

Udo Heinemann

List of Publications by Year in descending order

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246
papers

11,905
citations

26567

56
h-index

32761

100
g-index

257
all docs

257
docs citations

257
times ranked

12213
citing authors

#	ARTICLE	IF	CITATIONS
1	An Integrated Pharmacological, Structural, and Genetic Analysis of Extracellular Versus Intracellular ROS Production in Neutrophils. <i>Journal of Molecular Biology</i> , 2022, 434, 167533.	2.0	2
2	Cold-Shock Domains' Abundance, Structure, Properties, and Nucleic-Acid Binding. <i>Cancers</i> , 2021, 13, 190.	1.7	35
3	PIN and CCCH Zn-finger domains coordinate RNA targeting in ZC3H12 family endoribonucleases. <i>Nucleic Acids Research</i> , 2021, 49, 5369-5381.	6.5	9
4	Small-molecule inhibitors of the PDZ domain of Dishevelled proteins interrupt Wnt signalling. <i>Magnetic Resonance</i> , 2021, 2, 355-374.	0.8	5
5	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
6	<i>Pantoea stewartii</i> WceF is a glycan biofilm-modifying enzyme with a bacteriophage tailspike-like fold. <i>Journal of Biological Chemistry</i> , 2021, 296, 100286.	1.6	5
7	Technologies for profiling the impact of genomic variants on transcription factor binding. <i>Medizinische Genetik</i> , 2021, 33, 147-155.	0.1	1
8	Structure of the active GGEEF domain of a diguanylate cyclase from <i>Vibrio cholerae</i> . <i>Biochemical and Biophysical Research Communications</i> , 2020, 523, 287-292.	1.0	2
9	From Pyrazolones to Azaindoles: Evolution of Active-Site SHP2 Inhibitors Based on Scaffold Hopping and Bioisosteric Replacement. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 14780-14804.	2.9	16
10	Crystal structure of Q4D6Q6, a conserved kinetoplastid-specific protein from <i>Trypanosoma cruzi</i> . <i>Journal of Structural Biology</i> , 2020, 211, 107536.	1.3	2
11	Symmetry in Nucleic-Acid Double Helices. <i>Symmetry</i> , 2020, 12, 737.	1.1	15
12	Designed nanomolar small-molecule inhibitors of Ena/VASP EVH1 interaction impair invasion and extravasation of breast cancer cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 29684-29690.	3.3	21
13	Common Mode of Remodeling AAA ATPases p97/CDC48 by Their Disassembling Cofactors ASPL/PUX1. <i>Structure</i> , 2019, 27, 1830-1841.e3.	1.6	13
14	Structure-Based Screening of Tetrazolyhydrazide Inhibitors versus KDM4 Histone Demethylases. <i>ChemMedChem</i> , 2019, 14, 1828-1839.	1.6	11
15	Time-resolved DNA release from an O-antigen-specific <i>Salmonella</i> bacteriophage with a contractile tail. <i>Journal of Biological Chemistry</i> , 2019, 294, 11751-11761.	1.6	25
16	Structural Features of Tight-Junction Proteins. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6020.	1.8	98
17	Structural basis of gene regulation by the Grainyhead/CP2 transcription factor family. <i>Nucleic Acids Research</i> , 2018, 46, 2082-2095.	6.5	34
18	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

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19	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
20	Solvent Networks Tune Thermodynamics of Oligosaccharide Complex Formation in an Extended Protein Binding Site. <i>Journal of the American Chemical Society</i> , 2018, 140, 10447-10455.	6.6	11
21	Crystal Structures of the Single PDZ Domains from GRASP65 and their Interaction with the Golgin GM130. <i>Croatica Chemica Acta</i> , 2018, 91, .	0.1	4
22	Structural insight into protein-aided bacterial biofilm formation. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, e206-e206.	0.0	0
23	Structural basis of ASPL-mediated regulation of p97 methylation by METTL21D. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, e199-e200.	0.0	0
24	Internal Dynamics of the 3-Pyrroline-N-Oxide Ring in Spin-Labeled Proteins. <i>Journal of Physical Chemistry Letters</i> , 2017, 8, 1113-1117.	2.1	2
25	Tricellulin is a target of the ubiquitin ligase Itch. <i>Annals of the New York Academy of Sciences</i> , 2017, 1397, 157-168.	1.8	10
26	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
27	Combining EPR spectroscopy and X-ray crystallography to elucidate the structure and dynamics of conformationally constrained spin labels in T4 lysozyme single crystals. <i>Physical Chemistry Chemical Physics</i> , 2017, 19, 20723-20734.	1.3	5
28	Crystal structure of the tricellulin C-terminal coiled-coil domain reveals a unique mode of dimerization. <i>Annals of the New York Academy of Sciences</i> , 2017, 1405, 147-159.	1.8	9
29	Immune response regulation by paralogous endoribonucleases: ZC3H12C and N4BP1. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C452-C452.	0.0	0
30	Structural insight into protein-aided bacterial biofilm formation. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C391-C391.	0.0	0
31	Parsimonious DNA target-site recognition by Grh/CP2 transcription factors. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C298-C298.	0.0	0
32	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
33	Functional interaction of CCAAT/enhancer-binding-protein basic region mutants with E2F transcription factors and DNA. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 841-847.	0.9	1
34	XDSAPP2.0. <i>Journal of Applied Crystallography</i> , 2016, 49, 1085-1092.	1.9	219
35	Tracking Transient Conformational States of T4 Lysozyme at Room Temperature Combining X-ray Crystallography and Site-Directed Spin Labeling. <i>Journal of the American Chemical Society</i> , 2016, 138, 12868-12875.	6.6	13
36	Quantitative interaction mapping reveals an extended UBX domain in ASPL that disrupts functional p97 hexamers. <i>Nature Communications</i> , 2016, 7, 13047.	5.8	35

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37	AKAP18:PKA-RiI± structure reveals crucial anchor points for recognition of regulatory subunits of PKA. <i>Biochemical Journal</i> , 2016, 473, 1881-1894.	1.7	25
38	MCPIP3 (ZC3H12C) regulates the innate immune response by acting as a ribonuclease. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2016, 72, s249-s249.	0.0	0
39	Klf4 and Grhl1: two distinct ways of achieving DNA target site recognition. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2016, 72, s216-s216.	0.0	0
40	The automated expert processing system XDSAPP. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2016, 72, s191-s191.	0.0	2
41	Structural and biochemical insights into grainyhead-like 1 and its homolog grainyhead-like 3. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2015, 71, s243-s243.	0.0	0
42	Structural investigation of the small GTPase ARL4D. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2015, 71, s221-s221.	0.0	0
43	Translational regulation of gene expression by Lin28 and Roquin. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2015, 71, s29-s30.	0.0	0
44	Selective Inhibitors of the Protein Tyrosine Phosphatase SHP2 Block Cellular Motility and Growth of Cancer Cells inâ€...vitro and inâ€...vivo. <i>ChemMedChem</i> , 2015, 10, 815-826.	1.6	65
45	RC3H1 post-transcriptionally regulates A20 mRNA and modulates the activity of the IKK/NF-Î± pathway. <i>Nature Communications</i> , 2015, 6, 7367.	5.8	99
46	Roquin binding to target mRNAs involves a winged helix-turn-helix motif. <i>Nature Communications</i> , 2014, 5, 5701.	5.8	41
47	Structural Identification of the Vps18 Î±-Propeller Reveals a Critical Role in the HOPS Complex Stability and Function. <i>Journal of Biological Chemistry</i> , 2014, 289, 33503-33512.	1.6	13
48	Crystal structure of the yeast <sc>TRAPP</sc>-associated protein Tca17. <i>FEBS Journal</i> , 2014, 281, 4195-4206.	2.2	11
49	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
50	Enthalpic cost of water removal from a glucose binding cavity on HK620 TSP. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2014, 70, C1600-C1600.	0.0	0
51	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
52	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
53	Identification of LIN28B-bound mRNAs reveals features of target recognition and regulation. <i>RNA Biology</i> , 2013, 10, 1146-1159.	1.5	76
54	COLD-SHOCK DOMAINS â€“ VERSATILE MOLECULAR MODULES FOR SINGLE-STRANDED RNA BINDING AND REMODELING. , 2013, , 220-229.		0

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55	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
56	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
57	Structural studies of proteins involved in ER-associated protein degradation. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, s57-s57.	0.3	0
58	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
59	The SNF2-like helicase HELLS mediates E2F3-dependent transcription and cellular transformation. <i>EMBO Journal</i> , 2012, 31, 972-985.	3.5	68
60	The Lin28 cold-shock domain remodels pre-let-7 microRNA. <i>Nucleic Acids Research</i> , 2012, 40, 7492-7506.	6.5	80
61	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
62	Peptide Linkage to the β -Subunit of MHCII Creates a Stably Inverted Antigen Presentation Complex. <i>Journal of Molecular Biology</i> , 2012, 423, 294-302.	2.0	14
63	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. <i>Journal of Biological Chemistry</i> , 2012, 287, 8633-8640.	1.6	13
64	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
65	Flipped CLIP orientation in the MHC class II binding groove. <i>Molecular Immunology</i> , 2012, 51, 14.	1.0	0
66	XDSAPP: a graphical user interface for the convenient processing of diffraction data using XDS. <i>Journal of Applied Crystallography</i> , 2012, 45, 568-572.	1.9	260
67	Expression of protein complexes using multiple <i>Escherichia coli</i> protein co-expression systems: A benchmarking study. <i>Journal of Structural Biology</i> , 2011, 175, 159-170.	1.3	39
68	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
69	PAN-modular structure of microneme protein SML-2 from the parasite <i>Sarcocystis muris</i> at 1.95 Å resolution and its complex with 1-thio- β -D-galactose. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 936-944.	2.5	9
70	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
71	Structural and thermodynamic characterization of the adrenodoxin-like domain of the electron-transfer protein Etp1 from <i>Schizosaccharomyces pombe</i> . <i>Journal of Inorganic Biochemistry</i> , 2011, 105, 957-965.	1.5	11
72	Characterization of the self-palmitoylation activity of the transport protein particle component Bet3. <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 2653-2664.	2.4	8

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73	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.	2.2	29
74	Armadillo Motifs Involved in Vesicular Transport. PLoS ONE, 2010, 5, e8991.	1.1	20
75	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.	3.3	67
76	The Coxsackievirus Adenovirus Receptor Reveals Complex Homophilic and Heterophilic Interactions on Neural Cells. Journal of Neuroscience, 2010, 30, 2897-2910.	1.7	60
77	Repression of Transcriptional Activity of C/EBP β by E2F-Dimerization Partner Complexes. Molecular and Cellular Biology, 2010, 30, 2293-2304.	1.1	28
78	PSPF - a protein sample production facility for structural biologists. Acta Crystallographica Section A: Foundations and Advances, 2010, 66, s120-s121.	0.3	0
79	Self-association of quality control components in the ER. Acta Crystallographica Section A: Foundations and Advances, 2010, 66, s26-s26.	0.3	0
80	Unusual Armadillo Fold in the Human General Vesicular Transport Factor p115. PLoS ONE, 2009, 4, e4656.	1.1	25
81	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
82	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
83	Purification and preliminary X-ray crystallographic studies of β 2-microseminoprotein from human seminal plasma. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 518-521.	0.7	3
84	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.	1.5	14
85	Dimer Formation of a Stabilized G β 21 Variant: A Structural and Energetic Analysis. Journal of Molecular Biology, 2009, 391, 918-932.	2.0	16
86	Usa1 Functions as a Scaffold of the HRD-Ubiquitin Ligase. Molecular Cell, 2009, 36, 782-793.	4.5	114
87	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
88	Structural and functional characterization of human Iba proteins. FEBS Journal, 2008, 275, 4627-4640.	2.2	15
89	Protein production and purification. Nature Methods, 2008, 5, 135-146.	9.0	763
90	Crystal structure of <i>Escherichia coli</i> phage HK620 tailspike: podoviral tailspike endoglycosidase modules are evolutionarily related. Molecular Microbiology, 2008, 69, 303-316.	1.2	121

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91	Distinct isocomplexes of the TRAPP trafficking factor coexist inside human cells. FEBS Letters, 2008, 582, 3729-3733.	1.3	22
92	An Intersubunit Active Site between Supercoiled Parallel \hat{I}^2 Helices in the Trimeric Tailspike Endorhamnosidase of Shigella flexneri Phage Sf6. Structure, 2008, 16, 766-775.	1.6	83
93	An approach to quality management in structural biology: Biophysical selection of proteins for successful crystallization. Journal of Structural Biology, 2008, 162, 451-459.	1.3	14
94	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
95	Structural Genomics and Structural Proteomics: A Global Perspective. , 2008, , 505-537.		0
96	MolekÃ¼lmodelle und ModellmolekÃ¼le: Strukturanalyse groÃŸer biologischer MolekÃ¼le fÃ¼r die Medizin. , 2008, , 275-294.		0
97	Sequence specificity of single-stranded DNA-binding proteins: a novel DNA microarray approach. Nucleic Acids Research, 2007, 35, e75.	6.5	22
98	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.	2.0	20
99	Optimization of the G \hat{I}^2 1 Domain by Computational Design and by in Vitro Evolution: Structural and Energetic Basis of Stabilization. Journal of Molecular Biology, 2007, 373, 775-784.	2.0	19
100	Vectors for co-expression of an unrestricted number of proteins. Nucleic Acids Research, 2007, 35, e43-e43.	6.5	177
101	An idea whose time has come. Genome Biology, 2007, 8, 408.	13.9	6
102	Common mode of DNA binding to cold shock domains. FEBS Journal, 2007, 274, 1265-1279.	2.2	46
103	Light-Induced Reduction of Bovine Adrenodoxin via the Covalently Bound Ruthenium(II) Bipyridyl Complex:Ã Intra-molecular Electron Transfer and Crystal Structureâ€. Biochemistry, 2006, 45, 709-718.	1.2	8
104	Structural Basis for the Substrate Specificity of a Bacillus 1,3-1,4- \hat{I}^2 -Glucanase. Journal of Molecular Biology, 2006, 357, 1211-1225.	2.0	56
105	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.	2.0	64
106	Structure of the Bet3Ã“Tpc6B Core of TRAPP: Two Tpc6 Paralogs Form Trimeric Complexes with Bet3 and Mum2. Journal of Molecular Biology, 2006, 361, 22-32.	2.0	33
107	Low-resolution ab initio phasing of Sarcocystis muris lectin SML-2. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 533-540.	2.5	2
108	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

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109	Eukaryotic expression: developments for structural proteomics. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1114-1124.	2.5	79
110	Crystal structure of Homo sapiens PTDO12 reveals a zinc-containing hydrolase fold. <i>Protein Science</i> , 2006, 15, 914-920.	3.1	7
111	Building functional modules from molecular interactions. <i>Trends in Biochemical Sciences</i> , 2006, 31, 497-508.	3.7	42
112	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
113	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
114	Structure of palmitoylated BET3: insights into TRAPP complex assembly and membrane localization. <i>EMBO Journal</i> , 2005, 24, 875-884.	3.5	57
115	The structure of the TRAPP subunit TPC6 suggests a model for a TRAPP subcomplex. <i>EMBO Reports</i> , 2005, 6, 787-793.	2.0	39
116	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
117	X-ray structure of engineered human Aortic Preferentially Expressed Protein-1 (APEG-1). <i>BMC Structural Biology</i> , 2005, 5, 21.	2.3	8
118	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. <i>Biochemical and Biophysical Research Communications</i> , 2005, 338, 491-498.	1.0	14
119	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
120	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
121	Letter to the Editor: ^1H , ^{13}C and ^{15}N resonance assignments of the C-terminal BRCT domain from human BRCA1. <i>Journal of Biomolecular NMR</i> , 2004, 30, 221-222.	1.6	1
122	X-ray structure of human gankyrin, the product of a gene linked to hepatocellular carcinoma. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 214-217.	1.5	24
123	Crystal structure of Homo sapiens protein hp14.5. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 54, 797-800.	1.5	42
124	Structure of circularly permuted DsbAQ100T99: preserved global fold and local structural adjustments. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 304-309.	2.5	6
125	Single-stranded DNA bound to bacterial cold-shock proteins: preliminary crystallographic and Raman analysis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 755-757.	2.5	8
126	Solution Structure, Backbone Dynamics, and Association Behavior of the C-Terminal BRCT Domain from the Breast Cancer-Associated Protein BRCA1. <i>Biochemistry</i> , 2004, 43, 15983-15995.	1.2	26

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127	X-ray structure of fumarylacetoacetate hydrolase family member Homo sapiens FLJ36880. <i>Biological Chemistry</i> , 2004, 385, 935-942.	1.2	25
128	High-resolution Crystal Structures of Caldicellulosiruptor 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
129	Secure web book to store structural genomics research data. <i>Journal of Structural and Functional Genomics</i> , 2003, 4, 121-127.	1.2	1
130	Rapid purification and crystal structure analysis of a small protein carrying two terminal affinity tags. <i>Journal of Structural and Functional Genomics</i> , 2003, 4, 217-225.	1.2	6
131	Facilities and Methods for the High-Throughput Crystal Structural Analysis of Human Proteins. <i>ChemInform</i> , 2003, 34, no.	0.1	1
132	RP4 Repressor Protein KorB Binds to the Major Groove of the Operator DNA: A Raman Study. <i>Biochemistry</i> , 2003, 42, 14476-14482.	1.2	12
133	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
134	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
135	Molekülmolelle und Modellmoleküle: Strukturanalyse großer biologischer Moleküle für die Medizin. , 2003, , 340-359.		0
136	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
137	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
138	Linking Structural Biology With Genome Research. , 2002, , 179-189.		1
139	An Src Homology 3-like Domain Is Responsible for Dimerization of the Repressor Protein KorB Encoded by the Promiscuous IncP Plasmid RP4. <i>Journal of Biological Chemistry</i> , 2002, 277, 4191-4198.	1.6	40
140	Crystal structure of human nicotinamide mononucleotide adenylyltransferase in complex with NMN. <i>FEBS Letters</i> , 2002, 516, 239-244.	1.3	36
141	Corrigendum to: Crystal structure of human nicotinamide mononucleotide adenylyltransferase in complex with NMN (FEBS 25964). <i>FEBS Letters</i> , 2002, 523, 254-255.	1.3	0
142	Establishing a structural genomics platform: The Berlin-based Protein Structure Factory. <i>Gene Function & Disease</i> , 2002, 3, 25-32.	0.3	6
143	Crystallization and preliminary X-ray analysis of human nicotinamide mononucleotide adenylyltransferase (NMNAT). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 140-142.	2.5	2
144	Modeling of electrostatic recognition processes in the mammalian mitochondrial steroid hydroxylase system. <i>Biophysical Chemistry</i> , 2002, 100, 281-292.	1.5	10

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