

Helen M Berman

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3993556/publications.pdf>

Version: 2024-02-01

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	A new visual design language for biological structures in a cell. <i>Structure</i> , 2022, , .	3.3	2
2	Developing Community Resources for Nucleic Acid Structures. <i>Life</i> , 2022, 12, 540.	2.4	6
3	PDBx/mmCIF Ecosystem: Foundational Semantic Tools for Structural Biology. <i>Journal of Molecular Biology</i> , 2022, 434, 167599.	4.2	39
4	More than forty years of nucleic acid structural science. <i>Bioorganic and Medicinal Chemistry</i> , 2022, 69, 116887.	3.0	3
5	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDDataResource challenge. <i>Nature Methods</i> , 2021, 18, 156-164.	19.0	73
6	Synergies between the Protein Data Bank and the community. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 400-401.	8.2	7
7	Open-access data: A cornerstone for artificial intelligence approaches to protein structure prediction. <i>Structure</i> , 2021, 29, 515-520.	3.3	22
8	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
9	How the Protein Data Bank changed biology: An introduction to the JBC Reviews thematic series, part 2. <i>Journal of Biological Chemistry</i> , 2021, 296, 100748.	3.4	2
10	New system for archiving integrative structures. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1486-1496.	2.3	22
11	Insights from 20 years of the Molecule of the Month. <i>Biochemistry and Molecular Biology Education</i> , 2020, 48, 350-355.	1.2	16
12	Evolving data standards for cryo-EM structures. <i>Structural Dynamics</i> , 2020, 7, 014701.	2.3	26
13	The data universe of structural biology. <i>IUCr</i> , 2020, 7, 630-638.	2.2	16
14	Archiving and disseminating integrative structure models. <i>Journal of Biomolecular NMR</i> , 2019, 73, 385-398.	2.8	20
15	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
16	Open access to research artifacts: Implementing the next generation data management plan. <i>Proceedings of the Association for Information Science and Technology</i> , 2019, 56, 481-485.	0.6	2
17	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
18	Protein Data Bank: the single global archive for 3D macromolecular structure data. <i>Nucleic Acids Research</i> , 2019, 47, D520-D528.	14.5	671

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	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
22	Archiving of Integrative Structural Models. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1105, 261-272.	1.6	6
23	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
24	Anticipating innovations in structural biology. <i>Quarterly Reviews of Biophysics</i> , 2018, 51, e8.	5.7	6
25	New online curriculum: the PDB pipeline and data archiving. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, a243-a243.	0.1	0
26	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2017, 45, D271-D281.	14.5	619
27	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
28	DNAProDB: an interactive tool for structural analysis of DNA-protein complexes. <i>Nucleic Acids Research</i> , 2017, 45, W89-W97.	14.5	59
29	Protein Data Bank (PDB): The Single Global Macromolecular Structure Archive. <i>Methods in Molecular Biology</i> , 2017, 1607, 627-641.	0.9	592
30	PDB-Dev: a Prototype System for Depositing Integrative/Hybrid Structural Models. <i>Structure</i> , 2017, 25, 1317-1318.	3.3	84
31	Validation of Structures in the Protein Data Bank. <i>Structure</i> , 2017, 25, 1916-1927.	3.3	210
32	<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
33	The archiving and dissemination of biological structure data. <i>Current Opinion in Structural Biology</i> , 2016, 40, 17-22.	5.7	28
34	EMDataBank unified data resource for 3DEM. <i>Nucleic Acids Research</i> , 2016, 44, D396-D403.	14.5	230
35	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
36	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

#	ARTICLE	IF	CITATIONS
37	Data to knowledge: how to get meaning from your result. IUCr, 2015, 2, 45-58.	2.2	12
38	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. Structure, 2015, 23, 1156-1167.	3.3	159
39	The RCSB PDB "Molecule of the Month": Inspiring a Molecular View of Biology. PLoS Biology, 2015, 13, e1002140.	5.6	88
40	The RCSB Protein Data Bank: views of structural biology for basic and applied research and education. Nucleic Acids Research, 2015, 43, D345-D356.	14.5	461
41	Protein Structure Annotation Resources. Methods in Molecular Biology, 2015, 1261, 3-20.	0.9	1
42	The Protein Data Bank: Overview and Tools for Drug Discovery. NATO Science for Peace and Security Series A: Chemistry and Biology, 2015, , 93-106.	0.5	1
43	PSI SBKB Technology Portal: A Structural Biology Web Resource. FASEB Journal, 2015, 29, LB94.	0.5	0
44	The Protein Data Bank archive as an open data resource. Journal of Computer-Aided Molecular Design, 2014, 28, 1009-1014.	2.9	114
45	Improving the representation of peptide-like inhibitor and antibiotic molecules in the Protein Data Bank. Biopolymers, 2014, 101, 659-668.	2.4	31
46	The Nucleic Acid Database: new features and capabilities. Nucleic Acids Research, 2014, 42, D114-D122.	14.5	194
47	Response to On prompt update of literature references in the Protein Data Bank. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2780-2780.	2.5	1
48	Establishing the Next Generation of the Protein Data Bank. The Winnower, 2014, , .	0.0	1
49	How Community Has Shaped the Protein Data Bank. Structure, 2013, 21, 1485-1491.	3.3	33
50	The future of the protein data bank. Biopolymers, 2013, 99, 218-222.	2.4	65
51	Recommendations of the wwPDB NMR Validation Task Force. Structure, 2013, 21, 1563-1570.	3.3	151
52	Trendspotting in the Protein Data Bank. FEBS Letters, 2013, 587, 1036-1045.	2.8	74
53	Report of the wwPDB Small-Angle Scattering Task Force: Data Requirements for Biomolecular Modeling and the PDB. Structure, 2013, 21, 875-881.	3.3	77
54	AN OVERVIEW OF STRUCTURAL STUDIES OF THE COLLAGEN TRIPLE HELIX. , 2013, , 17-37.		2

#	ARTICLE	IF	CITATIONS
55	Chemical annotation of small and peptide-like molecules at the Protein Data Bank. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat079.	3.0	14
56	Comment on<i>On the propagation of errors</i>by Jaskolski (2013). Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2297-2297.	2.5	4
57	Comment onTimely deposition of macromolecular structures is necessary for peer reviewby Joosten et al.(2013). Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2296-2296.	2.5	1
58	Revealing structural views of biology. Biopolymers, 2013, 99, 817-824.	2.4	4
59	The RCSB Protein Data Bank: new resources for research and education. Nucleic Acids Research, 2012, 41, D475-D482.	14.5	418
60	Creating a community resource for protein science. Protein Science, 2012, 21, 1587-1596.	7.6	3
61	The 2010 cryo-EM modeling challenge. Biopolymers, 2012, 97, 651-654.	2.4	22
62	The Protein Structure Initiative Structural Biology Knowledgebase Technology Portal: a structural biology web resource. Journal of Structural and Functional Genomics, 2012, 13, 57-62.	1.2	20
63	The Protein Data Bank at 40: Reflecting on the Past to Prepare for the Future. Structure, 2012, 20, 391-396.	3.3	120
64	Structural Biology Knowledgebase: a biologists resource for protein structure and sample information. FASEB Journal, 2012, 26, lb194.	0.5	0
65	The evolution of the RCSB Protein Data Bank website. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2011, 1, 782-789.	14.6	7
66	The Structural Biology Knowledgebase: a portal to protein structures, sequences, functions, and methods. Journal of Structural and Functional Genomics, 2011, 12, 45-54.	1.2	65
67	Target highlights in CASP9: Experimental target structures for the critical assessment of techniques for protein structure prediction. Proteins: Structure, Function and Bioinformatics, 2011, 79, 6-20.	2.6	19
68	The RCSB Protein Data Bank: redesigned web site and web services. Nucleic Acids Research, 2011, 39, D392-D401.	14.5	549
69	EMDataBank.org: unified data resource for CryoEM. Nucleic Acids Research, 2011, 39, D456-D464.	14.5	246
70	Quality assurance for the query and distribution systems of the RCSB Protein Data Bank. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar003-bar003.	3.0	7
71	Promoting a structural view of biology for varied audiences: an overview of RCSB PDB resources and experiences. Journal of Applied Crystallography, 2010, 43, 1224-1229.	4.5	41
72	Safeguarding the integrity of protein archive. Nature, 2010, 463, 425-425.	27.8	7

#	ARTICLE	IF	CITATIONS
73	HOW TO USE THE PSI STRUCTURAL GENOMICS KNOWLEDGEBASE TO ENABLE RESEARCH. FASEB Journal, 2010, 24, 902.2.	0.5	0
74	The protein structure initiative structural genomics knowledgebase. Nucleic Acids Research, 2009, 37, D365-D368.	14.5	94
75	Three-dimensional EM structure of an intact activator-dependent transcription initiation complex. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 19830-19835.	7.1	76
76	The Protein Model Portal. Journal of Structural and Functional Genomics, 2009, 10, 1-8.	1.2	130
77	Data Deposition and Annotation at the Worldwide Protein Data Bank. Molecular Biotechnology, 2009, 42, 1-13.	2.4	113
78	Signatures of Protein-DNA Recognition in Free DNA Binding Sites. Journal of Molecular Biology, 2009, 386, 1054-1065.	4.2	40
79	The Protein Structure Initiative Structural Genomics Knowledgebase. FASEB Journal, 2009, 23, 858.10.	0.5	0
80	BioMagResBank (BMRB) as a partner in the Worldwide Protein Data Bank (wwPDB): new policies affecting biomolecular NMR depositions. Journal of Biomolecular NMR, 2008, 40, 153-155.	2.8	117
81	The Protein Data Bank: a historical perspective. Acta Crystallographica Section A: Foundations and Advances, 2008, 64, 88-95.	0.3	342
82	Representation of viruses in the remediated PDB archive. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 874-882.	2.5	35
83	Harnessing Knowledge from Structural Genomics. Structure, 2008, 16, 16-18.	3.3	7
84	Data Deposition and Annotation at the Worldwide Protein Data Bank. Methods in Molecular Biology, 2008, 426, 81-101.	0.9	17
85	RNA backbone: Consensus all-angle conformers and modular string nomenclature (an RNA Ontology) Tj ETQq1 1 0,784314 rgBT /Ove 3.5 216	3.5	216
86	The worldwide Protein Data Bank (wwPDB): ensuring a single, uniform archive of PDB data. Nucleic Acids Research, 2007, 35, D301-D303.	14.5	992
87	Remediation of the protein data bank archive. Nucleic Acids Research, 2007, 36, D426-D433.	14.5	136
88	Using the Tools and Resources of the RCSB Protein Data Bank. Current Protocols in Bioinformatics, 2007, 20, Unit1.9.	25.8	12
89	Realism about PDB. Nature Biotechnology, 2007, 25, 845-846.	17.5	17
90	Reply to: Building meaningful models of glycoproteins. Nature Structural and Molecular Biology, 2007, 14, 354-355.	8.2	24

#	ARTICLE	IF	CITATIONS
91	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
92	Conformational Effects of Gly-X-Gly Interruptions in the Collagen Triple Helix. <i>Journal of Molecular Biology</i> , 2006, 362, 298-311.	4.2	61
93	Reply to: Is one solution good enough?. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 185-185.	8.2	3
94	Outcome of a Workshop on Archiving Structural Models of Biological Macromolecules. <i>Structure</i> , 2006, 14, 1211-1217.	3.3	60
95	The RNA Ontology Consortium: An open invitation to the RNA community. <i>Rna</i> , 2006, 12, 533-541.	3.5	59
96	The RCSB PDB information portal for structural genomics. <i>Nucleic Acids Research</i> , 2006, 34, D302-D305.	14.5	334
97	Basics of Nucleic Acid Structure. , 2006, , 1-44.		0
98	Educational Resources for Structural Biology at the RCSB Protein Data Bank. <i>FASEB Journal</i> , 2006, 20, A541.	0.5	0
99	Using the Tools and Resources of the RCSB Protein Data Bank. <i>Current Protocols in Bioinformatics</i> , 2005, 9, 1.9.1.	25.8	1
100	The Protein Data Bank (PDB) and the Worldwide PDB http://www ww p d b . o r g . , 2005, , .		2
101	Reply to "Giving credit where credit is due". <i>Nature Structural and Molecular Biology</i> , 2005, 12, 634-634.	8.2	3
102	Large Macromolecular Complexes in the Protein Data Bank: A Status Report. <i>Structure</i> , 2005, 13, 381-388.	3.3	77
103	A structure-based method for identifying DNA-binding proteins and their sites of DNA-interaction. <i>Journal of Structural and Functional Genomics</i> , 2005, 5, 255-265.	1.2	2
104	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
105	PDBML: the representation of archival macromolecular structure data in XML. <i>Bioinformatics</i> , 2005, 21, 988-992.	4.1	154
106	Fundamentals of DNA and RNA Structure. <i>Methods of Biochemical Analysis</i> , 2005, , 41-73.	0.2	2
107	The Nucleic Acid Database. <i>Methods of Biochemical Analysis</i> , 2005, , 199-216.	0.2	4
108	TargetDB: a target registration database for structural genomics projects. <i>Bioinformatics</i> , 2004, 20, 2860-2862.	4.1	182

#	ARTICLE	IF	CITATIONS
109	Ligand Depot: a data warehouse for ligands bound to macromolecules. <i>Bioinformatics</i> , 2004, 20, 2153-2155.	4.1	189
110	The distribution and query systems of the RCSB Protein Data Bank. <i>Nucleic Acids Research</i> , 2004, 32, 223D-225.	14.5	108
111	RNA conformational classes. <i>Nucleic Acids Research</i> , 2004, 32, 1666-1677.	14.5	123
112	E. coli trp Repressor Forms a Domain-Swapped Array in Aqueous Alcohol. <i>Structure</i> , 2004, 12, 1099-1108.	3.3	13
113	Catabolite activator protein: DNA binding and transcription activation. <i>Current Opinion in Structural Biology</i> , 2004, 14, 10-20.	5.7	291
114	A structure-based method for identifying DNA-binding proteins and their sites of DNA-interaction. <i>Journal of Structural and Functional Genomics</i> , 2004, 5, 255-265.	1.2	1
115	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
116	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
117	The Impact of Structural Genomics on the Protein Data Bank. <i>Molecular Diagnosis and Therapy</i> , 2004, 4, 247-252.	3.3	26
118	The Protein Data Bank: A Case Study in Management of Community Data. <i>Current Proteomics</i> , 2004, 1, 49-57.	0.3	16
119	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
120	Announcing the worldwide Protein Data Bank. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 980-980.	8.2	2,355
121	Tools for the automatic identification and classification of RNA base pairs. <i>Nucleic Acids Research</i> , 2003, 31, 3450-3460.	14.5	240
122	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
123	The Protein Data Bank and structural genomics. <i>Nucleic Acids Research</i> , 2003, 31, 489-491.	14.5	331
124	Using electrostatic potentials to predict DNA-binding sites on DNA-binding proteins. <i>Nucleic Acids Research</i> , 2003, 31, 7189-7198.	14.5	186
125	The Need for Dictionaries, Ontologies, and Controlled Vocabularies. <i>OMICS A Journal of Integrative Biology</i> , 2003, 7, 9-10.	2.0	2
126	Validation of Protein Structures for Protein Data Bank. <i>Methods in Enzymology</i> , 2003, 374, 370-385.	1.0	43

#	ARTICLE	IF	CITATIONS
127	The nucleic acid database. <i>Methods of Biochemical Analysis</i> , 2003, 44, 199-216.	0.2	10
128	Structural Basis of Transcription Activation: The CAP-alpha CTD-DNA Complex. <i>Science</i> , 2002, 297, 1562-1566.	12.6	234
129	The Protein Data Bank: unifying the archive. <i>Nucleic Acids Research</i> , 2002, 30, 245-248.	14.5	261
130	The Protein Data Bank. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 899-907.	2.5	2,023
131	The Nucleic Acid Database. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 889-898.	2.5	57
132	Protein Structures: From Famine to Feast. <i>American Scientist</i> , 2002, 90, 350.	0.1	8
133	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
134	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
135	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
136	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
137	The Protein Data Bank and the challenge of structural genomics. <i>Nature Structural Biology</i> , 2000, 7, 957-959.	9.7	511
138	Integrin-collagen complex: a metal-glutamate handshake. <i>Structure</i> , 2000, 8, R121-R126.	3.3	36
139	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
140	An overview of the structures of protein-DNA complexes. <i>Genome Biology</i> , 2000, 1, reviews001.1.	9.6	531
141	The Protein Data Bank. <i>Nucleic Acids Research</i> , 2000, 28, 235-242.	14.5	31,087
142	The past and future of structure databases. <i>Current Opinion in Biotechnology</i> , 1999, 10, 76-80.	6.6	12
143	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
144	Sequence dependent conformational variations of collagen triple-helical structure. <i>Nature Structural Biology</i> , 1999, 6, 454-457.	9.7	277

#	ARTICLE	IF	CITATIONS
145	Protein-DNA interactions: a structural analysis. <i>Journal of Molecular Biology</i> , 1999, 287, 877-896.	4.2	397
146	Protein-DNA Interactions. <i>Biochemical Society Transactions</i> , 1999, 27, A88-A88.	3.4	1
147	Patterns of Hydration In Crystalline Collagen Peptides. <i>Journal of Biomolecular Structure and Dynamics</i> , 1998, 16, 367-380.	3.5	17
148	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
149	An Analysis of the Relationship between Hydration and Protein-DNA Interactions. <i>Biophysical Journal</i> , 1998, 75, 2170-2177.	0.5	75
150	Hydration of the Phosphate Group in Double-Helical DNA. <i>Biophysical Journal</i> , 1998, 75, 2422-2434.	0.5	201
151	[30] Macromolecular crystallographic information file. <i>Methods in Enzymology</i> , 1997, 277, 571-590.	1.0	148
152	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
153	Crystal studies of B-DNA: The answers and the questions. , 1997, 44, 23-44.		89
154	Conformations of the sugar-phosphate backbone in helical DNA crystal structures. , 1997, 42, 113-124.		198
155	Conformations of the sugar-phosphate backbone in helical DNA crystal structures. <i>Biopolymers</i> , 1997, 42, 113-124.	2.4	3
156	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
157	Geometric Parameters in Nucleic Acids: Sugar and Phosphate Constituents. <i>Journal of the American Chemical Society</i> , 1996, 118, 519-529.	13.7	215
158	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
159	Crystallographic Evidence for C-H...O=C Hydrogen Bonds in a Collagen Triple Helix. <i>Journal of Molecular Biology</i> , 1996, 264, 734-742.	4.2	209
160	Geometric Parameters in Nucleic Acids: Nitrogenous Bases. <i>Journal of the American Chemical Society</i> , 1996, 118, 509-518.	13.7	191
161	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
162	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

#	ARTICLE	IF	CITATIONS
163	Aromatic hydrogen bond in sequence-specific protein DNA recognition. <i>Nature Structural and Molecular Biology</i> , 1996, 3, 837-841.	8.2	66
164	The Nucleic Acid Database: Present and future. <i>Journal of Research of the National Institute of Standards and Technology</i> , 1996, 101, 243.	1.2	2
165	Hydration structure of a collagen peptide. <i>Structure</i> , 1995, 3, 893-906.	3.3	570
166	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
167	Crystal and molecular structure of a new Z-DNA crystal form: d[CGT(2-NH2-A)CG] and its platinated derivative. <i>Biochemistry</i> , 1995, 34, 15487-15495.	2.5	27
168	Hydration of the DNA bases is local. <i>Biophysical Journal</i> , 1995, 69, 2661-2669.	0.5	219
169	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
170	Title is missing!. <i>Machine Learning</i> , 1995, 21, 81-101.	5.4	7
171	DEXTER: A system that experiments with choices of training data using expert knowledge in the domain of DNA hydration. <i>Machine Learning</i> , 1995, 21, 81-101.	5.4	2
172	Crystal structure and nmr conformation of a cyclic pseudotetrapeptide containing urethane backbone linkages. <i>Biopolymers</i> , 1994, 34, 403-414.	2.4	3
173	Hydration of DNA: take 2. <i>Current Opinion in Structural Biology</i> , 1994, 4, 345-350.	5.7	132
174	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
175	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
176	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
177	Low temperature structures of dCpG-proflavine. Conformational and hydration effects. <i>Biophysical Journal</i> , 1992, 63, 1572-1578.	0.5	19
178	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
179	Hydration of DNA bases: Analysis of crystallographic data. <i>Biopolymers</i> , 1992, 32, 725-750.	2.4	127
180	Hydration of DNA. <i>Current Opinion in Structural Biology</i> , 1991, 1, 423-427.	5.7	86

#	ARTICLE	IF	CITATIONS
181	Crystal and molecular structure of a DNA fragment: d(CGTGAATTCACG). <i>Biochemistry</i> , 1991, 30, 4449-4455.	2.5	46
182	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
183	Crystal and molecular structure of a DNA duplex containing the carcinogenic lesion O6-methylguanine. <i>Biochemistry</i> , 1990, 29, 10461-10465.	2.5	50
184	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
185	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
186	Hydration of Nucleic Acid Crystals. <i>Annals of the New York Academy of Sciences</i> , 1986, 482, 166-178.	3.8	13
187	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
188	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
189	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
190	Crystal structures of fragments of DNA and RNA. , 1981, , 17-32.		6
191	Highly structured water network in crystals of a deoxydinucleoside drug complex. <i>Nature</i> , 1980, 288, 129-133.	27.8	134
192	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
193	Molecular and crystal structure of an intercalation complex: Proflavine-cytidylyl-(3?,5?)-guanosine. <i>Biopolymers</i> , 1979, 18, 2405-2429.	2.4	67
194	Biochemical Method. <i>Science</i> , 1977, 196, 50-50.	12.6	0
195	A crystallographic determination of a chemical structure: 6-amino-10-(l ² -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
196	The synthesis of 4-amino-8-(l ² -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
197	Crystal structure of a naturally occurring dinucleoside phosphate: Uridylyl 3â€²,5â€²-adenosine phosphate model for RNA chain folding. <i>Journal of Molecular Biology</i> , 1972, 66, 403-421.	4.2	188
198	A second determination of the structure of hydroxyurea. <i>Acta Crystallographica</i> , 1967, 23, 180-181.	0.5	26