

Udo Heinemann

List of Publications by Year in descending order

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246
papers

11,905
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26567

56
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32761

100
g-index

257
all docs

257
docs citations

257
times ranked

12213
citing authors

#	ARTICLE	IF	CITATIONS
1	Protein production and purification. <i>Nature Methods</i> , 2008, 5, 135-146.	9.0	763
2	A standard reference frame for the description of nucleic acid base-pair geometry 1 Edited by P. E. Wright 2 This 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.. <i>Journal of Molecular Biology</i> , 2001, 313, 229-237.	2.0	533
3	Helix geometry, hydration, and G.A mismatch in a B-DNA decamer. <i>Science</i> , 1987, 238, 498-504.	6.0	428
4	Universal nucleic acid-binding domain revealed by crystal structure of the <i>B. subtilis</i> major cold-shock protein. <i>Nature</i> , 1993, 364, 164-168.	13.7	357
5	Crystal structure of CspA, the major cold shock protein of <i>Escherichia coli</i> .. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 5119-5123.	3.3	342
6	Specific protein-nucleic acid recognition in ribonuclease T1â€™2â€™-guanylic acid complex: an X-ray study. <i>Nature</i> , 1982, 299, 27-31.	13.7	304
7	Two exposed amino acid residues confer thermostability on a cold shock protein. <i>Nature Structural Biology</i> , 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>. <i>Journal of Applied Crystallography</i> , 2012, 45, 568-572.	1.9	260
9	Structure of the DLM-1-Z-DNA complex reveals a conserved family of Z-DNA-binding proteins. <i>Nature Structural Biology</i> , 2001, 8, 761-765.	9.7	254
10	<i>XDSAPP2.0</i>. <i>Journal of Applied Crystallography</i> , 2016, 49, 1085-1092.	1.9	219
11	Molecular and active-site structure of a <i>Bacillus</i> 1,3-1,4-beta-glucanase.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993, 90, 5287-5291.	3.3	209
12	Adrenodoxin: Structure, stability, and electron transfer properties. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 40, 590-612.	1.5	194
13	Vectors for co-expression of an unrestricted number of proteins. <i>Nucleic Acids Research</i> , 2007, 35, e43-e43.	6.5	177
14	New aspects of electron transfer revealed by the crystal structure of a truncated bovine adrenodoxin, Adx(4â€™108). <i>Structure</i> , 1998, 6, 269-280.	1.6	167
15	Adrenodoxin Reductase-Adrenodoxin Complex Structure Suggests Electron Transfer Path in Steroid Biosynthesis. <i>Journal of Biological Chemistry</i> , 2001, 276, 2786-2789.	1.6	152
16	The structural and sequence homology of a family of microbial ribonucleases. <i>Trends in Biochemical Sciences</i> , 1983, 8, 364-369.	3.7	150
17	Ribonuclease T1 with free recognition and catalytic site: Crystal structure analysis at 1.5 Å... resolution. <i>Journal of Molecular Biology</i> , 1991, 222, 335-352.	2.0	146
18	Crystallographic study of one turn of G/C-rich B-DNA. <i>Journal of Molecular Biology</i> , 1989, 210, 369-381.	2.0	144

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19	Ribonuclease T1: Structure, Function, and Stability. <i>Angewandte Chemie International Edition in English</i> , 1991, 30, 343-360.	4.4	144
20	Involvement of a Bifunctional, Paired-like DNA-binding Domain and a Transpositional Enhancer in Sleeping Beauty Transposition. <i>Journal of Biological Chemistry</i> , 2002, 277, 34581-34588.	1.6	131
21	The DNA-bending protein HMGB1 is a cellular cofactor of Sleeping Beauty transposition. <i>Nucleic Acids Research</i> , 2003, 31, 2313-2322.	6.5	128
22	Thermal stability and atomic-resolution crystal structure of the <i>Bacillus caldolyticus</i> cold shock protein 1. Edited by D. C. Rees. <i>Journal of Molecular Biology</i> , 2000, 297, 975-988.	2.0	122
23	Crystal structure of <i>Escherichia coli</i> phage HK620 tailspike: podoviral tailspike endoglycosidase modules are evolutionarily related. <i>Molecular Microbiology</i> , 2008, 69, 303-316.	1.2	121
24	Usa1 Functions as a Scaffold of the HRD-Ubiquitin Ligase. <i>Molecular Cell</i> , 2009, 36, 782-793.	4.5	114
25	Crystal structure of guanosine-free ribonuclease T1, complexed with vanadate(V), suggests conformational change upon substrate binding. <i>Biochemistry</i> , 1989, 28, 7592-7600.	1.2	113
26	Mechanisms of Lin28-Mediated miRNA and mRNA Regulation – A Structural and Functional Perspective. <i>International Journal of Molecular Sciences</i> , 2013, 14, 16532-16553.	1.8	110
27	Crystal Structure and Site-directed Mutagenesis of <i>Bacillus macerans</i> Endo-1,3- β -glucanase. <i>Journal of Biological Chemistry</i> , 1995, 270, 3081-3088.	1.6	108
28	Crystal structure analysis of an A-DNA fragment at 1.8 Å resolution: d(GCCCGGGC). <i>Nucleic Acids Research</i> , 1987, 15, 9531-9550.	6.5	105
29	Crystal structures of recombinant histones HMfA and HMfB from the hyperthermophilic archaeon <i>Methanothermus fervidus</i> . <i>Journal of Molecular Biology</i> , 2000, 303, 35-47.	2.0	105
30	Three-dimensional structure of ribonuclease T1 complexed with guanylyl-2',5'-guanosine at 1.8 Å resolution. <i>Journal of Molecular Biology</i> , 1989, 206, 475-488.	2.0	103
31	Constitutive Activation of Mitogen-activated Protein Kinase-activated Protein Kinase 2 by Mutation of Phosphorylation Sites and an A-helix Motif. <i>Journal of Biological Chemistry</i> , 1995, 270, 27213-27221.	1.6	102
32	RC3H1 post-transcriptionally regulates A20 mRNA and modulates the activity of the IKK/NF- κ B pathway. <i>Nature Communications</i> , 2015, 6, 7367.	5.8	99
33	Structural Features of Tight-Junction Proteins. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6020.	1.8	98
34	Structural changes of TasA in biofilm formation of <i>Bacillus subtilis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3237-3242.	3.3	97
35	Facilities and Methods for the High-Throughput Crystal Structural Analysis of Human Proteins. <i>Accounts of Chemical Research</i> , 2003, 36, 157-163.	7.6	96
36	An Intersubunit Active Site between Supercoiled Parallel β Helices in the Trimeric Tailspike Endorhamnosidase of <i>Shigella flexneri</i> Phage Sf6. <i>Structure</i> , 2008, 16, 766-775.	1.6	83

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37	Circular permutation of polypeptide chains: Implications for protein folding and stability. <i>Progress in Biophysics and Molecular Biology</i> , 1995, 64, 121-143.	1.4	82
38	The Lin28 cold-shock domain remodels pre-let-7 microRNA. <i>Nucleic Acids Research</i> , 2012, 40, 7492-7506.	6.5	80
39	Eukaryotic expression: developments for structural proteomics. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1114-1124.	2.5	79
40	Detection of dynamic water molecules in a microcrystalline sample of the SH3 domain of β -spectrin by MAS solid-state NMR. <i>Journal of Biomolecular NMR</i> , 2005, 31, 295-310.	1.6	78
41	Native-like in vivo folding of a circularly permuted jellyroll protein shown by crystal structure analysis.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 10417-10421.	3.3	77
42	Identification of LIN28B-bound mRNAs reveals features of target recognition and regulation. <i>RNA Biology</i> , 2013, 10, 1146-1159.	1.5	76
43	Molecular cloning, nucleotide sequence, and characterization of the <i>Bacillus subtilis</i> gene encoding the DNA-binding protein HBSu. <i>Journal of Bacteriology</i> , 1991, 173, 3191-3198.	1.0	74
44	Crystal structure of <i>Bacillus licheniformis</i> 1,3-1,4- β -D-glucan 4-glucanohydrolase at 1.8 Å... resolution. <i>FEBS Letters</i> , 1995, 374, 221-224.	1.3	74
45	RNA single strands bind to a conserved surface of the major cold shock protein in crystals and solution. <i>Rna</i> , 2012, 18, 65-76.	1.6	72
46	Sequence-specific DNA binding determined by contacts outside the helix-turn-helix motif of the ParB homolog KorB. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 656-663.	3.6	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.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1991, 88, 593-597.	3.3	70
48	Crystal structure of acceptor stem of tRNA ^{Ala} from <i>Escherichia coli</i> shows unique G \leftrightarrow C wobble base pair at 1.16 Å resolution. <i>Rna</i> , 1999, 5, 670-677.	1.6	69
49	The structure of the Klf4 DNA-binding domain links to self-renewal and macrophage differentiation. <i>Cellular and Molecular Life Sciences</i> , 2011, 68, 3121-3131.	2.4	69
50	The SNF2-like helicase HELLS mediates E2F3-dependent transcription and cellular transformation. <i>EMBO Journal</i> , 2012, 31, 972-985.	3.5	68
51	Bidirectional binding of invariant chain peptides to an MHC class II molecule. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 22219-22224.	3.3	67
52	Structure and function of the <i>Bacillus</i> hybrid enzyme GluXyn-1: Native-like jellyroll fold preserved after insertion of autonomous globular domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 6613-6618.	3.3	66
53	Crystal Structure of an RNA Dodecamer Containing the <i>Escherichia coli</i> Shine-Dalgarno Sequence. <i>Journal of Molecular Biology</i> , 1995, 249, 595-603.	2.0	65
54	Selective Inhibitors of the Protein Tyrosine Phosphatase SHP2 Block Cellular Motility and Growth of Cancer Cells in <i>in vitro</i> and <i>in vivo</i> . <i>ChemMedChem</i> , 2015, 10, 815-826.	1.6	65

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55	T-rich DNA Single Strands Bind to a Prefomed Site on the Bacterial Cold Shock Protein Bs-CspB. <i>Journal of Molecular Biology</i> , 2006, 360, 702-714.	2.0	64
56	The Coxsackievirus Adenovirus Receptor Reveals Complex Homophilic and Heterophilic Interactions on Neural Cells. <i>Journal of Neuroscience</i> , 2010, 30, 2897-2910.	1.7	60
57	Structure of palmitoylated BET3: insights into TRAPP complex assembly and membrane localization. <i>EMBO Journal</i> , 2005, 24, 875-884.	3.5	57
58	Structural Basis for the Substrate Specificity of a Bacillus 1,3-1,4- β -Glucanase. <i>Journal of Molecular Biology</i> , 2006, 357, 1211-1225.	2.0	56
59	An integrated approach to structural genomics. <i>Progress in Biophysics and Molecular Biology</i> , 2000, 73, 347-362.	1.4	54
60	Tail morphology controls DNA release in two <i>Salmonella</i> phages with one lipopolysaccharide receptor recognition system. <i>Molecular Microbiology</i> , 2012, 83, 1244-1253.	1.2	53
61	Detection of a Monomeric Intermediate Associated with Dimerization of Protein Hu by Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 1998, 120, 6427-6428.	6.6	52
62	High-throughput three-dimensional protein structure determination. <i>Current Opinion in Biotechnology</i> , 2001, 12, 348-354.	3.3	52
63	Structural genomics of human proteins--target selection and generation of a public catalogue of expression clones. <i>Microbial Cell Factories</i> , 2005, 4, 21.	1.9	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. <i>Circulation: Cardiovascular Genetics</i> , 2012, 5, 400-411.	5.1	49
66	Three-dimensional structure of d(GGGATCCC) in the crystalline state. <i>Nucleic Acids Research</i> , 1988, 16, 7799-7816.	6.5	48
67	Circular permutations of protein sequence: not so rare?. <i>Trends in Biochemical Sciences</i> , 1995, 20, 349-350.	3.7	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). <i>FEBS Journal</i> , 1995, 232, 849-858.	0.2	47
69	Effect of a single β -methylene phosphonate linkage on the conformation of an A-DNA octamer double helix. <i>Nucleic Acids Research</i> , 1991, 19, 427-433.	6.5	46
70	Cation binding to a Bacillus (1,3-1,4)-beta-glucanase Geometry, affinity and effect on protein stability. <i>FEBS Journal</i> , 1994, 222, 203-214.	0.2	46
71	Crystal Structure of NblA from <i>Anabaena</i> sp. PCC 7120, a Small Protein Playing a Key Role in Phycobilisome Degradation. <i>Journal of Biological Chemistry</i> , 2006, 281, 5216-5223.	1.6	46
72	Unique self-palmitoylation activity of the transport protein particle component Bet3: A mechanism required for protein stability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 12701-12706.	3.3	46

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73	Common mode of DNA binding to cold shock domains. FEBS Journal, 2007, 274, 1265-1279.	2.2	46
74	Overproduction, crystallization, and preliminary X-ray diffraction studies of the major cold shock protein from <i>Bacillus subtilis</i> , CspB. Proteins: Structure, Function and Bioinformatics, 1992, 14, 120-124.	1.5	45
75	Vertebrate-type and plant-type ferredoxins: crystal structure comparison and electron transfer pathway modelling. Journal of Molecular Biology, 1999, 294, 501-513.	2.0	44
76	Crystal and molecular structure of the sulfhydryl protease calotropin DI at 3.2 Å resolution. Journal of Molecular Biology, 1982, 161, 591-606.	2.0	43
77	Crystallographic Study of Mechanism of Ribonuclease T1-Catalysed Specific RNA Hydrolysis. Journal of Biomolecular Structure and Dynamics, 1983, 1, 523-538.	2.0	43
78	pH-induced change in nucleotide binding geometry in the ribonuclease T1-2'-guanylic acid complex. FEBS Letters, 1985, 181, 129-132.	1.3	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.	1.7	43
80	Crystal structure of Homo sapiens protein hp14.5. Proteins: Structure, Function and Bioinformatics, 2004, 54, 797-800.	1.5	42
81	Building functional modules from molecular interactions. Trends in Biochemical Sciences, 2006, 31, 497-508.	3.7	42
82	Roquin binding to target mRNAs involves a winged helix-turn-helix motif. Nature Communications, 2014, 5, 5701.	5.8	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.	1.6	40
84	Restrained least-squares refinement of the crystal structure of the ribonuclease T1*2'-guanylic acid complex at 1.9 Å 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.	2.0	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.	1.3	39
87	Crystal structures of mutant forms of the <i>Bacillus caldolyticus</i> cold shock protein differing in thermal stability. Journal of Molecular Biology, 2001, 313, 359-369.	2.0	38
88	Crystal Structure of Barley 1,3-β-D-Glucanase at 2.0 Å Resolution and Comparison with <i>Bacillus</i> 1,3-β-D-Glucanase. Journal of Biological Chemistry, 1998, 273, 3438-3446.	1.6	37
89	Crystal structure of human nicotinamide mononucleotide adenylyltransferase in complex with NMN. FEBS Letters, 2002, 516, 239-244.	1.3	36
90	Quantitative interaction mapping reveals an extended UBX domain in ASPL that disrupts functional p97 hexamers. Nature Communications, 2016, 7, 13047.	5.8	35

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91	Cold-Shock Domains' Abundance, Structure, Properties, and Nucleic-Acid Binding. <i>Cancers</i> , 2021, 13, 190.	1.7	35
92	Molecular dynamics simulations of ribonuclease T1: Comparison of the free enzyme and 2' GMP-enzyme complex. <i>Proteins: Structure, Function and Bioinformatics</i> , 1989, 6, 20-31.	1.5	34
93	Salt-dependent and protein-concentration-dependent changes in the solution structure of the DNA-binding histone-like protein, HBSu, from <i>Bacillus subtilis</i> . <i>FEBS Journal</i> , 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. <i>ChemMedChem</i> , 2011, 6, 1411-1422.	1.6	34
95	Structural basis of gene regulation by the Grainyhead/CP2 transcription factor family. <i>Nucleic Acids Research</i> , 2018, 46, 2082-2095.	6.5	34
96	Electrochemical analysis of the self-complementary B-DNA decamer d(CCAGGCCTGG). <i>Bioelectrochemistry</i> , 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. <i>Journal of Molecular Biology</i> , 2006, 361, 22-32.	2.0	33
98	A novel form of RNA double helix based on G'U and C' A ⁺ wobble base pairing. <i>Rna</i> , 2018, 24, 209-218.	1.6	33
99	Crystallographic studies of DNA helix structure. <i>Biophysical Chemistry</i> , 1994, 50, 157-167.	1.5	32
100	High resolution crystal structure of domain I of the <i>Saccharomyces cerevisiae</i> homing endonuclease PI-SceI. <i>Nucleic Acids Research</i> , 2002, 30, 3962-3971.	6.5	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 P450 _{sc} . <i>FEBS Journal</i> , 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. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 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. <i>FEBS Journal</i> , 2010, 277, 1284-1296.	2.2	29
105	Crystal structure of native and a mutant of <i>Lampyris turkestanicus</i> luciferase implicate in bioluminescence color shift. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 2729-2735.	1.1	29
106	Bacteriophage P22 tailspike: structure of the complete protein and function of the interdomain linker. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1336-1345.	2.5	29
107	Repression of Transcriptional Activity of C/EBP β by E2F-Dimerization Partner Complexes. <i>Molecular and Cellular Biology</i> , 2010, 30, 2293-2304.	1.1	28
108	RNase T1 mutant Glu46Gln binds the inhibitors 2'GMP and 2'AMP at the 3' subsite. <i>Journal of Molecular Biology</i> , 1992, 225, 533-542.	2.0	26

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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 BRCA1. Biochemistry, 2004, 43, 15983-15995.	1.2	26
111	X-ray structure of fumarylacetoacetate hydrolase family member Homo sapiens FLJ36880. Biological Chemistry, 2004, 385, 935-942.	1.2	25
112	Unusual Armadillo Fold in the Human General Vesicular Transport Factor p115. PLoS ONE, 2009, 4, e4656.	1.1	25
113	AKAP18:PKA-RiI± structure reveals crucial anchor points for recognition of regulatory subunits of PKA. Biochemical Journal, 2016, 473, 1881-1894.	1.7	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.	1.6	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.	2.0	24
116	Crystal structure of chloromuconate cycloisomerase from Alcaligenes eutrophus JMP134 (pJP4) at 3 Å 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.	1.5	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.	0.7	23
119	Raison d'être and structural model for the B-Z transition of poly d(G-C) — poly d(G-C). FEBS Letters, 1989, 257, 223-227.	1.3	22
120	Ribonuclease T1: Struktur, Funktion und Stabilität. Angewandte Chemie, 1991, 103, 351-369.	1.6	22
121	Sequence specificity of single-stranded DNA-binding proteins: a novel DNA microarray approach. Nucleic Acids Research, 2007, 35, e75.	6.5	22
122	Distinct isocomplexes of the TRAPP trafficking factor coexist inside human cells. FEBS Letters, 2008, 582, 3729-3733.	1.3	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-tRNA ^{fMet} with the C-terminal domain of translational initiation factor IF2 from Bacillus stearothermophilus. FEBS Letters, 2000, 471, 128-132.	1.3	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.	6.5	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.	3.3	21

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127	Role of histidine-40 in ribonuclease T1 catalysis: three-dimensional structures of the partially active His40Lys mutant. <i>Biochemistry</i> , 1992, 31, 11317-11325.	1.2	20
128	Optimized Variants of the Cold Shock Protein from in Vitro Selection: Structural Basis of Their High Thermostability. <i>Journal of Molecular Biology</i> , 2007, 369, 1087-1097.	2.0	20
129	Armadillo Motifs Involved in Vesicular Transport. <i>PLoS ONE</i> , 2010, 5, e8991.	1.1	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. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 14266-14282.	2.9	20
131	Optimization of the G $\hat{1}$ 21 Domain by Computational Design and by in Vitro Evolution: Structural and Energetic Basis of Stabilization. <i>Journal of Molecular Biology</i> , 2007, 373, 775-784.	2.0	19
132	Structural and functional studies of ribonuclease T1. , 1989, , 111-141.		19
133	DNA-binding properties and primary structure of HB protein from <i>Bacillus globigii</i> . <i>FEBS Journal</i> , 1987, 165, 547-552.	0.2	18
134	Disorder and twin refinement of RNA heptamer double helices. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 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. <i>Glycobiology</i> , 2013, 23, 59-68.	1.3	18
136	An essential serotype recognition pocket on phage P22 tailspike protein forces <i>Salmonella enterica</i> serovar Paratyphi A O-antigen fragments to bind as nonsolution conformers. <i>Glycobiology</i> , 2013, 23, 486-494.	1.3	18
137	X-ray analysis of cubic crystals of the complex formed between ribonuclease T1 and guanosine-3',5'-bisphosphate. <i>Acta Crystallographica Section B: Structural Science</i> , 1991, 47, 521-527.	1.8	17
138	His92Ala mutation in ribonuclease T1 induces segmental flexibility. <i>Journal of Molecular Biology</i> , 1992, 224, 701-713.	2.0	17
139	DNA helix structure and refinement algorithm: comparison of models for d(CCAGGCm5CTGG) derived from NUCLSQ, TNT and X-PLOR. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1993, 49, 468-477.	2.5	17
140	High-resolution Crystal Structures of <i>Caldicellulosiruptor</i> Strain Rt8B.4 Carbohydrate-binding Module CBM27-1 and its Complex with Mannoheptaose. <i>Journal of Molecular Biology</i> , 2004, 340, 543-554.	2.0	17
141	Bacteriophage Tailspikes and Bacterial O-Antigens as a Model System to Study Weak-Affinity Protein-Polysaccharide Interactions. <i>Journal of the American Chemical Society</i> , 2016, 138, 9109-9118.	6.6	17
142	Dimer Formation of a Stabilized G $\hat{1}$ 21 Variant: A Structural and Energetic Analysis. <i>Journal of Molecular Biology</i> , 2009, 391, 918-932.	2.0	16
143	Identification of a Novel Benzimidazole Pyrazolone Scaffold That Inhibits KDM4 Lysine Demethylases and Reduces Proliferation of Prostate Cancer Cells. <i>SLAS Discovery</i> , 2017, 22, 801-812.	1.4	16
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