

# Mark J Van Raaij

## List of Publications by Year in descending order

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122  
papers

4,339  
citations

109321

35  
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118850

62  
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127  
all docs

127  
docs citations

127  
times ranked

4188  
citing authors

#	ARTICLE	IF	CITATIONS
1	Monomodular <i>Pseudomonas aeruginosa</i> phage JG004 lysozyme (Pae87) contains a bacterial surface-active antimicrobial peptide-like region and a possible substrate-binding subdomain. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 435-454.	2.3	7
2	Submission of structural biology data for review purposes. <i>IUCrJ</i> , 2022, 9, 1-2.	2.2	3
3	Structure and Function of Bacteriophages. , 2021, , 19-91.		6
4	Bacteriophage Tail Fibres, Tailspikes, and Bacterial Receptor Interaction. , 2021, , 194-205.		1
5	Topical Reviews in <i>Acta Crystallographica F Structural Biology Communications</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021, 77, 385-385.	0.8	0
6	Submission of structural biology data for review purposes. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021, 77, 435-436.	0.8	0
7	Submission of structural biology data for review purposes. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1477-1478.	2.3	1
8	Self-immolation of a Bacterial Dehydratase Enzyme by its Epoxide Product. <i>Chemistry - A European Journal</i> , 2020, 26, 8035-8044.	3.3	2
9	Innovation versus practice in biological crystallization. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 290-291.	0.8	0
10	Contamination or serendipity “doing the wrong thing by chance. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 391-391.	0.8	0
11	Hydroxylammonium derivatives for selective active-site lysine modification in the anti-virulence bacterial target DHQ1 enzyme. <i>Organic Chemistry Frontiers</i> , 2019, 6, 3127-3135.	4.5	4
12	Still Something to Discover: Novel Insights into Escherichia coli Phage Diversity and Taxonomy. <i>Viruses</i> , 2019, 11, 454.	3.3	77
13	Molecular anatomy of the receptor binding module of a bacteriophage long tail fiber. <i>PLoS Pathogens</i> , 2019, 15, e1008193.	4.7	38
14	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. <i>Journal of Applied Crystallography</i> , 2019, 52, 495-497.	4.5	1
15	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. <i>IUCrJ</i> , 2019, 6, 341-343.	2.2	8
16	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 321-323.	0.8	3
17	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 455-457.	2.3	10
18	Structure and Function of Bacteriophages. , 2019, , 1-73.		3

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19	Acta Crystallographica Section F “another home for cryo-electron microscopy contributions. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 1-2.	0.8	1
20	Welcoming Janet Newman with a BLAST on crystallization strategy. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 147-147.	0.8	0
21	Introducing Methods Communications, a new category of contributions to Acta Crystallographica F. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 529-530.	0.8	0
22	Taking biological structure communications into the third dimension. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 663-664.	0.8	0
23	Contractile injection systems of bacteriophages and related systems. Molecular Microbiology, 2018, 108, 6-15.	2.5	119
24	Bacteriophage T4 long tail fiber domains. Biophysical Reviews, 2018, 10, 463-471.	3.2	47
25	Target highlights from the first post-PSI CASP experiment (CASP12, May-August 2016). Proteins: Structure, Function and Bioinformatics, 2018, 86, 27-50.	2.6	11
26	The so far farthest reaches of the double jelly roll capsid protein fold. Virology Journal, 2018, 15, 181.	3.4	17
27	Carbohydrate structure hits the groove. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 441-442.	0.8	0
28	A novel amyloid designable scaffold and potential inhibitor inspired by <sc>GAIIG</sc> of amyloid beta and the <sc>HIV</sc> V3 loop. FEBS Letters, 2018, 592, 1777-1788.	2.8	18
29	Structure and N-acetylglucosamine binding of the distal domain of mouse adenovirus 2 fibre. Journal of General Virology, 2018, 99, 1494-1508.	2.9	8
30	Quo vadis, Acta Crystallographica F?. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 688-689.	0.8	0
31	Structure of a Reptilian Adenovirus Reveals a Phage Tailspike Fold Stabilizing a Vertebrate Virus Capsid. Structure, 2017, 25, 1562-1573.e5.	3.3	19
32	Crystal Structure of the Carboxy-Terminal Region of the Bacteriophage T4 Proximal Long Tail Fiber Protein Gp34. Viruses, 2017, 9, 168.	3.3	24
33	Some of the most interesting <sc>CASP</sc>11 targets through the eyes of their authors. Proteins: Structure, Function and Bioinformatics, 2016, 84, 34-50.	2.6	16
34	Fasciola hepatica calcium-binding protein FhCaBP2: structure of the dynein light chain-like domain. Parasitology Research, 2016, 115, 2879-2886.	1.6	7
35	Crystal structure of raptor adenovirus 1 fibre head and role of the beta-hairpin in siadenovirus fibre head domains. Virology Journal, 2016, 13, 106.	3.4	6
36	Characterization of a Bacteriophage-Derived Murein Peptidase for Elimination of Antibiotic-Resistant Staphylococcus aureus. Current Protein and Peptide Science, 2016, 17, 183-190.	1.4	20

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37	Crystal structure of the fibre head domain of bovine adenovirus 4, a ruminant atadenovirus. <i>Virology Journal</i> , 2015, 12, 81.	3.4	6
38	Structure of the Receptor-Binding Carboxy-Terminal Domain of the Bacteriophage T5 L-Shaped Tail Fibre with and without Its Intra-Molecular Chaperone. <i>Viruses</i> , 2015, 7, 6424-6440.	3.3	46
39	Structure and Sialyllactose Binding of the Carboxy-Terminal Head Domain of the Fibre from a Siadenovirus, Turkey Adenovirus 3. <i>PLoS ONE</i> , 2015, 10, e0139339.	2.5	25
40	Conformational Changes Leading to T7 DNA Delivery upon Interaction with the Bacterial Receptor. <i>Journal of Biological Chemistry</i> , 2015, 290, 10038-10044.	3.4	57
41	Chemical Modification of a Dehydratase Enzyme Involved in Bacterial Virulence by an Ammonium Derivative: Evidence of its Active Site Covalent Adduct. <i>Journal of the American Chemical Society</i> , 2015, 137, 9333-9343.	13.7	12
42	Irreversible covalent modification of type I dehydroquinase with a stable Schiff base. <i>Organic and Biomolecular Chemistry</i> , 2015, 13, 706-716.	2.8	8
43	Interplay between the mechanics of bacteriophage fibers and the strength of virus-host links. <i>Physical Review E</i> , 2014, 89, 052710.	2.1	9
44	Crystallization of the carboxy-terminal region of the bacteriophage T4 proximal long tail fibre protein gp34. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 970-975.	0.8	4
45	Exploring the Water-Binding Pocket of the Type II Dehydroquinase Enzyme in the Structure-Based Design of Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2014, 57, 3494-3510.	6.4	8
46	Molecular Characterization of a Lizard Adenovirus Reveals the First Atadenovirus with Two Fiber Genes and the First Adenovirus with Either One Short or Three Long Fibers per Penton. <i>Journal of Virology</i> , 2014, 88, 11304-11314.	3.4	36
47	Challenging the state of the art in protein structure prediction: Highlights of experimental target structures for the 10th Critical Assessment of Techniques for Protein Structure Prediction Experiment CASP10. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 26-42.	2.6	53
48	Insights into substrate binding and catalysis in bacterial type I dehydroquinase. <i>Biochemical Journal</i> , 2014, 462, 415-424.	3.7	8
49	Crystal structure of the lytic CHAPK domain of the endolysin LysK from <i>Staphylococcus aureus</i> bacteriophage K. <i>Virology Journal</i> , 2014, 11, 133.	3.4	47
50	Crystal Structure of the Fibre Head Domain of the Atadenovirus Snake Adenovirus 1. <i>PLoS ONE</i> , 2014, 9, e114373.	2.5	16
51	<i>Mycobacterium tuberculosis</i> Shikimate Kinase Inhibitors: Design and Simulation Studies of the Catalytic Turnover. <i>Journal of the American Chemical Society</i> , 2013, 135, 12366-12376.	13.7	51
52	Crystallization of the CHAP domain of the endolysin from <i>Staphylococcus aureus</i> bacteriophage K. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1393-1396.	0.7	14
53	Structural Characterization of the Bacteriophage T7 Tail Machinery. <i>Journal of Biological Chemistry</i> , 2013, 288, 26290-26299.	3.4	75
54	Mechanistic Basis of the Inhibition of Type II Dehydroquinase by (2 <i>S</i> )- and (2 <i>R</i> )-2-Benzyl-3-dehydroquinic Acids. <i>ACS Chemical Biology</i> , 2013, 8, 568-577.	3.4	11

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55	Crystallization of the C-terminal domain of the bacteriophage T5 L-shaped fibre. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1363-1367.	0.7	4
56	Design, Synthesis, and Structural Analysis of Turn Modified $\beta$ -Cyclodextrin-( $\beta$ -Cyclodextrin) <sub>2</sub> Peptide Derivatives toward Crystalline Hexagon-Shaped Cationic Nanochannel Assemblies. <i>Crystal Growth and Design</i> , 2013, 13, 4355-4367.	3.0	6
57	Crystallization of the C-terminal domain of the fibre protein from snake adenovirus 1, an atadenovirus. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1374-1379.	0.7	5
58	Bacteriophage Receptor Recognition and Nucleic Acid Transfer. <i>Sub-Cellular Biochemistry</i> , 2013, 68, 489-518.	2.4	18
59	Crystallization of the C-terminal head domain of the fibre protein from a siadenovirus, turkey adenovirus 3. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1135-1139.	0.7	7
60	High-resolution structures of <i>Thermus thermophilus</i> enoyl-acyl carrier protein reductase in the apo form, in complex with NAD <sup>+</sup> and in complex with NAD <sup>+</sup> and triclosan. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1139-1148.	0.7	7
61	$\beta$ -Inverted analogs of the antibiotic gramicidin S with an improved biological profile. <i>Bioorganic and Medicinal Chemistry</i> , 2012, 20, 6059-6062.	3.0	8
62	Crystallization of the C-terminal domain of the bacteriophage T7 fibre protein gp17. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 166-171.	0.7	11
63	Structure of the receptor-binding carboxy-terminal domain of bacteriophage T7 tail fibers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 9390-9395.	7.1	95
64	Design, synthesis and structural analysis of mixed $\beta$ -peptides that adopt stable cyclic hairpin-like conformations. <i>Tetrahedron</i> , 2012, 68, 2391-2400.	1.9	12
65	A Prodrug Approach for Improving Antituberculosis Activity of Potent Mycobacterium tuberculosis Type II Dehydroquinase Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2011, 54, 6063-6084.	6.4	32
66	Target highlights in CASP9: Experimental target structures for the critical assessment of techniques for protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 6-20.	2.6	19
67	Tetrahydrobenzothiophene Derivatives: Conformationally Restricted Inhibitors of Type II Dehydroquinase. <i>ChemMedChem</i> , 2011, 6, 266-272.	3.2	15
68	Evaluation of Readily Accessible Azoles as Mimics of the Aromatic Ring of <i>D</i> -Phenylalanine in the Turn Region of Gramicidin S. <i>ChemMedChem</i> , 2011, 6, 840-847.	3.2	17
69	Exploring the Conformational and Biological Versatility of Turn-Modified Gramicidin S by Using Sugar Amino Acid Homologues that Vary in Ring Size. <i>Chemistry - A European Journal</i> , 2011, 17, 3995-4004.	3.3	33
70	Synthesis and evaluation of strand and turn modified ring-extended gramicidin S derivatives. <i>Bioorganic and Medicinal Chemistry</i> , 2011, 19, 3402-3409.	3.0	9
71	Understanding the Key Factors that Control the Inhibition of Type II Dehydroquinase by (2 <i>R</i> )- $\beta$ -Benzyl- $\beta$ -dehydroquinic Acids. <i>ChemMedChem</i> , 2010, 5, 1726-1733.	3.2	22
72	Gramicidin S Derivatives Containing <i>cis</i> - and <i>trans</i> -Morpholine Amino Acids (MAAs) as Turn Mimetics. <i>Chemistry - A European Journal</i> , 2010, 16, 4259-4265.	3.3	15

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73	An Adamantyl Amino Acid Containing Gramicidin S Analogue with Broad Spectrum Antibacterial Activity and Reduced Hemolytic Activity. <i>Chemistry - A European Journal</i> , 2010, 16, 12174-12181.	3.3	33
74	Guest authors: for contributors only. <i>Nature</i> , 2010, 468, 765-765.	27.8	1
75	Crystallographic Structure of Porcine Adenovirus Type 4 Fiber Head and Galectin Domains. <i>Journal of Virology</i> , 2010, 84, 10558-10568.	3.4	19
76	Spain's Budget Neglects Research. <i>Science</i> , 2010, 327, 1078-1079.	12.6	3
77	Morphogenesis of the T4 tail and tail fibers. <i>Virology Journal</i> , 2010, 7, 355.	3.4	197
78	Structure of the bacteriophage T4 long tail fiber receptor-binding tip. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 20287-20292.	7.1	159
79	Synthesis and Biological Evaluation of New Nanomolar Competitive Inhibitors of Helicobacter pylori Type II Dehydroquinase. Structural Details of the Role of the Aromatic Moieties with Essential Residues. <i>Journal of Medicinal Chemistry</i> , 2010, 53, 191-200.	6.4	21
80	Two-chaperone assisted soluble expression and purification of the bacteriophage T4 long tail fibre protein gp37. <i>Protein Expression and Purification</i> , 2010, 70, 116-121.	1.3	43
81	Crystallographic structure of the $\hat{A}$ -helical triple coiled-coil domain of avian reovirus S1133 fibre. <i>Journal of General Virology</i> , 2009, 90, 672-677.	2.9	23
82	Bisphosphine-Functionalized Cyclic Decapeptides Based on the Natural Product Gramicidin S: A Potential Scaffold for Transition-Metal Coordination. <i>Chemistry - A European Journal</i> , 2009, 15, 8134-8145.	3.3	17
83	Crystallization of the head and galectin-like domains of porcine adenovirus isolate NADC-1 fibre. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1149-1152.	0.7	4
84	Synthesis and biological evaluation of asymmetric gramicidin S analogues containing modified d-phenylalanine residues. <i>Bioorganic and Medicinal Chemistry</i> , 2009, 17, 6318-6328.	3.0	14
85	Creation of Hybrid Nanorods From Sequences of Natural Trimeric Fibrous Proteins Using the Fibrin Trimerization Motif. <i>Methods in Molecular Biology</i> , 2008, 474, 15-33.	0.9	6
86	Structure of the Receptor-Binding Protein of Bacteriophage Det7: a Podoviral Tail Spike in a Myovirus. <i>Journal of Virology</i> , 2008, 82, 2265-2273.	3.4	98
87	Crystal Structure of the Avian Reovirus Inner Capsid Protein $\hat{I}fA$ . <i>Journal of Virology</i> , 2008, 82, 11208-11216.	3.4	20
88	Structure of the C-terminal head domain of the fowl adenovirus type 1 long fiber. <i>Journal of General Virology</i> , 2007, 88, 2407-2416.	2.9	27
89	Double-stranded helical twisted $\hat{I}^2$ -sheet channels in crystals of gramicidin S grown in the presence of trifluoroacetic and hydrochloric acids. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 401-407.	2.5	46
90	Crystallization of the avian reovirus double-stranded RNA-binding and core protein $\hat{I}fA$ . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 426-429.	0.7	3

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91	$\beta$ -Turn Modified Gramicidin S Analogues Containing Arylated Sugar Amino Acids Display Antimicrobial and Hemolytic Activity Comparable to the Natural Product. <i>Journal of the American Chemical Society</i> , 2006, 128, 7559-7565.	13.7	58
92	Crystallization of the C-terminal head domain of the avian adenovirus CELO long fibre. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 449-452.	0.7	5
93	Natural Triple $\beta$ -Stranded Fibrous Folds1. <i>Advances in Protein Chemistry</i> , 2006, 73, 97-124.	4.4	35
94	Crystallization of the C-terminal globular domain of avian reovirus fibre. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 651-654.	0.7	6
95	Structure of the Carboxy-terminal Receptor-binding Domain of Avian Reovirus Fibre SigmaC. <i>Journal of Molecular Biology</i> , 2005, 354, 137-149.	4.2	56
96	Folding of $\beta$ -Structured Fibrous Proteins and Self-Assembling Peptides. , 2005, 300, 125-140.		10
97	New law does little to ease research pain in Spain. <i>Nature</i> , 2004, 428, 365-365.	27.8	1
98	An Unusual Reverse Turn Structure Adopted by a Furanoid Sugar Amino Acid Incorporated in Gramicidin S. <i>Journal of the American Chemical Society</i> , 2004, 126, 3444-3446.	13.7	90
99	Beta-structured viral fibres: assembly, structure and implications for materials design. <i>Current Opinion in Solid State and Materials Science</i> , 2004, 8, 151-156.	11.5	11
100	Adenovirus Fibre Shaft Sequences Fold into the Native Triple Beta-Spiral Fold when N-terminally Fused to the Bacteriophage T4 Fibrin Foldon Trimerisation Motif. <i>Journal of Molecular Biology</i> , 2004, 342, 219-227.	4.2	31
101	Three-dimensional structure of bacteriophage T4 baseplate. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 688-693.	8.2	165
102	Conformational Analysis of Furanoid $\beta$ -Sugar Amino Acid Containing Cyclic Peptides by NMR Spectroscopy, Molecular Dynamics Simulation, and X-ray Crystallography: Evidence for a Novel Turn Structure. <i>Journal of the American Chemical Society</i> , 2003, 125, 10822-10829.	13.7	56
103	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
104	Review: Conformation and Folding of Novel Beta-Structural Elements in Viral Fiber Proteins: The Triple Beta-Spiral and Triple Beta-Helix. <i>Journal of Structural Biology</i> , 2002, 137, 236-247.	2.8	50
105	Structure, Folding and Assembly of Adenovirus Fibers. , 2002, , 221-234.		1
106	Crystal structure of a heat and protease-stable part of the bacteriophage T4 short tail fibre. <i>Journal of Molecular Biology</i> , 2001, 314, 1137-1146.	4.2	95
107	Influence of adenoviral fiber mutations on viral encapsidation, infectivity and in vivo tropism. <i>Gene Therapy</i> , 2001, 8, 49-57.	4.5	97
108	Dimeric Structure of the Coxsackievirus and Adenovirus Receptor D1 Domain at 1.7 Å... Resolution. <i>Structure</i> , 2001, 9, 1.	3.3	1

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109	Identification and Crystallisation of a Heat- and Protease-Stable Fragment of the Bacteriophage T4 Short Tail Fibre. <i>Biological Chemistry</i> , 2001, 382, 1049-55.	2.5	19
110	Kinetic Analysis of Adenovirus Fiber Binding to Its Receptor Reveals an Avidity Mechanism for Trimeric Receptor-Ligand Interactions. <i>Journal of Biological Chemistry</i> , 2001, 276, 9009-9015.	3.4	66
111	Dimeric Structure of the Coxsackievirus and Adenovirus Receptor D1 Domain at 1.7 Å... Resolution. <i>Structure</i> , 2000, 8, 1147-1155.	3.3	142
112	A triple $\beta$ -spiral in the adenovirus fibre shaft reveals a new structural motif for a fibrous protein. <i>Nature</i> , 1999, 401, 935-938.	27.8	310
113	Structure of the Human Adenovirus Serotype 2 Fiber Head Domain at 1.5 Å... Resolution. <i>Virology</i> , 1999, 262, 333-343.	2.4	87
114	The structure of bovine mitochondrial F1-ATPase: an example of rotary catalysis. <i>Biochemical Society Transactions</i> , 1999, 27, 37-42.	3.4	31
115	The ATPase Inhibitor Protein from Bovine Heart Mitochondria: The Minimal Inhibitory Sequence. <i>Biochemistry</i> , 1996, 35, 15618-15625.	2.5	79
116	The structure of bovine F1-ATPase complexed with the peptide antibiotic efrapeptin.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 9420-9424.	7.1	148
117	The structure of bovine F1-ATPase complexed with the antibiotic inhibitor aurovertin B. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 6913-6917.	7.1	173
118	[11] Structural analysis of ATP synthase from bovine heart mitochondria. <i>Methods in Enzymology</i> , 1995, 260, 163-190.	1.0	35
119	ATP Synthase from Bovine Heart Mitochondria. <i>Journal of Molecular Biology</i> , 1994, 242, 408-421.	4.2	52
120	F0 Membrane Domain of ATP Synthase from Bovine Heart Mitochondria: Purification, Subunit Composition, and Reconstitution with F1-ATPase. <i>Biochemistry</i> , 1994, 33, 7971-7978.	2.5	180
121	Crystallization of F1-ATPase from Bovine Heart Mitochondria. <i>Journal of Molecular Biology</i> , 1993, 229, 787-790.	4.2	75
122	Kirromycin drastically reduces the affinity of Escherichia coli elongation factor Tu for aminoacyl-tRNA. <i>Biochemistry</i> , 1991, 30, 6705-6710.	2.5	27