

Joachim Frank

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

149
papers

13,698
citations

57
h-index

117
g-index

170
ext. papers

15,385
ext. citations

10.3
avg, IF

6.71
L-index

#	Paper	IF	Citations
149	Recovery of Conformational Continuum from Single-particle Cryo-EM Images: Optimization of ManifoldEM Informed by Ground Truth. <i>IEEE Transactions on Computational Imaging</i> , 2022 , 1-1	4.5	0
148	Contributions of single-particle cryoelectron microscopy toward fighting COVID-19. <i>Trends in Biochemical Sciences</i> , 2021 ,	10.3	1
147	Interaction Networks of Ribosomal Expansion Segments in Kinetoplastids. <i>Sub-Cellular Biochemistry</i> , 2021 , 96, 433-450	5.5	1
146	"Just in Time": The Role of Cryo-Electron Microscopy in Combating Recent Pandemics. <i>Biochemistry</i> , 2021 , 60, 3449-3451	3.2	2
145	A Time-Resolved Cryo-EM Study of <i>Saccharomyces cerevisiae</i> 80S Ribosome Protein Composition in Response to a Change in Carbon Source. <i>Proteomics</i> , 2021 , 21, e2000125	4.8	3
144	Alexander Spirin's Vision of the Ribosome as a Thermal Ratchet Machine. <i>Biochemistry (Moscow)</i> , 2021 , 86, 910-912	2.9	
143	A glycan gate controls opening of the SARS-CoV-2 spike protein. <i>Nature Chemistry</i> , 2021 , 13, 963-968	17.6	63
142	What is in the black box? - A perspective on software in cryoelectron microscopy. <i>Biophysical Journal</i> , 2021 , 120, 4307-4311	2.9	
141	Symmetric activation and modulation of the human calcium-sensing receptor.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	7
140	Mechanism of ligand activation of a eukaryotic cyclic nucleotide-gated channel. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 625-634	17.6	22
139	Structure of human GABA receptor in an inactive state. <i>Nature</i> , 2020 , 584, 304-309	50.4	32
138	Propagation of Conformational Coordinates Across Angular Space in Mapping the Continuum of States from Cryo-EM Data by Manifold Embedding. <i>Journal of Chemical Information and Modeling</i> , 2020 , 60, 2484-2491	6.1	13
137	POLARIS: Path of Least Action Analysis on Energy Landscapes. <i>Journal of Chemical Information and Modeling</i> , 2020 , 60, 2581-2590	6.1	4
136	Ribosome-associated vesicles: A dynamic subcompartment of the endoplasmic reticulum in secretory cells. <i>Science Advances</i> , 2020 , 6, eaay9572	14.3	20
135	<i>Escherichia coli</i> NusG Links the Lead Ribosome with the Transcription Elongation Complex. <i>iScience</i> , 2020 , 23, 101352	6.1	17
134	Retrieving functional pathways of biomolecules from single-particle snapshots. <i>Nature Communications</i> , 2020 , 11, 4734	17.4	33
133	The structural basis for release-factor activation during translation termination revealed by time-resolved cryogenic electron microscopy. <i>Nature Communications</i> , 2019 , 10, 2579	17.4	25

132	Late steps in bacterial translation initiation visualized using time-resolved cryo-EM. <i>Nature</i> , 2019 , 570, 400-404	50.4	48
131	New Insights into Ribosome Structure and Function. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019 , 11,	10.2	24
130	Studying Kinetics by Counting Particles in Time-Resolved Cryo-EM. <i>Microscopy and Microanalysis</i> , 2019 , 25, 2-3	0.5	1
129	The Israeli acute paralysis virus IRES captures host ribosomes by mimicking a ribosomal state with hybrid tRNAs. <i>EMBO Journal</i> , 2019 , 38, e102226	13	8
128	Ryanodine Receptor Structure and Function in Health and Disease. <i>Sub-Cellular Biochemistry</i> , 2018 , 87, 329-352	5.5	65
127	New Opportunities Created by Single-Particle Cryo-EM: The Mapping of Conformational Space. <i>Biochemistry</i> , 2018 , 57, 888	3.2	21
126	Time-Resolved Cryo-electron Microscopy Using a Microfluidic Chip. <i>Methods in Molecular Biology</i> , 2018 , 1764, 59-71	1.4	24
125	Identification of ions in experimental electrostatic potential maps. <i>IUCrJ</i> , 2018 , 5, 375-381	4.7	14
124	Cryo-EM shows stages of initial codon selection on the ribosome by aa-tRNA in ternary complex with GTP and the GTPase-deficient EF-TuH84A. <i>Nucleic Acids Research</i> , 2018 , 46, 5861-5874	20.1	18
123	Key Intermediates in Ribosome Recycling Visualized by Time-Resolved Cryoelectron Microscopy. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2018 , 516-525	0.5	
122	The process of mRNA-tRNA translocation. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2018 , 405-412	0.5	
121	Structure of the 80S Ribosome from <i>Saccharomyces cerevisiae</i> tRNA-Ribosome and Subunit-Subunit Interactions. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2018 , 286-299	0.5	
120	The structure of the 80S ribosome from <i>Trypanosoma cruzi</i> reveals unique rRNA components. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2018 , 383-388	0.5	
119	Structure and assembly model for the <i>Trypanosoma cruzi</i> 60S ribosomal subunit. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2018 , 526-531	0.5	
118	Architecture of the Protein-Conducting Channel Associated with the Translating 80S Ribosome. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2018 , 274-285	0.5	
117	Exploration of parameters in cryo-EM leading to an improved density map of the <i>E. coli</i> ribosome. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2018 , 424-432	0.5	
116	Flexible Fitting of Atomic Structures into Electron Microscopy Maps Using Molecular Dynamics. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2018 , 433-443	0.5	
115	Quantitative Connection between Ensemble Thermodynamics and Single-Molecule Kinetics: A Case Study Using Cryogenic Electron Microscopy and Single-Molecule Fluorescence Resonance Energy Transfer Investigations of the Ribosome. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2018 , 476-489	0.5	

114	Incorporation of aminoacyl-tRNA into the ribosome as seen by cryo-electron microscopy. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2018 , 339-346	0.5	
113	A twisted tRNA intermediate sets the threshold for decoding. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2018 , 359-360	0.5	
112	Structural characterization of mRNA-tRNA translocation intermediates. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2018 , 450-455	0.5	
111	Channel opening and gating mechanism in AMPA-subtype glutamate receptors. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2018 , 542-558	0.5	0
110	Quantitative Characterization of Domain Motions in Molecular Machines. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2018 , 532-541	0.5	
109	Domain movements of elongation factor eEF2 and the eukaryotic 80S ribosome facilitate tRNA translocation. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2018 , 361-372	0.5	
108	Trajectories of the ribosome as a Brownian nanomachine. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2018 , 463-475	0.5	0
107	The Cryo-EM Structure of a Translation Initiation Complex from Escherichia coli. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2018 , 373-382	0.5	
106	Disentangling conformational states of macromolecules in 3D-EM through likelihood optimization. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2018 , 413-415	0.5	
105	Structural Basis for Gating and Activation of RyR1. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2018 , 497-515	0.5	
104	High-resolution cryo-electron microscopy structure of the Trypanosoma brucei ribosome. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2018 , 456-462	0.5	
103	Activation of GTP hydrolysis in mRNA-tRNA translocation by elongation factor G. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2018 , 490-496	0.5	
102	Locking and Unlocking of Ribosomal Motions. <i>journal of hand surgery Asian-Pacific volume, The</i> , 2018 , 347-358	0.5	
101	Einzelpartikel-Rekonstruktion biologischer Moleküle [Geschichte in einer Probe (Nobel-Aufsatz). <i>Angewandte Chemie</i> , 2018 , 130, 10990-11006	3.6	
100	Single-Particle Reconstruction of Biological Molecules-Story in a Sample (Nobel Lecture). <i>Angewandte Chemie - International Edition</i> , 2018 , 57, 10826-10841	16.4	24
99	Structure and activity of lipid bilayer within a membrane-protein transporter. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 12985-12990	11.5	80
98	Critical Role for Saccharomyces cerevisiae Asc1p in Translational Initiation at Elevated Temperatures. <i>Proteomics</i> , 2018 , 18, e1800208	4.8	1
97	Three-Dimensional Analysis of Mitochondrial Crista Ultrastructure in a Patient with Leigh Syndrome by In Situ Cryoelectron Tomography. <i>IScience</i> , 2018 , 6, 83-91	6.1	36

96	Quantitative Characterization of Domain Motions in Molecular Machines. <i>Journal of Physical Chemistry B</i> , 2017 , 121, 3747-3756	3.4	8
95	A Fast and Effective Microfluidic Spraying-Plunging Method for High-Resolution Single-Particle Cryo-EM. <i>Structure</i> , 2017 , 25, 663-670.e3	5.2	77
94	Nmd3 is a structural mimic of eIF5A, and activates the cpGTPase Lsg1 during 60S ribosome biogenesis. <i>EMBO Journal</i> , 2017 , 36, 854-868	13	46
93	The translation elongation cycle-capturing multiple states by cryo-electron microscopy. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017 , 372,	5.8	17
92	Structural Bases of Desensitization in AMPA Receptor-Auxiliary Subunit Complexes. <i>Neuron</i> , 2017 , 94, 569-580.e5	13.9	56
91	Time-resolved cryo-electron microscopy: Recent progress. <i>Journal of Structural Biology</i> , 2017 , 200, 303-306	3.4	68
90	Advances in the field of single-particle cryo-electron microscopy over the last decade. <i>Nature Protocols</i> , 2017 , 12, 209-212	18.8	96
89	Channel opening and gating mechanism in AMPA-subtype glutamate receptors. <i>Nature</i> , 2017 , 549, 60-65	50.4	125
88	Determination of the ribosome structure to a resolution of 2.5 Å by single-particle cryo-EM. <i>Protein Science</i> , 2017 , 26, 82-92	6.3	23
87	The mechanism of translation. <i>F1000Research</i> , 2017 , 6, 198	3.6	9
86	Structure of the STRA6 receptor for retinol uptake. <i>Science</i> , 2016 , 353,	33.3	73
85	Structural Basis for Gating and Activation of RyR1. <i>Cell</i> , 2016 , 167, 145-157.e17	56.2	204
84	Key Intermediates in Ribosome Recycling Visualized by Time-Resolved Cryoelectron Microscopy. <i>Structure</i> , 2016 , 24, 2092-2101	5.2	52
83	Elucidation of AMPA receptor-stargazin complexes by cryo-electron microscopy. <i>Science</i> , 2016 , 353, 83-89	33.3	89
82	Generalized single-particle cryo-EM—a historical perspective. <i>Microscopy (Oxford, England)</i> , 2016 , 65, 3-8	1.3	31
81	Two promising future developments of cryo-EM: capturing short-lived states and mapping a continuum of states of a macromolecule. <i>Microscopy (Oxford, England)</i> , 2016 , 65, 69-79	1.3	30
80	Continuous changes in structure mapped by manifold embedding of single-particle data in cryo-EM. <i>Methods</i> , 2016 , 100, 61-7	4.6	114
79	Whither Ribosome Structure and Dynamics Research? (A Perspective). <i>Journal of Molecular Biology</i> , 2016 , 428, 3565-9	6.5	10

78	Structure and assembly model for the <i>Trypanosoma cruzi</i> 60S ribosomal subunit. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 12174-12179	11.5	48
77	CTF Challenge: Result summary. <i>Journal of Structural Biology</i> , 2015 , 190, 348-59	3.4	29
76	Efficient estimation of three-dimensional covariance and its application in the analysis of heterogeneous samples in cryo-electron microscopy. <i>Structure</i> , 2015 , 23, 1129-37	5.2	24
75	Quantitative Connection between Ensemble Thermodynamics and Single-Molecule Kinetics: A Case Study Using Cryogenic Electron Microscopy and Single-Molecule Fluorescence Resonance Energy Transfer Investigations of the Ribosome. <i>Journal of Physical Chemistry B</i> , 2015 , 119, 10888-10901	3.4	9
74	Structure of mammalian eIF3 in the context of the 43S preinitiation complex. <i>Nature</i> , 2015 , 525, 491-5	50.4	142
73	Structure of a mammalian ryanodine receptor. <i>Nature</i> , 2015 , 517, 44-9	50.4	276
72	Structural dynamics of ribosome subunit association studied by mixing-spraying time-resolved cryogenic electron microscopy. <i>Structure</i> , 2015 , 23, 1097-105	5.2	60
71	Activation of GTP hydrolysis in mRNA-tRNA translocation by elongation factor G. <i>Science Advances</i> , 2015 , 1,	14.3	40
70	Dynamical features of the <i>Plasmodium falciparum</i> ribosome during translation. <i>Nucleic Acids Research</i> , 2015 , 43, 10515-24	20.1	38
69	The ABC-F protein EttA gates ribosome entry into the translation elongation cycle. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 143-51	17.6	77
68	EttA regulates translation by binding the ribosomal E site and restricting ribosome-tRNA dynamics. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 152-9	17.6	61
67	Particle migration analysis in iterative classification of cryo-EM single-particle data. <i>Journal of Structural Biology</i> , 2014 , 188, 267-73	3.4	8
66	Trajectories of the ribosome as a Brownian nanomachine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 17492-7	11.5	160
65	Automated particle picking for low-contrast macromolecules in cryo-electron microscopy. <i>Journal of Structural Biology</i> , 2014 , 186, 1-7	3.4	36
64	Hepatitis-C-virus-like internal ribosome entry sites displace eIF3 to gain access to the 40S subunit. <i>Nature</i> , 2013 , 503, 539-43	50.4	133
63	High-resolution cryo-electron microscopy structure of the <i>Trypanosoma brucei</i> ribosome. <i>Nature</i> , 2013 , 494, 385-9	50.4	102
62	Story in a sample—the potential (and limitations) of cryo-electron microscopy applied to molecular machines. <i>Biopolymers</i> , 2013 , 99, 832-6	2.2	18
61	Intermediate states during mRNA-tRNA translocation. <i>Current Opinion in Structural Biology</i> , 2012 , 22, 778-85	8.1	26

60	Integrity of the P-site is probed during maturation of the 60S ribosomal subunit. <i>Journal of Cell Biology</i> , 2012 , 197, 747-59	7.3	62
59	Structural characterization of mRNA-tRNA translocation intermediates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 6094-9	11.5	79
58	Structural insights into cognate versus near-cognate discrimination during decoding. <i>EMBO Journal</i> , 2011 , 30, 1497-507	13	47
57	Molecular dynamics of EF-G during translocation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79, 1478-86	4.2	33
56	Cryoelectron microscopy structures of the ribosome complex in intermediate states during tRNA translocation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 4817-21	11.5	32
55	Dynamics of the base of ribosomal A-site finger revealed by molecular dynamics simulations and Cryo-EM. <i>Nucleic Acids Research</i> , 2010 , 38, 1325-40	20.1	43
54	Characterization of the nuclear export adaptor protein Nmd3 in association with the 60S ribosomal subunit. <i>Journal of Cell Biology</i> , 2010 , 189, 1079-86	7.3	54
53	Structure and dynamics of a processive Brownian motor: the translating ribosome. <i>Annual Review of Biochemistry</i> , 2010 , 79, 381-412	29.1	197
52	The Ribosome Comes Alive. <i>Israel Journal of Chemistry</i> , 2010 , 50, 95-98	3.4	8
51	Ribosome-induced changes in elongation factor Tu conformation control GTP hydrolysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 1063-8	11.5	199
50	Elongation in translation as a dynamic interaction among the ribosome, tRNA, and elongation factors EF-G and EF-Tu. <i>Quarterly Reviews of Biophysics</i> , 2009 , 42, 159-200	7	92
49	Single-particle reconstruction of biological macromolecules in electron microscopy--30 years. <i>Quarterly Reviews of Biophysics</i> , 2009 , 42, 139-58	7	105
48	Comprehensive molecular structure of the eukaryotic ribosome. <i>Structure</i> , 2009 , 17, 1591-1604	5.2	130
47	Determination of signal-to-noise ratios and spectral SNRs in cryo-EM low-dose imaging of molecules. <i>Journal of Structural Biology</i> , 2009 , 166, 126-32	3.4	63
46	SPIDER image processing for single-particle reconstruction of biological macromolecules from electron micrographs. <i>Nature Protocols</i> , 2008 , 3, 1941-74	18.8	371
45	Flexible fitting of atomic structures into electron microscopy maps using molecular dynamics. <i>Structure</i> , 2008 , 16, 673-83	5.2	678
44	Visualization of the hybrid state of tRNA binding promoted by spontaneous ratcheting of the ribosome. <i>Molecular Cell</i> , 2008 , 32, 190-7	17.6	203
43	Recognition of aminoacyl-tRNA: a common molecular mechanism revealed by cryo-EM. <i>EMBO Journal</i> , 2008 , 27, 3322-31	13	44

42	Disentangling conformational states of macromolecules in 3D-EM through likelihood optimization. <i>Nature Methods</i> , 2007 , 4, 27-9	21.6	333
41	Preparation of macromolecular complexes for cryo-electron microscopy. <i>Nature Protocols</i> , 2007 , 2, 3239-46	14.8	165
40	Structures of modified eEF2 80S ribosome complexes reveal the role of GTP hydrolysis in translocation. <i>EMBO Journal</i> , 2007 , 26, 2421-31	13	145
39	The process of mRNA-tRNA translocation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 19671-8	11.5	178
38	Three-Dimensional Electron Microscopy of Macromolecular Assemblies 2006 ,		369
37	The ribosome and the mechanism of protein synthesis. <i>Reports on Progress in Physics</i> , 2006 , 69, 1383-1417	14.4	51
36	A method of focused classification, based on the bootstrap 3D variance analysis, and its application to EF-G-dependent translocation. <i>Journal of Structural Biology</i> , 2006 , 154, 184-94	3.4	136
35	Estimation of variance in single-particle reconstruction using the bootstrap technique. <i>Journal of Structural Biology</i> , 2006 , 154, 168-83	3.4	107
34	The role of tRNA as a molecular spring in decoding, accommodation, and peptidyl transfer. <i>FEBS Letters</i> , 2005 , 579, 959-62	3.8	82
33	The structure of the 80S ribosome from <i>Trypanosoma cruzi</i> reveals unique rRNA components. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 10206-11	11.5	51
32	Domain movements of elongation factor eEF2 and the eukaryotic 80S ribosome facilitate tRNA translocation. <i>EMBO Journal</i> , 2004 , 23, 1008-19	13	333
31	Regulation of eukaryotic translation by the RACK1 protein: a platform for signalling molecules on the ribosome. <i>EMBO Reports</i> , 2004 , 5, 1137-41	6.5	217
30	Dynamics of EF-G interaction with the ribosome explored by classification of a heterogeneous cryo-EM dataset. <i>Journal of Structural Biology</i> , 2004 , 147, 283-90	3.4	73
29	Time-resolved imaging of macromolecular processes and interactions. <i>Journal of Structural Biology</i> , 2004 , 147, 209-10	3.4	3
28	Electron microscopy of functional ribosome complexes. <i>Biopolymers</i> , 2003 , 68, 223-33	2.2	51
27	Incorporation of aminoacyl-tRNA into the ribosome as seen by cryo-electron microscopy. <i>Nature Structural and Molecular Biology</i> , 2003 , 10, 899-906	17.6	296
26	Locking and unlocking of ribosomal motions. <i>Cell</i> , 2003 , 114, 123-34	56.2	529
25	Toward an understanding of the structural basis of translation. <i>Genome Biology</i> , 2003 , 4, 237	18.3	28

24	A twisted tRNA intermediate sets the threshold for decoding. <i>Rna</i> , 2003 , 9, 384-5	5.8	33
23	Dynamic reorganization of the functionally active ribosome explored by normal mode analysis and cryo-electron microscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 9319-23	11.5	299
22	A cold look at transcription. <i>Structure</i> , 2002 , 10, 1156-7	5.2	
21	Cryo-EM reveals an active role for aminoacyl-tRNA in the accommodation process. <i>EMBO Journal</i> , 2002 , 21, 3557-67	13	248
20	Single-particle imaging of macromolecules by cryo-electron microscopy. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2002 , 31, 303-19		258
19	Three-dimensional imaging of biological complexity. <i>Journal of Structural Biology</i> , 2002 , 138, 85-91	3.4	82
18	Cryo-electron microscopy as an investigative tool: the ribosome as an example. <i>BioEssays</i> , 2001 , 23, 725-32	3.1	37
17	Hepatitis C virus IRES RNA-induced changes in the conformation of the 40s ribosomal subunit. <i>Science</i> , 2001 , 291, 1959-62	33.3	433
16	A ratchet-like inter-subunit reorganization of the ribosome during translocation. <i>Nature</i> , 2000 , 406, 318-24	32.4	693
15	Visualization of tRNA movements on the Escherichia coli 70S ribosome during the elongation cycle. <i>Journal of Cell Biology</i> , 2000 , 150, 447-60	7.3	146
14	Domain motions of EF-G bound to the 70S ribosome: insights from a hand-shaking between multi-resolution structures. <i>Biophysical Journal</i> , 2000 , 79, 1670-8	2.9	64
13	EF-G-dependent GTP hydrolysis induces translocation accompanied by large conformational changes in the 70S ribosome. <i>Nature Structural Biology</i> , 1999 , 6, 643-7		260
12	SPIDER and WEB: processing and visualization of images in 3D electron microscopy and related fields. <i>Journal of Structural Biology</i> , 1996 , 116, 190-9	3.4	1867
11	Estimation of variance distribution in three-dimensional reconstruction. II. Applications. <i>Journal of the Optical Society of America A: Optics and Image Science, and Vision</i> , 1995 , 12, 2628-35	1.8	8
10	A model of the translational apparatus based on a three-dimensional reconstruction of the Escherichia coli ribosome. <i>Biochemistry and Cell Biology</i> , 1995 , 73, 757-65	3.6	96
9	SPIDER: a modular software system for electron image processing. <i>Ultramicroscopy</i> , 1981 , 6, 343-357	3.1	147
8	Spider: a modular software system for electron image processing. <i>Ultramicroscopy</i> , 1981 , 6, 343-357	3.1	262
7	Averaging of low exposure electron micrographs of non-periodic objects. <i>Ultramicroscopy</i> , 1975 , 1, 159-62	6.1	131

6	The Ribosome as a Brownian Ratchet Machine158-190	6
5	Studies of Elongation Factor G-Dependent tRNA Translocation by Three-Dimensional Cryo-Electron Microscopy53-62	5
4	Visualization of Molecular Machines by Cryo-Electron Microscopy20-37	4
3	Identification of changing ribosome protein compositions using cryo-EM and mass spectrometry	1
2	Simulation of cryo-EM ensembles from atomic models of molecules exhibiting continuous conformations	4
1	Geometric machine learning informed by ground truth: Recovery of conformational continuum from single-particle cryo-EM data of biomolecules	2