

# Miquel Coll

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/9322526/miquel-coll-publications-by-citations.pdf>

**Version:** 2024-04-10

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	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
145	The bacterial conjugation protein TrwB resembles ring helicases and F1-ATPase. <i>Nature</i> , <b>2001</b> , 409, 637-41	40.4	279
144	Bacterial conjugation: a two-step mechanism for DNA transport. <i>Molecular Microbiology</i> , <b>2002</b> , 45, 1-8	4.1	268
143	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
142	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
141	Tandem DNA recognition by PhoB, a two-component signal transduction transcriptional activator. <i>Structure</i> , <b>2002</b> , 10, 701-13	5.2	241
140	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
139	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
138	Crystal structure of a DNA Holliday junction. <i>Nature Structural Biology</i> , <b>1999</b> , 6, 913-7		168
137	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
136	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
135	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
134	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
133	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
132	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
131	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
130	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

129	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
128	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
127	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
126	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
125	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
124	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
123	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
122	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
121	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
120	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
119	Coupling factors in macromolecular type-IV secretion machineries. <i>Current Pharmaceutical Design</i> , <b>2004</b> , 10, 1551-65	3.3	83
118	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
117	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
116	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
115	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
114	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
113	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> , <b>2005</b> , 187, 4957-66	3.5	63
112	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

111	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
110	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
109	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
108	The propeller DNA conformation of poly(dA).poly(dT). <i>Nucleic Acids Research</i> , <b>1989</b> , 17, 3229-45	20.1	61
107	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
106	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
105	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
104	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
103	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
102	Reinforced protein crystals. <i>Materials Research Bulletin</i> , <b>1998</b> , 33, 1593-1598	5.1	57
101	Molecular structure of an A-DNA decamer d(ACCGGCCGGT). <i>FEBS Journal</i> , <b>1989</b> , 181, 295-307		52
100	The structure of a transcription activation subcomplex reveals how $\lambda$ 70 is recruited to PhoB promoters. <i>EMBO Journal</i> , <b>2011</b> , 30, 3776-85	13	47
99	Molecular structure of a complete turn of A-DNA. <i>Journal of Molecular Biology</i> , <b>1991</b> , 221, 623-35	6.5	46
98	Plasmid Rolling-Circle Replication. <i>Microbiology Spectrum</i> , <b>2015</b> , 3, PLAS-0035-2014	8.9	45
97	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
96	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
95	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
94	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

93	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
92	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
91	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
90	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
89	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
88	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
87	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
86	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
85	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
84	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
83	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
82	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
81	Structure and role of coupling proteins in conjugal DNA transfer. <i>Research in Microbiology</i> , <b>2002</b> , 153, 199-204	4	31
80	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
79	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
78	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
77	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
76	Crystal structure of a Z-DNA fragment containing thymine/2-aminoadenine base pairs. <i>Journal of Biomolecular Structure and Dynamics</i> , <b>1986</b> , 4, 157-72	3.6	28

75	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
74	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
73	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
72	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
71	The X-ray crystal structures of two constitutively active mutants of the Escherichia coli PhoB receiver domain give insights into activation. <i>Journal of Molecular Biology</i> , <b>2007</b> , 366, 626-41	6.5	23
70	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
69	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
68	Three-dimensional structure of human tubulin chaperone cofactor A. <i>Journal of Molecular Biology</i> , <b>2002</b> , 318, 1139-49	6.5	22
67	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
66	Atomic structure of the Epstein-Barr virus portal. <i>Nature Communications</i> , <b>2019</b> , 10, 3891	17.4	20
65	Quaternary structural transitions in the DeoR-type repressor UlaR control transcriptional readout from the L-ascorbate utilization regulon in Escherichia coli. <i>Biochemistry</i> , <b>2008</b> , 47, 11424-33	3.2	20
64	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
63	Structure of xylanase Xys1delta from Streptomyces halstedii. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2003</b> , 59, 1447-53		20
62	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
61	The VIZIER project: preparedness against pathogenic RNA viruses. <i>Antiviral Research</i> , <b>2008</b> , 78, 37-46	10.8	19
60	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
59	PhoB transcriptional activator binds hierarchically to pho box promoters. <i>Biological Chemistry</i> , <b>2012</b> , 393, 1165-71	4.5	18
58	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

57	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
56	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
55	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
54	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
53	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
52	Structure and non-structure of centrosomal proteins. <i>PLoS ONE</i> , <b>2013</b> , 8, e62633	3.7	16
51	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
50	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
49	Alkynyl complexes of manganese(I) as ligands. Synthesis and x-ray structure of {[2-ButMn(CO)3(dppe)]2Cu}(PF6). <i>Journal of Organometallic Chemistry</i> , <b>1986</b> , 299, C43-C46	2.3	15
48	Intercalative DNA binding of the marine anticancer drug variolin B. <i>Scientific Reports</i> , <b>2017</b> , 7, 39680	4.9	13
47	Structural insights into transcription complexes. <i>Journal of Structural Biology</i> , <b>2011</b> , 175, 135-46	3.4	13
46	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
45	New data on the synaptic process of <i>Mesocricetus auratus</i> : connecting fibers, telomere association and heterosynapsis. <i>Genetica</i> , <b>1987</b> , 74, 105-12	1.5	13
44	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
43	Structure and mechanism of a cysteine sulfinatase engineered on the aspartate aminotransferase scaffold. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2012</b> , 1824, 339-49	4	12
42	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
41	Shaped protein single crystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>1995</b> , 51, 278-81		11
40	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



39	The cofactor-induced pre-active conformation in PhoB. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2006</b> , 62, 1046-57		10
38	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
37	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
36	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
35	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
34	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
33	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
32	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
31	On the reaction mechanism of class Pi glutathione S-transferase		8
30	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
29	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
28	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
27	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
26	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
25	Φ0 and PhoB activator: getting a better grip. <i>Transcription</i> , <b>2012</b> , 3, 160-4	4.8	7
24	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, 272-81	5.7	7
23	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
22	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



21	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> , <b>2002</b> , 58, 312-3		6
20	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
19	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
18	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
17	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
16	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
15	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
14	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
13	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
12	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
11	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
10	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
9	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
8	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
7	Plasmid Rolling-Circle Replication		2
6	Structure-Driven Discovery of $\beta$ -Diketoacid Inhibitors Against UL89 Herpesvirus Terminase. <i>ACS Omega</i> , <b>2018</b> , 3, 8497-8505	3.9	1
5	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
4	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

- 3 Insights into the inhibited form of the redox-sensitive SufE-like sulfur acceptor CsdE. *PLoS ONE*, **2017**, 12, e0186286 3.7
- 2 Advances in metallo-procarboxypeptidases **1994**, 19-27
- 1 Structures of Tailed Phages and Herpesviruses (Herpesviridae) **2021**, 318-328