Joachim Frank

List of Publications by Year
in descending order

147	16,648	58	121
papers	citations	h-index	g-index
		27035	20023

170	170	170	14176
all docs	docs citations	times ranked	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.	1.3	1,997
2	Flexible Fitting of Atomic Structures into Electron Microscopy Maps Using Molecular Dynamics. Structure, 2008, 16, 673-683.	1.6	833
3	A ratchet-like inter-subunit reorganization of the ribosome during translocation. Nature, 2000, 406, 318-322.	13.7	781
4	Locking and Unlocking of Ribosomal Motions. Cell, 2003, 114, 123-134.	13.5	579
5	Hepatitis C Virus IRES RNA-Induced Changes in the Conformation of the 40S Ribosomal Subunit. Science, 2001, 291, 1959-1962.	6.0	463
6	SPIDER image processing for single-particle reconstruction of biological macromolecules from electron micrographs. Nature Protocols, 2008, 3, 1941-1974.	5.5	435
7	Disentangling conformational states of macromolecules in 3D-EM through likelihood optimization. Nature Methods, 2007, 4, 27-29.	9.0	387
8	Domain movements of elongation factor eEF2 and the eukaryotic 80S ribosome facilitate tRNA translocation. EMBO Journal, 2004, 23, 1008-1019.	3.5	373
9	Structure of a mammalian ryanodine receptor. Nature, 2015, 517, 44-49.	13.7	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.	3.3	332
11	Incorporation of aminoacyl-tRNA into the ribosome as seen by cryo-electron microscopy. Nature Structural and Molecular Biology, 2003, 10, 899-906.	3.6	317
12	Structural Basis for Gating and Activation of RyR1. Cell, 2016, 167, 145-157.e17.	13.5	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	Spiderâ€"A modular software system for electron image processing. Ultramicroscopy, 1981, 6, 343-357.	0.8	281
16	Cryo-EM reveals an active role for aminoacyl-tRNA in the accommodation process. EMBO Journal, 2002, 21, 3557-3567.	3.5	272
17	A glycan gate controls opening of the SARS-CoV-2 spike protein. Nature Chemistry, 2021, 13, 963-968.	6.6	254
18	Regulation of eukaryotic translation by the RACK1 protein: a platform for signalling molecules on the ribosome. EMBO Reports, 2004, 5, 1137-1141.	2.0	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.	5.0	230
20	Visualization of the Hybrid State of tRNA Binding Promoted by Spontaneous Ratcheting of the Ribosome. Molecular Cell, 2008, 32, 190-197.	4.5	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.	3.3	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.	3.3	218
23	Structure of mammalian eIF3 in the context of the 43S preinitiation complex. Nature, 2015, 525, 491-495.	13.7	204
24	The process of mRNAâ€"tRNA translocation. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 19671-19678.	3.3	198
25	Preparation of macromolecular complexes for cryo-electron microscopy. Nature Protocols, 2007, 2, 3239-3246.	5.5	197
26	Channel opening and gating mechanism in AMPA-subtype glutamate receptors. Nature, 2017, 549, 60-65.	13.7	183
27	SPIDERâ€"A modular software system for electron image processing. Ultramicroscopy, 1981, 6, 343-357.	0.8	172
28	Structures of modified eEF2Â·80S ribosome complexes reveal the role of GTP hydrolysis in translocation. EMBO Journal, 2007, 26, 2421-2431.	3.5	171
29	Continuous changes in structure mapped by manifold embedding of single-particle data in cryo-EM. Methods, 2016, 100, 61-67.	1.9	162
30	Visualization of Trna Movements on the Escherichia coli 70s Ribosome during the Elongation Cycle. Journal of Cell Biology, 2000, 150, 447-460.	2.3	158
31	Hepatitis-C-virus-like internal ribosome entry sites displace eIF3 to gain access to the 40S subunit. Nature, 2013, 503, 539-543.	13.7	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.	1.3	155
33	Averaging of low exposure electron micrographs of non-periodic objects. Ultramicroscopy, 1975, 1, 159-162.	0.8	153
34	Comprehensive Molecular Structure of the Eukaryotic Ribosome. Structure, 2009, 17, 1591-1604.	1.6	140
35	Advances in the field of single-particle cryo-electron microscopy over the last decade. Nature Protocols, 2017, 12, 209-212.	5.5	127
36	Single-particle reconstruction of biological macromolecules in electron microscopy â€" 30 years. Quarterly Reviews of Biophysics, 2009, 42, 139-158.	2.4	126

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37	High-resolution cryo-electron microscopy structure of the Trypanosoma brucei ribosome. Nature, 2013, 494, 385-389.	13.7	122
38	Time-resolved cryo-electron microscopy: Recent progress. Journal of Structural Biology, 2017, 200, 303-306.	1.3	120
39	Structure and activity of lipid bilayer within a membrane-protein transporter. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 12985-12990.	3.3	119
40	Estimation of variance in single-particle reconstruction using the bootstrap technique. Journal of Structural Biology, 2006, 154, 168-183.	1.3	114
41	Elucidation of AMPA receptorâ€“stargazin complexes by cryoâ€“electron microscopy. Science, 2016, 353, 83-86.	6.0	112
42	A Fast and Effective Microfluidic Spraying-Plunging Method for High-Resolution Single-Particle Cryo-EM. Structure, 2017, 25, 663-670.e3.	1.6	112
43	The ABC-F protein EttA gates ribosome entry into the translation elongation cycle. Nature Structural and Molecular Biology, 2014, 21, 143-151.	3.6	109
44	Ryanodine Receptor Structure and Function in Health and Disease. Sub-Cellular Biochemistry, 2018, 87, 329-352.	1.0	104
45	Structure of the STRA6 receptor for retinol uptake. Science, 2016, 353, .	6.0	103
46	Late steps in bacterial translation initiation visualized using time-resolved cryo-EM. Nature, 2019, 570, 400-404.	13.7	103
47	Elongation in translation as a dynamic interaction among the ribosome, tRNA, and elongation factors EF-G and EF-Tu. Quarterly Reviews of Biophysics, 2009, 42, 159-200.	2.4	102
48	A model of the translational apparatus based on a three-dimensional reconstruction of the<i>Escherichia coli</i>ribosome. Biochemistry and Cell Biology, 1995, 73, 757-765.	0.9	101
49	Structural characterization of mRNA-tRNA translocation intermediates. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6094-6099.	3.3	96
50	Three-dimensional imaging of biological complexity. Journal of Structural Biology, 2002, 138, 85-91.	1.3	93
51	The role of tRNA as a molecular spring in decoding, accommodation, and peptidyl transfer. FEBS Letters, 2005, 579, 959-962.	1.3	93
52	Structural Bases of Desensitization in AMPA Receptor-Auxiliary Subunit Complexes. Neuron, 2017, 94, 569-580.e5.	3.8	89
53	Dynamics of EF-G interaction with the ribosome explored by classification of a heterogeneous cryo-EM dataset. Journal of Structural Biology, 2004, 147, 283-290.	1.3	88
54	Determination of signal-to-noise ratios and spectral SNRs in cryo-EM low-dose imaging of molecules. Journal of Structural Biology, 2009, 166, 126-132.	1.3	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.	3.6	80
56	Structural Dynamics of Ribosome Subunit Association Studied by Mixing-Spraying Time-Resolved Cryogenic Electron Microscopy. Structure, 2015, 23, 1097-1105.	1.6	78
57	Retrieving functional pathways of biomolecules from single-particle snapshots. Nature Communications, 2020, 11, 4734.	5.8	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.	0.2	75
59	Integrity of the P-site is probed during maturation of the 60S ribosomal subunit. Journal of Cell Biology, 2012, 197, 747-759.	2.3	68
60	Key Intermediates in Ribosome Recycling Visualized by Time-Resolved Cryoelectron Microscopy. Structure, 2016, 24, 2092-2101.	1.6	68
61	Nmd3 is a structural mimic of <scp>eIF</scp> 5A, and activates the cp <scp>GTP</scp> ase Lsg1 during 60S ribosome biogenesis. EMBO Journal, 2017, 36, 854-868.	3.5	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.	3.3	63
63	The structure of the 80S ribosome from Trypanosoma cruzi reveals unique rRNA components. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10206-10211.	3.3	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.	1.9	60
65	Structure of human GABAB receptor in an inactive state. Nature, 2020, 584, 304-309.	13.7	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.	2.3	58
67	The ribosome and the mechanism of protein synthesis. Reports on Progress in Physics, 2006, 69, 1383-1417.	8.1	56
68	Electron microscopy of functional ribosome complexes. Biopolymers, 2003, 68, 223-233.	1.2	54
69	Activation of GTP hydrolysis in mRNA-tRNA translocation by elongation factor G. Science Advances, 2015, 1, .	4.7	53
70	Structural insights into cognate versus near-cognate discrimination during decoding. EMBO Journal, 2011, 30, 1497-1507.	3.5	52
71	Automated particle picking for low-contrast macromolecules in cryo-electron microscopy. Journal of Structural Biology, 2014, 186, 1-7.	1.3	52
72	Recognition of aminoacyl-tRNA: a common molecular mechanism revealed by cryo-EM. EMBO Journal, 2008, 27, 3322-3331.	3.5	49

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73	Dynamics of the base of ribosomal A-site finger revealed by molecular dynamics simulations and Cryo-EM. Nucleic Acids Research, 2010, 38, 1325-1340.	6.5	48
74	Dynamical features of the<i>Plasmodium falciparum</i>ribosome during translation. Nucleic Acids Research, 2015, 43, gkv991.	6.5	48
75	Cryo-electron microscopy as an investigative tool: the ribosome as an example. BioEssays, 2001, 23, 725-732.	1.2	47
76	New Insights into Ribosome Structure and Function. Cold Spring Harbor Perspectives in Biology, 2019, 11, a032615.	2.3	45
77	Two promising future developments of cryo-EM: capturing short-lived states and mapping a continuum of states of a macromolecule. Microscopy (Oxford, England), 2016, 65, 69-79.	0.7	44
78	The structural basis for release-factor activation during translation termination revealed by time-resolved cryogenic electron microscopy. Nature Communications, 2019, 10, 2579.	5.8	43
79	Escherichia coli NusG Links the Lead Ribosome with the Transcription Elongation Complex. IScience, 2020, 23, 101352.	1.9	43
80	Ribosome-associated vesicles: A dynamic subcompartment of the endoplasmic reticulum in secretory cells. Science Advances, 2020, 6, eaay9572.	4.7	42
81	Mechanism of ligand activation of a eukaryotic cyclic nucleotideâˆ’gated channel. Nature Structural and Molecular Biology, 2020, 27, 625-634.	3.6	40
82	Time-Resolved Cryo-electron Microscopy Using a Microfluidic Chip. Methods in Molecular Biology, 2018, 1764, 59-71.	0.4	39
83	A twisted tRNA intermediate sets the threshold for decoding. Rna, 2003, 9, 384-385.	1.6	38
84	Generalized single-particle cryo-EM â€“ a historical perspective. Microscopy (Oxford, England), 2016, 65, 3-8.	0.7	38
85	Cryoelectron microscopy structures of the ribosome complex in intermediate states during tRNA translocation. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4817-4821.	3.3	35
86	Efficient Estimation of Three-Dimensional Covariance and its Application in the Analysis of Heterogeneous Samples in Cryo-Electron Microscopy. Structure, 2015, 23, 1129-1137.	1.6	35
87	Singleâ€Particle Reconstruction of Biological Moleculesâ€"Story in a Sample (Nobel Lecture). Angewandte Chemie - International Edition, 2018, 57, 10826-10841.	7.2	35
88	Molecular dynamics of EFâ€G during translocation. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1478-1486.	1.5	34
89	CTF Challenge: Result summary. Journal of Structural Biology, 2015, 190, 348-359.	1.3	34
90	Toward an understanding of the structural basis of translation. Genome Biology, 2003, 4, 237.	13.9	32

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91	New Opportunities Created by Single-Particle Cryo-EM: The Mapping of Conformational Space. Biochemistry, 2018, 57, 888-888.	1.2	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. Nucleic Acids Research, 2018, 46, 5861-5874.	6.5	29
93	Intermediate states during mRNAâ€"tRNA translocation. Current Opinion in Structural Biology, 2012, 22, 778-785.	2.6	28
94	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
95	Determination of the ribosome structure to a resolution of 2.5 Ã… by singleâ€particle cryoâ€EM. Protein Science, 2017, 26, 82-92.	3.1	26
96	The translation elongation cycleâ€"capturing multiple states by cryo-electron microscopy. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160180.	1.8	24
97	Story in a sampleâ€"the potential (and limitations) of cryoâ€electron microscopy applied to molecular machines. Biopolymers, 2013, 99, 832-836.	1.2	23
98	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
99	Identification of ions in experimental electrostatic potential maps. IUCrJ, 2018, 5, 375-381.	1.0	22
100	The Israeli acute paralysis virus IRES captures host ribosomes by mimicking a ribosomal state with hybrid tRNAs. EMBO Journal, 2019, 38, e102226.	3.5	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. Journal of Physical Chemistry B, 2015, 119, 10888-10901.	1.2	15
102	The Ribosome Comes Alive. Israel Journal of Chemistry, 2010, 50, 95-98.	1.0	12
103	Whither Ribosome Structure and Dynamics Research? (A Perspective). Journal of Molecular Biology, 2016, 428, 3565-3569.	2.0	11
104	POLARIS: Path of Least Action Analysis on Energy Landscapes. Journal of Chemical Information and Modeling, 2020, 60, 2581-2590.	2.5	11
105	The mechanism of translation. F1000Research, 2017, 6, 198.	0.8	11
106	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
107	Particle migration analysis in iterative classification of cryo-EM single-particle data. Journal of Structural Biology, 2014, 188, 267-273.	1.3	10
108	Quantitative Characterization of Domain Motions in Molecular Machines. Journal of Physical Chemistry B, 2017, 121, 3747-3756.	1.2	10

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109	Molecular architecture of <scp>40S</scp> translation initiation complexes on the hepatitis C virus <scp>IRES</scp>. EMBO Journal, 2022, 41, .	3.5	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.	0.8	9
111	The Ribosome as a Brownian Ratchet Machine. , 2011, , 158-190.		9
112	A Timeâ€Resolved Cryoâ€EM Study of Saccharomyces cerevisiae 80S Ribosome Protein Composition in Response to a Change in Carbon Source. Proteomics, 2021, 21, 2000125.	1.3	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.	3.7	6
115	Time-resolved imaging of macromolecular processes and interactions. Journal of Structural Biology, 2004, 147, 209-210.	1.3	4
116	Critical Role for <i>Saccharomyces cerevisiae</i> Asc1p in Translational Initiation at Elevated Temperatures. Proteomics, 2018, 18, e1800208.	1.3	4
117	â€œJust in Timeâ€ The Role of Cryo-Electron Microscopy in Combating Recent Pandemics. Biochemistry, 2021, 60, 3449-3451.	1.2	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.	0.2	3
120	Interaction Networks of Ribosomal Expansion Segments in Kinetoplastids. Sub-Cellular Biochemistry, 2021, 96, 433-450.	1.0	3
121	Trajectories of the ribosome as a Brownian nanomachine. journal of hand surgery Asian-Pacific volume, The, 2018, , 463-475.	0.2	2
122	A Cold Look at Transcription. Structure, 2002, 10, 1156-1157.	1.6	1
123	Studying Kinetics by Counting Particles in Time-Resolved Cryo-EM. Microscopy and Microanalysis, 2019, 25, 2-3.	0.2	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.	0.2	1
125	Cryo-Electron Microscopy Training at the Wadsworth Center. Microscopy and Microanalysis, 2000, 6, 278-279.	0.2	0
126	Einzelpartikelâ€Rekonstruktion biologischer MolekÃ¼le â€“ Geschichte in einer Probe (Nobelâ€Aufsatz). Angewandte Chemie, 2018, 130, 10990-11006.	1.6	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.	0.2	0
128	Alexander Spirinâ€™s Vision of the Ribosome as a Thermal Ratchet Machine. Biochemistry (Moscow), 2021, 86, 910-912.	0.7	0
129	What is in the black box? â€“ A perspective on software in cryoelectron microscopy. Biophysical Journal, 2021, 120, 4307-4311.	0.2	0
130	The process of mRNAâ€“tRNA translocation. journal of hand surgery Asian-Pacific volume, The, 2018, , 405-412.	0.2	0
131	Structure of the 80S Ribosome from <i>Saccharomyces cerevisiae</i>â€“tRNA-Ribosome and Subunit-Subunit Interactions. journal of hand surgery Asian-Pacific volume, The, 2018, , 286-299.	0.2	0
132	Structure and assembly model for the Trypanosoma cruzi 60S ribosomal subunit. journal of hand surgery Asian-Pacific volume, The, 2018, , 526-531.	0.2	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.	0.2	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.	0.2	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.	0.2	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.	0.2	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.	0.2	0
138	A twisted tRNA intermediate sets the threshold for decoding. journal of hand surgery Asian-Pacific volume, The, 2018, , 359-360.	0.2	0
139	Structural characterization of mRNA-tRNA translocation intermediates. journal of hand surgery Asian-Pacific volume, The, 2018, , 450-455.	0.2	0
140	Quantitative Characterization of Domain Motions in Molecular Machines. journal of hand surgery Asian-Pacific volume, The, 2018, , 532-541.	0.2	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.	0.2	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.	0.2	0
143	Disentangling conformational states of macromolecules in 3D-EM through likelihood optimization. journal of hand surgery Asian-Pacific volume, The, 2018, , 413-415.	0.2	0
144	Structural Basis for Gating and Activation of RyR1. journal of hand surgery Asian-Pacific volume, The, 2018, , 497-515.	0.2	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.	0.2	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.	0.2	0
147	Locking and Unlocking of Ribosomal Motions. journal of hand surgery Asian-Pacific volume, The, 2018, , 347-358.	0.2	0