

Jan Pieter Abrahams

List of Publications by Year in descending order

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136
papers

10,721
citations

61984

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31849

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144
all docs

144
docs citations

144
times ranked

10001
citing authors

#	ARTICLE	IF	CITATIONS
1	Statistically correcting dynamical electron scattering improves the refinement of protein nanocrystals, including charge refinement of coordinated metals. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 75-85.	2.3	8
2	Fabrication of low aspect ratio three-element Boersch phase shifters for voltage-controlled three electron beam interference. <i>Journal of Applied Physics</i> , 2020, 128, 134502.	2.5	7
3	2D Crystal Engineering of Nanosheets Assembled from Helical Peptide Building Blocks. <i>Angewandte Chemie</i> , 2019, 131, 13641-13646.	2.0	11
4	3D Electron Diffraction: The Nanocrystallography Revolution. <i>ACS Central Science</i> , 2019, 5, 1315-1329.	11.3	286
5	2D Crystal Engineering of Nanosheets Assembled from Helical Peptide Building Blocks. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 13507-13512.	13.8	39
6	Supramolecular architectures of molecularly thin yet robust free-standing layers. <i>Science Advances</i> , 2019, 5, eaav4489.	10.3	9
7	The wild-type flagellar filament of the Firmicute <i>Kurthia</i> at 2.8 Å resolution in vivo. <i>Scientific Reports</i> , 2019, 9, 14948.	3.3	12
8	Seeded Heteroepitaxial Growth of Crystallizable Collagen Triple Helices: Engineering Multifunctional Two-Dimensional Core-Shell Nanostructures. <i>Journal of the American Chemical Society</i> , 2019, 141, 20107-20117.	13.7	42
9	Inelastic scattering and solvent scattering reduce dynamical diffraction in biological crystals. <i>Acta Crystallographica Section B: Structural Science, Crystal Engineering and Materials</i> , 2019, 75, 523-531.	1.1	30
10	Reducing dynamical electron scattering reveals hydrogen atoms. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2019, 75, 82-93.	0.1	50
11	The Neuronal Tau Protein Blocks <i>in Vitro</i> Fibrillation of the Amyloid- β (A β) Peptide at the Oligomeric Stage. <i>Journal of the American Chemical Society</i> , 2018, 140, 8138-8146.	13.7	49
12	Electron diffraction and three-dimensional crystallography for structural biology. <i>Crystallography Reviews</i> , 2018, 24, 176-204.	1.5	43
13	Electron diffraction data processing with <i>DIALS</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 506-518.	2.3	103
14	A Molecular Level Approach To Elucidate the Supramolecular Packing of Light-Harvesting Antenna Systems. <i>Chemistry - A European Journal</i> , 2018, 24, 14989-14993.	3.3	3
15	Electron crystallography with the EIGER detector. <i>IUCr</i> , 2018, 5, 190-199.	2.2	33
16	Purification of Biotinylated Proteins Using Single Walled Carbon Nanotube-Streptavidin Complexes. <i>Journal of Nanoscience and Nanotechnology</i> , 2017, 17, 926-931.	0.9	0
17	A Novel Capturing Method for Quantification of Extra-Cellular Nanovesicles. <i>Journal of Nanoscience and Nanotechnology</i> , 2017, 17, 908-913.	0.9	2
18	Protein structure determination by electron diffraction using a single three-dimensional nanocrystal. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 738-748.	2.3	85

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19	Testing and Comparison of Imaging Detectors for Electrons in the Energy Range 10–20 keV. <i>Journal of Instrumentation</i> , 2017, 12, C11016-C11016.	1.2	2
20	Neutravidin-Mediated Extraction of Isolated Small Diameter Single Walled Carbon Nanotubes for Bio-Recognition. <i>Journal of Nanoscience and Nanotechnology</i> , 2017, 17, 3588-3596.	0.9	1
21	Specific Binding of Cu(II) Ions to Amyloid-Beta Peptides Bound to Aggregation-Inhibiting Molecules or SDS Micelles Creates Complexes that Generate Radical Oxygen Species. <i>Journal of Alzheimer's Disease</i> , 2016, 54, 971-982.	2.6	34
22	Characterization of Mn(II) ion binding to the amyloid- β peptide in Alzheimer's disease. <i>Journal of Trace Elements in Medicine and Biology</i> , 2016, 38, 183-193.	3.0	60
23	<i>Ab initio</i> structure determination of nanocrystals of organic pharmaceutical compounds by electron diffraction at room temperature using a Timepix quantum area direct electron detector. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2016, 72, 236-242.	0.1	127
24	Cross-interactions between the Alzheimer Disease Amyloid- β Peptide and Other Amyloid Proteins: A Further Aspect of the Amyloid Cascade Hypothesis. <i>Journal of Biological Chemistry</i> , 2016, 291, 16485-16493.	3.4	117
25	Reciprocal Molecular Interactions between the $A\beta$ Peptide Linked to Alzheimer's Disease and Insulin Linked to Diabetes Mellitus Type II. <i>ACS Chemical Neuroscience</i> , 2016, 7, 269-274.	3.5	37
26	Lattice filter for processing image data of three-dimensional protein nanocrystals. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 34-39.	2.3	9
27	A posteriori correction of camera characteristics from large image data sets. <i>Scientific Reports</i> , 2015, 5, 10317.	3.3	22
28	Cyclic Peptides as Inhibitors of Amyloid Fibrillation. <i>Chemistry - A European Journal</i> , 2014, 20, 2410-2419.	3.3	44
29	The $A\beta$ peptide forms non-amyloid fibrils in the presence of carbon nanotubes. <i>Nanoscale</i> , 2014, 6, 6720-6726.	5.6	43
30	Additions and corrections for <i>Journal of Materials Chemistry B</i> published 11th November 2013 to 10th June 2014. <i>Journal of Materials Chemistry B</i> , 2014, 2, 5478.	5.8	1
31	Endogenous Polyamines Reduce the Toxicity of Soluble $A\beta$ Peptide Aggregates Associated with Alzheimer's Disease. <i>Biomacromolecules</i> , 2014, 15, 1985-1991.	5.4	30
32	Alzheimer Peptides Aggregate into Transient Nanoglobules That Nucleate Fibrils. <i>Biochemistry</i> , 2014, 53, 6302-6308.	2.5	32
33	The hairpin conformation of the amyloid β peptide is an important structural motif along the aggregation pathway. <i>Journal of Biological Inorganic Chemistry</i> , 2014, 19, 623-634.	2.6	88
34	Non-chaperone Proteins Can Inhibit Aggregation and Cytotoxicity of Alzheimer Amyloid β Peptide. <i>Journal of Biological Chemistry</i> , 2014, 289, 27766-27775.	3.4	53
35	Capture of unstable protein complex on the streptavidin-coated single-walled carbon nanotubes. <i>Journal of Nanoparticle Research</i> , 2013, 15, 1.	1.9	1
36	Inhibiting and Reversing Amyloid- β Peptide (1–40) Fibril Formation with Gramicidin-S and Engineered Analogues. <i>Chemistry - A European Journal</i> , 2013, 19, 17338-17348.	3.3	39

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37	Visualizing the localization of transfection complexes during graphene nanoparticle-based transfection. <i>Journal of Materials Chemistry B</i> , 2013, 1, 6353.	5.8	2
38	Cellular Polyamines Promote Amyloid-Beta (A β) Peptide Fibrillation and Modulate the Aggregation Pathways. <i>ACS Chemical Neuroscience</i> , 2013, 4, 454-462.	3.5	89
39	Human lysozyme inhibits the in vitro aggregation of A β peptides, which in vivo are associated with Alzheimer's disease. <i>Chemical Communications</i> , 2013, 49, 6507.	4.1	44
40	An efficient nanolitre-volume multi-channel device for highly viscous materials used in membrane protein crystallization. <i>Journal of Applied Crystallography</i> , 2013, 46, 829-831.	4.5	0
41	A Medipix quantum area detector allows rotation electron diffraction data collection from submicrometre three-dimensional protein crystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1223-1230.	2.5	143
42	Imaging protein three-dimensional nanocrystals with cryo-EM. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 852-859.	2.5	33
43	Ultra-small graphene oxide functionalized with polyethylenimine (PEI) for very efficient gene delivery in cell and zebrafish embryos. <i>Nano Research</i> , 2012, 5, 703-709.	10.4	79
44	Single-Walled Carbon Nanotubes as Scaffolds to Concentrate DNA for the Study of DNA-Protein Interactions. <i>ChemPhysChem</i> , 2012, 13, 1569-1575.	2.1	3
45	Characterisation of a counting imaging detector for electron detection in the energy range 10-20keV. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 2012, 681, 21-24.	1.6	6
46	Structure of a post-translationally processed heterodimeric double-headed Kunitz-type serine protease inhibitor from potato. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 794-799.	2.5	22
47	A Straightforward and Robust Method for Introducing Human Hair as a Nucleant into High Throughput Crystallization Trials. <i>Crystal Growth and Design</i> , 2011, 11, 1170-1176.	3.0	15
48	Image Processing and Lattice Determination for Three-Dimensional Nanocrystals. <i>Microscopy and Microanalysis</i> , 2011, 17, 879-885.	0.4	10
49	Evaluation of Medipix2 detector for recording electron diffraction data in low dose conditions. <i>Journal of Instrumentation</i> , 2011, 6, C01033-C01033.	1.2	21
50	<i>EDIFF</i>: a program for automated unit-cell determination and indexing of electron diffraction data. <i>Journal of Applied Crystallography</i> , 2011, 44, 1132-1136.	4.5	9
51	Recent advances in the <i>CRANK</i> software suite for experimental phasing. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 331-337.	2.5	87
52	â€œ4D Biology for health and diseaseâ€•workshop report. <i>New Biotechnology</i> , 2011, 28, 291-293.	4.4	2
53	Low energy electron microscopy imaging using Medipix2 detector. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 2011, 633, S239-S242.	1.6	15
54	A Graphene Oxide-Streptavidin Complex for Biorecognition â€• Towards Affinity Purification. <i>Advanced Functional Materials</i> , 2010, 20, 2857-2865.	14.9	63

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55	A novel approximation method of CTF amplitude correction for 3D single particle reconstruction. <i>Ultramicroscopy</i> , 2010, 110, 350-358.	1.9	8
56	Stable Single-Walled Carbon Nanotube-Streptavidin Complex for Biorecognition. <i>Journal of Physical Chemistry C</i> , 2010, 114, 4345-4352.	3.1	25
57	The strong phase object approximation may allow extending crystallographic phases of dynamical electron diffraction patterns of 3D protein nano-crystals. <i>Zeitschrift für Kristallographie</i> , 2010, 225, 67-76.	1.1	7
58	IMPROVED IMAGING IN LOW ENERGY ELECTRON MICROSCOPY AND PHOTO EMISSION ELECTRON MICROSCOPY USING MEDIPIX2 PIXEL DETECTOR. , 2010, , .		0
59	An Intelligent Peak Search Program for Digital Electron Diffraction Images of 3D Nano-Crystals. , 2009, , .		3
60	Mammalian Navigators are microtubule plus-end tracking proteins that can reorganize the cytoskeleton to induce neurite-like extensions. <i>Cytoskeleton</i> , 2009, 66, 824-838.	4.4	49
61	Characterization of a diagnostic Fab fragment binding trimeric Lewis X. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 439-447.	2.6	10
62	Involvement of a carboxylated lysine in UV damage endonuclease. <i>Protein Science</i> , 2009, 18, 549-558.	7.6	4
63	Unit-cell determination from randomly oriented electron-diffraction patterns. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 625-632.	2.5	28
64	The Max-Inf2/Lorentz Center workshop on New algorithms in macromolecular crystallography and electron microscopy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 623-624.	2.5	0
65	Medipix 2 detector applied to low energy electron microscopy. <i>Ultramicroscopy</i> , 2009, 110, 33-35.	1.9	40
66	Recycling of Aborted Ribosomal 50S Subunit-Nascent Chain-tRNA Complexes by the Heat Shock Protein Hsp15. <i>Journal of Molecular Biology</i> , 2009, 386, 1357-1367.	4.2	38
67	Crystal Structure of Chlorite Dismutase, a Detoxifying Enzyme Producing Molecular Oxygen. <i>Journal of Molecular Biology</i> , 2009, 387, 192-206.	4.2	68
68	Recent advances in CRANK. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2009, 65, s160-s160.	0.3	0
69	Macromolecular electron crystallography. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2009, 65, s7-s7.	0.3	0
70	Cloning, expression, purification, crystallization and preliminary X-ray diffraction analysis of chlorite dismutase: a detoxifying enzyme producing molecular oxygen. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 730-732.	0.7	7
71	Microtubule Plus-End Conformations and Dynamics in the Periphery of Interphase Mouse Fibroblasts. <i>Molecular Biology of the Cell</i> , 2008, 19, 3138-3146.	2.1	28
72	Cyclops: New modular software suite for cryo-EM. <i>Journal of Structural Biology</i> , 2007, 157, 19-27.	2.8	12

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73	Heterogeneous nucleation of three-dimensional protein nanocrystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 564-570.	2.5	52
74	Crystal Structure of the DNA Repair Enzyme Ultraviolet Damage Endonuclease. <i>Structure</i> , 2007, 15, 1316-1324.	3.3	22
75	Phase refinement through density modification. , 2007, , 143-154.		0
76	The Impact of Single Amino Acid Substitutions in CD3 β on the CD3 β Interaction and T-Cell Receptor α CD3 Complex Formation. <i>Human Immunology</i> , 2006, 67, 579-588.	2.4	9
77	Structure of the E. coli signal recognition particle bound to a translating ribosome. <i>Nature</i> , 2006, 444, 503-506.	27.8	126
78	Nano-dispensing by electrospray for biotechnology. <i>Biotechnology Journal</i> , 2006, 1, 969-975.	3.5	23
79	Protein Nanocrystallization. , 2006, , 1-25.		2
80	The protein structure of recombinant human lactoferrin produced in the milk of transgenic cows closely matches the structure of human milk-derived lactoferrin. <i>Transgenic Research</i> , 2005, 14, 397-405.	2.4	37
81	Relevance of Apoptin's Integrity for Its Functional Behavior. <i>Journal of Virology</i> , 2005, 79, 1337-1338.	3.4	34
82	Structure of an Anti-Lewis X Fab Fragment in Complex with Its Lewis X Antigen. <i>Structure</i> , 2004, 12, 1227-1236.	3.3	48
83	Crank. <i>Structure</i> , 2004, 12, 1753-1761.	3.3	115
84	Crystallization and preliminary X-ray crystallographic studies on a Kunitz-type potato serine protease inhibitor. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1464-1466.	2.5	1
85	TYSON: Robust searching, sorting, and selecting of single particles in electron micrographs. <i>Journal of Structural Biology</i> , 2004, 145, 76-83.	2.8	14
86	Apoptin's functional N- and C-termini independently bind DNA. <i>FEBS Letters</i> , 2004, 557, 155-158.	2.8	24
87	Crystal Structure of an Empty Capsid of Turnip Yellow Mosaic Virus. <i>Journal of Molecular Biology</i> , 2004, 341, 1205-1214.	4.2	22
88	Effect of reactive site loop elongation on the inhibitory activity of C1-inhibitor. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2004, 1699, 139-144.	2.3	3
89	Mechanism of Thrombin's Enigmatic Sodium Switch Revealed. <i>Structure</i> , 2003, 11, 363-364.	3.3	3
90	Prevalent conformations and subunit exchange in the biologically active apoptin protein multimer. <i>FEBS Journal</i> , 2003, 270, 3619-3627.	0.2	9

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91	Crystallization and preliminary X-ray analysis of an anti-LewisX Fab fragment with and without its LewisX antigen. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1306-1309.	2.5	5
92	ATP-induced conformational changes of the nucleotide-binding domain of Na,K-ATPase. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 468-474.	8.2	97
93	Area detectors in structural biology. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 2003, 509, 274-282.	1.6	9
94	Importance of Nuclear Localization of Apoptin for Tumor-specific Induction of Apoptosis. <i>Journal of Biological Chemistry</i> , 2003, 278, 27729-27736.	3.4	123
95	Structure of \hat{I}^2 -Antithrombin and the Effect of Glycosylation on Antithrombin's Heparin Affinity and Activity. <i>Journal of Molecular Biology</i> , 2003, 326, 823-833.	4.2	121
96	The Structure of the Receptor-binding Domain of the Bacteriophage T4 Short Tail Fibre Reveals a Knitted Trimeric Metal-binding Fold. <i>Journal of Molecular Biology</i> , 2003, 331, 361-373.	4.2	108
97	Visualization by Cryo-electron Microscopy of Genomic RNA that Binds to the Protein Capsid Inside Bacteriophage MS2. <i>Journal of Molecular Biology</i> , 2003, 332, 415-422.	4.2	52
98	Recombinant apoptin multimers kill tumor cells but are nontoxic and epitope-shielded in a normal-cell-specific fashion. <i>Experimental Cell Research</i> , 2003, 289, 36-46.	2.6	51
99	Apoptin Induces Tumor-specific Apoptosis as a Globular Multimer. <i>Journal of Biological Chemistry</i> , 2003, 278, 9042-9051.	3.4	56
100	Apoptin protein multimers form distinct higher-order nucleoprotein complexes with DNA. <i>Nucleic Acids Research</i> , 2003, 31, 4805-4813.	14.5	36
101	The Functional Integrity of the Serpin Domain of C1-inhibitor Depends on the Unique N-terminal Domain, as Revealed by a Pathological Mutant. <i>Journal of Biological Chemistry</i> , 2003, 278, 29463-29470.	3.4	39
102	X-Ray Crystallographic Structure Determination of Large Asymmetric Macromolecular Assemblies. <i>Methods in Enzymology</i> , 2003, 374, 163-188.	1.0	9
103	Structural and Functional Aspects of C1-Inhibitor. <i>Immunobiology</i> , 2002, 205, 518-533.	1.9	62
104	A novel pH-dependent dimerization motif in \hat{I}^2 -lactoglobulin from pig (<i>Sus scrofa</i>). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 480-486.	2.5	23
105	Screening crystallisation conditions using fluorescence correlation spectroscopy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1536-1541.	2.5	3
106	The prospects of protein nanocrystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1901-1906.	2.5	42
107	Protein nano-crystallogenesis. <i>Enzyme and Microbial Technology</i> , 2002, 30, 262-265.	3.2	10
108	Structure elucidation of \hat{I}^2 -mannanase: from the electron-density map to the DNA sequence. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 37-43.	2.5	7

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109	Matrix methods for solving protein substructures of chlorine and sulfur from anomalous data. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1857-1862.	2.5	39
110	Crystal structure of the C-terminal SH2 domain of the p85 $\hat{1}\pm$ regulatory subunit of phosphoinositide 3-kinase: an SH2 domain mimicking its own substrate. Journal of Molecular Biology, 1999, 292, 763-770.	4.2	31
111	The structure of bovine mitochondrial F1-ATPase: an example of rotary catalysis. Biochemical Society Transactions, 1999, 27, 37-42.	3.4	31
112	P3 2.6 ?? Structure of beta antithrombin and complete structure of latent antithrombin. Blood Coagulation and Fibrinolysis, 1999, 10, 538.	1.0	0
113	New developments in phase refinement. Current Opinion in Structural Biology, 1998, 8, 601-605.	5.7	15
114	Wild-type $\hat{1}\pm$ -antitrypsin is in the canonical inhibitory conformation. Journal of Molecular Biology, 1998, 275, 419-425.	4.2	138
115	Implications for function and therapy of a 2.9 Å structure of binary-complexed antithrombin. Journal of Molecular Biology, 1998, 283, 9-14.	4.2	99
116	The anticoagulant activation of antithrombin by heparin. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 14683-14688.	7.1	683
117	The 2.6 Å... structure of antithrombin indicates a conformational change at the heparin binding site 1 Edited by R. Huber. Journal of Molecular Biology, 1997, 266, 601-609.	4.2	188
118	The crystal structure of the nucleotide-free $\hat{1}\pm 3\hat{1}^2 3$ subcomplex of F1-ATPase from the thermophilic Bacillus PS3 is a symmetric trimer. Structure, 1997, 5, 825-836.	3.3	241
119	Bias Reduction in Phase Refinement by Modified Interference Functions: Introducing the $\hat{1}^3$ Correction. Acta Crystallographica Section D: Biological Crystallography, 1997, 53, 371-376.	2.5	58
120	Improved diffraction of antithrombin crystals grown in microgravity. Acta Crystallographica Section D: Biological Crystallography, 1997, 53, 622-625.	2.5	12
121	The structure of bovine F1-ATPase complexed with the peptide antibiotic efrapeptin.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 9420-9424.	7.1	148
122	The structure of bovine F1-ATPase complexed with the antibiotic inhibitor aurovertin B.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 6913-6917.	7.1	173
123	Methods used in the structure determination of bovine mitochondrial F1 ATPase. Acta Crystallographica Section D: Biological Crystallography, 1996, 52, 30-42.	2.5	999
124	Inhibitory conformation of the reactive loop of $\hat{1}\pm$ -antitrypsin. Nature Structural and Molecular Biology, 1996, 3, 676-681.	8.2	240
125	Structure at 2.8 Å, resolution of F1-ATPase from bovine heart mitochondria. Nature, 1994, 370, 621-628.	27.8	3,138
126	Crystallization of F1-ATPase from Bovine Heart Mitochondria. Journal of Molecular Biology, 1993, 229, 787-790.	4.2	75

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127	Crystallization and Preliminary X-ray Diffraction Analysis of Two Conformations of Intact Human Antithrombin. <i>Journal of Molecular Biology</i> , 1993, 234, 1253-1258.	4.2	22
128	Porting and optimising star. <i>APL Quote Quad</i> , 1992, 23, 265-274.	0.1	0
129	Kirromycin drastically reduces the affinity of <i>Escherichia coli</i> elongation factor Tu for aminoacyl-tRNA. <i>Biochemistry</i> , 1991, 30, 6705-6710.	2.5	27
130	The influence of tRNA located at the P-site on the turnover of EF-Tu-GTP on ribosomes. <i>Biochimie</i> , 1991, 73, 1089-1092.	2.6	4
131	Isolation and stability of ternary complexes of elongation factor Tu, GTP and aminoacyl-tRNA. <i>Nucleic Acids Research</i> , 1991, 19, 553-556.	14.5	10
132	Prediction of RNA secondary structure, including pseudoknotting, by computer simulation. <i>Nucleic Acids Research</i> , 1990, 18, 3035-3035.	14.5	229
133	The interaction between aminoacyl-tRNA and the mutant elongation factors Tu AR and B0. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1990, 1050, 226-229.	2.4	4
134	Effects of Kirromycin on the Elongation Factor EF-Tu and its Interactions with GDP or GTP and tRNA. The Application of zone-Interference Gel Electrophoresis, a New Method for the Analysis of Weak Complexes. , 1989, , 121-129.		2
135	Zone-interference gel electrophoresis: a new method for studying weak protein-nucleic acid complexes under native equilibrium conditions. <i>Nucleic Acids Research</i> , 1988, 16, 10099-10108.	14.5	33
136	Five pseudoknots are present at the 204 nucleotides long 3' noncoding region of tobacco mosaic virus RNA. <i>Nucleic Acids Research</i> , 1985, 13, 7673-7686.	14.5	150