

John Helliwell

List of Publications by Year in descending order

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361
papers

7,176
citations

66315

42
h-index

85498

71
g-index

462
all docs

462
docs citations

462
times ranked

5475
citing authors

#	ARTICLE	IF	CITATIONS
1	Protein hydration dynamics in solution: a critical survey. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2004, 359, 1207-1224.	1.8	475
2	The recording and analysis of synchrotron X-radiation Laue diffraction photographs. <i>Journal of Applied Crystallography</i> , 1989, 22, 483-497.	1.9	190
3	The molecular basis of the coloration mechanism in lobster shell: \hat{A} -Crustacyanin at 3.2- \hat{A} resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 9795-9800.	3.3	177
4	Three-dimensional structure of human erythrocytic purine nucleoside phosphorylase at 3.2 \hat{A} resolution.. <i>Journal of Biological Chemistry</i> , 1990, 265, 1812-1820.	1.6	168
5	Synchrotron X-radiation protein crystallography: instrumentation, methods and applications. <i>Reports on Progress in Physics</i> , 1984, 47, 1403-1497.	8.1	155
6	X-Ray and molecular dynamics studies of concanavalin-A glucoside and mannoside complexes Relating structure to thermodynamics of binding. <i>Journal of the Chemical Society, Faraday Transactions</i> , 1998, 94, 1603-1611.	1.7	143
7	Protein crystal perfection and the nature of radiation damage. <i>Journal of Crystal Growth</i> , 1988, 90, 259-272.	0.7	136
8	The structure of concanavalin A and its bound solvent determined with small-molecule accuracy at 0.94 [Aring]resolution. <i>Journal of the Chemical Society, Faraday Transactions</i> , 1997, 93, 4305-4312.	1.7	132
9	Active site of trypanothione reductase. <i>Journal of Molecular Biology</i> , 1992, 227, 322-333.	2.0	129
10	THREE-DIMENSIONAL STRUCTURE OF HUMAN ERYTHROCYTIC PURINE NUCLEOSIDE PHOSPHORYLASE AT 3.2 ANGSTROMS RESOLUTION. , 1990, 265, 1812-20.		127
11	Laue crystallography: coming of age. <i>Journal of Synchrotron Radiation</i> , 1999, 6, 891-917.	1.0	122
12	Crystal Structure of Peach Pru p 3, the Prototypic Member of the Family of Plant Non-specific Lipid Transfer Protein Pan-allergens. <i>Journal of Molecular Biology</i> , 2006, 356, 684-694.	2.0	122
13	Refined structure of concanavalin A complexed with methyl \hat{I} -D-mannopyranoside at 2.0 \hat{A} ... resolution and comparison with the saccharide-free structure. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1994, 50, 847-858.	2.5	121
14	LSCALE \hat{e} “ the new normalization, scaling and absorption correction program in the DaresburyLauesoftware suite. <i>Journal of Applied Crystallography</i> , 1999, 32, 554-562.	1.9	102
15	Multiplicity distribution of reflections in Laue diffraction. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 1987, 43, 656-674.	0.3	96
16	Improvements in lysozyme protein crystal perfection through microgravity growth. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995, 51, 1099-1102.	2.5	86
17	Macromolecular crystallization in microgravity. <i>Reports on Progress in Physics</i> , 2005, 68, 799-853.	8.1	83
18	<i>Online_DPI</i>: a web server to calculate the diffraction precision index for a protein structure. <i>Journal of Applied Crystallography</i> , 2015, 48, 939-942.	1.9	79

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19	Piperazine silicate (EU 19): the structure of a very small crystal determined with synchrotron radiation. <i>Acta Crystallographica Section B: Structural Science</i> , 1988, 44, 73-77.	1.8	75
20	Distal pocket polarity in ligand binding to myoglobin: Deoxy and carbonmonoxy forms of a threonine68(E11) mutant investigated by x-ray crystallography and infrared spectroscopy. <i>Biochemistry</i> , 1993, 32, 13061-13070.	1.2	74
21	Self-association of a DNA loop creates a quadruplex: crystal structure of d(GCATGCT) at 1.8 Å resolution. <i>Structure</i> , 1995, 3, 335-340.	1.6	72
22	Trends and Challenges in Experimental Macromolecular Crystallography. <i>Quarterly Reviews of Biophysics</i> , 1996, 29, 227-278.	2.4	72
23	The X-ray diffraction station at the ADONE wiggler facility: preliminary results (including crystal) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.9	68
24	The 15-K neutron structure of saccharide-free concanavalin A. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 16405-16410.	3.3	68
25	The determination of protonation states in proteins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 906-922.	2.5	66
26	Unravelling the structural chemistry of the colouration mechanism in lobster shell. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 2072-2082.	2.5	65
27	The structure of the saccharide-binding site of concanavalin A. <i>EMBO Journal</i> , 1989, 8, 2189-93.	3.5	65
28	Structural studies of the effect that dimethyl sulfoxide (DMSO) has on cisplatin and carboplatin binding to histidine in a protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 601-612.	2.5	60
29	Synchrotron X-ray reciprocal-space mapping, topography and diffraction resolution studies of macromolecular crystal quality. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 868-880.	2.5	59
30	Protein microcrystal diffraction and the effects of radiation damage with ultra-high-flux synchrotron radiation.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1985, 82, 7604-7607.	3.3	56
31	Protein crystallography with synchrotron radiation. <i>Journal of Molecular Structure</i> , 1985, 130, 63-91.	1.8	55
32	Direct determination of the positions of the deuterium atoms of the bound water in concanavalin A by neutron Laue crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 541-550.	2.5	55
33	Do we see what we should see? Describing non-covalent interactions in protein structures including precision. <i>IUCrj</i> , 2014, 1, 74-81.	1.0	55
34	Optimized anomalous dispersion in crystallography: a synchrotron X-ray polychromatic simultaneous profile method. <i>Nature</i> , 1982, 298, 835-838.	13.7	54
35	CCD video observation of microgravity crystallization: apocrustacyanin C1. <i>Journal of Crystal Growth</i> , 1997, 171, 219-225.	0.7	54
36	Facilities for solution scattering and fibre diffraction at the Daresbury SRS. <i>Journal of Applied Crystallography</i> , 1985, 18, 396-403.	1.9	52

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37	Thermal motion in protein crystals estimated using laser-generated ultrasound and Young's modulus measurements. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 1990, 46, 315-320.	0.3	50
38	Unravelling the chemical basis of the bathochromic shift in the lobster carapace; new crystal structures of unbound astaxanthin, canthaxanthin and zeaxanthin. <i>Acta Crystallographica Section B: Structural Science</i> , 2007, 63, 328-337.	1.8	48
39	Neutron Laue diffraction study of concanavalin A The proton of Asp28. <i>Journal of the Chemical Society, Faraday Transactions</i> , 1997, 93, 4313-4317.	1.7	47
40	The variety of X-ray diffuse scattering from macromolecular crystals and its respective components. <i>Acta Crystallographica Section B: Structural Science</i> , 1991, 47, 960-968.	1.8	45
41	Bound-solvent structures for microgravity-, ground control-, gel- and microbatch-grown hen egg-white lysozyme crystals at 1.8 Å... resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 745-752.	2.5	45
42	The 1.2 Å... resolution structure of the con A-dimannose complex. <i>Journal of Molecular Biology</i> , 2001, 310, 875-884.	2.0	44
43	Softer and soft X-rays in macromolecular crystallography. <i>Journal of Synchrotron Radiation</i> , 2005, 12, 410-419.	1.0	44
44	Anomalous scattering in structural chemistry and biology. <i>Crystallography Reviews</i> , 2005, 11, 245-335.	0.4	44
45	An investigation into structural changes due to deuteration. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2008, 64, 359-367.	0.3	43
46	Angular distribution of reflections in Laue diffraction. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 1991, 47, 352-373.	0.3	42
47	The interdependence of wavelength, redundancy and dose in sulfur SAD experiments. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 1196-1209.	2.5	42
48	Central data collection facility for protein crystallography, small angle diffraction and scattering at the Daresbury Laboratory Synchrotron Radiation Source (SRS), England. <i>Journal of Physics E: Scientific Instruments</i> , 1982, 15, 1363-1372.	0.7	40
49	A high-throughput structural biology/proteomics beamline at the SRS on a new multipole wiggler. <i>Journal of Synchrotron Radiation</i> , 2005, 12, 455-466.	1.0	39
50	Protonation-state determination in proteins using high-resolution X-ray crystallography: effects of resolution and completeness. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 800-809.	2.5	39
51	The use of MULTAN to locate the positions of anomalous scatterers. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 1989, 45, 715-718.	0.3	38
52	Time-resolved structures of hydroxymethylbilane synthase (Lys59Gln mutant) as it is loaded with substrate in the crystal determined by Laue diffraction. <i>Journal of the Chemical Society, Faraday Transactions</i> , 1998, 94, 2615-2622.	1.7	38
53	Structure of lobster apocrustacyanin A1 using softer X-rays. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1219-1229.	2.5	38
54	S-SWAT (softer single-wavelength anomalous technique): potential in high-throughput protein crystallography. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2003, 59, 327-334.	0.3	38

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55	High-resolution crystallographic studies of native concanavalin A using rapid Laue data collection methods and the introduction of a monochromatic large-angle oscillation technique (LOT). <i>Journal of the Chemical Society, Faraday Transactions</i> , 1993, 89, 2667.	1.7	37
56	Room-temperature X-ray diffraction studies of cisplatin and carboplatin binding to His15 of HEWL after prolonged chemical exposure. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1300-1306.	0.7	37
57	Crystal Structure of the C1 domain of Cardiac Myosin Binding Protein-C: Implications for Hypertrophic Cardiomyopathy. <i>Journal of Molecular Biology</i> , 2008, 378, 387-397.	2.0	36
58	Neutron Laue diffraction does it faster. <i>Nature Structural and Molecular Biology</i> , 1997, 4, 874-876.	3.6	35
59	On the origin and variation of colors in lobster carapace. <i>Physical Chemistry Chemical Physics</i> , 2015, 17, 16723-16732.	1.3	35
60	Synchrotron Radiation and Crystallography: the First 50 Years. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 1998, 54, 738-749.	0.3	34
61	The crystal structure analysis of the relative binding of cisplatin and carboplatin in a mixture with histidine in a protein studied at 100 and 300 K with repeated X-ray irradiation. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 121-125.	2.5	34
62	Safeguarding Structural Data Repositories against Bad Apples. <i>Structure</i> , 2016, 24, 216-220.	1.6	34
63	Synchrotron radiation macromolecular crystallography: science and spin-offs. <i>IUCrJ</i> , 2015, 2, 283-291.	1.0	34
64	Raw diffraction data preservation and reuse: overview, update on practicalities and metadata requirements. <i>IUCrJ</i> , 2017, 4, 87-99.	1.0	34
65	Carboplatin binding to histidine. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1135-1142.	0.4	33
66	Oscillation camera data processing: reflecting range and prediction of partiality. I. Conventional X-ray sources. <i>Journal of Applied Crystallography</i> , 1982, 15, 338-351.	1.9	31
67	Report of the Working Group on Synchrotron Radiation Nomenclature "brightness, spectral brightness or brilliance?". <i>Journal of Synchrotron Radiation</i> , 2005, 12, 385-385.	1.0	31
68	Macromolecular crystal twinning, lattice disorders and multiple crystals1. <i>Crystallography Reviews</i> , 2008, 14, 189-250.	0.4	31
69	Correcting the record of structural publications requires joint effort of the community and journal editors. <i>FEBS Journal</i> , 2016, 283, 4452-4457.	2.2	31
70	Principles and methods used to grow and optimize crystals of protein-metallo-drug adducts, to determine metal binding sites and to assign metal ligands. <i>Metallomics</i> , 2017, 9, 1534-1547.	1.0	31
71	Synchrotron and neutron techniques in biological crystallography. <i>Chemical Society Reviews</i> , 2004, 33, 548.	18.7	30
72	High-resolution structures of single-metal-substituted concanavalin A: the Co,Ca-protein at 1.6 Å... and the Ni,Ca-protein at 2.0 Å.... <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1994, 50, 749-756.	2.5	29

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73	Structure solution of a cubic crystal of concanavalin A complexed with methyl α -D-glucopyranoside. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1996, 52, 143-155.	2.5	28
74	Experience with exchange and archiving of raw data: comparison of data from two diffractometers and four software packages on a series of lysozyme crystals. <i>Journal of Applied Crystallography</i> , 2013, 46, 108-119.	1.9	28
75	Crystallography and Databases. <i>Data Science Journal</i> , 2017, 16, .	0.6	28
76	Oscillation camera data processing: reflecting range and prediction of partiality. 2. Monochromatized synchrotron X-radiation from a singly bent triangular monochromator. <i>Journal of Applied Crystallography</i> , 1982, 15, 493-508.	1.9	27
77	Experiences with making diffraction image data available: what metadata do we need to archive?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2502-2509.	2.5	26
78	The science is in the data. <i>IUCrJ</i> , 2017, 4, 714-722.	1.0	26
79	Binding of Coenzyme and Substrate and Coenzyme Analogues to 6-Phosphogluconate Dehydrogenase from Sheep Liver. An X-Ray Study at 0.6-nm Resolution. <i>FEBS Journal</i> , 1979, 98, 121-130.	0.2	25
80	The uses of synchrotron x-radiation in the crystallography of molecular biology. <i>Progress in Biophysics and Molecular Biology</i> , 1983, 41, 67-123.	1.4	25
81	Refined structure of cadmium-substituted concanavalin A at 2.0 Å... resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1993, 49, 561-571.	2.5	25
82	Synchrotron radiation facilities. <i>Nature Structural Biology</i> , 1998, 5, 614-617.	9.7	25
83	Structure of 6-phosphogluconate dehydrogenase from sheep liver at 6 Å... resolution. <i>Journal of Molecular Biology</i> , 1977, 112, 183-197.	2.0	24
84	The location of manganese and calcium ion cofactors in pea lectin crystals by use of anomalous dispersion and tuneable synchrotron X-radiation. <i>Acta Crystallographica Section B: Structural Science</i> , 1985, 41, 336-341.	1.8	24
85	Towards the measurement of ideal data for macromolecular crystallography using synchrotron sources. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1993, 49, 120-128.	2.5	24
86	An evaluation review of the prediction of protonation states in proteins versus crystallographic experiment. <i>Crystallography Reviews</i> , 2009, 15, 231-259.	0.4	24
87	The sensitivity of the synchrotron Laue method to small structural changes: binding studies of human carbonic anhydrase II (HCAII). <i>Acta Crystallographica Section B: Structural Science</i> , 1992, 48, 281-285.	1.8	23
88	Time-resolved and static-ensemble structural chemistry of hydroxymethylbilane synthase. <i>Faraday Discussions</i> , 2003, 122, 131-144.	1.6	23
89	Properties of a new crystal form of the complex of concanavalin a with methyl α -d-glucopyranoside. <i>Journal of Molecular Biology</i> , 1987, 195, 759-760.	2.0	22
90	Initiating a crystallographic study of trypanothione reductase. <i>Journal of Molecular Biology</i> , 1990, 216, 235-237.	2.0	22

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91	Experiences with archived raw diffraction images data: capturing cisplatin after chemical conversion of carboplatin in high salt conditions for a protein crystal. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 880-883.	1.0	21
92	X-ray Structure of the Carboplatin-Loaded Apo-Ferritin Nanocage. <i>ACS Medicinal Chemistry Letters</i> , 2017, 8, 433-437.	1.3	21
93	A new macromolecular crystallography Station (9.5) on the SRS wiggler beam line for very rapid Laue and rapidly tunable monochromatic measurements: Commissioning and first results. <i>Review of Scientific Instruments</i> , 1992, 63, 1062-1064.	0.6	20
94	Partial Improvement of Crystal Quality for Microgravity-Grown Apocrustacyanin C1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1997, 53, 231-239.	2.5	20
95	New leads for fragment-based design of rhenium/technetium radiopharmaceutical agents. <i>IUCrj</i> , 2017, 4, 283-290.	1.0	20
96	X-ray Crystal Structure and Time-Resolved Spectroscopy of the Blue Carotenoid Violerythrin. <i>Journal of Physical Chemistry B</i> , 2010, 114, 8760-8769.	1.2	19
97	New developments in crystallography: exploring its technology, methods and scope in the molecular biosciences. <i>Bioscience Reports</i> , 2017, 37, .	1.1	19
98	Crystallization and preliminary x-ray investigation of purine-nucleoside phosphorylase from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 1985, 260, 12968-12969.	1.6	19
99	Oscillation camera data processing. 3. General diffraction spot size, shape and energy profile: formalism for polychromatic diffraction experiments with monochromatized synchrotron X-radiation from a singly bent triangular monochromator. <i>Journal of Applied Crystallography</i> , 1983, 16, 242-250.	1.9	18
100	The effect of metal ion homogeneity on the diffraction limit of orthorhombic (I222) crystals of concanavalin A. <i>Journal of Crystal Growth</i> , 1988, 88, 537-540.	0.7	18
101	Calibration tests and use of a Nicolet/Xentronics imaging proportional chamber mounted on a conventional source for protein crystallography. <i>Journal of Applied Crystallography</i> , 1989, 22, 123-137.	1.9	18
102	MAD Phasing Strategies Explored with a Brominated Oligonucleotide Crystal at 1.65Å... Resolution. <i>Journal of Synchrotron Radiation</i> , 1996, 3, 24-34.	1.0	18
103	Determination of the structure of selenomethionine-labelled hydroxymethylbilane synthase in its active form by multi-wavelength anomalous dispersion. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 631-643.	2.5	18
104	Overview and new developments in softer X-ray ($2\text{\AA} \dots < \hat{\nu} > 5\text{\AA}$...) protein crystallography. <i>Journal of Synchrotron Radiation</i> , 2004, 11, 1-3.	1.0	18
105	Instrumentation for Laue diffraction (invited). <i>Review of Scientific Instruments</i> , 1989, 60, 1531-1536.	0.6	17
106	Protein crystal movements and fluid flows during microgravity growth. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 1998, 356, 1045-1061.	1.6	17
107	Determination of the site of incorporation of cobalt in CoZnPO-CZP by multiple-wavelength anomalous-dispersion crystallography. <i>Acta Crystallographica Section B: Structural Science</i> , 1999, 55, 327-332.	1.8	17
108	Development of instrumentation and methods for MAD and structural genomics at the SRS, ESRF, CHESS and Elettra facilities. <i>Journal of Synchrotron Radiation</i> , 1999, 6, 822-833.	1.0	17

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109	An investigation into the protonation states of the C1 domain of cardiac myosin-binding protein C. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 658-664.	2.5	17
110	How to Solve Protein Structures with an X-ray Laser. <i>Science</i> , 2013, 339, 146-147.	6.0	17
111	A 2D MWPC area detector for use with synchrotron X-radiation at the Daresbury laboratory for small angle diffraction and scattering. <i>Nuclear Instruments & Methods in Physics Research</i> , 1982, 201, 175-180.	0.9	16
112	A down-to-Earth approach. <i>Nature</i> , 2007, 448, 658-659.	13.7	16
113	X-ray crystal structures of diacetates of 6- <i>s-cis</i> and 6- <i>s-trans</i> astaxanthin and of 7,8-didehydroastaxanthin and 7,8,7,8-tetrahydroastaxanthin: comparison with free and protein-bound astaxanthins. <i>Acta Crystallographica Section B: Structural Science</i> , 2009, 65, 238-247.	1.8	16
114	Chemical conversion of cisplatin and carboplatin with histidine in a model protein crystallized under sodium iodide conditions. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1127-1131.	0.4	16
115	FACT and FAIR with Big Data allows objectivity in science: The view of crystallography. <i>Structural Dynamics</i> , 2019, 6, 054306.	0.9	16
116	Isomorphous replacement with optimized anomalous scattering applied to protein crystallography. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 1990, 46, 721-725.	0.3	15
117	Accurate and highly complete synchrotron protein crystal Laue diffraction data using the ESRF CCD and the Daresbury Laue software. <i>Journal of Synchrotron Radiation</i> , 1999, 6, 995-1006.	1.0	15
118	Space-grown crystals may prove their worth. <i>Nature</i> , 1999, 398, 20-20.	13.7	15
119	The combination of molecular dynamics with crystallography for elucidating protein-ligand interactions: a case study involving peanut lectin complexes with T-antigen and lactose. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1584-1594.	2.5	15
120	Carotenoid-Protein Interactions. , 2008, , 99-118.		15
121	Structural dynamics of cisplatin binding to histidine in a protein. <i>Structural Dynamics</i> , 2014, 1, 034701.	0.9	15
122	What is the structural chemistry of the living organism at its temperature and pressure?. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 87-93.	1.1	15
123	Crystallization and preliminary x-ray investigation of purine-nucleoside phosphorylase from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 1985, 260, 12968-9.	1.6	15
124	Protein dynamics: use of computer graphics and protein crystal diffuse scattering recorded with synchrotron X-radiation. <i>Biochemical Society Transactions</i> , 1986, 14, 653-655.	1.6	14
125	A two-wavelength crystallographic study of a new aluminophosphate containing nickel. <i>Acta Crystallographica Section B: Structural Science</i> , 1993, 49, 420-428.	1.8	14
126	Lysozyme Crystal Growth Kinetics Monitored Using a Mach-Zehnder Interferometer. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1996, 52, 529-533.	2.5	14

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127	Determination of zinc incorporation in the Zn-substituted gallophosphate ZnULM-5 by multiple wavelength anomalous dispersion techniques. <i>Acta Crystallographica Section B: Structural Science</i> , 2010, 66, 345-357.	1.8	14
128	The use of electronic area detectors for synchrotron X-radiation protein crystallography with particular reference to the Daresbury SRS. <i>Nuclear Instruments & Methods in Physics Research</i> , 1982, 201, 153-174.	0.9	13
129	A comparison of Laue and monochromatic X-ray analyses of a small-molecule crystal. <i>Acta Crystallographica Section B: Structural Science</i> , 1989, 45, 482-488.	1.8	13
130	A comparison of Laue and monochromatic X-ray analyses: the determination of the hydrogen-atom positions of an organic small-molecule crystal. <i>Acta Crystallographica Section B: Structural Science</i> , 1989, 45, 591-596.	1.8	13
131	Time-resolved synchrotron Laue diffraction and its application in structural molecular biology and materials science. <i>Phase Transitions</i> , 1992, 39, 145-160.	0.6	13
132	X-Ray crystallography in structural chemistry and molecular biology. <i>Chemical Communications</i> , 1996, , 1595.	2.2	13
133	Protein crystal perfection and its application. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 793-798.	2.5	13
134	The structural chemistry and structural biology of colouration in marine crustacea. <i>Crystallography Reviews</i> , 2010, 16, 231-242.	0.4	13
135	SR instrumentation for optimized anomalous scattering and high resolution structure studies of proteins and nucleic acids (invited). <i>Review of Scientific Instruments</i> , 1995, 66, 1287-1292.	0.6	12
136	[14] Overview of synchrotron radiation and macromolecular crystallography. <i>Methods in Enzymology</i> , 1997, 276, 203-217.	0.4	12
137	CCD Video Observation of Microgravity Crystallization of Lysozyme and Correlation with Accelerometer Data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1997, 53, 747-755.	2.5	12
138	Deriving the ultrastructure of β -crustacyanin using lower-resolution structural and biophysical methods. <i>Journal of Synchrotron Radiation</i> , 2011, 18, 79-83.	1.0	12
139	The binding of platinum hexahalides (Cl, Br and I) to hen egg-white lysozyme and the chemical transformation of the PtI ₆ octahedral complex to a PtI ₃ moiety bound to His15. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1132-1134.	0.4	12
140	Data science skills for referees: I biological X-ray crystallography. <i>Crystallography Reviews</i> , 2018, 24, 263-272.	0.4	12
141	Absorption of x-radiation by single crystals of proteins containing labile metal components: the determination of the number of iron atoms within the central core of ferritin. <i>Inorganica Chimica Acta</i> , 1985, 106, 193-196.	1.2	11
142	The laue method and its use in time-resolved crystallography. <i>Topics in Current Chemistry</i> , 1989, , 61-74.	4.0	11
143	Evaluation of reflection intensities for the components of multiple Laue diffraction spots by direct methods. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 1993, 49, 528-531.	0.3	11
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