

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
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130
all docs

130
docs citations

130
times ranked

5120
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Submission of structural biology data for review purposes. IUCrJ, 2022, 9, 1-2.	2.2	3
3	Insights Into Drug Repurposing, as Well as Specificity and Compound Properties of Piperidine-Based SARS-CoV-2 PLpro Inhibitors. Frontiers in Chemistry, 2022, 10, 861209.	3.6	11
4	Crystal structure of fungal tannase from <i>Aspergillus niger</i> . Acta Crystallographica Section D: Structural Biology, 2021, 77, 267-277.	2.3	6
5	Structure-guided selection of puromycin N-acetyltransferase mutants with enhanced selection stringency for deriving mammalian cell lines expressing recombinant proteins. Scientific Reports, 2021, 11, 5247.	3.3	2
6	Data- and diversity-driven development of a Shotgun crystallization screen using the Protein Data Bank. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1437-1450.	2.3	3
7	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
8	Submission of structural biology data for review purposes. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 435-436.	0.8	0
9	Design of a methotrexate-controlled chemical dimerization system and its use in bio-electronic devices. Nature Communications, 2021, 12, 7137.	12.8	17
10	Submission of structural biology data for review purposes. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1477-1478.	2.3	1
11	Mechanism and inhibition of the papain-like protease, PLpro, of SARS-CoV-2. EMBO Journal, 2020, 39, e106275.	7.8	330
12	Predicting the Effect of Chemical Factors on the pH of Crystallization Trials. IScience, 2020, 23, 101219.	4.1	3
13	Bacterial catabolism of s-triazine herbicides: biochemistry, evolution and application. Advances in Microbial Physiology, 2020, 76, 129-186.	2.4	10
14	Tools to Ease the Choice and Design of Protein Crystallisation Experiments. Crystals, 2020, 10, 95.	2.2	7
15	Crystal structures of human ENPP1 in apo and bound forms. Acta Crystallographica Section D: Structural Biology, 2020, 76, 889-898.	2.3	24
16	Innovation versus practice in biological crystallization. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 290-291.	0.8	0
17	Contamination or serendipity – “doing the wrong thing by chance. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 391-391.	0.8	0
18	The X-ray crystal structure of the N-terminal domain of Ssr4, a <i>Schizosaccharomyces pombe</i> chromatin-remodelling protein. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 583-589.	0.8	3

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19	<i>BLAST</i>ing away preconceptions in crystallization trials. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 184-192.	0.8	12
20	Fragment screening for a protein-protein interaction inhibitor to WDR5. Structural Dynamics, 2019, 6, 064701.	2.3	6
21	A Crystal/Clear Pipeline for Applied Image Processing. Lecture Notes in Computer Science, 2019, , 19-37.	1.3	2
22	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. Journal of Applied Crystallography, 2019, 52, 495-497.	4.5	1
23	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. IUCrJ, 2019, 6, 341-343.	2.2	8
24	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 321-323.	0.8	3
25	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. Acta Crystallographica Section D: Structural Biology, 2019, 75, 455-457.	2.3	10
26	Structures of the transcriptional regulator BgaR, a lactose sensor. Acta Crystallographica Section D: Structural Biology, 2019, 75, 639-646.	2.3	7
27	The evolving story of AtzT, a periplasmic binding protein. Acta Crystallographica Section D: Structural Biology, 2019, 75, 995-1002.	2.3	1
28	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
29	Taking biological structure communications into the third dimension. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 663-664.	0.8	0
30	Structural characterization of a novel monotreme-specific protein with antimicrobial activity from the milk of the platypus. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 39-45.	0.8	10
31	An unexpected vestigial protein complex reveals the evolutionary origins of an s-triazine catabolic enzyme. Journal of Biological Chemistry, 2018, 293, 7880-7891.	3.4	18
32	Organizing a crystallization laboratory. Journal of Applied Crystallography, 2018, 51, 47-54.	4.5	1
33	A novel decarboxylating amidohydrolase involved in avoiding metabolic dead ends during cyanuric acid catabolism in Pseudomonas sp. strain ADP. PLoS ONE, 2018, 13, e0206949.	2.5	11
34	<i>Cinder</i>: keeping crystallographers app-y. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 410-418.	0.8	7
35	Structural and biochemical characterization of the biuret hydrolase (BiuH) from the cyanuric acid catabolism pathway of Rhizobium leguminosarum bv. viciae 3841. PLoS ONE, 2018, 13, e0192736.	2.5	12
36	Classification of crystallization outcomes using deep convolutional neural networks. PLoS ONE, 2018, 13, e0198883.	2.5	54

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37	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
38	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
39	Understanding the control of grape berry ripening and developing opportunities for its manipulation. <i>Acta Horticulturae</i> , 2017, , 1-10.	0.2	1
40	Parallel and antiparallel cyclic α -peptide nanotubes. <i>Chemical Communications</i> , 2017, 53, 6613-6616.	4.1	36
41	The nanoscience behind the art of in-meso crystallization of membrane proteins. <i>Nanoscale</i> , 2017, 9, 754-763.	5.6	30
42	Reverse engineering: transaminase biocatalyst development using ancestral sequence reconstruction. <i>Green Chemistry</i> , 2017, 19, 5375-5380.	9.0	36
43	Lipidic Cubic Phase-Induced Membrane Protein Crystallization: Interplay Between Lipid Molecular Structure, Mesophase Structure and Properties, and Crystallogenesis. <i>Crystal Growth and Design</i> , 2017, 17, 5667-5674.	3.0	16
44	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
45	A 12 C-Alanine Catabolism Pathway Containing a Highly Promiscuous α -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
46	Some of the most interesting α -CASP11 targets through the eyes of their authors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 34-50.	2.6	16
47	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
48	Structural and functional characterisation of ferret interleukin-2. <i>Developmental and Comparative Immunology</i> , 2016, 55, 32-38.	2.3	2
49	Multi-view Learning for Classification of X-Ray Crystallography Images. <i>Lecture Notes in Computer Science</i> , 2016, , 446-458.	1.3	0
50	X-Ray Structure and Mutagenesis Studies of the N-Isopropylammelide Isopropylaminohydrolase, AtzC. <i>PLoS ONE</i> , 2015, 10, e0137700.	2.5	5
51	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
52	Rational engineering of a mesohalophilic carbonic anhydrase to an extreme halotolerant biocatalyst. <i>Nature Communications</i> , 2015, 6, 10278.	12.8	80
53	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
54	The structure of the hexameric atrazine chlorohydrolase AtzA. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 710-720.	2.5	19

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55	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
56	Transmembrane Complexes of DAP12 Crystallized in Lipid Membranes Provide Insights into Control of Oligomerization in Immunoreceptor Assembly. Cell Reports, 2015, 11, 1184-1192.	6.4	20
57	Crystallization: Digging into the Past to Learn Lessons for the Future. Methods in Molecular Biology, 2015, 1261, 141-156.	0.9	4
58	What's in a Name? Moving Towards a Limited Vocabulary for Macromolecular Crystallisation. Australian Journal of Chemistry, 2014, 67, 1813.	0.9	10
59	Nitrate in the active site of protein tyrosine phosphatase 1B is a putative mimetic of the transition state. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 565-571.	2.5	2
60	Crystallization screening: the influence of history on current practice. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 835-853.	0.8	54
61	The structure of vanin 1: a key enzyme linking metabolic disease and inflammation. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 3320-3329.	2.5	37
62	Crystallization and preliminary X-ray diffraction analysis of the amidase domain of allophanate hydrolase from <i>Pseudomonas</i> sp. strain ADP. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 310-315.	0.8	8
63	Interrogating HIV integrase for compounds that bind- a SAMPL challenge. Journal of Computer-Aided Molecular Design, 2014, 28, 347-362.	2.9	25
64	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
65	A drunken search in crystallization space. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1303-1311.	0.8	38
66	Identifying, studying and making good use of macromolecular crystals. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 993-1008.	0.8	23
67	Using Time Courses To Enrich the Information Obtained from Images of Crystallization Trials. Crystal Growth and Design, 2014, 14, 261-269.	3.0	15
68	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
69	Quantifying the quality of the experiments used to grow protein crystals: theiQCsuite. Journal of Applied Crystallography, 2014, 47, 1097-1106.	4.5	1
70	Parallel Screening of Low Molecular Weight Fragment Libraries: Do Differences in Methodology Affect Hit Identification?. Journal of Biomolecular Screening, 2013, 18, 147-159.	2.6	61
71	Using Graphs to Represent Crystallization Conditions. Crystal Growth and Design, 2013, 13, 1290-1294.	3.0	2
72	High-Throughput Thermal Scanning for Protein Stability: Making a Good Technique More Robust. ACS Combinatorial Science, 2013, 15, 387-392.	3.8	62

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73	Crystallization reports are the backbone of <i>Acta Cryst. F</i> , but do they have any spine?. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 712-718.	0.7	11
74	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
75	Cyanuric acid hydrolase: evolutionary innovation by structural concatenation. <i>Molecular Microbiology</i> , 2013, 88, 1149-1163.	2.5	31
76	Classification of protein crystallisation images using texture-based statistical features. , 2013, , .		1
77	Fragment Screening for the Modelling Community: SPR, ITC, and Crystallography. <i>Australian Journal of Chemistry</i> , 2013, 66, 1507.	0.9	6
78	Determination of the Structure of the Catabolic N-Succinylornithine Transaminase (AstC) from <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2013, 8, e58298.	2.5	17
79	Exploring the Chemical Space around 8-Mercaptoguanine as a Route to New Inhibitors of the Folate Biosynthesis Enzyme HPPK. <i>PLoS ONE</i> , 2013, 8, e59535.	2.5	17
80	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
81	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
82	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
83	A universal indicator dye pH assay for crystallization solutions and other high-throughput applications. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1003-1009.	2.5	13
84	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
85	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
86	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
87	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
88	An Observation about Circular Shortest Paths: Dealing with Additional Constraints Using Branch and Bound. , 2011, , .		0
89	Evaluating Protic Ionic Liquids as Protein Crystallization Additives. <i>Crystal Growth and Design</i> , 2011, 11, 1777-1785.	3.0	46
90	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

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91	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
92	Cloning, expression, purification and crystallization of dihydrodipicolinate synthase from the grapevine <i>Vitis vinifera</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1537-1541.	0.7	11
93	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
94	Structural Basis for a New Mechanism of Inhibition of HIV-1 Integrase Identified by Fragment Screening and Structure-Based Design. <i>Antiviral Chemistry and Chemotherapy</i> , 2011, 21, 155-168.	0.6	49
95	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
96	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
97	A new crystal form of human vascular adhesion protein 1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1572-1578.	0.7	16
98	Germline humanization of a murine $\text{A}\beta^2$ antibody and crystal structure of the humanized recombinant Fab fragment. <i>Protein Science</i> , 2010, 19, 299-308.	7.6	25
99	Identification and characterization of two families of $\text{F}_{420}\text{H}_{20}$ -dependent reductases from <i>Mycobacteria</i> that catalyse aflatoxin degradation. <i>Molecular Microbiology</i> , 2010, 78, 561-575.	2.5	132
100	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
101	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
102	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
103	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
104	Crystallization and preliminary X-ray analysis of dihydrodipicolinate synthase from <i>Clostridium botulinum</i> in the presence of its substrate pyruvate. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 253-255.	0.7	14
105	Crystallization and preliminary X-ray analysis of the complexes between a Fab and two forms of human insulin-like growth factor II. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 945-948.	0.7	1
106	The purification, crystallization and preliminary X-ray diffraction analysis of dihydrodipicolinate synthase from <i>Clostridium botulinum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 206-208.	0.7	14
107	Phoenito experiments: combining the strengths of commercial crystallization automation. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 991-996.	0.7	31
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	Improved Success of Sparse Matrix Protein Crystallization Screening with Heterogeneous Nucleating Agents. <i>PLoS ONE</i> , 2007, 2, e1091.	2.5	49
110	Initial evaluations of the reproducibility of vapor-diffusion crystallization. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 826-832.	2.5	36
111	A review of techniques for maximizing diffraction from a protein crystal in still. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 27-31.	2.5	42
112	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
113	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
114	Tapping the Protein Data Bank for crystallization information. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1662-1669.	2.5	29
115	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
116	Novel buffer systems for macromolecular crystallization. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 610-612.	2.5	111
117	Structural Studies of <i>Salmonella typhimurium</i> ArnB (PmrH) Aminotransferase. <i>Structure</i> , 2002, 10, 1569-1580.	3.3	73
118	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
119	Crystal Structure of the Haloalkane Dehalogenase from <i>Sphingomonas paucimobilis</i> UT26. <i>Biochemistry</i> , 2000, 39, 14082-14086.	2.5	118
120	Haloalkane Dehalogenases: Structure of a <i>Rhodococcus</i> Enzyme. <i>Biochemistry</i> , 1999, 38, 16105-16114.	2.5	150
121	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
122	Class-directed structure determination: Foundation for a protein structure initiative. <i>Protein Science</i> , 1998, 7, 1851-1856.	7.6	89
123	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
124	The crystal structures of Rubisco and opportunities for manipulating photosynthesis. <i>Journal of Experimental Botany</i> , 1995, 46, 1261-1267.	4.8	8
125	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
126	Redetermination of the crystal structure of hexaamminecobalt(II) chloride. <i>Inorganic Chemistry</i> , 1991, 30, 3499-3502.	4.0	16

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127	Predicting the Effect of Chemical Factors on the pH of Crystallisation Trials. SSRN Electronic Journal, 0, , .	0.4	0