

Friedrich Foerster

List of Publications by Year in descending order

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103
papers

10,415
citations

34016

52
h-index

38300

95
g-index

116
all docs

116
docs citations

116
times ranked

9090
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	Visualizing the molecular sociology at the HeLa cell nuclear periphery. Science, 2016, 351, 969-972.	6.0	493
3	Nuclear Pore Complex Structure and Dynamics Revealed by Cryoelectron Tomography. Science, 2004, 306, 1387-1390.	6.0	451
4	TOM software toolbox: acquisition and analysis for electron tomography. Journal of Structural Biology, 2005, 149, 227-234.	1.3	424
5	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
6	Snapshots of nuclear pore complexes in action captured by cryo-electron tomography. Nature, 2007, 449, 611-615.	13.7	330
7	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
8	The Eukaryotic CO ₂ -Concentrating Organelle Is Liquid-like and Exhibits Dynamic Reorganization. Cell, 2017, 171, 148-162.e19.	13.5	298
9	A molecular census of 26 <i>S</i> proteasomes in intact neurons. Science, 2015, 347, 439-442.	6.0	287
10	False discovery rate estimation for cross-linked peptides identified by mass spectrometry. Nature Methods, 2012, 9, 901-903.	9.0	273
11	Expanding the Chemical Cross-Linking Toolbox by the Use of Multiple Proteases and Enrichment by Size Exclusion Chromatography. Molecular and Cellular Proteomics, 2012, 11, M111.014126.	2.5	264
12	Identification of macromolecular complexes in cryoelectron tomograms of phantom cells. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 14153-14158.	3.3	246
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.	3.3	242
14	Chemical cross-linking/mass spectrometry targeting acidic residues in proteins and protein complexes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 9455-9460.	3.3	213
15	Integrating Diverse Data for Structure Determination of Macromolecular Assemblies. Annual Review of Biochemistry, 2008, 77, 443-477.	5.0	204
16	PyTom: A python-based toolbox for localization of macromolecules in cryo-electron tomograms and subtomogram analysis. Journal of Structural Biology, 2012, 178, 177-188.	1.3	202
17	The Mechanism of HIV-1 Core Assembly: Insights from Three-Dimensional Reconstructions of Authentic Virions. Structure, 2006, 14, 15-20.	1.6	188
18	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

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19	Structural basis for coupling protein transport and N-glycosylation at the mammalian endoplasmic reticulum. <i>Science</i> , 2018, 360, 215-219.	6.0	177
20	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
21	Structure of the native Sec61 protein-conducting channel. <i>Nature Communications</i> , 2015, 6, 8403.	5.8	169
22	Classification of cryo-electron sub-tomograms using constrained correlation. <i>Journal of Structural Biology</i> , 2008, 161, 276-286.	1.3	161
23	Multiple Conformations of <i>E. coli</i> Hsp90 in Solution: Insights into the Conformational Dynamics of Hsp90. <i>Structure</i> , 2008, 16, 755-765.	1.6	154
24	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
25	Structure of the 26S proteasome with ATP- γ -S bound provides insights into the mechanism of nucleotide-dependent substrate translocation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 7264-7269.	3.3	148
26	Equally sloped tomography with oversampling reconstruction. <i>Physical Review B</i> , 2005, 72, .	1.1	144
27	Integration of Small-Angle X-Ray Scattering Data into Structural Modeling of Proteins and Their Assemblies. <i>Journal of Molecular Biology</i> , 2008, 382, 1089-1106.	2.0	139
28	The proteasomal subunit Rpn6 is a molecular clamp holding the core and regulatory subcomplexes together. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 149-154.	3.3	136
29	Mapping 70S ribosomes in intact cells by cryoelectron tomography and pattern recognition. <i>Journal of Structural Biology</i> , 2006, 156, 334-341.	1.3	135
30	Dissecting the molecular organization of the translocon-associated protein complex. <i>Nature Communications</i> , 2017, 8, 14516.	5.8	131
31	Structure of the 26S proteasome from <i>Schizosaccharomyces pombe</i> at subnanometer resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 20992-20997.	3.3	130
32	Structure of the mammalian oligosaccharyl-transferase complex in the native ER protein translocon. <i>Nature Communications</i> , 2014, 5, 3072.	5.8	127
33	Crystal structure of the proteasomal deubiquitylation module Rpn8-Rpn11. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2984-2989.	3.3	120
34	An Update on Sec61 Channel Functions, Mechanisms, and Related Diseases. <i>Frontiers in Physiology</i> , 2017, 8, 887.	1.3	117
35	Insights into the molecular architecture of the 26S proteasome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 11943-11947.	3.3	116
36	Organization of the mitochondrial translation machinery studied in situ by cryoelectron tomography. <i>Nature Communications</i> , 2015, 6, 6019.	5.8	115

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37	Localization of the proteasomal ubiquitin receptors Rpn10 and Rpn13 by electron cryomicroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 1479-1484.	3.3	114
38	Structures of the cyanobacterial circadian oscillator frozen in a fully assembled state. Science, 2017, 355, 1181-1184.	6.0	106
39	Morphological Characterization of Molecular Complexes Present in the Synaptic Cleft. Structure, 2005, 13, 423-434.	1.6	98
40	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
41	Structure Determination In Situ by Averaging of Tomograms. Methods in Cell Biology, 2007, 79, 741-767.	0.5	97
42	Structure and 3D Arrangement of Endoplasmic Reticulum Membrane-Associated Ribosomes. Structure, 2012, 20, 1508-1518.	1.6	79
43	Structure of the Human Mitochondrial Ribosome Studied In Situ by Cryoelectron Tomography. Structure, 2017, 25, 1574-1581.e2.	1.6	73
44	Protein Transport into the Human Endoplasmic Reticulum. Journal of Molecular Biology, 2015, 427, 1159-1175.	2.0	71
45	Subtomogram analysis using the Volta phase plate. Journal of Structural Biology, 2017, 197, 94-101.	1.3	71
46	Fast and accurate reference-free alignment of subtomograms. Journal of Structural Biology, 2013, 182, 235-245.	1.3	70
47	Computational exploration of structural information from cryo-electron tomograms. Current Opinion in Structural Biology, 2004, 14, 325-331.	2.6	68
48	Visual Proteomics. Methods in Enzymology, 2010, 483, 215-243.	0.4	68
49	Proteomics reveals signal peptide features determining the client specificity in human TRAP-dependent ER protein import. Nature Communications, 2018, 9, 3765.	5.8	68
50	The Catalytic Activity of Ubp6 Enhances Maturation of the Proteasomal Regulatory Particle. Molecular Cell, 2011, 42, 637-649.	4.5	64
51	A clearer picture of the ER translocon complex. Journal of Cell Science, 2020, 133, .	1.2	64
52	Unveiling the Long-Held Secrets of the 26S Proteasome. Structure, 2013, 21, 1551-1562.	1.6	59
53	An atomic model AAA-ATPase/20S core particle sub-complex of the 26S proteasome. Biochemical and Biophysical Research Communications, 2009, 388, 228-233.	1.0	54
54	Structure of the human signal peptidase complex reveals the determinants for signal peptide cleavage. Molecular Cell, 2021, 81, 3934-3948.e11.	4.5	51

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55	Toward an Integrated Structural Model of the 26S Proteasome. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1666-1677.	2.5	50
56	Autofocused 3D Classification of Cryoelectron Subtomograms. <i>Structure</i> , 2014, 22, 1528-1537.	1.6	43
57	Structural insights into the cross-neutralization of SARS-CoV and SARS-CoV-2 by the human monoclonal antibody 47D11. <i>Science Advances</i> , 2021, 7, .	4.7	42
58	Organization of the native ribosomeâ€“translocon complex at the mammalian endoplasmic reticulum membrane. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 2122-2129.	1.1	40
59	Cryo-EM structures of human STEAP4 reveal mechanism of iron(III) reduction. <i>Nature Communications</i> , 2018, 9, 4337.	5.8	40
60	Identification of signal peptide features for substrate specificity in human Sec62/Sec63â€“dependent ER protein import. <i>FEBS Journal</i> , 2020, 287, 4612-4640.	2.2	40
61	In vivo veritas: electron cryotomography of cells. <i>Trends in Biotechnology</i> , 2002, 20, S40-S44.	4.9	35
62	Iterative reconstruction of cryo-electron tomograms using nonuniform fast Fourier transforms. <i>Journal of Structural Biology</i> , 2014, 185, 309-316.	1.3	35
63	Nucleotideâ€“dependent conformational changes of the AAA+ ATPase p97 revisited. <i>FEBS Letters</i> , 2016, 590, 595-604.	1.3	35
64	SHREC 2020: Classification in cryo-electron tomograms. <i>Computers and Graphics</i> , 2020, 91, 279-289.	1.4	33
65	Allosteric Effects in the Regulation of 26S Proteasome Activities. <i>Journal of Molecular Biology</i> , 2013, 425, 1415-1423.	2.0	28
66	Localization of the regulatory particle subunit Sem1 in the 26S proteasome. <i>Biochemical and Biophysical Research Communications</i> , 2013, 435, 250-254.	1.0	28
67	Arginine Î€-stacking drives binding to fibrils of the Alzheimer protein Tau. <i>Nature Communications</i> , 2020, 11, 571.	5.8	28
68	Structural disorder and its role in proteasomal degradation. <i>FEBS Letters</i> , 2015, 589, 2552-2560.	1.3	27
69	Take Me Home, Protein Roads: Structural Insights into Signal Peptide Interactions during ER Translocation. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11871.	1.8	27
70	How to build a ribosome from RNA fragments in <i>Chlamydomonas</i> mitochondria. <i>Nature Communications</i> , 2021, 12, 7176.	5.8	27
71	Structural impact of K63 ubiquitin on yeast translocating ribosomes under oxidative stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 22157-22166.	3.3	21
72	New insights into the structure of the MHC class I peptide-loading complex and mechanisms of TAP inhibition by viral immune evasion proteins. <i>Molecular Immunology</i> , 2019, 113, 103-114.	1.0	20

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73	Direct observation of dynamic protein interactions involving human microtubules using solid-state NMR spectroscopy. <i>Nature Communications</i> , 2020, 11, 18.	5.8	20
74	The Structure of Human Tripeptidyl Peptidase II as Determined by a Hybrid Approach. <i>Structure</i> , 2012, 20, 593-603.	1.6	19
75	Structural basis for recognition and remodeling of the TBP:DNA:NC2 complex by Mot1. <i>ELife</i> , 2015, 4, .	2.8	19
76	Orientation-Selective Incorporation of Transmembrane F ₀ F ₁ ATP Synthase Complex from <i>Micrococcus luteus</i> in Polymer-Supported Membranes. <i>Macromolecular Bioscience</i> , 2008, 8, 1034-1043.	2.1	16
77	ZNF365 Promotes Stability of Fragile Sites and Telomeres. <i>Cancer Discovery</i> , 2013, 3, 798-811.	7.7	15
78	Molecular architecture of the HerA-NurA DNA double-strand break resection complex. <i>FEBS Letters</i> , 2014, 588, 4637-4644.	1.3	15
79	Functions and Mechanisms of the Human Ribosome-Translocon Complex. <i>Sub-Cellular Biochemistry</i> , 2019, 93, 83-141.	1.0	15
80	Quantitative Proteomics and Differential Protein Abundance Analysis after Depletion of Putative mRNA Receptors in the ER Membrane of Human Cells Identifies Novel Aspects of mRNA Targeting to the ER. <i>Molecules</i> , 2021, 26, 3591.	1.7	14
81	TRAM1 protein may support ER protein import by modulating the phospholipid bilayer near the lateral gate of the Sec61-channel. <i>Channels</i> , 2020, 14, 28-44.	1.5	13
82	Integration of Cryo-EM with Atomic and Protein-Protein Interaction Data. <i>Methods in Enzymology</i> , 2010, 483, 47-72.	0.4	12
83	Detection and identification of macromolecular complexes in cryo-electron tomograms using support vector machines. , 2012, , .		11
84	Emerging Mechanistic Insights into AAA Complexes Regulating Proteasomal Degradation. <i>Biomolecules</i> , 2014, 4, 774-794.	1.8	11
85	Fluoxetine targets an allosteric site in the enterovirus 2C AAA+ ATPase and stabilizes a ring-shaped hexameric complex. <i>Science Advances</i> , 2022, 8, eabj7615.	4.7	11
86	Quantitative Proteomics and Differential Protein Abundance Analysis after the Depletion of PEX3 from Human Cells Identifies Additional Aspects of Protein Targeting to the ER. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13028.	1.8	7
87	Cryo-electron tomography for the structural study of mitochondrial translation. <i>Tissue and Cell</i> , 2019, 57, 129-138.	1.0	6
88	Bimodal endocytic probe for three-dimensional correlative light and electron microscopy. <i>Cell Reports Methods</i> , 2022, 2, 100220.	1.4	6
89	Automatic particle picking and multi-class classification in cryo-electron tomograms. , 2014, , .		5
90	Sec61: A static framework for membrane-protein insertion. <i>Channels</i> , 2016, 10, 167-169.	1.5	5

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91	Recent advances in electron tomography. <i>Journal of Structural Biology</i> , 2017, 197, 71-72.	1.3	3
92	Structural Biology in Situ Using Cryo-Electron Subtomogram Analysis. <i>Biological and Medical Physics Series</i> , 2018, , 237-259.	0.3	3
93	“4D Biology for health and disease”-workshop report. <i>New Biotechnology</i> , 2011, 28, 291-293.	2.4	2
94	1.14 Structure Determination of Macromolecular Complexes by Cryo-Electron Microscopy in vitro and in situ. , 2012, , 245-276.		1
95	Automated detection of polysomes in cryoelectron tomography. , 2014, , .		1
96	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
97	Towards High Resolution in Cryo-Electron Tomography Subtomogram Analysis. <i>Microscopy and Microanalysis</i> , 2017, 23, 812-813.	0.2	1
98	In Situ Studies of Mitochondrial Translation by Cryo-Electron Tomography. <i>Methods in Molecular Biology</i> , 2021, 2192, 243-268.	0.4	1
99	Subtomogram analysis: The sum of a tomogram’s particles reveals molecular structure in situ. <i>Journal of Structural Biology: X</i> , 2022, 6, 100063.	0.7	1
100	2.5 Studying the Macromolecular Machinery of Cells in situ by Cryo-Electron Tomography. , 2012, , 59-89.		0
101	The 26S Proteasome. , 2013, , 3691-3700.		0
102	26S Proteasome: Structure and Function. , 2019, , .		0
103	Protein Turnover 26S Proteasome: Structure and Function. , 2021, , 229-235.		0