

Henning Stahlberg

List of Publications by Year in descending order

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Version: 2024-02-01

217
papers

14,683
citations

20817

60
h-index

24982

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. | 7.8 | 842 |
| 2 | Lewy pathology in Parkinsonâ€™s disease consists of crowded organelles and lipid membranes. Nature Neuroscience, 2019, 22, 1099-1109. | 14.8 | 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. | 7.1 | 499 |
| 4 | Proton-powered turbine of a plant motor. Nature, 2000, 405, 418-419. | 27.8 | 478 |
| 5 | Cryo-EM structure of alpha-synuclein fibrils. ELife, 2018, 7, . | 6.0 | 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. | 2.8 | 376 |
| 7 | X-ray structure of the mouse serotonin 5-HT3 receptor. Nature, 2014, 512, 276-281. | 27.8 | 358 |
| 8 | Structure of the human multidrug transporter ABCG2. Nature, 2017, 546, 504-509. | 27.8 | 332 |
| 9 | Structural basis of small-molecule inhibition of human multidrug transporter ABCG2. Nature Structural and Molecular Biology, 2018, 25, 333-340. | 8.2 | 258 |
| 10 | Coassembly of Mgm1 isoforms requires cardiolipin and mediates mitochondrial inner membrane fusion. Journal of Cell Biology, 2009, 186, 793-803. | 5.2 | 243 |
| 11 | Structure of the T4 baseplate and its function in triggering sheath contraction. Nature, 2016, 533, 346-352. | 27.8 | 231 |
| 12 | Two new polymorphic structures of human full-length alpha-synuclein fibrils solved by cryo-electron microscopy. ELife, 2019, 8, . | 6.0 | 220 |
| 13 | Structure of the Type VI Secretion System Contractile Sheath. Cell, 2015, 160, 952-962. | 28.9 | 216 |
| 14 | Disease Modeling and Phenotypic Drug Screening for Diabetic Cardiomyopathy using Human Induced Pluripotent Stem Cells. Cell Reports, 2014, 9, 810-820. | 6.4 | 206 |
| 15 | Focus: The interface between data collection and data processing in cryo-EM. Journal of Structural Biology, 2017, 198, 124-133. | 2.8 | 192 |
| 16 | Cryo-EM structures of a human ABCG2 mutant trapped in ATP-bound and substrate-bound states. Nature, 2018, 563, 426-430. | 27.8 | 188 |
| 17 | Bacterial Na ⁺ ATP synthase has an undecameric rotor. EMBO Reports, 2001, 2, 229-233. | 4.5 | 185 |
| 18 | Oocyte CD9 is enriched on the microvillar membrane and required for normal microvillar shape and distribution. Developmental Biology, 2007, 304, 317-325. | 2.0 | 185 |

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|----|--|------|-----------|
| 19 | 2dxâ€™User-friendly image processing for 2D crystals. <i>Journal of Structural Biology</i> , 2007, 157, 64-72. | 2.8 | 184 |
| 20 | Characterization of the motion of membrane proteins using high-speed atomic force microscopy. <i>Nature Nanotechnology</i> , 2012, 7, 525-529. | 31.5 | 184 |
| 21 | Rad51 paralogues Rad55â€™Rad57 balance the antirecombinase Srs2 in Rad51 filament formation. <i>Nature</i> , 2011, 479, 245-248. | 27.8 | 183 |
| 22 | Molecular assembly of the aerolysin pore reveals a swirling membrane-insertion mechanism. <i>Nature Chemical Biology</i> , 2013, 9, 623-629. | 8.0 | 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, . | 12.4 | 178 |
| 24 | High resolution AFM topographs of the Escherichia coli water channel aquaporin Z. <i>EMBO Journal</i> , 1999, 18, 4981-4987. | 7.8 | 176 |
| 25 | Cullinâ€™RING ubiquitin E3 ligase regulation by the COP9 signalosome. <i>Nature</i> , 2016, 531, 598-603. | 27.8 | 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. | 7.1 | 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. | 7.1 | 153 |
| 28 | Friction Anisotropy and Asymmetry of a Compliant Monolayer Induced by a Small Molecular Tilt. <i>Science</i> , 1998, 280, 273-275. | 12.6 | 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. | 4.2 | 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. | 14.8 | 143 |
| 31 | RNAi Screening Reveals Proteasome- and Cullin3-Dependent Stages in Vaccinia Virus Infection. <i>Cell Reports</i> , 2012, 2, 1036-1047. | 6.4 | 139 |
| 32 | Structural basis for regulation of human acetyl-CoA carboxylase. <i>Nature</i> , 2018, 558, 470-474. | 27.8 | 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. | 7.1 | 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. | 7.1 | 125 |
| 35 | A Homotetrameric Kinesin-5, KLP61F, Bundles Microtubules and Antagonizes Ncd in Motility Assays. <i>Current Biology</i> , 2006, 16, 2293-2302. | 3.9 | 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. | 5.2 | 117 |

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|----|---|------|-----------|
| 37 | A helical inner scaffold provides a structural basis for centriole cohesion. <i>Science Advances</i> , 2020, 6, eaaz4137. | 10.3 | 116 |
| 38 | Domain structure of secretin PulD revealed by limited proteolysis and electron microscopy. <i>EMBO Journal</i> , 2000, 19, 2229-2236. | 7.8 | 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. | 6.0 | 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. | 2.8 | 108 |
| 42 | Cryo-EM structure of the extended type VI secretion system sheathâ€“tube complex. <i>Nature Microbiology</i> , 2017, 2, 1507-1512. | 13.3 | 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. | 8.2 | 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. | 2.8 | 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. | 2.5 | 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. | 2.5 | 85 |
| 47 | Graphene: Substrate preparation and introduction. <i>Journal of Structural Biology</i> , 2011, 174, 234-238. | 2.8 | 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. | 2.8 | 83 |
| 49 | The application of graphene as a sample support in transmission electron microscopy. <i>Solid State Communications</i> , 2012, 152, 1375-1382. | 1.9 | 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. | 6.4 | 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. | 7.1 | 78 |
| 52 | ATP synthase: constrained stoichiometry of the transmembrane rotor. <i>FEBS Letters</i> , 2001, 504, 219-222. | 2.8 | 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. | 2.8 | 74 |

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| 55 | The 4.5Å... Structure of Human AQP2. <i>Journal of Molecular Biology</i> , 2005, 350, 278-289. | 4.2 | 74 |
| 56 | Cell-free reconstitution reveals centriole cartwheel assembly mechanisms. <i>Nature Communications</i> , 2017, 8, 14813. | 12.8 | 74 |
| 57 | Cryo-EM reconstruction of Type VI secretion system baseplate and sheath distal end. <i>EMBO Journal</i> , 2018, 37, . | 7.8 | 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. | 4.2 | 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. | 4.2 | 70 |
| 60 | Sampling the conformational space of membrane protein surfaces with the AFM. <i>European Biophysics Journal</i> , 2002, 31, 172-178. | 2.2 | 70 |
| 61 | Structure and Function of Purified Monoclonal Antibody Dimers Induced by Different Stress Conditions. <i>Pharmaceutical Research</i> , 2012, 29, 2047-2059. | 3.5 | 68 |
| 62 | Molecular Electron Microscopy: State of the Art and Current Challenges. <i>ACS Chemical Biology</i> , 2008, 3, 268-281. | 3.4 | 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. | 7.1 | 64 |
| 64 | 2dx_merge: Data management and merging for 2D crystal images. <i>Journal of Structural Biology</i> , 2007, 160, 375-384. | 2.8 | 63 |
| 65 | Membrane Association Landscape of Myelin Basic Protein Portrays Formation of the Myelin Major Dense Line. <i>Scientific Reports</i> , 2017, 7, 4974. | 3.3 | 63 |
| 66 | Type III Protein Translocase. <i>Journal of Biological Chemistry</i> , 2003, 278, 25816-25824. | 3.4 | 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. | 3.8 | 60 |
| 68 | Ligand-induced structural changes in the cyclic nucleotide-modulated potassium channel MloK1. <i>Nature Communications</i> , 2014, 5, 3106. | 12.8 | 59 |
| 69 | Structural basis for chirality and directional motility of <i>Plasmodium</i> sporozoites. <i>Cellular Microbiology</i> , 2012, 14, 1757-1768. | 2.1 | 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. | 9.9 | 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. | 2.3 | 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. | 4.2 | 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. | 4.2 | 52 |
| 74 | Oxidative Doping Renders Graphene Hydrophilic, Facilitating Its Use As a Support in Biological TEM. <i>Nano Letters</i> , 2011, 11, 4319-4323. | 9.1 | 52 |
| 75 | Structural Basis of Drug Recognition by the Multidrug Transporter ABCG2. <i>Journal of Molecular Biology</i> , 2021, 433, 166980. | 4.2 | 52 |
| 76 | Cryo-EM structure of the rhodopsin-G β γ complex reveals binding of the rhodopsin C-terminal tail to the g β subunit. <i>ELife</i> , 2019, 8, . | 6.0 | 52 |
| 77 | The Structure of the Prokaryotic Cyclic Nucleotide-Modulated Potassium Channel MloK1 at 16 Å... Resolution. <i>Structure</i> , 2007, 15, 1053-1064. | 3.3 | 51 |
| 78 | Cryo-EM analysis of homodimeric full-length LRRK2 and LRRK1 protein complexes. <i>Scientific Reports</i> , 2017, 7, 8667. | 3.3 | 51 |
| 79 | Preparation and Characterization of Stable β -Synuclein Lipoprotein Particles. <i>Journal of Biological Chemistry</i> , 2016, 291, 8516-8527. | 3.4 | 49 |
| 80 | Three-Dimensional Imaging of Biological Tissue by Cryo X-Ray Ptychography. <i>Scientific Reports</i> , 2017, 7, 6291. | 3.3 | 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. | 7.6 | 48 |
| 82 | Lipid Internal Dynamics Probed in Nanodiscs. <i>ChemPhysChem</i> , 2017, 18, 2651-2657. | 2.1 | 47 |
| 83 | Structural basis of Focal Adhesion Kinase activation on lipid membranes. <i>EMBO Journal</i> , 2020, 39, e104743. | 7.8 | 47 |
| 84 | Low-dose aberration corrected cryo-electron microscopy of organic specimens. <i>Ultramicroscopy</i> , 2008, 108, 1636-1644. | 1.9 | 46 |
| 85 | Structures of ABCG2 under turnover conditions reveal a key step in the drug transport mechanism. <i>Nature Communications</i> , 2021, 12, 4376. | 12.8 | 46 |
| 86 | Double hexameric ring assembly of the type III protein translocase ATPase HrcN. <i>Molecular Microbiology</i> , 2006, 61, 119-125. | 2.5 | 45 |
| 87 | Cryo-electron tomography reveals four-membrane architecture of the <i>Plasmodium</i> apicoplast. <i>Malaria Journal</i> , 2013, 12, 25. | 2.3 | 44 |
| 88 | An iris diaphragm mechanism to gate a cyclic nucleotide-gated ion channel. <i>Nature Communications</i> , 2018, 9, 3978. | 12.8 | 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. | 12.8 | 43 |
| 90 | Characterization of mAb dimers reveals predominant dimer forms common in therapeutic mAbs. <i>MAbs</i> , 2016, 8, 928-940. | 5.2 | 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. | 2.6 | 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. | 7.1 | 41 |
| 93 | Molecular structure and function of myelin protein PO in membrane stacking. <i>Scientific Reports</i> , 2019, 9, 642. | 3.3 | 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. | 11.4 | 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, . | 2.0 | 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. | 12.8 | 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. | 4.5 | 38 |
| 98 | Diverse roles of TssA-like proteins in the assembly of bacterial type VI secretion systems. <i>EMBO Journal</i> , 2019, 38, e100825. | 7.8 | 38 |
| 99 | A maximum likelihood approach to two-dimensional crystals. <i>Journal of Structural Biology</i> , 2007, 160, 362-374. | 2.8 | 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. | 4.2 | 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. | 3.3 | 37 |
| 102 | The Structure of the Mouse Serotonin 5-HT ₃ Receptor in Lipid Vesicles. <i>Structure</i> , 2016, 24, 165-170. | 3.3 | 36 |
| 103 | Structural basis of the activation of the CC chemokine receptor 5 by a chemokine agonist. <i>Science Advances</i> , 2021, 7, . | 10.3 | 36 |
| 104 | Image processing library and toolkit for the electron microscopy community. <i>Journal of Structural Biology</i> , 2003, 144, 4-12. | 2.8 | 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. | 2.6 | 34 |
| 106 | CTF Challenge: Result summary. <i>Journal of Structural Biology</i> , 2015, 190, 348-359. | 2.8 | 34 |
| 107 | Femtosecond X-ray coherent diffraction of aligned amyloid fibrils on low background graphene. <i>Nature Communications</i> , 2018, 9, 1836. | 12.8 | 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. | 10.3 | 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. | 3.3 | 33 |
| 110 | Protocols for Subtomogram Averaging of Membrane Proteins in the Dynamo Software Package. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 82. | 3.5 | 33 |
| 111 | Milestones in electron crystallography. <i>Journal of Computer-Aided Molecular Design</i> , 2006, 20, 519-527. | 2.9 | 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. | 2.8 | 32 |
| 113 | Architecture of the centriole cartwheel-containing region revealed by cryo-electron tomography. <i>EMBO Journal</i> , 2020, 39, e106246. | 7.8 | 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. | 2.8 | 30 |
| 115 | Rendering graphene supports hydrophilic with non-covalent aromatic functionalization for transmission electron microscopy. <i>Applied Physics Letters</i> , 2014, 104, . | 3.3 | 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. | 2.5 | 30 |
| 117 | Chloroplast FOF1ATP Synthase Imaged by Atomic Force Microscopy. <i>Journal of Structural Biology</i> , 1997, 119, 139-148. | 2.8 | 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. | 2.8 | 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. | 8.2 | 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. | 7.3 | 28 |
| 121 | LIMITING FACTORS IN SINGLE PARTICLE CRYO ELECTRON TOMOGRAPHY. <i>Computational and Structural Biotechnology Journal</i> , 2012, 1, e201207002. | 4.1 | 28 |
| 122 | Single-cell lysis for visual analysis by electron microscopy. <i>Journal of Structural Biology</i> , 2013, 183, 467-473. | 2.8 | 28 |
| 123 | 3D reconstruction of two-dimensional crystals. <i>Archives of Biochemistry and Biophysics</i> , 2015, 581, 68-77. | 3.0 | 27 |
| 124 | Cryo-electron Microscopy of Membrane Proteins. <i>Methods in Molecular Biology</i> , 2014, 1117, 325-341. | 0.9 | 27 |
| 125 | Real-time visualization of conformational changes within single MloK1 cyclic nucleotide-modulated channels. <i>Nature Communications</i> , 2016, 7, 12789. | 12.8 | 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. | 1.0 | 25 |

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|-----|--|------|-----------|
| 127 | Connecting $\hat{1}/4$ -fluidics to electron microscopy. <i>Journal of Structural Biology</i> , 2012, 177, 128-134. | 2.8 | 25 |
| 128 | Retrieving high-resolution information from disordered 2D crystals by single-particle cryo-EM. <i>Nature Communications</i> , 2019, 10, 1722. | 12.8 | 25 |
| 129 | Automatic lattice determination for two-dimensional crystal images. <i>Journal of Structural Biology</i> , 2007, 160, 353-361. | 2.8 | 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. | 2.1 | 23 |
| 131 | Total Sample Conditioning and Preparation of Nanoliter Volumes for Electron Microscopy. <i>ACS Nano</i> , 2016, 10, 4981-4988. | 14.6 | 23 |
| 132 | Robust image alignment for cryogenic transmission electron microscopy. <i>Journal of Structural Biology</i> , 2017, 197, 279-293. | 2.8 | 23 |
| 133 | Self-Assembly of a Designed Nucleoprotein Architecture through Multimodal Interactions. <i>ACS Central Science</i> , 2018, 4, 1578-1586. | 11.3 | 22 |
| 134 | Cerebral Corpora amylacea are dense membranous labyrinths containing structurally preserved cell organelles. <i>Scientific Reports</i> , 2018, 8, 18046. | 3.3 | 21 |
| 135 | The aquaporin sidedness revisited. <i>Journal of Molecular Biology</i> , 2000, 299, 1271-1278. | 4.2 | 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. | 5.7 | 20 |
| 137 | 3D Reconstruction from 2D Crystal Image and Diffraction Data. <i>Methods in Enzymology</i> , 2010, 482, 101-129. | 1.0 | 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. | 1.0 | 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. | 3.4 | 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. | 3.3 | 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. | 4.2 | 17 |
| 143 | Single particle 3D reconstruction for 2D crystal images of membrane proteins. <i>Journal of Structural Biology</i> , 2014, 185, 267-277. | 2.8 | 17 |
| 144 | High-resolution cryo-EM structure of urease from the pathogen <i>Yersinia enterocolitica</i> . <i>Nature Communications</i> , 2020, 11, 5101. | 12.8 | 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. | 2.4 | 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. | 4.5 | 16 |
| 147 | Pharmacokinetic evaluation of tapentadol extended-release tablets in healthy subjects. <i>Journal of Opioid Management</i> , 2013, 9, 291-300. | 0.5 | 16 |
| 148 | 2.4-Å... structure of the double-ring <i>Gemmatimonas phototrophica</i> photosystem. <i>Science Advances</i> , 2022, 8, eabk3139. | 10.3 | 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. | 3.4 | 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. | 1.0 | 14 |
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