

Fei Sun

List of Publications by Year in descending order

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138
papers

7,009
citations

94433

37
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66911

78
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155
all docs

155
docs citations

155
times ranked

12600
citing authors

#	ARTICLE	IF	CITATIONS
1	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, 13, 760-777.	11.0	23
2	Imaging biological samples by integrated differential phase contrast (iDPC) STEM technique. <i>Journal of Structural Biology</i> , 2022, 214, 107837.	2.8	13
3	Cryo-EM structure and electrophysiological characterization of ALMT from <i>Glycine max</i> reveal a previously uncharacterized class of anion channels. <i>Science Advances</i> , 2022, 8, eabm3238.	10.3	13
4	Novel cleavage sites identified in SARS-CoV-2 spike protein reveal mechanism for cathepsin L-facilitated viral infection and treatment strategies. <i>Cell Discovery</i> , 2022, 8, .	6.7	40
5	Structural insights into membrane remodeling by SNX1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	11
6	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.	2.9	3
7	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.	13.8	5
8	The Unusual Homodimer of a Heme-Copper Terminal Oxidase Allows Itself to Utilize Two Electron Donors. <i>Angewandte Chemie</i> , 2021, 133, 13435-13442.	2.0	0
9	Structures of human mGlu2 and mGlu7 homo- and heterodimers. <i>Nature</i> , 2021, 594, 589-593.	27.8	66
10	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.	17.1	38
11	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.	2.8	15
12	Cellular 3D-reconstruction and analysis in the human cerebral cortex using automatic serial sections. <i>Communications Biology</i> , 2021, 4, 1030.	4.4	6
13	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.	6.7	17
14	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, .	7.1	30
15	A cryo-electron microscopy support film formed by 2D crystals of hydrophobin HFBI. <i>Nature Communications</i> , 2021, 12, 7257.	12.8	23
16	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.	4.9	20
17	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.	2.0	4
18	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.	13.8	11

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19	Minireview of progress in the structural study of SARS-CoV-2 proteins. <i>Current Research in Microbial Sciences</i> , 2020, 1, 53-61.	2.3	43
20	Editorial overview: New insights into membrane protein machineries from technology revolution. <i>Current Opinion in Structural Biology</i> , 2020, 63, iii-v.	5.7	0
21	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.	2.9	33
22	Isolated Heme A Synthase from <i>Aquifex aeolicus</i> Is a Trimer. <i>MBio</i> , 2020, 11, .	4.1	6
23	Cryo-EM structures of the air-oxidized and dithionite-reduced photosynthetic alternative complex III from <i>Roseiflexus castenholzii</i> . <i>Science Advances</i> , 2020, 6, eaba2739.	10.3	10
24	Molecular mechanism of mitochondrial phosphatidate transfer by Ups1. <i>Communications Biology</i> , 2020, 3, 468.	4.4	6
25	A single-cell transcriptomic landscape of primate arterial aging. <i>Nature Communications</i> , 2020, 11, 2202.	12.8	95
26	Structural basis of G _s and G _i recognition by the human glucagon receptor. <i>Science</i> , 2020, 367, 1346-1352.	12.6	117
27	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.	12.0	1,083
28	Frontispiz: A 3.3-Å Resolution Structure of Hyperthermophilic Respiratory Complex III Reveals the Mechanism of Its Thermal Stability. <i>Angewandte Chemie</i> , 2020, 132, .	2.0	0
29	Frontispiece: 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, .	13.8	0
30	NLRP6 self-assembles into a linear molecular platform following LPS binding and ATP stimulation. <i>Scientific Reports</i> , 2020, 10, 198.	3.3	23
31	Cryo-EM structures of S-OPA1 reveal its interactions with membrane and changes upon nucleotide binding. <i>ELife</i> , 2020, 9, .	6.0	38
32	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.	4.1	15
33	ACAP1 assembles into an unusual protein lattice for membrane deformation through multiple stages. <i>PLoS Computational Biology</i> , 2019, 15, e1007081.	3.2	2
34	Synthetic Multienzyme Complexes, Catalytic Nanomachineries for Cascade Biosynthesis <i>In Vivo</i> . <i>ACS Nano</i> , 2019, 13, 9895-9906.	14.6	65
35	The late stage of COPI vesicle fission requires shorter forms of phosphatidic acid and diacylglycerol. <i>Nature Communications</i> , 2019, 10, 3409.	12.8	11
36	Cryo-EM Structure of Actin Filaments from <i>Zea mays</i> Pollen. <i>Plant Cell</i> , 2019, 31, 2855-2867.	6.6	18

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37	SmartBac, a new baculovirus system for large protein complex production. <i>Journal of Structural Biology</i> : X, 2019, 1, 100003.	1.3	14
38	Atlastin-1 regulates morphology and function of endoplasmic reticulum in dendrites. <i>Nature Communications</i> , 2019, 10, 568.	12.8	41
39	New interfaces on MiD51 for Drp1 recruitment and regulation. <i>PLoS ONE</i> , 2019, 14, e0211459.	2.5	15
40	Cryo-EM structure of the RC-LH core complex from an early branching photosynthetic prokaryote. <i>Nature Communications</i> , 2018, 9, 1568.	12.8	59
41	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.	1.6	3
42	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.	2.8	27
43	Thermodynamics of voltage-gated ion channels. <i>Biophysics Reports</i> , 2018, 4, 300-319.	0.8	22
44	In situ protein micro-crystal fabrication by cryo-FIB for electron diffraction. <i>Biophysics Reports</i> , 2018, 4, 339-347.	0.8	38
45	An electron transfer path connects subunits of a mycobacterial respiratory supercomplex. <i>Science</i> , 2018, 362, .	12.6	117
46	Orienting the future of bio-macromolecular electron microscopy. <i>Chinese Physics B</i> , 2018, 27, 063601.	1.4	14
47	Autogdeterm: automatic geometry determination for electron tomography. <i>Tsinghua Science and Technology</i> , 2018, 23, 369-376.	6.1	1
48	Molecular Details of the PH Domain of ACAP1^{BAR-PH} Protein Binding to PIP-Containing Membrane. <i>Journal of Physical Chemistry B</i> , 2017, 121, 3586-3596.	2.6	17
49	Structural Insight into the Specific DNA Template Binding to DnaG primase in Bacteria. <i>Scientific Reports</i> , 2017, 7, 659.	3.3	10
50	Molecular insights into the enzyme promiscuity of an aromatic prenyltransferase. <i>Nature Chemical Biology</i> , 2017, 13, 226-234.	8.0	100
51	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.	2.8	28
52	AuTom: A novel automatic platform for electron tomography reconstruction. <i>Journal of Structural Biology</i> , 2017, 199, 196-208.	2.8	25
53	Accelerating electron tomography reconstruction algorithm ICON with GPU. <i>Biophysics Reports</i> , 2017, 3, 36-42.	0.8	17
54	Determining the target protein localization in 3D using the combination of FIB-SEM and APEX2. <i>Biophysics Reports</i> , 2017, 3, 92-99.	0.8	14

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55	Crystal structure of E. coli apolipoprotein N-acyl transferase. Nature Communications, 2017, 8, 15948.	12.8	31
56	Using integrated correlative cryo-light and electron microscopy to directly observe syntaphilin-immobilized neuronal mitochondria in situ. Biophysics Reports, 2017, 3, 8-16.	0.8	12
57	A Fully Automatic Geometric Parameters Determining Method for Electron Tomography. Lecture Notes in Computer Science, 2017, , 385-389.	1.3	1
58	Accelerating Electron Tomography Reconstruction Algorithm ICON Using the Intel Xeon Phi Coprocessor on Tianhe-2 Supercomputer. Lecture Notes in Computer Science, 2017, , 258-269.	1.3	1
59	Fabrication of Frozen-Hydrated Sections by Focused Ion Beam(FIB) Method. Microscopy and Microanalysis, 2016, 22, 182-183.	0.4	0
60	An improved cryo-FIB method for fabrication of frozen hydrated lamella. Journal of Structural Biology, 2016, 194, 218-223.	2.8	42
61	Structural insights into Ca ²⁺ -activated long-range allosteric channel gating of RyR1. Cell Research, 2016, 26, 977-994.	12.0	84
62	Structural characterization of coatomer in its cytosolic state. Protein and Cell, 2016, 7, 586-600.	11.0	12
63	ICON: 3D reconstruction with "missing-information"™ restoration in biological electron tomography. Journal of Structural Biology, 2016, 195, 100-112.	2.8	75
64	Three-dimensional visualization of arsenic stimulated mouse liver sinusoidal by FIB-SEM approach. Protein and Cell, 2016, 7, 227-232.	11.0	2
65	FIRT: Filtered iterative reconstruction technique with information restoration. Journal of Structural Biology, 2016, 195, 49-61.	2.8	26
66	Crystal structure of E. coli lipoprotein diacylglyceryl transferase. Nature Communications, 2016, 7, 10198.	12.8	81
67	A local-optimization refinement algorithm in single particle analysis for macromolecular complex with multiple rigid modules. Protein and Cell, 2016, 7, 46-62.	11.0	13
68	Three-dimensional super-resolution protein localization correlated with vitrified cellular context. Scientific Reports, 2015, 5, 13017.	3.3	94
69	A novel fully automatic scheme for fiducial marker-based alignment in electron tomography. Journal of Structural Biology, 2015, 192, 403-417.	2.8	39
70	BrkAutoDisplay: functional display of multiple exogenous proteins on the surface of Escherichia coli by using BrkA autotransporter. Microbial Cell Factories, 2015, 14, 129.	4.0	9
71	Acyl-CoA Dehydrogenase Drives Heat Adaptation by Sequestering Fatty Acids. Cell, 2015, 161, 1152-1163.	28.9	105
72	A novel mitochondrial carrier protein Mme1 acts as a yeast mitochondrial magnesium exporter. Biochimica Et Biophysica Acta - Molecular Cell Research, 2015, 1853, 724-732.	4.1	19

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73	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, 889-894.	0.8	5
74	Dimerization Interface of 3-Hydroxyacyl-CoA Dehydrogenase Tunes the Formation of Its Catalytic Intermediate. <i>PLoS ONE</i> , 2014, 9, e95965.	2.5	10
75	Molecular insights into the membrane-associated phosphatidylinositol 4-kinase III β . <i>Nature Communications</i> , 2014, 5, 3552.	12.8	52
76	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, 596-599.	0.8	1
77	A marker-free automatic alignment method based on scale-invariant features. <i>Journal of Structural Biology</i> , 2014, 186, 167-180.	2.8	35
78	A PH Domain in ACAP1 Possesses Key Features of the BAR Domain in Promoting Membrane Curvature. <i>Developmental Cell</i> , 2014, 31, 73-86.	7.0	32
79	Identification of neurons responsible for feeding behavior in the <i>Drosophila</i> brain. <i>Science China Life Sciences</i> , 2014, 57, 391-402.	4.9	7
80	Puzzle out the regulation mechanism of PI4KIII β activity. <i>Science China Life Sciences</i> , 2014, 57, 636-638.	4.9	3
81	Cryo-EM structures of two bovine adenovirus type 3 intermediates. <i>Virology</i> , 2014, 450-451, 174-181.	2.4	31
82	C-terminal motif within Sec7 domain regulates guanine nucleotide exchange activity via tuning protein conformation. <i>Biochemical and Biophysical Research Communications</i> , 2014, 446, 380-386.	2.1	1
83	Flexible interwoven termini determine the thermal stability of thermosomes. <i>Protein and Cell</i> , 2013, 4, 432-444.	11.0	13
84	Revealing various coupling of electron transfer and proton pumping in mitochondrial respiratory chain. <i>Current Opinion in Structural Biology</i> , 2013, 23, 526-538.	5.7	35
85	A fast calculation strategy of density function in ISAF reconstruction algorithm. <i>Science China Information Sciences</i> , 2013, 56, 1-12.	4.3	4
86	Expression, purification and preliminary characterization of glucagon receptor extracellular domain. <i>Protein Expression and Purification</i> , 2013, 89, 232-240.	1.3	4
87	Identification of SERPINB1 As a Physiological Inhibitor of Human Granzyme H. <i>Journal of Immunology</i> , 2013, 190, 1319-1330.	0.8	31
88	MicroRNA-124 reduces caveolar density by targeting caveolin-1 in porcine kidney epithelial PK15 cells. <i>Molecular and Cellular Biochemistry</i> , 2013, 384, 213-219.	3.1	17
89	Structural Insights into the Intrinsic Self-Assembly of Par-3 N-Terminal Domain. <i>Structure</i> , 2013, 21, 997-1006.	3.3	34
90	Coexistence of ribbon and helical fibrils originating from hIAPP 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, 2798-2803.	7.1	104

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91	Atomic Model of Rabbit Hemorrhagic Disease Virus by Cryo-Electron Microscopy and Crystallography. PLoS Pathogens, 2013, 9, e1003132.	4.7	94
92	Purification, crystallization and preliminary crystallographic analysis of 3-hydroxyacyl-CoA dehydrogenase from <i>Caenorhabditis elegans</i> . Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 515-519.	0.7	1
93	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 α -crystallin domain. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120327.	4.0	18
94	Research of Mitochondrial Calcium Transportation. Sheng Wu Wu Li Hsueh Bao, 2013, 29, 167.	0.1	1
95	Electron Microscopy Reconstruction of Helical Assemblies. Sheng Wu Wu Li Hsueh Bao, 2013, 29, 879.	0.1	0
96	Interference microscopy volume illustration for biomedical data. , 2012, , .		0
97	The p53-induced Gene E124 Is an Essential Component of the Basal Autophagy Pathway. Journal of Biological Chemistry, 2012, 287, 42053-42063.	3.4	68
98	Mechanistic Insights into Regulated Cargo Binding by ACAP1 Protein. Journal of Biological Chemistry, 2012, 287, 28675-28685.	3.4	25
99	Structural Insights into the Substrate Specificity of Human Granzyme H: The Functional Roles of a Novel RKR Motif. Journal of Immunology, 2012, 188, 765-773.	0.8	19
100	Structural insights into the peroxidase activity and inactivation of human peroxiredoxin 4. Biochemical Journal, 2012, 441, 113-118.	3.7	77
101	The Intra-S Phase Checkpoint Targets Dna2 to Prevent Stalled Replication Forks from Reversing. Cell, 2012, 149, 1221-1232.	28.9	149
102	Cryo-EM structure of a transcribing cyovirus. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6118-6123.	7.1	52
103	Three-dimensional reconstruction using an adaptive simultaneous algebraic reconstruction technique in electron tomography. Journal of Structural Biology, 2011, 175, 277-287.	2.8	43
104	Single-particle reconstruction using L2-gradient flow. Journal of Structural Biology, 2011, 176, 259-267.	2.8	14
105	Autotransporter passenger domain secretion requires a hydrophobic cavity at the extracellular entrance of the β -domain pore. Biochemical Journal, 2011, 435, 577-587.	3.7	39
106	Thiabendazole inhibits ubiquinone reduction activity of mitochondrial respiratory complex II via a water molecule mediated binding feature. Protein and Cell, 2011, 2, 531-542.	11.0	45
107	Atomic model of a cyovirus built from cryo-EM structure provides insight into the mechanism of mRNA capping. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1373-1378.	7.1	65
108	A fast mapping method in the ISAF reconstruction algorithm. , 2011, 2011, 3930-3.		0

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109	Crystal Structure of a Novel Esterase Rv0045c from <i>Mycobacterium tuberculosis</i> . PLoS ONE, 2011, 6, e20506.	2.5	20
110	Substrate Binding Properties of Thermosome ATcpn ² From <i>Acidianus Tengchongensis</i> . Progress in Biochemistry and Biophysics, 2011, 38, 151-158.	0.3	1
111	Cryo-electron microscopy reconstructions of two types of wild rabbit hemorrhagic disease viruses characterized the structural features of Lagovirus. Protein and Cell, 2010, 1, 48-58.	11.0	27
112	Crystal Structure of Group II Chaperonin in the Open State. Structure, 2010, 18, 1270-1279.	3.3	38
113	Expression, purification and preliminary biochemical studies of the N-terminal domain of leucine-rich repeat kinase 2. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2010, 1804, 1780-1784.	2.3	10
114	Purification, crystallization and preliminary crystallographic analysis of very-long-chain acyl-CoA dehydrogenase from <i>Caenorhabditis elegans</i> . Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 426-430.	0.7	7
115	The Role and Structure of the Carboxyl-terminal Domain of the Human Voltage-gated Proton Channel Hv1. Journal of Biological Chemistry, 2010, 285, 12047-12054.	3.4	56
116	Secreted Monocytic miR-150 Enhances Targeted Endothelial Cell Migration. Molecular Cell, 2010, 39, 133-144.	9.7	1,059
117	Distinct symmetry and limited peptide refolding activity of the thermosomes from the acidothermophilic archaea <i>Acidianus tengchongensis</i> S5T. Biochemical and Biophysical Research Communications, 2010, 393, 228-234.	2.1	9
118	Five mutations in N-terminus confer thermostability on mesophilic xylanase. Biochemical and Biophysical Research Communications, 2010, 395, 200-206.	2.1	59
119	Prokaryotic Expression of Active Mitochondrial Uncoupling Protein 1*. Progress in Biochemistry and Biophysics, 2010, 37, 56-62.	0.3	4
120	Structural Basis for Proteolytic Specificity of the Human Apoptosis-Inducing Granzyme M. Journal of Immunology, 2009, 183, 421-429.	0.8	25
121	D Structural Investigation of Caveolae From Porcine Aorta Endothelial Cell by Electron Tomography*. Progress in Biochemistry and Biophysics, 2009, 2009, 729-735.	0.3	3
122	Crystal structure of human ERp44 shows a dynamic functional modulation by its carboxy-terminal tail. EMBO Reports, 2008, 9, 642-647.	4.5	66
123	Crystal structure and mutagenic analysis of GDOsp, a gentisate 1,2-dioxygenase from <i>Silicibacter pomeroyi</i> . Protein Science, 2008, 17, 1362-1373.	7.6	46
124	The Crystal Structure of Human Isopentenyl Diphosphate Isomerase at 1.7Å Resolution Reveals its Catalytic Mechanism in Isoprenoid Biosynthesis. Journal of Molecular Biology, 2007, 366, 1447-1458.	4.2	29
125	Preliminary molecular characterization and crystallization of mitochondrial respiratory complex II from porcine heart. FEBS Journal, 2007, 274, 1524-1529.	4.7	10
126	Crystal structure of the N-terminal SH3 domain of mouse PIX, p21-activated kinase-interacting exchange factor. Biochemical and Biophysical Research Communications, 2006, 339, 407-414.	2.1	8

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127	New Antiviral Target Revealed by the Hexameric Structure of Mouse Hepatitis Virus Nonstructural Protein nsp15. <i>Journal of Virology</i> , 2006, 80, 7909-7917.	3.4	85
128	Dodecamer Structure of Severe Acute Respiratory Syndrome Coronavirus Nonstructural Protein nsp10. <i>Journal of Virology</i> , 2006, 80, 7902-7908.	3.4	95
129	Insights into SARS-CoV transcription and replication from the structure of the nsp7â€“nsp8 hexadecamer. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 980-986.	8.2	255
130	Crystal Structure of Mitochondrial Respiratory Membrane Protein Complex II. <i>Cell</i> , 2005, 121, 1043-1057.	28.9	689
131	Structural Basis for the Specific Recognition of RET by the Dok1 Phosphotyrosine Binding Domain. <i>Journal of Biological Chemistry</i> , 2004, 279, 4962-4969.	3.4	32
132	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, 334-336.	2.5	2
133	Crystal Structure of Tabtoxin Resistance Protein Complexed with Acetyl Coenzyme A Reveals the Mechanism for Î²-Lactam Acetylation. <i>Journal of Molecular Biology</i> , 2003, 325, 1019-1030.	4.2	46
134	Structure Based Hyperthermostability of Archaeal Histone HPhA from <i>Pyrococcus horikoshii</i> . <i>Journal of Molecular Biology</i> , 2003, 325, 1031-1037.	4.2	18
135	Design and Structure-Based Study of New Potential FKBP12 Inhibitors. <i>Biophysical Journal</i> , 2003, 85, 3194-3201.	0.5	37
136	Site-Directed Mutagenesis and Preliminary X-Ray Crystallographic Studies of the Tabtoxin Resistance Protein. <i>Protein and Peptide Letters</i> , 2003, 10, 255-263.	0.9	1
137	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, 870-871.	2.5	4
138	Developing Graphene Grids for Cryoelectron Microscopy. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	3.5	3