

Joachim Frank

List of Publications by Year in descending order

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147
papers

16,648
citations

27035

58
h-index

20023

121
g-index

170
all docs

170
docs citations

170
times ranked

14176
citing authors

#	ARTICLE	IF	CITATIONS
1	Contributions of single-particle cryoelectron microscopy toward fighting COVID-19. Trends in Biochemical Sciences, 2022, 47, 117-123.	3.7	6
2	Recovery of Conformational Continuum From Single-Particle Cryo-EM Images: Optimization of ManifoldEM Informed by Ground Truth. IEEE Transactions on Computational Imaging, 2022, 8, 462-478.	2.6	11
3	Molecular architecture of <sc>40S</sc> translation initiation complexes on the hepatitis C virus <sc>IRES</sc>. EMBO Journal, 2022, 41, .	3.5	10
4	A Time-Resolved Cryo-EM Study of Saccharomyces cerevisiae 80S Ribosome Protein Composition in Response to a Change in Carbon Source. Proteomics, 2021, 21, 2000125.	1.3	7
5	“Just in Time”: The Role of Cryo-Electron Microscopy in Combating Recent Pandemics. Biochemistry, 2021, 60, 3449-3451.	1.2	4
6	Alexander Spirin’s Vision of the Ribosome as a Thermal Ratchet Machine. Biochemistry (Moscow), 2021, 86, 910-912.	0.7	0
7	A glycan gate controls opening of the SARS-CoV-2 spike protein. Nature Chemistry, 2021, 13, 963-968.	6.6	254
8	What is in the black box? “ A perspective on software in cryoelectron microscopy. Biophysical Journal, 2021, 120, 4307-4311.	0.2	0
9	Interaction Networks of Ribosomal Expansion Segments in Kinetoplastids. Sub-Cellular Biochemistry, 2021, 96, 433-450.	1.0	3
10	Symmetric activation and modulation of the human calcium-sensing receptor. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	23
11	Escherichia coli NusG Links the Lead Ribosome with the Transcription Elongation Complex. IScience, 2020, 23, 101352.	1.9	43
12	Retrieving functional pathways of biomolecules from single-particle snapshots. Nature Communications, 2020, 11, 4734.	5.8	76
13	Mechanism of ligand activation of a eukaryotic cyclic nucleotide-gated channel. Nature Structural and Molecular Biology, 2020, 27, 625-634.	3.6	40
14	Structure of human GABAB receptor in an inactive state. Nature, 2020, 584, 304-309.	13.7	59
15	Propagation of Conformational Coordinates Across Angular Space in Mapping the Continuum of States from Cryo-EM Data by Manifold Embedding. Journal of Chemical Information and Modeling, 2020, 60, 2484-2491.	2.5	27
16	POLARIS: Path of Least Action Analysis on Energy Landscapes. Journal of Chemical Information and Modeling, 2020, 60, 2581-2590.	2.5	11
17	Ribosome-associated vesicles: A dynamic subcompartment of the endoplasmic reticulum in secretory cells. Science Advances, 2020, 6, eaay9572.	4.7	42
18	New Insights into Ribosome Structure and Function. Cold Spring Harbor Perspectives in Biology, 2019, 11, a032615.	2.3	45

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19	Studying Kinetics by Counting Particles in Time-Resolved Cryo-EM. <i>Microscopy and Microanalysis</i> , 2019, 25, 2-3.	0.2	1
20	The structural basis for release-factor activation during translation termination revealed by time-resolved cryogenic electron microscopy. <i>Nature Communications</i> , 2019, 10, 2579.	5.8	43
21	Late steps in bacterial translation initiation visualized using time-resolved cryo-EM. <i>Nature</i> , 2019, 570, 400-404.	13.7	103
22	The Israeli acute paralysis virus IRES captures host ribosomes by mimicking a ribosomal state with hybrid tRNAs. <i>EMBO Journal</i> , 2019, 38, e102226.	3.5	16
23	Ryanodine Receptor Structure and Function in Health and Disease. <i>Sub-Cellular Biochemistry</i> , 2018, 87, 329-352.	1.0	104
24	New Opportunities Created by Single-Particle Cryo-EM: The Mapping of Conformational Space. <i>Biochemistry</i> , 2018, 57, 888-888.	1.2	31
25	Time-Resolved Cryo-electron Microscopy Using a Microfluidic Chip. <i>Methods in Molecular Biology</i> , 2018, 1764, 59-71.	0.4	39
26	Einzelpartikel-Rekonstruktion biologischer Moleküle – Geschichte in einer Probe (Nobel-Aufsatz). <i>Angewandte Chemie</i> , 2018, 130, 10990-11006.	1.6	0
27	Single-Particle Reconstruction of Biological Molecules – Story in a Sample (Nobel Lecture). <i>Angewandte Chemie - International Edition</i> , 2018, 57, 10826-10841.	7.2	35
28	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.	3.3	119
29	Critical Role for <i>Saccharomyces cerevisiae</i> Asc1p in Translational Initiation at Elevated Temperatures. <i>Proteomics</i> , 2018, 18, e1800208.	1.3	4
30	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.	1.9	60
31	Identification of ions in experimental electrostatic potential maps. <i>IUCr</i> , 2018, 5, 375-381.	1.0	22
32	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.	6.5	29
33	Key Intermediates in Ribosome Recycling Visualized by Time-Resolved Cryoelectron Microscopy. <i>Journal of Hand Surgery Asian-Pacific volume, The</i> , 2018, , 516-525.	0.2	0
34	The process of mRNA-tRNA translocation. <i>Journal of Hand Surgery Asian-Pacific volume, The</i> , 2018, , 405-412.	0.2	0
35	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.	0.2	0
36	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.	0.2	1

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37	Structure and assembly model for the Trypanosoma cruzi 60S ribosomal subunit. journal of hand surgery Asian-Pacific volume, The, 2018, , 526-531.	0.2	0
38	Architecture of the Protein-Conducting Channel Associated with the Translating 80S Ribosome. journal of hand surgery Asian-Pacific volume, The, 2018, , 274-285.	0.2	0
39	Exploration of parameters in cryo-EM leading to an improved density map of the <i>E. coli</i> ribosome. journal of hand surgery Asian-Pacific volume, The, 2018, , 424-432.	0.2	0
40	Flexible Fitting of Atomic Structures into Electron Microscopy Maps Using Molecular Dynamics. journal of hand surgery Asian-Pacific volume, The, 2018, , 433-443.	0.2	0
41	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. journal of hand surgery Asian-Pacific volume, The, 2018, , 476-489.	0.2	0
42	Incorporation of aminoacyl-tRNA into the ribosome as seen by cryo-electron microscopy. journal of hand surgery Asian-Pacific volume, The, 2018, , 339-346.	0.2	0
43	A twisted tRNA intermediate sets the threshold for decoding. journal of hand surgery Asian-Pacific volume, The, 2018, , 359-360.	0.2	0
44	Structural characterization of mRNA-tRNA translocation intermediates. journal of hand surgery Asian-Pacific volume, The, 2018, , 450-455.	0.2	0
45	Channel opening and gating mechanism in AMPA-subtype glutamate receptors. journal of hand surgery Asian-Pacific volume, The, 2018, , 542-558.	0.2	3
46	Quantitative Characterization of Domain Motions in Molecular Machines. journal of hand surgery Asian-Pacific volume, The, 2018, , 532-541.	0.2	0
47	Domain movements of elongation factor eEF2 and the eukaryotic 80S ribosome facilitate tRNA translocation. journal of hand surgery Asian-Pacific volume, The, 2018, , 361-372.	0.2	0
48	Trajectories of the ribosome as a Brownian nanomachine. journal of hand surgery Asian-Pacific volume, The, 2018, , 463-475.	0.2	2
49	The Cryo-EM Structure of a Translation Initiation Complex from Escherichia coli. journal of hand surgery Asian-Pacific volume, The, 2018, , 373-382.	0.2	0
50	Disentangling conformational states of macromolecules in 3D-EM through likelihood optimization. journal of hand surgery Asian-Pacific volume, The, 2018, , 413-415.	0.2	0
51	Structural Basis for Gating and Activation of RyR1. journal of hand surgery Asian-Pacific volume, The, 2018, , 497-515.	0.2	0
52	High-resolution cryo-electron microscopy structure of the Trypanosoma brucei ribosome. journal of hand surgery Asian-Pacific volume, The, 2018, , 456-462.	0.2	0
53	Activation of GTP hydrolysis in mRNA-tRNA translocation by elongation factor G. journal of hand surgery Asian-Pacific volume, The, 2018, , 490-496.	0.2	0
54	Locking and Unlocking of Ribosomal Motions. journal of hand surgery Asian-Pacific volume, The, 2018, , 347-358.	0.2	0

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55	Quantitative Characterization of Domain Motions in Molecular Machines. <i>Journal of Physical Chemistry B</i> , 2017, 121, 3747-3756.	1.2	10
56	A Fast and Effective Microfluidic Spraying-Plunging Method for High-Resolution Single-Particle Cryo-EM. <i>Structure</i> , 2017, 25, 663-670.e3.	1.6	112
57	Nmd3 is a structural mimic of $eIF5A$, and activates the $capGTPase$ Lsg1 during 60S ribosome biogenesis. <i>EMBO Journal</i> , 2017, 36, 854-868.	3.5	67
58	The translation elongation cycle—capturing multiple states by cryo-electron microscopy. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160180.	1.8	24
59	Structural Bases of Desensitization in AMPA Receptor-Auxiliary Subunit Complexes. <i>Neuron</i> , 2017, 94, 569-580.e5.	3.8	89
60	Time-resolved cryo-electron microscopy: Recent progress. <i>Journal of Structural Biology</i> , 2017, 200, 303-306.	1.3	120
61	Advances in the field of single-particle cryo-electron microscopy over the last decade. <i>Nature Protocols</i> , 2017, 12, 209-212.	5.5	127
62	Channel opening and gating mechanism in AMPA-subtype glutamate receptors. <i>Nature</i> , 2017, 549, 60-65.	13.7	183
63	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.	3.1	26
64	The mechanism of translation. <i>F1000Research</i> , 2017, 6, 198.	0.8	11
65	Continuous changes in structure mapped by manifold embedding of single-particle data in cryo-EM. <i>Methods</i> , 2016, 100, 61-67.	1.9	162
66	Whither Ribosome Structure and Dynamics Research? (A Perspective). <i>Journal of Molecular Biology</i> , 2016, 428, 3565-3569.	2.0	11
67	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.	3.3	63
68	Structure of the STRA6 receptor for retinol uptake. <i>Science</i> , 2016, 353, .	6.0	103
69	Structural Basis for Gating and Activation of RyR1. <i>Cell</i> , 2016, 167, 145-157.e17.	13.5	301
70	Key Intermediates in Ribosome Recycling Visualized by Time-Resolved Cryoelectron Microscopy. <i>Structure</i> , 2016, 24, 2092-2101.	1.6	68
71	Elucidation of AMPA receptor–stargazin complexes by cryo-electron microscopy. <i>Science</i> , 2016, 353, 83-86.	6.0	112
72	Generalized single-particle cryo-EM—a historical perspective. <i>Microscopy (Oxford, England)</i> , 2016, 65, 3-8.	0.7	38

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73	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.	0.7	44
74	Structural Dynamics of Ribosome Subunit Association Studied by Mixing-Spraying Time-Resolved Cryogenic Electron Microscopy. <i>Structure</i> , 2015, 23, 1097-1105.	1.6	78
75	Activation of GTP hydrolysis in mRNA-tRNA translocation by elongation factor G. <i>Science Advances</i> , 2015, 1, .	4.7	53
76	Dynamical features of the <i>Plasmodium falciparum</i> ribosome during translation. <i>Nucleic Acids Research</i> , 2015, 43, gkv991.	6.5	48
77	CTF Challenge: Result summary. <i>Journal of Structural Biology</i> , 2015, 190, 348-359.	1.3	34
78	Efficient Estimation of Three-Dimensional Covariance and its Application in the Analysis of Heterogeneous Samples in Cryo-Electron Microscopy. <i>Structure</i> , 2015, 23, 1129-1137.	1.6	35
79	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.	1.2	15
80	Structure of mammalian eIF3 in the context of the 43S preinitiation complex. <i>Nature</i> , 2015, 525, 491-495.	13.7	204
81	Structure of a mammalian ryanodine receptor. <i>Nature</i> , 2015, 517, 44-49.	13.7	350
82	Particle migration analysis in iterative classification of cryo-EM single-particle data. <i>Journal of Structural Biology</i> , 2014, 188, 267-273.	1.3	10
83	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, 17492-17497.	3.3	218
84	Automated particle picking for low-contrast macromolecules in cryo-electron microscopy. <i>Journal of Structural Biology</i> , 2014, 186, 1-7.	1.3	52
85	The ABC-F protein EttA gates ribosome entry into the translation elongation cycle. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 143-151.	3.6	109
86	EttA regulates translation by binding the ribosomal E site and restricting ribosome-tRNA dynamics. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 152-159.	3.6	80
87	Hepatitis-C-virus-like internal ribosome entry sites displace eIF3 to gain access to the 40S subunit. <i>Nature</i> , 2013, 503, 539-543.	13.7	158
88	High-resolution cryo-electron microscopy structure of the <i>Trypanosoma brucei</i> ribosome. <i>Nature</i> , 2013, 494, 385-389.	13.7	122
89	Story in a sample—the potential (and limitations) of cryo-electron microscopy applied to molecular machines. <i>Biopolymers</i> , 2013, 99, 832-836.	1.2	23
90	Structural characterization of mRNA-tRNA translocation intermediates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 6094-6099.	3.3	96

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91	Intermediate states during mRNA-tRNA translocation. <i>Current Opinion in Structural Biology</i> , 2012, 22, 778-785.	2.6	28
92	Integrity of the P-site is probed during maturation of the 60S ribosomal subunit. <i>Journal of Cell Biology</i> , 2012, 197, 747-759.	2.3	68
93	The Ribosome as a Brownian Ratchet Machine. , 2011, , 158-190.		9
94	Structural insights into cognate versus near-cognate discrimination during decoding. <i>EMBO Journal</i> , 2011, 30, 1497-1507.	3.5	52
95	Molecular dynamics of EF-G during translocation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1478-1486.	1.5	34
96	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, 4817-4821.	3.3	35
97	Visualization of Molecular Machines by Cryo-Electron Microscopy. , 2011, , 20-37.		4
98	The Ribosome Comes Alive. <i>Israel Journal of Chemistry</i> , 2010, 50, 95-98.	1.0	12
99	Dynamics of the base of ribosomal A-site finger revealed by molecular dynamics simulations and Cryo-EM. <i>Nucleic Acids Research</i> , 2010, 38, 1325-1340.	6.5	48
100	Characterization of the nuclear export adaptor protein Nmd3 in association with the 60S ribosomal subunit. <i>Journal of Cell Biology</i> , 2010, 189, 1079-1086.	2.3	58
101	Structure and Dynamics of a Processive Brownian Motor: The Translating Ribosome. <i>Annual Review of Biochemistry</i> , 2010, 79, 381-412.	5.0	230
102	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, 1063-1068.	3.3	219
103	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.	2.4	102
104	Single-particle reconstruction of biological macromolecules in electron microscopy - 30 years. <i>Quarterly Reviews of Biophysics</i> , 2009, 42, 139-158.	2.4	126
105	Comprehensive Molecular Structure of the Eukaryotic Ribosome. <i>Structure</i> , 2009, 17, 1591-1604.	1.6	140
106	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, 126-132.	1.3	86
107	SPIDER image processing for single-particle reconstruction of biological macromolecules from electron micrographs. <i>Nature Protocols</i> , 2008, 3, 1941-1974.	5.5	435
108	Flexible Fitting of Atomic Structures into Electron Microscopy Maps Using Molecular Dynamics. <i>Structure</i> , 2008, 16, 673-683.	1.6	833

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109	Visualization of the Hybrid State of tRNA Binding Promoted by Spontaneous Ratcheting of the Ribosome. <i>Molecular Cell</i> , 2008, 32, 190-197.	4.5	224
110	Recognition of aminoacyl-tRNA: a common molecular mechanism revealed by cryo-EM. <i>EMBO Journal</i> , 2008, 27, 3322-3331.	3.5	49
111	The process of mRNA-tRNA translocation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 19671-19678.	3.3	198
112	Disentangling conformational states of macromolecules in 3D-EM through likelihood optimization. <i>Nature Methods</i> , 2007, 4, 27-29.	9.0	387
113	Preparation of macromolecular complexes for cryo-electron microscopy. <i>Nature Protocols</i> , 2007, 2, 3239-3246.	5.5	197
114	Structures of modified eEF2-80S ribosome complexes reveal the role of GTP hydrolysis in translocation. <i>EMBO Journal</i> , 2007, 26, 2421-2431.	3.5	171
115	The ribosome and the mechanism of protein synthesis. <i>Reports on Progress in Physics</i> , 2006, 69, 1383-1417.	8.1	56
116	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, 184-194.	1.3	155
117	Estimation of variance in single-particle reconstruction using the bootstrap technique. <i>Journal of Structural Biology</i> , 2006, 154, 168-183.	1.3	114
118	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, 10206-10211.	3.3	61
119	The role of tRNA as a molecular spring in decoding, accommodation, and peptidyl transfer. <i>FEBS Letters</i> , 2005, 579, 959-962.	1.3	93
120	Domain movements of elongation factor eEF2 and the eukaryotic 80S ribosome facilitate tRNA translocation. <i>EMBO Journal</i> , 2004, 23, 1008-1019.	3.5	373
121	Regulation of eukaryotic translation by the RACK1 protein: a platform for signalling molecules on the ribosome. <i>EMBO Reports</i> , 2004, 5, 1137-1141.	2.0	241
122	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, 283-290.	1.3	88
123	Time-resolved imaging of macromolecular processes and interactions. <i>Journal of Structural Biology</i> , 2004, 147, 209-210.	1.3	4
124	Electron microscopy of functional ribosome complexes. <i>Biopolymers</i> , 2003, 68, 223-233.	1.2	54
125	Incorporation of aminoacyl-tRNA into the ribosome as seen by cryo-electron microscopy. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 899-906.	3.6	317
126	Locking and Unlocking of Ribosomal Motions. <i>Cell</i> , 2003, 114, 123-134.	13.5	579

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127	Toward an understanding of the structural basis of translation. <i>Genome Biology</i> , 2003, 4, 237.	13.9	32
128	A twisted tRNA intermediate sets the threshold for decoding. <i>Rna</i> , 2003, 9, 384-385.	1.6	38
129	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, 9319-9323.	3.3	332
130	Single-Particle Imaging of Macromolecules by Cryo-Electron Microscopy. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2002, 31, 303-319.	18.3	282
131	Three-dimensional imaging of biological complexity. <i>Journal of Structural Biology</i> , 2002, 138, 85-91.	1.3	93
132	A Cold Look at Transcription. <i>Structure</i> , 2002, 10, 1156-1157.	1.6	1
133	Cryo-EM reveals an active role for aminoacyl-tRNA in the accommodation process. <i>EMBO Journal</i> , 2002, 21, 3557-3567.	3.5	272
134	Hepatitis C Virus IRES RNA-Induced Changes in the Conformation of the 40S Ribosomal Subunit. <i>Science</i> , 2001, 291, 1959-1962.	6.0	463
135	Cryo-electron microscopy as an investigative tool: the ribosome as an example. <i>BioEssays</i> , 2001, 23, 725-732.	1.2	47
136	A ratchet-like inter-subunit reorganization of the ribosome during translocation. <i>Nature</i> , 2000, 406, 318-322.	13.7	781
137	Cryo-Electron Microscopy Training at the Wadsworth Center. <i>Microscopy and Microanalysis</i> , 2000, 6, 278-279.	0.2	0
138	Visualization of Trna Movements on the Escherichia coli 70s Ribosome during the Elongation Cycle. <i>Journal of Cell Biology</i> , 2000, 150, 447-460.	2.3	158
139	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, 1670-1678.	0.2	75
140	EF-G-dependent GTP hydrolysis induces translocation accompanied by large conformational changes in the 70S ribosome. <i>Nature Structural Biology</i> , 1999, 6, 643-647.	9.7	282
141	SPIDER and WEB: Processing and Visualization of Images in 3D Electron Microscopy and Related Fields. <i>Journal of Structural Biology</i> , 1996, 116, 190-199.	1.3	1,997
142	Estimation of variance distribution in threedimensional reconstruction II Applications. <i>Journal of the Optical Society of America A: Optics and Image Science, and Vision</i> , 1995, 12, 2628.	0.8	9
143	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, 757-765.	0.9	101
144	SPIDER—A modular software system for electron image processing. <i>Ultramicroscopy</i> , 1981, 6, 343-357.	0.8	172

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145	Spider – A modular software system for electron image processing. Ultramicroscopy, 1981, 6, 343-357.	0.8	281
146	Averaging of low exposure electron micrographs of non-periodic objects. Ultramicroscopy, 1975, 1, 159-162.	0.8	153
147	Studies of Elongation Factor G-Dependent tRNA Translocation by Three-Dimensional Cryo-Electron Microscopy. , 0, , 53-62.		7