

Fei Sun

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.

138
papers

5,171
citations

32
h-index

70
g-index

155
ext. papers

6,231
ext. citations

9
avg, IF

5.39
L-index

#	Paper	IF	Citations
138	Imaging biological samples by integrated differential phase contrast (iDPC) STEM technique.. <i>Journal of Structural Biology</i> , 2022 , 214, 107837	3.4	0
137	8 Å structure of the outer rings of the <i>Xenopus laevis</i> nuclear pore complex obtained by cryo-EM and AI.. <i>Protein and Cell</i> , 2022 , 1	7.2	4
136	Cryo-EM structure and electrophysiological characterization of ALMT from reveal a previously uncharacterized class of anion channels.. <i>Science Advances</i> , 2022 , 8, eabm3238	14.3	0
135	Structure-based evidence for the enhanced transmissibility of the dominant SARS-CoV-2 B.1.1.7 variant (Alpha). <i>Cell Discovery</i> , 2021 , 7, 109	22.3	8
134	Nanometer-resolution in situ structure of the SARS-CoV-2 postfusion spike protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	7
133	Reprint of "Amorphous nickel titanium alloy film: A new choice for cryo electron microscopy sample preparation". <i>Progress in Biophysics and Molecular Biology</i> , 2021 , 160, 5-15	4.7	1
132	The Unusual Homodimer of a Heme-Copper Terminal Oxidase Allows Itself to Utilize Two Electron Donors. <i>Angewandte Chemie - International Edition</i> , 2021 , 60, 13323-13330	16.4	1
131	The Unusual Homodimer of a Heme-Copper Terminal Oxidase Allows Itself to Utilize Two Electron Donors. <i>Angewandte Chemie</i> , 2021 , 133, 13435-13442	3.6	
130	Structures of human mGlu2 and mGlu7 homo- and heterodimers. <i>Nature</i> , 2021 , 594, 589-593	50.4	22
129	Structural and functional basis for pan-CoV fusion inhibitors against SARS-CoV-2 and its variants with preclinical evaluation. <i>Signal Transduction and Targeted Therapy</i> , 2021 , 6, 288	21	13
128	VHUT-cryo-FIB, a method to fabricate frozen hydrated lamellae from tissue specimens for in situ cryo-electron tomography. <i>Journal of Structural Biology</i> , 2021 , 213, 107763	3.4	2
127	Cellular 3D-reconstruction and analysis in the human cerebral cortex using automatic serial sections. <i>Communications Biology</i> , 2021 , 4, 1030	6.7	0
126	A cryo-electron microscopy support film formed by 2D crystals of hydrophobin HFBI.. <i>Nature Communications</i> , 2021 , 12, 7257	17.4	1
125	A single-cell transcriptomic landscape of primate arterial aging. <i>Nature Communications</i> , 2020 , 11, 2202	17.4	36
124	Structural basis of G and G recognition by the human glucagon receptor. <i>Science</i> , 2020 , 367, 1346-1352	33.3	53
123	Inhibition of SARS-CoV-2 (previously 2019-nCoV) infection by a highly potent pan-coronavirus fusion inhibitor targeting its spike protein that harbors a high capacity to mediate membrane fusion. <i>Cell Research</i> , 2020 , 30, 343-355	24.7	745
122	NLRP6 self-assembles into a linear molecular platform following LPS binding and ATP stimulation. <i>Scientific Reports</i> , 2020 , 10, 198	4.9	18

121	Cryo-EM structures of S-OPA1 reveal its interactions with membrane and changes upon nucleotide binding. <i>ELife</i> , 2020 , 9,	8.9	16
120	A 3.3 Å Resolution Structure of Hyperthermophilic Respiratory Complex III Reveals the Mechanism of Its Thermal Stability. <i>Angewandte Chemie</i> , 2020 , 132, 351-359	3.6	2
119	A 3.3 Å Resolution Structure of Hyperthermophilic Respiratory Complex III Reveals the Mechanism of Its Thermal Stability. <i>Angewandte Chemie - International Edition</i> , 2020 , 59, 343-351	16.4	7
118	Minireview of progress in the structural study of SARS-CoV-2 proteins. <i>Current Research in Microbial Sciences</i> , 2020 , 1, 53-61	3.3	23
117	Amorphous nickel titanium alloy film: A new choice for cryo electron microscopy sample preparation. <i>Progress in Biophysics and Molecular Biology</i> , 2020 , 156, 3-13	4.7	9
116	Isolated Heme A Synthase from <i>Aquifex aeolicus</i> Is a Trimer. <i>MBio</i> , 2020 , 11,	7.8	3
115	Cryo-EM structures of the air-oxidized and dithionite-reduced photosynthetic alternative complex III from. <i>Science Advances</i> , 2020 , 6, eaba2739	14.3	5
114	Molecular mechanism of mitochondrial phosphatidate transfer by Ups1. <i>Communications Biology</i> , 2020 , 3, 468	6.7	1
113	Three-dimensional reconstruction of <i>Picea wilsonii</i> Mast. pollen grains using automated electron microscopy. <i>Science China Life Sciences</i> , 2020 , 63, 171-179	8.5	7
112	SmartBac, a new baculovirus system for large protein complex production. <i>Journal of Structural Biology: X</i> , 2019 , 1, 100003	2.9	7
111	Atlastin-1 regulates morphology and function of endoplasmic reticulum in dendrites. <i>Nature Communications</i> , 2019 , 10, 568	17.4	26
110	New interfaces on MiD51 for Drp1 recruitment and regulation. <i>PLoS ONE</i> , 2019 , 14, e0211459	3.7	8
109	AuTom-dualx: a toolkit for fully automatic fiducial marker-based alignment of dual-axis tilt series with simultaneous reconstruction. <i>Bioinformatics</i> , 2019 , 35, 319-328	7.2	10
108	ACAP1 assembles into an unusual protein lattice for membrane deformation through multiple stages. <i>PLoS Computational Biology</i> , 2019 , 15, e1007081	5	1
107	Synthetic Multienzyme Complexes, Catalytic Nanomachineries for Cascade Biosynthesis. <i>ACS Nano</i> , 2019 , 13, 9895-9906	16.7	32
106	The late stage of COPI vesicle fission requires shorter forms of phosphatidic acid and diacylglycerol. <i>Nature Communications</i> , 2019 , 10, 3409	17.4	5
105	Cryo-EM Structure of Actin Filaments from Pollen. <i>Plant Cell</i> , 2019 , 31, 2855-2867	11.6	12
104	Cryo-EM structure of the RC-LH core complex from an early branching photosynthetic prokaryote. <i>Nature Communications</i> , 2018 , 9, 1568	17.4	29

103	Autogdeterm: automatic geometry determination for electron tomography. <i>Tsinghua Science and Technology</i> , 2018 , 23, 369-376	3.4	1
102	ICON-MIC: Implementing a CPU/MIC Collaboration Parallel Framework for ICON on Tianhe-2 Supercomputer. <i>Journal of Computational Biology</i> , 2018 , 25, 270-281	1.7	3
101	High-vacuum optical platform for cryo-CLEM (HOPE): A new solution for non-integrated multiscale correlative light and electron microscopy. <i>Journal of Structural Biology</i> , 2018 , 201, 63-75	3.4	14
100	Thermodynamics of voltage-gated ion channels. <i>Biophysics Reports</i> , 2018 , 4, 300-319	3.5	16
99	protein micro-crystal fabrication by cryo-FIB for electron diffraction. <i>Biophysics Reports</i> , 2018 , 4, 339-347	3.5	22
98	An electron transfer path connects subunits of a mycobacterial respiratory supercomplex. <i>Science</i> , 2018 , 362,	33.3	76
97	Orienting the future of bio-macromolecular electron microscopy. <i>Chinese Physics B</i> , 2018 , 27, 063601	1.2	6
96	Molecular Details of the PH Domain of ACAP1 Protein Binding to PIP-Containing Membrane. <i>Journal of Physical Chemistry B</i> , 2017 , 121, 3586-3596	3.4	11
95	Structural Insight into the Specific DNA Template Binding to DnaG primase in Bacteria. <i>Scientific Reports</i> , 2017 , 7, 659	4.9	6
94	Molecular insights into the enzyme promiscuity of an aromatic prenyltransferase. <i>Nature Chemical Biology</i> , 2017 , 13, 226-234	11.7	68
93	Large scale three-dimensional reconstruction of an entire <i>Caenorhabditis elegans</i> larva using AutoCUTS-SEM. <i>Journal of Structural Biology</i> , 2017 , 200, 87-96	3.4	17
92	AuTom: A novel automatic platform for electron tomography reconstruction. <i>Journal of Structural Biology</i> , 2017 , 199, 196-208	3.4	20
91	Accelerating electron tomography reconstruction algorithm ICON with GPU. <i>Biophysics Reports</i> , 2017 , 3, 36-42	3.5	11
90	Determining the target protein localization in 3D using the combination of FIB-SEM and APEX2. <i>Biophysics Reports</i> , 2017 , 3, 92-99	3.5	9
89	Crystal structure of <i>E. coli</i> apolipoprotein N-acyl transferase. <i>Nature Communications</i> , 2017 , 8, 15948	17.4	24
88	Using integrated correlative cryo-light and electron microscopy to directly observe syntaphilin-immobilized neuronal mitochondria. <i>Biophysics Reports</i> , 2017 , 3, 8-16	3.5	10
87	A Fully Automatic Geometric Parameters Determining Method for Electron Tomography. <i>Lecture Notes in Computer Science</i> , 2017 , 385-389	0.9	1
86	Accelerating Electron Tomography Reconstruction Algorithm ICON Using the Intel Xeon Phi Coprocessor on Tianhe-2 Supercomputer. <i>Lecture Notes in Computer Science</i> , 2017 , 258-269	0.9	1

85	Structural characterization of coatamer in its cytosolic state. <i>Protein and Cell</i> , 2016 , 7, 586-600	7.2	9
84	ICON: 3D reconstruction with missing-information restoration in biological electron tomography. <i>Journal of Structural Biology</i> , 2016 , 195, 100-12	3.4	51
83	Three-dimensional visualization of arsenic stimulated mouse liver sinusoidal by FIB-SEM approach. <i>Protein and Cell</i> , 2016 , 7, 227-32	7.2	2
82	FIRT: Filtered iterative reconstruction technique with information restoration. <i>Journal of Structural Biology</i> , 2016 , 195, 49-61	3.4	22
81	Crystal structure of E. coli lipoprotein diacylglyceryl transferase. <i>Nature Communications</i> , 2016 , 7, 10198	17.4	62
80	A local-optimization refinement algorithm in single particle analysis for macromolecular complex with multiple rigid modules. <i>Protein and Cell</i> , 2016 , 7, 46-62	7.2	11
79	Fabrication of Frozen-Hydrated Sections by Focused Ion Beam(FIB) Method. <i>Microscopy and Microanalysis</i> , 2016 , 22, 182-183	0.5	
78	An improved cryo-FIB method for fabrication of frozen hydrated lamella. <i>Journal of Structural Biology</i> , 2016 , 194, 218-23	3.4	29
77	Structural insights into Ca(2+)-activated long-range allosteric channel gating of RyR1. <i>Cell Research</i> , 2016 , 26, 977-94	24.7	71
76	Expression, purification, crystallization and crystallographic study of the <i>Aspergillus terreus</i> aromatic prenyltransferase AtaPT. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015 , 71, 889-94	1.1	4
75	Three-dimensional super-resolution protein localization correlated with vitrified cellular context. <i>Scientific Reports</i> , 2015 , 5, 13017	4.9	67
74	A novel fully automatic scheme for fiducial marker-based alignment in electron tomography. <i>Journal of Structural Biology</i> , 2015 , 192, 403-417	3.4	31
73	BrkAutoDisplay: functional display of multiple exogenous proteins on the surface of <i>Escherichia coli</i> by using BrkA autotransporter. <i>Microbial Cell Factories</i> , 2015 , 14, 129	6.4	9
72	Acyl-CoA Dehydrogenase Drives Heat Adaptation by Sequestering Fatty Acids. <i>Cell</i> , 2015 , 161, 1152-1163	36.2	65
71	A novel mitochondrial carrier protein Mme1 acts as a yeast mitochondrial magnesium exporter. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2015 , 1853, 724-32	4.9	17
70	A PH domain in ACAP1 possesses key features of the BAR domain in promoting membrane curvature. <i>Developmental Cell</i> , 2014 , 31, 73-86	10.2	25
69	Identification of neurons responsible for feeding behavior in the <i>Drosophila</i> brain. <i>Science China Life Sciences</i> , 2014 , 57, 391-402	8.5	6
68	Puzzle out the regulation mechanism of PI4KIII α activity. <i>Science China Life Sciences</i> , 2014 , 57, 636-8	8.5	2

67	Cryo-EM structures of two bovine adenovirus type 3 intermediates. <i>Virology</i> , 2014 , 450-451, 174-81	3.6	26
66	C-terminal motif within Sec7 domain regulates guanine nucleotide exchange activity via tuning protein conformation. <i>Biochemical and Biophysical Research Communications</i> , 2014 , 446, 380-6	3.4	1
65	Dimerization interface of 3-hydroxyacyl-CoA dehydrogenase tunes the formation of its catalytic intermediate. <i>PLoS ONE</i> , 2014 , 9, e95965	3.7	6
64	Molecular insights into the membrane-associated phosphatidylinositol 4-kinase II. <i>Nature Communications</i> , 2014 , 5, 3552	17.4	38
63	Expression, purification, crystallization and preliminary crystallographic study of the cytoplasmic domain of the mitochondrial dynamics protein MiD51. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 596-9	1.1	1
62	A marker-free automatic alignment method based on scale-invariant features. <i>Journal of Structural Biology</i> , 2014 , 186, 167-80	3.4	26
61	Flexible interwoven termini determine the thermal stability of thermosomes. <i>Protein and Cell</i> , 2013 , 4, 432-44	7.2	12
60	Revealing various coupling of electron transfer and proton pumping in mitochondrial respiratory chain. <i>Current Opinion in Structural Biology</i> , 2013 , 23, 526-38	8.1	29
59	A fast calculation strategy of density function in ISAF reconstruction algorithm. <i>Science China Information Sciences</i> , 2013 , 56, 1-12	3.4	1
58	Expression, purification and preliminary characterization of glucagon receptor extracellular domain. <i>Protein Expression and Purification</i> , 2013 , 89, 232-40	2	3
57	Identification of SERPINB1 as a physiological inhibitor of human granzyme H. <i>Journal of Immunology</i> , 2013 , 190, 1319-30	5.3	21
56	MicroRNA-124 reduces caveolar density by targeting caveolin-1 in porcine kidney epithelial PK15 cells. <i>Molecular and Cellular Biochemistry</i> , 2013 , 384, 213-9	4.2	16
55	Structural insights into the intrinsic self-assembly of Par-3 N-terminal domain. <i>Structure</i> , 2013 , 21, 997-1006	9.6	26
54	Coexistence of ribbon and helical fibrils originating from hIAPP(20-29) revealed by quantitative nanomechanical atomic force microscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 2798-803	11.5	83
53	Atomic model of rabbit hemorrhagic disease virus by cryo-electron microscopy and crystallography. <i>PLoS Pathogens</i> , 2013 , 9, e1003132	7.6	80
52	Purification, crystallization and preliminary crystallographic analysis of 3-hydroxyacyl-CoA dehydrogenase from <i>Caenorhabditis elegans</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013 , 69, 515-9		1
51	Changes in the quaternary structure and function of MjHSP16.5 attributable to deletion of the IXI motif and introduction of the substitution, R107G, in the Crystallin domain. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013 , 368, 20120327	5.8	14
50	The intra-S phase checkpoint targets Dna2 to prevent stalled replication forks from reversing. <i>Cell</i> , 2012 , 149, 1221-32	56.2	124

49	Cryo-EM structure of a transcribing cypovirus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 6118-23	11.5	41
48	The p53-induced gene Ei24 is an essential component of the basal autophagy pathway. <i>Journal of Biological Chemistry</i> , 2012 , 287, 42053-63	5.4	53
47	Mechanistic insights into regulated cargo binding by ACAP1 protein. <i>Journal of Biological Chemistry</i> , 2012 , 287, 28675-85	5.4	21
46	Structural insights into the substrate specificity of human granzyme H: the functional roles of a novel RKR motif. <i>Journal of Immunology</i> , 2012 , 188, 765-73	5.3	16
45	Structural insights into the peroxidase activity and inactivation of human peroxiredoxin 4. <i>Biochemical Journal</i> , 2012 , 441, 113-8	3.8	69
44	Three-dimensional reconstruction using an adaptive simultaneous algebraic reconstruction technique in electron tomography. <i>Journal of Structural Biology</i> , 2011 , 175, 277-87	3.4	33
43	Single-particle reconstruction using L(2)-gradient flow. <i>Journal of Structural Biology</i> , 2011 , 176, 259-67	3.4	10
42	Mitochondrial Respiratory Complex II 2011 ,		1
41	Autotransporter passenger domain secretion requires a hydrophobic cavity at the extracellular entrance of the β domain pore. <i>Biochemical Journal</i> , 2011 , 435, 577-87	3.8	37
40	Thiabendazole inhibits ubiquinone reduction activity of mitochondrial respiratory complex II via a water molecule mediated binding feature. <i>Protein and Cell</i> , 2011 , 2, 531-42	7.2	29
39	Atomic model of a cypovirus built from cryo-EM structure provides insight into the mechanism of mRNA capping. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 1373-8	11.5	55
38	A fast mapping method in the ISAF reconstruction algorithm. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2011 , 2011, 3930-3	0.9	
37	Crystal structure of a novel esterase Rv0045c from <i>Mycobacterium tuberculosis</i> . <i>PLoS ONE</i> , 2011 , 6, e20506	3.96	19
36	Substrate Binding Properties of Thermosome ATcpnBrom <i>Acidianus Tengchongensis</i> . <i>Progress in Biochemistry and Biophysics</i> , 2011 , 38, 151-158		1
35	The role and structure of the carboxyl-terminal domain of the human voltage-gated proton channel Hv1. <i>Journal of Biological Chemistry</i> , 2010 , 285, 12047-54	5.4	48
34	Secreted monocytic miR-150 enhances targeted endothelial cell migration. <i>Molecular Cell</i> , 2010 , 39, 133-46	4.46	944
33	Distinct symmetry and limited peptide refolding activity of the thermosomes from the acidothermophilic archaea <i>Acidianus tengchongensis</i> S5(T). <i>Biochemical and Biophysical Research Communications</i> , 2010 , 393, 228-34	3.4	9
32	Five mutations in N-terminus confer thermostability on mesophilic xylanase. <i>Biochemical and Biophysical Research Communications</i> , 2010 , 395, 200-6	3.4	55

31	Cryo-electron microscopy reconstructions of two types of wild rabbit hemorrhagic disease viruses characterized the structural features of Lagovirus. <i>Protein and Cell</i> , 2010 , 1, 48-58	7.2	23
30	Crystal structure of group II chaperonin in the open state. <i>Structure</i> , 2010 , 18, 1270-9	5.2	34
29	Expression, purification and preliminary biochemical studies of the N-terminal domain of leucine-rich repeat kinase 2. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010 , 1804, 1780-4	4	10
28	Purification, crystallization and preliminary crystallographic analysis of very-long-chain acyl-CoA dehydrogenase from <i>Caenorhabditis elegans</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 426-30		7
27	Prokaryotic Expression of Active Mitochondrial Uncoupling Protein 1*. <i>Progress in Biochemistry and Biophysics</i> , 2010 , 37, 56-62		4
26	Structural basis for proteolytic specificity of the human apoptosis-inducing granzyme M. <i>Journal of Immunology</i> , 2009 , 183, 421-9	5.3	23
25	Mitochondrial Respiratory Complex II 2009 ,		1
24	D Structural Investigation of Caveolae From Porcine Aorta Endothelial Cell by Electron Tomography*. <i>Progress in Biochemistry and Biophysics</i> , 2009 , 2009, 729-735		3
23	Crystal structure of human ERp44 shows a dynamic functional modulation by its carboxy-terminal tail. <i>EMBO Reports</i> , 2008 , 9, 642-7	6.5	63
22	Crystal structure and mutagenic analysis of GDOsp, a gentisate 1,2-dioxygenase from <i>Silicibacter pomeroyi</i> . <i>Protein Science</i> , 2008 , 17, 1362-73	6.3	42
21	Preliminary molecular characterization and crystallization of mitochondrial respiratory complex II from porcine heart. <i>FEBS Journal</i> , 2007 , 274, 1524-9	5.7	10
20	The crystal structure of human isopentenyl diphosphate isomerase at 1.7 Å resolution reveals its catalytic mechanism in isoprenoid biosynthesis. <i>Journal of Molecular Biology</i> , 2007 , 366, 1447-58	6.5	27
19	New antiviral target revealed by the hexameric structure of mouse hepatitis virus nonstructural protein nsp15. <i>Journal of Virology</i> , 2006 , 80, 7909-17	6.6	70
18	Dodecamer structure of severe acute respiratory syndrome coronavirus nonstructural protein nsp10. <i>Journal of Virology</i> , 2006 , 80, 7902-8	6.6	83
17	Crystal structure of the N-terminal SH3 domain of mouse betaPIX, p21-activated kinase-interacting exchange factor. <i>Biochemical and Biophysical Research Communications</i> , 2006 , 339, 407-14	3.4	5
16	Crystal structure of mitochondrial respiratory membrane protein complex II. <i>Cell</i> , 2005 , 121, 1043-57	56.2	558
15	Insights into SARS-CoV transcription and replication from the structure of the nsp7-nsp8 hexadecamer. <i>Nature Structural and Molecular Biology</i> , 2005 , 12, 980-6	17.6	202
14	Structural basis for the specific recognition of RET by the Dok1 phosphotyrosine binding domain. <i>Journal of Biological Chemistry</i> , 2004 , 279, 4962-9	5.4	26

13	Expression, crystallization and preliminary X-ray studies of the recombinant PTB domain of mouse dok1 protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004 , 60, 334-6		2
12	Crystal structure of tabtoxin resistance protein complexed with acetyl coenzyme A reveals the mechanism for beta-lactam acetylation. <i>Journal of Molecular Biology</i> , 2003 , 325, 1019-30	6.5	46
11	Structure based hyperthermostability of archaeal histone HPhA from <i>Pyrococcus horikoshii</i> . <i>Journal of Molecular Biology</i> , 2003 , 325, 1031-7	6.5	17
10	Design and structure-based study of new potential FKBP12 inhibitors. <i>Biophysical Journal</i> , 2003 , 85, 3194-301	4.301	32
9	Site-directed mutagenesis and preliminary x-ray crystallographic studies of the tabtoxin resistance protein. <i>Protein and Peptide Letters</i> , 2003 , 10, 255-63	1.9	1
8	Crystallization and preliminary X-ray analysis of recombinant histone HPhA from the hyperthermophilic archaeon <i>Pyrococcus horikoshii</i> OT3. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002 , 58, 870-1		4
7	Determining the architecture of nuclear ring of <i>Xenopus laevis</i> nuclear pore complex using integrated approaches		1
6	8 Å structure of the cytoplasmic ring of the <i>Xenopus laevis</i> nuclear pore complex solved by cryo-EM and AI		1
5	8 Å structure of the nuclear ring of the <i>Xenopus laevis</i> nuclear pore complex solved by cryo-EM and AI		1
4	Cryo-EM structures reveal a conformational change of SOPA1 during mitochondrial inner membrane fusion		1
3	VHUT-cryo-FIB, a method to fabricate frozen-hydrated lamella of tissue specimen for in situ cryo-electron tomography		2
2	Inhibition of SARS-CoV-2 infection (previously 2019-nCoV) by a highly potent pan-coronavirus fusion inhibitor targeting its spike protein that harbors a high capacity to mediate membrane fusion		4
1	Large protein complex production using the SmartBac System - Strategies and Applications		2