.e5	5.2	28
107	Proteasomes: unfoldase-assisted protein degradation machines. <i>Biological Chemistry</i> , 2019 , 401, 183-199	4.5	15
106	An integrated workflow for crosslinking mass spectrometry. <i>Molecular Systems Biology</i> , 2019 , 15, e8994	12.2	58
105	Single Particle Imaging with the Volta Phase Plate. <i>Microscopy and Microanalysis</i> , 2019 , 25, 7-8	0.5	1

104	The persuasive power of Ernesto Carafoli. <i>Biochemical and Biophysical Research Communications</i> , 2019 , 520, 657-658	3.4	
103	Tricalbin-Mediated Contact Sites Control ER Curvature to Maintain Plasma Membrane Integrity. <i>Developmental Cell</i> , 2019 , 51, 476-487.e7	10.2	43
102	Cryo-EM structures of the archaeal PAN-proteasome reveal an around-the-ring ATPase cycle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 534-539	11.5	51
101	Phase-plate cryo-EM structure of a biased agonist-bound human GLP-1 receptor-Gs complex. <i>Nature</i> , 2018 , 555, 121-125	50.4	190
100	The cryo-electron microscopy structure of huntingtin. <i>Nature</i> , 2018 , 555, 117-120	50.4	70
99	In Situ Structure of Neuronal C9orf72 Poly-GA Aggregates Reveals Proteasome Recruitment. <i>Cell</i> , 2018 , 172, 696-705.e12	56.2	196
98	Phase separation of a yeast prion protein promotes cellular fitness. <i>Science</i> , 2018 , 359,	33.3	344
97	Molecular and structural architecture of polyQ aggregates in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E3446-E3453	11.5	40
96	Expanded Coverage of the 26S Proteasome Conformational Landscape Reveals Mechanisms of Peptidase Gating. <i>Cell Reports</i> , 2018 , 24, 1301-1315.e5	10.6	65
95	Connectivity of centermost chromatophores in <i>Rhodobacter sphaeroides</i> bacteria. <i>Molecular Microbiology</i> , 2018 , 109, 812-825	4.1	16
94	In situ architecture of the algal nuclear pore complex. <i>Nature Communications</i> , 2018 , 9, 2361	17.4	76
93	Structure of the adenosine-bound human adenosine A receptor-G complex. <i>Nature</i> , 2018 , 558, 559-563	50.4	188
92	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	0.5	0
91	Pleomorphic linkers as ubiquitous structural organizers of vesicles in axons. <i>PLoS ONE</i> , 2018 , 13, e0197886	3.7	21
90	Cryo-EM structure of the active, G-protein complexed, human CGRP receptor. <i>Nature</i> , 2018 , 561, 492-497	50.4	141
89	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	11.5	108
88	Phase-plate cryo-EM structure of a class B GPCR-G-protein complex. <i>Nature</i> , 2017 , 546, 118-123	50.4	334
87	Dissecting the molecular organization of the translocon-associated protein complex. <i>Nature Communications</i> , 2017 , 8, 14516	17.4	82

86	Molecular Details Underlying Dynamic Structures and Regulation of the Human 26S Proteasome. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, 840-854	7.6	67
85	Challenges of Integrating Stochastic Dynamics and Cryo-Electron Tomograms in Whole-Cell Simulations. <i>Journal of Physical Chemistry B</i> , 2017 , 121, 3871-3881	3.4	9
84	Cryo-FIB Lift-out Sample Preparation Using a Novel Cryo-gripper Tool. <i>Microscopy and Microanalysis</i> , 2017 , 23, 844-845	0.5	2
83	In Situ Architecture and Cellular Interactions of PolyQ Inclusions. <i>Cell</i> , 2017 , 171, 179-187.e10	56.2	177
82	Revisiting the Structure of Hemoglobin and Myoglobin with Cryo-Electron Microscopy. <i>Journal of Molecular Biology</i> , 2017 , 429, 2611-2618	6.5	20
81	Morphologies of synaptic protein membrane fusion interfaces. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 9110-9115	11.5	33
80	Charting Molecular Landscapes Using Cryo-Electron Tomography. <i>Microscopy Today</i> , 2017 , 25, 26-31	0.4	
79	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	11.5	79
78	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	11.5	21
77	Expanding the boundaries of cryo-EM with phase plates. <i>Current Opinion in Structural Biology</i> , 2017 , 46, 87-94	8.1	66
76	Cryo-EM structure of haemoglobin at 3.2 Å determined with the Volta phase plate. <i>Nature Communications</i> , 2017 , 8, 16099	17.4	171
75	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	3.4	143
74	The structure of the COPI coat determined within the cell. <i>ELife</i> , 2017 , 6,	8.9	94
73	Using the Volta phase plate with defocus for cryo-EM single particle analysis. <i>ELife</i> , 2017 , 6,	8.9	87
72	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	1.3	0
71	1S-B2-1Single Particle Analysis Applications of the Volta Phase Plate. <i>Microscopy (Oxford, England)</i> , 2017 , 66, i9-i9	1.3	0
70	In Situ Cryo-Electron Tomography: A Post-Reductionist Approach to Structural Biology. <i>Journal of Molecular Biology</i> , 2016 , 428, 332-343	6.5	112
69	Enabling and doing structural biology in situ 2016 , 113-113		

68	Volta phase plate cryo-EM of the small protein complex Prx3. <i>Nature Communications</i> , 2016 , 7, 10534	17.4	58
67	Hierarchical detection and analysis of macromolecular complexes in cryo-electron tomograms using Pyto software. <i>Journal of Structural Biology</i> , 2016 , 196, 503-514	3.4	14
66	Actin Organization in Cells Responding to a Perforated Surface, Revealed by Live Imaging and Cryo-Electron Tomography. <i>Structure</i> , 2016 , 24, 1031-43	5.2	38
65	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, 7816-21	11.5	143
64	Structure of transcribing mammalian RNA polymerase II. <i>Nature</i> , 2016 , 529, 551-4	50.4	136
63	Structure-Driven Developments of 26S Proteasome Inhibitors. <i>Annual Review of Pharmacology and Toxicology</i> , 2016 , 56, 191-209	17.9	20
62	Removing Contamination-Induced Reconstruction Artifacts from Cryo-electron Tomograms. <i>Biophysical Journal</i> , 2016 , 110, 850-9	2.9	12
61	Site-Specific Cryo-focused Ion Beam Sample Preparation Guided by 3D Correlative Microscopy. <i>Biophysical Journal</i> , 2016 , 110, 860-9	2.9	122
60	Visualizing the molecular sociology at the HeLa cell nuclear periphery. <i>Science</i> , 2016 , 351, 969-72	33.3	344
59	Cryo-FIB Sample Preparation for Cryo-ET With the Volta Phase Plate. <i>Microscopy and Microanalysis</i> , 2016 , 22, 72-73	0.5	
58	Cryo-EM single particle analysis with the Volta phase plate. <i>ELife</i> , 2016 , 5,	8.9	102
57	Single Particle Analysis with the Volta Phase Plate. <i>Microscopy and Microanalysis</i> , 2016 , 22, 82-83	0.5	1
56	Lipoprotein-like particles in a prokaryote: quinone droplets of <i>Thermoplasma acidophilum</i> . <i>FEMS Microbiology Letters</i> , 2016 , 363,	2.9	3
55	Cryo-Electron Tomography: Can it Reveal the Molecular Sociology of Cells in Atomic Detail?. <i>Trends in Cell Biology</i> , 2016 , 26, 825-837	18.3	189
54	Proteasomes. A molecular census of 26S proteasomes in intact neurons. <i>Science</i> , 2015 , 347, 439-42	33.3	239
53	Structural characterization of the interaction of Ubp6 with the 26S proteasome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 8626-31	11.5	86
52	Electron cryotomography of vitrified cells with a Volta phase plate. <i>Journal of Structural Biology</i> , 2015 , 190, 143-54	3.4	108
51	Centrosomes. Regulated assembly of a supramolecular centrosome scaffold in vitro. <i>Science</i> , 2015 , 348, 808-12	33.3	125

50	In situ structural analysis of Golgi intracisternal protein arrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 11264-9	11.5	83
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, 262-9	3.4	96
48	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	0.5	2
47	Practical Aspects and Usage Tips for the Volta Phase Plate. <i>Microscopy and Microanalysis</i> , 2015 , 21, 1391-1392	0.5	0
46	Native architecture of the Chlamydomonas chloroplast revealed by in situ cryo-electron tomography. <i>ELife</i> , 2015 , 4,	8.9	166
45	In situ studies of cellular architecture by Electron Cryo-Tomography with Volta Phase Plate. <i>Microscopy and Microanalysis</i> , 2015 , 21, 1835-1836	0.5	1
44	Cryo-focused Ion Beam Sample Preparation for Imaging Vitreous Cells by Cryo-electron Tomography. <i>Bio-protocol</i> , 2015 , 5,	0.9	72
43	Volta potential phase plate for in-focus phase contrast transmission electron microscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 15635-40	11.5	341
42	Coordinate transformation based cryo-correlative methods for electron tomography and focused ion beam milling. <i>Ultramicroscopy</i> , 2014 , 143, 15-23	3.1	26
41	Automated Cryo-tomography and Single Particle Analysis with a New Type of Phase Plate. <i>Microscopy and Microanalysis</i> , 2014 , 20, 206-207	0.5	4
40	Phase-Contrast Cryo-Electron Tomography of Primary Cultured Neuronal Cells. <i>Microscopy and Microanalysis</i> , 2014 , 20, 208-209	0.5	
39	Phase Contrast Cryo-Electron Tomography and Single Particle Analysis with a New Phase Plate. <i>Microscopy and Microanalysis</i> , 2014 , 20, 232-233	0.5	1
38	Structural Cell Biology: Preparing Specimens for Cryo-Electron Tomography Using Focused-Ion-Beam Milling. <i>Microscopy and Microanalysis</i> , 2014 , 20, 1222-1223	0.5	
37	Quantitative live-cell imaging reveals spatio-temporal dynamics and cytoplasmic assembly of the 26S proteasome. <i>Nature Communications</i> , 2014 , 5, 3396	17.4	71
36	Opening windows into the cell: focused-ion-beam milling for cryo-electron tomography. <i>Current Opinion in Structural Biology</i> , 2013 , 23, 771-7	8.1	127
35	Cryo-electron tomography: the challenge of doing structural biology in situ. <i>Journal of Cell Biology</i> , 2013 , 202, 407-19	7.3	266
34	Molecular architecture of the 26S proteasome holocomplex determined by an integrative approach. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 1380-7	11.5	380
33	Automated segmentation of electron tomograms for a quantitative description of actin filament networks. <i>Journal of Structural Biology</i> , 2012 , 177, 135-44	3.4	122

32	Electron Microscopy of Biological Materials at the Nanometer Scale. <i>Annual Review of Materials Research</i> , 2012 , 42, 33-58	12.8	91
31	Focused ion beam micromachining of eukaryotic cells for cryoelectron tomography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 4449-54	11.5	260
30	Maximum likelihood based classification of electron tomographic data. <i>Journal of Structural Biology</i> , 2011 , 173, 77-85	3.4	47
29	Micromachining tools and correlative approaches for cellular cryo-electron tomography. <i>Journal of Structural Biology</i> , 2010 , 172, 169-79	3.4	178
28	Structural Genomics and Structural Proteomics: A Global Perspective 2008 , 505-537		
27	Organization of actin networks in intact filopodia. <i>Current Biology</i> , 2007 , 17, 79-84	6.3	127
26	Three-dimensional architecture of murine rod outer segments determined by cryoelectron tomography. <i>Journal of Cell Biology</i> , 2007 , 177, 917-25	7.3	171
25	Mass spectrometry reveals the missing links in the assembly pathway of the bacterial 20 S proteasome. <i>Journal of Biological Chemistry</i> , 2007 , 282, 18448-18457	5.4	44
24	Localization of protein complexes by pattern recognition. <i>Methods in Cell Biology</i> , 2007 , 79, 615-38	1.8	21
23	Correlative microscopy: bridging the gap between fluorescence light microscopy and cryo-electron tomography. <i>Journal of Structural Biology</i> , 2007 , 160, 135-45	3.4	305
22	A visual approach to proteomics. <i>Nature Reviews Molecular Cell Biology</i> , 2006 , 7, 225-30	48.7	196
21	A voyage to the inner space of cells. <i>Protein Science</i> , 2005 , 14, 257-69	6.3	27
20	TOM software toolbox: acquisition and analysis for electron tomography. <i>Journal of Structural Biology</i> , 2005 , 149, 227-34	3.4	367
19	From proteomic inventory to architecture. <i>FEBS Letters</i> , 2005 , 579, 933-7	3.8	70
18	Structural studies by electron tomography: from cells to molecules. <i>Annual Review of Biochemistry</i> , 2005 , 74, 833-65	29.1	551
17	Retrovirus envelope protein complex structure in situ studied by cryo-electron tomography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 4729-34	11.5	263
16	Mapping molecular landscapes inside cells. <i>Biological Chemistry</i> , 2004 , 385, 865-72	4.5	43
15	Nuclear pore complex structure and dynamics revealed by cryoelectron tomography. <i>Science</i> , 2004 , 306, 1387-90	33.3	408

14	Exploring the Inner Space of Cells by Cryoelectron-Tomography. <i>Microscopy and Microanalysis</i> , 2004 , 10, 152-153	0.5	1
13	Three-dimensional structure of herpes simplex virus from cryo-electron tomography. <i>Science</i> , 2003 , 302, 1396-8	33.3	441
12	From words to literature in structural proteomics. <i>Nature</i> , 2003 , 422, 216-25	50.4	412
11	Electron tomography: towards visualizing the molecular organization of the cytoplasm. <i>Current Opinion in Structural Biology</i> , 2002 , 12, 679-84	8.1	191
10	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, 14153-8	11.5	207
9	The regulatory complex of <i>Drosophila melanogaster</i> 26S proteasomes. Subunit composition and localization of a deubiquitylating enzyme. <i>Journal of Cell Biology</i> , 2000 , 150, 119-30	7.3	124
8	Cryo-electron tomography of neurospora mitochondria. <i>Journal of Structural Biology</i> , 2000 , 129, 48-56	3.4	170
7	Perspectives of molecular and cellular electron tomography. <i>Journal of Structural Biology</i> , 1997 , 120, 276-308	3.4	355
6	Molecular Biology of Assemblies and Machines		24
5	In situ architecture of the ciliary base reveals the stepwise assembly of IFT trains		2
4	A selective autophagy pathway for phase separated endocytic protein deposits		1
3	Amyloid-like aggregates cause lysosomal defects in neurons via gain-of-function toxicity		4
2	Structural basis for VIPP1 oligomerization and maintenance of thylakoid membrane integrity		7
1	Gel-like inclusions of C-terminal fragments of TDP-43 sequester and inhibit proteasomes in neurons		1