

Mark J Van Raaij

List of Publications by Year in descending order

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122
papers

4,339
citations

109321

35
h-index

118850

62
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127
all docs

127
docs citations

127
times ranked

4188
citing authors

#	ARTICLE	IF	CITATIONS
1	A triple \hat{I}^2 -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
2	Morphogenesis of the T4 tail and tail fibers. <i>Virology Journal</i> , 2010, 7, 355.	3.4	197
3	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
4	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
5	Three-dimensional structure of bacteriophage T4 baseplate. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 688-693.	8.2	165
6	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
7	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
8	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
9	Contractile injection systems of bacteriophages and related systems. <i>Molecular Microbiology</i> , 2018, 108, 6-15.	2.5	119
10	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
11	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
12	Influence of adenoviral fiber mutations on viral encapsidation, infectivity and in vivo tropism. <i>Gene Therapy</i> , 2001, 8, 49-57.	4.5	97
13	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
14	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
15	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
16	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
17	The ATPase Inhibitor Protein from Bovine Heart Mitochondria: The Minimal Inhibitory Sequence. <i>Biochemistry</i> , 1996, 35, 15618-15625.	2.5	79
18	Still Something to Discover: Novel Insights into Escherichia coli Phage Diversity and Taxonomy. <i>Viruses</i> , 2019, 11, 454.	3.3	77

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19	Crystallization of F1-ATPase from Bovine Heart Mitochondria. <i>Journal of Molecular Biology</i> , 1993, 229, 787-790.	4.2	75
20	Structural Characterization of the Bacteriophage T7 Tail Machinery. <i>Journal of Biological Chemistry</i> , 2013, 288, 26290-26299.	3.4	75
21	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
22	β -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
23	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
24	Conformational Analysis of Furanoid β -Sugar Amino Acid Containing Cyclic Peptides by NMR Spectroscopy, Molecular Dynamics Simulation, and X-ray Crystallography: A Evidence for a Novel Turn Structure. <i>Journal of the American Chemical Society</i> , 2003, 125, 10822-10829.	13.7	56
25	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
26	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
27	ATP Synthase from Bovine Heart Mitochondria. <i>Journal of Molecular Biology</i> , 1994, 242, 408-421.	4.2	52
28	Mycobacterium tuberculosis 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
29	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
30	Crystal structure of the lytic CHAPK domain of the endolysin LysK from Staphylococcus aureus bacteriophage K. <i>Virology Journal</i> , 2014, 11, 133.	3.4	47
31	Bacteriophage T4 long tail fiber domains. <i>Biophysical Reviews</i> , 2018, 10, 463-471.	3.2	47
32	Double-stranded helical twisted β -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
33	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
34	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
35	Molecular anatomy of the receptor binding module of a bacteriophage long tail fiber. <i>PLoS Pathogens</i> , 2019, 15, e1008193.	4.7	38
36	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

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37	[11] Structural analysis of ATP synthase from bovine heart mitochondria. <i>Methods in Enzymology</i> , 1995, 260, 163-190.	1.0	35
38	Natural Triple β -Stranded Fibrous Folds1. <i>Advances in Protein Chemistry</i> , 2006, 73, 97-124.	4.4	35
39	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
40	Exploring the Conformational and Biological Versatility of β -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
41	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
42	The structure of bovine mitochondrial F1-ATPase: an example of rotary catalysis. <i>Biochemical Society Transactions</i> , 1999, 27, 37-42.	3.4	31
43	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
44	Kirromycin drastically reduces the affinity of Escherichia coli elongation factor Tu for aminoacyl-tRNA. <i>Biochemistry</i> , 1991, 30, 6705-6710.	2.5	27
45	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
46	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
47	Crystal Structure of the Carboxy-Terminal Region of the Bacteriophage T4 Proximal Long Tail Fiber Protein Gp34. <i>Viruses</i> , 2017, 9, 168.	3.3	24
48	Crystallographic structure of the β -helical triple coiled-coil domain of avian reovirus S1133 fibre. <i>Journal of General Virology</i> , 2009, 90, 672-677.	2.9	23
49	Understanding the Key Factors that Control the Inhibition of Type II Dehydroquinase by (2 <i>R</i> ,3 <i>R</i>)-Benzyl- β -dehydroquinic Acids. <i>ChemMedChem</i> , 2010, 5, 1726-1733.	3.2	22
50	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
51	Crystal Structure of the Avian Reovirus Inner Capsid Protein σ A. <i>Journal of Virology</i> , 2008, 82, 11208-11216.	3.4	20
52	Characterization of a Bacteriophage-Derived Murein Peptidase for Elimination of Antibiotic-Resistant Staphylococcus aureus. <i>Current Protein and Peptide Science</i> , 2016, 17, 183-190.	1.4	20
53	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
54	Crystallographic Structure of Porcine Adenovirus Type 4 Fiber Head and Galectin Domains. <i>Journal of Virology</i> , 2010, 84, 10558-10568.	3.4	19

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55	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
56	Structure of a Reptilian Adenovirus Reveals a Phage Tailspike Fold Stabilizing a Vertebrate Virus Capsid. <i>Structure</i> , 2017, 25, 1562-1573.e5.	3.3	19
57	A novel amyloid designable scaffold and potential inhibitor inspired by <scp>GAILG</scp> of amyloid beta and the <scp>HIV</scp>â€1 V3 loop. <i>FEBS Letters</i> , 2018, 592, 1777-1788.	2.8	18
58	Bacteriophage Receptor Recognition and Nucleic Acid Transfer. <i>Sub-Cellular Biochemistry</i> , 2013, 68, 489-518.	2.4	18
59	Bisphosphineâ€Functionalized Cyclic Decapeptides Based on the Natural Product Gramicidinâ€S: A Potential Scaffold for Transitionâ€Metal Coordination. <i>Chemistry - A European Journal</i> , 2009, 15, 8134-8145.	3.3	17
60	Evaluation of Readily Accessible Azoles as Mimics of the Aromatic Ring of <scp>D</scp>â€Phenylalanine in the Turn Region of Gramicidinâ€S. <i>ChemMedChem</i> , 2011, 6, 840-847.	3.2	17
61	The so far farthest reaches of the double jelly roll capsid protein fold. <i>Virology Journal</i> , 2018, 15, 181.	3.4	17
62	Some of the most interesting <scp>CASP</scp>11 targets through the eyes of their authors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 34-50.	2.6	16
63	Crystal Structure of the Fibre Head Domain of the Atadenovirus Snake Adenovirus 1. <i>PLoS ONE</i> , 2014, 9, e114373.	2.5	16
64	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
65	Tetrahydrobenzothiophene Derivatives: Conformationally Restricted Inhibitors of Typeâ€II Dehydroquinase. <i>ChemMedChem</i> , 2011, 6, 266-272.	3.2	15
66	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
67	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
68	Design, synthesis and structural analysis of mixed $\hat{I}\pm/\hat{I}^2$ -peptides that adopt stable cyclic hairpin-like conformations. <i>Tetrahedron</i> , 2012, 68, 2391-2400.	1.9	12
69	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
70	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
71	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
72	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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73	Target highlights from the first post-PSI CASP experiment (CASP12, May-August 2016). <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 27-50.	2.6	11
74	Folding of β -Structured Fibrous Proteins and Self-Assembling Peptides. , 2005, 300, 125-140.		10
75	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
76	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
77	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
78	β -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
79	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
80	Insights into substrate binding and catalysis in bacterial type I dehydroquinase. <i>Biochemical Journal</i> , 2014, 462, 415-424.	3.7	8
81	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
82	Structure and N-acetylglucosamine binding of the distal domain of mouse adenovirus 2 fibre. <i>Journal of General Virology</i> , 2018, 99, 1494-1508.	2.9	8
83	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. <i>IUCr</i> , 2019, 6, 341-343.	2.2	8
84	High-resolution structures of <i>Thermus thermophilus</i> enoyl-acyl carrier protein reductase in the apo form, in complex with NAD ⁺ and in complex with NAD ⁺ and triclosan. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1139-1148.	0.7	7
85	<i>Fasciola hepatica</i> calcium-binding protein FhCaBP2: structure of the dynein light chain-like domain. <i>Parasitology Research</i> , 2016, 115, 2879-2886.	1.6	7
86	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
87	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
88	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
89	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
90	Design, Synthesis, and Structural Analysis of Turn Modified β -Cyclodextrin-(β -Cyclodextrin) ₃ -(β -Cyclodextrin) ₂ -(β -Cyclodextrin) ₂ Peptide Derivatives toward Crystalline Hexagon-Shaped Cationic Nanochannel Assemblies. <i>Crystal Growth and Design</i> , 2013, 13, 4355-4367.	3.0	6

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91	Crystal structure of the fibre head domain of bovine adenovirus 4, a ruminant atadenovirus. <i>Virology Journal</i> , 2015, 12, 81.	3.4	6
92	Crystal structure of raptor adenovirus 1 fibre head and role of the beta-hairpin in siadenovirus fibre head domains. <i>Virology Journal</i> , 2016, 13, 106.	3.4	6
93	Structure and Function of Bacteriophages. , 2021, , 19-91.		6
94	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
95	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
96	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
97	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
98	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
99	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
100	Crystallization of the avian reovirus double-stranded RNA-binding and core protein σ A. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 426-429.	0.7	3
101	Spain's Budget Neglects Research. <i>Science</i> , 2010, 327, 1078-1079.	12.6	3
102	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
103	Structure and Function of Bacteriophages. , 2019, , 1-73.		3
104	Submission of structural biology data for review purposes. <i>IUCr</i> , 2022, 9, 1-2.	2.2	3
105	Self-immolation of a Bacterial Dehydratase Enzyme by its Epoxide Product. <i>Chemistry - A European Journal</i> , 2020, 26, 8035-8044.	3.3	2
106	Dimeric Structure of the Coxsackievirus and Adenovirus Receptor D1 Domain at 1.7 Å... Resolution. <i>Structure</i> , 2001, 9, 1.	3.3	1
107	New law does little to ease research pain in Spain. <i>Nature</i> , 2004, 428, 365-365.	27.8	1
108	Guest authors: for contributors only. <i>Nature</i> , 2010, 468, 765-765.	27.8	1

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109	Bacteriophage Tail Fibres, Tailspikes, and Bacterial Receptor Interaction. , 2021, , 194-205.		1
110	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. Journal of Applied Crystallography, 2019, 52, 495-497.	4.5	1
111	Structure, Folding and Assembly of Adenovirus Fibers. , 2002, , 221-234.		1
112	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
113	Submission of structural biology data for review purposes. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1477-1478.	2.3	1
114	Carbohydrate structure hits the groove. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 441-442.	0.8	0
115	Quo vadis, Acta Crystallographica F?. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 688-689.	0.8	0
116	Welcoming Janet Newman with a BLAST on crystallization strategy. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 147-147.	0.8	0
117	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
118	Taking biological structure communications into the third dimension. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 663-664.	0.8	0
119	Innovation versus practice in biological crystallization. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 290-291.	0.8	0
120	Contamination or serendipity “doing the wrong thing by chance. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 391-391.	0.8	0
121	Topical Reviews in <i>Acta Crystallographica F Structural Biology Communications</i>. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 385-385.	0.8	0
122	Submission of structural biology data for review purposes. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 435-436.	0.8	0