

# Miquel Coll

## List of Publications by Year in descending order

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142  
papers

8,741  
citations

38660

50  
h-index

46693

89  
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all docs

151  
docs citations

151  
times ranked

8687  
citing authors

#	ARTICLE	IF	CITATIONS
1	Using a partial atomic model from medium-resolution cryo-EM to solve a large crystal structure. Acta Crystallographica Section D: Structural Biology, 2021, 77, 11-18.	1.1	4
2	Structures of Tailed Phages and Herpesviruses (Herpesviridae). , 2021, , 318-328.		0
3	Structures of T7 bacteriophage portal and tail suggest a viral DNA retention and ejection mechanism. Nature Communications, 2019, 10, 3746.	5.8	61
4	Atomic structure of the Epstein-Barr virus portal. Nature Communications, 2019, 10, 3891.	5.8	28
5	Structure-Driven Discovery of Î±,Î³-Diketoacid Inhibitors Against UL99 Herpesvirus Terminase. ACS Omega, 2018, 3, 8497-8505.	1.6	7
6	Intercalative DNA binding of the marine anticancer drug variolin B. Scientific Reports, 2017, 7, 39680.	1.6	19
7	Insights into the inhibited form of the redox-sensitive SufE-like sulfur acceptor CsdE. PLoS ONE, 2017, 12, e0186286.	1.1	0
8	Structural basis of a histidine-DNA nicking/joining mechanism for gene transfer and promiscuous spread of antibiotic resistance. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E6526-E6535.	3.3	27
9	Conformational plasticity of RepB, the replication initiator protein of promiscuous streptococcal plasmid pMV158. Scientific Reports, 2016, 6, 20915.	1.6	11
10	A C2HC zinc finger is essential for the RING-E2 interaction of the ubiquitin ligase RNF125. Scientific Reports, 2016, 6, 29232.	1.6	20
11	Mechanism of Sulfur Transfer Across Protein-Protein Interfaces: The Cysteine Desulfurase Model System. ACS Catalysis, 2016, 6, 3975-3984.	5.5	12
12	Irreversible inhibitors of the 3C protease of Coxsackie virus through templated assembly of protein-binding fragments. Nature Communications, 2016, 7, 12761.	5.8	30
13	Plasmid Rolling-Circle Replication. Microbiology Spectrum, 2015, 3, PLAS-0035-2014.	1.2	69
14	The Crystal Structure and Small-Angle X-Ray Analysis of CsdL/TcdA Reveal a New tRNA Binding Motif in the MoeB/E1 Superfamily. PLoS ONE, 2015, 10, e0118606.	1.1	10
15	The structure of the TBCE/TBCB chaperones and Î±-tubulin complex shows a tubulin dimer dissociation mechanism. Journal of Cell Science, 2015, 128, 1824-34.	1.2	27
16	Structural Analysis and Mutant Growth Properties Reveal Distinctive Enzymatic and Cellular Roles for the Three Major L-Alanine Transaminases of Escherichia coli. PLoS ONE, 2014, 9, e102139.	1.1	16
17	Thread Insertion of a Bis(dipyridophenazine) Diruthenium Complex into the DNA Double Helix by the Extrusion of AT Base Pairs and Cross-Linking of DNA Duplexes. Angewandte Chemie - International Edition, 2014, 53, 1949-1952.	7.2	42
18	Structural Basis for DNA Binding Specificity by the Auxin-Dependent ARF Transcription Factors. Cell, 2014, 156, 577-589.	13.5	348

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19	Nicking activity of the pMV158 MobM relaxase on cognate and heterologous origins of transfer. <i>Plasmid</i> , 2013, 70, 120-130.	0.4	12
20	Functional Properties and Structural Requirements of the Plasmid pMV158-Encoded MobM Relaxase Domain. <i>Journal of Bacteriology</i> , 2013, 195, 3000-3008.	1.0	7
21	Structure and Non-Structure of Centrosomal Proteins. <i>PLoS ONE</i> , 2013, 8, e62633.	1.1	25
22	Structure and mechanism of a cysteine sulfinate desulfinate engineered on the aspartate aminotransferase scaffold. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 339-349.	1.1	17
23	Œf70 and PhoB activator. <i>Transcription</i> , 2012, 3, 160-164.	1.7	9
24	PhoB transcriptional activator binds hierarchically to <i>pho box</i> promoters. <i>Biological Chemistry</i> , 2012, 393, 1165-1171.	1.2	20
25	Structural insights into transcription complexes. <i>Journal of Structural Biology</i> , 2011, 175, 135-146.	1.3	14
26	Human mitochondrial transcription factor A induces a U-turn structure in the light strand promoter. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1281-1289.	3.6	168
27	Site-directed mutagenesis of mouse glutathione transferase P1 unlocks masked cooperativity, introduces a novel mechanism for ping pong kinetic behaviour, and provides further structural evidence for participation of a water molecule in proton abstraction from glutathione. <i>FEBS Journal</i> , 2011, 278, 273-281.	2.2	7
28	Picornavirus non-structural proteins as targets for new anti-virals with broad activity. <i>Antiviral Research</i> , 2011, 89, 204-218.	1.9	76
29	The UlaG protein family defines novel structural and functional motifs grafted on an ancient RNase fold. <i>BMC Evolutionary Biology</i> , 2011, 11, 273.	3.2	7
30	Structural Basis for Antiviral Inhibition of the Main Protease, 3C, from Human Enterovirus 93. <i>Journal of Virology</i> , 2011, 85, 10764-10773.	1.5	20
31	The MobM relaxase domain of plasmid pMV158: thermal stability and activity upon Mn <sup>2+</sup> and specific DNA binding. <i>Nucleic Acids Research</i> , 2011, 39, 4315-4329.	6.5	29
32	The structure of a transcription activation subcomplex reveals how Œf <sup>70</sup> is recruited to PhoB promoters. <i>EMBO Journal</i> , 2011, 30, 3776-3785.	3.5	63
33	Self-Assembly of Functionalizable Two-Component 3D DNA Arrays through the Induced Formation of DNA Three-Way Junction Branch Points by Supramolecular Cylinders. <i>Angewandte Chemie - International Edition</i> , 2010, 49, 2336-2339.	7.2	65
34	Human mitochondrial mTERF wraps around DNA through a left-handed superhelical tandem repeat. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 891-893.	3.6	46
35	Structure and inhibition of herpesvirus DNA packaging terminase nuclease domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 16078-16083.	3.3	102
36	Molecular Architecture of the Mn <sup>2+</sup> -dependent Lactonase UlaG Reveals an RNase-like Metallo-Œ <sup>2</sup> -lactamase Fold and a Novel Quaternary Structure. <i>Journal of Molecular Biology</i> , 2010, 398, 715-729.	2.0	31

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37	The Structure of RNA-Free Rho Termination Factor Indicates a Dynamic Mechanism of Transcript Capture. <i>Journal of Molecular Biology</i> , 2010, 400, 16-23.	2.0	11
38	Plasmid replication initiator RepB forms a hexamer reminiscent of ring helicases and has mobile nuclease domains. <i>EMBO Journal</i> , 2009, 28, 1666-1678.	3.5	45
39	Cloning, expression, purification and crystallization of the Rho transcription termination factor from <i>Thermotoga maritima</i> . <i>Protein Expression and Purification</i> , 2009, 65, 174-178.	0.6	2
40	DNA-binding drugs caught in action: the latest 3D pictures of drug-DNA complexes. <i>Dalton Transactions</i> , 2009, , 399-414.	1.6	153
41	Overproduction, crystallization and preliminary X-ray analysis of the putative <i>Escherichia coli</i> ascorbate-6-phosphate lactonase UlaG from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 36-38.	0.7	3
42	The VIZIER project: Preparedness against pathogenic RNA viruses. <i>Antiviral Research</i> , 2008, 78, 37-46.	1.9	26
43	Quaternary Structural Transitions in the DeoR-Type Repressor UlaR Control Transcriptional Readout from the Ascorbate Utilization Regulon in <i>Escherichia coli</i> . <i>Biochemistry</i> , 2008, 47, 11424-11433.	1.2	30
44	The X-ray Crystal Structures of Two Constitutively Active Mutants of the <i>Escherichia coli</i> PhoB Receiver Domain Give Insights into Activation. <i>Journal of Molecular Biology</i> , 2007, 366, 626-641.	2.0	23
45	Unveiling the Molecular Mechanism of a Conjugative Relaxase: The Structure of TrwC Complexed with a 27-mer DNA Comprising the Recognition Hairpin and the Cleavage Site. <i>Journal of Molecular Biology</i> , 2006, 358, 857-869.	2.0	68
46	The Structure of Phage $\phi$ 29 Transcription Regulator p4-DNA Complex Reveals an N-Hook Motif for DNA Binding. <i>Molecular Cell</i> , 2006, 22, 73-81.	4.5	15
47	The cofactor-induced pre-active conformation in PhoB. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1046-1057.	2.5	12
48	Application of the use of high-throughput technologies to the determination of protein structures of bacterial and viral pathogens. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1196-1207.	2.5	23
49	Cut and move: protein machinery for DNA processing in bacterial conjugation. <i>Current Opinion in Structural Biology</i> , 2006, 16, 744-752.	2.6	37
50	Molecular Recognition of a Three-Way DNA Junction by a Metallo-supramolecular Helicate. <i>Angewandte Chemie - International Edition</i> , 2006, 45, 1227-1231.	7.2	278
51	Molecular Recognition of a Three-Way DNA Junction by a Metallo-supramolecular Helicate. <i>Angewandte Chemie - International Edition</i> , 2006, 45, 1834-1834.	7.2	2
52	X-ray crystallographic studies of two transthyretin variants: further insights into amyloidogenesis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 333-339.	2.5	12
53	The anticancer agent ellipticine unwinds DNA by intercalative binding in an orientation parallel to base pairs. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1009-1012.	2.5	107
54	Crystal Structure of an Iron-Dependent Group III Dehydrogenase That Interconverts L-Lactaldehyde and L-1,2-Propanediol in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2005, 187, 4957-4966.	1.0	76

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55	On the Transcriptional Regulation of Methicillin Resistance. <i>Journal of Biological Chemistry</i> , 2004, 279, 17888-17896.	1.6	67
56	Coupling Factors in Macromolecular Type-IV Secretion Machineries. <i>Current Pharmaceutical Design</i> , 2004, 10, 1551-1565.	0.9	94
57	Structure of xylanase Xys1 <sup>HP</sup> from <i>Streptomyces halstedii</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1447-1453.	2.5	22
58	Recognition and processing of the origin of transfer DNA by conjugative relaxase TrwC. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 1002-1010.	3.6	132
59	Three-dimensional Structure of Mecl. <i>Journal of Biological Chemistry</i> , 2003, 278, 39897-39905.	1.6	46
60	The Structure of Human Prokallikrein 6 Reveals a Novel Activation Mechanism for the Kallikrein Family. <i>Journal of Biological Chemistry</i> , 2002, 277, 27273-27281.	1.6	74
61	Conjugative Plasmid Protein TrwB, an Integral Membrane Type IV Secretion System Coupling Protein. <i>Journal of Biological Chemistry</i> , 2002, 277, 7556-7566.	1.6	75
62	A Genetically Economical Family of Plasmid-Encoded Transcriptional Repressors Involved in Control of Plasmid Copy Number. <i>Journal of Bacteriology</i> , 2002, 184, 4943-4951.	1.0	46
63	Detailed architecture of a DNA translocating machine: the high-resolution structure of the bacteriophage $\phi$ 29 connector particle 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2002, 315, 663-676.	2.0	205
64	Three-dimensional Structure of Human Tubulin Chaperone Cofactor A. <i>Journal of Molecular Biology</i> , 2002, 318, 1139-1149.	2.0	23
65	The Inherent Properties of DNA Four-way Junctions: Comparing the Crystal Structures of Holliday Junctions. <i>Journal of Molecular Biology</i> , 2002, 320, 1037-1051.	2.0	44
66	Note to the Paper by Guasch et al. (2002) Detailed Architecture of a DNA Translocating Machine: The High-resolution Structure of the Bacteriophage $\phi$ 29 Connector Particle. <i>Journal of Molecular Biology</i> , 2002, 321, 379-380.	2.0	2
67	Human Procarboxypeptidase B: Three-dimensional Structure and Implications for Thrombin-activatable Fibrinolysis Inhibitor (TAFI). <i>Journal of Molecular Biology</i> , 2002, 321, 537-547.	2.0	66
68	Structure and role of coupling proteins in conjugal DNA transfer. <i>Research in Microbiology</i> , 2002, 153, 199-204.	1.0	37
69	Structure of the DNA-Bound T-Box Domain of Human TBX3, a Transcription Factor Responsible for Ulnar-Mammary Syndrome. <i>Structure</i> , 2002, 10, 343-356.	1.6	105
70	Tandem DNA Recognition by PhoB, a Two-Component Signal Transduction Transcriptional Activator. <i>Structure</i> , 2002, 10, 701-713.	1.6	266
71	Bacterial conjugation: a two-step mechanism for DNA transport. <i>Molecular Microbiology</i> , 2002, 45, 1-8.	1.2	341
72	Crystallization and preliminary X-ray analysis of the DNA decamers d(CCGGATCCGG) and d(CCGGCGCCGG). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 310-311.	2.5	3

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73	Crystallization and preliminary X-ray analysis of the antimalarial and cytotoxic alkaloid cryptolepine complexed with the DNA fragment d(CCTAGG) <sub>2</sub> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 312-313.	2.5	11
74	The antimalarial and cytotoxic drug cryptolepine intercalates into DNA at cytosine-cytosine sites. <i>Nature Structural Biology</i> , 2002, 9, 57-60.	9.7	164
75	<i>Trypanosoma cruzi</i> macrophage infectivity potentiator has a rotamase core and a highly exposed $\alpha$ -helix. <i>EMBO Reports</i> , 2002, 3, 88-94.	2.0	42
76	Plasmid transcriptional repressor CopG oligomerises to render helical superstructures unbound and in complexes with oligonucleotides. <i>Journal of Molecular Biology</i> , 2001, 310, 403-417.	2.0	25
77	Review: Postchaperonin Tubulin Folding Cofactors and Their Role in Microtubule Dynamics. <i>Journal of Structural Biology</i> , 2001, 135, 219-229.	1.3	134
78	Structure of TrwB, a gatekeeper in bacterial conjugation. <i>International Journal of Biochemistry and Cell Biology</i> , 2001, 33, 839-843.	1.2	33
79	Three-dimensional structure of human RNase 1 <sup>N7</sup> at 1.9 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 498-505.	2.5	20
80	Solving a 300 kDa multimeric protein by low-resolution MAD phasing and averaging/phase extension. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 800-805.	2.5	3
81	Structure of human biliverdin IXbeta reductase, an early fetal bilirubin IXbeta producing enzyme. <i>Nature Structural Biology</i> , 2001, 8, 215-220.	9.7	99
82	The bacterial conjugation protein TrwB resembles ring helicases and F1-ATPase. <i>Nature</i> , 2001, 409, 637-641.	13.7	318
83	The Structure of an Engineered Domain-Swapped Ribonuclease Dimer and Its Implications for the Evolution of Proteins toward Oligomerization. <i>Structure</i> , 2001, 9, 967-976.	1.6	45
84	The Crystal Structure of the Inhibitor-complexed Carboxypeptidase D Domain II and the Modeling of Regulatory Carboxypeptidases. <i>Journal of Biological Chemistry</i> , 2001, 276, 16177-16184.	1.6	71
85	Three-dimensional crystal structure of human eosinophil cationic protein (RNase 3) at 1.75 Å resolution. Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2000, 300, 1297-1307.	2.0	56
86	Three-dimensional structure of a human pancreatic ribonuclease variant, a step forward in the design of cytotoxic ribonucleases. <i>Journal of Molecular Biology</i> , 2000, 303, 49-59.	2.0	30
87	Towards understanding a molecular switch mechanism: thermodynamic and crystallographic studies of the signal transduction protein CheY. <i>Journal of Molecular Biology</i> , 2000, 303, 213-225.	2.0	27
88	Cloning, overexpression, crystallization and preliminary X-ray analysis of a family 1 $\beta$ -glucosidase from <i>Streptomyces</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 679-682.	2.5	6
89	Two-wavelength MAD phasing: in search of the optimal choice of wavelengths. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1449-1458.	2.5	9
90	Crystal structure of a DNA Holliday junction. <i>Nature Structural Biology</i> , 1999, 6, 913-917.	9.7	196

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91	Crystal structure of avian carboxypeptidase D domain II: a prototype for the regulatory metallo-carboxypeptidase subfamily. EMBO Journal, 1999, 18, 5817-5826.	3.5	71
92	The three-dimensional structure of human RNase 4, unliganded and complexed with d(up), reveals the basis for its uridine selectivity 1 Edited by R. Huber. Journal of Molecular Biology, 1999, 285, 205-214.	2.0	48
93	Three-dimensional crystal structure of the transcription factor PhoB receiver domain 1 Edited by R. Huber. Journal of Molecular Biology, 1999, 285, 675-687.	2.0	120
94	The structure of plasmid-encoded transcriptional repressor CopG unliganded and bound to its operator. EMBO Journal, 1998, 17, 7404-7415.	3.5	150
95	Reinforced protein crystals. Materials Research Bulletin, 1998, 33, 1593-1598.	2.7	60
96	Structure Analysis of Two CheY Mutants: Importance of the Hydrogen-Bond Contribution to Protein Stability. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 378-385.	2.5	8
97	Overexpression, purification, crystallization and preliminary X-ray diffraction analysis of the receiver domain of PhoB. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 1460-1463.	2.5	2
98	A modification of the hanging drop method of protein crystallisation suitable for an undergraduate class practical. Biochemical Education, 1998, 26, 173-175.	0.1	2
99	Overexpression, purification, crystallization and preliminary X-ray diffraction analysis of the pMV158-encoded plasmid transcriptional repressor protein CopG. FEBS Letters, 1998, 425, 161-165.	1.3	5
100	Purification, crystallization and preliminary X-ray diffraction studies of the bacteriophage $\phi$ 29 connector particle. FEBS Letters, 1998, 430, 283-287.	1.3	9
101	Crystallographic analysis reveals the 12-fold symmetry of the bacteriophage $\phi$ 29 connector particle. Journal of Molecular Biology, 1998, 281, 219-225.	2.0	39
102	The Three-dimensional Structure of Cys-47-modified Mouse Liver Glutathione S-Transferase P1-1. Journal of Biological Chemistry, 1998, 273, 2844-2850.	1.6	41
103	The three-dimensional structure of a class-Pi glutathione S-transferase complexed with glutathione: the active-site hydration provides insights into the reaction mechanism. Biochemical Journal, 1998, 333, 811-816.	1.7	23
104	Characterisation and preliminary X-ray diffraction analysis of human pancreatic procarboxypeptidase A2. FEBS Letters, 1997, 420, 7-10.	1.3	19
105	The three-dimensional structure of human procarboxypeptidase A2. Deciphering the basis of the inhibition, activation and intrinsic activity of the zymogen. EMBO Journal, 1997, 16, 6906-6913.	3.5	92
106	On the reaction mechanism of class Pi glutathione S-transferase. , 1997, 28, 530-542.		11
107	The Three-dimensional Structure of Two Mutants of the Signal Transduction Protein CheY Suggest its Molecular Activation Mechanism. Journal of Molecular Biology, 1996, 257, 116-128.	2.0	30
108	Intrinsic Conformational Preferences of the Hoechst Dye Family and their Influence on DNA Binding. FEBS Journal, 1996, 239, 376-383.	0.2	14

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109	Shaped protein single crystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995, 51, 278-281.	2.5	13
110	Investigating the Structural Determinants of the p21-like Triphosphate and Mg <sup>2+</sup> -Binding Site. <i>Journal of Molecular Biology</i> , 1995, 249, 654-664.	2.0	18
111	Dichlorobis(pentachlorophenyl) germane and derivatives; synthesis of bis(pentachlorophenyl) germanediol and molecular structure of diiodobis(pentachlorophenyl) germane. <i>Journal of Organometallic Chemistry</i> , 1994, 474, 89-95.	0.8	9
112	Three-dimensional crystal structure of the A-tract DNA dodecamer d(CGCAAATTTGCG) complexed with the minor-groove-binding drug Hoechst 33258. <i>FEBS Journal</i> , 1994, 222, 721-726.	0.2	105
113	Molecular Structure at 1.8 Å... of Mouse Liver Class Pi Glutathione S-transferase Complexed with S-(p-Nitrobenzyl)glutathione and Other Inhibitors. <i>Journal of Molecular Biology</i> , 1994, 237, 298-314.	2.0	128
114	Magnesium Binding to the Bacterial Chemotaxis Protein CheY Results in Large Conformational Changes Involving its Functional Surface. <i>Journal of Molecular Biology</i> , 1994, 238, 489-495.	2.0	131
115	Advances in metallo-procarboxypeptidases. , 1994, , 19-27.		0
116	Advances in metallo-procarboxypeptidases. Emerging details on the inhibition mechanism and on the activation process. <i>FEBS Journal</i> , 1993, 211, 381-389.	0.2	77
117	Crystal quality of lysozyme single crystals grown by the gel acupuncture method. <i>Materials Research Bulletin</i> , 1993, 28, 541-546.	2.7	39
118	Structure Analysis of Cytochrome c3 From <i>Desulfovibrio vulgaris</i> Hildenborough at 1.9 Å... Resolution. <i>Journal of Molecular Biology</i> , 1993, 234, 680-699.	2.0	100
119	Molecular structure of the A-tract DNA dodecamer d(CGCAAATTTGCG) complexed with the minor groove binding drug netropsin. <i>Biochemistry</i> , 1993, 32, 8403-8410.	1.2	110
120	Pancreatic Procarboxypeptidases: Their Activation Processes Related to the Structural Features of the Zymogens and Activation Segments. <i>Biological Chemistry Hoppe-Seyler</i> , 1992, 373, 387-392.	1.4	12
121	Three-dimensional structure of porcine pancreatic procarboxypeptidase A. <i>Journal of Molecular Biology</i> , 1992, 224, 141-157.	2.0	117
122	Comparison of the NMR solution structure with the X-ray crystal structure of the activation domain from procarboxypeptidase B. <i>Journal of Biomolecular NMR</i> , 1992, 2, 1-10.	1.6	20
123	Molecular structure of a complete turn of A-DNA. <i>Journal of Molecular Biology</i> , 1991, 221, 623-635.	2.0	51
124	Molecular structure of nicked DNA: a substrate for DNA repair enzymes.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1990, 87, 2526-2530.	3.3	76
125	Molecular Structure of the Complex Formed Between the Anticancer Drug Cisplatin and d(pGpG): C222<sub>1</sub> Crystal Form. <i>Journal of Biomolecular Structure and Dynamics</i> , 1990, 8, 315-330.	2.0	43
126	Enzymatic mechanism of creatine amidinohydrolase as deduced from crystal structures. <i>Journal of Molecular Biology</i> , 1990, 214, 597-610.	2.0	72



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127	The propeller DNA conformation of poly(dA).poly(dT). <i>Nucleic Acids Research</i> , 1989, 17, 3229-3245.	6.5	67
128	Molecular structure of an A-DNA decamer d(ACCGGCCGGT). <i>FEBS Journal</i> , 1989, 181, 295-307.	0.2	57
129	Preliminary crystallographic studies of the Fab fragment of an anti-azophenylarsonate antibody. <i>Journal of Molecular Biology</i> , 1989, 206, 789-790.	2.0	1
130	Molecular structure of the netropsin-d(CGCGATATCGCG) complex: DNA conformation in an alternating AT segment. <i>Biochemistry</i> , 1989, 28, 310-320.	1.2	226
131	Binding of a Hoechst dye to d(CGCGATATCGCG) and its influence on the conformation of the DNA fragment. <i>Biochemistry</i> , 1989, 28, 7849-7859.	1.2	172
132	Effects of 5-fluorouracil/guanine wobble base pairs in Z-DNA: molecular and crystal structure of d(CGCGFG). <i>Nucleic Acids Research</i> , 1989, 17, 911-923.	6.5	32
133	Trivalent behavior during prophase I in male mice heterozygous for three Robertsonian translocations: an electron-microscopic study. <i>Cytogenetic and Genome Research</i> , 1989, 52, 105-110.	0.6	16
134	Structure of the dipeptide L-prolyl-L-lysine acetate. A new conformation of the lysine side chain. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 1988, 44, 281-285.	0.4	3
135	Crystal and molecular structure of the dipeptide l-Tyr-l-Lys. <i>International Journal of Biological Macromolecules</i> , 1988, 10, 55-59.	3.6	13
136	Structure of d(CACGTG), a Z-DNA hexamer containing AT base pairs. <i>Nucleic Acids Research</i> , 1988, 16, 8695-8705.	6.5	33
137	Crystal and Molecular Structure of the Sodium Salt of the Dinucleotide Duplex d(CpG). <i>Journal of Biomolecular Structure and Dynamics</i> , 1987, 4, 797-811.	2.0	40
138	A bifurcated hydrogen-bonded conformation in the d(A.T) base pairs of the DNA dodecamer d(CGCAAATTTGCG) and its complex with distamycin.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1987, 84, 8385-8389.	3.3	722
139	New data on the synaptic process of <i>Mesocricetus auratus</i> : connecting fibers, telomere association and heterosynapsis. <i>Genetica</i> , 1987, 74, 105-112.	0.5	14
140	Œf-Alkynyl complexes of manganese(I) as ligands. Synthesis and x-ray structure of {[Œ-2-ButMn(CO)3(dppe)]2Cu}(PF6). <i>Journal of Organometallic Chemistry</i> , 1986, 299, C43-C46.	0.8	15
141	Crystal Structure of A Z-DNA Fragment Containing Thymine/2-Amino adenine Base Pairs. <i>Journal of Biomolecular Structure and Dynamics</i> , 1986, 4, 157-172.	2.0	34
142	Plasmid Rolling-Circle Replication. , 0 , 45-69.		3