

# Miquel Coll

## List of Publications by Year in descending order

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142  
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8,741  
citations

38660  
50  
h-index

46693  
89  
g-index

151  
all docs

151  
docs citations

151  
times ranked

8687  
citing authors

#	ARTICLE	IF	CITATIONS
1	A bifurcated hydrogen-bonded conformation in the d(A.T) base pairs of the DNA dodecamer d(CGCAAATTTGCG) and its complex with distamycin.. Proceedings of the National Academy of Sciences of the United States of America, 1987, 84, 8385-8389.	3.3	722
2	Structural Basis for DNA Binding Specificity by the Auxin-Dependent ARF Transcription Factors. Cell, 2014, 156, 577-589.	13.5	348
3	Bacterial conjugation: a two-step mechanism for DNA transport. Molecular Microbiology, 2002, 45, 1-8.	1.2	341
4	The bacterial conjugation protein TrwB resembles ring helicases and F1-ATPase. Nature, 2001, 409, 637-641.	13.7	318
5	Molecular Recognition of a Three-Way DNA Junction by a Metallo-supramolecular Helicate. Angewandte Chemie - International Edition, 2006, 45, 1227-1231.	7.2	278
6	Tandem DNA Recognition by PhoB, a Two-Component Signal Transduction Transcriptional Activator. Structure, 2002, 10, 701-713.	1.6	266
7	Molecular structure of the netropsin-d(CGCGATATCGCG) complex: DNA conformation in an alternating AT segment. Biochemistry, 1989, 28, 310-320.	1.2	226
8	Detailed architecture of a DNA translocating machine: the high-resolution structure of the bacteriophage $\phi$ 29 connector particle 1 Edited by R. Huber. Journal of Molecular Biology, 2002, 315, 663-676.	2.0	205
9	Crystal structure of a DNA Holliday junction. Nature Structural Biology, 1999, 6, 913-917.	9.7	196
10	Binding of a Hoechst dye to d(CGCGATATCGCG) and its influence on the conformation of the DNA fragment. Biochemistry, 1989, 28, 7849-7859.	1.2	172
11	Human mitochondrial transcription factor A induces a U-turn structure in the light strand promoter. Nature Structural and Molecular Biology, 2011, 18, 1281-1289.	3.6	168
12	The antimalarial and cytotoxic drug cryptolepine intercalates into DNA at cytosine-cytosine sites. Nature Structural Biology, 2002, 9, 57-60.	9.7	164
13	DNA-binding drugs caught in action: the latest 3D pictures of drug-DNA complexes. Dalton Transactions, 2009, , 399-414.	1.6	153
14	The structure of plasmid-encoded transcriptional repressor CopG unliganded and bound to its operator. EMBO Journal, 1998, 17, 7404-7415.	3.5	150
15	Review: Postchaperonin Tubulin Folding Cofactors and Their Role in Microtubule Dynamics. Journal of Structural Biology, 2001, 135, 219-229.	1.3	134
16	Recognition and processing of the origin of transfer DNA by conjugative relaxase TrwC. Nature Structural and Molecular Biology, 2003, 10, 1002-1010.	3.6	132
17	Magnesium Binding to the Bacterial Chemotaxis Protein CheY Results in Large Conformational Changes Involving its Functional Surface. Journal of Molecular Biology, 1994, 238, 489-495.	2.0	131
18	Molecular Structure at 1.8 Å... of Mouse Liver Class Pi Glutathione S-transferase Complexed with S-(p-Nitrobenzyl)glutathione and Other Inhibitors. Journal of Molecular Biology, 1994, 237, 298-314.	2.0	128

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19	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
20	Three-dimensional structure of porcine pancreatic procarboxypeptidase A. Journal of Molecular Biology, 1992, 224, 141-157.	2.0	117
21	Molecular structure of the A-tract DNA dodecamer d(CGCAAATTTGCG) complexed with the minor groove binding drug netropsin. Biochemistry, 1993, 32, 8403-8410.	1.2	110
22	The anticancer agent ellipticine unwinds DNA by intercalative binding in an orientation parallel to base pairs. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 1009-1012.	2.5	107
23	Three-dimensional crystal structure of the A-tract DNA dodecamer d(CGCAAATTTGCG) complexed with the minor-groove-binding drug Hoechst 33258. FEBS Journal, 1994, 222, 721-726.	0.2	105
24	Structure of the DNA-Bound T-Box Domain of Human TBX3, a Transcription Factor Responsible for Ulnar-Mammary Syndrome. Structure, 2002, 10, 343-356.	1.6	105
25	Structure and inhibition of herpesvirus DNA packaging terminase nuclease domain. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 16078-16083.	3.3	102
26	Structure Analysis of Cytochrome c3 From Desulfovibrio vulgaris Hildenborough at 1.9 Å... Resolution. Journal of Molecular Biology, 1993, 234, 680-699.	2.0	100
27	Structure of human biliverdin IXbeta reductase, an early fetal bilirubin IXbeta producing enzyme. Nature Structural Biology, 2001, 8, 215-220.	9.7	99
28	Coupling Factors in Macromolecular Type-IV Secretion Machineries. Current Pharmaceutical Design, 2004, 10, 1551-1565.	0.9	94
29	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
30	Advances in metallo-procarboxypeptidases. Emerging details on the inhibition mechanism and on the activation process. FEBS Journal, 1993, 211, 381-389.	0.2	77
31	Molecular structure of nicked DNA: a substrate for DNA repair enzymes.. Proceedings of the National Academy of Sciences of the United States of America, 1990, 87, 2526-2530.	3.3	76
32	Crystal Structure of an Iron-Dependent Group III Dehydrogenase That Interconverts L-Lactaldehyde and L-1,2-Propanediol in Escherichia coli. Journal of Bacteriology, 2005, 187, 4957-4966.	1.0	76
33	Picornavirus non-structural proteins as targets for new anti-virals with broad activity. Antiviral Research, 2011, 89, 204-218.	1.9	76
34	Conjugative Plasmid Protein TrwB, an Integral Membrane Type IV Secretion System Coupling Protein. Journal of Biological Chemistry, 2002, 277, 7556-7566.	1.6	75
35	The Structure of Human Prokallikrein 6 Reveals a Novel Activation Mechanism for the Kallikrein Family. Journal of Biological Chemistry, 2002, 277, 27273-27281.	1.6	74
36	Enzymatic mechanism of creatine amidinohydrolase as deduced from crystal structures. Journal of Molecular Biology, 1990, 214, 597-610.	2.0	72

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37	Crystal structure of avian carboxypeptidase D domain II: a prototype for the regulatory metallocarboxypeptidase subfamily. EMBO Journal, 1999, 18, 5817-5826.	3.5	71
38	The Crystal Structure of the Inhibitor-complexed Carboxypeptidase D Domain II and the Modeling of Regulatory Carboxypeptidases. Journal of Biological Chemistry, 2001, 276, 16177-16184.	1.6	71
39	Plasmid Rolling-Circle Replication. Microbiology Spectrum, 2015, 3, PLAS-0035-2014.	1.2	69
40	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. Journal of Molecular Biology, 2006, 358, 857-869.	2.0	68
41	The propeller DNA conformation of poly(dA).poly(dT). Nucleic Acids Research, 1989, 17, 3229-3245.	6.5	67
42	On the Transcriptional Regulation of Methicillin Resistance. Journal of Biological Chemistry, 2004, 279, 17888-17896.	1.6	67
43	Human Procarboxypeptidase B: Three-dimensional Structure and Implications for Thrombin-activatable Fibrinolysis Inhibitor (TAFI). Journal of Molecular Biology, 2002, 321, 537-547.	2.0	66
44	Self-Assembly of Functionalizable Two-Component 3D DNA Arrays through the Induced Formation of DNA Three-Way Junction Branch Points by Supramolecular Cylinders. Angewandte Chemie - International Edition, 2010, 49, 2336-2339.	7.2	65
45	The structure of a transcription activation subcomplex reveals how $\sigma^{70}$ is recruited to PhoB promoters. EMBO Journal, 2011, 30, 3776-3785.	3.5	63
46	Structures of T7 bacteriophage portal and tail suggest a viral DNA retention and ejection mechanism. Nature Communications, 2019, 10, 3746.	5.8	61
47	Reinforced protein crystals. Materials Research Bulletin, 1998, 33, 1593-1598.	2.7	60
48	Molecular structure of an A-DNA decamer d(ACCGGCCGGT). FEBS Journal, 1989, 181, 295-307.	0.2	57
49	Three-dimensional crystal structure of human eosinophil cationic protein (RNase 3) at 1.75 Å... resolution11Edited by R. Huber. Journal of Molecular Biology, 2000, 300, 1297-1307.	2.0	56
50	Molecular structure of a complete turn of A-DNA. Journal of Molecular Biology, 1991, 221, 623-635.	2.0	51
51	The three-dimensional structure of human RNase 4, unliganded and complexed with d(up), reveals the basis for its uridine selectivity 11Edited by R. Huber. Journal of Molecular Biology, 1999, 285, 205-214.	2.0	48
52	A Genetically Economical Family of Plasmid-Encoded Transcriptional Repressors Involved in Control of Plasmid Copy Number. Journal of Bacteriology, 2002, 184, 4943-4951.	1.0	46
53	Three-dimensional Structure of Mecl. Journal of Biological Chemistry, 2003, 278, 39897-39905.	1.6	46
54	Human mitochondrial mTERF wraps around DNA through a left-handed superhelical tandem repeat. Nature Structural and Molecular Biology, 2010, 17, 891-893.	3.6	46

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55	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
56	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
57	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
58	Molecular Structure of the Complex Formed Between the Anticancer Drug Cisplatin and d(pCpG): C222<sub>1</sub>Crystal Form. <i>Journal of Biomolecular Structure and Dynamics</i> , 1990, 8, 315-330.	2.0	43
59	<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
60	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> , 2014, 53, 1949-1952.	7.2	42
61	The Three-dimensional Structure of Cys-47-modified Mouse Liver Glutathione S-Transferase P1-1. <i>Journal of Biological Chemistry</i> , 1998, 273, 2844-2850.	1.6	41
62	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
63	Crystal quality of lysozyme single crystals grown by the gel acupuncture method. <i>Materials Research Bulletin</i> , 1993, 28, 541-546.	2.7	39
64	Crystallographic analysis reveals the 12-fold symmetry of the bacteriophage $\phi$ 29 connector particle. <i>Journal of Molecular Biology</i> , 1998, 281, 219-225.	2.0	39
65	Structure and role of coupling proteins in conjugal DNA transfer. <i>Research in Microbiology</i> , 2002, 153, 199-204.	1.0	37
66	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
67	Crystal Structure of A Z-DNA Fragment Containing Thymine/2-Aminoadenine Base Pairs. <i>Journal of Biomolecular Structure and Dynamics</i> , 1986, 4, 157-172.	2.0	34
68	Structure of d(CACGTG), a Z-DNA hexamer containing AT base pairs. <i>Nucleic Acids Research</i> , 1988, 16, 8695-8705.	6.5	33
69	Structure of TrwB, a gatekeeper in bacterial conjugation. <i>International Journal of Biochemistry and Cell Biology</i> , 2001, 33, 839-843.	1.2	33
70	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
71	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> , 2010, 398, 715-729.	2.0	31
72	The Three-dimensional Structure of Two Mutants of the Signal Transduction Protein CheY Suggest its Molecular Activation Mechanism. <i>Journal of Molecular Biology</i> , 1996, 257, 116-128.	2.0	30

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73	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
74	Quaternary Structural Transitions in the DeoR-Type Repressor UlaR Control Transcriptional Readout from the <scp> </scp>-Ascorbate Utilization Regulon in <i>Escherichia coli</i>. <i>Biochemistry</i> , 2008, 47, 11424-11433.	1.2	30
75	Irreversible inhibitors of the 3C protease of Coxsackie virus through templated assembly of protein-binding fragments. <i>Nature Communications</i> , 2016, 7, 12761.	5.8	30
76	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
77	Atomic structure of the Epstein-Barr virus portal. <i>Nature Communications</i> , 2019, 10, 3891.	5.8	28
78	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
79	The structure of the TBCE/TBCB chaperones and $\hat{1}\pm$ -tubulin complex shows a tubulin dimer dissociation mechanism. <i>Journal of Cell Science</i> , 2015, 128, 1824-34.	1.2	27
80	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> , 2017, 114, E6526-E6535.	3.3	27
81	The VIZIER project: Preparedness against pathogenic RNA viruses. <i>Antiviral Research</i> , 2008, 78, 37-46.	1.9	26
82	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
83	Structure and Non-Structure of Centrosomal Proteins. <i>PLoS ONE</i> , 2013, 8, e62633.	1.1	25
84	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> , 1998, 333, 811-816.	1.7	23
85	Three-dimensional Structure of Human Tubulin Chaperone Cofactor A. <i>Journal of Molecular Biology</i> , 2002, 318, 1139-1149.	2.0	23
86	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
87	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
88	Structure of xylanase Xys1 <sup>17</sup> from <i>Streptomyces halstedii</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1447-1453.	2.5	22
89	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
90	Three-dimensional structure of human RNase 1 <sup>17</sup> N7 at 1.9Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 498-505.	2.5	20

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91	Structural Basis for Antiviral Inhibition of the Main Protease, 3C, from Human Enterovirus 93. Journal of Virology, 2011, 85, 10764-10773.	1.5	20
92	PhoB transcriptional activator binds hierarchically to <i>pho box</i> promoters. Biological Chemistry, 2012, 393, 1165-1171.	1.2	20
93	A C2HC zinc finger is essential for the RING-E2 interaction of the ubiquitin ligase RNF125. Scientific Reports, 2016, 6, 29232.	1.6	20
94	Characterisation and preliminary X-ray diffraction analysis of human pancreatic procarboxypeptidase A2. FEBS Letters, 1997, 420, 7-10.	1.3	19
95	Intercalative DNA binding of the marine anticancer drug variolin B. Scientific Reports, 2017, 7, 39680.	1.6	19
96	Investigating the Structural Determinants of the p21-like Triphosphate and Mg <sup>2+</sup> -Binding Site. Journal of Molecular Biology, 1995, 249, 654-664.	2.0	18
97	Structure and mechanism of a cysteine sulfinate desulfinate engineered on the aspartate aminotransferase scaffold. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2012, 1824, 339-349.	1.1	17
98	Trivalent behavior during prophase I in male mice heterozygous for three Robertsonian translocations: an electron-microscopic study. Cytogenetic and Genome Research, 1989, 52, 105-110.	0.6	16
99	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
100	Œf-Alkynyl complexes of manganese(I) as ligands. Synthesis and x-ray structure of {[Œ-2-ButMn(CO)3(dppe)]2Cu}(PF6). Journal of Organometallic Chemistry, 1986, 299, C43-C46.	0.8	15
101	The Structure of Phage Œ29 Transcription Regulator p4-DNA Complex Reveals an N-Hook Motif for DNA Binding. Molecular Cell, 2006, 22, 73-81.	4.5	15
102	New data on the synaptic process of Mesocricetus auratus: connecting fibers, telomere association and heterosynapsis. Genetica, 1987, 74, 105-112.	0.5	14
103	Intrinsic Conformational Preferences of the Hoechst Dye Family and their Influence on DNA Binding. FEBS Journal, 1996, 239, 376-383.	0.2	14
104	Structural insights into transcription complexes. Journal of Structural Biology, 2011, 175, 135-146.	1.3	14
105	Crystal and molecular structure of the dipeptide L-Tyr-L-Lys. International Journal of Biological Macromolecules, 1988, 10, 55-59.	3.6	13
106	Shaped protein single crystals. Acta Crystallographica Section D: Biological Crystallography, 1995, 51, 278-281.	2.5	13
107	Pancreatic Procarboxypeptidases: Their Activation Processes Related to the Structural Features of the Zymogens and Activation Segments. Biological Chemistry Hoppe-Seyler, 1992, 373, 387-392.	1.4	12
108	X-ray crystallographic studies of two transthyretin variants: further insights into amyloidogenesis. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 333-339.	2.5	12



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109	The cofactor-induced pre-active conformation in PhoB. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1046-1057.	2.5	12
110	Nicking activity of the pMV158 MobM relaxase on cognate and heterologous origins of transfer. <i>Plasmid</i> , 2013, 70, 120-130.	0.4	12
111	Mechanism of Sulfur Transfer Across Protein-Protein Interfaces: The Cysteine Desulfurase Model System. <i>ACS Catalysis</i> , 2016, 6, 3975-3984.	5.5	12
112	On the reaction mechanism of class Pi glutathione S-transferase. , 1997, 28, 530-542.		11
113	Crystallization and preliminary X-ray analysis of the antimalarial and cytotoxic alkaloid cryptolepine complexed with the DNA fragment d(CCTAGC)2. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 312-313.	2.5	11
114	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
115	Conformational plasticity of RepB, the replication initiator protein of promiscuous streptococcal plasmid pMV158. <i>Scientific Reports</i> , 2016, 6, 20915.	1.6	11
116	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> , 2015, 10, e0118606.	1.1	10
117	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
118	Purification, crystallization and preliminary X-ray diffraction studies of the bacteriophage $\phi$ 29 connector particle. <i>FEBS Letters</i> , 1998, 430, 283-287.	1.3	9
119	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
120	$\phi$ 70 and PhoB activator. <i>Transcription</i> , 2012, 3, 160-164.	1.7	9
121	Structure Analysis of Two CheY Mutants: Importance of the Hydrogen-Bond Contribution to Protein Stability. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 378-385.	2.5	8
122	Site-directed mutagenesis of mouse glutathione transferase P1 unlocks masked cooperativity, introduces a novel mechanism for $\alpha$ -pinopong <sup>TM</sup> 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
123	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
124	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
125	Structure-Driven Discovery of $\beta$ , $\gamma$ -Diketoacid Inhibitors Against UL89 Herpesvirus Terminase. <i>ACS Omega</i> , 2018, 3, 8497-8505.	1.6	7
126	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



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127	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
128	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
129	Structure of the dipeptide L-prolyl-L-lysine acetate. A new conformation of the lysine side chain. Acta Crystallographica Section C: Crystal Structure Communications, 1988, 44, 281-285.	0.4	3
130	Solving a 300â€¦kDa multimeric protein by low-resolution MAD phasing and averaging/phase extension. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 800-805.	2.5	3
131	Crystallization and preliminary X-ray analysis of the DNA decamers d(CCGGATCCGG) and d(CCGGCGCCGG). Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 310-311.	2.5	3
132	Overproduction, crystallization and preliminary X-ray analysis of the putative<scp>L</scp>-ascorbate-6-phosphate lactonase UlaG from<i>Escherichia coli</i>. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 36-38.	0.7	3
133	Plasmid Rolling-Circle Replication. , 0, , 45-69.		3
134	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
135	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
136	Note to the Paper by Guasch et al. (2002) Detailed Architecture of a DNA Translocating Machine: The High-resolution Structure of the Bacteriophage Î†29 Connector Particle. Journal of Molecular Biology, 2002, 321, 379-380.	2.0	2
137	Molecular Recognition of a Three-Way DNA Junction by a Metallosupramolecular Helicate. Angewandte Chemie - International Edition, 2006, 45, 1834-1834.	7.2	2
138	Cloning, expression, purification and crystallization of the Rho transcription termination factor from Thermotoga maritima. Protein Expression and Purification, 2009, 65, 174-178.	0.6	2
139	Preliminary crystallographic studies of the Fab fragment of an anti-azophenylarsonate antibody. Journal of Molecular Biology, 1989, 206, 789-790.	2.0	1
140	Insights into the inhibited form of the redox-sensitive SufE-like sulfur acceptor CsdE. PLoS ONE, 2017, 12, e0186286.	1.1	0
141	Structures of Tailed Phages and Herpesviruses (Herpesviridae). , 2021, , 318-328.		0
142	Advances in metallo-procarboxypeptidases. , 1994, , 19-27.		0