

Janet M Newman

List of Publications by Year in descending order

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127
papers

3,688
citations

126907

33
h-index

149698

56
g-index

130
all docs

130
docs citations

130
times ranked

5120
citing authors

#	ARTICLE	IF	CITATIONS
1	Mechanism and inhibition of the papain-like protease, PLpro, of SARS-CoV-2. <i>EMBO Journal</i> , 2020, 39, e106275.	7.8	330
2	Towards rationalization of crystallization screening for small- to medium-sized academic laboratories: the PACT/JCSG+ strategy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1426-1431.	2.5	228
3	Structural analysis of a set of proteins resulting from a bacterial genomics project. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 787-796.	2.6	217
4	Haloalkane Dehalogenases: Structure of a Rhodococcus Enzyme. <i>Biochemistry</i> , 1999, 38, 16105-16114.	2.5	150
5	Identification and characterization of two families of F ₄₂₀ H ₂ -dependent reductases from <i>Mycobacteria</i> that catalyse aflatoxin degradation. <i>Molecular Microbiology</i> , 2010, 78, 561-575.	2.5	132
6	Crystal Structure of the Haloalkane Dehalogenase from <i>Sphingomonas paucimobilis</i> UT26. <i>Biochemistry</i> , 2000, 39, 14082-14086.	2.5	118
7	Novel buffer systems for macromolecular crystallization. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 610-612.	2.5	111
8	Structure of translation initiation factor 5A from <i>Pyrobaculum aerophilum</i> at 1.75 Å resolution. <i>Structure</i> , 1998, 6, 1207-1214.	3.3	109
9	Class-directed structure determination: Foundation for a protein structure initiative. <i>Protein Science</i> , 1998, 7, 1851-1856.	7.6	89
10	Rational engineering of a mesohalophilic carbonic anhydrase to an extreme halotolerant biocatalyst. <i>Nature Communications</i> , 2015, 6, 10278.	12.8	80
11	Structural and Functional Basis of Resistance to Neuraminidase Inhibitors of Influenza B Viruses. <i>Journal of Medicinal Chemistry</i> , 2010, 53, 6421-6431.	6.4	75
12	Structural Studies of <i>Salmonella typhimurium</i> ArnB (PmrH) Aminotransferase. <i>Structure</i> , 2002, 10, 1569-1580.	3.3	73
13	Crystal Structure of an Indole-3-Acetic Acid Amido Synthetase from Grapevine Involved in Auxin Homeostasis. <i>Plant Cell</i> , 2012, 24, 4525-4538.	6.6	70
14	High-Throughput Thermal Scanning for Protein Stability: Making a Good Technique More Robust. <i>ACS Combinatorial Science</i> , 2013, 15, 387-392.	3.8	62
15	Parallel Screening of Low Molecular Weight Fragment Libraries: Do Differences in Methodology Affect Hit Identification?. <i>Journal of Biomolecular Screening</i> , 2013, 18, 147-159.	2.6	61
16	Crystallization screening: the influence of history on current practice. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 835-853.	0.8	54
17	Classification of crystallization outcomes using deep convolutional neural networks. <i>PLoS ONE</i> , 2018, 13, e0198883.	2.5	54
18	Improved Success of Sparse Matrix Protein Crystallization Screening with Heterogeneous Nucleating Agents. <i>PLoS ONE</i> , 2007, 2, e1091.	2.5	49

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19	Structural Basis for a New Mechanism of Inhibition of H I V-1 Integrase Identified by Fragment Screening and Structure-Based Design. <i>Antiviral Chemistry and Chemotherapy</i> , 2011, 21, 155-168.	0.6	49
20	Small Molecule Inhibitors of the LEDGF Site of Human Immunodeficiency Virus Integrase Identified by Fragment Screening and Structure Based Design. <i>PLoS ONE</i> , 2012, 7, e40147.	2.5	49
21	Evaluating Protic Ionic Liquids as Protein Crystallization Additives. <i>Crystal Growth and Design</i> , 2011, 11, 1777-1785.	3.0	46
22	Structure of an effector-induced inactivated state of ribulose 1,5-bisphosphate carboxylase/oxygenase: the binary complex between enzyme and xylulose 1,5-bisphosphate. <i>Structure</i> , 1994, 2, 495-502.	3.3	44
23	Meltdown: A Tool to Help in the Interpretation of Thermal Melt Curves Acquired by Differential Scanning Fluorimetry. <i>Journal of Biomolecular Screening</i> , 2015, 20, 898-905.	2.6	44
24	A review of techniques for maximizing diffraction from a protein crystal in stilla. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 27-31.	2.5	42
25	High-Throughput Production and Structural Characterization of Libraries of Self-Assembly Lipidic Cubic Phase Materials. <i>ACS Combinatorial Science</i> , 2012, 14, 247-252.	3.8	42
26	A Human Monoclonal Antibody against Insulin-Like Growth Factor-II Blocks the Growth of Human Hepatocellular Carcinoma Cell Lines <i>in vitro</i> and <i>in vivo</i> . <i>Molecular Cancer Therapeutics</i> , 2010, 9, 1809-1819.	4.1	39
27	The C6 Web Tool: A Resource for the Rational Selection of Crystallization Conditions. <i>Crystal Growth and Design</i> , 2010, 10, 2785-2792.	3.0	39
28	On the need for an international effort to capture, share and use crystallization screening data. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 253-258.	0.7	38
29	A drunken search in crystallization space. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1303-1311.	0.8	38
30	The structure of vanin 1: a key enzyme linking metabolic disease and inflammation. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 3320-3329.	2.5	37
31	Initial evaluations of the reproducibility of vapor-diffusion crystallization. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 826-832.	2.5	36
32	Parallel and antiparallel cyclic α -helix peptide nanotubes. <i>Chemical Communications</i> , 2017, 53, 6613-6616.	4.1	36
33	Reverse engineering: transaminase biocatalyst development using ancestral sequence reconstruction. <i>Green Chemistry</i> , 2017, 19, 5375-5380.	9.0	36
34	Expanding screening space through the use of alternative reservoirs in vapor-diffusion experiments. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 490-493.	2.5	34
35	Some practical guidelines for UV imaging in the protein crystallization laboratory. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 201-208.	0.7	32
36	Phoenix experiments: combining the strengths of commercial crystallization automation. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 991-996.	0.7	31

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37	Cyanuric acid hydrolase: evolutionary innovation by structural concatenation. <i>Molecular Microbiology</i> , 2013, 88, 1149-1163.	2.5	31
38	Crystal Structures of Novel Allosteric Peptide Inhibitors of HIV Integrase Identify New Interactions at the LEDGF Binding Site. <i>ChemBioChem</i> , 2011, 12, 2311-2315.	2.6	30
39	The nanoscience behind the art of in-meso crystallization of membrane proteins. <i>Nanoscale</i> , 2017, 9, 754-763.	5.6	30
40	Tapping the Protein Data Bank for crystallization information. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1662-1669.	2.5	29
41	Structural basis for ligand recognition by a Cache chemosensory domain that mediates carboxylate sensing in <i>Pseudomonas syringae</i> . <i>Scientific Reports</i> , 2016, 6, 35198.	3.3	28
42	One plate, two plates, a thousand plates. How crystallisation changes with large numbers of samples. <i>Methods</i> , 2011, 55, 73-80.	3.8	26
43	Germline humanization of a murine $\text{A}\hat{1}^2$ antibody and crystal structure of the humanized recombinant Fab fragment. <i>Protein Science</i> , 2010, 19, 299-308.	7.6	25
44	Interrogating HIV integrase for compounds that bind- a SAMPL challenge. <i>Journal of Computer-Aided Molecular Design</i> , 2014, 28, 347-362.	2.9	25
45	Structure of <i>S. aureus</i> HPPK and the Discovery of a New Substrate Site Inhibitor. <i>PLoS ONE</i> , 2012, 7, e29444.	2.5	24
46	Crystal structures of human ENPP1 in apo and bound forms. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 889-898.	2.3	24
47	Identifying, studying and making good use of macromolecular crystals. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 993-1008.	0.8	23
48	A $\hat{1}^2$ -Alanine Catabolism Pathway Containing a Highly Promiscuous $\hat{1}^2$ -Transaminase in the 12-Aminododecanate-Degrading <i>Pseudomonas</i> sp. Strain AAC. <i>Applied and Environmental Microbiology</i> , 2016, 82, 3846-3856.	3.1	21
49	Transmembrane Complexes of DAP12 Crystallized in Lipid Membranes Provide Insights into Control of Oligomerization in Immunoreceptor Assembly. <i>Cell Reports</i> , 2015, 11, 1184-1192.	6.4	20
50	The DINGO dataset: a comprehensive set of data for the SAMPL challenge. <i>Journal of Computer-Aided Molecular Design</i> , 2012, 26, 497-503.	2.9	19
51	The structure of the hexameric atrazine chlorohydrolase AtzA. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 710-720.	2.5	19
52	X-Ray Structure of the Amidase Domain of AtzF, the Allophanate Hydrolase from the Cyanuric Acid-Mineralizing Multienzyme Complex. <i>Applied and Environmental Microbiology</i> , 2015, 81, 470-480.	3.1	18
53	An unexpected vestigial protein complex reveals the evolutionary origins of an s-triazine catabolic enzyme. <i>Journal of Biological Chemistry</i> , 2018, 293, 7880-7891.	3.4	18
54	Practical Aspects of the SAMPL Challenge: Providing an Extensive Experimental Data Set for the Modeling Community. <i>Journal of Biomolecular Screening</i> , 2009, 14, 1245-1250.	2.6	17

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55	Determination of the Structure of the Catabolic N-Succinylornithine Transaminase (AstC) from <i>Escherichia coli</i> . PLoS ONE, 2013, 8, e58298.	2.5	17
56	Exploring the Chemical Space around 8-Mercaptoguanine as a Route to New Inhibitors of the Folate Biosynthesis Enzyme HPPK. PLoS ONE, 2013, 8, e59535.	2.5	17
57	Design of a methotrexate-controlled chemical dimerization system and its use in bio-electronic devices. Nature Communications, 2021, 12, 7137.	12.8	17
58	Redetermination of the crystal structure of hexaamminecobalt(II) chloride. Inorganic Chemistry, 1991, 30, 3499-3502.	4.0	16
59	A new crystal form of human vascular adhesion protein 1. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1572-1578.	0.7	16
60	Formulation screening by differential scanning fluorimetry: how often does it work?. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1359-1364.	0.8	16
61	Some of the most interesting <scp>CASP</scp>11 targets through the eyes of their authors. Proteins: Structure, Function and Bioinformatics, 2016, 84, 34-50.	2.6	16
62	Lipidic Cubic Phase-Induced Membrane Protein Crystallization: Interplay Between Lipid Molecular Structure, Mesophase Structure and Properties, and Crystallogenesis. Crystal Growth and Design, 2017, 17, 5667-5674.	3.0	16
63	Using Time Courses To Enrich the Information Obtained from Images of Crystallization Trials. Crystal Growth and Design, 2014, 14, 261-269.	3.0	15
64	The purification, crystallization and preliminary X-ray diffraction analysis of dihydrodipicolinate synthase from <i>Clostridium botulinum</i> . Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 206-208.	0.7	14
65	Crystallization and preliminary X-ray analysis of dihydrodipicolinate synthase from <i>Clostridium botulinum</i> in the presence of its substrate pyruvate. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 253-255.	0.7	14
66	Structure-Based Design and Development of Functionalized Mercaptoguanine Derivatives as Inhibitors of the Folate Biosynthesis Pathway Enzyme 6-Hydroxymethyl-7,8-dihydropterin Pyrophosphokinase from <i>Staphylococcus aureus</i> . Journal of Medicinal Chemistry, 2014, 57, 9612-9626.	6.4	14
67	300-Fold Increase in Production of the Zn ²⁺ -Dependent Dechlorinase TrzN in Soluble Form via Apoenzyme Stabilization. Applied and Environmental Microbiology, 2014, 80, 4003-4011.	3.1	14
68	A universal indicator dye pH assay for crystallization solutions and other high-throughput applications. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1003-1009.	2.5	13
69	Structural and biochemical characterization of the biuret hydrolase (BiuH) from the cyanuric acid catabolism pathway of <i>Rhizobium leguminosorum</i> bv. <i>viciae</i> 3841. PLoS ONE, 2018, 13, e0192736.	2.5	12
70	<i>BLAST</i>ing away preconceptions in crystallization trials. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 184-192.	0.8	12
71	Cloning, expression, purification and crystallization of dihydrodipicolinate synthase from the grapevine <i>Vitis vinifera</i> . Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1537-1541.	0.7	11
72	Crystallization reports are the backbone of <i>Acta Cryst. F</i>, but do they have any spine?. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 712-718.	0.7	11

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73	A novel decarboxylating amidohydrolase involved in avoiding metabolic dead ends during cyanuric acid catabolism in <i>Pseudomonas</i> sp. strain ADP. <i>PLoS ONE</i> , 2018, 13, e0206949.	2.5	11
74	Insights Into Drug Repurposing, as Well as Specificity and Compound Properties of Piperidine-Based SARS-CoV-2 PLpro Inhibitors. <i>Frontiers in Chemistry</i> , 2022, 10, 861209.	3.6	11
75	DroplIT, an improved image analysis method for droplet identification in high-throughput crystallization trials. <i>Journal of Applied Crystallography</i> , 2010, 43, 1548-1552.	4.5	10
76	What's in a Name? Moving Towards a Limited Vocabulary for Macromolecular Crystallisation. <i>Australian Journal of Chemistry</i> , 2014, 67, 1813.	0.9	10
77	Structural characterization of a novel monotreme-specific protein with antimicrobial activity from the milk of the platypus. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 39-45.	0.8	10
78	Bacterial catabolism of s-triazine herbicides: biochemistry, evolution and application. <i>Advances in Microbial Physiology</i> , 2020, 76, 129-186.	2.4	10
79	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
80	The crystal structures of Rubisco and opportunities for manipulating photosynthesis. <i>Journal of Experimental Botany</i> , 1995, 46, 1261-1267.	4.8	8
81	Crystallization and preliminary X-ray diffraction analysis of the amidase domain of allophanate hydrolase from <i>Pseudomonas</i> sp. strain ADP. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 310-315.	0.8	8
82	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. <i>IUCr</i> , 2019, 6, 341-343.	2.2	8
83	<i>Cinder</i> : keeping crystallographers app-y. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 410-418.	0.8	7
84	Tools to Ease the Choice and Design of Protein Crystallisation Experiments. <i>Crystals</i> , 2020, 10, 95.	2.2	7
85	Structures of the transcriptional regulator BgaR, a lactose sensor. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 639-646.	2.3	7
86	Fragment Screening for the Modelling Community: SPR, ITC, and Crystallography. <i>Australian Journal of Chemistry</i> , 2013, 66, 1507.	0.9	6
87	High-Resolution X-Ray Structures of Two Functionally Distinct Members of the Cyclic Amide Hydrolase Family of Toblerone Fold Enzymes. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	6
88	Fragment screening for a protein-protein interaction inhibitor to WDR5. <i>Structural Dynamics</i> , 2019, 6, 064701.	2.3	6
89	Crystal structure of fungal tannase from <i>Aspergillus niger</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 267-277.	2.3	6
90	A Nondenaturing Purification Scheme for the DNA-Binding Domain of Poly(ADP-Ribose) Polymerase, a Structure-Specific DNA-Binding Protein. <i>Protein Expression and Purification</i> , 1998, 14, 79-86.	1.3	5

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91	From information management to protein annotation: preparing protein structures for drug discovery. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1968-1970.	2.5	5
92	Crystallization and preliminary X-ray analysis of 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase from <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 575-578.	0.7	5
93	13th International Conference on the Crystallization of Biological Macromolecules (ICCBM13) Proceedings Overview. <i>Crystal Growth and Design</i> , 2012, 12, 3-7.	3.0	5
94	X-Ray Structure and Mutagenesis Studies of the N-Isopropylammelide Isopropylaminohydrolase, <i>AtzC</i> . <i>PLoS ONE</i> , 2015, 10, e0137700.	2.5	5
95	Crystallization of an apo form of human arginase: using all the tools in the toolbox simultaneously. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 90-93.	0.7	4
96	Crystallization: Digging into the Past to Learn Lessons for the Future. <i>Methods in Molecular Biology</i> , 2015, 1261, 141-156.	0.9	4
97	Crystal structure of a putrescine aminotransferase from <i>Pseudomonas</i> sp. strain AAC. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 29-35.	0.8	3
98	Predicting the Effect of Chemical Factors on the pH of Crystallization Trials. <i>IScience</i> , 2020, 23, 101219.	4.1	3
99	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
100	Data- and diversity-driven development of a Shotgun crystallization screen using the Protein Data Bank. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1437-1450.	2.3	3
101	The X-ray crystal structure of the N-terminal domain of Ssr4, a chromatin-remodelling protein. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 583-589.	0.8	3
102	Submission of structural biology data for review purposes. <i>IUCr</i> , 2022, 9, 1-2.	2.2	3
103	Using Graphs to Represent Crystallization Conditions. <i>Crystal Growth and Design</i> , 2013, 13, 1290-1294.	3.0	2
104	Nitrate in the active site of protein tyrosine phosphatase 1B is a putative mimetic of the transition state. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 565-571.	2.5	2
105	Structural and functional characterisation of ferret interleukin-2. <i>Developmental and Comparative Immunology</i> , 2016, 55, 32-38.	2.3	2
106	X-ray crystal structure of a malonate-semialdehyde dehydrogenase from <i>Pseudomonas</i> sp. strain AAC. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 24-28.	0.8	2
107	Structure-guided selection of puromycin N-acetyltransferase mutants with enhanced selection stringency for deriving mammalian cell lines expressing recombinant proteins. <i>Scientific Reports</i> , 2021, 11, 5247.	3.3	2
108	Increasing Protein Crystallization Screening Success with Heterogeneous Nucleating Agents. <i>Methods in Molecular Biology</i> , 2008, 426, 403-409.	0.9	2

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109	A Crystal/Clear Pipeline for Applied Image Processing. Lecture Notes in Computer Science, 2019, , 19-37.	1.3	2
110	Over the rainbow: structural characterization of the chromoproteins gfasPurple, amilCP, spisPink and eforRed. Acta Crystallographica Section D: Structural Biology, 2022, 78, 599-612.	2.3	2
111	Crystallization and preliminary X-ray analysis of the complexes between a Fab and two forms of human insulin-like growth factor II. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 945-948.	0.7	1
112	Classification of protein crystallisation images using texture-based statistical features. , 2013, , .		1
113	Understanding the control of grape berry ripening and developing opportunities for its manipulation. Acta Horticulturae, 2017, , 1-10.	0.2	1
114	Organizing a crystallization laboratory. Journal of Applied Crystallography, 2018, 51, 47-54.	4.5	1
115	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. Journal of Applied Crystallography, 2019, 52, 495-497.	4.5	1
116	The evolving story of AtzT, a periplasmic binding protein. Acta Crystallographica Section D: Structural Biology, 2019, 75, 995-1002.	2.3	1
117	Quantifying the quality of the experiments used to grow protein crystals: theiQCsuite. Journal of Applied Crystallography, 2014, 47, 1097-1106.	4.5	1
118	Submission of structural biology data for review purposes. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1477-1478.	2.3	1
119	An Observation about Circular Shortest Paths: Dealing with Additional Constraints Using Branch and Bound. , 2011, , .		0
120	Multi-view Learning for Classification of X-Ray Crystallography Images. Lecture Notes in Computer Science, 2016, , 446-458.	1.3	0
121	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
122	Taking biological structure communications into the third dimension. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 663-664.	0.8	0
123	Innovation versus practice in biological crystallization. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 290-291.	0.8	0
124	Contamination or serendipity “doing the wrong thing by chance. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 391-391.	0.8	0
125	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
126	Predicting the Effect of Chemical Factors on the pH of Crystallisation Trials. SSRN Electronic Journal, 0, , .	0.4	0

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127	Submission of structural biology data for review purposes. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 435-436.	0.8	0