

# Helen M Berman

## List of Publications by Year in descending order

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198  
papers

58,201  
citations

8181

76  
h-index

2895

190  
g-index

219  
all docs

219  
docs citations

219  
times ranked

51503  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Protein Data Bank. <i>Nucleic Acids Research</i> , 2000, 28, 235-242.	14.5	31,087
2	Announcing the worldwide Protein Data Bank. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 980-980.	8.2	2,355
3	The Protein Data Bank. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 899-907.	2.5	2,023
4	The worldwide Protein Data Bank (wwPDB): ensuring a single, uniform archive of PDB data. <i>Nucleic Acids Research</i> , 2007, 35, D301-D303.	14.5	992
5	The nucleic acid database. A comprehensive relational database of three-dimensional structures of nucleic acids. <i>Biophysical Journal</i> , 1992, 63, 751-759.	0.5	963
6	RCSB Protein Data Bank: biological macromolecular structures enabling research and education in fundamental biology, biomedicine, biotechnology and energy. <i>Nucleic Acids Research</i> , 2019, 47, D464-D474.	14.5	918
7	Protein Data Bank: the single global archive for 3D macromolecular structure data. <i>Nucleic Acids Research</i> , 2019, 47, D520-D528.	14.5	671
8	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2017, 45, D271-D281.	14.5	619
9	Protein Data Bank (PDB): The Single Global Macromolecular Structure Archive. <i>Methods in Molecular Biology</i> , 2017, 1607, 627-641.	0.9	592
10	Hydration structure of a collagen peptide. <i>Structure</i> , 1995, 3, 893-906.	3.3	570
11	The RCSB Protein Data Bank: redesigned web site and web services. <i>Nucleic Acids Research</i> , 2011, 39, D392-D401.	14.5	549
12	A standard reference frame for the description of nucleic acid base-pair geometry 1 Edited by P. E. Wright 2 This is a document of the Nomenclature Committee of IUBMB (NC-IUBMB)/IUPAC-IUBMB Joint Commission on Biochemical Nomenclature (JCBN), whose members are R. Cammack (chairman), A. Bairoch, H.M. Berman, S. Boyce, C.R. Cantor, K. Elliott, D. Horton, M. Kanehisa, A. Kotyk, G.P. Moss, N. Sharon and K.F. Tipton.. <i>Journal of Molecular Biology</i> , 2001, 313, 229-237.	4.2	533
13	An overview of the structures of protein-DNA complexes. <i>Genome Biology</i> , 2000, 1, reviews001.1.	9.6	531
14	The Protein Data Bank and the challenge of structural genomics. <i>Nature Structural Biology</i> , 2000, 7, 957-959.	9.7	511
15	The RCSB Protein Data Bank: views of structural biology for basic and applied research and education. <i>Nucleic Acids Research</i> , 2015, 43, D345-D356.	14.5	461
16	The RCSB Protein Data Bank: new resources for research and education. <i>Nucleic Acids Research</i> , 2012, 41, D475-D482.	14.5	418
17	Protein-DNA interactions: a structural analysis. <i>Journal of Molecular Biology</i> , 1999, 287, 877-896.	4.2	397
18	The Protein Data Bank: a historical perspective. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2008, 64, 88-95.	0.3	342

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19	The RCSB PDB information portal for structural genomics. <i>Nucleic Acids Research</i> , 2006, 34, D302-D305.	14.5	334
20	The Protein Data Bank and structural genomics. <i>Nucleic Acids Research</i> , 2003, 31, 489-491.	14.5	331
21	The RCSB Protein Data Bank: a redesigned query system and relational database based on the mmCIF schema. <i>Nucleic Acids Research</i> , 2004, 33, D233-D237.	14.5	303
22	Catabolite activator protein: DNA binding and transcription activation. <i>Current Opinion in Structural Biology</i> , 2004, 14, 10-20.	5.7	291
23	Sequence dependent conformational variations of collagen triple-helical structure. <i>Nature Structural Biology</i> , 1999, 6, 454-457.	9.7	277
24	Structure of the CAP-DNA Complex at 2.5 Å... Resolution: A Complete Picture of the Protein-DNA Interface. <i>Journal of Molecular Biology</i> , 1996, 260, 395-408.	4.2	262
25	The Protein Data Bank: unifying the archive. <i>Nucleic Acids Research</i> , 2002, 30, 245-248.	14.5	261
26	EMDataBank.org: unified data resource for CryoEM. <i>Nucleic Acids Research</i> , 2011, 39, D456-D464.	14.5	246
27	Tools for the automatic identification and classification of RNA base pairs. <i>Nucleic Acids Research</i> , 2003, 31, 3450-3460.	14.5	240
28	Automated and accurate deposition of structures solved by X-ray diffraction to the Protein Data Bank. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1833-1839.	2.5	236
29	Structural Basis of Transcription Activation: The CAP-alpha CTD-DNA Complex. <i>Science</i> , 2002, 297, 1562-1566.	12.6	234
30	EMDataBank unified data resource for 3DEM. <i>Nucleic Acids Research</i> , 2016, 44, D396-D403.	14.5	230
31	Hydration of the DNA bases is local. <i>Biophysical Journal</i> , 1995, 69, 2661-2669.	0.5	219
32	RCSB Protein Data Bank: Sustaining a living digital data resource that enables breakthroughs in scientific research and biomedical education. <i>Protein Science</i> , 2018, 27, 316-330.	7.6	219
33	New parameters for the refinement of nucleic acid-containing structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1996, 52, 57-64.	2.5	217
34	RNA backbone: Consensus all-angle conformers and modular string nomenclature (an RNA Ontology) <i>Tj ETQq0 0 0,rgBT /Overlock 10 Tf</i>	3.5	216
35	Geometric Parameters in Nucleic Acids: Å Sugar and Phosphate Constituents. <i>Journal of the American Chemical Society</i> , 1996, 118, 519-529.	13.7	215
36	Validation of Structures in the Protein Data Bank. <i>Structure</i> , 2017, 25, 1916-1927.	3.3	210

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37	Crystallographic Evidence for C $\alpha$ -H $\cdots$ O=C Hydrogen Bonds in a Collagen Triple Helix. <i>Journal of Molecular Biology</i> , 1996, 264, 734-742.	4.2	209
38	Hydration of the Phosphate Group in Double-Helical DNA. <i>Biophysical Journal</i> , 1998, 75, 2422-2434.	0.5	201
39	Conformations of the sugar-phosphate backbone in helical DNA crystal structures. , 1997, 42, 113-124.		198
40	Staggered molecular packing in crystals of a collagen-like peptide with a single charged pair. <i>Journal of Molecular Biology</i> , 2000, 301, 1191-1205.	4.2	197
41	The Nucleic Acid Database: new features and capabilities. <i>Nucleic Acids Research</i> , 2014, 42, D114-D122.	14.5	194
42	Geometric Parameters in Nucleic Acids: Nitrogenous Bases. <i>Journal of the American Chemical Society</i> , 1996, 118, 509-518.	13.7	191
43	The cAMP binding domain: An ancient signaling module. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 45-50.	7.1	190
44	Ligand Depot: a data warehouse for ligands bound to macromolecules. <i>Bioinformatics</i> , 2004, 20, 2153-2155.	4.1	189
45	Crystal structure of a naturally occurring dinucleoside phosphate: Uridyl 3',5'-adenosine phosphate model for RNA chain folding. <i>Journal of Molecular Biology</i> , 1972, 66, 403-421.	4.2	188
46	Using electrostatic potentials to predict DNA-binding sites on DNA-binding proteins. <i>Nucleic Acids Research</i> , 2003, 31, 7189-7198.	14.5	186
47	TargetDB: a target registration database for structural genomics projects. <i>Bioinformatics</i> , 2004, 20, 2860-2862.	4.1	182
48	The crystal and molecular structure of a collagen-like peptide with A biologically relevant sequence. <i>Journal of Molecular Biology</i> , 2001, 311, 131-147.	4.2	179
49	X-ray crystallographic determination of a collagen-like peptide with the repeating sequence (Pro-Pro-Gly). <i>Journal of Molecular Biology</i> , 1998, 280, 623-638.	4.2	166
50	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015, 23, 1156-1167.	3.3	159
51	PDBML: the representation of archival macromolecular structure data in XML. <i>Bioinformatics</i> , 2005, 21, 988-992.	4.1	154
52	Recommendations of the wwPDB NMR Validation Task Force. <i>Structure</i> , 2013, 21, 1563-1570.	3.3	151
53	[30] Macromolecular crystallographic information file. <i>Methods in Enzymology</i> , 1997, 277, 571-590.	1.0	148
54	The structure of drug-deoxydinucleoside phosphate complex; generalized conformational behavior of intercalation complexes with RNA and DNA fragments. <i>Nucleic Acids Research</i> , 1980, 8, 85-98.	14.5	146

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55	Remediation of the protein data bank archive. <i>Nucleic Acids Research</i> , 2007, 36, D426-D433.	14.5	136
56	A systematic method for studying the spatial distribution of water molecules around nucleic acid bases. <i>Biophysical Journal</i> , 1993, 65, 2291-2303.	0.5	135
57	Highly structured water network in crystals of a deoxydinucleoside-drug complex. <i>Nature</i> , 1980, 288, 129-133.	27.8	134
58	Hydration of DNA: take 2. <i>Current Opinion in Structural Biology</i> , 1994, 4, 345-350.	5.7	132
59	The Protein Model Portal. <i>Journal of Structural and Functional Genomics</i> , 2009, 10, 1-8.	1.2	130
60	OneDep: Unified wwPDB System for Deposition, Biocuration, and Validation of Macromolecular Structures in the PDB Archive. <i>Structure</i> , 2017, 25, 536-545.	3.3	130
61	Hydration of DNA bases: Analysis of crystallographic data. <i>Biopolymers</i> , 1992, 32, 725-750.	2.4	127
62	RNA conformational classes. <i>Nucleic Acids Research</i> , 2004, 32, 1666-1677.	14.5	123
63	Crystal structure of the unique RNA-binding domain of the influenza virus NS1 protein. <i>Nature Structural and Molecular Biology</i> , 1997, 4, 896-899.	8.2	120
64	The Protein Data Bank at 40: Reflecting on the Past to Prepare for the Future. <i>Structure</i> , 2012, 20, 391-396.	3.3	120
65	The structure of a pseudo intercalated complex between actinomycin and the DNA binding sequence d(GpC). <i>Nature</i> , 1982, 296, 466-469.	27.8	117
66	BioMagResBank (BMRB) as a partner in the Worldwide Protein Data Bank (wwPDB): new policies affecting biomolecular NMR depositions. <i>Journal of Biomolecular NMR</i> , 2008, 40, 153-155.	2.8	117
67	The Protein Data Bank archive as an open data resource. <i>Journal of Computer-Aided Molecular Design</i> , 2014, 28, 1009-1014.	2.9	114
68	Analysis of local helix bending in crystal structures of DNA oligonucleotides and DNA-protein complexes. <i>Biophysical Journal</i> , 1995, 68, 2454-2468.	0.5	113
69	Data Deposition and Annotation at the Worldwide Protein Data Bank. <i>Molecular Biotechnology</i> , 2009, 42, 1-13.	2.4	113
70	The distribution and query systems of the RCSB Protein Data Bank. <i>Nucleic Acids Research</i> , 2004, 32, 223D-225.	14.5	108
71	The protein structure initiative structural genomics knowledgebase. <i>Nucleic Acids Research</i> , 2009, 37, D365-D368.	14.5	94
72	Crystal studies of B-DNA: The answers and the questions. , 1997, 44, 23-44.		89

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73	The RCSB PDB "Molecule of the Month" Inspiring a Molecular View of Biology. <i>PLoS Biology</i> , 2015, 13, e1002140.	5.6	88
74	Hydration of DNA. <i>Current Opinion in Structural Biology</i> , 1991, 1, 423-427.	5.7	86
75	PDB-Dev: a Prototype System for Depositing Integrative/Hybrid Structural Models. <i>Structure</i> , 2017, 25, 1317-1318.	3.3	84
76	Development of a Prototype System for Archiving Integrative/Hybrid Structure Models of Biological Macromolecules. <i>Structure</i> , 2018, 26, 894-904.e2.	3.3	81
77	Large Macromolecular Complexes in the Protein Data Bank: A Status Report. <i>Structure</i> , 2005, 13, 381-388.	3.3	77
78	Report of the wwPDB Small-Angle Scattering Task Force: Data Requirements for Biomolecular Modeling and the PDB. <i>Structure</i> , 2013, 21, 875-881.	3.3	77
79	Three-dimensional EM structure of an intact activator-dependent transcription initiation complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 19830-19835.	7.1	76
80	An Analysis of the Relationship between Hydration and Protein-DNA Interactions. <i>Biophysical Journal</i> , 1998, 75, 2170-2177.	0.5	75
81	Trendspotting in the Protein Data Bank. <i>FEBS Letters</i> , 2013, 587, 1036-1045.	2.8	74
82	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDDataResource challenge. <i>Nature Methods</i> , 2021, 18, 156-164.	19.0	73
83	Molecular and crystal structure of an intercalation complex: Proflavine-cytidylyl-(3',5?)-guanosine. <i>Biopolymers</i> , 1979, 18, 2405-2429.	2.4	67
84	Aromatic hydrogen bond in sequence-specific protein DNA recognition. <i>Nature Structural and Molecular Biology</i> , 1996, 3, 837-841.	8.2	66
85	The Structural Biology Knowledgebase: a portal to protein structures, sequences, functions, and methods. <i>Journal of Structural and Functional Genomics</i> , 2011, 12, 45-54.	1.2	65
86	The future of the protein data bank. <i>Biopolymers</i> , 2013, 99, 218-222.	2.4	65
87	Conformational Effects of Glycine-Gly Interruptions in the Collagen Triple Helix. <i>Journal of Molecular Biology</i> , 2006, 362, 298-311.	4.2	61
88	Outcome of a Workshop on Archiving Structural Models of Biological Macromolecules. <i>Structure</i> , 2006, 14, 1211-1217.	3.3	60
89	The RNA Ontology Consortium: An open invitation to the RNA community. <i>Rna</i> , 2006, 12, 533-541.	3.5	59
90	DNAProDB: an interactive tool for structural analysis of DNA-protein complexes. <i>Nucleic Acids Research</i> , 2017, 45, W89-W97.	14.5	59

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91	Indirect readout of DNA sequence at the primary-kink site in the CAP-DNA complex: alteration of DNA binding specificity through alteration of DNA kinking. <i>Journal of Molecular Biology</i> , 2001, 314, 75-82.	4.2	57
92	The Nucleic Acid Database. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 889-898.	2.5	57
93	Indirect readout of DNA sequence at the primary-kink site in the CAP-DNA complex: DNA binding specificity based on energetics of DNA kinking. <i>Journal of Molecular Biology</i> , 2001, 314, 63-74.	4.2	52
94	Crystal and molecular structure of a DNA duplex containing the carcinogenic lesion O6-methylguanine. <i>Biochemistry</i> , 1990, 29, 10461-10465.	2.5	50
95	Crystal and molecular structure of a DNA fragment: d(CGTGAATTCACG). <i>Biochemistry</i> , 1991, 30, 4449-4455.	2.5	46
96	Announcing mandatory submission of PDBx/mmCIF format files for crystallographic depositions to the Protein Data Bank (PDB). <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 451-454.	2.3	46
97	Worldwide Protein Data Bank biocuration supporting open access to high-quality 3D structural biology data. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	45
98	Validation of Protein Structures for Protein Data Bank. <i>Methods in Enzymology</i> , 2003, 374, 370-385.	1.0	43
99	Indirect Readout of DNA Sequence at the Primary-kink Site in the CAP-DNA Complex: Recognition of Pyrimidine-Purine and Purine-Purine Steps. <i>Journal of Molecular Biology</i> , 2006, 357, 173-183.	4.2	43
100	Promoting a structural view of biology for varied audiences: an overview of RCSB PDB resources and experiences. <i>Journal of Applied Crystallography</i> , 2010, 43, 1224-1229.	4.5	41
101	DNAproDB: an expanded database and web-based tool for structural analysis of DNA-protein complexes. <i>Nucleic Acids Research</i> , 2019, 48, D277-D287.	14.5	41
102	Signatures of Protein-DNA Recognition in Free DNA Binding Sites. <i>Journal of Molecular Biology</i> , 2009, 386, 1054-1065.	4.2	40
103	NMR Exchange Format: a unified and open standard for representation of NMR restraint data. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 433-434.	8.2	40
104	Structural studies of a new antitumor and antiviral agent: selenazofurin and its .alpha. anomer. <i>Journal of the American Chemical Society</i> , 1985, 107, 1394-1400.	13.7	39
105	PDBx/mmCIF Ecosystem: Foundational Semantic Tools for Structural Biology. <i>Journal of Molecular Biology</i> , 2022, 434, 167599.	4.2	39
106	Crystal and molecular structure of a DNA fragment containing a 2-aminoadenine modification: the relationship between conformation, packing, and hydration in Z-DNA hexamers. <i>Biochemistry</i> , 1992, 31, 9622-9628.	2.5	36
107	Integrin-collagen complex: a metal-glutamate handshake. <i>Structure</i> , 2000, 8, R121-R126.	3.3	36
108	Representation of viruses in the remediated PDB archive. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 874-882.	2.5	35

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109	How Community Has Shaped the Protein Data Bank. <i>Structure</i> , 2013, 21, 1485-1491.	3.3	33
110	Improving the representation of peptide-like inhibitor and antibiotic molecules in the Protein Data Bank. <i>Biopolymers</i> , 2014, 101, 659-668.	2.4	31
111	Disrupted Collagen Architecture in the Crystal Structure of a Triple-Helical Peptide with a Gly → Ala Substitution. <i>Connective Tissue Research</i> , 1996, 35, 401-406.	2.3	30
112	The crystal and molecular structure of the anticancer drug actinomycin D?some explanations for its unusual properties. <i>Biopolymers</i> , 1988, 27, 843-864.	2.4	29
113	Monte Carlo Studies on Water in the dCpG/Proflavin Crystal Hydrate. <i>Journal of Biomolecular Structure and Dynamics</i> , 1983, 1, 287-297.	3.5	28
114	The archiving and dissemination of biological structure data. <i>Current Opinion in Structural Biology</i> , 2016, 40, 17-22.	5.7	28
115	Crystal and molecular structure of a new Z-DNA crystal form: d[CGT(2-NH <sub>2</sub> -A)CG] and its platinated derivative. <i>Biochemistry</i> , 1995, 34, 15487-15495.	2.5	27
116	Design of a data model for developing laboratory information management and analysis systems for protein production. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 278-284.	2.6	27
117	A second determination of the structure of hydroxyurea. <i>Acta Crystallographica</i> , 1967, 23, 180-181.	0.5	26
118	The Impact of Structural Genomics on the Protein Data Bank. <i>Molecular Diagnosis and Therapy</i> , 2004, 4, 247-252.	3.3	26
119	Evolving data standards for cryo-EM structures. <i>Structural Dynamics</i> , 2020, 7, 014701.	2.3	26
120	A crystallographic determination of a chemical structure: 6-amino-10-(1 <sup>2</sup> -d-ribofuranosylamino)pyrimido-[5,4-d]pyrimidine, an example of an unusual d-ribose conformation. <i>Carbohydrate Research</i> , 1975, 44, 169-180.	2.3	25
121	Reply to: Building meaningful models of glycoproteins. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 354-355.	8.2	24
122	The 2010 cryo-EM modeling challenge. <i>Biopolymers</i> , 2012, 97, 651-654.	2.4	22
123	<i>DCC</i> : a Swiss army knife for structure factor analysis and validation. <i>Journal of Applied Crystallography</i> , 2016, 49, 1081-1084.	4.5	22
124	Open-access data: A cornerstone for artificial intelligence approaches to protein structure prediction. <i>Structure</i> , 2021, 29, 515-520.	3.3	22
125	New system for archiving integrative structures. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1486-1496.	2.3	22
126	Statistical Models for Discerning Protein Structures Containing the DNA-binding Helix-Turn-Helix Motif. <i>Journal of Molecular Biology</i> , 2003, 330, 43-55.	4.2	21



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127	The Protein Structure Initiative Structural Biology Knowledgebase Technology Portal: a structural biology web resource. <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 57-62.	1.2	20
128	Archiving and disseminating integrative structure models. <i>Journal of Biomolecular NMR</i> , 2019, 73, 385-398.	2.8	20
129	The synthesis of 4-amino-8-( $\beta$ -ribofuranosyl)aminopyrimido[5,4-]pyrimidine from a purine nucleoside: a novel rearrangement of the purine ring. <i>Tetrahedron Letters</i> , 1973, 14, 3099-3101.	1.4	19
130	Low temperature structures of dCpG-proflavine. Conformational and hydration effects. <i>Biophysical Journal</i> , 1992, 63, 1572-1578.	0.5	19
131	Target highlights in CASP9: Experimental target structures for the critical assessment of techniques for protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 6-20.	2.6	19
132	A Systematic Study of Patterns of Hydration in Nucleic Acids:(I) Guanine and Cytosine. <i>Journal of Biomolecular Structure and Dynamics</i> , 1988, 5, 1101-1110.	3.5	18
133	Structure of a new crystal form of a DNA dodecamer containing T.cntdot.(O6Me)G base pairs. <i>Biochemistry</i> , 1995, 34, 16632-16640.	2.5	18
134	Patterns of Hydration In Crystalline Collagen Peptides. <i>Journal of Biomolecular Structure and Dynamics</i> , 1998, 16, 367-380.	3.5	17
135	Realism about PDB. <i>Nature Biotechnology</i> , 2007, 25, 845-846.	17.5	17
136	Data Deposition and Annotation at the Worldwide Protein Data Bank. <i>Methods in Molecular Biology</i> , 2008, 426, 81-101.	0.9	17
137	The Protein Data Bank: A Case Study in Management of Community Data. <i>Current Proteomics</i> , 2004, 1, 49-57.	0.3	16
138	Insights from 20 years of the Molecule of the Month. <i>Biochemistry and Molecular Biology Education</i> , 2020, 48, 350-355.	1.2	16
139	The data universe of structural biology. <i>IUCr</i> , 2020, 7, 630-638.	2.2	16
140	Crystallization, X-ray studies, and site-directed cysteine mutagenesis of the DNA-binding domain of OmpR. <i>Protein Science</i> , 1996, 5, 1429-1433.	7.6	15
141	Chemical annotation of small and peptide-like molecules at the Protein Data Bank. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat079.	3.0	14
142	How the Protein Data Bank changed biology: An introduction to the JBC Reviews thematic series, part 1. <i>Journal of Biological Chemistry</i> , 2021, 296, 100608.	3.4	14
143	Hydration of Nucleic Acid Crystals. <i>Annals of the New York Academy of Sciences</i> , 1986, 482, 166-178.	3.8	13
144	E. coli trp Repressor Forms a Domain-Swapped Array in Aqueous Alcohol. <i>Structure</i> , 2004, 12, 1099-1108.	3.3	13

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145	The past and future of structure databases. <i>Current Opinion in Biotechnology</i> , 1999, 10, 76-80.	6.6	12
146	Using the Tools and Resources of the RCSB Protein Data Bank. <i>Current Protocols in Bioinformatics</i> , 2007, 20, Unit1.9.	25.8	12
147	RCSB PDB <i>Mobile</i> : iOS and Android mobile apps to provide data access and visualization to the RCSB Protein Data Bank. <i>Bioinformatics</i> , 2015, 31, 126-127.	4.1	12
148	Data to knowledge: how to get meaning from your result. <i>IUCr</i> , 2015, 2, 45-58.	2.2	12
149	The nucleic acid database. <i>Methods of Biochemical Analysis</i> , 2003, 44, 199-216.	0.2	10
150	Protein Structures: From Famine to Feast. <i>American Scientist</i> , 2002, 90, 350.	0.1	8
151	A Structural Model For Sequence-Specific Proflavin-DNA Interactions During In Vitro Frameshift Mutagenesis. <i>Journal of Biomolecular Structure and Dynamics</i> , 1992, 10, 317-331.	3.5	7
152	Title is missing!. <i>Machine Learning</i> , 1995, 21, 81-101.	5.4	7
153	Harnessing Knowledge from Structural Genomics. <i>Structure</i> , 2008, 16, 16-18.	3.3	7
154	Safeguarding the integrity of protein archive. <i>Nature</i> , 2010, 463, 425-425.	27.8	7
155	The evolution of the RCSB Protein Data Bank website. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2011, 1, 782-789.	14.6	7
156	Quality assurance for the query and distribution systems of the RCSB Protein Data Bank. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar003-bar003.	3.0	7
157	Synergies between the Protein Data Bank and the community. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 400-401.	8.2	7
158	A Monte Carlo simulation study of the aqueous hydration of r(GpC)2: Comparison with crystallographic ordered water sites. <i>Biopolymers</i> , 1990, 29, 771-783.	2.4	6
159	CIF Applications. XI.A La Mode: a ligand and monomer object data environment. I. Automated construction of mmCIF monomer and ligand models. <i>Journal of Applied Crystallography</i> , 1999, 32, 125-133.	4.5	6
160	Archiving of Integrative Structural Models. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1105, 261-272.	1.6	6
161	Anticipating innovations in structural biology. <i>Quarterly Reviews of Biophysics</i> , 2018, 51, e8.	5.7	6
162	Crystal structures of fragments of DNA and RNA. , 1981, , 17-32.		6

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163	Developing Community Resources for Nucleic Acid Structures. <i>Life</i> , 2022, 12, 540.	2.4	6
164	The Nucleic Acid Database. <i>Methods of Biochemical Analysis</i> , 2005, , 199-216.	0.2	4
165	Comment on<i>On the propagation of errors</i> by Jaskolski (2013). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2297-2297.	2.5	4
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