# Steven J Ludtke

## List of Publications by Year
## in descending order

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|---|---|---|---|
| 128<br>papers | 16,114<br>citations | 19657<br>61<br>h-index | 19749<br>117<br>g-index |
| 141<br>all docs | 141<br>docs citations | 141<br>times ranked | 17278<br>citing authors |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1 | EMAN2: An extensible image processing suite for electron microscopy. Journal of Structural Biology, 2007, 157, 38-46. | 2.8 | 2,798 |
| 2 | EMAN: Semiautomated Software for High-Resolution Single-Particle Reconstructions. Journal of Structural Biology, 1999, 128, 82-97. | 2.8 | 2,320 |
| 3 | Integrative structure and functional anatomy of a nuclear pore complex. Nature, 2018, 555, 475-482. | 27.8 | 435 |
| 4 | SPARX, a new environment for Cryo-EM image processing. Journal of Structural Biology, 2007, 157, 47-55. | 2.8 | 356 |
| 5 | Superparamagnetic gadonanotubes are high-performance MRI contrast agents. Chemical Communications, 2005, , 3915. | 4.1 | 310 |
| 6 | Convolutional neural networks for automated annotation of cellular cryo-electron tomograms. Nature Methods, 2017, 14, 983-985. | 19.0 | 298 |
| 7 | Bridging the information gap: computational tools for intermediate resolution structure interpretation. Journal of Molecular Biology, 2001, 308, 1033-1044. | 4.2 | 282 |
| 8 | The Molecular Architecture of the Eukaryotic Chaperonin TRiC/CCT. Structure, 2012, 20, 814-825. | 3.3 | 261 |
| 9 | EMDataBank.org: unified data resource for CryoEM. Nucleic Acids Research, 2011, 39, D456-D464. | 14.5 | 246 |
| 10 | Improvement of cryo-EM maps by density modification. Nature Methods, 2020, 17, 923-927. | 19.0 | 243 |
| 11 | Close membrane-membrane proximity induced by Ca2+-dependent multivalent binding of synaptotagmin-1 to phospholipids. Nature Structural and Molecular Biology, 2006, 13, 209-217. | 8.2 | 235 |
| 12 | EMDataBank unified data resource for 3DEM. Nucleic Acids Research, 2016, 44, D396-D403. | 14.5 | 230 |
| 13 | Neutron scattering in the plane of membranes: structure of alamethicin pores. Biophysical Journal, 1996, 70, 2659-2666. | 0.5 | 226 |
| 14 | Mechanism of alamethicin insertion into lipid bilayers. Biophysical Journal, 1996, 71, 2669-2679. | 0.5 | 213 |
| 15 | Gating machinery of InsP3R channels revealed by electron cryomicroscopy. Nature, 2015, 527, 336-341. | 27.8 | 199 |
| 16 | Mechanism of folding chamber closure in a group II chaperonin. Nature, 2010, 463, 379-383. | 27.8 | 196 |
| 17 | Mitochondrial ATP Synthasome. Journal of Biological Chemistry, 2004, 279, 31761-31768. | 3.4 | 193 |
| 18 | X-ray diffraction study of lipid bilayer membranes interacting with amphiphilic helical peptides: diphytanoyl phosphatidylcholine with alamethicin at low concentrations. Biophysical Journal, 1995, 68, 2361-2369. | 0.5 | 192 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 19 | Seeing GroEL at 6 Ã… Resolution by Single Particle Electron Cryomicroscopy. Structure, 2004, 12, 1129-1136. | 3.3 | 187 |
| 20 | A complete data processing workflow for cryo-ET and subtomogram averaging. Nature Methods, 2019, 16, 1161-1168. | 19.0 | 174 |
| 21 | De Novo Backbone Trace of GroEL from Single Particle Electron Cryomicroscopy. Structure, 2008, 16, 441-448. | 3.3 | 164 |
| 22 | High resolution single particle refinement in EMAN2.1. Methods, 2016, 100, 25-34. | 3.8 | 163 |
| 23 | 4.0-â„« resolution cryo-EM structure of the mammalian chaperonin TRiC/CCT reveals its unique subunit arrangement. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 4967-4972. | 7.1 | 152 |
| 24 | Interprotofilament interactions between Alzheimer's AÎ² <sub>1â€"42</sub> peptides in amyloid fibrils revealed by cryoEM. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 4653-4658. | 7.1 | 147 |
| 25 | A Structure of the Human Apoptosome at 12.8 Ã… Resolution Provides Insights into This Cell Death Platform. Structure, 2005, 13, 1725-1735. | 3.3 | 145 |
| 26 | Cooperative membrane insertion of magainin correlated with its cytolytic activity. Biochimica Et Biophysica Acta - Biomembranes, 1994, 1190, 181-184. | 2.6 | 144 |
| 27 | The Pore Structure of the Closed RyR1 Channel. Structure, 2005, 13, 1203-1211. | 3.3 | 142 |
| 28 | Structure of the SecY channel during initiation of protein translocation. Nature, 2014, 506, 102-106. | 27.8 | 138 |
| 29 | Structure of a Biologically Active Estrogen Receptor-Coactivator Complex on DNA. Molecular Cell, 2015, 57, 1047-1058. | 9.7 | 137 |
| 30 | Automatic particle selection: results of a comparative study. Journal of Structural Biology, 2004, 145, 3-14. | 2.8 | 129 |
| 31 | Architecture of the Ribosomeâ€"Channel Complex Derived from Native Membranes. Journal of Molecular Biology, 2005, 348, 445-457. | 4.2 | 126 |
| 32 | Visualizing virus assembly intermediates inside marine cyanobacteria. Nature, 2013, 502, 707-710. | 27.8 | 123 |
| 33 | Structural diversity of supercoiled DNA. Nature Communications, 2015, 6, 8440. | 12.8 | 122 |
| 34 | A 11.5 Ã… single particle reconstruction of GroEL using EMAN. Journal of Molecular Biology, 2001, 314, 253-262. | 4.2 | 119 |
| 35 | Structure of an Apoptosome-Procaspase-9 CARD Complex. Structure, 2010, 18, 571-583. | 3.3 | 118 |
| 36 | Subnanometer-resolution electron cryomicroscopy-based domain models for the cytoplasmic region of skeletal muscle RyR channel. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 9610-9615. | 7.1 | 106 |

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|---|---|---|---|
| 37 | Effect of changing the size of lipid headgroup on peptide insertion into membranes. Biophysical Journal, 1997, 73, 239-244. | 0.5 | 105 |
| 38 | An atomic model of brome mosaic virus using direct electron detection and real-space optimization. Nature Communications, 2014, 5, 4808. | 12.8 | 105 |
| 39 | Deep learning-based mixed-dimensional Gaussian mixture model for characterizing variability in cryo-EM. Nature Methods, 2021, 18, 930-936. | 19.0 | 102 |
| 40 | Single particle tomography in EMAN2. Journal of Structural Biology, 2015, 190, 279-290. | 2.8 | 98 |
| 41 | Fourier Amplitude Decay of Electron Cryomicroscopic Images of Single Particles and Effects on Structure Determination. Journal of Structural Biology, 2001, 133, 32-42. | 2.8 | 95 |
| 42 | In situ structure and assembly of the multidrug efflux pump AcrAB-TolC. Nature Communications, 2019, 10, 2635. | 12.8 | 95 |
| 43 | Structural Insights of Transcriptionally Active, Full-Length Androgen Receptor Coactivator Complexes. Molecular Cell, 2020, 79, 812-823.e4. | 9.7 | 94 |
| 44 | Ribosome Binding of a Single Copy of the SecY Complex: Implications for Protein Translocation. Molecular Cell, 2007, 28, 1083-1092. | 9.7 | 92 |
| 45 | Mechanism of lid closure in the eukaryotic chaperonin TRiC/CCT. Nature Structural and Molecular Biology, 2008, 15, 746-753. | 8.2 | 91 |
| 46 | Comprehensive structure and functional adaptations of the yeast nuclear pore complex. Cell, 2022, 185, 361-378.e25. | 28.9 | 87 |
| 47 | Structure of the Type 1 Inositol 1,4,5-Trisphosphate Receptor Revealed by Electron Cryomicroscopy. Journal of Biological Chemistry, 2003, 278, 21319-21322. | 3.4 | 85 |
| 48 | Single-Particle Refinement and Variability Analysis in EMAN2.1. Methods in Enzymology, 2016, 579, 159-189. | 1.0 | 85 |
| 49 | The Holo-Apoptosome: Activation of Procaspase-9 and Interactions with Caspase-3. Structure, 2011, 19, 1084-1096. | 3.3 | 83 |
| 50 | Structural Analysis of the Anaphase-Promoting Complex Reveals Multiple Active Sites and Insights into Polyubiquitylation. Molecular Cell, 2005, 20, 855-866. | 9.7 | 81 |
| 51 | Flexible Architecture of IP3R1 by Cryo-EM. Structure, 2011, 19, 1192-1199. | 3.3 | 80 |
| 52 | Symmetry-free cryo-EM structures of the chaperonin TRiC along its ATPase-driven conformational cycle. EMBO Journal, 2012, 31, 720-730. | 7.8 | 80 |
| 53 | Cryo-EM of macromolecular assemblies at near-atomic resolution. Nature Protocols, 2010, 5, 1697-1708. | 12.0 | 79 |
| 54 | Experimental Verification of Conformational Variation of Human Fatty Acid Synthase as Predicted by Normal Mode Analysis. Structure, 2004, 12, 185-191. | 3.3 | 78 |

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|---|---|---|---|
| 55 | Structure of the voltage-gated L-type Ca2+ channel by electron cryomicroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 10370-10375. | 7.1 | 76 |
| 56 | Structure of Ca2+ Release Channel at 14Ã… Resolution. Journal of Molecular Biology, 2005, 345, 427-431. | 4.2 | 76 |
| 57 | Structure of the Drosophila Apoptosome at 6.9ÂÃ… Resolution. Structure, 2011, 19, 128-140. | 3.3 | 73 |
| 58 | TRiCâ€™s tricks inhibit huntingtin aggregation. ELife, 2013, 2, e00710. | 6.0 | 73 |
| 59 | Structural and Functional Impacts of ER Coactivator Sequential Recruitment. Molecular Cell, 2017, 67, 733-743.e4. | 9.7 | 69 |
| 60 | De Novo modeling in cryo-EM density maps with Pathwalking. Journal of Structural Biology, 2016, 196, 289-298. | 2.8 | 68 |
| 61 | Cryoelectron Microscopy Structures of Rotavirus NSP2-NSP5 and NSP2-RNA Complexes: Implications for Genome Replication. Journal of Virology, 2006, 80, 10829-10835. | 3.4 | 66 |
| 62 | Model of human low-density lipoprotein and bound receptor based on CryoEM. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 1059-1064. | 7.1 | 65 |
| 63 | A 9Ã… single particle reconstruction from CCD captured images on a 200kV electron cryomicroscope. Journal of Structural Biology, 2004, 147, 116-127. | 2.8 | 64 |
| 64 | Visualizing Individual RuBisCO and Its Assembly into Carboxysomes in Marine Cyanobacteria by Cryo-Electron Tomography. Journal of Molecular Biology, 2018, 430, 4156-4167. | 4.2 | 63 |
| 65 | Structural Mechanism of SDS-Induced Enzyme Activity of Scorpion Hemocyanin Revealed by Electron Cryomicroscopy. Structure, 2009, 17, 749-758. | 3.3 | 61 |
| 66 | The skeletal muscle Ca2+ release channel has an oxidoreductase-like domain. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 12155-12160. | 7.1 | 60 |
| 67 | An Expanded Conformation of Single-Ring GroEL-GroES Complex Encapsulates an 86 kDa Substrate. Structure, 2006, 14, 1711-1722. | 3.3 | 59 |
| 68 | MRC2014: Extensions to the MRC format header for electron cryo-microscopy and tomography. Journal of Structural Biology, 2015, 192, 146-150. | 2.8 | 59 |
| 69 | Quaternary structure of human fatty acid synthase by electron cryomicroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 138-143. | 7.1 | 57 |
| 70 | Human CCT4 and CCT5 Chaperonin Subunits Expressed in Escherichia coli Form Biologically Active Homo-oligomers. Journal of Biological Chemistry, 2013, 288, 17734-17744. | 3.4 | 54 |
| 71 | 3-D Structures of Macromolecules Using Single-Particle Analysis in EMAN. Methods in Molecular Biology, 2010, 673, 157-173. | 0.9 | 52 |
| 72 | EMEN2: An Object Oriented Database and Electronic Lab Notebook. Microscopy and Microanalysis, 2013, 19, 1-10. | 0.4 | 52 |

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|---|---|---|---|
| 73 | Structure of the 30ÂkDa HIV-1 RNA Dimerization Signal by a Hybrid Cryo-EM, NMR, and Molecular Dynamics Approach. Structure, 2018, 26, 490-498.e3. | 3.3 | 52 |
| 74 | Structural basis of amino acid surveillance by higher-order tRNA-mRNA interactions. Nature Structural and Molecular Biology, 2019, 26, 1094-1105. | 8.2 | 52 |
| 75 | Data management challenges in three-dimensional EM. Nature Structural and Molecular Biology, 2012, 19, 1203-1207. | 8.2 | 49 |
| 76 | Cryo-EM reveals ligand induced allostery underlying InsP3R channel gating. Cell Research, 2018, 28, 1158-1170. | 12.0 | 48 |
| 77 | Cross-neutralizing human anti-poliovirus antibodies bind the recognition site for cellular receptor. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20242-20247. | 7.1 | 45 |
| 78 | Electron cryomicroscopy of single particles at subnanometer resolution. Current Opinion in Structural Biology, 2005, 15, 571-577. | 5.7 | 43 |
| 79 | Validation of Cryo-EM Structure of IP3R1 Channel. Structure, 2013, 21, 900-909. | 3.3 | 43 |
| 80 | Alignment algorithms and per-particle CTF correction for single particle cryo-electron tomography. Journal of Structural Biology, 2016, 194, 383-394. | 2.8 | 42 |
| 81 | The advent of structural biology in situ by single particle cryo-electron tomography. Biophysics Reports, 2017, 3, 17-35. | 0.8 | 41 |
| 82 | New software tools in EMAN2 inspired by EMDatabank map challenge. Journal of Structural Biology, 2018, 204, 283-290. | 2.8 | 40 |
| 83 | Constructing and Validating Initial CÎ± Models from Subnanometer Resolution Density Maps with Pathwalking. Structure, 2012, 20, 450-463. | 3.3 | 38 |
| 84 | X-ray scattering with momentum transfer in the plane of membrane. Application to gramicidin organization. Biophysical Journal, 1993, 64, 157-162. | 0.5 | 37 |
| 85 | Closed state of gramicidin channel detected by X-ray in-plane scattering. Biophysical Chemistry, 1994, 49, 83-89. | 2.8 | 34 |
| 86 | CTF Challenge: Result summary. Journal of Structural Biology, 2015, 190, 348-359. | 2.8 | 34 |
| 87 | Cryo-EM Structure of a Molluscan Hemocyanin Suggests Its Allosteric Mechanism. Structure, 2013, 21, 604-613. | 3.3 | 30 |
| 88 | Domain organization of membraneâ€bound factor VIII. Biopolymers, 2013, 99, 448-459. | 2.4 | 30 |
| 89 | Discrete Structure of an RNA Folding Intermediate Revealed by Cryo-electron Microscopy. Journal of the American Chemical Society, 2010, 132, 16352-16353. | 13.7 | 29 |
| 90 | Single Particle Analysis at High Resolution. Methods in Enzymology, 2010, 482, 211-235. | 1.0 | 29 |

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|---|---|---|---|
| 91 | Structural and functional analyses of photosystem II in the marine diatom <i>Phaeodactylum tricornutum</i>. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17316-17322. | 7.1 | 29 |
| 92 | In situ structure of the AcrAB-TolC efflux pump at subnanometer resolution. Structure, 2022, 30, 107-113.e3. | 3.3 | 28 |
| 93 | Structure of the bifunctional and Golgi-associated formiminotransferase cyclodeaminase octamer. EMBO Journal, 2004, 23, 2963-2971. | 7.8 | 26 |
| 94 | Characterization of Antibiotic Peptide Pores Using Cryo-EM and Comparison to Neutron Scattering. Biophysical Journal, 2009, 97, 164-172. | 0.5 | 26 |
| 95 | Cryo-ET of <i>Toxoplasma</i> parasites gives subnanometer insight into tubulin-based structures. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, . | 7.1 | 26 |
| 96 | Zernike phase-contrast electron cryotomography applied to marine cyanobacteria infected with cyanophages. Nature Protocols, 2014, 9, 2630-2642. | 12.0 | 24 |
| 97 | A Near-Atomic Structure of the Dark Apoptosome Provides Insight into Assembly and Activation. Structure, 2017, 25, 40-52. | 3.3 | 23 |
| 98 | Disruption of Human Plasma High-Density Lipoproteins by Streptococcal Serum Opacity Factor Requires Labile Apolipoprotein A-I. Biochemistry, 2009, 48, 1481-1487. | 2.5 | 22 |
| 99 | The 2010 cryoâ€em modeling challenge. Biopolymers, 2012, 97, 651-654. | 2.4 | 22 |
| 100 | Details of ssDNA annealing revealed by an HSV-1 ICP8â€“ssDNA binary complex. Nucleic Acids Research, 2013, 41, 5927-5937. | 14.5 | 22 |
| 101 | Single-particle Cryo-EM of calcium release channels: structural validation. Current Opinion in Structural Biology, 2013, 23, 755-762. | 5.7 | 19 |
| 102 | Object Oriented Database and Electronic Notebook for Transmission Electron Microscopy. Microscopy and Microanalysis, 2003, 9, 556-565. | 0.4 | 16 |
| 103 | Preliminary Structural Elucidation of Î²-(1,3)-glucan Synthase from Candida glabrata Using Cryo-Electron Tomography. Journal of Fungi (Basel, Switzerland), 2021, 7, 120. | 3.5 | 16 |
| 104 | Direct Measurement of the Structure of Reconstituted High-Density Lipoproteins by Cryo-EM. Biophysical Journal, 2016, 110, 810-816. | 0.5 | 15 |
| 105 | Focal pair merging for contrast enhancement of single particles. Journal of Structural Biology, 2003, 144, 73-78. | 2.8 | 14 |
| 106 | Singleâ€Particle Electron Cryomicroscopy of the Ion Channels in the Excitationâ€“Contraction Coupling Junction. Methods in Cell Biology, 2007, 79, 407-435. | 1.1 | 12 |
| 107 | The Electron Microscopy eXchange (EMX) initiative. Journal of Structural Biology, 2016, 194, 156-163. | 2.8 | 12 |
| 108 | 3D Structure of IP3 Receptor. Current Topics in Membranes, 2010, 66, 171-189. | 0.9 | 7 |

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|---|---|---|---|
| 109 | Computational Tools to Improve Visualization by Cryo-Electron Tomography. Biophysical Journal, 2016, 110, 159a. | 0.5 | 2 |
| 110 | A Complete Workflow for Cellular Tomography and Subtomogram Averaging in EMAN2. Microscopy and Microanalysis, 2018, 24, 866-867. | 0.4 | 2 |
| 111 | Using Cryo-ET to distinguish platelets during pre-acute myeloid leukemia from steady state hematopoiesis. Communications Biology, 2022, 5, 72. | 4.4 | 2 |
| 112 | Building and Validating Atomic Models for Cryo-EM Density Maps. Microscopy and Microanalysis, 2016, 22, 2080-2081. | 0.4 | 1 |
| 113 | New Strategies for Improving CryoEM Single Particle Analysis in EMAN2.2. Microscopy and Microanalysis, 2017, 23, 810-811. | 0.4 | 1 |
| 114 | In Situ Structure and Assembly of the Bacterial Multidrug Efflux Pump. Microscopy and Microanalysis, 2019, 25, 1304-1305. | 0.4 | 1 |
| 115 | Estimates of the Fourier Amplitude Decay of Electron Micrographs of Single Particles. Microscopy and Microanalysis, 2000, 6, 256-257. | 0.4 | 0 |
| 116 | Merging Focal Pairs for Improved Particle Selection and Orientation Determination. Microscopy and Microanalysis, 2002, 8, 216-217. | 0.4 | 0 |
| 117 | Imaging Ice Embedded Single Particles With A 16 Megapixel CCD Camera. Microscopy and Microanalysis, 2003, 9, 962-963. | 0.4 | 0 |
| 118 | GroEL Structure at 6 Ã… Resolution Using Electron Cryomicroscopy and EMAN. Microscopy and Microanalysis, 2004, 10, 1494-1495. | 0.4 | 0 |
| 119 | Modeling Protein Structure in Macromolecular Assemblies at Near Atomic Resolutions. Microscopy and Microanalysis, 2015, 21, 541-542. | 0.4 | 0 |
| 120 | IP3R1 - Assessing Map Interpretability at Near Atomic Resolution. Microscopy and Microanalysis, 2015, 21, 543-544. | 0.4 | 0 |
| 121 | Going Deeper in Cryo Electron Tomography with Neural Networks. Microscopy and Microanalysis, 2017, 23, 814-815. | 0.4 | 0 |
| 122 | A Complete Workflow for Subnanometer Resolution Subtomogram Averaging In Situ. Microscopy and Microanalysis, 2020, 26, 1616-1616. | 0.4 | 0 |
| 123 | Explore the complexity of proteins with an expanded CryoET data processing pipeline. Microscopy and Microanalysis, 2021, 27, 2816-2817. | 0.4 | 0 |
| 124 | Conformational Changes of Eukaryotic Chaperonin TRiC/CCT in the Nucleotide Cycle Revealed by CryoEM. FASEB Journal, 2009, 23, 850.12. | 0.5 | 0 |
| 125 | Rocking Motion of the Equatorial Domains of a Group II Chaperonin between Two Biochemical States Revealed by Singleâ€Particle Cryoâ€EM at Nearâ€atomic and Subnanometer Resolutions. FASEB Journal, 2009, 23, 673.12. | 0.5 | 0 |
| 126 | 4.0 Ã… Resolution Cryoâ€EM Structure of the Mammalian Chaperonin TRiC/CCT Reveals its Unique Subunit Arrangement. FASEB Journal, 2010, 24, 684.5. | 0.5 | 0 |

| # | Article | IF | Citations |
|---|---|---|---|
| 127 | In Situ Investigations of the Bacterial Type II Secretion System. Microscopy and Microanalysis, 2020, 26, 2734-2735. | 0.4 | 0 |
| 128 | Precision requirements and data compression in CryoEM/CryoET. Journal of Structural Biology, 2022, 214, 107875. | 2.8 | 0 |