

Steven J Ludtke

List of Publications by Year in descending order

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128
papers

16,114
citations

19657

61
h-index

19749

117
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141
all docs

141
docs citations

141
times ranked

17278
citing authors

#	ARTICLE	IF	CITATIONS
1	In situ structure of the AcrAB-TolC efflux pump at subnanometer resolution. <i>Structure</i> , 2022, 30, 107-113.e3.	3.3	28
2	Using Cryo-ET to distinguish platelets during pre-acute myeloid leukemia from steady state hematopoiesis. <i>Communications Biology</i> , 2022, 5, 72.	4.4	2
3	Comprehensive structure and functional adaptations of the yeast nuclear pore complex. <i>Cell</i> , 2022, 185, 361-378.e25.	28.9	87
4	Cryo-ET of <i>Toxoplasma</i> parasites gives subnanometer insight into tubulin-based structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	26
5	Precision requirements and data compression in CryoEM/CryoET. <i>Journal of Structural Biology</i> , 2022, 214, 107875.	2.8	0
6	Preliminary Structural Elucidation of β -(1,3)-glucan Synthase from <i>Candida glabrata</i> Using Cryo-Electron Tomography. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 120.	3.5	16
7	Explore the complexity of proteins with an expanded CryoET data processing pipeline. <i>Microscopy and Microanalysis</i> , 2021, 27, 2816-2817.	0.4	0
8	Deep learning-based mixed-dimensional Gaussian mixture model for characterizing variability in cryo-EM. <i>Nature Methods</i> , 2021, 18, 930-936.	19.0	102
9	Structural Insights of Transcriptionally Active, Full-Length Androgen Receptor Coactivator Complexes. <i>Molecular Cell</i> , 2020, 79, 812-823.e4.	9.7	94
10	Improvement of cryo-EM maps by density modification. <i>Nature Methods</i> , 2020, 17, 923-927.	19.0	243
11	A Complete Workflow for Subnanometer Resolution Subtomogram Averaging In Situ. <i>Microscopy and Microanalysis</i> , 2020, 26, 1616-1616.	0.4	0
12	In Situ Investigations of the Bacterial Type II Secretion System. <i>Microscopy and Microanalysis</i> , 2020, 26, 2734-2735.	0.4	0
13	Structural and functional analyses of photosystem II in the marine diatom <i>Phaeodactylum tricornutum</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17316-17322.	7.1	29
14	A complete data processing workflow for cryo-ET and subtomogram averaging. <i>Nature Methods</i> , 2019, 16, 1161-1168.	19.0	174
15	In Situ Structure and Assembly of the Bacterial Multidrug Efflux Pump. <i>Microscopy and Microanalysis</i> , 2019, 25, 1304-1305.	0.4	1
16	In situ structure and assembly of the multidrug efflux pump AcrAB-TolC. <i>Nature Communications</i> , 2019, 10, 2635.	12.8	95
17	Structural basis of amino acid surveillance by higher-order tRNA-mRNA interactions. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 1094-1105.	8.2	52
18	Structure of the 30 kDa HIV-1 RNA Dimerization Signal by a Hybrid Cryo-EM, NMR, and Molecular Dynamics Approach. <i>Structure</i> , 2018, 26, 490-498.e3.	3.3	52

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19	Integrative structure and functional anatomy of a nuclear pore complex. <i>Nature</i> , 2018, 555, 475-482.	27.8	435
20	A Complete Workflow for Cellular Tomography and Subtomogram Averaging in EMAN2. <i>Microscopy and Microanalysis</i> , 2018, 24, 866-867.	0.4	2
21	Cryo-EM reveals ligand induced allostery underlying InsP3R channel gating. <i>Cell Research</i> , 2018, 28, 1158-1170.	12.0	48
22	New software tools in EMAN2 inspired by EMDatabank map challenge. <i>Journal of Structural Biology</i> , 2018, 204, 283-290.	2.8	40
23	Visualizing Individual RuBisCO and Its Assembly into Carboxysomes in Marine Cyanobacteria by Cryo-Electron Tomography. <i>Journal of Molecular Biology</i> , 2018, 430, 4156-4167.	4.2	63
24	The advent of structural biology in situ by single particle cryo-electron tomography. <i>Biophysics Reports</i> , 2017, 3, 17-35.	0.8	41
25	A Near-Atomic Structure of the Dark Apoptosome Provides Insight into Assembly and Activation. <i>Structure</i> , 2017, 25, 40-52.	3.3	23
26	Structural and Functional Impacts of ER Coactivator Sequential Recruitment. <i>Molecular Cell</i> , 2017, 67, 733-743.e4.	9.7	69
27	Convolutional neural networks for automated annotation of cellular cryo-electron tomograms. <i>Nature Methods</i> , 2017, 14, 983-985.	19.0	298
28	New Strategies for Improving CryoEM Single Particle Analysis in EMAN2.2. <i>Microscopy and Microanalysis</i> , 2017, 23, 810-811.	0.4	1
29	Going Deeper in Cryo Electron Tomography with Neural Networks. <i>Microscopy and Microanalysis</i> , 2017, 23, 814-815.	0.4	0
30	Single-Particle Refinement and Variability Analysis in EMAN2.1. <i>Methods in Enzymology</i> , 2016, 579, 159-189.	1.0	85
31	Building and Validating Atomic Models for Cryo-EM Density Maps. <i>Microscopy and Microanalysis</i> , 2016, 22, 2080-2081.	0.4	1
32	Alignment algorithms and per-particle CTF correction for single particle cryo-electron tomography. <i>Journal of Structural Biology</i> , 2016, 194, 383-394.	2.8	42
33	High resolution single particle refinement in EMAN2.1. <i>Methods</i> , 2016, 100, 25-34.	3.8	163
34	De Novo modeling in cryo-EM density maps with Pathwalking. <i>Journal of Structural Biology</i> , 2016, 196, 289-298.	2.8	68
35	EMDataBank unified data resource for 3DEM. <i>Nucleic Acids Research</i> , 2016, 44, D396-D403.	14.5	230
36	The Electron Microscopy eXchange (EMX) initiative. <i>Journal of Structural Biology</i> , 2016, 194, 156-163.	2.8	12

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37	Computational Tools to Improve Visualization by Cryo-Electron Tomography. <i>Biophysical Journal</i> , 2016, 110, 159a.	0.5	2
38	Direct Measurement of the Structure of Reconstituted High-Density Lipoproteins by Cryo-EM. <i>Biophysical Journal</i> , 2016, 110, 810-816.	0.5	15
39	Modeling Protein Structure in Macromolecular Assemblies at Near Atomic Resolutions. <i>Microscopy and Microanalysis</i> , 2015, 21, 541-542.	0.4	0
40	IP3R1 - Assessing Map Interpretability at Near Atomic Resolution. <i>Microscopy and Microanalysis</i> , 2015, 21, 543-544.	0.4	0
41	Structure of a Biologically Active Estrogen Receptor-Coactivator Complex on DNA. <i>Molecular Cell</i> , 2015, 57, 1047-1058.	9.7	137
42	Single particle tomography in EMAN2. <i>Journal of Structural Biology</i> , 2015, 190, 279-290.	2.8	98
43	CTF Challenge: Result summary. <i>Journal of Structural Biology</i> , 2015, 190, 348-359.	2.8	34
44	MRC2014: Extensions to the MRC format header for electron cryo-microscopy and tomography. <i>Journal of Structural Biology</i> , 2015, 192, 146-150.	2.8	59
45	Gating machinery of InsP3R channels revealed by electron cryomicroscopy. <i>Nature</i> , 2015, 527, 336-341.	27.8	199
46	Structural diversity of supercoiled DNA. <i>Nature Communications</i> , 2015, 6, 8440.	12.8	122
47	An atomic model of brome mosaic virus using direct electron detection and real-space optimization. <i>Nature Communications</i> , 2014, 5, 4808.	12.8	105
48	Zernike phase-contrast electron cryotomography applied to marine cyanobacteria infected with cyanophages. <i>Nature Protocols</i> , 2014, 9, 2630-2642.	12.0	24
49	Structure of the SecY channel during initiation of protein translocation. <i>Nature</i> , 2014, 506, 102-106.	27.8	138
50	Cryo-EM Structure of a Molluscan Hemocyanin Suggests Its Allosteric Mechanism. <i>Structure</i> , 2013, 21, 604-613.	3.3	30
51	Visualizing virus assembly intermediates inside marine cyanobacteria. <i>Nature</i> , 2013, 502, 707-710.	27.8	123
52	Cross-neutralizing human anti-poliovirus antibodies bind the recognition site for cellular receptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20242-20247.	7.1	45
53	Single-particle Cryo-EM of calcium release channels: structural validation. <i>Current Opinion in Structural Biology</i> , 2013, 23, 755-762.	5.7	19
54	Validation of Cryo-EM Structure of IP3R1 Channel. <i>Structure</i> , 2013, 21, 900-909.	3.3	43

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55	Domain organization of membrane-bound factor VIII. <i>Biopolymers</i> , 2013, 99, 448-459.	2.4	30
56	Details of ssDNA annealing revealed by an HSV-1 ICP8-ssDNA binary complex. <i>Nucleic Acids Research</i> , 2013, 41, 5927-5937.	14.5	22
57	Human CCT4 and CCT5 Chaperonin Subunits Expressed in <i>Escherichia coli</i> Form Biologically Active Homo-oligomers. <i>Journal of Biological Chemistry</i> , 2013, 288, 17734-17744.	3.4	54
58	EMEN2: An Object Oriented Database and Electronic Lab Notebook. <i>Microscopy and Microanalysis</i> , 2013, 19, 1-10.	0.4	52
59	TRiC™s tricks inhibit huntingtin aggregation. <i>ELife</i> , 2013, 2, e00710.	6.0	73
60	Symmetry-free cryo-EM structures of the chaperonin TRiC along its ATPase-driven conformational cycle. <i>EMBO Journal</i> , 2012, 31, 720-730.	7.8	80
61	Data management challenges in three-dimensional EM. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1203-1207.	8.2	49
62	The 2010 cryo-EM modeling challenge. <i>Biopolymers</i> , 2012, 97, 651-654.	2.4	22
63	Constructing and Validating Initial Cl± Models from Subnanometer Resolution Density Maps with Pathwalking. <i>Structure</i> , 2012, 20, 450-463.	3.3	38
64	The Molecular Architecture of the Eukaryotic Chaperonin TRiC/CCT. <i>Structure</i> , 2012, 20, 814-825.	3.3	261
65	Structure of the <i>Drosophila</i> Apoptosome at 6.9Å... Resolution. <i>Structure</i> , 2011, 19, 128-140.	3.3	73
66	Flexible Architecture of IP3R1 by Cryo-EM. <i>Structure</i> , 2011, 19, 1192-1199.	3.3	80
67	The Holo-Apoptosome: Activation of Procaspase-9 and Interactions with Caspase-3. <i>Structure</i> , 2011, 19, 1084-1096.	3.3	83
68	EMDataBank.org: unified data resource for CryoEM. <i>Nucleic Acids Research</i> , 2011, 39, D456-D464.	14.5	246
69	Structure of an Apoptosome-Procaspase-9 CARD Complex. <i>Structure</i> , 2010, 18, 571-583.	3.3	118
70	Mechanism of folding chamber closure in a group II chaperonin. <i>Nature</i> , 2010, 463, 379-383.	27.8	196
71	Cryo-EM of macromolecular assemblies at near-atomic resolution. <i>Nature Protocols</i> , 2010, 5, 1697-1708.	12.0	79
72	4.0-Å resolution cryo-EM structure of the mammalian chaperonin TRiC/CCT reveals its unique subunit arrangement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4967-4972.	7.1	152

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73	3D Structure of IP3 Receptor. <i>Current Topics in Membranes</i> , 2010, 66, 171-189.	0.9	7
74	Discrete Structure of an RNA Folding Intermediate Revealed by Cryo-electron Microscopy. <i>Journal of the American Chemical Society</i> , 2010, 132, 16352-16353.	13.7	29
75	Single Particle Analysis at High Resolution. <i>Methods in Enzymology</i> , 2010, 482, 211-235.	1.0	29
76	3-D Structures of Macromolecules Using Single-Particle Analysis in EMAN. <i>Methods in Molecular Biology</i> , 2010, 673, 157-173.	0.9	52
77	Model of human low-density lipoprotein and bound receptor based on CryoEM. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 1059-1064.	7.1	65
78	4.0 Å... Resolution Cryo-EM Structure of the Mammalian Chaperonin TRiC/CCT Reveals its Unique Subunit Arrangement. <i>FASEB Journal</i> , 2010, 24, 684.5.	0.5	0
79	Interprotofilament interactions between Alzheimer's A β peptides in amyloid fibrils revealed by cryoEM. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 4653-4658.	7.1	147
80	Structural Mechanism of SDS-Induced Enzyme Activity of Scorpion Hemocyanin Revealed by Electron Cryomicroscopy. <i>Structure</i> , 2009, 17, 749-758.	3.3	61
81	Disruption of Human Plasma High-Density Lipoproteins by Streptococcal Serum Opacity Factor Requires Labile Apolipoprotein A-I. <i>Biochemistry</i> , 2009, 48, 1481-1487.	2.5	22
82	Characterization of Antibiotic Peptide Pores Using Cryo-EM and Comparison to Neutron Scattering. <i>Biophysical Journal</i> , 2009, 97, 164-172.	0.5	26
83	Conformational Changes of Eukaryotic Chaperonin TRiC/CCT in the Nucleotide Cycle Revealed by CryoEM. <i>FASEB Journal</i> , 2009, 23, 850.12.	0.5	0
84	Rocking Motion of the Equatorial Domains of a Group II Chaperonin between Two Biochemical States Revealed by Single-Particle Cryo-EM at Near-atomic and Subnanometer Resolutions. <i>FASEB Journal</i> , 2009, 23, 673.12.	0.5	0
85	Mechanism of lid closure in the eukaryotic chaperonin TRiC/CCT. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 746-753.	8.2	91
86	De Novo Backbone Trace of GroEL from Single Particle Electron Cryomicroscopy. <i>Structure</i> , 2008, 16, 441-448.	3.3	164
87	Subnanometer-resolution electron cryomicroscopy-based domain models for the cytoplasmic region of skeletal muscle RyR channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 9610-9615.	7.1	106
88	EMAN2: An extensible image processing suite for electron microscopy. <i>Journal of Structural Biology</i> , 2007, 157, 38-46.	2.8	2,798
89	SPARX, a new environment for Cryo-EM image processing. <i>Journal of Structural Biology</i> , 2007, 157, 47-55.	2.8	356
90	Ribosome Binding of a Single Copy of the SecY Complex: Implications for Protein Translocation. <i>Molecular Cell</i> , 2007, 28, 1083-1092.	9.7	92

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91	Single-Particle Electron Cryomicroscopy of the Ion Channels in the Excitation-Contraction Coupling Junction. <i>Methods in Cell Biology</i> , 2007, 79, 407-435.	1.1	12
92	Close membrane-membrane proximity induced by Ca ²⁺ -dependent multivalent binding of synaptotagmin-1 to phospholipids. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 209-217.	8.2	235
93	An Expanded Conformation of Single-Ring GroEL-GroES Complex Encapsulates an 86 kDa Substrate. <i>Structure</i> , 2006, 14, 1711-1722.	3.3	59
94	Cryoelectron Microscopy Structures of Rotavirus NSP2-NSP5 and NSP2-RNA Complexes: Implications for Genome Replication. <i>Journal of Virology</i> , 2006, 80, 10829-10835.	3.4	66
95	The Pore Structure of the Closed RyR1 Channel. <i>Structure</i> , 2005, 13, 1203-1211.	3.3	142
96	A Structure of the Human Apoptosome at 12.8 Å... Resolution Provides Insights into This Cell Death Platform. <i>Structure</i> , 2005, 13, 1725-1735.	3.3	145
97	Electron cryomicroscopy of single particles at subnanometer resolution. <i>Current Opinion in Structural Biology</i> , 2005, 15, 571-577.	5.7	43
98	Structure of Ca ²⁺ Release Channel at 14 Å... Resolution. <i>Journal of Molecular Biology</i> , 2005, 345, 427-431.	4.2	76
99	Architecture of the Ribosome-Channel Complex Derived from Native Membranes. <i>Journal of Molecular Biology</i> , 2005, 348, 445-457.	4.2	126
100	Structural Analysis of the Anaphase-Promoting Complex Reveals Multiple Active Sites and Insights into Polyubiquitylation. <i>Molecular Cell</i> , 2005, 20, 855-866.	9.7	81
101	Superparamagnetic gadonanotubes are high-performance MRI contrast agents. <i>Chemical Communications</i> , 2005, , 3915.	4.1	310
102	Mitochondrial ATP Synthasome. <i>Journal of Biological Chemistry</i> , 2004, 279, 31761-31768.	3.4	193
103	Structure of the bifunctional and Golgi-associated formiminotransferase cyclodeaminase octamer. <i>EMBO Journal</i> , 2004, 23, 2963-2971.	7.8	26
104	Experimental Verification of Conformational Variation of Human Fatty Acid Synthase as Predicted by Normal Mode Analysis. <i>Structure</i> , 2004, 12, 185-191.	3.3	78
105	Seeing GroEL at 6 Å... Resolution by Single Particle Electron Cryomicroscopy. <i>Structure</i> , 2004, 12, 1129-1136.	3.3	187
106	Automatic particle selection: results of a comparative study. <i>Journal of Structural Biology</i> , 2004, 145, 3-14.	2.8	129
107	A 9 Å... single particle reconstruction from CCD captured images on a 200kV electron cryomicroscope. <i>Journal of Structural Biology</i> , 2004, 147, 116-127.	2.8	64
108	GroEL Structure at 6 Å... Resolution Using Electron Cryomicroscopy and EMAN. <i>Microscopy and Microanalysis</i> , 2004, 10, 1494-1495.	0.4	0

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109	Focal pair merging for contrast enhancement of single particles. <i>Journal of Structural Biology</i> , 2003, 144, 73-78.	2.8	14
110	Structure of the Type 1 Inositol 1,4,5-Trisphosphate Receptor Revealed by Electron Cryomicroscopy. <i>Journal of Biological Chemistry</i> , 2003, 278, 21319-21322.	3.4	85
111	Object Oriented Database and Electronic Notebook for Transmission Electron Microscopy. <i>Microscopy and Microanalysis</i> , 2003, 9, 556-565.	0.4	16
112	Imaging Ice Embedded Single Particles With A 16 Megapixel CCD Camera. <i>Microscopy and Microanalysis</i> , 2003, 9, 962-963.	0.4	0
113	Quaternary structure of human fatty acid synthase by electron cryomicroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 138-143.	7.1	57
114	The skeletal muscle Ca ²⁺ release channel has an oxidoreductase-like domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12155-12160.	7.1	60
115	Structure of the voltage-gated L-type Ca ²⁺ channel by electron cryomicroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 10370-10375.	7.1	76
116	Merging Focal Pairs for Improved Particle Selection and Orientation Determination. <i>Microscopy and Microanalysis</i> , 2002, 8, 216-217.	0.4	0
117	Bridging the information gap: computational tools for intermediate resolution structure interpretation. <i>Journal of Molecular Biology</i> , 2001, 308, 1033-1044.	4.2	282
118	A 11.5 Å... single particle reconstruction of GroEL using EMAN. <i>Journal of Molecular Biology</i> , 2001, 314, 253-262.	4.2	119
119	Fourier Amplitude Decay of Electron Cryomicroscopic Images of Single Particles and Effects on Structure Determination. <i>Journal of Structural Biology</i> , 2001, 133, 32-42.	2.8	95
120	Estimates of the Fourier Amplitude Decay of Electron Micrographs of Single Particles. <i>Microscopy and Microanalysis</i> , 2000, 6, 256-257.	0.4	0
121	EMAN: Semiautomated Software for High-Resolution Single-Particle Reconstructions. <i>Journal of Structural Biology</i> , 1999, 128, 82-97.	2.8	2,320
122	Effect of changing the size of lipid headgroup on peptide insertion into membranes. <i>Biophysical Journal</i> , 1997, 73, 239-244.	0.5	105
123	Mechanism of alamethicin insertion into lipid bilayers. <i>Biophysical Journal</i> , 1996, 71, 2669-2679.	0.5	213
124	Neutron scattering in the plane of membranes: structure of alamethicin pores. <i>Biophysical Journal</i> , 1996, 70, 2659-2666.	0.5	226
125	X-ray diffraction study of lipid bilayer membranes interacting with amphiphilic helical peptides: diphytanoyl phosphatidylcholine with alamethicin at low concentrations. <i>Biophysical Journal</i> , 1995, 68, 2361-2369.	0.5	192
126	Closed state of gramicidin channel detected by X-ray in-plane scattering. <i>Biophysical Chemistry</i> , 1994, 49, 83-89.	2.8	34

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127	Cooperative membrane insertion of magainin correlated with its cytolytic activity. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1994, 1190, 181-184.	2.6	144
128	X-ray scattering with momentum transfer in the plane of membrane. Application to gramicidin organization. <i>Biophysical Journal</i> , 1993, 64, 157-162.	0.5	37