

Joachim Frank

List of Publications by Year in descending order

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147
papers

16,648
citations

23567
58
h-index

17592
121
g-index

170
all docs

170
docs citations

170
times ranked

12594
citing authors

#	ARTICLE	IF	CITATIONS
1	SPIDER and WEB: Processing and Visualization of Images in 3D Electron Microscopy and Related Fields. Journal of Structural Biology, 1996, 116, 190-199.	2.8	1,997
2	Flexible Fitting of Atomic Structures into Electron Microscopy Maps Using Molecular Dynamics. Structure, 2008, 16, 673-683.	3.3	833
3	A ratchet-like inter-subunit reorganization of the ribosome during translocation. Nature, 2000, 406, 318-322.	27.8	781
4	Locking and Unlocking of Ribosomal Motions. Cell, 2003, 114, 123-134.	28.9	579
5	Hepatitis C Virus IRES RNA-Induced Changes in the Conformation of the 40S Ribosomal Subunit. Science, 2001, 291, 1959-1962.	12.6	463
6	SPIDER image processing for single-particle reconstruction of biological macromolecules from electron micrographs. Nature Protocols, 2008, 3, 1941-1974.	12.0	435
7	Disentangling conformational states of macromolecules in 3D-EM through likelihood optimization. Nature Methods, 2007, 4, 27-29.	19.0	387
8	Domain movements of elongation factor eEF2 and the eukaryotic 80S ribosome facilitate tRNA translocation. EMBO Journal, 2004, 23, 1008-1019.	7.8	373
9	Structure of a mammalian ryanodine receptor. Nature, 2015, 517, 44-49.	27.8	350
10	Dynamic reorganization of the functionally active ribosome explored by normal mode analysis and cryo-electron microscopy. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 9319-9323.	7.1	332
11	Incorporation of aminoacyl-tRNA into the ribosome as seen by cryo-electron microscopy. Nature Structural and Molecular Biology, 2003, 10, 899-906.	8.2	317
12	Structural Basis for Gating and Activation of RyR1. Cell, 2016, 167, 145-157.e17.	28.9	301
13	EF-G-dependent GTP hydrolysis induces translocation accompanied by large conformational changes in the 70S ribosome. Nature Structural Biology, 1999, 6, 643-647.	9.7	282
14	Single-Particle Imaging of Macromolecules by Cryo-Electron Microscopy. Annual Review of Biophysics and Biomolecular Structure, 2002, 31, 303-319.	18.3	282
15	Spider – A modular software system for electron image processing. Ultramicroscopy, 1981, 6, 343-357.	1.9	281
16	Cryo-EM reveals an active role for aminoacyl-tRNA in the accommodation process. EMBO Journal, 2002, 21, 3557-3567.	7.8	272
17	A glycan gate controls opening of the SARS-CoV-2 spike protein. Nature Chemistry, 2021, 13, 963-968.	13.6	254
18	Regulation of eukaryotic translation by the RACK1 protein: a platform for signalling molecules on the ribosome. EMBO Reports, 2004, 5, 1137-1141.	4.5	241

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19	Structure and Dynamics of a Processive Brownian Motor: The Translating Ribosome. Annual Review of Biochemistry, 2010, 79, 381-412.	11.1	230
20	Visualization of the Hybrid State of tRNA Binding Promoted by Spontaneous Ratcheting of the Ribosome. Molecular Cell, 2008, 32, 190-197.	9.7	224
21	Ribosome-induced changes in elongation factor Tu conformation control GTP hydrolysis. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1063-1068.	7.1	219
22	Trajectories of the ribosome as a Brownian nanomachine. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17492-17497.	7.1	218
23	Structure of mammalian eIF3 in the context of the 43S preinitiation complex. Nature, 2015, 525, 491-495.	27.8	204
24	The process of mRNA-tRNA translocation. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 19671-19678.	7.1	198
25	Preparation of macromolecular complexes for cryo-electron microscopy. Nature Protocols, 2007, 2, 3239-3246.	12.0	197
26	Channel opening and gating mechanism in AMPA-subtype glutamate receptors. Nature, 2017, 549, 60-65.	27.8	183
27	SPIDER-A modular software system for electron image processing. Ultramicroscopy, 1981, 6, 343-357.	1.9	172
28	Structures of modified eEF2-80S ribosome complexes reveal the role of GTP hydrolysis in translocation. EMBO Journal, 2007, 26, 2421-2431.	7.8	171
29	Continuous changes in structure mapped by manifold embedding of single-particle data in cryo-EM. Methods, 2016, 100, 61-67.	3.8	162
30	Visualization of Trna Movements on the Escherichia coli 70s Ribosome during the Elongation Cycle. Journal of Cell Biology, 2000, 150, 447-460.	5.2	158
31	Hepatitis-C-virus-like internal ribosome entry sites displace eIF3 to gain access to the 40S subunit. Nature, 2013, 503, 539-543.	27.8	158
32	A method of focused classification, based on the bootstrap 3D variance analysis, and its application to EF-G-dependent translocation. Journal of Structural Biology, 2006, 154, 184-194.	2.8	155
33	Averaging of low exposure electron micrographs of non-periodic objects. Ultramicroscopy, 1975, 1, 159-162.	1.9	153
34	Comprehensive Molecular Structure of the Eukaryotic Ribosome. Structure, 2009, 17, 1591-1604.	3.3	140
35	Advances in the field of single-particle cryo-electron microscopy over the last decade. Nature Protocols, 2017, 12, 209-212.	12.0	127
36	Single-particle reconstruction of biological macromolecules in electron microscopy - 30 years. Quarterly Reviews of Biophysics, 2009, 42, 139-158.	5.7	126

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37	High-resolution cryo-electron microscopy structure of the <i>Trypanosoma brucei</i> ribosome. <i>Nature</i> , 2013, 494, 385-389.	27.8	122
38	Time-resolved cryo-electron microscopy: Recent progress. <i>Journal of Structural Biology</i> , 2017, 200, 303-306.	2.8	120
39	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.	7.1	119
40	Estimation of variance in single-particle reconstruction using the bootstrap technique. <i>Journal of Structural Biology</i> , 2006, 154, 168-183.	2.8	114
41	Elucidation of AMPA receptor–stargazin complexes by cryo–electron microscopy. <i>Science</i> , 2016, 353, 83-86.	12.6	112
42	A Fast and Effective Microfluidic Spraying-Plunging Method for High-Resolution Single-Particle Cryo-EM. <i>Structure</i> , 2017, 25, 663-670.e3.	3.3	112
43	The ABC-F protein EttA gates ribosome entry into the translation elongation cycle. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 143-151.	8.2	109
44	Ryanodine Receptor Structure and Function in Health and Disease. <i>Sub-Cellular Biochemistry</i> , 2018, 87, 329-352.	2.4	104
45	Structure of the STRA6 receptor for retinol uptake. <i>Science</i> , 2016, 353, .	12.6	103
46	Late steps in bacterial translation initiation visualized using time-resolved cryo-EM. <i>Nature</i> , 2019, 570, 400-404.	27.8	103
47	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.	5.7	102
48	A model of the translational apparatus based on a three-dimensional reconstruction of the <i>Escherichia coli</i> ribosome. <i>Biochemistry and Cell Biology</i> , 1995, 73, 757-765.	2.0	101
49	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.	7.1	96
50	Three-dimensional imaging of biological complexity. <i>Journal of Structural Biology</i> , 2002, 138, 85-91.	2.8	93
51	The role of tRNA as a molecular spring in decoding, accommodation, and peptidyl transfer. <i>FEBS Letters</i> , 2005, 579, 959-962.	2.8	93
52	Structural Bases of Desensitization in AMPA Receptor-Auxiliary Subunit Complexes. <i>Neuron</i> , 2017, 94, 569-580.e5.	8.1	89
53	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.	2.8	88
54	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.	2.8	86

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55	EttA regulates translation by binding the ribosomal E site and restricting ribosome-tRNA dynamics. Nature Structural and Molecular Biology, 2014, 21, 152-159.	8.2	80
56	Structural Dynamics of Ribosome Subunit Association Studied by Mixing-Spraying Time-Resolved Cryogenic Electron Microscopy. Structure, 2015, 23, 1097-1105.	3.3	78
57	Retrieving functional pathways of biomolecules from single-particle snapshots. Nature Communications, 2020, 11, 4734.	12.8	76
58	Domain Motions of EF-G Bound to the 70S Ribosome: Insights from a Hand-Shaking between Multi-Resolution Structures. Biophysical Journal, 2000, 79, 1670-1678.	0.5	75
59	Integrity of the P-site is probed during maturation of the 60S ribosomal subunit. Journal of Cell Biology, 2012, 197, 747-759.	5.2	68
60	Key Intermediates in Ribosome Recycling Visualized by Time-Resolved Cryoelectron Microscopy. Structure, 2016, 24, 2092-2101.	3.3	68
61	Nmd3 is a structural mimic of $\text{eIF}5\text{A}$, and activates the cpGTPase Lsg1 during 60S ribosome biogenesis. EMBO Journal, 2017, 36, 854-868.	7.8	67
62	Structure and assembly model for the <i>Trypanosoma cruzi</i> 60S ribosomal subunit. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12174-12179.	7.1	63
63	The structure of the 80S ribosome from <i>Trypanosoma cruzi</i> reveals unique rRNA components. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10206-10211.	7.1	61
64	Three-Dimensional Analysis of Mitochondrial Crista Ultrastructure in a Patient with Leigh Syndrome by In Situ Cryoelectron Tomography. IScience, 2018, 6, 83-91.	4.1	60
65	Structure of human GABAB receptor in an inactive state. Nature, 2020, 584, 304-309.	27.8	59
66	Characterization of the nuclear export adaptor protein Nmd3 in association with the 60S ribosomal subunit. Journal of Cell Biology, 2010, 189, 1079-1086.	5.2	58
67	The ribosome and the mechanism of protein synthesis. Reports on Progress in Physics, 2006, 69, 1383-1417.	20.1	56
68	Electron microscopy of functional ribosome complexes. Biopolymers, 2003, 68, 223-233.	2.4	54
69	Activation of GTP hydrolysis in mRNA-tRNA translocation by elongation factor G. Science Advances, 2015, 1, .	10.3	53
70	Structural insights into cognate versus near-cognate discrimination during decoding. EMBO Journal, 2011, 30, 1497-1507.	7.8	52
71	Automated particle picking for low-contrast macromolecules in cryo-electron microscopy. Journal of Structural Biology, 2014, 186, 1-7.	2.8	52
72	Recognition of aminoacyl-tRNA: a common molecular mechanism revealed by cryo-EM. EMBO Journal, 2008, 27, 3322-3331.	7.8	49

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73	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.	14.5	48
74	Dynamical features of the <i>Plasmodium falciparum</i> ribosome during translation. <i>Nucleic Acids Research</i> , 2015, 43, gkv991.	14.5	48
75	Cryo-electron microscopy as an investigative tool: the ribosome as an example. <i>BioEssays</i> , 2001, 23, 725-732.	2.5	47
76	New Insights into Ribosome Structure and Function. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a032615.	5.5	45
77	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.	1.5	44
78	The structural basis for release-factor activation during translation termination revealed by time-resolved cryogenic electron microscopy. <i>Nature Communications</i> , 2019, 10, 2579.	12.8	43
79	<i>Escherichia coli</i> NusG Links the Lead Ribosome with the Transcription Elongation Complex. <i>IScience</i> , 2020, 23, 101352.	4.1	43
80	Ribosome-associated vesicles: A dynamic subcompartment of the endoplasmic reticulum in secretory cells. <i>Science Advances</i> , 2020, 6, eaay9572.	10.3	42
81	Mechanism of ligand activation of a eukaryotic cyclic nucleotide-gated channel. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 625-634.	8.2	40
82	Time-Resolved Cryo-electron Microscopy Using a Microfluidic Chip. <i>Methods in Molecular Biology</i> , 2018, 1764, 59-71.	0.9	39
83	A twisted tRNA intermediate sets the threshold for decoding. <i>Rna</i> , 2003, 9, 384-385.	3.5	38
84	Generalized single-particle cryo-EM – a historical perspective. <i>Microscopy (Oxford, England)</i> , 2016, 65, 3-8.	1.5	38
85	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.	7.1	35
86	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.	3.3	35
87	Single-Particle Reconstruction of Biological Molecules – Story in a Sample (Nobel Lecture). <i>Angewandte Chemie - International Edition</i> , 2018, 57, 10826-10841.	13.8	35
88	Molecular dynamics of EF-G during translocation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1478-1486.	2.6	34
89	CTF Challenge: Result summary. <i>Journal of Structural Biology</i> , 2015, 190, 348-359.	2.8	34
90	Toward an understanding of the structural basis of translation. <i>Genome Biology</i> , 2003, 4, 237.	9.6	32

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91	New Opportunities Created by Single-Particle Cryo-EM: The Mapping of Conformational Space. <i>Biochemistry</i> , 2018, 57, 888-888.	2.5	31
92	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.	14.5	29
93	Intermediate states during mRNA-tRNA translocation. <i>Current Opinion in Structural Biology</i> , 2012, 22, 778-785.	5.7	28
94	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.	5.4	27
95	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.	7.6	26
96	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.	4.0	24
97	Story in a sample—the potential (and limitations) of cryo-electron microscopy applied to molecular machines. <i>Biopolymers</i> , 2013, 99, 832-836.	2.4	23
98	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, .	7.1	23
99	Identification of ions in experimental electrostatic potential maps. <i>IUCr</i> , 2018, 5, 375-381.	2.2	22
100	The Israeli acute paralysis virus IRES captures host ribosomes by mimicking a ribosomal state with hybrid tRNAs. <i>EMBO Journal</i> , 2019, 38, e102226.	7.8	16
101	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.	2.6	15
102	The Ribosome Comes Alive. <i>Israel Journal of Chemistry</i> , 2010, 50, 95-98.	2.3	12
103	Whither Ribosome Structure and Dynamics Research? (A Perspective). <i>Journal of Molecular Biology</i> , 2016, 428, 3565-3569.	4.2	11
104	POLARIS: Path of Least Action Analysis on Energy Landscapes. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 2581-2590.	5.4	11
105	The mechanism of translation. <i>F1000Research</i> , 2017, 6, 198.	1.6	11
106	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, 8, 462-478.	4.4	11
107	Particle migration analysis in iterative classification of cryo-EM single-particle data. <i>Journal of Structural Biology</i> , 2014, 188, 267-273.	2.8	10
108	Quantitative Characterization of Domain Motions in Molecular Machines. <i>Journal of Physical Chemistry B</i> , 2017, 121, 3747-3756.	2.6	10

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109	Molecular architecture of 40S translation initiation complexes on the hepatitis C virus IRES. EMBO Journal, 2022, 41, .	7.8	10
110	Estimation of variance distribution in threedimensional reconstruction II Applications. Journal of the Optical Society of America A: Optics and Image Science, and Vision, 1995, 12, 2628.	1.5	9
111	The Ribosome as a Brownian Ratchet Machine. , 2011, , 158-190.		9
112	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.	2.2	7
113	Studies of Elongation Factor G-Dependent tRNA Translocation by Three-Dimensional Cryo-Electron Microscopy. , 0, , 53-62.		7
114	Contributions of single-particle cryoelectron microscopy toward fighting COVID-19. Trends in Biochemical Sciences, 2022, 47, 117-123.	7.5	6
115	Time-resolved imaging of macromolecular processes and interactions. Journal of Structural Biology, 2004, 147, 209-210.	2.8	4
116	Critical Role for <i>Saccharomyces cerevisiae</i> Asc1p in Translational Initiation at Elevated Temperatures. Proteomics, 2018, 18, e1800208.	2.2	4
117	Just in Time: The Role of Cryo-Electron Microscopy in Combating Recent Pandemics. Biochemistry, 2021, 60, 3449-3451.	2.5	4
118	Visualization of Molecular Machines by Cryo-Electron Microscopy. , 2011, , 20-37.		4
119	Channel opening and gating mechanism in AMPA-subtype glutamate receptors. journal of hand surgery Asian-Pacific volume, The, 2018, , 542-558.	0.4	3
120	Interaction Networks of Ribosomal Expansion Segments in Kinetoplastids. Sub-Cellular Biochemistry, 2021, 96, 433-450.	2.4	3
121	Trajectories of the ribosome as a Brownian nanomachine. journal of hand surgery Asian-Pacific volume, The, 2018, , 463-475.	0.4	2
122	A Cold Look at Transcription. Structure, 2002, 10, 1156-1157.	3.3	1
123	Studying Kinetics by Counting Particles in Time-Resolved Cryo-EM. Microscopy and Microanalysis, 2019, 25, 2-3.	0.4	1
124	The structure of the 80S ribosome from Trypanosoma cruzi reveals unique rRNA components. journal of hand surgery Asian-Pacific volume, The, 2018, , 383-388.	0.4	1
125	Cryo-Electron Microscopy Training at the Wadsworth Center. Microscopy and Microanalysis, 2000, 6, 278-279.	0.4	0
126	Einzelpartikel-Rekonstruktion biologischer Moleküle – Geschichte in einer Probe (Nobel-Aufsatz). Angewandte Chemie, 2018, 130, 10990-11006.	2.0	0

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127	Key Intermediates in Ribosome Recycling Visualized by Time-Resolved Cryoelectron Microscopy. journal of hand surgery Asian-Pacific volume, The, 2018, , 516-525.	0.4	0
128	Alexander Spirin's Vision of the Ribosome as a Thermal Ratchet Machine. Biochemistry (Moscow), 2021, 86, 910-912.	1.5	0
129	What is in the black box? – A perspective on software in cryoelectron microscopy. Biophysical Journal, 2021, 120, 4307-4311.	0.5	0
130	The process of mRNA-tRNA translocation. journal of hand surgery Asian-Pacific volume, The, 2018, , 405-412.	0.4	0
131	Structure of the 80S Ribosome from <i>Saccharomyces cerevisiae</i> – tRNA-Ribosome and Subunit-Subunit Interactions. journal of hand surgery Asian-Pacific volume, The, 2018, , 286-299.	0.4	0
132	Structure and assembly model for the Trypanosoma cruzi 60S ribosomal subunit. journal of hand surgery Asian-Pacific volume, The, 2018, , 526-531.	0.4	0
133	Architecture of the Protein-Conducting Channel Associated with the Translating 80S Ribosome. journal of hand surgery Asian-Pacific volume, The, 2018, , 274-285.	0.4	0
134	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.	0.4	0
135	Flexible Fitting of Atomic Structures into Electron Microscopy Maps Using Molecular Dynamics. journal of hand surgery Asian-Pacific volume, The, 2018, , 433-443.	0.4	0
136	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.	0.4	0
137	Incorporation of aminoacyl-tRNA into the ribosome as seen by cryo-electron microscopy. journal of hand surgery Asian-Pacific volume, The, 2018, , 339-346.	0.4	0
138	A twisted tRNA intermediate sets the threshold for decoding. journal of hand surgery Asian-Pacific volume, The, 2018, , 359-360.	0.4	0
139	Structural characterization of mRNA-tRNA translocation intermediates. journal of hand surgery Asian-Pacific volume, The, 2018, , 450-455.	0.4	0
140	Quantitative Characterization of Domain Motions in Molecular Machines. journal of hand surgery Asian-Pacific volume, The, 2018, , 532-541.	0.4	0
141	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.	0.4	0
142	The Cryo-EM Structure of a Translation Initiation Complex from Escherichia coli. journal of hand surgery Asian-Pacific volume, The, 2018, , 373-382.	0.4	0
143	Disentangling conformational states of macromolecules in 3D-EM through likelihood optimization. journal of hand surgery Asian-Pacific volume, The, 2018, , 413-415.	0.4	0
144	Structural Basis for Gating and Activation of RyR1. journal of hand surgery Asian-Pacific volume, The, 2018, , 497-515.	0.4	0

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145	High-resolution cryo-electron microscopy structure of the Trypanosoma brucei ribosome. journal of hand surgery Asian-Pacific volume, The, 2018, , 456-462.	0.4	0
146	Activation of GTP hydrolysis in mRNA-tRNA translocation by elongation factor G. journal of hand surgery Asian-Pacific volume, The, 2018, , 490-496.	0.4	0
147	Locking and Unlocking of Ribosomal Motions. journal of hand surgery Asian-Pacific volume, The, 2018, , 347-358.	0.4	0