

# Rolf Boelens

## List of Publications by Year in descending order

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243  
papers

15,121  
citations

22099

59  
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22764

112  
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272  
all docs

272  
docs citations

272  
times ranked

16907  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural anomalies in a published NMR-derived structure of IRAK-M. <i>Journal of Molecular Graphics and Modelling</i> , 2022, 111, 108061.	1.3	1
2	Introduction to a special issue of <i>Magnetic Resonance</i> ; in honour of Robert Kaptein at the occasion of his 80th birthday. <i>Magnetic Resonance</i> , 2021, 2, 465-474.	0.8	0
3	HERMES – A Software Tool for the Prediction and Analysis of Magnetic-Induced Residual Dipolar Couplings in Nucleic Acids. <i>ChemPlusChem</i> , 2020, 85, 2177-2185.	1.3	0
4	Diubiquitin-Based NMR Analysis: Interactions Between Lys6-Linked diUb and UBA Domain of UBXN1. <i>Frontiers in Chemistry</i> , 2019, 7, 921.	1.8	3
5	Function and Interactions of ERCC1-XPF in DNA Damage Response. <i>Molecules</i> , 2018, 23, 3205.	1.7	59
6	Disordered Peptides Looking for Their Native Environment: Structural Basis of CB1 Endocannabinoid Receptor Binding to Peptides. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 100.	1.6	11
7	iNEXT: a European facility network to stimulate translational structural biology. <i>FEBS Letters</i> , 2018, 592, 1909-1917.	1.3	4
8	Identification of a diagnostic structural motif reveals a new reaction intermediate and condensation pathway in kraft lignin formation. <i>Chemical Science</i> , 2018, 9, 6348-6360.	3.7	143
9	DNA repair factor APLF acts as a H2A-H2B histone chaperone through binding its DNA interaction surface. <i>Nucleic Acids Research</i> , 2018, 46, 7138-7152.	6.5	36
10	Single-stranded DNA Binding by the Helix-Hairpin-Helix Domain of XPF Protein Contributes to the Substrate Specificity of the ERCC1-XPF Protein Complex. <i>Journal of Biological Chemistry</i> , 2017, 292, 2842-2853.	1.6	13
11	VirB7 and VirB9 Interactions Are Required for the Assembly and Antibacterial Activity of a Type IV Secretion System. <i>Structure</i> , 2016, 24, 1707-1718.	1.6	14
12	A model for the interaction of the G3 subdomain of <i>Geobacillus stearothermophilus</i> IF2 with the 30S ribosomal subunit. <i>Protein Science</i> , 2016, 25, 1722-1733.	3.1	3
13	Impact of nucleic acid self-alignment in a strong magnetic field on the interpretation of indirect spin-spin interactions. <i>Journal of Biomolecular NMR</i> , 2016, 64, 53-62.	1.6	6
14	Molecular Basis of the Receptor Interactions of Polysialic Acid (polySia), polySia Mimetics, and Sulfated Polysaccharides. <i>ChemMedChem</i> , 2016, 11, 990-1002.	1.6	11
15	New insights into the structure and composition of technical lignins: a comparative characterisation study. <i>Green Chemistry</i> , 2016, 18, 2651-2665.	4.6	648
16	Axin cancer mutants form nanoaggregates to rewire the Wnt signaling network. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 324-332.	3.6	31
17	Conformational Plasticity of the POTRA 5 Domain in the Outer Membrane Protein Assembly Factor BamA. <i>Structure</i> , 2015, 23, 1317-1324.	1.6	25
18	Insight into the conformational stability of membrane-embedded BamA using a combined solution and solid-state NMR approach. <i>Journal of Biomolecular NMR</i> , 2015, 61, 321-332.	1.6	19

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19	<i>E. coli</i> MG1655 modulates its phospholipid composition through the cell cycle. <i>FEBS Letters</i> , 2015, 589, 2726-2730.	1.3	28
20	Estrogen Receptor Folding Modulates cSrc Kinase SH2 Interaction via a Helical Binding Mode. <i>ACS Chemical Biology</i> , 2015, 10, 2624-2632.	1.6	6
21	The Cerebro-oculo-facio-skeletal Syndrome Point Mutation F231L in the ERCC1 DNA Repair Protein Causes Dissociation of the ERCC1-XPF Complex. <i>Journal of Biological Chemistry</i> , 2015, 290, 20541-20555.	1.6	14
22	Block Copolymer Micelles with an Intermediate Star-Flower-Like Structure Studied by <sup>1</sup> H NMR Relaxometry. <i>Macromolecular Chemistry and Physics</i> , 2014, 215, 915-919.	1.1	7
23	Structure, stability, and IgE binding of the peach allergen <i>P</i> eamaclein (Pru p 7). <i>Biopolymers</i> , 2014, 102, 416-425.	1.2	43
24	The basic helix-loop-helix region of the transcriptional repressor hairy and enhancer of split 1 is preorganized to bind DNA. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 537-545.	1.5	4
25	Structural basis of nucleic acid binding by <i>Nicotiana tabacum</i> glycine-rich RNA-binding protein: implications for its RNA chaperone function. <i>Nucleic Acids Research</i> , 2014, 42, 8705-8718.	6.5	19
26	Proteins Feel More Than They See: Fine-Tuning of Binding Affinity by Properties of the Non-Interacting Surface. <i>Journal of Molecular Biology</i> , 2014, 426, 2632-2652.	2.0	103
27	Mechanism of <i>D</i> domain swapping in bovine seminal ribonuclease. <i>FEBS Journal</i> , 2014, 281, 842-850.	2.2	7
28	Hsp90-Tau Complex Reveals Molecular Basis for Specificity in Chaperone Action. <i>Cell</i> , 2014, 156, 963-974.	13.5	269
29	A Natural Product Switch for a Dynamic Protein Interface. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 6443-6448.	7.2	32
30	Binding Hotspots of BAZ2B Bromodomain: Histone Interaction Revealed by Solution NMR Driven Docking. <i>Biochemistry</i> , 2014, 53, 6706-6716.	1.2	23
31	Absolute MR thermometry using nanocarriers. <i>Contrast Media and Molecular Imaging</i> , 2014, 9, 283-290.	0.4	4
32	Protein Plasticity and Protein-Lipid Interactions of the Beta-Barrel Assembly Machinery. <i>Biophysical Journal</i> , 2014, 106, 47a.	0.2	0
33	Nucleosomal DNA binding drives the recognition of H3K36-methylated nucleosomes by the PSIP1-PWWP domain. <i>Epigenetics and Chromatin</i> , 2013, 6, 12.	1.8	141
34	A NMR guided approach for CsrA RNA crystallization. <i>Journal of Biomolecular NMR</i> , 2013, 56, 31-39.	1.6	2
35	Sliding and target location of DNA-binding proteins: an NMR view of the lac repressor system. <i>Journal of Biomolecular NMR</i> , 2013, 56, 41-49.	1.6	10
36	<sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N resonance assignments of wild-type <i>Bacillus subtilis</i> Lipase A and its mutant evolved towards thermostability. <i>Biomolecular NMR Assignments</i> , 2013, 7, 249-252.	0.4	5

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37	Influence of the O-phosphorylation of serine, threonine and tyrosine in proteins on the amidic <sup>15</sup> N chemical shielding anisotropy tensors. <i>Journal of Biomolecular NMR</i> , 2013, 55, 59-70.	1.6	2
38	Redox-Dependent Control of FOXO/DAF-16 by Transportin-1. <i>Molecular Cell</i> , 2013, 49, 730-742.	4.5	138
39	Structure of the O-glycosylated Conopeptide CcTx from <i>Conus consors</i> Venom. <i>Chemistry - A European Journal</i> , 2013, 19, 870-879.	1.7	21
40	Dynamic Readers for 5-(Hydroxy)Methylcytosine and Its Oxidized Derivatives. <i>Cell</i> , 2013, 152, 1146-1159.	13.5	888
41	Identification, structural and pharmacological characterization of $\tilde{I}_1$ -CnVA, a conopeptide that selectively interacts with somatostatin sst3 receptor. <i>Biochemical Pharmacology</i> , 2013, 85, 1663-1671.	2.0	34
42	$\tilde{I}_2$ TrCP interacts with the ubiquitin-dependent endocytosis motif of the GH receptor in an unconventional manner. <i>Biochemical Journal</i> , 2013, 453, 291-301.	1.7	6
43	The Fanconi anemia associated protein FAAP24 uses two substrate specific binding surfaces for DNA recognition. <i>Nucleic Acids Research</i> , 2013, 41, 6739-6749.	6.5	4
44	Some notes on fatal acquired multiple acyl-CoA dehydrogenase deficiency (MADD) in a two-year-old warmblood stallion and European tar spot ( <i>Rhytisma acerinum</i> ). <i>Veterinary Quarterly</i> , 2013, 33, 47-51.	3.0	3
45	Glycosylation of Conotoxins. <i>Marine Drugs</i> , 2013, 11, 623-642.	2.2	25
46	3D DOSY-TROSY to determine the translational diffusion coefficient of large protein complexes. <i>Protein Engineering, Design and Selection</i> , 2012, 25, 319-319.	1.0	1
47	Structural Dynamics of Bacterial Translation Initiation Factor IF2. <i>Journal of Biological Chemistry</i> , 2012, 287, 10922-10932.	1.6	24
48	WeNMR: Structural Biology on the Grid. <i>Journal of Grid Computing</i> , 2012, 10, 743-767.	2.5	170
49	Binding of Hydrogen-Citrate to Photoactive Yellow Protein Is Affected by the Structural Changes Related to Signaling State Formation. <i>Journal of Physical Chemistry B</i> , 2012, 116, 13172-13182.	1.2	2
50	A novel $\tilde{I}_1$ -conopeptide, CnIIIC, exerts potent and preferential inhibition of Na <sup>v</sup> 1.2/1.4 channels and blocks neuronal nicotinic acetylcholine receptors. <i>British Journal of Pharmacology</i> , 2012, 166, 1654-1668.	2.7	55
51	Sulforaphane inhibits pancreatic cancer through disrupting Hsp90-p50Cdc37 complex and direct interactions with amino acids residues of Hsp90. <i>Journal of Nutritional Biochemistry</i> , 2012, 23, 1617-1626.	1.9	49
52	In support of the BMRB. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 854-860.	3.6	6
53	NMR Studies on Structure and Dynamics of the Monomeric Derivative of BS-RNase: New Insights for 3D Domain Swapping. <i>PLoS ONE</i> , 2012, 7, e29076.	1.1	13
54	Biophysical characterization of mutants of <i>Bacillus subtilis</i> lipase evolved for thermostability: Factors contributing to increased activity retention. <i>Protein Science</i> , 2012, 21, 487-497.	3.1	49

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55	Molecular Organization of Various Collagen Fragments as Revealed by Atomic Force Microscopy and Diffusion-Ordered NMR Spectroscopy. <i>ChemPhysChem</i> , 2012, 13, 3117-3125.	1.0	16
56	The Structure of the XPF-ssDNA Complex Underscores the Distinct Roles of the XPF and ERCC1 Helix-Hairpin-Helix Domains in ss/ds DNA Recognition. <i>Structure</i> , 2012, 20, 667-675.	1.6	28
57	Temperature dependence of the magnetic volume susceptibility of human breast fat tissue: an NMR study. <i>Magnetic Resonance Materials in Physics, Biology, and Medicine</i> , 2012, 25, 33-39.	1.1	24
58	N-terminal domain of human Hsp90 triggers binding to the cochaperone p23. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 580-585.	3.3	109
59	Structural insights into transcription complexes. <i>Journal of Structural Biology</i> , 2011, 175, 135-146.	1.3	14
60	Critical Scaffolding Regions of the Tumor Suppressor Axin1 Are Natively Unfolded. <i>Journal of Molecular Biology</i> , 2011, 405, 773-786.	2.0	58
61	Symmetry and Asymmetry of the RING-RING Dimer of Rad18. <i>Journal of Molecular Biology</i> , 2011, 410, 424-435.	2.0	41
62	Cys-Ph-TAHA: a lanthanide binding tag for RDC and PCS enhanced protein NMR. <i>Journal of Biomolecular NMR</i> , 2011, 51, 329-337.	1.6	43
63	NMR resonance assignments of NarE, a putative ADP-ribosylating toxin from <i>Neisseria meningitidis</i> . <i>Biomolecular NMR Assignments</i> , 2011, 5, 35-38.	0.4	5
64	<sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N assignment of the GNA1946 outer membrane lipoprotein from <i>Neisseria meningitidis</i> . <i>Biomolecular NMR Assignments</i> , 2011, 5, 135-138.	0.4	4
65	Quantitative use of chemical shifts for the modeling of protein complexes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2662-2670.	1.5	20
66	E3 ligase Rad18 promotes monoubiquitination rather than ubiquitin chain formation by E2 enzyme Rad6. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5590-5595.	3.3	104
67	Structural and Biochemical Characterization of NarE, an Iron-containing ADP-ribosyltransferase from <i>Neisseria meningitidis</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 14842-14851.	1.6	16
68	3D DOSY-TROSY to determine the translational diffusion coefficient of large protein complexes. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 99-103.	1.0	25
69	Crystal structure and collagen-binding site of immune inhibitory receptor LAIR-1: unexpected implications for collagen binding by platelet receptor GPVI. <i>Blood</i> , 2010, 115, 1364-1373.	0.6	62
70	SAMPLEX: Automatic mapping of perturbed and unperturbed regions of proteins and complexes. <i>BMC Bioinformatics</i> , 2010, 11, 51.	1.2	24
71	<i>parD</i> toxin-antitoxin system of plasmid R1 – basic contributions, biotechnological applications and relationships with closely related toxin-antitoxin systems. <i>FEBS Journal</i> , 2010, 277, 3097-3117.	2.2	32
72	NMR characterization of foldedness for the production of E3 RING domains. <i>Journal of Structural Biology</i> , 2010, 172, 120-127.	1.3	5

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73	Protein interactions regulate ubiquitin and SUMO conjugation. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2010, 66, s2-s2.	0.3	0
74	Sequence-specific Recognition of DNA by the C-terminal Domain of Nucleoid-associated Protein H-NS. <i>Journal of Biological Chemistry</i> , 2009, 284, 30453-30462.	1.6	34
75	A comprehensive framework of E2â€“RING E3 interactions of the human ubiquitinâ€“proteasome system. <i>Molecular Systems Biology</i> , 2009, 5, 295.	3.2	126
76	A comprehensive framework of E2â€“RING E3 interactions of the human ubiquitinâ€“proteasome system. <i>Molecular Systems Biology</i> , 2009, 5, .	3.2	21
77	MINOES: A new approach to select a representative ensemble of structures in NMR studies of (partially) unfolded states. Application to Î”25â€“PYP. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 895-904.	1.5	13
78	A mutagenic analysis of the RNase mechanism of the bacterial Kid toxin by mass spectrometry. <i>FEBS Journal</i> , 2009, 276, 4973-4986.	2.2	13
79	Novel strategies to overcome expression problems encountered with toxic proteins: Application to the production of Lac repressor proteins for NMR studies. <i>Protein Expression and Purification</i> , 2009, 67, 104-112.	0.6	9
80	E2â€“c-Cbl Recognition Is Necessary but not Sufficient for Ubiquitination Activity. <i>Journal of Molecular Biology</i> , 2009, 385, 507-519.	2.0	37
81	Specificity and Affinity of Lac Repressor for the Auxiliary Operators O2 and O3 Are Explained by the Structures of Their Proteinâ€“DNA Complexes. <i>Journal of Molecular Biology</i> , 2009, 390, 478-489.	2.0	46
82	The HhH domain of the human DNA repair protein XPF forms stable homodimers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 1551-1563.	1.5	19
83	High-level expression of biologically active glycoprotein hormones in <i>Pichia pastoris</i> strainsâ€“selection of strain GS115, and not X-33, for the production of biologically active N-glycosylated 15N-labeled phCG. <i>Glycoconjugate Journal</i> , 2008, 25, 245-257.	1.4	28
84	Structural Insight into the Recognition of the H3K4me3 Mark by the TFIID Subunit TAF3. <i>Structure</i> , 2008, 16, 1245-1256.	1.6	123
85	The Structural Basis of the Difference in Sensitivity for PNGase F in the De-N-glycosylation of the Native Bovine Pancreatic Ribonucleases B and BS. <i>Biochemistry</i> , 2008, 47, 3435-3446.	1.2	18
86	The Solution Structure of DNA-free Pax-8 Paired Box Domain Accounts for Redox Regulation of Transcriptional Activity in the Pax Protein Family. <i>Journal of Biological Chemistry</i> , 2008, 283, 33321-33328.	1.6	21
87	Structural Dynamics in the Activation of Epac. <i>Journal of Biological Chemistry</i> , 2008, 283, 6501-6508.	1.6	29
88	Structure and Function of Bacterial Kid-Kis and Related Toxin-Antitoxin Systems. <i>Protein and Peptide Letters</i> , 2007, 14, 113-124.	0.4	31
89	Analysis of the XPA and ssDNA-binding surfaces on the central domain of human ERCC1 reveals evidence for subfunctionalization. <i>Nucleic Acids Research</i> , 2007, 35, 5789-5798.	6.5	39
90	Interactions of Kidâ€“Kis toxinâ€“antitoxin complexes with the parD operator-promoter region of plasmid R1 are piloted by the Kis antitoxin and tuned by the stoichiometry of Kidâ€“Kis oligomers. <i>Nucleic Acids Research</i> , 2007, 35, 1737-1749.	6.5	51

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91	Modeling Protein-Protein Complexes Involved in the Cytochrome Oxidase Copper-Delivery Pathway. <i>Journal of Proteome Research</i> , 2007, 6, 1530-1539.	1.8	27
92	On the Role of Aromatic Side Chains in the Photoactivation of BLUF Domains. <i>Biochemistry</i> , 2007, 46, 7405-7415.	1.2	106
93	Interactions between the toxin Kid of the bacterial parD system and the antitoxins Kis and MazE. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 219-231.	1.5	29
94	The Intrinsically Unstructured Domain of PC4 Modulates the Activity of the Structured Core through Inter- and Intramolecular Interactions. <i>Biochemistry</i> , 2006, 45, 5067-5081.	1.2	20
95	Cooperative $\alpha$ -helix unfolding in a protein-DNA complex from hydrogen-deuterium exchange. <i>Protein Science</i> , 2006, 15, 1752-1759.	3.1	1
96	Solution Structure of a Chemosensory Protein from the Desert Locust <i>Schistocerca gregaria</i> . <i>Biochemistry</i> , 2006, 45, 10606-10613.	1.2	111
97	Information-driven protein-DNA docking using HADDOCK: it is a matter of flexibility. <i>Nucleic Acids Research</i> , 2006, 34, 3317-3325.	6.5	169
98	Model for RNA Binding and the Catalytic Site of the RNase Kid of the Bacterial parD Toxin-Antitoxin System. <i>Journal of Molecular Biology</i> , 2006, 357, 115-126.	2.0	48
99	Light-Induced Flipping of a Conserved Glutamine Sidechain and Its Orientation in the AppA BLUF Domain. <i>Journal of the American Chemical Society</i> , 2006, 128, 15066-15067.	6.6	75
100	Direct Use of Unassigned Resonances in NMR Structure Calculations with Proxy Residues. <i>Journal of the American Chemical Society</i> , 2006, 128, 7566-7571.	6.6	15
101	Comparative NMR study on the impact of point mutations on protein stability of <i>Pseudomonas mendocinalipase</i> . <i>Protein Science</i> , 2006, 15, 1915-1927.	3.1	14
102	Combining NMR Relaxation with Chemical Shift Perturbation Data to Drive Protein-protein Docking. <i>Journal of Biomolecular NMR</i> , 2006, 34, 237-244.	1.6	39
103	The Solution Structure of the AppA BLUF Domain: Insight into the Mechanism of Light-Induced Signaling. <i>ChemBioChem</i> , 2006, 7, 187-193.	1.3	111
104	The nucleotide-binding site of bacterial translation initiation factor 2 (IF2) as a metabolic sensor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 13962-13967.	3.3	155
105	NMR analysis of protein interactions. <i>Current Opinion in Chemical Biology</i> , 2005, 9, 501-508.	2.8	109
106	Solution structure of the C1-subdomain of <i>Bacillus stearotherophilus</i> translation initiation factor IF2. <i>Protein Science</i> , 2005, 14, 2461-2468.	3.1	23
107	Data-driven docking for the study of biomolecular complexes. <i>FEBS Journal</i> , 2005, 272, 293-312.	2.2	125
108	The Solution Structure of a Transient Photoreceptor Intermediate: $\lambda$ 25 Photoactive Yellow Protein. <i>Structure</i> , 2005, 13, 953-962.	1.6	71



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109	The Structure of the Human ERCC1/XPF Interaction Domains Reveals a Complementary Role for the Two Proteins in Nucleotide Excision Repair. <i>Structure</i> , 2005, 13, 1849-1858.	1.6	116
110	Altered Specificity in DNA Binding by the lac Repressor: A Mutant lac Headpiece that Mimics the gal Repressor. <i>ChemBioChem</i> , 2005, 6, 1628-1637.	1.3	14
111	Describing Partially Unfolded States of Proteins from Sparse NMR Ddata. <i>Journal of Biomolecular NMR</i> , 2005, 33, 175-186.	1.6	17
112	Solution Structure of the C-terminal Domain of TFIH P44 Subunit Reveals a Novel Type of C4C4 Ring Domain Involved in Protein-Protein Interactions. <i>Journal of Biological Chemistry</i> , 2005, 280, 20785-20792.	1.6	28
113	Structural Properties of the Promiscuous VP16 Activation Domain. <i>Biochemistry</i> , 2005, 44, 827-839.	1.2	63
114	Dynamics and Metal Exchange Properties of C4C4 RING Domains from CNOT4 and the p44 Subunit of TFIH. <i>Journal of Molecular Biology</i> , 2005, 349, 621-637.	2.0	21
115	Structural Model of the UbcH5B/CNOT4 Complex Revealed by Combining NMR, Mutagenesis, and Docking Approaches. <i>Structure</i> , 2004, 12, 633-644.	1.6	113
116	Side chain dynamics monitored by <sup>13</sup> C- <sup>13</sup> C cross-relaxation. <i>Journal of Biomolecular NMR</i> , 2004, 29, 151-166.	1.6	11
117	Toward an Integrated Model of Protein-DNA Recognition as Inferred from NMR Studies on the Lac Repressor System. <i>ChemInform</i> , 2004, 35, no.	0.1	0
118	Toward an Integrated Model of Protein-DNA Recognition as Inferred from NMR Studies on the Lac Repressor System. <i>Chemical Reviews</i> , 2004, 104, 3567-3586.	23.0	74
119	Structure and Flexibility Adaptation in Nonspecific and Specific Protein-DNA Complexes. <i>Science</i> , 2004, 305, 386-389.	6.0	506
120	An Altered-specificity Ubiquitin-conjugating Enzyme/Ubiquitin-Protein Ligase Pair. <i>Journal of Molecular Biology</i> , 2004, 337, 157-165.	2.0	35
121	Solution Structure of the Ubiquitin-conjugating Enzyme UbcH5B. <i>Journal of Molecular Biology</i> , 2004, 344, 513-526.	2.0	31
122	An alternate conformation of the hyperthermostable HU protein from <i>Thermotoga maritima</i> has unexpectedly high flexibility. <i>FEBS Letters</i> , 2004, 563, 49-54.	1.3	13
123	HADDOCK: A Protein-Protein Docking Approach Based on Biochemical or Biophysical Information. <i>Journal of the American Chemical Society</i> , 2003, 125, 1731-1737.	6.6	2,642
124	Use of very long-distance NOEs in a fully deuterated protein: an approach for rapid protein fold determination. <i>Journal of Magnetic Resonance</i> , 2003, 163, 228-235.	1.2	25
125	X-ray absorption spectroscopic studies of zinc in the N-terminal domain of HIV-2 integrase and model compounds. <i>Journal of Synchrotron Radiation</i> , 2003, 10, 86-95.	1.0	23
126	Lack of Negative Charge in the E46Q Mutant of Photoactive Yellow Protein Prevents Partial Unfolding of the Blue-Shifted Intermediate. <i>Biochemistry</i> , 2003, 42, 14501-14506.	1.2	33



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127	Structural and Functional Analysis of the Kid Toxin Protein from E. coli Plasmid R1. <i>Structure</i> , 2002, 10, 1425-1433.	1.6	77
128	Crystallization and preliminary X-ray crystallographic studies on the parD-encoded protein Kid from <i>Escherichia coli</i> plasmid R1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 355-358.	2.5	10
129	A residue-specific view of the association and dissociation pathway in protein-DNA recognition. <i>Nature Structural Biology</i> , 2002, 9, 193-7.	9.7	30
130	Identification of a ubiquitin-protein ligase subunit within the CCR4-NOT transcription repressor complex. <i>EMBO Journal</i> , 2002, 21, 355-364.	3.5	186
131	Plasticity in protein-DNA recognition: lac repressor interacts with its natural operator O1 through alternative conformations of its DNA-binding domain. <i>EMBO Journal</i> , 2002, 21, 2866-2876.	3.5	117
132	Rapid protein fold determination using secondary chemical shifts and cross-hydrogen bond <sup>15</sup> N- <sup>13</sup> C' scalar couplings (3hbJNC'). <i>Journal of Biomolecular NMR</i> , 2001, 21, 221-233.	1.6	23
133	The Structure of the C4C4RING Finger of Human NOT4 Reveals Features Distinct from Those of C3HC4 RING Fingers. <i>Journal of Biological Chemistry</i> , 2001, 276, 10185-10190.	1.6	80
134	Refined solution structure of the dimeric N-terminal HHCC domain of HIV-2 integrase. <i>Journal of Biomolecular NMR</i> , 2000, 18, 119-128.	1.6	27
135	Mapping the fMet-tRNA <sup>fMet</sup> binding site of initiation factor IF2. <i>EMBO Journal</i> , 2000, 19, 5233-5240.	3.5	94
136	Hydration dynamics of the collagen triple helix by NMR. Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 2000, 300, 1041-1048.	2.0	103
137	Mutations in the glucocorticoid receptor DNA-binding domain mimic an allosteric effect of DNA. Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 2000, 301, 947-958.	2.0	45
138	Changes in Dynamical Behavior of the Retinoid X Receptor DNA-Binding Domain upon Binding to a 14 Base-Pair DNA Half Site. <i>Biochemistry</i> , 2000, 39, 8747-8757.	1.2	15
139	Structure and Dynamics of the Tetrameric Mnt Repressor and a Model for its DNA Complex. <i>Journal of Biomolecular Structure and Dynamics</i> , 2000, 17, 113-122.	2.0	2
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