

# Elsbeth F Garman

## List of Publications by Year in descending order

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149  
papers

9,223  
citations

38660

50  
h-index

42291

92  
g-index

150  
all docs

150  
docs citations

150  
times ranked

9650  
citing authors

#	ARTICLE	IF	CITATIONS
1	Blu-Ice and the Distributed Control System: software for data acquisition and instrument control at macromolecular crystallography beamlines. <i>Journal of Synchrotron Radiation</i> , 2002, 9, 401-406.	1.0	1,018
2	Experimental determination of the radiation dose limit for cryocooled protein crystals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 4912-4917.	3.3	366
3	Architecture of a protein central to iron homeostasis: crystal structure and spectroscopic analysis of the ferric uptake regulator. <i>Molecular Microbiology</i> , 2003, 47, 903-915.	1.2	304
4	Radiation damage in macromolecular crystallography: what is it and why should we care?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 339-351.	2.5	299
5	Haem-ligand switching during catalysis in crystals of a nitrogen-cycle enzyme. <i>Nature</i> , 1997, 389, 406-412.	13.7	294
6	HDAC6 <p>97/VCP controlled polyubiquitin chain turnover. <i>EMBO Journal</i>, 2006, 25, 3357-3366.</p>	3.5	248
7	Macromolecular Cryocrystallography. <i>Journal of Applied Crystallography</i> , 1997, 30, 211-237.	1.9	242
8	Crystal structure of <i>Vibrio cholerae</i> neuraminidase reveals dual lectin-like domains in addition to the catalytic domain. <i>Structure</i> , 1994, 2, 535-544.	1.6	207
9	Identification of Novel Purine and Pyrimidine Cyclin-Dependent Kinase Inhibitors with Distinct Molecular Interactions and Tumor Cell Growth Inhibition Profiles. <i>Journal of Medicinal Chemistry</i> , 2000, 43, 2797-2804.	2.9	203
10	<i>RADDOSE-3D</i> : time- and space-resolved modelling of dose in macromolecular crystallography. <i>Journal of Applied Crystallography</i> , 2013, 46, 1225-1230.	1.9	200
11	The crystal structure of cyclin A. <i>Structure</i> , 1995, 3, 1235-1247.	1.6	183
12	X-ray absorption by macromolecular crystals: the effects of wavelength and crystal composition on absorbed dose. <i>Journal of Applied Crystallography</i> , 2004, 37, 513-522.	1.9	178
13	Plant cysteine oxidases are dioxygenases that directly enable arginyl transferase-catalysed arginylation of N-end rule targets. <i>Nature Communications</i> , 2017, 8, 14690.	5.8	171
14	Two structures of the catalytic domain of phosphorylase kinase: an active protein kinase complexed with substrate analogue and product. <i>Structure</i> , 1995, 3, 467-482.	1.6	162
15	Cryocooling and radiation damage in macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 32-47.	2.5	144
16	Radiation damage in macromolecular cryocrystallography. <i>Current Opinion in Structural Biology</i> , 2006, 16, 624-629.	2.6	134
17	Absorbed dose calculations for macromolecular crystals: improvements to <i>RADDOSE</i> . <i>Journal of Synchrotron Radiation</i> , 2009, 16, 152-162.	1.0	129
18	Towards an understanding of radiation damage in cryocooled macromolecular crystals. <i>Journal of Synchrotron Radiation</i> , 2005, 12, 257-260.	1.0	121

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19	Crystal Structure and Function of the Zinc Uptake Regulator FurB from <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 9914-9922.	1.6	121
20	Observation of Decreased Radiation Damage at Higher Dose Rates in Room Temperature Protein Crystallography. <i>Structure</i> , 2007, 15, 1531-1541.	1.6	121
21	Cool data: quantity AND quality. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1641-1653.	2.5	119
22	'Cool' crystals: macromolecular cryocrystallography and radiation damage. <i>Current Opinion in Structural Biology</i> , 2003, 13, 545-551.	2.6	119
23	Developments in X-ray Crystallographic Structure Determination of Biological Macromolecules. <i>Science</i> , 2014, 343, 1102-1108.	6.0	119
24	Crystal structures of fibronectin-binding sites from <i>Staphylococcus aureus</i> FnBPA in complex with fibronectin domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 12254-12258.	3.3	116
25	X-ray crystallographic structure of a papain-leupeptin complex. <i>FEBS Letters</i> , 1993, 315, 38-42.	1.3	114
26	Mutations at Critical N-Glycosylation Sites Reduce Tyrosinase Activity by Altering Folding and Quality Control. <i>Journal of Biological Chemistry</i> , 2000, 275, 8169-8175.	1.6	113
27	VARP Is Recruited on to Endosomes by Direct Interaction with Retromer, Where Together They Function in Export to the Cell Surface. <i>Developmental Cell</i> , 2014, 29, 591-606.	3.1	110
28	Crystal structure of a berenil-d(CGCAAATTTGCCG) complex. <i>Journal of Molecular Biology</i> , 1992, 226, 481-490.	2.0	103
29	Multigrain crystallography. <i>Zeitschrift für Kristallographie</i> , 2012, 227, 63-78.	1.1	95
30	Estimate your dose: RADDPOSE3D. <i>Protein Science</i> , 2018, 27, 217-228.	3.1	93
31	Effect of Irradiation-Induced Disorder on the Conductivity and Critical Temperature of the Organic Superconductor (BEDT-TTF) <sub>2</sub> Cu(SCN) <sub>2</sub> . <i>Physical Review Letters</i> , 2006, 96, 177002.	2.9	86
32	The structure of a glycogen phosphorylase glucopyranose spirohydantoin complex at 1.8 Å... resolution and 100 K: The role of the water structure and its contribution to binding. <i>Protein Science</i> , 1998, 7, 915-927.	3.1	85
33	Know your dose: RADDPOSE. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 381-388.	2.5	84
34	Radiation damage and dose limits in serial synchrotron crystallography at cryo- and room temperatures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 4142-4151.	3.3	84
35	The Structures of <i>Salmonella typhimurium</i> LT2 Neuraminidase and its Complexes with Three Inhibitors at High Resolution. <i>Journal of Molecular Biology</i> , 1996, 259, 264-280.	2.0	83
36	Physical and chemical considerations of damage induced in protein crystals by synchrotron radiation: a radiation chemical perspective. <i>Journal of Synchrotron Radiation</i> , 2002, 9, 329-332.	1.0	83

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37	Investigation of possible free-radical scavengers and metrics for radiation damage in protein cryocrystallography. <i>Journal of Synchrotron Radiation</i> , 2002, 9, 347-354.	1.0	81
38	Elemental analysis of proteins by microPIXE. <i>Progress in Biophysics and Molecular Biology</i> , 2005, 89, 173-205.	1.4	81
39	Determination of X-ray flux using silicon pin diodes. <i>Journal of Synchrotron Radiation</i> , 2009, 16, 143-151.	1.0	81
40	A complex iron-calcium cofactor catalyzing phosphotransfer chemistry. <i>Science</i> , 2014, 345, 1170-1173.	6.0	80
41	The Structures of Frataxin Oligomers Reveal the Mechanism for the Delivery and Detoxification of Iron. <i>Structure</i> , 2006, 14, 1535-1546.	1.6	78
42	The Crystal Structure of the Escherichia coli RNase E Apoprotein and a Mechanism for RNA Degradation. <i>Structure</i> , 2008, 16, 1238-1244.	1.6	74
43	Parameters affecting the X-ray dose absorbed by macromolecular crystals. <i>Journal of Synchrotron Radiation</i> , 2005, 12, 268-275.	1.0	70
44	Colouring cryo-cooled crystals: online microspectrophotometry. <i>Journal of Synchrotron Radiation</i> , 2009, 16, 163-172.	1.0	69
45	Predicting the X-ray lifetime of protein crystals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20551-20556.	3.3	65
46	A 1.8 Å... resolution structure of pig muscle 3-phosphoglycerate kinase with bound MgADP and 3-phosphoglycerate in open conformation: new insight into the role of the nucleotide in domain closure11Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2001, 306, 499-511.	2.0	60
47	The Three-dimensional Structure of the N-Acetylglucosamine-6-phosphate Deacetylase, NagA, from <i>Bacillus subtilis</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 2809-2816.	1.6	60
48	Radioprotectant screening for cryocrystallography. <i>Journal of Synchrotron Radiation</i> , 2007, 14, 73-83.	1.0	60
49	Controlling Influenza by Inhibiting the Viruss Neuraminidase. <i>Current Drug Targets</i> , 2004, 5, 119-136.	1.0	59
50	Structure of monoclinic papain at 1.60 Å... resolution. <i>Acta Crystallographica Section B: Structural Science</i> , 1992, 48, 59-67.	1.8	54
51	X-ray radiation damage to biological macromolecules: further insights. <i>Journal of Synchrotron Radiation</i> , 2017, 24, 1-6.	1.0	53
52	Insights into the mechanism of X-ray-induced disulfide-bond cleavage in lysozyme crystals based on EPR, optical absorption and X-ray diffraction studies. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2381-2394.	2.5	51
53	Identifying and quantifying radiation damage at the atomic level. <i>Journal of Synchrotron Radiation</i> , 2015, 22, 201-212.	1.0	51
54	Heavy-atom derivatization. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1903-1913.	2.5	48

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55	Structural changes caused by radiation-induced reduction and radiolysis: the effect of X-ray absorbed dose in a fungal multicopper oxidase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 564-577.	2.5	48
56	â€œZn-Linkâ€ A Metal-Sharing Interface that Organizes the Quaternary Structure and Catalytic Site of the Endoribonuclease, RNase Eâ€. <i>Biochemistry</i> , 2005, 44, 4667-4675.	1.2	47
57	Radiation Damage in Macromolecular Crystallography. <i>Methods in Molecular Biology</i> , 2017, 1607, 467-489.	0.4	47
58	VIROLOGY: Enhanced: The Origin and Control of Pandemic Influenza. <i>Science</i> , 2001, 293, 1776-1777.	6.0	46
59	A Single Sequence Change Destabilizes the Influenza Virus Neuraminidase Tetramer. <i>Virology</i> , 1997, 236, 66-75.	1.1	42
60	An overview of heavy-atom derivatization of protein crystals. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 303-318.	1.1	40
61	Effective scavenging at cryotemperatures: furtherâ€increasing the dose tolerance of protein crystals. <i>Journal of Synchrotron Radiation</i> , 2011, 18, 346-357.	1.0	39
62	Leaving no element of doubt: analysis of proteins using microPIXE. <i>Structure</i> , 1999, 7, R291-R299.	1.6	38
63	Mechanism for the Hydrolysis of a Sulfur-Sulfur Bond Based on the Crystal Structure of the Thiosulfohydrolase SoxB. <i>Journal of Biological Chemistry</i> , 2009, 284, 21707-21718.	1.6	37
64	Pandemic influenza: its origin and control. <i>Microbes and Infection</i> , 2002, 4, 1309-1316.	1.0	36
65	Room-temperature scavengers for macromolecular crystallography: increased lifetimes and modified dose dependence of the intensity decay. <i>Journal of Synchrotron Radiation</i> , 2009, 16, 205-216.	1.0	36
66	Radiation damage in protein crystals examined under various conditions by different methods. <i>Journal of Synchrotron Radiation</i> , 2009, 16, 129-132.	1.0	36
67	Optimizing the spatial distribution of dose in X-ray macromolecular crystallography. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 49-57.	1.0	35
68	The Solution and Crystal Structures of a Module Pair from the Staphylococcus aureus-Binding Site of Human Fibronectinâ€A Tale with a Twist. <i>Journal of Molecular Biology</i> , 2007, 368, 833-844.	2.0	34
69	Progress in research into radiation damage in cryo-cooled macromolecular crystals. <i>Journal of Synchrotron Radiation</i> , 2007, 14, 1-3.	1.0	34
70	Purification, crystallization and preliminary crystallographic study of neuraminidase from <i>Vibrio cholerae</i> and <i>Salmonella typhimurium</i> LT2. <i>Journal of Molecular Biology</i> , 1992, 226, 1287-1290.	2.0	33
71	Cryocooling of Macromolecular Crystals: Optimization Methods. <i>Methods in Enzymology</i> , 2003, 368, 188-216.	0.4	33
72	To scavenge or not to scavenge, that is STILL theâ€question. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 23-36.	1.0	33

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73	Radiation damage in small-molecule crystallography: fact not fiction. <i>IUCr</i> , 2019, 6, 703-713.	1.0	32
74	Insights into an unusual Auxiliary Activity 9 family member lacking the histidine brace motif of lytic polysaccharide monoxygenases. <i>Journal of Biological Chemistry</i> , 2019, 294, 17117-17130.	1.6	30
75	Crystallization and preliminary X-ray study of a lipase from <i>Pseudomonas glumae</i> . <i>Journal of Molecular Biology</i> , 1992, 224, 281-282.	2.0	28
76	Development of tools to automate quantitative analysis of radiation damage in SAXS experiments. <i>Journal of Synchrotron Radiation</i> , 2017, 24, 63-72.	1.0	28
77	Piperidinols That Show Anti-Tubercular Activity as Inhibitors of Arylamine N-Acetyltransferase: An Essential Enzyme for Mycobacterial Survival Inside Macrophages. <i>PLoS ONE</i> , 2012, 7, e52790.	1.1	27
78	Radiation damage to macromolecules: kill or cure?. <i>Journal of Synchrotron Radiation</i> , 2015, 22, 195-200.	1.0	26
79	X-ray radiation damage to biological samples: recent progress. <i>Journal of Synchrotron Radiation</i> , 2019, 26, 907-911.	1.0	25
80	Probing the architecture of the <i>Mycobacterium marinum</i> arylamine N-acetyltransferase active site. <i>Protein and Cell</i> , 2010, 1, 384-392.	4.8	24
81	Structure of arylamine N-acetyltransferase from <i>Mycobacterium tuberculosis</i> determined by cross-seeding with the homologous protein from <i>M. marinum</i> : triumph over adversity. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1433-1446.	2.5	24
82	High-Throughput PIXE as an Essential Quantitative Assay for Accurate Metalloprotein Structural Analysis: Development and Application. <i>Journal of the American Chemical Society</i> , 2020, 142, 185-197.	6.6	24
83	Radiation damage to crystalline biological molecules: current view. <i>Journal of Synchrotron Radiation</i> , 2002, 9, 327-328.	1.0	23
84	A previously unobserved conformation for the human Pex5p receptor suggests roles for intrinsic flexibility and rigid domain motions in ligand binding. <i>BMC Structural Biology</i> , 2007, 7, 24.	2.3	23
85	RADDSE-XFEL: femtosecond time-resolved dose estimates for macromolecular X-ray free-electron laser experiments. <i>Journal of Applied Crystallography</i> , 2020, 53, 549-560.	1.9	23
86	Heterotypic interactions drive antibody synergy against a malaria vaccine candidate. <i>Nature Communications</i> , 2022, 13, 933.	5.8	23
87	Radiation damage to biological macromolecules: some answers and more questions. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 1-6.	1.0	21
88	Radiation damage to nucleoprotein complexes in macromolecular crystallography. <i>Journal of Synchrotron Radiation</i> , 2015, 22, 213-224.	1.0	21
89	The binding of haem and zinc in the 1.9 Å X-ray structure of <i>Escherichia coli</i> bacterioferritin. <i>Journal of Biological Inorganic Chemistry</i> , 2009, 14, 201-207.	1.1	20
90	Structure of the trypanosome transferrin receptor reveals mechanisms of ligand recognition and immune evasion. <i>Nature Microbiology</i> , 2019, 4, 2074-2081.	5.9	20

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91	Crystallization and Preliminary X-ray Studies of Influenza A Virus Neuraminidase of Subtypes N5, N6, N8 and N9. <i>Journal of Molecular Biology</i> , 1993, 230, 345-348.	2.0	19
92	OH cleavage from tyrosine: debunking a myth. <i>Journal of Synchrotron Radiation</i> , 2017, 24, 7-18.	1.0	19
93	<i>RABDAM</i> : quantifying specific radiation damage in individual protein crystal structures. <i>Journal of Applied Crystallography</i> , 2018, 51, 552-559.	1.9	19
94	Demystifying the synchrotron trip: a first time user's guide. <i>Structure</i> , 1999, 7, R111-R121.	1.6	18
95	Cryocrystallography of Macromolecules: Practice and Optimization. , 2007, 364, 1-18.		18
96	RNA protects a nucleoprotein complex against radiation damage. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 648-657.	1.1	18
97	Quantifying and comparing radiation damage in the Protein Data Bank. <i>Nature Communications</i> , 2022, 13, 1314.	5.8	18
98	The Structure, Function, and Inhibition of Influenza Virus Neuraminidase. , 2005, , 247-267.		17
99	Macromolecular crystallography radiation damage research: what's new?. <i>Journal of Synchrotron Radiation</i> , 2011, 18, 313-317.	1.0	15
100	<i>RIDL</i> : a tool to investigate radiation-induced density loss. <i>Journal of Applied Crystallography</i> , 2018, 51, 952-962.	1.9	15
101	The potential benefits of using higher X-ray energies for macromolecular crystallography. <i>Journal of Synchrotron Radiation</i> , 2019, 26, 922-930.	1.0	15
102	Zinc determines dynamical properties and aggregation kinetics of human insulin. <i>Biophysical Journal</i> , 2021, 120, 886-898.	0.2	15
103	The Nobel Science: One Hundred Years of Crystallography. <i>Interdisciplinary Science Reviews</i> , 2015, 40, 244-264.	1.0	14
104	A design of crystal mounting cell that allows the controlled variation of humidity at the protein crystal during X-ray diffraction. <i>Journal of Applied Crystallography</i> , 1993, 26, 465-466.	1.9	13
105	Modelling heating effects in cryocooled protein crystals. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 2001, 467-468, 1380-1383.	0.7	13
106	Simultaneous X-ray diffraction from multiple single crystals of macromolecules. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 608-618.	2.5	13
107	A new method for predetermining the diffraction quality of protein crystals: using SOAP as a selection tool. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 130-140.	2.5	12
108	Structural knowledge or X-ray damage? A case study on xylose isomerase illustrating both. <i>Journal of Synchrotron Radiation</i> , 2019, 26, 931-944.	1.0	12

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109	High-resolution mapping of metal ions reveals principles of surface layer assembly in <i>Caulobacter crescentus</i> cells. <i>Structure</i> , 2022, 30, 215-228.e5.	1.6	12
110	Structural and Electronic Effects of X-ray Irradiation on Prototypical [M(COD)Cl] <sub>2</sub> Catalysts. <i>Journal of Physical Chemistry A</i> , 2021, 125, 7473-7488.	1.1	11
111	The growth and characterization of crystals of human immunodeficiency virus (HIV) reverse transcriptase. <i>Journal of Crystal Growth</i> , 1993, 126, 261-269.	0.7	10
112	Crystallization, microPIXE and preliminary crystallographic analysis of the complex between the third KH domain of hnRNP K and single-stranded DNA. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 784-787.	2.5	10
113	The topology, structure and PE interaction of LITAF underpin a Charcot-Marie-Tooth disease type 1C. <i>BMC Biology</i> , 2016, 14, 109.	1.7	10
114	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 455-457.	1.1	10
115	Resolving the subtle details of human DNA alkyltransferase lesion search and repair mechanism by single-molecule studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2116218119.	3.3	10
116	Glucocorticoid Receptor-like Zn(Cys) <sub>4</sub> Motifs in BslI Restriction Endonuclease. <i>Journal of Molecular Biology</i> , 2003, 334, 595-603.	2.0	8
117	X-ray crystal structure analysis of magnetically oriented microcrystals of lysozyme at 1.8 Å resolution. <i>Journal of Applied Crystallography</i> , 2016, 49, 457-461.	1.9	8
118	“To Cross-Seed or Not To Cross-Seed”: A Pilot Study Using Metallo-β-lactamases. <i>Crystal Growth and Design</i> , 2017, 17, 913-924.	1.4	8
119	Radiation damage to biological samples: still a pertinent issue. <i>Journal of Synchrotron Radiation</i> , 2021, 28, 1278-1283.	1.0	8
120	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. <i>IUCr</i> , 2019, 6, 341-343.	1.0	8
121	Radiation-damage investigation of a DNA 16-mer. <i>Journal of Synchrotron Radiation</i> , 2019, 26, 998-1009.	1.0	7
122	RECENT BIOMEDICAL APPLICATIONS OF THE OXFORD SCANNING PROTON MICROPROBE. <i>International Journal of PIXE</i> , 1999, 09, 199-216.	0.4	6
123	Temperature characteristics of crystal storage devices in a CP100 dry shipping Dewar. <i>Journal of Applied Crystallography</i> , 2004, 37, 1000-1003.	1.9	6
124	Radiation Damage in Macromolecular Crystallography. <i>Synchrotron Radiation News</i> , 2015, 28, 15-19.	0.2	5
125	Twinned or not twinned, that is the question: crystallization and preliminary crystallographic analysis of the 2F13F1 module pair of human fibronectin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1341-1345.	2.5	4
126	Radiation damage within nucleoprotein complexes studied by macromolecular X-ray crystallography. <i>Radiation Physics and Chemistry</i> , 2016, 128, 118-125.	1.4	4



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127	Doses for experiments with microbeams and microcrystals: Monte Carlo simulations in RADDOSÉ3D. Protein Science, 2021, 30, 8-19.	3.1	4
128	X-Ray Data Collection From Macromolecular Crystals. , 2007, 364, 63-94.		3
129	Antiviral adhesion molecular mechanisms for influenza: W. G. Laver's lifetime obsession. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140034.	1.8	3
130	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 321-323.	0.4	3
131	Radiation Damage in Macromolecular Crystallography: What Is It and Why Do We Care?. NATO Science for Peace and Security Series A: Chemistry and Biology, 2013, , 69-77.	0.5	3
132	Submission of structural biology data for review purposes. IUCrJ, 2022, 9, 1-2.	1.0	3
133	Summary of lecture at biophysics and structural biology at synchrotrons workshop Crystallography 101: diffraction theory and space groups. Biophysical Reviews, 2019, 11, 525-528.	1.5	2
134	Summary of lecture and practical session at Biophysics and Structural Biology at Synchrotrons workshop: cryo-cooling in macromolecular crystallographyâ€”why and how?. Biophysical Reviews, 2019, 11, 539-541.	1.5	2
135	Macromolecular cryo-crystallography. NATO Science Series Series II, Mathematics, Physics and Chemistry, 2007, , 25-40.	0.1	2
136	Summary of case study lecture at Biophysics and Structural Biology at Synchrotrons Workshop Triumph over Adversity: structure of arylamine N-acetyltransferase from M. tuberculosis. Biophysical Reviews, 2019, 11, 535-537.	1.5	1
137	Elemental Analysis of Proteins by Proton Induced X-ray Emission (microPIXE). NATO Science for Peace and Security Series A: Chemistry and Biology, 2013, , 79-89.	0.5	1
138	Chapter 4. Radiation Damage in Macromolecular Crystallography. Chemical Biology, 2018, , 88-116.	0.1	1
139	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. Journal of Applied Crystallography, 2019, 52, 495-497.	1.9	1
140	Rosalind Franklin 1920â€”1958. Acta Crystallographica Section D: Structural Biology, 2020, 76, 698-701.	1.1	1
141	Submission of structural biology data for review purposes. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1477-1478.	1.1	1
142	Limitations in macromolecular crystallography due to radiation damage. AIP Conference Proceedings, 2000, , .	0.3	0
143	SARS Proteomics Reveals Viral Secrets. Structure, 2005, 13, 1582-1583.	1.6	0
144	Response to Krumrey's Comments on Determination of X-ray flux using silicon pin diodes by R. L. Owen et al. (2009). J. Synchrotron Rad. 16, 143â€”153. Journal of Synchrotron Radiation, 2009, 16, 691-692.	1.0	0

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145	Characterisation of the membrane topology and molecular structure of LITAF to provide insights into the molecular pathogenesis of Charcot-Marie-Tooth disease type 1C. <i>Lancet, The</i> , 2016, 387, S87.	6.3	0
146	Louise Napier Johnson (1940â€“2012). <i>Biochemist</i> , 2012, 34, 43-44.	0.2	0
147	New Section Editor of Acta Cryst. D. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 702-702.	1.1	0
148	Three new Co-editors appointed to Acta Crystallographica Section D, Structural Biology. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 612-612.	1.1	0
149	Submission of structural biology data for review purposes. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021, 77, 435-436.	0.4	0