

John Helliwell

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#	Paper	IF	Citations
290	Protein hydration dynamics in solution: a critical survey. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2004 , 359, 1207-23; discussion 1223-4, 1323-8	5.8	419
289	Three-dimensional structure of human erythrocytic purine nucleoside phosphorylase at 3.2 Å resolution. <i>Journal of Biological Chemistry</i> , 1990 , 265, 1812-1820	5.4	145
288	The molecular basis of the coloration mechanism in lobster shell: beta-crustacyanin at 3.2-Å resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 9795-800	11.5	143
287	Synchrotron X-radiation protein crystallography: instrumentation, methods and applications. <i>Reports on Progress in Physics</i> , 1984 , 47, 1403-1497	14.4	134
286	The recording and analysis of synchrotron X-radiation Laue diffraction photographs. <i>Journal of Applied Crystallography</i> , 1989 , 22, 483-497	3.8	130
285	Three-dimensional structure of human erythrocytic purine nucleoside phosphorylase at 3.2 Å resolution. <i>Journal of Biological Chemistry</i> , 1990 , 265, 1812-20	5.4	126
284	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		119
283	Active site of trypanothione reductase. A target for rational drug design. <i>Journal of Molecular Biology</i> , 1992 , 227, 322-33	6.5	119
282	The structure of concanavalin A and its bound solvent determined with small-molecule accuracy at 0.94 Å resolution. <i>Journal of the Chemical Society, Faraday Transactions</i> , 1997 , 93, 4305-4312		114
281	Protein crystal perfection and the nature of radiation damage. <i>Journal of Crystal Growth</i> , 1988 , 90, 259-278		111
280	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, 684-94	6.5	103
279	Laue crystallography: coming of age. <i>Journal of Synchrotron Radiation</i> , 1999 , 6, 891-917	2.4	102
278	Refined structure of concanavalin A complexed with methyl alpha-D-mannopyranoside at 2.0 Å resolution and comparison with the saccharide-free structure. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1994 , 50, 847-58		98
277	Improvements in lysozyme protein crystal perfection through microgravity growth. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995 , 51, 1099-102		78
276	How To Be a Better Scientist. By Andrew C. Johnson and John P. Sumpter. Taylor and Francis, 2018. Pp. 248. Price GBP 15.19 ISBN 9781138731295 (paperback), GBP 76.00 ISBN 9781138731219 (hardback), GBP 12.34 ISBN 9781315189079 (ebook). <i>Journal of Applied Crystallography</i> , 2020 , 53, 863-864	3.8	78
275	Macromolecular crystallization in microgravity. <i>Reports on Progress in Physics</i> , 2005 , 68, 799-853	14.4	77
274	LSCALE—the new normalization, scaling and absorption correction program in the Daresbury Laue software suite. <i>Journal of Applied Crystallography</i> , 1999 , 32, 554-562	3.8	75

273	Multiplicity distribution of reflections in Laue diffraction. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 1987 , 43, 656-674		69
272	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, 13061-70	3.2	66
271	Self-association of a DNA loop creates a quadruplex: crystal structure of d(GCATGCT) at 1.8 Å resolution. <i>Structure</i> , 1995 , 3, 335-40	5.2	66
270	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		65
269	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, 16405-10	11.5	64
268	Macromolecular Crystallography with Synchrotron Radiation 1992 ,		64
267	Trends and challenges in experimental macromolecular crystallography. <i>Quarterly Reviews of Biophysics</i> , 1996 , 29, 227-78	7	61
266	The determination of protonation states in proteins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007 , 63, 906-22		57
265	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, 601-12		54
264	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, 7604-7	11.5	53
263	Online_DPI: a web server to calculate the diffraction precision index for a protein structure. <i>Journal of Applied Crystallography</i> , 2015 , 48, 939-942	3.8	51
262	CCD video observation of microgravity crystallization: apocrustacyanin C1. <i>Journal of Crystal Growth</i> , 1997 , 171, 219-225	1.6	49
261	Protein crystallography with synchrotron radiation. <i>Journal of Molecular Structure</i> , 1985 , 130, 63-91	3.4	48
260	Facilities for solution scattering and fibre diffraction at the Daresbury SRS. <i>Journal of Applied Crystallography</i> , 1985 , 18, 396-403	3.8	48
259	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		44
258	Do we see what we should see? Describing non-covalent interactions in protein structures including precision. <i>IUCrJ</i> , 2014 , 1, 74-81	4.7	43
257	Unravelling the structural chemistry of the colouration mechanism in lobster shell. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 2072-82		43
256	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, 541-50		43

255	Optimized anomalous dispersion in crystallography: a synchrotron X-ray polychromatic simultaneous profile method. <i>Nature</i> , 1982 , 298, 835-838	50.4	43
254	The structure of the saccharide-binding site of concanavalin A. <i>EMBO Journal</i> , 1989 , 8, 2189-93	13	43
253	The interdependence of wavelength, redundancy and dose in sulfur SAD experiments. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008 , 64, 1196-209		40
252	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, 745-52		40
251	The 1.2 Å resolution structure of the Con A-dimannose complex. <i>Journal of Molecular Biology</i> , 2001 , 310, 875-84	6.5	39
250	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, 328-37		38
249	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		38
248	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, 800-9		36
247	Anomalous scattering in structural chemistry and biology View all notes . <i>Crystallography Reviews</i> , 2005 , 11, 245-335	1.3	36
246	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, 1300-6		35
245	The X-ray diffraction station at the ADONE wiggler facility: preliminary results (including crystal perfection). <i>Journal of Applied Crystallography</i> , 1992 , 25, 192-194	3.8	35
244	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, 121-5		33
243	An investigation into structural changes due to deuteration. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2008 , 64, 359-67		33
242	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		33
241	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		33
240	Macromolecular Crystallization and Crystal Perfection 2010 ,		32
239	Crystal structure of the C1 domain of cardiac myosin binding protein-C: implications for hypertrophic cardiomyopathy. <i>Journal of Molecular Biology</i> , 2008 , 378, 387-97	6.5	32
238	Carboplatin binding to histidine. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 1135-42	1.1	31

237	Structure of lobster apocrustacyanin A1 using softer X-rays. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001 , 57, 1219-29		30
236	Angular distribution of reflections in Laue diffraction. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 1991 , 47, 352-373		30
235	Safeguarding Structural Data Repositories against Bad Apples. <i>Structure</i> , 2016 , 24, 216-20	5.2	29
234	Neutron Laue diffraction study of concanavalin A. <i>Journal of the Chemical Society, Faraday Transactions</i> , 1997 , 93, 4313-4317		29
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232	A high-throughput structural biology/proteomics beamline at the SRS on a new multipole wiggler. <i>Journal of Synchrotron Radiation</i> , 2005 , 12, 455-66	2.4	29
231	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, 868-80		29
230	Synchrotron radiation macromolecular crystallography: science and spin-offs. <i>IUCrJ</i> , 2015 , 2, 283-91	4.7	29
229	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		27
228	On the origin and variation of colors in lobster carapace. <i>Physical Chemistry Chemical Physics</i> , 2015 , 17, 16723-32	3.6	26
227	Macromolecular crystal twinning, lattice disorders and multiple crystals1View all notes. <i>Crystallography Reviews</i> , 2008 , 14, 189-250	1.3	26
226	Principles and methods used to grow and optimize crystals of protein-metallodrug adducts, to determine metal binding sites and to assign metal ligands. <i>Metallomics</i> , 2017 , 9, 1534-1547	4.5	24
225	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	3.8	24
224	Structure solution of a cubic crystal of concanavalin A complexed with methyl alpha-D-glucopyranoside. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1996 , 52, 143-55		24
223	Raw diffraction data preservation and reuse: overview, update on practicalities and metadata requirements. <i>IUCrJ</i> , 2017 , 4, 87-99	4.7	24
222	Correcting the record of structural publications requires joint effort of the community and journal editors. <i>FEBS Journal</i> , 2016 , 283, 4452-4457	5.7	24
221	Report of the Working Group on Synchrotron Radiation Nomenclature - brightness, spectral brightness or brilliance?. <i>Journal of Synchrotron Radiation</i> , 2005 , 12, 385	2.4	23
220	The uses of synchrotron X-radiation in the crystallography of molecular biology. <i>Progress in Biophysics and Molecular Biology</i> , 1983 , 41, 67-123	4.7	22

219	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, 880-3	2.4	21
218	Synchrotron and neutron techniques in biological crystallography. <i>Chemical Society Reviews</i> , 2004 , 33, 548-57	58.5	21
217	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, 749-56		21
216	Initiating a crystallographic study of trypanothione reductase. <i>Journal of Molecular Biology</i> , 1990 , 216, 235-7	6.5	21
215	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		21
214	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, 121-30		21
213	Structure of 6-phosphogluconate dehydrogenase from sheep liver at 6 Å resolution. <i>Journal of Molecular Biology</i> , 1977 , 112, 183-97	6.5	21
212	X-ray Structure of the Carboplatin-Loaded Apo-Ferritin Nanocage. <i>ACS Medicinal Chemistry Letters</i> , 2017 , 8, 433-437	4.3	20
211	Time-resolved and static-ensemble structural chemistry of hydroxymethylbilane synthase. <i>Faraday Discussions</i> , 2003 , 122, 131-44; discussion 171-90	3.6	20
210	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		20
209	Towards the measurement of ideal data for macromolecular crystallography using synchrotron sources. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1993 , 49, 120-8		20
208	Refined structure of cadmium-substituted concanavalin A at 2.0 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1993 , 49, 561-71		20
207	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	3.8	20
206	New leads for fragment-based design of rhenium/technetium radiopharmaceutical agents. <i>IUCrJ</i> , 2017 , 4, 283-290	4.7	20
205	Experiences with making diffraction image data available: what metadata do we need to archive?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 2502-9		19
204	An evaluation review of the prediction of protonation states in proteins versus crystallographic experiment. <i>Crystallography Reviews</i> , 2009 , 15, 231-259	1.3	19
203	Partial improvement of crystal quality for microgravity-grown apocrustacyanin C1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1997 , 53, 231-9		19
202	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	1.7	19

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200	Synchrotron radiation facilities. <i>Nature Structural Biology</i> , 1998 , 5 Suppl, 614-7		18
199	The use of MULTAN to locate the positions of anomalous scatterers. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 1989 , 45, 715-718		18
198	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	3.8	18
197	Crystallography and Databases. <i>Data Science Journal</i> , 2017 , 16,	2	18
196	The science is in the data. <i>IUCrJ</i> , 2017 , 4, 714-722	4.7	17
195	X-ray crystal structure and time-resolved spectroscopy of the blue carotenoid violerythrin. <i>Journal of Physical Chemistry B</i> , 2010 , 114, 8760-9	3.4	17
194	S-SWAT (softer single-wavelength anomalous technique): potential in high-throughput protein crystallography. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2003 , 59, 327-34		17
193	MAD Phasing Strategies Explored with a Brominated Oligonucleotide Crystal at 1.65Å Resolution. <i>Journal of Synchrotron Radiation</i> , 1996 , 3, 24-34	2.4	17
192	Instrumentation for Laue diffraction (invited). <i>Review of Scientific Instruments</i> , 1989 , 60, 1531-1536	1.7	17
191	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	3.8	17
190	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, 1127-31	1.1	16
189	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		16
188	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	5.4	16
187	Protein crystal movements and fluid flows during microgravity growth. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 1998 , 356, 1045-1061	3	15
186	New developments in crystallography: exploring its technology, methods and scope in the molecular biosciences. <i>Bioscience Reports</i> , 2017 , 37,	4.1	14
185	Structural dynamics of cisplatin binding to histidine in a protein. <i>Structural Dynamics</i> , 2014 , 1, 034701	3.2	14
184	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, 658-64		14

183	Determination of the structure of seleno-methionine-labelled hydroxymethylbilane synthase in its active form by multi-wavelength anomalous dispersion. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 631-43		14
182	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	2.4	14
181	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	1.6	14
180	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		14
179	X-ray crystal structures of diacetates of 6-s-cis and 6-s-trans 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, 238-47		13
178	Overview and new developments in softer X-ray (2A <i>Journal of Synchrotron Radiation</i> , 2004 , 11, 1-3	2.4	13
177	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, 1584-94		13
176	Lysozyme crystal growth kinetics monitored using a Mach-Zehnder interferometer. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1996 , 52, 529-33		13
175	A two-wavelength crystallographic study of a new aluminophosphate containing nickel. <i>Acta Crystallographica Section B: Structural Science</i> , 1993 , 49, 420-428		13
174	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		13
173	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	3.8	13
172	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	5.4	13
171	Biochemistry. How to solve protein structures with an X-ray laser. <i>Science</i> , 2013 , 339, 146-7	33.3	12
170	The structural chemistry and structural biology of colouration in marine crustacea. <i>Crystallography Reviews</i> , 2010 , 16, 231-242	1.3	12
169	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, 345-57		12
168	CCD video observation of microgravity crystallization of lysozyme and correlation with accelerometer data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1997 , 53, 747-55		12
167	Protein crystal perfection and its application. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005 , 61, 793-8		12
166	X-Ray crystallography in structural chemistry and molecular biology. <i>Chemical Communications</i> , 1996 , 1595	5.8	12

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157	Time-dependent analysis of K ₂ PtBr ₆ binding to lysozyme studied by protein powder and single crystal X-ray analysis. <i>Zeitschrift für Kristallographie</i> , 2010 , 225, 570-575		10
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153	The evolution of synchrotron radiation and the growth of its importance in crystallography. <i>Crystallography Reviews</i> , 2012 , 18, 33-93	1.3	9
152	Deriving the ultrastructure of β -crustacyanin using lower-resolution structural and biophysical methods. <i>Journal of Synchrotron Radiation</i> , 2011 , 18, 79-83	2.4	9
151	Crystallographic analysis of counterion effects on subtilisin enzymatic action in acetonitrile. <i>Journal of the American Chemical Society</i> , 2010 , 132, 2293-300	16.4	9
150	Microgravity protein crystallization: are we reaping the full benefit of outer space?. <i>Annals of the New York Academy of Sciences</i> , 2002 , 974, 591-7	6.5	9
149	Apocrustacyanin C(1) crystals grown in space and on earth using vapour-diffusion geometry: protein structure refinements and electron-density map comparisons. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 1117-23		9
148	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	1.7	9

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146	Formation of a highly dense tetra-rhenium cluster in a protein crystal and its implications in medical imaging. <i>IUCrJ</i> , 2019 , 6, 695-702	4.7	9
145	FACT and FAIR with Big Data allows objectivity in science: The view of crystallography. <i>Structural Dynamics</i> , 2019 , 6, 054306	3.2	8
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