

# Miquel Coll

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

146 papers	7,499 citations	47 h-index	83 g-index
151 ext. papers	8,141 ext. citations	7.9 avg, IF	5.23 L-index

#	Paper	IF	Citations
146	Using a partial atomic model from medium-resolution cryo-EM to solve a large crystal structure. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2021</b> , 77, 11-18	5.5	0
145	Structures of Tailed Phages and Herpesviruses (Herpesviridae) <b>2021</b> , 318-328		
144	Atomic structure of the Epstein-Barr virus portal. <i>Nature Communications</i> , <b>2019</b> , 10, 3891	17.4	20
143	Structures of T7 bacteriophage portal and tail suggest a viral DNA retention and ejection mechanism. <i>Nature Communications</i> , <b>2019</b> , 10, 3746	17.4	22
142	Structure-Driven Discovery of $\beta$ -Diketoacid Inhibitors Against UL89 Herpesvirus Terminase. <i>ACS Omega</i> , <b>2018</b> , 3, 8497-8505	3.9	1
141	Intercalative DNA binding of the marine anticancer drug variolin B. <i>Scientific Reports</i> , <b>2017</b> , 7, 39680	4.9	13
140	Insights into the inhibited form of the redox-sensitive SufE-like sulfur acceptor CsdE. <i>PLoS ONE</i> , <b>2017</b> , 12, e0186286	3.7	
139	Structural basis of a histidine-DNA nicking/joining mechanism for gene transfer and promiscuous spread of antibiotic resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E6526-E6535	11.5	17
138	Irreversible inhibitors of the 3C protease of Coxsackie virus through templated assembly of protein-binding fragments. <i>Nature Communications</i> , <b>2016</b> , 7, 12761	17.4	22
137	Conformational plasticity of RepB, the replication initiator protein of promiscuous streptococcal plasmid pMV158. <i>Scientific Reports</i> , <b>2016</b> , 6, 20915	4.9	9
136	A C2HC zinc finger is essential for the RING-E2 interaction of the ubiquitin ligase RNF125. <i>Scientific Reports</i> , <b>2016</b> , 6, 29232	4.9	9
135	Mechanism of Sulfur Transfer Across Protein-Protein Interfaces: The Cysteine Desulfurase Model System. <i>ACS Catalysis</i> , <b>2016</b> , 6, 3975-3984	13.1	9
134	Plasmid Rolling-Circle Replication. <i>Microbiology Spectrum</i> , <b>2015</b> , 3, PLAS-0035-2014	8.9	45
133	The crystal structure and small-angle X-ray analysis of CsdL/TcdA reveal a new tRNA binding motif in the MoeB/E1 superfamily. <i>PLoS ONE</i> , <b>2015</b> , 10, e0118606	3.7	7
132	The structure of the complex between $\beta$ -tubulin, TBCE and TBCB reveals a tubulin dimer dissociation mechanism. <i>Journal of Cell Science</i> , <b>2015</b> , 128, 1824-34	5.3	19
131	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. <i>Angewandte Chemie - International Edition</i> , <b>2014</b> , 53, 1949-52	16.4	38
130	Structural basis for DNA binding specificity by the auxin-dependent ARF transcription factors. <i>Cell</i> , <b>2014</b> , 156, 577-89	56.2	243

129	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. <i>Angewandte Chemie</i> , <b>2014</b> , 126, 1980-1983	3.6	7
128	Structural analysis and mutant growth properties reveal distinctive enzymatic and cellular roles for the three major L-alanine transaminases of Escherichia coli. <i>PLoS ONE</i> , <b>2014</b> , 9, e102139	3.7	8
127	Nicking activity of the pMV158 MobM relaxase on cognate and heterologous origins of transfer. <i>Plasmid</i> , <b>2013</b> , 70, 120-30	3.3	12
126	Functional properties and structural requirements of the plasmid pMV158-encoded MobM relaxase domain. <i>Journal of Bacteriology</i> , <b>2013</b> , 195, 3000-8	3.5	6
125	Structure and non-structure of centrosomal proteins. <i>PLoS ONE</i> , <b>2013</b> , 8, e62633	3.7	16
124	Structure and mechanism of a cysteine sulfinate desulfinate engineered on the aspartate aminotransferase scaffold. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2012</b> , 1824, 339-49	4	12
123	PhoB and PhoB activator: getting a better grip. <i>Transcription</i> , <b>2012</b> , 3, 160-4	4.8	7
122	PhoB transcriptional activator binds hierarchically to pho box promoters. <i>Biological Chemistry</i> , <b>2012</b> , 393, 1165-71	4.5	18
121	Structural insights into transcription complexes. <i>Journal of Structural Biology</i> , <b>2011</b> , 175, 135-46	3.4	13
120	Human mitochondrial transcription factor A induces a U-turn structure in the light strand promoter. <i>Nature Structural and Molecular Biology</i> , <b>2011</b> , 18, 1281-9	17.6	134
119	Site-directed mutagenesis of mouse glutathione transferase P1-1 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> , <b>2011</b> , 278, 273-81	5.7	7
118	Picornavirus non-structural proteins as targets for new anti-virals with broad activity. <i>Antiviral Research</i> , <b>2011</b> , 89, 204-18	10.8	59
117	The UlaG protein family defines novel structural and functional motifs grafted on an ancient RNase fold. <i>BMC Evolutionary Biology</i> , <b>2011</b> , 11, 273	3	5
116	Structural basis for antiviral inhibition of the main protease, 3C, from human enterovirus 93. <i>Journal of Virology</i> , <b>2011</b> , 85, 10764-73	6.6	16
115	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> , <b>2011</b> , 39, 4315-29	20.1	26
114	The structure of a transcription activation subcomplex reveals how $\Phi$ 70 is recruited to PhoB promoters. <i>EMBO Journal</i> , <b>2011</b> , 30, 3776-85	13	47
113	Human mitochondrial mTERF wraps around DNA through a left-handed superhelical tandem repeat. <i>Nature Structural and Molecular Biology</i> , <b>2010</b> , 17, 891-3	17.6	38
112	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> , <b>2010</b> , 107, 16078-83	11.5	82

111	Correction for Nadal et al., 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> , <b>2010</b> , 107, 17059-17059	11.5	3
110	Molecular architecture of the Mn <sup>2+</sup> -dependent lactonase UlaG reveals an RNase-like metallo-beta-lactamase fold and a novel quaternary structure. <i>Journal of Molecular Biology</i> , <b>2010</b> , 398, 715-29	6.5	26
109	The structure of RNA-free Rho termination factor indicates a dynamic mechanism of transcript capture. <i>Journal of Molecular Biology</i> , <b>2010</b> , 400, 16-23	6.5	9
108	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</i> , <b>2010</b> , 122, 2386-2389	3.6	16
107	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> , <b>2010</b> , 49, 2336-9	16.4	57
106	Plasmid replication initiator RepB forms a hexamer reminiscent of ring helicases and has mobile nuclease domains. <i>EMBO Journal</i> , <b>2009</b> , 28, 1666-78	13	36
105	Cloning, expression, purification and crystallization of the Rho transcription termination factor from <i>Thermotoga maritima</i> . <i>Protein Expression and Purification</i> , <b>2009</b> , 65, 174-8	2	2
104	DNA-binding drugs caught in action: the latest 3D pictures of drug-DNA complexes. <i>Dalton Transactions</i> , <b>2009</b> , 399-414	4.3	139
103	The VIZIER project: preparedness against pathogenic RNA viruses. <i>Antiviral Research</i> , <b>2008</b> , 78, 37-46	10.8	19
102	Quaternary structural transitions in the DeoR-type repressor UlaR control transcriptional readout from the L-ascorbate utilization regulon in <i>Escherichia coli</i> . <i>Biochemistry</i> , <b>2008</b> , 47, 11424-33	3.2	20
101	Overproduction, crystallization and preliminary X-ray analysis of the putative L-ascorbate-6-phosphate lactonase UlaG from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2008</b> , 64, 36-8		2
100	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> , <b>2007</b> , 366, 626-41	6.5	23
99	Cut and move: protein machinery for DNA processing in bacterial conjugation. <i>Current Opinion in Structural Biology</i> , <b>2006</b> , 16, 744-52	8.1	35
98	Molecular recognition of a three-way DNA junction by a metallosupramolecular helicate. <i>Angewandte Chemie - International Edition</i> , <b>2006</b> , 45, 1227-31	16.4	248
97	Molecular Recognition of a Three-Way DNA Junction by a Metallosupramolecular Helicate. <i>Angewandte Chemie - International Edition</i> , <b>2006</b> , 45, 1834-1834	16.4	2
96	Molecular Recognition of a Three-Way DNA Junction by a Metallosupramolecular Helicate. <i>Angewandte Chemie</i> , <b>2006</b> , 118, 1249-1253	3.6	85
95	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> , <b>2006</b> , 358, 857-69	6.5	58
94	The structure of phage phi29 transcription regulator p4-DNA complex reveals an N-hook motif for DNA. <i>Molecular Cell</i> , <b>2006</b> , 22, 73-81	17.6	15

93	The cofactor-induced pre-active conformation in PhoB. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2006</b> , 62, 1046-57		10
92	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> , <b>2006</b> , 62, 1196-207		20
91	Crystal structure of an iron-dependent group III dehydrogenase that interconverts L-lactaldehyde and L-1,2-propanediol in Escherichia coli. <i>Journal of Bacteriology</i> , <b>2005</b> , 187, 4957-66	3.5	63
90	X-ray crystallographic studies of two transthyretin variants: further insights into amyloidogenesis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2005</b> , 61, 333-9		10
89	The anticancer agent ellipticine unwinds DNA by intercalative binding in an orientation parallel to base pairs. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2005</b> , 61, 1009-12		83
88	On the transcriptional regulation of methicillin resistance: Mecl repressor in complex with its operator. <i>Journal of Biological Chemistry</i> , <b>2004</b> , 279, 17888-96	5.4	60
87	Coupling factors in macromolecular type-IV secretion machineries. <i>Current Pharmaceutical Design</i> , <b>2004</b> , 10, 1551-65	3.3	83
86	Structure of xylanase Xys1delta from Streptomyces halstedii. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2003</b> , 59, 1447-53		20
85	Recognition and processing of the origin of transfer DNA by conjugative relaxase TrwC. <i>Nature Structural and Molecular Biology</i> , <b>2003</b> , 10, 1002-10	17.6	118
84	Three-dimensional structure of Mecl. Molecular basis for transcriptional regulation of staphylococcal methicillin resistance. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 39897-905	5.4	42
83	Structure of the DNA-bound T-box domain of human TBX3, a transcription factor responsible for ulnar-mammary syndrome. <i>Structure</i> , <b>2002</b> , 10, 343-56	5.2	91
82	Tandem DNA recognition by PhoB, a two-component signal transduction transcriptional activator. <i>Structure</i> , <b>2002</b> , 10, 701-13	5.2	241
81	Bacterial conjugation: a two-step mechanism for DNA transport. <i>Molecular Microbiology</i> , <b>2002</b> , 45, 1-8	4.1	268
80	Crystallization and preliminary X-ray analysis of the DNA decamers d(CCGGATCCGG) and d(CCGGCGCCGG). <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2002</b> , 58, 310-1		3
79	Crystallization and preliminary X-ray analysis of the antimalarial and cytotoxic alkaloid cryptolepine complexed with the DNA fragment d(CCTAGG)2. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2002</b> , 58, 312-3		6
78	The antimalarial and cytotoxic drug cryptolepine intercalates into DNA at cytosine-cytosine sites. <i>Nature Structural Biology</i> , <b>2002</b> , 9, 57-60		138
77	Trypanosoma cruzi macrophage infectivity potentiator has a rotamase core and a highly exposed alpha-helix. <i>EMBO Reports</i> , <b>2002</b> , 3, 88-94	6.5	36
76	The structure of human prokallikrein 6 reveals a novel activation mechanism for the kallikrein family. <i>Journal of Biological Chemistry</i> , <b>2002</b> , 277, 27273-81	5.4	64

75	Conjugative plasmid protein TrwB, an integral membrane type IV secretion system coupling protein. Detailed structural features and mapping of the active site cleft. <i>Journal of Biological Chemistry</i> , <b>2002</b> , 277, 7556-66	5.4	63
74	A genetically economical family of plasmid-encoded transcriptional repressors involved in control of plasmid copy number. <i>Journal of Bacteriology</i> , <b>2002</b> , 184, 4943-51	3.5	39
73	Detailed architecture of a DNA translocating machine: the high-resolution structure of the bacteriophage phi29 connector particle. <i>Journal of Molecular Biology</i> , <b>2002</b> , 315, 663-76	6.5	192
72	Three-dimensional structure of human tubulin chaperone cofactor A. <i>Journal of Molecular Biology</i> , <b>2002</b> , 318, 1139-49	6.5	22
71	The inherent properties of DNA four-way junctions: comparing the crystal structures of holliday junctions. <i>Journal of Molecular Biology</i> , <b>2002</b> , 320, 1037-51	6.5	41
70	Note to the Paper by Guasch . (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> , <b>2002</b> , 321, 379-380	6.5	2
69	Human procarboxypeptidase B: three-dimensional structure and implications for thrombin-activatable fibrinolysis inhibitor (TAFI). <i>Journal of Molecular Biology</i> , <b>2002</b> , 321, 537-47	6.5	61
68	Structure and role of coupling proteins in conjugal DNA transfer. <i>Research in Microbiology</i> , <b>2002</b> , 153, 199-204	4	31
67	Three-dimensional structure of human RNase 1 delta N7 at 1.9 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2001</b> , 57, 498-505		18
66	Solving a 300 kDa multimeric protein by low-resolution MAD phasing and averaging/phase extension. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2001</b> , 57, 800-5		3
65	Structure of human biliverdin IXbeta reductase, an early fetal bilirubin IXbeta producing enzyme. <i>Nature Structural Biology</i> , <b>2001</b> , 8, 215-20		85
64	The bacterial conjugation protein TrwB resembles ring helicases and F1-ATPase. <i>Nature</i> , <b>2001</b> , 409, 637-41	5.4	279
63	The structure of an engineered domain-swapped ribonuclease dimer and its implications for the evolution of proteins toward oligomerization. <i>Structure</i> , <b>2001</b> , 9, 967-76	5.2	43
62	The crystal structure of the inhibitor-complexed carboxypeptidase D domain II and the modeling of regulatory carboxypeptidases. <i>Journal of Biological Chemistry</i> , <b>2001</b> , 276, 16177-84	5.4	67
61	Plasmid transcriptional repressor CopG oligomerises to render helical superstructures unbound and in complexes with oligonucleotides. <i>Journal of Molecular Biology</i> , <b>2001</b> , 310, 403-17	6.5	19
60	Review: postchaperonin tubulin folding cofactors and their role in microtubule dynamics. <i>Journal of Structural Biology</i> , <b>2001</b> , 135, 219-29	3.4	116
59	Structure of TrwB, a gatekeeper in bacterial conjugation. <i>International Journal of Biochemistry and Cell Biology</i> , <b>2001</b> , 33, 839-43	5.6	30
58	Three-dimensional crystal structure of human eosinophil cationic protein (RNase 3) at 1.75 Å resolution. <i>Journal of Molecular Biology</i> , <b>2000</b> , 300, 1297-307	6.5	45



57	Three-dimensional structure of a human pancreatic ribonuclease variant, a step forward in the design of cytotoxic ribonucleases. <i>Journal of Molecular Biology</i> , <b>2000</b> , 303, 49-60	6.5	28
56	Towards understanding a molecular switch mechanism: thermodynamic and crystallographic studies of the signal transduction protein CheY. <i>Journal of Molecular Biology</i> , <b>2000</b> , 303, 213-25	6.5	25
55	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> , <b>1999</b> , 55, 679-82		6
54	Two-wavelength MAD phasing: in search of the optimal choice of wavelengths. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>1999</b> , 55, 1449-58		8
53	Crystal structure of a DNA Holliday junction. <i>Nature Structural Biology</i> , <b>1999</b> , 6, 913-7		168
52	Crystal structure of avian carboxypeptidase D domain II: a prototype for the regulatory metallocarboxypeptidase subfamily. <i>EMBO Journal</i> , <b>1999</b> , 18, 5817-26	13	63
51	The three-dimensional structure of human RNase 4, unliganded and complexed with d(Up), reveals the basis for its uridine selectivity. <i>Journal of Molecular Biology</i> , <b>1999</b> , 285, 205-14	6.5	44
50	Three-dimensional crystal structure of the transcription factor PhoB receiver domain. <i>Journal of Molecular Biology</i> , <b>1999</b> , 285, 675-87	6.5	113
49	The structure of plasmid-encoded transcriptional repressor CopG unliganded and bound to its operator. <i>EMBO Journal</i> , <b>1998</b> , 17, 7404-15	13	130
48	Reinforced protein crystals. <i>Materials Research Bulletin</i> , <b>1998</b> , 33, 1593-1598	5.1	57
47	Structure analysis of two CheY mutants: importance of the hydrogen-bond contribution to protein stability. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>1998</b> , 54, 378-85		8
46	Overexpression, purification, crystallization and preliminary X-ray diffraction analysis of the receiver domain of PhoB. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>1998</b> , 54, 1460-3		2
45	A modification of the hanging drop method of protein crystallisation suitable for an undergraduate class practical. <i>Biochemical Education</i> , <b>1998</b> , 26, 173-175		2
44	Overexpression, purification, crystallization and preliminary X-ray diffraction analysis of the pMV158-encoded plasmid transcriptional repressor protein CopG. <i>FEBS Letters</i> , <b>1998</b> , 425, 161-5	3.8	5
43	Purification, crystallization and preliminary X-ray diffraction studies of the bacteriophage phi29 connector particle. <i>FEBS Letters</i> , <b>1998</b> , 430, 283-7	3.8	8
42	Crystallographic analysis reveals the 12-fold symmetry of the bacteriophage phi29 connector particle. <i>Journal of Molecular Biology</i> , <b>1998</b> , 281, 219-25	6.5	33
41	The three-dimensional structure of Cys-47-modified mouse liver glutathione S-transferase P1-1. Carboxymethylation dramatically decreases the affinity for glutathione and is associated with a loss of electron density in the alphaB-310B region. <i>Journal of Biological Chemistry</i> , <b>1998</b> , 273, 2844-50	5.4	35
40	The three-dimensional structure of a class-Pi glutathione S-transferase complexed with glutathione: the active-site hydration provides insights into the reaction mechanism. <i>Biochemical Journal</i> , <b>1998</b> , 333 ( Pt 3), 811-6	3.8	21

39	Characterisation and preliminary X-ray diffraction analysis of human pancreatic procarboxypeptidase A2. <i>FEBS Letters</i> , <b>1997</b> , 420, 7-10	3.8	17
38	The three-dimensional structure of human procarboxypeptidase A2. Deciphering the basis of the inhibition, activation and intrinsic activity of the zymogen. <i>EMBO Journal</i> , <b>1997</b> , 16, 6906-13	13	80
37	On the reaction mechanism of class Pi glutathione S-transferase <b>1997</b> , 28, 530-542		8
36	The three-dimensional structure of two mutants of the signal transduction protein CheY suggest its molecular activation mechanism. <i>Journal of Molecular Biology</i> , <b>1996</b> , 257, 116-28	6.5	29
35	Intrinsic conformational preferences of the Hoechst dye family and their influence of DNA binding. <i>FEBS Journal</i> , <b>1996</b> , 239, 376-83		13
34	Investigating the structural determinants of the p21-like triphosphate and Mg <sup>2+</sup> binding site. <i>Journal of Molecular Biology</i> , <b>1995</b> , 249, 654-64	6.5	15
33	Shaped protein single crystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>1995</b> , 51, 278-81		11
32	Dichlorobis(pentachlorophenyl) germane and derivatives; synthesis of bis(pentachlorophenyl) germanediol and molecular structure of diiodobis(pentachlorophenyl) germane. <i>Journal of Organometallic Chemistry</i> , <b>1994</b> , 474, 89-95	2.3	7
31	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> , <b>1994</b> , 222, 721-6		90
30	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> , <b>1994</b> , 237, 298-314	6.5	119
29	Magnesium binding to the bacterial chemotaxis protein CheY results in large conformational changes involving its functional surface. <i>Journal of Molecular Biology</i> , <b>1994</b> , 238, 489-95	6.5	122
28	Advances in metallo-procarboxypeptidases <b>1994</b> , 19-27		
27	Structure analysis of cytochrome c3 from <i>Desulfovibrio vulgaris</i> Hildenborough at 1.9 Å resolution. <i>Journal of Molecular Biology</i> , <b>1993</b> , 234, 680-99	6.5	88
26	Molecular structure of the A-tract DNA dodecamer d(CGCAAATTTGCG) complexed with the minor groove binding drug netropsin. <i>Biochemistry</i> , <b>1993</b> , 32, 8403-10	3.2	100
25	Advances in metallo-procarboxypeptidases. Emerging details on the inhibition mechanism and on the activation process. <i>FEBS Journal</i> , <b>1993</b> , 211, 381-9		63
24	Crystal quality of lysozyme single crystals grown by the gel acupuncture method. <i>Materials Research Bulletin</i> , <b>1993</b> , 28, 541-546	5.1	37
23	Pancreatic procarboxypeptidases: their activation processes related to the structural features of the zymogens and activation segments. <i>Biological Chemistry Hoppe-Seyler</i> , <b>1992</b> , 373, 387-92		10
22	Three-dimensional structure of porcine pancreatic procarboxypeptidase A. A comparison of the A and B zymogens and their determinants for inhibition and activation. <i>Journal of Molecular Biology</i> , <b>1992</b> , 224, 141-57	6.5	109



21	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> , <b>1992</b> , 2, 1-10	3	17
20	Molecular structure of a complete turn of A-DNA. <i>Journal of Molecular Biology</i> , <b>1991</b> , 221, 623-35	6.5	46
19	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> , <b>1990</b> , 87, 2526-30	11.5	66
18	Molecular structure of the complex formed between the anticancer drug cisplatin and d(pGpG): C222(1) crystal form. <i>Journal of Biomolecular Structure and Dynamics</i> , <b>1990</b> , 8, 315-30	3.6	39
17	Enzymatic mechanism of creatine amidinohydrolase as deduced from crystal structures. <i>Journal of Molecular Biology</i> , <b>1990</b> , 214, 597-610	6.5	61
16	The propeller DNA conformation of poly(dA).poly(dT). <i>Nucleic Acids Research</i> , <b>1989</b> , 17, 3229-45	20.1	61
15	Molecular structure of an A-DNA decamer d(ACCGGCCGGT). <i>FEBS Journal</i> , <b>1989</b> , 181, 295-307		52
14	Preliminary crystallographic studies of the Fab fragment of an anti-azophenylarsonate antibody. <i>Journal of Molecular Biology</i> , <b>1989</b> , 206, 789-90	6.5	1
13	Molecular structure of the netropsin-d(CGCGATATCGCG) complex: DNA conformation in an alternating AT segment. <i>Biochemistry</i> , <b>1989</b> , 28, 310-20	3.2	204
12	Binding of a Hoechst dye to d(CGCGATATCGCG) and its influence on the conformation of the DNA fragment. <i>Biochemistry</i> , <b>1989</b> , 28, 7849-59	3.2	152
11	Effects of 5-fluorouracil/guanine wobble base pairs in Z-DNA: molecular and crystal structure of d(CGCGFG). <i>Nucleic Acids Research</i> , <b>1989</b> , 17, 911-23	20.1	29
10	Trivalent behavior during prophase I in male mice heterozygous for three Robertsonian translocations: an electron-microscopic study. <i>Cytogenetic and Genome Research</i> , <b>1989</b> , 52, 105-10	1.9	11
9	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> , <b>1988</b> , 44, 281-285		3
8	Crystal and molecular structure of the dipeptide l-Tyr-l-Lys. <i>International Journal of Biological Macromolecules</i> , <b>1988</b> , 10, 55-59	7.9	12
7	Structure of d(CACGTG), a Z-DNA hexamer containing AT base pairs. <i>Nucleic Acids Research</i> , <b>1988</b> , 16, 8695-705	20.1	28
6	Crystal and molecular structure of the sodium salt of the dinucleotide duplex d(CpG). <i>Journal of Biomolecular Structure and Dynamics</i> , <b>1987</b> , 4, 797-811	3.6	34
5	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> , <b>1987</b> , 84, 8385-9	11.5	655
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1	Plasmid Rolling-Circle Replication45-69		2