

Wolfgang Baumeister

List of Publications by Citations

Source: <https://exaly.com/author-pdf/1511530/wolfgang-baumeister-publications-by-citations.pdf>

Version: 2024-04-26

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Structural studies by electron tomography: from cells to molecules. <i>Annual Review of Biochemistry</i> , 2005 , 74, 833-65	29.1	551
138	Three-dimensional structure of herpes simplex virus from cryo-electron tomography. <i>Science</i> , 2003 , 302, 1396-8	33.3	441
137	From words to literature in structural proteomics. <i>Nature</i> , 2003 , 422, 216-25	50.4	412
136	Nuclear pore complex structure and dynamics revealed by cryoelectron tomography. <i>Science</i> , 2004 , 306, 1387-90	33.3	408
135	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
134	TOM software toolbox: acquisition and analysis for electron tomography. <i>Journal of Structural Biology</i> , 2005 , 149, 227-34	3.4	367
133	Perspectives of molecular and cellular electron tomography. <i>Journal of Structural Biology</i> , 1997 , 120, 276-308	3.4	355
132	Phase separation of a yeast prion protein promotes cellular fitness. <i>Science</i> , 2018 , 359,	33.3	344
131	Visualizing the molecular sociology at the HeLa cell nuclear periphery. <i>Science</i> , 2016 , 351, 969-72	33.3	344
130	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
129	Phase-plate cryo-EM structure of a class B GPCR-G-protein complex. <i>Nature</i> , 2017 , 546, 118-123	50.4	334
128	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
127	Cryo-electron tomography: the challenge of doing structural biology in situ. <i>Journal of Cell Biology</i> , 2013 , 202, 407-19	7.3	266
126	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
125	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
124	Proteasomes. A molecular census of 26S proteasomes in intact neurons. <i>Science</i> , 2015 , 347, 439-42	33.3	239
123	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

122	In Situ Structure of Neuronal C9orf72 Poly-GA Aggregates Reveals Proteasome Recruitment. <i>Cell</i> , 2018 , 172, 696-705.e12	56.2	196
121	A visual approach to proteomics. <i>Nature Reviews Molecular Cell Biology</i> , 2006 , 7, 225-30	48.7	196
120	Electron tomography: towards visualizing the molecular organization of the cytoplasm. <i>Current Opinion in Structural Biology</i> , 2002 , 12, 679-84	8.1	191
119	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
118	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
117	Structure of the adenosine-bound human adenosine A receptor-G complex. <i>Nature</i> , 2018 , 558, 559-563	50.4	188
116	Micromachining tools and correlative approaches for cellular cryo-electron tomography. <i>Journal of Structural Biology</i> , 2010 , 172, 169-79	3.4	178
115	In Situ Architecture and Cellular Interactions of PolyQ Inclusions. <i>Cell</i> , 2017 , 171, 179-187.e10	56.2	177
114	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
113	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
112	Cryo-electron tomography of neurospora mitochondria. <i>Journal of Structural Biology</i> , 2000 , 129, 48-56	3.4	170
111	Native architecture of the Chlamydomonas chloroplast revealed by in situ cryo-electron tomography. <i>ELife</i> , 2015 , 4,	8.9	166
110	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
109	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
108	Cryo-EM structure of the active, G-protein complexed, human CGRP receptor. <i>Nature</i> , 2018 , 561, 492-497	50.4	141
107	Structure of transcribing mammalian RNA polymerase II. <i>Nature</i> , 2016 , 529, 551-4	50.4	136
106	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
105	Organization of actin networks in intact filopodia. <i>Current Biology</i> , 2007 , 17, 79-84	6.3	127

104	Centrosomes. Regulated assembly of a supramolecular centrosome scaffold in vitro. <i>Science</i> , 2015 , 348, 808-12	33.3	125
103	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
102	Site-Specific Cryo-focused Ion Beam Sample Preparation Guided by 3D Correlative Microscopy. <i>Biophysical Journal</i> , 2016 , 110, 860-9	2.9	122
101	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
100	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
99	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
98	Electron cryotomography of vitrified cells with a Volta phase plate. <i>Journal of Structural Biology</i> , 2015 , 190, 143-54	3.4	108
97	Cryo-EM single particle analysis with the Volta phase plate. <i>ELife</i> , 2016 , 5,	8.9	102
96	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
95	The structure of the COPI coat determined within the cell. <i>ELife</i> , 2017 , 6,	8.9	94
94	Stress- and ubiquitylation-dependent phase separation of the proteasome. <i>Nature</i> , 2020 , 578, 296-300	50.4	92
93	Electron Microscopy of Biological Materials at the Nanometer Scale. <i>Annual Review of Materials Research</i> , 2012 , 42, 33-58	12.8	91
92	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
91	Using the Volta phase plate with defocus for cryo-EM single particle analysis. <i>ELife</i> , 2017 , 6,	8.9	87
90	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
89	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
88	Dissecting the molecular organization of the translocon-associated protein complex. <i>Nature Communications</i> , 2017 , 8, 14516	17.4	82
87	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

86	In situ architecture of the algal nuclear pore complex. <i>Nature Communications</i> , 2018 , 9, 2361	17.4	76
85	Cryo-focused Ion Beam Sample Preparation for Imaging Vitreous Cells by Cryo-electron Tomography. <i>Bio-protocol</i> , 2015 , 5,	0.9	72
84	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
83	The cryo-electron microscopy structure of huntingtin. <i>Nature</i> , 2018 , 555, 117-120	50.4	70
82	From proteomic inventory to architecture. <i>FEBS Letters</i> , 2005 , 579, 933-7	3.8	70
81	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
80	Expanding the boundaries of cryo-EM with phase plates. <i>Current Opinion in Structural Biology</i> , 2017 , 46, 87-94	8.1	66
79	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
78	Volta phase plate cryo-EM of the small protein complex Prx3. <i>Nature Communications</i> , 2016 , 7, 10534	17.4	58
77	An integrated workflow for crosslinking mass spectrometry. <i>Molecular Systems Biology</i> , 2019 , 15, e8994	12.2	58
76	The promise and the challenges of cryo-electron tomography. <i>FEBS Letters</i> , 2020 , 594, 3243-3261	3.8	51
75	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
74	Maximum likelihood based classification of electron tomographic data. <i>Journal of Structural Biology</i> , 2011 , 173, 77-85	3.4	47
73	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
72	Mapping molecular landscapes inside cells. <i>Biological Chemistry</i> , 2004 , 385, 865-72	4.5	43
71	Tricalbin-Mediated Contact Sites Control ER Curvature to Maintain Plasma Membrane Integrity. <i>Developmental Cell</i> , 2019 , 51, 476-487.e7	10.2	43
70	Charting the native architecture of thylakoid membranes with single-molecule precision. <i>ELife</i> , 2020 , 9,	8.9	41
69	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

68	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
67	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
66	Cryo-EM structure of the native rhodopsin dimer in nanodiscs. <i>Journal of Biological Chemistry</i> , 2019 , 294, 14215-14230	5.4	34
65	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
64	A Selective Autophagy Pathway for Phase-Separated Endocytic Protein Deposits. <i>Molecular Cell</i> , 2020 , 80, 764-778.e7	17.6	33
63	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
62	The Architecture of Traveling Actin Waves Revealed by Cryo-Electron Tomography. <i>Structure</i> , 2019 , 27, 1211-1223.e5	5.2	28
61	A voyage to the inner space of cells. <i>Protein Science</i> , 2005 , 14, 257-69	6.3	27
60	Coordinate transformation based cryo-correlative methods for electron tomography and focused ion beam milling. <i>Ultramicroscopy</i> , 2014 , 143, 15-23	3.1	26
59	Template-free detection and classification of membrane-bound complexes in cryo-electron tomograms. <i>Nature Methods</i> , 2020 , 17, 209-216	21.6	25
58	Molecular Biology of Assemblies and Machines		24
57	In situ architecture of neuronal β synuclein inclusions. <i>Nature Communications</i> , 2021 , 12, 2110	17.4	24
56	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
55	Localization of protein complexes by pattern recognition. <i>Methods in Cell Biology</i> , 2007 , 79, 615-38	1.8	21
54	Pleomorphic linkers as ubiquitous structural organizers of vesicles in axons. <i>PLoS ONE</i> , 2018 , 13, e0197886	3.7	21
53	Structure-Driven Developments of 26S Proteasome Inhibitors. <i>Annual Review of Pharmacology and Toxicology</i> , 2016 , 56, 191-209	17.9	20
52	Revisiting the Structure of Hemoglobin and Myoglobin with Cryo-Electron Microscopy. <i>Journal of Molecular Biology</i> , 2017 , 429, 2611-2618	6.5	20
51	Structural basis for VIPP1 oligomerization and maintenance of thylakoid membrane integrity. <i>Cell</i> , 2021 , 184, 3643-3659.e23	56.2	17

50	Connectivity of centermost chromatophores in <i>Rhodobacter sphaeroides</i> bacteria. <i>Molecular Microbiology</i> , 2018 , 109, 812-825	4.1	16
49	Proteasomes: unfoldase-assisted protein degradation machines. <i>Biological Chemistry</i> , 2019 , 401, 183-199.	4.5	15
48	Molecular and cellular dynamics of the 26S proteasome. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2021 , 1869, 140583	4	15
47	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
46	Three-dimensional organization of the cytoskeleton: A cryo-electron tomography perspective. <i>Protein Science</i> , 2020 , 29, 1302-1320	6.3	13
45	Removing Contamination-Induced Reconstruction Artifacts from Cryo-electron Tomograms. <i>Biophysical Journal</i> , 2016 , 110, 850-9	2.9	12
44	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
43	Towards Visual Proteomics at High Resolution. <i>Journal of Molecular Biology</i> , 2021 , 433, 167187	6.5	12
42	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
41	Deep learning improves macromolecule identification in 3D cellular cryo-electron tomograms. <i>Nature Methods</i> , 2021 , 18, 1386-1394	21.6	9
40	Molecular-scale visualization of sarcomere contraction within native cardiomyocytes. <i>Nature Communications</i> , 2021 , 12, 4086	17.4	9
39	STOPGAP: A Software Package for Subtomogram Averaging and Refinement. <i>Microscopy and Microanalysis</i> , 2020 , 26, 2516-2516	0.5	8
38	Investigating the Structure of Neurotoxic Protein Aggregates Inside Cells. <i>Trends in Cell Biology</i> , 2020 , 30, 951-966	18.3	8
37	Structural basis for VIPP1 oligomerization and maintenance of thylakoid membrane integrity		7
36	Reliable estimation of membrane curvature for cryo-electron tomography. <i>PLoS Computational Biology</i> , 2020 , 16, e1007962	5	6
35	In situ cryo-electron tomography reveals gradient organization of ribosome biogenesis in intact nucleoli. <i>Nature Communications</i> , 2021 , 12, 5364	17.4	6
34	The evolution of the huntingtin-associated protein 40 (HAP40) in conjunction with huntingtin. <i>BMC Evolutionary Biology</i> , 2020 , 20, 162	3	4
33	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

32	Amyloid-like aggregates cause lysosomal defects in neurons via gain-of-function toxicity		4
31	Trans-synaptic assemblies link synaptic vesicles and neuroreceptors. <i>Science Advances</i> , 2021 , 7,	14.3	4
30	Amyloid-like aggregating proteins cause lysosomal defects in neurons via gain-of-function toxicity.. <i>Life Science Alliance</i> , 2022 , 5,	5.8	4
29	Lipoprotein-like particles in a prokaryote: quinone droplets of <i>Thermoplasma acidophilum</i> . <i>FEMS Microbiology Letters</i> , 2016 , 363,	2.9	3
28	Pathological polyQ expansion does not alter the conformation of the Huntingtin-HAP40 complex. <i>Structure</i> , 2021 , 29, 804-809.e5	5.2	3
27	Determinants shaping the nanoscale architecture of the mouse rod outer segment.. <i>ELife</i> , 2021 , 10,	8.9	3
26	Cryo-FIB Lift-out Sample Preparation Using a Novel Cryo-gripper Tool. <i>Microscopy and Microanalysis</i> , 2017 , 23, 844-845	0.5	2
25	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
24	In situ architecture of the ciliary base reveals the stepwise assembly of IFT trains		2
23	Interphase epichromatin: last refuge for the 30-nm chromatin fiber?. <i>Chromosoma</i> , 2021 , 130, 91-102	2.8	2
22	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
21	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
20	Exploring the Inner Space of Cells by Cryoelectron-Tomography. <i>Microscopy and Microanalysis</i> , 2004 , 10, 152-153	0.5	1
19	A selective autophagy pathway for phase separated endocytic protein deposits		1
18	Single Particle Analysis with the Volta Phase Plate. <i>Microscopy and Microanalysis</i> , 2016 , 22, 82-83	0.5	1
17	Single Particle Imaging with the Volta Phase Plate. <i>Microscopy and Microanalysis</i> , 2019 , 25, 7-8	0.5	1
16	Gel-like inclusions of C-terminal fragments of TDP-43 sequester and inhibit proteasomes in neurons		1
15	Statistical spatial analysis for cryo-electron tomography.. <i>Computer Methods and Programs in Biomedicine</i> , 2022 , 218, 106693	6.9	1

14	Gel-like inclusions of C-terminal fragments of TDP-43 sequester stalled proteasomes in neurons.. <i>EMBO Reports</i> , 2022 , e53890	6.5	1
13	Practical Aspects and Usage Tips for the Volta Phase Plate. <i>Microscopy and Microanalysis</i> , 2015 , 21, 1391-1392	1.3	0
12	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
11	1S-B2-1Single Particle Analysis Applications of the Volta Phase Plate. <i>Microscopy (Oxford, England)</i> , 2017 , 66, i9-i9	1.3	0
10	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
9	A feature-guided, focused 3D signal permutation method for subtomogram averaging.. <i>Journal of Structural Biology</i> , 2022 , 107851	3.4	0
8	Enabling and doing structural biology in situ 2016 , 113-113		
7	Phase-Contrast Cryo-Electron Tomography of Primary Cultured Neuronal Cells. <i>Microscopy and Microanalysis</i> , 2014 , 20, 208-209	0.5	
6	Charting Molecular Landscapes Using Cryo-Electron Tomography. <i>Microscopy Today</i> , 2017 , 25, 26-31	0.4	
5	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	
4	Structural Genomics and Structural Proteomics: A Global Perspective 2008 , 505-537		
3	Cryo-FIB Sample Preparation for Cryo-ET With the Volta Phase Plate. <i>Microscopy and Microanalysis</i> , 2016 , 22, 72-73	0.5	
2	The persuasive power of Ernesto Carafoli. <i>Biochemical and Biophysical Research Communications</i> , 2019 , 520, 657-658	3.4	
1	Autophagy ENDing unproductive phase-separated endocytic protein deposits. <i>Autophagy</i> , 2021 , 17, 3264-3265	3.2	0