

Paul Langan

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2513084/publications.pdf>

Version: 2024-02-01

155
papers

13,517
citations

57758

44
h-index

21540

114
g-index

183
all docs

183
docs citations

183
times ranked

12725
citing authors

#	ARTICLE	IF	CITATIONS
1	Capturing the Catalytic Proton of Dihydrofolate Reductase: Implications for General Acid-Base Catalysis. <i>ACS Catalysis</i> , 2021, 11, 5873-5884.	11.2	8
2	BraggNet: integrating Bragg peaks using neural networks. <i>Journal of Applied Crystallography</i> , 2019, 52, 854-863.	4.5	25
3	Tension wood structure and morphology conducive for better enzymatic digestion. <i>Biotechnology for Biofuels</i> , 2018, 11, 44.	6.2	26
4	Neutron scattering in the biological sciences: progress and prospects. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 1129-1168.	2.3	47
5	Evaluation of models determined by neutron diffraction and proposed improvements to their validation and deposition. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 800-813.	2.3	15
6	Improving the accuracy and resolution of neutron crystallographic data by three-dimensional profile fitting of Bragg peaks in reciprocal space. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 1085-1095.	2.3	27
7	Understanding Multiscale Structural Changes During Dilute Acid Pretreatment of Switchgrass and Poplar. <i>ACS Sustainable Chemistry and Engineering</i> , 2017, 5, 426-435.	6.7	29
8	Responses to 'Atomic resolution': a badly abused term in structural biology. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 381-383.	2.3	7
9	Dynamics of water bound to crystalline cellulose. <i>Scientific Reports</i> , 2017, 7, 11840.	3.3	82
10	Long-Range Electrostatics-Induced Two-Proton Transfer Captured by Neutron Crystallography in an Enzyme Catalytic Site. <i>Angewandte Chemie</i> , 2016, 128, 5008-5011.	2.0	6
11	Long-Range Electrostatics-Induced Two-Proton Transfer Captured by Neutron Crystallography in an Enzyme Catalytic Site. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 4924-4927.	13.8	42
12	Structural Studies of Plant CESA Support Eighteen CESAs in the Plant CSC. <i>Biophysical Journal</i> , 2016, 110, 27a.	0.5	0
13	Molecular Interactions in an α -Chitin/Hydrazine Complex: Dynamic Hydrogen Bonds and Improvement of Polymeric Crystallinity. <i>Crystal Growth and Design</i> , 2016, 16, 3345-3352.	3.0	6
14	Visualizing the Bohr effect in hemoglobin: neutron structure of equine cyanomethemoglobin in the R state and comparison with human deoxyhemoglobin in the T state. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 892-903.	2.3	7
15	A Structural Study of CESA1 Catalytic Domain of Arabidopsis Cellulose Synthesis Complex: Evidence for CESA Trimers. <i>Plant Physiology</i> , 2016, 170, 123-135.	4.8	104
16	Production of Bacterial Cellulose with Controlled Deuterium-Hydrogen Substitution for Neutron Scattering Studies. <i>Methods in Enzymology</i> , 2015, 565, 123-146.	1.0	11
17	MARTINI Coarse-Grained Model for Crystalline Cellulose Microfibers. <i>Journal of Physical Chemistry B</i> , 2015, 119, 465-473.	2.6	54
18	Phosphoryl Transfer Reaction Snapshots in Crystals. <i>Journal of Biological Chemistry</i> , 2015, 290, 15538-15548.	3.4	22

#	ARTICLE	IF	CITATIONS
19	Direct determination of protonation states and visualization of hydrogen bonding in a glycoside hydrolase with neutron crystallography. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 12384-12389.	7.1	35
20	Why genetic modification of lignin leads to low-recalcitrance biomass. Physical Chemistry Chemical Physics, 2015, 17, 358-364.	2.8	38
21	Protein Kinase A Catalytic Subunit Primed for Action: Time-Lapse Crystallography of Michaelis Complex Formation. Structure, 2015, 23, 2331-2340.	3.3	22
22	The Macromolecular Neutron Diffractometer MaNDi at the Spallation Neutron Source. Journal of Applied Crystallography, 2015, 48, 1302-1306.	4.5	64
23	Determination of cellulose crystallinity from powder diffraction diagrams. Biopolymers, 2015, 103, 67-73.	2.4	15
24	Thermal green protein, an extremely stable, nonaggregating fluorescent protein created by structure-guided surface engineering. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1225-1237.	2.6	18
25	Effect of lignin content on changes occurring in poplar cellulose ultrastructure during dilute acid pretreatment. Biotechnology for Biofuels, 2014, 7, 150.	6.2	113
26	Toward resolving the catalytic mechanism of dihydrofolate reductase using neutron and ultrahigh-resolution X-ray crystallography. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 18225-18230.	7.1	72
27	Preliminary joint X-ray and neutron protein crystallographic studies of ecDHFR complexed with folate and NADP ⁺ . Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 814-818.	0.8	7
28	Morphological changes in the cellulose and lignin components of biomass occur at different stages during steam pretreatment. Cellulose, 2014, 21, 873-878.	4.9	37
29	Lignin Valorization: Improving Lignin Processing in the Biorefinery. Science, 2014, 344, 1246843.	12.6	2,994
30	Common processes drive the thermochemical pretreatment of lignocellulosic biomass. Green Chemistry, 2014, 16, 63-68.	9.0	198
31	Hydration Control of the Mechanical and Dynamical Properties of Cellulose. Biomacromolecules, 2014, 15, 4152-4159.	5.4	44
32	L-Arabinose Binding, Isomerization, and Epimerization by D-Xylose Isomerase: X-Ray/Neutron Crystallographic and Molecular Simulation Study. Structure, 2014, 22, 1287-1300.	3.3	22
33	Controlled incorporation of deuterium into bacterial cellulose. Cellulose, 2014, 21, 927-936.	4.9	30
34	Structural coarsening of aspen wood by hydrothermal pretreatment monitored by small- and wide-angle scattering of X-rays and neutrons on oriented specimens. Cellulose, 2014, 21, 1015-1024.	4.9	56
35	Solid-state solvent molecular interactions observed in crystal structures of β -chitin complexes. Cellulose, 2014, 21, 1007-1014.	4.9	5
36	The initial structure of cellulose during ammonia pretreatment. Cellulose, 2014, 21, 1117-1126.	4.9	14

#	ARTICLE	IF	CITATIONS
37	100 Years of cellulose fiber diffraction and the emergence of complementary techniques. <i>Cellulose</i> , 2014, 21, 1087-1089.	4.9	3
38	Metal-Free cAMP-Dependent Protein Kinase Can Catalyze Phosphoryl Transfer. <i>Biochemistry</i> , 2014, 53, 3179-3186.	2.5	18
39	Engineering acidic <i>Streptomyces rubiginosus</i> D-xylose isomerase by rational enzyme design. <i>Protein Engineering, Design and Selection</i> , 2014, 27, 59-64.	2.1	19
40	Comparison of changes in cellulose ultrastructure during different pretreatments of poplar. <i>Cellulose</i> , 2014, 21, 2419-2431.	4.9	47
41	Hydrolysis of DFP and the Nerve Agent (<i>S</i>)-Sarin by DFPase Proceeds along Two Different Reaction Pathways: Implications for Engineering Bioscavengers. <i>Journal of Physical Chemistry B</i> , 2014, 118, 4479-4489.	2.6	42
42	X-ray crystallographic studies of family 11 xylanase Michaelis and product complexes: implications for the catalytic mechanism. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 11-23.	2.5	34
43	Structure and dynamics of a complex of cellulose with EDA: insights into the action of amines on cellulose. <i>Cellulose</i> , 2013, 20, 1563-1571.	4.9	18
44	Seeing the chemistry in biology with neutron crystallography. <i>Physical Chemistry Chemical Physics</i> , 2013, 15, 13705.	2.8	21
45	Insights into the Phosphoryl Transfer Catalyzed by cAMP-Dependent Protein Kinase: An X-ray Crystallographic Study of Complexes with Various Metals and Peptide Substrate SP20. <i>Biochemistry</i> , 2013, 52, 3721-3727.	2.5	24
46	The crystal structure of mono-ethylenediamine β -chitin from synchrotron X-ray fiber diffraction. <i>Carbohydrate Polymers</i> , 2013, 92, 1737-1742.	10.2	18
47	Joint X-ray/Neutron Crystallographic Study of HIV-1 Protease with Clinical Inhibitor Amprenavir: Insights for Drug Design. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 5631-5635.	6.4	61
48	Heterologous expression, purification, crystallization and preliminary X-ray analysis of <i>Trichoderma reesei</i> xylanase II and four variants. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 320-323.	0.7	2
49	Neutron Technologies for Bioenergy Research. <i>Industrial Biotechnology</i> , 2012, 8, 209-216.	0.8	17
50	Direct observation of hydrogen atom dynamics and interactions by ultrahigh resolution neutron protein crystallography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15301-15306.	7.1	51
51	Inhibition of D-xylose isomerase by polyols: atomic details by joint X-ray/neutron crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1201-1206.	2.5	18
52	Evidence for Complex Molecular Architectures for Solvent-Extracted Lignins. <i>ACS Macro Letters</i> , 2012, 1, 568-573.	4.8	33
53	Coarse-Grained Model for the Interconversion between Native and Liquid Ammonia-Treated Crystalline Cellulose. <i>Journal of Physical Chemistry B</i> , 2012, 116, 8031-8037.	2.6	27
54	A coarse-grained model for synergistic action of multiple enzymes on cellulose. <i>Biotechnology for Biofuels</i> , 2012, 5, 55.	6.2	39

#	ARTICLE	IF	CITATIONS
55	Direct Determination of the Hydrogen Bonding Arrangement in Anhydrous β -D-Glucan by Neutron Fiber Diffraction. <i>Biomacromolecules</i> , 2012, 13, 288-291.	5.4	39
56	Inorganic pyrophosphatase crystals from <i>Thermococcus thio-reducens</i> for X-ray and neutron diffraction. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1482-1487.	0.7	19
57	Water in Crystalline Fibers of Dihydrate β -D-Glucan Results in Unexpected Absence of Intramolecular Hydrogen Bonding. <i>PLoS ONE</i> , 2012, 7, e39376.	2.5	55
58	Room-temperature ultrahigh-resolution time-of-flight neutron and X-ray diffraction studies of H/D-exchanged crambin. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 119-123.	0.7	9
59	Low- and room-temperature X-ray structures of protein kinase A ternary complexes shed new light on its activity. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 854-860.	2.5	26
60	Exploring new strategies for cellulosic biofuels production. <i>Energy and Environmental Science</i> , 2011, 4, 3820.	30.8	79
61	Neutron Structure of Human Carbonic Anhydrase II: A Hydrogen-Bonded Water Network Observed between pH 7.8 and 10.0. <i>Biochemistry</i> , 2011, 50, 9421-9423.	2.5	52
62	Restructuring the Crystalline Cellulose Hydrogen Bond Network Enhances Its Depolymerization Rate. <i>Journal of the American Chemical Society</i> , 2011, 133, 11163-11174.	13.7	321
63	Probing the Early Events Associated with Liquid Ammonia Pretreatment of Native Crystalline Cellulose. <i>Journal of Physical Chemistry B</i> , 2011, 115, 9782-9788.	2.6	33
64	Ionic-Liquid Induced Changes in Cellulose Structure Associated with Enhanced Biomass Hydrolysis. <i>Biomacromolecules</i> , 2011, 12, 3091-3098.	5.4	113
65	Multiresolution Molecular Dynamics Simulations of Crystalline Nanofibrils. <i>Biophysical Journal</i> , 2011, 100, 310a.	0.5	0
66	Regioselectivity of Enzymatic and Photochemical Single Electron Transfer Promoted Carbon-Carbon Bond Fragmentation Reactions of Tetrameric Lignin Model Compounds. <i>Journal of Organic Chemistry</i> , 2011, 76, 2840-2852.	3.2	40
67	Insights into Hydrogen Bonding and Stacking Interactions in Cellulose. <i>Journal of Physical Chemistry A</i> , 2011, 115, 14191-14202.	2.5	122
68	Reintroducing Electrostatics into Macromolecular Crystallographic Refinement: Application to Neutron Crystallography and DNA Hydration. <i>Structure</i> , 2011, 19, 523-533.	3.3	36
69	Neutron crystallographic and molecular dynamics studies of the structure of ammonia-cellulose I: rearrangement of hydrogen bonding during the treatment of cellulose with ammonia. <i>Cellulose</i> , 2011, 18, 191-206.	4.9	39
70	High-resolution neutron crystallographic studies of the hydration of the coenzyme cob(II)alamin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 584-591.	2.5	30
71	Preliminary joint X-ray and neutron protein crystallographic studies of endoxylanase II from the fungus <i>Trichoderma longibrachiatum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 283-286.	0.7	6
72	Preliminary joint neutron time-of-flight and X-ray crystallographic study of human ABO(H) blood group A glycosyltransferase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 258-262.	0.7	4

#	ARTICLE	IF	CITATIONS
73	Time-of-flight neutron diffraction study of bovine \hat{I}^3 -chymotrypsin at the Protein Crystallography Station. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 587-590.	0.7	1
74	Identification of the Elusive Hydronium Ion Exchanging Roles with a Proton in an Enzyme at Lower pHâ€¦Values. <i>Angewandte Chemie - International Edition</i> , 2011, 50, 7520-7523.	13.8	62
75	Reversible swelling of the cell wall of poplar biomass by ionic liquid at room temperature. <i>Bioresource Technology</i> , 2011, 102, 4518-4523.	9.6	53
76	Time-resolved X-ray diffraction microprobe studies of the conversion of cellulose I to ethylenediamine-cellulose I. <i>Cellulose</i> , 2010, 17, 735-745.	4.9	30
77	Metal Ion Roles and the Movement of Hydrogen during Reaction Catalyzed by D-Xylose Isomerase: A Joint X-Ray and Neutron Diffraction Study. <i>Structure</i> , 2010, 18, 688-699.	3.3	139
78	Enzymes for carbon sequestration: neutron crystallographic studies of carbonic anhydrase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1178-1183.	2.5	10
79	Protonation states of histidine and other key residues in deoxy normal human adult hemoglobin by neutron protein crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1144-1152.	2.5	6
80	Hemoglobin redux: combining neutron and X-ray diffraction with mass spectrometry to analyse the quaternary state of oxidized hemoglobins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1249-1256.	2.5	1
81	Joint X-ray and neutron refinement with<i>phenix.refine</i>. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1153-1163.	2.5	259
82	Macromolecular neutron crystallography at the Protein Crystallography Station (PCS). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1206-1212.	2.5	11
83	Using neutron protein crystallography to understand enzyme mechanisms. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1257-1261.	2.5	5
84	In silicostudies of crystalline cellulose and its degradation by enzymes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1184-1188.	2.5	25
85	Looking at hydrogen bonds in cellulose. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1172-1177.	2.5	48
86	Neutron structure and mechanistic studies of diisopropyl fluorophosphatase (DFPase). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1131-1138.	2.5	18
87	Opportunities and challenges with the growth of neutron crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1121-1123.	2.5	5
88	X-ray structure of perdeuterated diisopropyl fluorophosphatase (DFPase): perdeuteration of proteins for neutron diffraction. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 379-385.	0.7	16
89	Preliminary neutron and X-ray crystallographic studies of equine cyanomethemoglobin. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 474-477.	0.7	4
90	A joint x-ray and neutron study on amicyanin reveals the role of protein dynamics in electron transfer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 6817-6822.	7.1	36

#	ARTICLE	IF	CITATIONS
91	Neutron Structure of Human Carbonic Anhydrase II: Implications for Proton Transfer. <i>Biochemistry</i> , 2010, 49, 415-421.	2.5	82
92	Direct Determination of Protonation States of Histidine Residues in a 2Å... Neutron Structure of Deoxy-Human Normal Adult Hemoglobin and Implications for the Bohr Effect. <i>Journal of Molecular Biology</i> , 2010, 398, 276-291.	4.2	35
93	Nature and Kinetic Analysis of Carbon-13 Carbon Bond Fragmentation Reactions of Cation Radicals Derived from SET-Oxidation of Lignin Model Compounds. <i>Journal of Organic Chemistry</i> , 2010, 75, 6549-6562.	3.2	88
94	Rapid determination of hydrogen positions and protonation states of diisopropyl fluorophosphatase by joint neutron and X-ray diffraction refinement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 713-718.	7.1	77
95	The structure of the complex of cellulose I with ethylenediamine by X-ray crystallography and cross-polarization/magic angle spinning ¹³ C nuclear magnetic resonance. <i>Cellulose</i> , 2009, 16, 943-957.	4.9	42
96	Generalized X-ray and neutron crystallographic analysis: more accurate and complete structures for biological macromolecules. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 567-573.	2.5	137
97	Preliminary joint neutron and X-ray crystallographic study of human carbonic anhydrase II. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 495-498.	0.7	13
98	X-ray structure of the ternary MTX- ¹⁴ NADPH complex of the anthrax dihydrofolate reductase: A pharmacophore for dual-site inhibitor design. <i>Journal of Structural Biology</i> , 2009, 166, 162-171.	2.8	25
99	X-ray Crystallographic, Scanning Microprobe X-ray Diffraction, and Cross-Polarized/Magic Angle Spinning ¹³ C NMR Studies of the Structure of Cellulose III _{II} . <i>Biomacromolecules</i> , 2009, 10, 302-309.	5.4	63
100	Conformational Flexibility of Soluble Cellulose Oligomers: Chain Length and Temperature Dependence. <i>Journal of the American Chemical Society</i> , 2009, 131, 14786-14794.	13.7	102
101	Protein structures by spallation neutron crystallography. <i>Journal of Synchrotron Radiation</i> , 2008, 15, 215-218.	2.4	35
102	Preliminary time-of-flight neutron diffraction study of human deoxyhemoglobin. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 270-273.	0.7	9
103	New sources and instrumentation for neutrons in biology. <i>Chemical Physics</i> , 2008, 345, 133-151.	1.9	53
104	Tailored instrumentation for long-pulse neutron spallation sources. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 2008, 589, 34-46.	1.6	29
105	Neutron crystallography: opportunities, challenges, and limitations. <i>Current Opinion in Structural Biology</i> , 2008, 18, 593-600.	5.7	136
106	Neutron Crystallography, Molecular Dynamics, and Quantum Mechanics Studies of the Nature of Hydrogen Bonding in Cellulose I _β . <i>Biomacromolecules</i> , 2008, 9, 3133-3140.	5.4	215
107	Hydrogen Location in Stages of an Enzyme-Catalyzed Reaction: Time-of-Flight Neutron Structure of d-Xylose Isomerase with Bound d-Xylulose. <i>Biochemistry</i> , 2008, 47, 7595-7597.	2.5	42
108	The structure of celluloses. <i>Powder Diffraction</i> , 2008, 23, 92-95.	0.2	33

#	ARTICLE	IF	CITATIONS
109	The effect of deuteration on protein structure: a high-resolution comparison of hydrogenous and perdeuterated haloalkane dehalogenase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 1000-1008.	2.5	42
110	Neutron and X-ray structural studies of short hydrogen bonds in photoactive yellow protein (PYP). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 1178-1184.	2.5	42
111	Preliminary time-of-flight neutron diffraction study on diisopropyl fluorophosphatase (DFPase) from <i>Loligo vulgaris</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 42-45.	0.7	21
112	Preliminary neutron and ultrahigh-resolution X-ray diffraction studies of the aspartic proteinase endothiapepsin cocrystallized with a gem-diol inhibitor. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 1080-1083.	0.7	10
113	X-ray Structure of Ammonia ⁺ Cellulose I: A New Insights into the Conversion of Cellulose I to Cellulose III. <i>Macromolecules</i> , 2006, 39, 2947-2952.	4.8	94
114	Synthesis, capillary crystallization and preliminary joint X-ray and neutron crystallographic study of Z-DNA without polyamine at low pH. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 453-456.	0.7	11
115	Locating active-site hydrogen atoms in D-xylose isomerase: Time-of-flight neutron diffraction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 8342-8347.	7.1	60
116	Neutron diffraction studies of <i>Escherichia coli</i> dihydrofolate reductase complexed with methotrexate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 18493-18498.	7.1	68
117	Synchrotron X-ray structures of cellulose II ² and regenerated cellulose II at ambient temperature and 100 ÅK. <i>Cellulose</i> , 2005, 12, 551-562.	4.9	102
118	A preliminary time-of-flight neutron diffraction study on amicyanin from <i>Paracoccus denitrificans</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 640-642.	2.5	14
119	Conceptual design of a macromolecular neutron diffractometer (MaNDi) for the SNS. <i>Journal of Applied Crystallography</i> , 2005, 38, 964-974.	4.5	31
120	Neutron diffraction from fibers. <i>Crystallography Reviews</i> , 2005, 11, 125-147.	1.5	9
121	W3Y single mutant of rubredoxin from <i>Pyrococcus furiosus</i> : a preliminary time-of-flight neutron study. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 200-202.	2.5	8
122	A preliminary time-of-flight neutron diffraction study of <i>Streptomyces rubiginosus</i> D-xylose isomerase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 241-249.	2.5	20
123	Protein crystallography with spallation neutrons. <i>Journal of Synchrotron Radiation</i> , 2004, 11, 80-82.	2.4	23
124	Protein crystallography with spallation neutrons: the user facility at Los Alamos Neutron Science Center. <i>Journal of Applied Crystallography</i> , 2004, 37, 24-31.	4.5	66
125	Protein crystallography with spallation neutrons: collecting and processing wavelength-resolved Laue protein data. <i>Journal of Applied Crystallography</i> , 2004, 37, 253-257.	4.5	45
126	Cellulose III Crystal Structure and Hydrogen Bonding by Synchrotron X-ray and Neutron Fiber Diffraction. <i>Macromolecules</i> , 2004, 37, 8548-8555.	4.8	267

#	ARTICLE	IF	CITATIONS
127	New Facilities Expand Protein Crystallography Opportunities. <i>Physics Today</i> , 2004, 57, 19-19.	0.3	2
128	Crystal Structure and Hydrogen Bonding System in Cellulose II from Synchrotron X-ray and Neutron Fiber Diffraction. <i>Journal of the American Chemical Society</i> , 2003, 125, 14300-14306.	13.7	1,274
129	Periodic Disorder along Ramie Cellulose Microfibrils. <i>Biomacromolecules</i> , 2003, 4, 1013-1017.	5.4	216
130	Preparation of Tunicin Cellulose II Samples for X-ray and Neutron Diffraction. <i>Fibre Diffraction Review</i> , 2003, 11, 75.	0.6	1
131	Structural characterization of crystals of L-glycine during anomalous electrical behaviour. <i>Acta Crystallographica Section B: Structural Science</i> , 2002, 58, 728-733.	1.8	70
132	Crystal Structure and Hydrogen-Bonding System in Cellulose II from Synchrotron X-ray and Neutron Fiber Diffraction. <i>Journal of the American Chemical Society</i> , 2002, 124, 9074-9082.	13.7	2,231
133	X-ray Structure of Mercerized Cellulose II at 1 Å... Resolution. <i>Biomacromolecules</i> , 2001, 2, 410-416.	5.4	457
134	<title>Device for cutting the time tail from spallation neutron pulses</title>. , 2001, , .		1
135	A low-temperature neutron diffraction study of Mn ²⁺ -acetate. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 2001, 57, 909-910.	0.4	7
136	Neutron Laue diffraction studies of coenzyme cob(II)alamin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 51-59.	2.5	17
137	High resolution neutron fibre diffraction data on hydrogenated and deuterated cellulose. <i>International Journal of Biological Macromolecules</i> , 1999, 26, 279-283.	7.5	35
138	A Revised Structure and Hydrogen-Bonding System in Cellulose II from a Neutron Fiber Diffraction Analysis. <i>Journal of the American Chemical Society</i> , 1999, 121, 9940-9946.	13.7	328
139	Need for Neutron Diffraction Instruments. <i>Science</i> , 1999, 286, 1089-1089.	12.6	0
140	New Developments in Instrumentation for X-ray and Neutron Fibre Diffraction Experiments. <i>Journal of Applied Crystallography</i> , 1998, 31, 758-766.	4.5	17
141	Neutron fibre diffraction: Recent advances at the ILL. <i>Physica B: Condensed Matter</i> , 1997, 234-236, 213-214.	2.7	3
142	The distribution of water in highly ordered fibres of hyaluronic acid. <i>Physica B: Condensed Matter</i> , 1997, 234-236, 215-216.	2.7	3
143	Neutron diffraction measurements on the C15 Laves phase TaV ₂ Dx. <i>Physica B: Condensed Matter</i> , 1997, 234-236, 945-948.	2.7	1
144	Neutron Laue diffraction in macromolecular crystallography. <i>Physica B: Condensed Matter</i> , 1997, 241-243, 1122-1130.	2.7	32

#	ARTICLE	IF	CITATIONS
145	Ordered water around deuterated A-DNA by neutron fibre diffraction. Physica B: Condensed Matter, 1997, 241-243, 1156-1158.	2.7	3
146	A high-angle neutron fibre diffraction study of the hydration of B-DNA. Physica B: Condensed Matter, 1997, 241-243, 1166-1168.	2.7	4
147	A high-angle neutron fibre diffraction study of the hydration of deuterated A-DNA. Biophysical Chemistry, 1997, 69, 85-96.	2.8	44
148	Collecting and Processing Neutron Fibre Diffraction Data from a Single-Crystal Diffractometer. Journal of Applied Crystallography, 1996, 29, 383-389.	4.5	19
149	Attenuation corrections for X-ray and neutron fibre diffraction studies. Journal of Applied Crystallography, 1995, 28, 49-52.	4.5	2
150	Neutron fibre diffraction studies of DNA hydration. Physica B: Condensed Matter, 1995, 213-214, 783-785.	2.7	6
151	High angle neutron fibre diffraction studies of the distribution of water around the D form of DNA. Physica B: Condensed Matter, 1992, 180-181, 737-739.	2.7	3
152	A neutron diffraction study of the distribution of water in the A form of the DNA double helix. Physica B: Condensed Matter, 1992, 180-181, 759-761.	2.7	7
153	Neutron diffraction studies of the structure of PEEK. Physica B: Condensed Matter, 1992, 180-181, 528-530.	2.7	8
154	The location of water around the DNA double-helix. Physica B: Condensed Matter, 1989, 156-157, 468-470.	2.7	18
155	Battery cell analysis via changes in the slope of the "as-found" data to identify marginal capacity cells. , 0, , .		2