

# Henning Stahlberg

## List of Publications by Year in descending order

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217  
papers

14,683  
citations

20797

60  
h-index

24961

109  
g-index

269  
all docs

269  
docs citations

269  
times ranked

19048  
citing authors

#	ARTICLE	IF	CITATIONS
1	Cryo-EM structure of native human thyroglobulin. <i>Nature Communications</i> , 2022, 13, 61.	5.8	9
2	2.4-Å... structure of the double-ring <i>Gemmatimonas phototrophica</i> photosystem. <i>Science Advances</i> , 2022, 8, eabk3139.	4.7	16
3	Cryo-EM structures of a LptDE transporter in complex with Pro-macrobodies offer insight into lipopolysaccharide translocation. <i>Nature Communications</i> , 2022, 13, 1826.	5.8	14
4	Coordination-Driven Monolayer-to-Bilayer Transition in Two-Dimensional Metal-Organic Networks. <i>Journal of Physical Chemistry B</i> , 2021, 125, 4204-4211.	1.2	1
5	Structural basis of the activation of the CC chemokine receptor 5 by a chemokine agonist. <i>Science Advances</i> , 2021, 7, .	4.7	36
6	Structural Basis of Drug Recognition by the Multidrug Transporter ABCG2. <i>Journal of Molecular Biology</i> , 2021, 433, 166980.	2.0	52
7	Structures of ABCG2 under turnover conditions reveal a key step in the drug transport mechanism. <i>Nature Communications</i> , 2021, 12, 4376.	5.8	46
8	Identification of a Dps contamination in Mitomycin-C-induced expression of Colicin Ia. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2021, 1863, 183607.	1.4	0
9	for High-Resolution. <i>Methods in Molecular Biology</i> , 2021, 2215, 267-284.	0.4	0
10	FTLD-τDP assemblies seed neoaggregates with subtype-specific features via a prion-like cascade. <i>EMBO Reports</i> , 2021, 22, e53877.	2.0	14
11	The Dynamo Software Package for Cryo-electron Tomography and Subtomogram Averaging. <i>Microscopy and Microanalysis</i> , 2020, 26, 3142-3145.	0.2	6
12	High-resolution cryo-EM structure of urease from the pathogen <i>Yersinia enterocolitica</i> . <i>Nature Communications</i> , 2020, 11, 5101.	5.8	17
13	Single particle cryo-EM of the complex between interphotoreceptor retinoid-binding protein and a monoclonal antibody. <i>FASEB Journal</i> , 2020, 34, 13918-13934.	0.2	6
14	Alterations in Sub-Axonal Architecture Between Normal Aging and Parkinson's Diseased Human Brains Using Label-Free Cryogenic X-ray Nanotomography. <i>Frontiers in Neuroscience</i> , 2020, 14, 570019.	1.4	2
15	The Contorsbody, an antibody format for agonism: Design, structure, and function. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1210-1220.	1.9	5
16	A helical inner scaffold provides a structural basis for centriole cohesion. <i>Science Advances</i> , 2020, 6, eaaz4137.	4.7	116
17	Protease-activation using anti-idiotypic masks enables tumor specificity of a folate receptor 1-T cell bispecific antibody. <i>Nature Communications</i> , 2020, 11, 3196.	5.8	43
18	Cryo-EM, X-ray diffraction, and atomistic simulations reveal determinants for the formation of a supramolecular myelin-like proteolipid lattice. <i>Journal of Biological Chemistry</i> , 2020, 295, 8692-8705.	1.6	15

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19	Grayscale e-beam lithography: Effects of a delayed development for well-controlled 3D patterning. <i>Microelectronic Engineering</i> , 2020, 225, 111272.	1.1	17
20	New insights on the structure of alpha-synuclein fibrils using cryo-electron microscopy. <i>Current Opinion in Neurobiology</i> , 2020, 61, 89-95.	2.0	72
21	Structural basis of Focal Adhesion Kinase activation on lipid membranes. <i>EMBO Journal</i> , 2020, 39, e104743.	3.5	47
22	Architecture of the centriole cartwheel-containing region revealed by cryo-electron tomography. <i>EMBO Journal</i> , 2020, 39, e106246.	3.5	32
23	“Differential Visual Proteomics” Enabling the Proteome-Wide Comparison of Protein Structures of Single-Cells. <i>Journal of Proteome Research</i> , 2019, 18, 3521-3531.	1.8	1
24	Imaging of post-mortem human brain tissue using electron and X-ray microscopy. <i>Current Opinion in Structural Biology</i> , 2019, 58, 138-148.	2.6	20
25	Microfluidic protein isolation and sample preparation for high-resolution cryo-EM. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15007-15012.	3.3	41
26	DuoMab: a novel CrossMab-based IgG-derived antibody format for enhanced antibody-dependent cell-mediated cytotoxicity. <i>MAbs</i> , 2019, 11, 1402-1414.	2.6	8
27	Molecular structure and function of myelin protein PO in membrane stacking. <i>Scientific Reports</i> , 2019, 9, 642.	1.6	41
28	Lewy pathology in Parkinson’s disease consists of crowded organelles and lipid membranes. <i>Nature Neuroscience</i> , 2019, 22, 1099-1109.	7.1	604
29	Tumor-targeted 4-1BB agonists for combination with T cell bispecific antibodies as off-the-shelf therapy. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	178
30	Retrieving high-resolution information from disordered 2D crystals by single-particle cryo-EM. <i>Nature Communications</i> , 2019, 10, 1722.	5.8	25
31	Cryo-EM structures of the pore-forming A subunit from the <i>Yersinia entomophaga</i> ABC toxin. <i>Nature Communications</i> , 2019, 10, 1952.	5.8	40
32	Cryo-EM structure of phosphodiesterase 6 reveals insights into the allosteric regulation of type I phosphodiesterases. <i>Science Advances</i> , 2019, 5, eaav4322.	4.7	34
33	Supramolecular architectures of molecularly thin yet robust free-standing layers. <i>Science Advances</i> , 2019, 5, eaav4489.	4.7	9
34	Diverse roles of TssA-like proteins in the assembly of bacterial type VI secretion systems. <i>EMBO Journal</i> , 2019, 38, e100825.	3.5	38
35	TDP-43 extracted from frontotemporal lobar degeneration subject brains displays distinct aggregate assemblies and neurotoxic effects reflecting disease progression rates. <i>Nature Neuroscience</i> , 2019, 22, 65-77.	7.1	143
36	Cryo-EM structure of the rhodopsin-G $\beta$ $\gamma$ complex reveals binding of the rhodopsin C-terminal tail to the G $\beta$ subunit. <i>ELife</i> , 2019, 8, .	2.8	52

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37	Two new polymorphic structures of human full-length alpha-synuclein fibrils solved by cryo-electron microscopy. <i>ELife</i> , 2019, 8, .	2.8	220
38	Direct protein crystallization on ultrathin membranes for diffraction measurements at X-ray free-electron lasers. Corrigendum. <i>Journal of Applied Crystallography</i> , 2019, 52, 1460-1460.	1.9	0
39	Miniaturizing EM Sample Preparation: Opportunities, Challenges, and "Visual Proteomics". <i>Proteomics</i> , 2018, 18, e1700176.	1.3	14
40	Structure of a zosuquidar and UIC2-bound human-mouse chimeric ABCB1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1973-E1982.	3.3	153
41	3D correlative electron microscopy reveals continuity of <i>Brucella</i> -containing vacuoles with the endoplasmic reticulum. <i>Journal of Cell Science</i> , 2018, 131, .	1.2	40
42	High-Resolution Cryoelectron Microscopy Structure of the Cyclic Nucleotide-Modulated Potassium Channel MloK1 in a Lipid Bilayer. <i>Structure</i> , 2018, 26, 20-27.e3.	1.6	18
43	Cryo-EM reconstruction of Type VI secretion system baseplate and sheath distal end. <i>EMBO Journal</i> , 2018, 37, .	3.5	74
44	Structural basis of small-molecule inhibition of human multidrug transporter ABCG2. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 333-340.	3.6	258
45	MRCZ "A file format for cryo-TEM data with fast compression. <i>Journal of Structural Biology</i> , 2018, 201, 252-257.	1.3	11
46	Self-Assembly of a Designed Nucleoprotein Architecture through Multimodal Interactions. <i>ACS Central Science</i> , 2018, 4, 1578-1586.	5.3	22
47	Cryo-EM structures of a human ABCG2 mutant trapped in ATP-bound and substrate-bound states. <i>Nature</i> , 2018, 563, 426-430.	13.7	188
48	Cerebral Corpora amylacea are dense membranous labyrinths containing structurally preserved cell organelles. <i>Scientific Reports</i> , 2018, 8, 18046.	1.6	21
49	Structure of a PSI-LHCI-cyt b <sub>6</sub> f supercomplex in <i>Chlamydomonas reinhardtii</i> promoting cyclic electron flow under anaerobic conditions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 10517-10522.	3.3	64
50	Demonstration of femtosecond X-ray pump X-ray probe diffraction on protein crystals. <i>Structural Dynamics</i> , 2018, 5, 054303.	0.9	11
51	An iris diaphragm mechanism to gate a cyclic nucleotide-gated ion channel. <i>Nature Communications</i> , 2018, 9, 3978.	5.8	44
52	Protocols for Subtomogram Averaging of Membrane Proteins in the Dynamo Software Package. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 82.	1.6	33
53	Miniaturized Sample Preparation for Transmission Electron Microscopy. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	7
54	Cryo-EM structure of alpha-synuclein fibrils. <i>ELife</i> , 2018, 7, .	2.8	444

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55	Image processing techniques for high-resolution structure determination from badly ordered 2D crystals. <i>Journal of Structural Biology</i> , 2018, 203, 120-134.	1.3	9
56	Femtosecond X-ray coherent diffraction of aligned amyloid fibrils on low background graphene. <i>Nature Communications</i> , 2018, 9, 1836.	5.8	34
57	Structural basis for regulation of human acetyl-CoA carboxylase. <i>Nature</i> , 2018, 558, 470-474.	13.7	135
58	Amyloid Fibril Polymorphism: Almost Identical on the Atomic Level, Mesoscopically Very Different. <i>Journal of Physical Chemistry B</i> , 2017, 121, 1783-1792.	1.2	41
59	Proteoliposomes – a system to study membrane proteins under buffer gradients by cryo-EM. <i>Nanotechnology Reviews</i> , 2017, 6, 57-74.	2.6	14
60	Membrane vesicle secretion and prophage induction in multidrug-resistant <i>Stenotrophomonas maltophilia</i> in response to ciprofloxacin stress. <i>Environmental Microbiology</i> , 2017, 19, 3930-3937.	1.8	60
61	Structure of the human multidrug transporter ABCG2. <i>Nature</i> , 2017, 546, 504-509.	13.7	332
62	Lipid Internal Dynamics Probed in Nanodiscs. <i>ChemPhysChem</i> , 2017, 18, 2651-2657.	1.0	47
63	Direct protein crystallization on ultrathin membranes for diffraction measurements at X-ray free-electron lasers. <i>Journal of Applied Crystallography</i> , 2017, 50, 909-918.	1.9	16
64	Monitoring the Conformational Changes of Individual Cyclic Nucleotide-Gated Ion Channels by High-Speed Atomic Force Microscopy. <i>Biophysical Journal</i> , 2017, 112, 422a.	0.2	0
65	Focus: The interface between data collection and data processing in cryo-EM. <i>Journal of Structural Biology</i> , 2017, 198, 124-133.	1.3	192
66	Cell-free reconstitution reveals centriole cartwheel assembly mechanisms. <i>Nature Communications</i> , 2017, 8, 14813.	5.8	74
67	Solution structure of discoidal high-density lipoprotein particles with a shortened apolipoprotein A-I. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 187-193.	3.6	105
68	Robust image alignment for cryogenic transmission electron microscopy. <i>Journal of Structural Biology</i> , 2017, 197, 279-293.	1.3	23
69	Cryo-EM structure of the extended type VI secretion system sheath-tube complex. <i>Nature Microbiology</i> , 2017, 2, 1507-1512.	5.9	107
70	Cryo-EM analysis of homodimeric full-length LRRK2 and LRRK1 protein complexes. <i>Scientific Reports</i> , 2017, 7, 8667.	1.6	51
71	Expression, Biochemistry, and Stabilization with Camel Antibodies of Membrane Proteins: Case Study of the Mouse 5-HT3 Receptor. <i>Methods in Molecular Biology</i> , 2017, 1635, 139-168.	0.4	5
72	Membrane Association Landscape of Myelin Basic Protein Portrays Formation of the Myelin Major Dense Line. <i>Scientific Reports</i> , 2017, 7, 4974.	1.6	63

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73	Three-Dimensional Imaging of Biological Tissue by Cryo X-Ray Ptychography. <i>Scientific Reports</i> , 2017, 7, 6291.	1.6	49
74	Two-dimensional crystallization of the mouse serotonin 5-HT <sub>3A</sub> receptor. <i>Micron</i> , 2017, 92, 19-24.	1.1	1
75	Dynamo Catalogue: Geometrical tools and data management for particle picking in subtomogram averaging of cryo-electron tomograms. <i>Journal of Structural Biology</i> , 2017, 197, 135-144.	1.3	108
76	Blotting-free and lossless cryo-electron microscopy grid preparation from nanoliter-sized protein samples and single-cell extracts. <i>Journal of Structural Biology</i> , 2017, 197, 220-226.	1.3	95
77	Thylakoid Ultrastructure: Visualizing the Photosynthetic Machinery. <i>Microbiology Monographs</i> , 2017, , 149-191.	0.3	0
78	<scp>GSDMD</scp> membrane pore formation constitutes the mechanism of pyroptotic cell death. <i>EMBO Journal</i> , 2016, 35, 1766-1778.	3.5	842
79	Cullinâ€“RING ubiquitin E3 ligase regulation by the COP9 signalosome. <i>Nature</i> , 2016, 531, 598-603.	13.7	173
80	Characterization of mAb dimers reveals predominant dimer forms common in therapeutic mAbs. <i>MAbs</i> , 2016, 8, 928-940.	2.6	42
81	Direct Visualization of Glutamate Transporter Transport Cycle. <i>Biophysical Journal</i> , 2016, 110, 178a-179a.	0.2	0
82	Structure of the T4 baseplate and its function in triggering sheath contraction. <i>Nature</i> , 2016, 533, 346-352.	13.7	231
83	Total Sample Conditioning and Preparation of Nanoliter Volumes for Electron Microscopy. <i>ACS Nano</i> , 2016, 10, 4981-4988.	7.3	23
84	Cholesteryl ester transfer between lipoproteins does not require a ternary tunnel complex with CETP. <i>Journal of Structural Biology</i> , 2016, 194, 191-198.	1.3	32
85	Biochemical and biophysical approaches to study the structure and function of the chloride channel (ClC) family of proteins. <i>Biochimie</i> , 2016, 128-129, 154-162.	1.3	7
86	Real-time visualization of conformational changes within single MloK1 cyclic nucleotide-modulated channels. <i>Nature Communications</i> , 2016, 7, 12789.	5.8	26
87	The lipidome associated with the Î³-secretase complex is required for its integrity and activity. <i>Biochemical Journal</i> , 2016, 473, 321-334.	1.7	12
88	The Structure of the Mouse Serotonin 5-HT <sub>3</sub> Receptor in Lipid Vesicles. <i>Structure</i> , 2016, 24, 165-170.	1.6	36
89	Preparation and Characterization of Stable Î±-Synuclein Lipoprotein Particles. <i>Journal of Biological Chemistry</i> , 2016, 291, 8516-8527.	1.6	49
90	Ultrathin membrane chips as X-ray transparent supports for serial crystallography. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2016, 72, s184-s184.	0.0	0

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91	Explorations of Lipid Effects in Cyclic Nucleotide-Gated Ion Channels using a Nanodisc Platform. Biophysical Journal, 2015, 108, 290a-291a.	0.2	0
92	Structure of the Type VI Secretion System Contractile Sheath. Cell, 2015, 160, 952-962.	13.5	216
93	3D reconstruction of two-dimensional crystals. Archives of Biochemistry and Biophysics, 2015, 581, 68-77.	1.4	27
94	CTF Challenge: Result summary. Journal of Structural Biology, 2015, 190, 348-359.	1.3	34
95	<i>Yersinia enterocolitica</i> type III secretion injectisomes form regularly spaced clusters, which incorporate new machines upon activation. Molecular Microbiology, 2015, 95, 875-884.	1.2	30
96	Structure and assembly of the mouse ASC inflammasome by combined NMR spectroscopy and cryo-electron microscopy. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13237-13242.	3.3	133
97	Translational arrest by a prokaryotic signal recognition particle is mediated by RNA interactions. Nature Structural and Molecular Biology, 2015, 22, 767-773.	3.6	29
98	Rendering graphene supports hydrophilic with non-covalent aromatic functionalization for transmission electron microscopy. Applied Physics Letters, 2014, 104, .	1.5	30
99	<i>Clostridium difficile</i> toxin CDT hijacks microtubule organization and reroutes vesicle traffic to increase pathogen adherence. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2313-2318.	3.3	78
100	Disease Modeling and Phenotypic Drug Screening for Diabetic Cardiomyopathy using Human Induced Pluripotent Stem Cells. Cell Reports, 2014, 9, 810-820.	2.9	206
101	(443) Relative bioavailability of a new tamper resistant extended-release oxycodone/naloxone combination product. Journal of Pain, 2014, 15, S86.	0.7	1
102	A KcsA/MloK1 Chimeric Ion Channel Has Lipid-dependent Ligand-binding Energetics. Journal of Biological Chemistry, 2014, 289, 9535-9546.	1.6	12
103	Exploring the Interactome: Microfluidic Isolation of Proteins and Interacting Partners for Quantitative Analysis by Electron Microscopy. Analytical Chemistry, 2014, 86, 4680-4687.	3.2	13
104	X-ray structure of the mouse serotonin 5-HT <sub>3</sub> receptor. Nature, 2014, 512, 276-281.	13.7	358
105	The ultrastructure of Chlorobaculum tepidum revealed by cryo-electron tomography. Biochimica Et Biophysica Acta - Bioenergetics, 2014, 1837, 1635-1642.	0.5	14
106	Ligand-induced structural changes in the cyclic nucleotide-modulated potassium channel MloK1. Nature Communications, 2014, 5, 3106.	5.8	59
107	openBEB: open biological experiment browser for correlative measurements. BMC Bioinformatics, 2014, 15, 84.	1.2	9
108	Single particle 3D reconstruction for 2D crystal images of membrane proteins. Journal of Structural Biology, 2014, 185, 267-277.	1.3	17

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109	Expression, Purification and Stabilization of the Mouse 5HT3 Receptor. <i>Biophysical Journal</i> , 2014, 106, 338a.	0.2	0
110	Structural and Mechanistic Paradigm of Leptin Receptor Activation Revealed by Complexes with Wild-Type and Antagonist Leptins. <i>Structure</i> , 2014, 22, 866-877.	1.6	37
111	2dx_automator: Implementation of a semiautomatic high-throughput high-resolution cryo-electron crystallography pipeline. <i>Journal of Structural Biology</i> , 2014, 186, 302-307.	1.3	29
112	Functional surface engineering by nucleotide-modulated potassium channel insertion into polymer membranes attached to solid supports. <i>Biomaterials</i> , 2014, 35, 7286-7294.	5.7	40
113	Cryo-Electron Microscopy of Potassium Channel Membrane Proteins. <i>Microscopy and Microanalysis</i> , 2014, 20, 1206-1207.	0.2	0
114	Cryo-electron Microscopy of Membrane Proteins. <i>Methods in Molecular Biology</i> , 2014, 1117, 325-341.	0.4	27
115	Molecular assembly of the aerolysin pore reveals a swirling membrane-insertion mechanism. <i>Nature Chemical Biology</i> , 2013, 9, 623-629.	3.9	183
116	Cryo-electron tomography reveals four-membrane architecture of the Plasmodium apicoplast. <i>Malaria Journal</i> , 2013, 12, 25.	0.8	44
117	Structure of the Dodecameric <i>Yersinia enterocolitica</i> Secretin YscC and Its Trypsin-Resistant Core. <i>Structure</i> , 2013, 21, 2152-2161.	1.6	33
118	Growth of Large and Highly Ordered 2D Crystals of a K <sup>+</sup> Channel, Structural Role of Lipidic Environment. <i>Biophysical Journal</i> , 2013, 105, 398-408.	0.2	8
119	Vaccinia Virus Entry Is Followed by Core Activation and Proteasome-Mediated Release of the Immunomodulatory Effector VH1 from Lateral Bodies. <i>Cell Reports</i> , 2013, 4, 464-476.	2.9	79
120	Single-cell lysis for visual analysis by electron microscopy. <i>Journal of Structural Biology</i> , 2013, 183, 467-473.	1.3	28
121	Bridging from conventional marketed immediate release formulations to new tamper resistant alternatives. <i>Journal of Pain</i> , 2013, 14, S70.	0.7	0
122	Structure and Substrate-Induced Conformational Changes of the Secondary Citrate/Sodium Symporter CitS Revealed by Electron Crystallography. <i>Structure</i> , 2013, 21, 1243-1250.	1.6	12
123	Thermal Unfolding of a Mammalian Pentameric Ligand-gated Ion Channel Proceeds at Consecutive, Distinct Steps*. <i>Journal of Biological Chemistry</i> , 2013, 288, 5756-5769.	1.6	18
124	Image Processing of 2D Crystal Images. <i>Methods in Molecular Biology</i> , 2013, 955, 171-194.	0.4	9
125	Merging of Image Data in Electron Crystallography. <i>Methods in Molecular Biology</i> , 2013, 955, 195-209.	0.4	6
126	Automation of Image Processing in Electron Crystallography. <i>Methods in Molecular Biology</i> , 2013, 955, 313-330.	0.4	5



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127	Pharmacokinetic evaluation of tapentadol extended-release tablets in healthy subjects. <i>Journal of Opioid Management</i> , 2013, 9, 291-300.	0.2	16
128	In situ structural analysis of the <i>Yersinia enterocolitica</i> injectisome. <i>ELife</i> , 2013, 2, e00792.	2.8	109
129	Mus81-Mms4 Functions as a Single Heterodimer To Cleave Nicked Intermediates in Recombinational DNA Repair. <i>Molecular and Cellular Biology</i> , 2012, 32, 3065-3080.	1.1	55
130	Ionic Liquids as Matrices in Microfluidic Sample Deposition for High-Mass Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry. <i>European Journal of Mass Spectrometry</i> , 2012, 18, 279-286.	0.5	19
131	Structural basis for chirality and directional motility of <i>Plasmodium</i> sporozoites. <i>Cellular Microbiology</i> , 2012, 14, 1757-1768.	1.1	58
132	RNAi Screening Reveals Proteasome- and Cullin3-Dependent Stages in Vaccinia Virus Infection. <i>Cell Reports</i> , 2012, 2, 1036-1047.	2.9	139
133	Interactions of CCR5, the Main HIV Coreceptor, with Rantes and Other Ligands. <i>Biophysical Journal</i> , 2012, 102, 239a-240a.	0.2	0
134	LIMITING FACTORS IN SINGLE PARTICLE CRYO ELECTRON TOMOGRAPHY. <i>Computational and Structural Biotechnology Journal</i> , 2012, 1, e201207002.	1.9	28
135	The application of graphene as a sample support in transmission electron microscopy. <i>Solid State Communications</i> , 2012, 152, 1375-1382.	0.9	80
136	Projection Structure of the Secondary Citrate/Sodium Symporter CitS at 6Å Resolution by Electron Crystallography. <i>Journal of Molecular Biology</i> , 2012, 418, 117-126.	2.0	5
137	Assessing the benefits of focal pair cryo-electron tomography. <i>Journal of Structural Biology</i> , 2012, 178, 88-97.	1.3	8
138	Connecting $\mu$ -fluidics to electron microscopy. <i>Journal of Structural Biology</i> , 2012, 177, 128-134.	1.3	25
139	Dynamo: A flexible, user-friendly development tool for subtomogram averaging of cryo-EM data in high-performance computing environments. <i>Journal of Structural Biology</i> , 2012, 178, 139-151.	1.3	376
140	Complete Lateral and Angular Diffusion and Protein-Protein Interaction Description of a Membrane Protein. <i>Biophysical Journal</i> , 2012, 102, 413a-414a.	0.2	0
141	1.15 Analysis of 2-D Crystals of Membrane Proteins by Electron Microscopy. , 2012, , 277-310.		5
142	The Application of Scanning Transmission Electron Microscopy (STEM) to the Study of Nanoscale Systems. <i>Nanostructure Science and Technology</i> , 2012, , 11-40.	0.1	6
143	Characterization of the motion of membrane proteins using high-speed atomic force microscopy. <i>Nature Nanotechnology</i> , 2012, 7, 525-529.	15.6	184
144	Structure and Function of Purified Monoclonal Antibody Dimers Induced by Different Stress Conditions. <i>Pharmaceutical Research</i> , 2012, 29, 2047-2059.	1.7	68

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145	Iterative Transform Algorithms for 3D Reconstruction of 2D Crystals. <i>Journal of Next Generation Information Technology</i> , 2012, 3, 28-35.	0.2	0
146	Oxidative Doping Renders Graphene Hydrophilic, Facilitating Its Use As a Support in Biological TEM. <i>Nano Letters</i> , 2011, 11, 4319-4323.	4.5	52
147	3D reconstruction of 2D crystals. , 2011, , .		0
148	Graphene: Substrate preparation and introduction. <i>Journal of Structural Biology</i> , 2011, 174, 234-238.	1.3	84
149	Polymer-based cell-free expression of ligand-binding family B G-protein coupled receptors without detergents. <i>Protein Science</i> , 2011, 20, 1030-1041.	3.1	48
150	Rad51 paralogues Rad55 and Rad57 balance the antirecombinase Srs2 in Rad51 filament formation. <i>Nature</i> , 2011, 479, 245-248.	13.7	183
151	Automatic recovery of missing amplitudes and phases in tilt-limited electron crystallography of two-dimensional crystals. <i>Physical Review E</i> , 2011, 84, 011916.	0.8	23
152	Interaction of complexes I, III, and IV within the bovine respirasome by single particle cryoelectron tomography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15196-15200.	3.3	170
153	An optical and microPET assessment of thermally-sensitive liposome biodistribution in the Met-1 tumor model: Importance of formulation. <i>Journal of Controlled Release</i> , 2010, 143, 13-22.	4.8	56
154	3D Reconstruction from 2D Crystal Image and Diffraction Data. <i>Methods in Enzymology</i> , 2010, 482, 101-129.	0.4	19
155	High-resolution low-dose scanning transmission electron microscopy. <i>Journal of Electron Microscopy</i> , 2010, 59, 103-112.	0.9	113
156	Preparation of 2D Crystals of Membrane Proteins for High-Resolution Electron Crystallography Data Collection. <i>Methods in Enzymology</i> , 2010, 481, 25-43.	0.4	25
157	Filling the missing cone: automatic recovery of data in tilt-limited microscopy. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2010, 66, s17-s17.	0.3	0
158	Coassembly of Mgm1 isoforms requires cardiolipin and mediates mitochondrial inner membrane fusion. <i>Journal of Cell Biology</i> , 2009, 186, 793-803.	2.3	243
159	Structural variability of edge dislocations in a SrTiO <sub>3</sub> low-angle [001] tilt grain boundary. <i>Journal of Materials Research</i> , 2009, 24, 2191-2199.	1.2	34
160	Membrane activity of a reactive protein. <i>FEBS Letters</i> , 2009, 583, 1001-1005.	1.3	6
161	2007 Annual progress report synopsis of the Center for Structures of Membrane Proteins. <i>Journal of Structural and Functional Genomics</i> , 2009, 10, 193-208.	1.2	17
162	Crystal Structures of Limulus SAP-Like Pentraxin Reveal Two Molecular Aggregations. <i>Journal of Molecular Biology</i> , 2009, 386, 1240-1254.	2.0	17

#	ARTICLE	IF	CITATIONS
163	Low-dose aberration corrected cryo-electron microscopy of organic specimens. <i>Ultramicroscopy</i> , 2008, 108, 1636-1644.	0.8	46
164	Molecular Electron Microscopy: State of the Art and Current Challenges. <i>ACS Chemical Biology</i> , 2008, 3, 268-281.	1.6	65
165	Bridging Across Length Scales: Multi-Scale Ordering of Supported Lipid Bilayers via Lipoprotein Self-assembly and Surface Patterning. <i>Journal of the American Chemical Society</i> , 2008, 130, 11164-11169.	6.6	13
166	The fold of Î±-synuclein fibrils. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8637-8642.	3.3	499
167	2dx - Automated 3D structure reconstruction from 2D crystal data. <i>Microscopy and Microanalysis</i> , 2008, 14, 1290-1291.	0.2	9
168	Membrane pore formation by pentraxin proteins from <i>Limulus</i> , the American horseshoe crab. <i>Biochemical Journal</i> , 2008, 413, 305-313.	1.7	13
169	Structural Analysis of the Cyclic Nucleotide Modulated Potassium Channel MloK1. <i>Microscopy and Microanalysis</i> , 2007, 13, .	0.2	0
170	Oocyte CD9 is enriched on the microvillar membrane and required for normal microvillar shape and distribution. <i>Developmental Biology</i> , 2007, 304, 317-325.	0.9	185
171	2dx – User-friendly image processing for 2D crystals. <i>Journal of Structural Biology</i> , 2007, 157, 64-72.	1.3	184
172	Automatic lattice determination for two-dimensional crystal images. <i>Journal of Structural Biology</i> , 2007, 160, 353-361.	1.3	24
173	2dx_merge: Data management and merging for 2D crystal images. <i>Journal of Structural Biology</i> , 2007, 160, 375-384.	1.3	63
174	A maximum likelihood approach to two-dimensional crystals. <i>Journal of Structural Biology</i> , 2007, 160, 362-374.	1.3	37
175	Electron crystallography of membrane proteins. <i>Journal of Structural Biology</i> , 2007, 160, 263-264.	1.3	7
176	Structural and Kinetic Studies of Induced Fit in Xylulose Kinase from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2007, 365, 783-798.	2.0	37
177	2dx – User Friendly Image Processing (and Merging) for 2D Crystals. <i>Microscopy and Microanalysis</i> , 2007, 13, 160-161.	0.2	1
178	The Structure of the Prokaryotic Cyclic Nucleotide-Modulated Potassium Channel MloK1 at 16 Å.. Resolution. <i>Structure</i> , 2007, 15, 1053-1064.	1.6	51
179	Electron Crystallography of Membrane Proteins. <i>Methods in Molecular Biology</i> , 2007, 369, 331-343.	0.4	7
180	Avoiding Charge Induced Drift In Vitrified Biological Specimens Through Scanning Transmission Electron Microscopy. <i>Microscopy and Microanalysis</i> , 2006, 12, 246-247.	0.2	3

#	ARTICLE	IF	CITATIONS
181	Applications of Atomic Scale Scanning Transmission Electron Microscopy. <i>Microscopy and Microanalysis</i> , 2006, 12, 134-135.	0.2	0
182	Cryo-Electron Microscopy Analysis of a 105 kDa Protein Particle: The Xylulose Kinase from E. Coli. <i>Microscopy and Microanalysis</i> , 2006, 12, 408-409.	0.2	1
183	Double hexameric ring assembly of the type III protein translocase ATPase HrcN. <i>Molecular Microbiology</i> , 2006, 61, 119-125.	1.2	45
184	Milestones in electron crystallography. <i>Journal of Computer-Aided Molecular Design</i> , 2006, 20, 519-527.	1.3	32
185	A Homotetrameric Kinesin-5, KLP61F, Bundles Microtubules and Antagonizes Ncd in Motility Assays. <i>Current Biology</i> , 2006, 16, 2293-2302.	1.8	124
186	Correction: Functional modulation of IFT kinesins extends the sensory repertoire of ciliated neurons in <i>Caenorhabditis elegans</i> . <i>Journal of Cell Biology</i> , 2006, 172, 949-949.	2.3	0
187	Correction: Functional modulation of IFT kinesins extends the sensory repertoire of ciliated neurons in <i>Caenorhabditis elegans</i> . <i>Journal of Cell Biology</i> , 2006, 175, 837-837.	2.3	0
188	Functional modulation of IFT kinesins extends the sensory repertoire of ciliated neurons in <i>Caenorhabditis elegans</i> . <i>Journal of Cell Biology</i> , 2006, 172, 663-669.	2.3	117
189	The 4.5Å... Structure of Human AQP2. <i>Journal of Molecular Biology</i> , 2005, 350, 278-289.	2.0	74
190	Oligomeric structure of the <i>Bacillus subtilis</i> cell division protein DivIVA determined by transmission electron microscopy. <i>Molecular Microbiology</i> , 2004, 52, 1281-1290.	1.2	89
191	Image processing library and toolkit for the electron microscopy community. <i>Journal of Structural Biology</i> , 2003, 144, 4-12.	1.3	35
192	Type III Protein Translocase. <i>Journal of Biological Chemistry</i> , 2003, 278, 25816-25824.	1.6	61
193	Assessing the structure of membrane proteins: combining different methods gives the full picture. <i>Biochemistry and Cell Biology</i> , 2002, 80, 563-568.	0.9	10
194	Aquaglyceroporins: Channel proteins with a conserved core, multiple functions, and variable surfaces. <i>International Review of Cytology</i> , 2002, 215, 75-104.	6.2	74
195	Progress in the analysis of membrane protein structure and function. <i>FEBS Letters</i> , 2002, 529, 65-72.	1.3	74
196	Sampling the conformational space of membrane protein surfaces with the AFM. <i>European Biophysics Journal</i> , 2002, 31, 172-178.	1.2	70
197	Charting and unzipping the surface layer of <i>Corynebacterium glutamicum</i> with the atomic force microscope. <i>Molecular Microbiology</i> , 2002, 44, 675-684.	1.2	85
198	ATP synthase: constrained stoichiometry of the transmembrane rotor. <i>FEBS Letters</i> , 2001, 504, 219-222.	1.3	76

#	ARTICLE	IF	CITATIONS
199	Two-dimensional crystals: a powerful approach to assess structure, function and dynamics of membrane proteins. <i>FEBS Letters</i> , 2001, 504, 166-172.	1.3	83
200	Chapter 2 The aquaporin superfamily: Structure and function. <i>Current Topics in Membranes</i> , 2001, 51, 39-119.	0.5	3
201	Bacterial Na <sup>+</sup> ATP synthase has an undecameric rotor. <i>EMBO Reports</i> , 2001, 2, 229-233.	2.0	185
202	Proton-powered turbine of a plant motor. <i>Nature</i> , 2000, 405, 418-419.	13.7	478
203	The 3.7 Å... projection map of the glycerol facilitator GlpF: a variant of the aquaporin tetramer. <i>EMBO Reports</i> , 2000, 1, 183-189.	2.0	38
204	The aquaporin sidedness revisited. <i>Journal of Molecular Biology</i> , 2000, 299, 1271-1278.	2.0	20
205	Surface Tongue-and-groove Contours on Lens MIP Facilitate Cell-to-cell Adherence. <i>Journal of Molecular Biology</i> , 2000, 300, 779-789.	2.0	149
206	The 6.9-Å... Structure of GlpF: A Basis for Homology Modeling of the Glycerol Channel from <i>Escherichia coli</i> . <i>Journal of Structural Biology</i> , 2000, 132, 133-141.	1.3	30
207	Domain structure of secretin PulD revealed by limited proteolysis and electron microscopy. <i>EMBO Journal</i> , 2000, 19, 2229-2236.	3.5	115
208	GLPF: A Structural Variant of the Aquaporin Tetramer. , 2000, , 13-21.		1
209	Mitochondrial Lon of <i>Saccharomyces cerevisiae</i> is a ring-shaped protease with seven flexible subunits. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 6787-6790.	3.3	125
210	High resolution AFM topographs of the <i>Escherichia coli</i> water channel aquaporin Z. <i>EMBO Journal</i> , 1999, 18, 4981-4987.	3.5	176
211	The reaction center complex from the green sulfur bacterium <i>Chlorobium tepidum</i> : a structural analysis by scanning transmission electron microscopy. <i>Journal of Molecular Biology</i> , 1999, 290, 851-858.	2.0	52
212	Structure of the water channel AqpZ from <i>Escherichia coli</i> revealed by electron crystallography. <i>Journal of Molecular Biology</i> , 1999, 291, 1181-1190.	2.0	70
213	Title is missing!. <i>Photosynthesis Research</i> , 1998, 55, 363-368.	1.6	7
214	Are the light-harvesting I complexes from <i>Rhodospirillum rubrum</i> arranged around the reaction centre in a square geometry? 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1998, 282, 819-831.	2.0	53
215	Friction Anisotropy and Asymmetry of a Compliant Monolayer Induced by a Small Molecular Tilt. <i>Science</i> , 1998, 280, 273-275.	6.0	151
216	Chloroplast FOF1ATP Synthase Imaged by Atomic Force Microscopy. <i>Journal of Structural Biology</i> , 1997, 119, 139-148.	1.3	29

#	ARTICLE	IF	CITATIONS
217	Sulphur-bearing lipids for the covalent attachment of supported lipid bilayers to gold surfaces: a detailed characterisation and analysis. <i>Materials Science and Engineering C</i> , 1996, 4, 7-18.	3.8	28