List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6315320/publications.pdf Version: 2024-02-01



LIDO HEINEMANN

#	Article	IF	CITATIONS
1	Protein production and purification. Nature Methods, 2008, 5, 135-146.	19.0	763
2	A standard reference frame for the description of nucleic acid base-pair geometry 1 1Edited by P. E. Wright 2 2This is a document of the Nomenclature Committee of IUBMB (NC-IUBMB)/IUPAC-IUBMB Joint Commission on Biochemical Nomenclature (JCBN), whose members are R. Cammack (chairman), A. Bairoch, H.M. Berman, S. Boyce, C.R. Cantor, K. Elliott, D. Horton, M. Kanehisa, A. Kotyk, G.P. Moss, N. Sharon and K.F. Tipton., Journal of Molecular Biology, 2001, 313, 229-237.	4.2	533
3	Helix geometry, hydration, and G.A mismatch in a B-DNA decamer. Science, 1987, 238, 498-504.	12.6	428
4	Universal nucleic acid-binding domain revealed by crystal structure of the B. subtilis major cold-shock protein. Nature, 1993, 364, 164-168.	27.8	357
5	Crystal structure of CspA, the major cold shock protein of Escherichia coli Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 5119-5123.	7.1	342
6	Specific protein-nucleic acid recognition in ribonuclease T1–2′-guanylic acid complex: an X-ray study. Nature, 1982, 299, 27-31.	27.8	304
7	Two exposed amino acid residues confer thermostability on a cold shock protein. Nature Structural Biology, 2000, 7, 380-383.	9.7	284
8	<i>XDSAPP</i> : a graphical user interface for the convenient processing of diffraction data using <i>XDS</i> . Journal of Applied Crystallography, 2012, 45, 568-572.	4.5	260
9	Structure of the DLM-1-Z-DNA complex reveals a conserved family of Z-DNA-binding proteins. Nature Structural Biology, 2001, 8, 761-765.	9.7	254
10	<i>XDSAPP2.0</i> . Journal of Applied Crystallography, 2016, 49, 1085-1092.	4.5	219
11	Molecular and active-site structure of a Bacillus 1,3-1,4-beta-glucanase Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 5287-5291.	7.1	209
12	Adrenodoxin: Structure, stability, and electron transfer properties. Proteins: Structure, Function and Bioinformatics, 2000, 40, 590-612.	2.6	194
13	Vectors for co-expression of an unrestricted number of proteins. Nucleic Acids Research, 2007, 35, e43-e43.	14.5	177
14	New aspects of electron transfer revealed by the crystal structure of a truncated bovine adrenodoxin, Adx(4–108). Structure, 1998, 6, 269-280.	3.3	167
15	Adrenodoxin Reductase-Adrenodoxin Complex Structure Suggests Electron Transfer Path in Steroid Biosynthesis. Journal of Biological Chemistry, 2001, 276, 2786-2789.	3.4	152
16	The structural and sequence homology of a family of microbial ribonucleases. Trends in Biochemical Sciences, 1983, 8, 364-369.	7.5	150
17	Ribonuclease T1 with free recognition and catalytic site: Crystal structure analysis at 1.5 Ã resolution. Journal of Molecular Biology, 1991, 222, 335-352.	4.2	146
18	Crystallographic study of one turn of G/C-rich B-DNA. Journal of Molecular Biology, 1989, 210, 369-381.	4.2	144

#	Article	IF	CITATIONS
19	Ribonuclease T1: Structure, Function, and Stability. Angewandte Chemie International Edition in English, 1991, 30, 343-360.	4.4	144
20	Involvement of a Bifunctional, Paired-like DNA-binding Domain and a Transpositional Enhancer in Sleeping BeautyTransposition. Journal of Biological Chemistry, 2002, 277, 34581-34588.	3.4	131
21	The DNA-bending protein HMGB1 is a cellular cofactor of Sleeping Beauty transposition. Nucleic Acids Research, 2003, 31, 2313-2322.	14.5	128
22	Thermal stability and atomic-resolution crystal structure of the Bacillus caldolyticus cold shock protein 1 1Edited by D. C. Rees. Journal of Molecular Biology, 2000, 297, 975-988.	4.2	122
23	Crystal structure of <i>Escherichia coli</i> phage HK620 tailspike: podoviral tailspike endoglycosidase modules are evolutionarily related. Molecular Microbiology, 2008, 69, 303-316.	2.5	121
24	Usa1 Functions as a Scaffold of the HRD-Ubiquitin Ligase. Molecular Cell, 2009, 36, 782-793.	9.7	114
25	Crystal structure of guanosine-free ribonuclease T1, complexed with vanadate(V), suggests conformational change upon substrate binding. Biochemistry, 1989, 28, 7592-7600.	2.5	113
26	Mechanisms of Lin28-Mediated miRNA and mRNA Regulation—A Structural and Functional Perspective. International Journal of Molecular Sciences, 2013, 14, 16532-16553.	4.1	110
27	Crystal Structure and Site-directed Mutagenesis of Bacillus macerans Endo-1,3 –1,4- β-glucanase. Journal of Biological Chemistry, 1995, 270, 3081-3088.	3.4	108
28	Crystal structure analysis of an A-DNA fragment at 1.8 Ã resolution: d(GCCCGGGC). Nucleic Acids Research, 1987, 15, 9531-9550.	14.5	105
29	Crystal structures of recombinant histones HMfA and HMfB from the hyperthermophilic archaeon Methanothermus fervidus. Journal of Molecular Biology, 2000, 303, 35-47.	4.2	105
30	Three-dimensional structure of ribonuclease T1 complexed with guanylyl-2′,5′-guanosine at 1.8 Ã resolution. Journal of Molecular Biology, 1989, 206, 475-488.	4.2	103
31	Constitutive Activation of Mitogen-activated Protein Kinase-activated Protein Kinase 2 by Mutation of Phosphorylation Sites and an A-helix Motif. Journal of Biological Chemistry, 1995, 270, 27213-27221.	3.4	102
32	RC3H1 post-transcriptionally regulates A20 mRNA and modulates the activity of the IKK/NF-κB pathway. Nature Communications, 2015, 6, 7367.	12.8	99
33	Structural Features of Tight-Junction Proteins. International Journal of Molecular Sciences, 2019, 20, 6020.	4.1	98
34	Structural changes of TasA in biofilm formation of <i>Bacillus subtilis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 3237-3242.	7.1	97
35	Facilities and Methods for the High-Throughput Crystal Structural Analysis of Human Proteins. Accounts of Chemical Research, 2003, 36, 157-163.	15.6	96
36	An Intersubunit Active Site between Supercoiled Parallel β Helices in the Trimeric Tailspike Endorhamnosidase of Shigella flexneri Phage Sf6. Structure, 2008, 16, 766-775.	3.3	83

#	Article	IF	CITATIONS
37	Circular permutation of polypeptide chains: Implications for protein folding and stability. Progress in Biophysics and Molecular Biology, 1995, 64, 121-143.	2.9	82
38	The Lin28 cold-shock domain remodels pre-let-7 microRNA. Nucleic Acids Research, 2012, 40, 7492-7506.	14.5	80
39	Eukaryotic expression: developments for structural proteomics. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1114-1124.	2.5	79
40	Detection of dynamic water molecules in a microcrystalline sample of the SH3 domain of α-spectrin by MAS solid-state NMR. Journal of Biomolecular NMR, 2005, 31, 295-310.	2.8	78
41	Native-like in vivo folding of a circularly permuted jellyroll protein shown by crystal structure analysis Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 10417-10421.	7.1	77
42	Identification of LIN28B-bound mRNAs reveals features of target recognition and regulation. RNA Biology, 2013, 10, 1146-1159.	3.1	76
43	Molecular cloning, nucleotide sequence, and characterization of the Bacillus subtilis gene encoding the DNA-binding protein HBsu. Journal of Bacteriology, 1991, 173, 3191-3198.	2.2	74
44	Crystal structure ofBacillus licheniformis1,3-1,4-β-d-glucan 4-glucanohydrolase at 1.8 à resolution. FEBS Letters, 1995, 374, 221-224.	2.8	74
45	RNA single strands bind to a conserved surface of the major cold shock protein in crystals and solution. Rna, 2012, 18, 65-76.	3.5	72
46	Sequence-specific DNA binding determined by contacts outside the helix-turn-helix motif of the ParB homolog KorB. Nature Structural and Molecular Biology, 2004, 11, 656-663.	8.2	71
47	Molecular dynamics simulation of the hydration shell of a B-DNA decamer reveals two main types of minor-groove hydration depending on groove width Proceedings of the National Academy of Sciences of the United States of America, 1991, 88, 593-597.	7.1	70
48	Crystal structure of acceptor stem of tRNAAla from Escherichia coli shows unique G•U wobble base pair at 1.16 â"« resolution. Rna, 1999, 5, 670-677.	3.5	69
49	The structure of the Klf4 DNA-binding domain links to self-renewal and macrophage differentiation. Cellular and Molecular Life Sciences, 2011, 68, 3121-3131.	5.4	69
50	The SNF2-like helicase HELLS mediates E2F3-dependent transcription and cellular transformation. EMBO Journal, 2012, 31, 972-985.	7.8	68
51	Bidirectional binding of invariant chain peptides to an MHC class II molecule. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 22219-22224.	7.1	67
52	Structure and function of the Bacillus hybrid enzyme GluXyn-1: Native-like jellyroll fold preserved after insertion of autonomous globular domain. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 6613-6618.	7.1	66
53	Crystal Structure of an RNA Dodecamer Containing theEscherichia coliShine-Dalgarno Sequence. Journal of Molecular Biology, 1995, 249, 595-603.	4.2	65
54	Selective Inhibitors of the Protein Tyrosine Phosphatase SHP2 Block Cellular Motility and Growth of Cancer Cells in vitro and in vivo. ChemMedChem, 2015, 10, 815-826.	3.2	65

#	Article	IF	CITATIONS
55	T-rich DNA Single Strands Bind to a Preformed Site on the Bacterial Cold Shock Protein Bs-CspB. Journal of Molecular Biology, 2006, 360, 702-714.	4.2	64
56	The Coxsackievirus–Adenovirus Receptor Reveals Complex Homophilic and Heterophilic Interactions on Neural Cells. Journal of Neuroscience, 2010, 30, 2897-2910.	3.6	60
57	Structure of palmitoylated BET3: insights into TRAPP complex assembly and membrane localization. EMBO Journal, 2005, 24, 875-884.	7.8	57
58	Structural Basis for the Substrate Specificity of a Bacillus 1,3-1,4-β-Glucanase. Journal of Molecular Biology, 2006, 357, 1211-1225.	4.2	56
59	An integrated approach to structural genomics. Progress in Biophysics and Molecular Biology, 2000, 73, 347-362.	2.9	54
60	Tail morphology controls DNA release in two <i>Salmonella</i> phages with one lipopolysaccharide receptor recognition system. Molecular Microbiology, 2012, 83, 1244-1253.	2.5	53
61	Detection of a Monomeric Intermediate Associated with Dimerization of Protein Hu by Mass Spectrometry. Journal of the American Chemical Society, 1998, 120, 6427-6428.	13.7	52
62	High-throughput three-dimensional protein structure determination. Current Opinion in Biotechnology, 2001, 12, 348-354.	6.6	52
63	Structural genomics of human proteinstarget selection and generation of a public catalogue of expression clones. Microbial Cell Factories, 2005, 4, 21.	4.0	50
64	Structural genomics in Europe: slow start, strong finish?. , 2000, 7, 940-942.		49
65	Molecular Insights into Arrhythmogenic Right Ventricular Cardiomyopathy Caused by Plakophilin-2 Missense Mutations. Circulation: Cardiovascular Genetics, 2012, 5, 400-411.	5.1	49
66	Three-dimensional structure of d(GGGATCCC) in the crystalline state. Nucleic Acids Research, 1988, 16, 7799-7816.	14.5	48
67	Circular permutations of protein sequence: not so rare?. Trends in Biochemical Sciences, 1995, 20, 349-350.	7.5	47
68	Crystal and Molecular Structure at 0.16-nm Resolution of the Hybrid Bacillus Endo-1,3-1,4-beta-D-Glucan 4-Glucanohydrolase H(A16-M). FEBS Journal, 1995, 232, 849-858.	0.2	47
69	Effect of a single 3′-methylene phosphonate linkage on the conformation of an A-DNA octamer double helix. Nucleic Acids Research, 1991, 19, 427-433.	14.5	46
70	Cation binding to a Bacillus (1,3-1,4)-beta-glucanase Geometry, affinity and effect on protein stability. FEBS Journal, 1994, 222, 203-214.	0.2	46
71	Crystal Structure of NblA from Anabaena sp. PCC 7120, a Small Protein Playing a Key Role in Phycobilisome Degradation. Journal of Biological Chemistry, 2006, 281, 5216-5223.	3.4	46
72	Unique self-palmitoylation activity of the transport protein particle component Bet3: A mechanism required for protein stability. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 12701-12706.	7.1	46

#	Article	IF	CITATIONS
73	Common mode of DNA binding to cold shock domains. FEBS Journal, 2007, 274, 1265-1279.	4.7	46
74	Overproduction, crystallization, and preliminary Xâ€ray diffraction studies of the major cold shock protein from <i>Bacillus subtilis</i> , CspB. Proteins: Structure, Function and Bioinformatics, 1992, 14, 120-124.	2.6	45
75	Vertebrate-type and plant-type ferredoxins: crystal structure comparison and electron transfer pathway modelling. Journal of Molecular Biology, 1999, 294, 501-513.	4.2	44
76	Crystal and molecular structure of the sulfhydryl protease calotropin DI at 3·2 à resolution. Journal of Molecular Biology, 1982, 161, 591-606.	4.2	43
77	Crystallographic Study of Mechanism of Ribonuclease Ti-Catalysed Specific RNA Hydrolysis. Journal of Biomolecular Structure and Dynamics, 1983, 1, 523-538.	3.5	43
78	pH-induced change in nucleotide binding geometry in the ribonuclease T1 -2'-guanylic acid complex. FEBS Letters, 1985, 181, 129-132.	2.8	43
79	Clinical variability in distal spinal muscular atrophy type 1 (DSMA1): determination of steady-state IGHMBP2 protein levels in five patients with infantile and juvenile disease. Journal of Molecular Medicine, 2009, 87, 31-41.	3.9	43
80	Crystal structure of Homo sapiens protein hp14.5. Proteins: Structure, Function and Bioinformatics, 2004, 54, 797-800.	2.6	42
81	Building functional modules from molecular interactions. Trends in Biochemical Sciences, 2006, 31, 497-508.	7.5	42
82	Roquin binding to target mRNAs involves a winged helix-turn-helix motif. Nature Communications, 2014, 5, 5701.	12.8	41
83	An Src Homology 3-like Domain Is Responsible for Dimerization of the Repressor Protein KorB Encoded by the Promiscuous IncP Plasmid RP4. Journal of Biological Chemistry, 2002, 277, 4191-4198.	3.4	40
84	Restrained least-squares refinement of the crystal structure of the ribonuclease T1*2'-guanylic acid complex at 1·9 à resolution. Acta Crystallographica Section B: Structural Science, 1987, 43, 548-554.	1.8	39
85	The structure of the TRAPP subunit TPC6 suggests a model for a TRAPP subcomplex. EMBO Reports, 2005, 6, 787-793.	4.5	39
86	Expression of protein complexes using multiple Escherichia coli protein co-expression systems: A benchmarking study. Journal of Structural Biology, 2011, 175, 159-170.	2.8	39
87	Crystal structures of mutant forms of the Bacillus caldolyticus cold shock protein differing in thermal stability. Journal of Molecular Biology, 2001, 313, 359-369.	4.2	38
88	Crystal Structure of Barley 1,3–1,4-β-Glucanase at 2.0-à Resolution and Comparison with Bacillus1,3–1,4-β-Glucanase. Journal of Biological Chemistry, 1998, 273, 3438-3446.	3.4	37
89	Crystal structure of human nicotinamide mononucleotide adenylyltransferase in complex with NMN. FEBS Letters, 2002, 516, 239-244.	2.8	36
90	Quantitative interaction mapping reveals an extended UBX domain in ASPL that disrupts functional p97 hexamers. Nature Communications, 2016, 7, 13047.	12.8	35

#	Article	IF	CITATIONS
91	Cold-Shock Domains—Abundance, Structure, Properties, and Nucleic-Acid Binding. Cancers, 2021, 13, 190.	3.7	35
92	Molecular dynamics simulations of ribonuclease T1: Comparison of the free enzyme and 2â€ <sup>2</sup> GMP-enzyme complex. Proteins: Structure, Function and Bioinformatics, 1989, 6, 20-31.	2.6	34
93	Salt-dependent and protein-concentration-dependent changes in the solution structure of the DNA-binding histone-like protein, HBsu, from Bacillus subtilis. FEBS Journal, 1992, 204, 1049-1055.	0.2	34
94	Discovery, Structure–Activity Relationship Studies, and Crystal Structure of Nonpeptide Inhibitors Bound to the Shank3 PDZ Domain. ChemMedChem, 2011, 6, 1411-1422.	3.2	34
95	Structural basis of gene regulation by the Grainyhead/CP2 transcription factor family. Nucleic Acids Research, 2018, 46, 2082-2095.	14.5	34
96	Electrochemical analysis of the self-complementary B-DNA decamer d(CCAGGCCTGG). Bioelectrochemistry, 1990, 23, 285-299.	1.0	33
97	Structure of the Bet3–Tpc6B Core of TRAPP: Two Tpc6 Paralogs Form Trimeric Complexes with Bet3 and Mum2. Journal of Molecular Biology, 2006, 361, 22-32.	4.2	33
98	A novel form of RNA double helix based on G·U and C·A <sup>+</sup> wobble base pairing. Rna, 2018, 24, 209-218.	3.5	33
99	Crystallographic studies of DNA helix structure. Biophysical Chemistry, 1994, 50, 157-167.	2.8	32
100	High resolution crystal structure of domain I of the Saccharomyces cerevisiae homing endonuclease Pl-Scel. Nucleic Acids Research, 2002, 30, 3962-3971.	14.5	32
101	Crystal structures and properties of de novo circularly permuted 1,3-1,4-β-glucanases. , 1998, 30, 155-167.		30
102	Covalently crosslinked complexes of bovine adrenodoxin with adrenodoxin reductase and cytochrome P450scc. FEBS Journal, 2001, 268, 1837-1843.	0.2	30
103	First steps towards effective methods in exploiting high-throughput technologies for the determination of human protein structures of high biomedical value. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1208-1217.	2.5	29
104	Crystal structure of <i>Klebsiella</i> sp. ASR1 phytase suggests substrate binding to a preformed active site that meets the requirements of a plant rhizosphere enzyme. FEBS Journal, 2010, 277, 1284-1296.	4.7	29
105	Crystal structure of native and a mutant of Lampyris turkestanicus luciferase implicate in bioluminescence color shift. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 2729-2735.	2.3	29
106	Bacteriophage P22 tailspike: structure of the complete protein and function of the interdomain linker. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1336-1345.	2.5	29
107	Repression of Transcriptional Activity of C/EBPα by E2F-Dimerization Partner Complexes. Molecular and Cellular Biology, 2010, 30, 2293-2304.	2.3	28
108	RNase T1 mutant Glu46Cln binds the inhibitors 2′CMP and 2′AMP at the 3′ subsite. Journal of Molecular Biology, 1992, 225, 533-542.	4.2	26

#	Article	IF	CITATIONS
109	Determination of DNA-binding parameters for the Bacillus subtilis histone-like HBsu protein through introduction of fluorophores by site-directed mutagenesis of a synthetic gene. FEBS Journal, 1992, 207, 677-685.	0.2	26
110	Solution Structure, Backbone Dynamics, and Association Behavior of the C-Terminal BRCT Domain from the Breast Cancer-Associated Protein BRCA1â€,‡. Biochemistry, 2004, 43, 15983-15995.	2.5	26
111	X-ray structure of fumarylacetoacetate hydrolase family member Homo sapiens FLJ36880. Biological Chemistry, 2004, 385, 935-942.	2.5	25
112	Unusual Armadillo Fold in the Human General Vesicular Transport Factor p115. PLoS ONE, 2009, 4, e4656.	2.5	25
113	AKAP18:PKA-RIIα structure reveals crucial anchor points for recognition of regulatory subunits of PKA. Biochemical Journal, 2016, 473, 1881-1894.	3.7	25
114	Time-resolved DNA release from an O-antigen–specific Salmonella bacteriophage with a contractile tail. Journal of Biological Chemistry, 2019, 294, 11751-11761.	3.4	25
115	A Note on Crystal Packing and Global Helix Structure in Short A-DNA Duplexes. Journal of Biomolecular Structure and Dynamics, 1991, 8, 801-811.	3.5	24
116	Crystal structure of chloromuconate cycloisomerase fromAlcaligenes eutrophusJMP134 (pJP4) at 3 Ã resolution. Acta Crystallographica Section D: Biological Crystallography, 1994, 50, 75-84.	2.5	24
117	X-ray structure of human gankyrin, the product of a gene linked to hepatocellular carcinoma. Proteins: Structure, Function and Bioinformatics, 2004, 55, 214-217.	2.6	24
118	Diversity in Structure and Function of Tethering Complexes: Evidence for Different Mechanisms in Vesicular Transport Regulation. Current Protein and Peptide Science, 2008, 9, 197-209.	1.4	23
119	Raison d'être and structural model for the B-Z transition of poly d(G-C)â^— poly d(G-C). FEBS Letters, 1989, 257, 223-227.	2.8	22
120	Ribonuclease T1: Struktur, Funktion und StabilitĤ Angewandte Chemie, 1991, 103, 351-369.	2.0	22
121	Sequence specificity of single-stranded DNA-binding proteins: a novel DNA microarray approach. Nucleic Acids Research, 2007, 35, e75.	14.5	22
122	Distinct isocomplexes of the TRAPP trafficking factor coexist inside human cells. FEBS Letters, 2008, 582, 3729-3733.	2.8	22
123	Crystallization of a Complex between Ribonuclease T1 and 2'-Guanylic Acid. FEBS Journal, 1980, 109, 109-114.	0.2	21
124	Interaction of fMet-tRNAfMetwith the C-terminal domain of translational initiation factor IF2 fromBacillus stearothermophilus. FEBS Letters, 2000, 471, 128-132.	2.8	21
125	Crystal structure of KorA bound to operator DNA: insight into repressor cooperation in RP4 gene regulation. Nucleic Acids Research, 2009, 37, 1915-1924.	14.5	21
126	Designed nanomolar small-molecule inhibitors of Ena/VASP EVH1 interaction impair invasion and extravasation of breast cancer cells. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 29684-29690.	7.1	21

#	Article	IF	CITATIONS
127	Role of histidine-40 in ribonuclease T1 catalysis: three-dimensional structures of the partially active His40Lys mutant. Biochemistry, 1992, 31, 11317-11325.	2.5	20
128	Optimized Variants of the Cold Shock Protein from in Vitro Selection: Structural Basis of Their High Thermostability. Journal of Molecular Biology, 2007, 369, 1087-1097.	4.2	20
129	Armadillo Motifs Involved in Vesicular Transport. PLoS ONE, 2010, 5, e8991.	2.5	20
130	Enhanced Properties of a Benzimidazole Benzylpyrazole Lysine Demethylase Inhibitor: Mechanism-of-Action, Binding Site Analysis, and Activity in Cellular Models of Prostate Cancer. Journal of Medicinal Chemistry, 2021, 64, 14266-14282.	6.4	20
131	Optimization of the Gβ1 Domain by Computational Design and by in Vitro Evolution: Structural and Energetic Basis of Stabilization. Journal of Molecular Biology, 2007, 373, 775-784.	4.2	19
132	Structural and functional studies of ribonuclease T1. , 1989, , 111-141.		19
133	DNA-binding properties and primary structure of HB protein from Bacillus globigii. FEBS Journal, 1987, 165, 547-552.	0.2	18
134	Disorder and twin refinement of RNA heptamer double helices. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1405-1413.	2.5	18
135	Single amino acid exchange in bacteriophage HK620 tailspike protein results in thousand-fold increase of its oligosaccharide affinity. Glycobiology, 2013, 23, 59-68.	2.5	18
136	An essential serotype recognition pocket on phage P22 tailspike protein forces Salmonella enterica serovar Paratyphi A O-antigen fragments to bind as nonsolution conformers. Glycobiology, 2013, 23, 486-494.	2.5	18
137	X-ray analysis of cubic crystals of the complex formed between ribonuclease T1 and guanosine-3',5'-bisphosphate. Acta Crystallographica Section B: Structural Science, 1991, 47, 521-527.	1.8	17
138	His92Ala mutation in ribonuclease T1 induces segmental flexibility. Journal of Molecular Biology, 1992, 224, 701-713.	4.2	17
139	DNA helix structure and refinement algorithm: comparison of models for d(CCAGGCm5CTGG) derived from NUCLSQ, TNT and X-PLOR. Acta Crystallographica Section D: Biological Crystallography, 1993, 49, 468-477.	2.5	17
140	High-resolution Crystal Structures of Caldicellulosiruptor Strain Rt8B.4 Carbohydrate-binding Module CBM27-1 and its Complex with Mannohexaose. Journal of Molecular Biology, 2004, 340, 543-554.	4.2	17
141	Bacteriophage Tailspikes and Bacterial O-Antigens as a Model System to Study Weak-Affinity Protein–Polysaccharide Interactions. Journal of the American Chemical Society, 2016, 138, 9109-9118.	13.7	17
142	Dimer Formation of a Stabilized Gβ1 Variant: A Structural and Energetic Analysis. Journal of Molecular Biology, 2009, 391, 918-932.	4.2	16
143	Identification of a Novel Benzimidazole Pyrazolone Scaffold That Inhibits KDM4 Lysine Demethylases and Reduces Proliferation of Prostate Cancer Cells. SLAS Discovery, 2017, 22, 801-812.	2.7	16
144	From Pyrazolones to Azaindoles: Evolution of Active-Site SHP2 Inhibitors Based on Scaffold Hopping and Bioisosteric Replacement. Journal of Medicinal Chemistry, 2020, 63, 14780-14804.	6.4	16

#	Article	IF	CITATIONS
145	Crystallographic Study of Glu58Ala RNase T1.cntdot.2'-Guanosine Monophosphate at 1.9ANG. Resolution. Biochemistry, 1994, 33, 1654-1662.	2.5	15
146	Structural and functional characterization of human Iba proteins. FEBS Journal, 2008, 275, 4627-4640.	4.7	15
147	Symmetry in Nucleic-Acid Double Helices. Symmetry, 2020, 12, 737.	2.2	15
148	Studies on the domain structure of the Salmonella/typhimurium AraC protein. FEBS Journal, 1989, 185, 319-325.	0.2	14
149	The interaction domain of the redox protein adrenodoxin is mandatory for binding of the electron acceptor CYP11A1, but is not required for binding of the electron donor adrenodoxin reductase. Biochemical and Biophysical Research Communications, 2005, 338, 491-498.	2.1	14
150	An approach to quality management in structural biology: Biophysical selection of proteins for successful crystallization. Journal of Structural Biology, 2008, 162, 451-459.	2.8	14
151	The dipole moment of the electron carrier adrenodoxin is not critical for redox partner interaction and electron transfer. Journal of Inorganic Biochemistry, 2009, 103, 997-1004.	3.5	14
152	Peptide Linkage to the α-Subunit of MHCII Creates a Stably Inverted Antigen Presentation Complex. Journal of Molecular Biology, 2012, 423, 294-302.	4.2	14
153	Preparation and crystallization of a cross-linked complex of bovine adrenodoxin and adrenodoxin reductase. Proteins: Structure, Function and Bioinformatics, 1997, 28, 289-292.	2.6	13
154	Structural and Biochemical Basis of Yos9 Protein Dimerization and Possible Contribution to Self-association of 3-Hydroxy-3-methylglutaryl-Coenzyme A Reductase Degradation Ubiquitin-Ligase Complex. Journal of Biological Chemistry, 2012, 287, 8633-8640.	3.4	13
155	Structural Identification of the Vps18 β-Propeller Reveals a Critical Role in the HOPS Complex Stability and Function. Journal of Biological Chemistry, 2014, 289, 33503-33512.	3.4	13
156	Tracking Transient Conformational States of T4 Lysozyme at Room Temperature Combining X-ray Crystallography and Site-Directed Spin Labeling. Journal of the American Chemical Society, 2016, 138, 12868-12875.	13.7	13
157	Common Mode of Remodeling AAA ATPases p97/CDC48 by Their Disassembling Cofactors ASPL/PUX1. Structure, 2019, 27, 1830-1841.e3.	3.3	13
158	Conformations and conformational changes of four Phe Trp variants of the DNA-binding histone-like protein, HBsu, from Bacillus subtilis studied by circular dichroism and fluorescence spectroscopy. FEBS Journal, 1993, 217, 849-856.	0.2	12
159	Three-dimensional structure of the ternary complex between ribonuclease T1, guanosine 3',5'-bisphosphate and inorganic phosphate at 0.19 nm resolution. FEBS Journal, 1993, 211, 311-316.	0.2	12
160	Trp59 to Tyr substitution enhances the catalytic activity of RNase T1 and of the Tyr to Trp variants in positions 24, 42 and 45. Protein Engineering, Design and Selection, 1993, 6, 739-744.	2.1	12
161	Conformation of d(GGGATCCC)2in crystals and in solution studied by X-ray diffraction, Raman spectroscopy and molecular modelling. Nucleic Acids Research, 1993, 21, 569-576.	14.5	12
162	Crystal Structure of an Eight-Base Pair Duplex Containing the 3â€~-DNAâ^'RNA-5â€~ Junction Formed during Initiation of Minus-Strand Synthesis of HIV Replicationâ€. Biochemistry, 1998, 37, 12005-12011.	2.5	12

#	Article	IF	CITATIONS
163	RP4 Repressor Protein KorB Binds to the Major Groove of the Operator DNA: A Raman Studyâ€. Biochemistry, 2003, 42, 14476-14482.	2.5	12
164	Crystallization of Barley (1-3, 1-4)-Î <sup>2</sup> -glucanase, Isoenzyme II. Journal of Molecular Biology, 1993, 232, 1003-1004.	4.2	11
165	Structural and thermodynamic characterization of the adrenodoxin-like domain of the electron-transfer protein Etp1 from Schizosaccharomyces pombe. Journal of Inorganic Biochemistry, 2011, 105, 957-965.	3.5	11
166	Crystal structure of the yeast <scp>TRAPP</scp> â€associated protein Tca17. FEBS Journal, 2014, 281, 4195-4206.	4.7	11
167	Solvent Networks Tune Thermodynamics of Oligosaccharide Complex Formation in an Extended Protein Binding Site. Journal of the American Chemical Society, 2018, 140, 10447-10455.	13.7	11
168	Structureâ€Based Screening of Tetrazolylhydrazide Inhibitors versus KDM4 Histone Demethylases. ChemMedChem, 2019, 14, 1828-1839.	3.2	11
169	Molecular dynamics simulations of ribonuclease T1. European Biophysics Journal, 1988, 16, 287-297.	2.2	10
170	Crystallization of the hybrid Bacillus (1–3, 1–4)-β-glucanase H(A16-M). Journal of Molecular Biology, 1991, 218, 703-704.	4.2	10
171	Modeling of electrostatic recognition processes in the mammalian mitochondrial steroid hydroxylase system. Biophysical Chemistry, 2002, 100, 281-292.	2.8	10
172	Tricellulin is a target of the ubiquitin ligase Itch. Annals of the New York Academy of Sciences, 2017, 1397, 157-168.	3.8	10
173	Mechanism of guanosine recognition and RNA hydrolysis by ribonuclease T1. Pure and Applied Chemistry, 1985, 57, 417-422.	1.9	9
174	Crystal and Molecular Structure at 0.16-nm Resolution of the Hybrid Bacillus Endo-1,3-1,4-beta-D-Glucan 4-Glucanohydrolase H(A16-M). FEBS Journal, 1995, 232, 849-858.	0.2	9
175	PAN-modular structure of microneme protein SML-2 from the parasite <i>Sarcocystis muris</i> at 1.95â€Ã resolution and its complex with 1-thio-l²- <scp>D</scp> -galactose. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 936-944.	2.5	9
176	Crystal structure of the tricellulin Câ€ŧerminal coiled oil domain reveals a unique mode of dimerization. Annals of the New York Academy of Sciences, 2017, 1405, 147-159.	3.8	9
177	PIN and CCCH Zn-finger domains coordinate RNA targeting in ZC3H12 family endoribonucleases. Nucleic Acids Research, 2021, 49, 5369-5381.	14.5	9
178	Single-stranded DNA bound to bacterial cold-shock proteins: preliminary crystallographic and Raman analysis. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 755-757.	2.5	8
179	X-ray structure of engineered human Aortic Preferentially Expressed Protein-1 (APEG-1). BMC Structural Biology, 2005, 5, 21.	2.3	8
180	Light-Induced Reduction of Bovine Adrenodoxin via the Covalently Bound Ruthenium(II) Bipyridyl Complex: Intramolecular Electron Transfer and Crystal Structureâ€. Biochemistry, 2006, 45, 709-718.	2.5	8

#	Article	IF	CITATIONS
181	Characterization of the self-palmitoylation activity of the transport protein particle component Bet3. Cellular and Molecular Life Sciences, 2010, 67, 2653-2664.	5.4	8
182	Chemical Synthesis and Cloning of a Gene Coding for Bacillus Subjilis Hbsu Protein. Nucleosides & Nucleotides, 1988, 7, 817-820.	0.5	7
183	Preliminary characterization by X-ray diffraction and Raman spectroscopy of a crystalline complex ofBacillus stearothermophilusinitiation factorÂ2â€C-domain and fMet-tRNAfMet. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 712-716.	2.5	7
184	Crystal structure of Homo sapiens PTD012 reveals a zinc-containing hydrolase fold. Protein Science, 2006, 15, 914-920.	7.6	7
185	Crystallization and preliminary X-ray characterization of theMethanothermus fervidus histones HMfA and HMfB. , 1996, 24, 269-271.		6
186	Establishing a structural genomics platform: The Berlin-based Protein Structure Factory. Gene Function & Disease, 2002, 3, 25-32.	0.3	6
187	Rapid purification and crystal structure analysis of a small protein carrying two terminal affinity tags. Journal of Structural and Functional Genomics, 2003, 4, 217-225.	1.2	6
188	Structure of circularly permuted DsbAQ100T99: preserved global fold and local structural adjustments. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 304-309.	2.5	6
189	An idea whose time has come. Genome Biology, 2007, 8, 408.	9.6	6
190	Combining EPR spectroscopy and X-ray crystallography to elucidate the structure and dynamics of conformationally constrained spin labels in T4 lysozyme single crystals. Physical Chemistry Chemical Physics, 2017, 19, 20723-20734.	2.8	5
191	Small-molecule inhibitors of the PDZ domain of Dishevelled proteins interrupt Wnt signalling. Magnetic Resonance, 2021, 2, 355-374.	1.9	5
192	Pantoea stewartii WceF is a glycan biofilm-modifying enzyme with a bacteriophage tailspike-like fold. Journal of Biological Chemistry, 2021, 296, 100286.	3.4	5
193	Covalently crosslinked complexes of bovine adrenodoxin with adrenodoxin reductase and cytochrome P450scc Mass spectrometry and Edman degradation of complexes of the steroidogenic hydroxylase system. FEBS Journal, 2001, 268, 1837-1843.	0.2	5
194	Conformational stability of the DNA-binding histone-like protein, HBsu, fromBacillus subtilis, and of the four HBsu variants [F29W], [F47W], [F50W] and [F79W]. Journal of Biomolecular Structure and Dynamics, 1993, 11, 381-394.	3.5	4
195	Structure of adrenodoxin and function in mitochondrial steroid hydroxylation. Endocrine Research, 1998, 24, 531-539.	1.2	4
196	Structural biology: the foundation of molecular medicine. Journal of Molecular Medicine, 2000, 78, 245-246.	3.9	4
197	Crystal Structures of the Single PDZ Domains from GRASP65 and their Interaction with the Golgin GM130. Croatica Chemica Acta, 2018, 91, .	0.4	4
198	Molekulare Basis der Genkontrolle. Nachrichten Aus Der Chemie, 1984, 32, 712-716.	0.0	3

#	Article	IF	CITATIONS
199	X-Ray Studies of DNA Aiming at Elucidating the Sequence-Structure Code. Nucleosides & Nucleotides, 1990, 9, 349-354.	0.5	3
200	Crystals of the chemically synthesized acceptor stem of tRNAAlafromEscherichia colidiffracting to high resolution. Acta Crystallographica Section D: Biological Crystallography, 1996, 52, 871-873.	2.5	3
201	Crystallization and X-ray diffraction data of a tRNASecacceptor-stem helix. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 664-666.	2.5	3
202	Characterization and crystallization of a novelSarcocystis murislectin, SML-2. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1042-1045.	2.5	3
203	Purification and preliminary X-ray crystallographic studies of β-microseminoprotein from human seminal plasma. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 518-521.	0.7	3
204	X-Ray Crystallographic Studies of the A-Form of DNA. Nucleosides & Nucleotides, 1988, 7, 699-702.	0.5	2
205	Synthesis of the Bacillus subtilis histone-like DNA-binding protein HBsu in Escherichia coli and secretion into the periplasm. Gene, 1993, 124, 99-103.	2.2	2
206	Crystallization and preliminary X-ray analysis of human nicotinamide mononucleotide adenylyltransferase (NMNAT). Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 140-142.	2.5	2
207	Low-resolutionab initiophasing ofSarcocystis murislectin SML-2. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 533-540.	2.5	2
208	Internal Dynamics of the 3-Pyrroline- <i>N</i> -Oxide Ring in Spin-Labeled Proteins. Journal of Physical Chemistry Letters, 2017, 8, 1113-1117.	4.6	2
209	Structure of the active GGEEF domain of a diguanylate cyclase from Vibrio cholerae. Biochemical and Biophysical Research Communications, 2020, 523, 287-292.	2.1	2
210	Crystal structure of Q4D6Q6, a conserved kinetoplastid-specific protein from Trypanosoma cruzi. Journal of Structural Biology, 2020, 211, 107536.	2.8	2
211	The automated expert processing system XDSAPP. Acta Crystallographica Section A: Foundations and Advances, 2016, 72, s191-s191.	0.1	2
212	An Integrated Pharmacological, Structural, and Genetic Analysis of Extracellular Versus Intracellular ROS Production in Neutrophils. Journal of Molecular Biology, 2022, 434, 167533.	4.2	2
213	Glass-capillary collimator for distance compensation and partial monochromatization at rotating-anode X-ray generators. Journal of Applied Crystallography, 1995, 28, 853-855.	4.5	1
214	Röntgenstrukturanalyse großer Biomoleküle. Chemie in Unserer Zeit, 1998, 32, 22-33.	0.1	1
215	Linking Structural Biology With Genome Research. , 2002, , 179-189.		1
216	Secure web book to store structural genomics research data. Journal of Structural and Functional Genomics, 2003, 4, 121-127.	1.2	1

#	Article	IF	CITATIONS
217	Facilities and Methods for the High-Throughput Crystal Structural Analysis of Human Proteins. ChemInform, 2003, 34, no.	0.0	1
218	Letter to the Editor:1H,13C and15N resonance assignments of the C-terminal BRCT domain from human BRCA1. Journal of Biomolecular NMR, 2004, 30, 221-222.	2.8	1
219	Functional interaction of CCAAT/enhancer-binding-protein-α basic region mutants with E2F transcription factors and DNA. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2016, 1859, 841-847.	1.9	1
220	Technologies for profiling the impact of genomic variants on transcription factor binding. Medizinische Genetik, 2021, 33, 147-155.	0.2	1
221	<title>Structural analysis of DNA oligomers in single crystals and in aqueous solutions by micro-FTIR and Raman spectroscopy</title> . , 1992, 1575, 459.		0
222	Linking structural biology with genome research: Beamlines for the Berlin "Protein Structure Factory―initiative. AlP Conference Proceedings, 2000, , .	0.4	0
223	Structural Studies of Model RNA Helices with Relevance to Aminoacyl-tRNA Synthetase Specificity and HIV Reverse Transcription. Journal of Biomolecular Structure and Dynamics, 2000, 17, 39-45.	3.5	0
224	Corrigendum to: Crystal structure of human nicotinamide mononucleotide adenylyltransferase in complex with NMN (FEBS 25964). FEBS Letters, 2002, 523, 254-255.	2.8	0
225	Crystal and Molecular Structure at 0.16â€nm Resolution of the Hybrid <i>Bacillus</i> Endoâ€1,3â€1,4â€Î²â€Dâ€Glucan 4â€Glucanohydrolase H(A16â€M). FEBS Journal, 1995, 232, 849-858.	0.2	0
226	Flipped CLIP orientation in the MHC class II binding groove. Molecular Immunology, 2012, 51, 14.	2.2	0
227	COLD-SHOCK DOMAINS – VERSATILE MOLECULAR MODULES FOR SINGLE-STRANDED RNA BINDING AND REMODELING. , 2013, , 220-229.		0
228	Structural and biochemical insights into grainyhead-like 1 and its homolog grainyhead-like 3. Acta Crystallographica Section A: Foundations and Advances, 2015, 71, s243-s243.	0.1	0
229	Structural investigation of the small GTPase ARL4D. Acta Crystallographica Section A: Foundations and Advances, 2015, 71, s221-s221.	0.1	0
230	Translational regulation of gene expression by Lin28 and Roquin. Acta Crystallographica Section A: Foundations and Advances, 2015, 71, s29-s30.	0.1	0
231	MolekÃ1⁄4lmodelle und ModellmolekÃ1⁄4le: Strukturanalyse großer biologischer MolekÃ1⁄4le fÃ1⁄4r die Medizin. , 2003, , 340-359.		0
232	Structural Genomics and Structural Proteomics: A Global Perspective. , 2008, , 505-537.		0
233	Conserved binding mode of single-stranded DNA and RNA to cold-shock domains. Acta Crystallographica Section A: Foundations and Advances, 2009, 65, s21-s21.	0.3	0
234	PSPF - a protein sample production facility for structural biologists. Acta Crystallographica Section A: Foundations and Advances, 2010, 66, s120-s121.	0.3	0

#	Article	IF	CITATIONS
235	Self-association of quality control components in the ER. Acta Crystallographica Section A: Foundations and Advances, 2010, 66, s26-s26.	0.3	0
236	Structural studies of proteins involved in ER-associated protein degradation. Acta Crystallographica Section A: Foundations and Advances, 2013, 69, s57-s57.	0.3	0
237	Enthalpic cost of water removal from a glucose binding cavity on HK620 TSP. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C1600-C1600.	0.1	0
238	MCPIP3 (ZC3H12C) regulates the innate immune response by acting as a ribonuclease. Acta Crystallographica Section A: Foundations and Advances, 2016, 72, s249-s249.	0.1	0
239	Klf4 and Grhl1: two distinct ways of achieving DNA target site recognition. Acta Crystallographica Section A: Foundations and Advances, 2016, 72, s216-s216.	0.1	0
240	Immune response regulation by paralogous endoribonucleases: ZC3H12C and N4BP1. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C452-C452.	0.1	0
241	Structural insight into protein-aided bacterial biofilm formation. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C391-C391.	0.1	0
242	Parsimonious DNA target-site recognition by Grh/CP2 transcription factors. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C298-C298.	0.1	0
243	Structural insight into protein-aided bacterial biofilm formation. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, e206-e206.	0.1	0
244	Structural basis of ASPL-mediated regulation of p97 methylation by METTL21D. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, e199-e200.	0.1	0
245	Ribonuclease T1: Mechanism of Specific Guanine Recognition and RNA Hydrolysis. Jerusalem Symposia on Quantum Chemistry and Biochemistry, 1983, , 265-276.	0.2	0
246	Molekülmodelle und Modellmoleküle: Strukturanalyse großer biologischer Moleküle für die Medizin. , 2008, , 275-294.		0