

Henning Stahlberg

List of Publications by Year in descending order

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217
papers

14,683
citations

20759

60
h-index

24915

109
g-index

269
all docs

269
docs citations

269
times ranked

19048
citing authors

#	ARTICLE	IF	CITATIONS
1	<scp>GSDMD</scp> membrane pore formation constitutes the mechanism of pyroptotic cell death. EMBO Journal, 2016, 35, 1766-1778.	3.5	842
2	Lewy pathology in Parkinsonâ€™s disease consists of crowded organelles and lipid membranes. Nature Neuroscience, 2019, 22, 1099-1109.	7.1	604
3	The fold of Î±-synuclein fibrils. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8637-8642.	3.3	499
4	Proton-powered turbine of a plant motor. Nature, 2000, 405, 418-419.	13.7	478
5	Cryo-EM structure of alpha-synuclein fibrils. ELife, 2018, 7, .	2.8	444
6	Dynamo: A flexible, user-friendly development tool for subtomogram averaging of cryo-EM data in high-performance computing environments. Journal of Structural Biology, 2012, 178, 139-151.	1.3	376
7	X-ray structure of the mouse serotonin 5-HT3 receptor. Nature, 2014, 512, 276-281.	13.7	358
8	Structure of the human multidrug transporter ABCG2. Nature, 2017, 546, 504-509.	13.7	332
9	Structural basis of small-molecule inhibition of human multidrug transporter ABCG2. Nature Structural and Molecular Biology, 2018, 25, 333-340.	3.6	258
10	Coassembly of Mgm1 isoforms requires cardiolipin and mediates mitochondrial inner membrane fusion. Journal of Cell Biology, 2009, 186, 793-803.	2.3	243
11	Structure of the T4 baseplate and its function in triggering sheath contraction. Nature, 2016, 533, 346-352.	13.7	231
12	Two new polymorphic structures of human full-length alpha-synuclein fibrils solved by cryo-electron microscopy. ELife, 2019, 8, .	2.8	220
13	Structure of the Type VI Secretion System Contractile Sheath. Cell, 2015, 160, 952-962.	13.5	216
14	Disease Modeling and Phenotypic Drug Screening for Diabetic Cardiomyopathy using Human Induced Pluripotent Stem Cells. Cell Reports, 2014, 9, 810-820.	2.9	206
15	Focus: The interface between data collection and data processing in cryo-EM. Journal of Structural Biology, 2017, 198, 124-133.	1.3	192
16	Cryo-EM structures of a human ABCG2 mutant trapped in ATP-bound and substrate-bound states. Nature, 2018, 563, 426-430.	13.7	188
17	Bacterial Na ⁺ -ATP synthase has an undecameric rotor. EMBO Reports, 2001, 2, 229-233.	2.0	185
18	Oocyte CD9 is enriched on the microvillar membrane and required for normal microvillar shape and distribution. Developmental Biology, 2007, 304, 317-325.	0.9	185

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19	2dxâ€™User-friendly image processing for 2D crystals. <i>Journal of Structural Biology</i> , 2007, 157, 64-72.	1.3	184
20	Characterization of the motion of membrane proteins using high-speed atomic force microscopy. <i>Nature Nanotechnology</i> , 2012, 7, 525-529.	15.6	184
21	Rad51 paralogues Rad55â€™Rad57 balance the antirecombinase Srs2 in Rad51 filament formation. <i>Nature</i> , 2011, 479, 245-248.	13.7	183
22	Molecular assembly of the aerolysin pore reveals a swirling membrane-insertion mechanism. <i>Nature Chemical Biology</i> , 2013, 9, 623-629.	3.9	183
23	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
24	High resolution AFM topographs of the Escherichia coli water channel aquaporin Z. <i>EMBO Journal</i> , 1999, 18, 4981-4987.	3.5	176
25	Cullinâ€™RING ubiquitin E3 ligase regulation by the COP9 signalosome. <i>Nature</i> , 2016, 531, 598-603.	13.7	173
26	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
27	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
28	Friction Anisotropy and Asymmetry of a Compliant Monolayer Induced by a Small Molecular Tilt. <i>Science</i> , 1998, 280, 273-275.	6.0	151
29	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
30	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
31	RNAi Screening Reveals Proteasome- and Cullin3-Dependent Stages in Vaccinia Virus Infection. <i>Cell Reports</i> , 2012, 2, 1036-1047.	2.9	139
32	Structural basis for regulation of human acetyl-CoA carboxylase. <i>Nature</i> , 2018, 558, 470-474.	13.7	135
33	Structure and assembly of the mouse ASC inflammasome by combined NMR spectroscopy and cryo-electron microscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13237-13242.	3.3	133
34	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
35	A Homotetrameric Kinesin-5, KLP61F, Bundles Microtubules and Antagonizes Ncd in Motility Assays. <i>Current Biology</i> , 2006, 16, 2293-2302.	1.8	124
36	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

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37	A helical inner scaffold provides a structural basis for centriole cohesion. <i>Science Advances</i> , 2020, 6, eaaz4137.	4.7	116
38	Domain structure of secretin PulD revealed by limited proteolysis and electron microscopy. <i>EMBO Journal</i> , 2000, 19, 2229-2236.	3.5	115
39	High-resolution low-dose scanning transmission electron microscopy. <i>Journal of Electron Microscopy</i> , 2010, 59, 103-112.	0.9	113
40	In situ structural analysis of the <i>Yersinia enterocolitica</i> injectisome. <i>ELife</i> , 2013, 2, e00792.	2.8	109
41	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
42	Cryo-EM structure of the extended type VI secretion system sheathâ€“tube complex. <i>Nature Microbiology</i> , 2017, 2, 1507-1512.	5.9	107
43	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
44	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
45	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
46	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
47	Graphene: Substrate preparation and introduction. <i>Journal of Structural Biology</i> , 2011, 174, 234-238.	1.3	84
48	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
49	The application of graphene as a sample support in transmission electron microscopy. <i>Solid State Communications</i> , 2012, 152, 1375-1382.	0.9	80
50	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
51	<i>Clostridium difficile</i> toxin CDT hijacks microtubule organization and reroutes vesicle traffic to increase pathogen adherence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2313-2318.	3.3	78
52	ATP synthase: constrained stoichiometry of the transmembrane rotor. <i>FEBS Letters</i> , 2001, 504, 219-222.	1.3	76
53	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
54	Progress in the analysis of membrane protein structure and function. <i>FEBS Letters</i> , 2002, 529, 65-72.	1.3	74

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55	The 4.5Å... Structure of Human AQP2. <i>Journal of Molecular Biology</i> , 2005, 350, 278-289.	2.0	74
56	Cell-free reconstitution reveals centriole cartwheel assembly mechanisms. <i>Nature Communications</i> , 2017, 8, 14813.	5.8	74
57	Cryo-EM reconstruction of Type VI secretion system baseplate and sheath distal end. <i>EMBO Journal</i> , 2018, 37, .	3.5	74
58	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
59	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
60	Sampling the conformational space of membrane protein surfaces with the AFM. <i>European Biophysics Journal</i> , 2002, 31, 172-178.	1.2	70
61	Structure and Function of Purified Monoclonal Antibody Dimers Induced by Different Stress Conditions. <i>Pharmaceutical Research</i> , 2012, 29, 2047-2059.	1.7	68
62	Molecular Electron Microscopy: State of the Art and Current Challenges. <i>ACS Chemical Biology</i> , 2008, 3, 268-281.	1.6	65
63	Structure of a PSI-LHCI-cyt b ₆ 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
64	2dx_merge: Data management and merging for 2D crystal images. <i>Journal of Structural Biology</i> , 2007, 160, 375-384.	1.3	63
65	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
66	Type III Protein Translocase. <i>Journal of Biological Chemistry</i> , 2003, 278, 25816-25824.	1.6	61
67	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
68	Ligand-induced structural changes in the cyclic nucleotide-modulated potassium channel MloK1. <i>Nature Communications</i> , 2014, 5, 3106.	5.8	59
69	Structural basis for chirality and directional motility of <i>Plasmodium</i> sporozoites. <i>Cellular Microbiology</i> , 2012, 14, 1757-1768.	1.1	58
70	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
71	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
72	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

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73	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
74	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
75	Structural Basis of Drug Recognition by the Multidrug Transporter ABCG2. <i>Journal of Molecular Biology</i> , 2021, 433, 166980.	2.0	52
76	Cryo-EM structure of the rhodopsin-G β - γ ² complex reveals binding of the rhodopsin C-terminal tail to the γ ² subunit. <i>ELife</i> , 2019, 8, .	2.8	52
77	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
78	Cryo-EM analysis of homodimeric full-length LRRK2 and LRRK1 protein complexes. <i>Scientific Reports</i> , 2017, 7, 8667.	1.6	51
79	Preparation and Characterization of Stable β -Synuclein Lipoprotein Particles. <i>Journal of Biological Chemistry</i> , 2016, 291, 8516-8527.	1.6	49
80	Three-Dimensional Imaging of Biological Tissue by Cryo X-Ray Ptychography. <i>Scientific Reports</i> , 2017, 7, 6291.	1.6	49
81	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
82	Lipid Internal Dynamics Probed in Nanodiscs. <i>ChemPhysChem</i> , 2017, 18, 2651-2657.	1.0	47
83	Structural basis of Focal Adhesion Kinase activation on lipid membranes. <i>EMBO Journal</i> , 2020, 39, e104743.	3.5	47
84	Low-dose aberration corrected cryo-electron microscopy of organic specimens. <i>Ultramicroscopy</i> , 2008, 108, 1636-1644.	0.8	46
85	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
86	Double hexameric ring assembly of the type III protein translocase ATPase HrcN. <i>Molecular Microbiology</i> , 2006, 61, 119-125.	1.2	45
87	Cryo-electron tomography reveals four-membrane architecture of the <i>Plasmodium</i> apicoplast. <i>Malaria Journal</i> , 2013, 12, 25.	0.8	44
88	An iris diaphragm mechanism to gate a cyclic nucleotide-gated ion channel. <i>Nature Communications</i> , 2018, 9, 3978.	5.8	44
89	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
90	Characterization of mAb dimers reveals predominant dimer forms common in therapeutic mAbs. <i>MAbs</i> , 2016, 8, 928-940.	2.6	42

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91	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
92	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
93	Molecular structure and function of myelin protein PO in membrane stacking. <i>Scientific Reports</i> , 2019, 9, 642.	1.6	41
94	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
95	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
96	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
97	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
98	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
99	A maximum likelihood approach to two-dimensional crystals. <i>Journal of Structural Biology</i> , 2007, 160, 362-374.	1.3	37
100	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
101	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
102	The Structure of the Mouse Serotonin 5-HT ₃ Receptor in Lipid Vesicles. <i>Structure</i> , 2016, 24, 165-170.	1.6	36
103	Structural basis of the activation of the CC chemokine receptor 5 by a chemokine agonist. <i>Science Advances</i> , 2021, 7, .	4.7	36
104	Image processing library and toolkit for the electron microscopy community. <i>Journal of Structural Biology</i> , 2003, 144, 4-12.	1.3	35
105	Structural variability of edge dislocations in a SrTiO ₃ low-angle [001] tilt grain boundary. <i>Journal of Materials Research</i> , 2009, 24, 2191-2199.	1.2	34
106	CTF Challenge: Result summary. <i>Journal of Structural Biology</i> , 2015, 190, 348-359.	1.3	34
107	Femtosecond X-ray coherent diffraction of aligned amyloid fibrils on low background graphene. <i>Nature Communications</i> , 2018, 9, 1836.	5.8	34
108	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

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109	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
110	Protocols for Subtomogram Averaging of Membrane Proteins in the Dynamo Software Package. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 82.	1.6	33
111	Milestones in electron crystallography. <i>Journal of Computer-Aided Molecular Design</i> , 2006, 20, 519-527.	1.3	32
112	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
113	Architecture of the centriole cartwheel-containing region revealed by cryo-electron tomography. <i>EMBO Journal</i> , 2020, 39, e106246.	3.5	32
114	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
115	Rendering graphene supports hydrophilic with non-covalent aromatic functionalization for transmission electron microscopy. <i>Applied Physics Letters</i> , 2014, 104, .	1.5	30
116	<i>Yersinia enterocolitica</i> type III secretion injectisomes form regularly spaced clusters, which incorporate new machines upon activation. <i>Molecular Microbiology</i> , 2015, 95, 875-884.	1.2	30
117	Chloroplast FOF1ATP Synthase Imaged by Atomic Force Microscopy. <i>Journal of Structural Biology</i> , 1997, 119, 139-148.	1.3	29
118	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
119	Translational arrest by a prokaryotic signal recognition particle is mediated by RNA interactions. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 767-773.	3.6	29
120	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
121	LIMITING FACTORS IN SINGLE PARTICLE CRYO ELECTRON TOMOGRAPHY. <i>Computational and Structural Biotechnology Journal</i> , 2012, 1, e201207002.	1.9	28
122	Single-cell lysis for visual analysis by electron microscopy. <i>Journal of Structural Biology</i> , 2013, 183, 467-473.	1.3	28
123	3D reconstruction of two-dimensional crystals. <i>Archives of Biochemistry and Biophysics</i> , 2015, 581, 68-77.	1.4	27
124	Cryo-electron Microscopy of Membrane Proteins. <i>Methods in Molecular Biology</i> , 2014, 1117, 325-341.	0.4	27
125	Real-time visualization of conformational changes within single MloK1 cyclic nucleotide-modulated channels. <i>Nature Communications</i> , 2016, 7, 12789.	5.8	26
126	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

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127	Connecting $\hat{1}/4$ -fluidics to electron microscopy. <i>Journal of Structural Biology</i> , 2012, 177, 128-134.	1.3	25
128	Retrieving high-resolution information from disordered 2D crystals by single-particle cryo-EM. <i>Nature Communications</i> , 2019, 10, 1722.	5.8	25
129	Automatic lattice determination for two-dimensional crystal images. <i>Journal of Structural Biology</i> , 2007, 160, 353-361.	1.3	24
130	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
131	Total Sample Conditioning and Preparation of Nanoliter Volumes for Electron Microscopy. <i>ACS Nano</i> , 2016, 10, 4981-4988.	7.3	23
132	Robust image alignment for cryogenic transmission electron microscopy. <i>Journal of Structural Biology</i> , 2017, 197, 279-293.	1.3	23
133	Self-Assembly of a Designed Nucleoprotein Architecture through Multimodal Interactions. <i>ACS Central Science</i> , 2018, 4, 1578-1586.	5.3	22
134	Cerebral Corpora amylacea are dense membranous labyrinths containing structurally preserved cell organelles. <i>Scientific Reports</i> , 2018, 8, 18046.	1.6	21
135	The aquaporin sidedness revisited. <i>Journal of Molecular Biology</i> , 2000, 299, 1271-1278.	2.0	20
136	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
137	3D Reconstruction from 2D Crystal Image and Diffraction Data. <i>Methods in Enzymology</i> , 2010, 482, 101-129.	0.4	19
138	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
139	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
140	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
141	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
142	Crystal Structures of Limulus SAP-Like Pentraxin Reveal Two Molecular Aggregations. <i>Journal of Molecular Biology</i> , 2009, 386, 1240-1254.	2.0	17
143	Single particle 3D reconstruction for 2D crystal images of membrane proteins. <i>Journal of Structural Biology</i> , 2014, 185, 267-277.	1.3	17
144	High-resolution cryo-EM structure of urease from the pathogen <i>Yersinia enterocolitica</i> . <i>Nature Communications</i> , 2020, 11, 5101.	5.8	17

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145	Grayscale e-beam lithography: Effects of a delayed development for well-controlled 3D patterning. <i>Microelectronic Engineering</i> , 2020, 225, 111272.	1.1	17
146	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
147	Pharmacokinetic evaluation of tapentadol extended-release tablets in healthy subjects. <i>Journal of Opioid Management</i> , 2013, 9, 291-300.	0.2	16
148	2.4-Å... structure of the double-ring <i>Gemmatimonas phototrophica</i> photosystem. <i>Science Advances</i> , 2022, 8, eabk3139.	4.7	16
149	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
150	The ultrastructure of <i>Chlorobaculum tepidum</i> revealed by cryo-electron tomography. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2014, 1837, 1635-1642.	0.5	14
151	Proteoliposomes – a system to study membrane proteins under buffer gradients by cryo-EM. <i>Nanotechnology Reviews</i> , 2017, 6, 57-74.	2.6	14
152	Miniaturizing EM Sample Preparation: Opportunities, Challenges, and “Visual Proteomics”. <i>Proteomics</i> , 2018, 18, e1700176.	1.3	14
153	FTLD- τ DP assemblies seed neoaggregates with subtype-specific features via a prion-like cascade. <i>EMBO Reports</i> , 2021, 22, e53877.	2.0	14
154	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
155	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
156	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
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158	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
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