

Rolf Boelens

List of Publications by Year in descending order

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papers

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272
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times ranked

16907
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Dynamic Readers for 5-(Hydroxy)Methylcytosine and Its Oxidized Derivatives. <i>Cell</i> , 2013, 152, 1146-1159.	13.5	888
3	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
4	Structure and Flexibility Adaptation in Nonspecific and Specific Protein-DNA Complexes. <i>Science</i> , 2004, 305, 386-389.	6.0	506
5	Hsp90-Tau Complex Reveals Molecular Basis for Specificity in Chaperone Action. <i>Cell</i> , 2014, 156, 963-974.	13.5	269
6	Altered flexibility in the substrate-binding site of related native and engineered high-alkaline <i>Bacillus subtilis</i> 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1999, 292, 111-123.	2.0	256
7	The DNA-binding domain of HIV-1 integrase has an SH3-like fold. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 807-810.	3.6	242
8	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
9	Structure of Arc repressor in solution: evidence for a family of β -sheet DNA-binding proteins. <i>Nature</i> , 1990, 346, 586-589.	13.7	180
10	WeNMR: Structural Biology on the Grid. <i>Journal of Grid Computing</i> , 2012, 10, 743-767.	2.5	170
11	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
12	Solution structure of the POU-specific DNA-binding domain of Oct-1. <i>Nature</i> , 1993, 362, 852-855.	13.7	161
13	Structural and dynamic changes of photoactive yellow protein during its photocycle in solution. <i>Nature Structural Biology</i> , 1998, 5, 568-570.	9.7	155
14	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
15	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
16	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
17	Redox-Dependent Control of FOXO/DAF-16 by Transportin-1. <i>Molecular Cell</i> , 2013, 49, 730-742.	4.5	138
18	The solution structure of the amino-terminal HHCC domain of HIV-2 integrase: a three-helix bundle stabilized by zinc. <i>Current Biology</i> , 1997, 7, 739-746.	1.8	134

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19	Solution Structure and Backbone Dynamics of the Photoactive Yellow Protein. <i>Biochemistry</i> , 1998, 37, 12689-12699.	1.2	129
20	An Off-resonance Rotating Frame Relaxation Experiment for the Investigation of Macromolecular Dynamics Using Adiabatic Rotations. <i>Journal of Magnetic Resonance</i> , 1998, 131, 351-357.	1.2	129
21	Gradient-enhanced HMQC and HSQC spectroscopy. Applications to ¹⁵ N-labeled Mnt repressor. <i>Journal of the American Chemical Society</i> , 1991, 113, 9688-9690.	6.6	128
22	A comprehensive framework of E2-RING E3 interactions of the human ubiquitin-proteasome system. <i>Molecular Systems Biology</i> , 2009, 5, 295.	3.2	126
23	Data-driven docking for the study of biomolecular complexes. <i>FEBS Journal</i> , 2005, 272, 293-312.	2.2	125
24	Structural Insight into the Recognition of the H3K4me3 Mark by the TFIID Subunit TAF3. <i>Structure</i> , 2008, 16, 1245-1256.	1.6	123
25	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
26	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
27	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
28	Solution Structure of a Chemosensory Protein from the Desert Locust <i>Schistocerca gregaria</i> . <i>Biochemistry</i> , 2006, 45, 10606-10613.	1.2	111
29	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
30	NMR analysis of protein interactions. <i>Current Opinion in Chemical Biology</i> , 2005, 9, 501-508.	2.8	109
31	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
32	On the Role of Aromatic Side Chains in the Photoactivation of BLUF Domains. <i>Biochemistry</i> , 2007, 46, 7405-7415.	1.2	106
33	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
34	Solution Structure of the HU Protein from <i>Bacillus stearothermophilus</i> . <i>Journal of Molecular Biology</i> , 1995, 254, 692-703.	2.0	103
35	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
36	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

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37	Quantitative Measurement of Relaxation Interference Effects between ^1H NCSA and ^1H - ^{15}N Dipolar Interaction: A Correlation with Secondary Structure. <i>Journal of the American Chemical Society</i> , 1997, 119, 8985-8990.	6.6	94
38	Mapping the fMet-tRNA ^{fMet} binding site of initiation factor IF2. <i>EMBO Journal</i> , 2000, 19, 5233-5240.	3.5	94
39	The solution structure of Lac repressor headpiece 62 complexed to a symmetrical lac operator. <i>Structure</i> , 1999, 7, 1483-53.	1.6	84
40	Refined solution structure of the c-terminal DNA-binding domain of human immunovirus-1 integrase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 36, 556-564.	1.5	83
41	Conformational changes in the oligonucleotide duplex d(GCGTTGCG). d(CGCAACGC) induced by formation of a cis-syn thymine dimer. A two-dimensional NMR study. <i>FEBS Journal</i> , 1987, 162, 37-43.	0.2	82
42	Probing the Nature of the Blue-Shifted Intermediate of Photoactive Yellow Protein in Solution by NMR: ^2H - ^1H Hydrogen-Deuterium Exchange Data and pH Studies. <i>Biochemistry</i> , 2000, 39, 14392-14399.	1.2	81
43	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
44	High-resolution Structure of the Phosphorylated Form of the Histidine-containing Phosphocarrier Protein HPr from <i>Escherichia coli</i> Determined by Restrained Molecular Dynamics from NMR-NOE Data. <i>Journal of Molecular Biology</i> , 1995, 246, 180-193.	2.0	78
45	Formation of the hinge helix in the lac repressor is induced upon binding to the lac operator. <i>Nature Structural Biology</i> , 1996, 3, 916-919.	9.7	77
46	Structural and Functional Analysis of the Kid Toxin Protein from <i>E. coli</i> Plasmid R1. <i>Structure</i> , 2002, 10, 1425-1433.	1.6	77
47	Rapid and simple approach for the NMR resonance assignment of the carbohydrate chains of an intact glycoprotein Application of gradient-enhanced natural abundance ^1H - ^{13}C HSQC and HSQC-TOCSY to the α -subunit of human chorionic gonadotropin. <i>FEBS Letters</i> , 1994, 348, 1-6.	1.3	75
48	PhoE Signal Peptide Inserts into Micelles as a Dynamic Helix-Break-Helix Structure, Which Is Modulated by the Environment. A Two-Dimensional ^1H NMR Study. <i>Biochemistry</i> , 1995, 34, 11617-11624.	1.2	75
49	NMR Studies of the Free α Subunit of Human Chorionic Gonadotropin. Structural Influences of N-Glycosylation and the β Subunit on the Conformation of the α Subunit. <i>FEBS Journal</i> , 1996, 241, 229-242.	0.2	75
50	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
51	μ -Ensemble iterative relaxation matrix approach: A new NMR refinement protocol applied to the solution structure of crambin. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 15, 385-400.	1.5	74
52	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
53	NMR structures of phospholipase A2 reveal conformational changes during interfacial activation. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 402-406.	3.6	72
54	The Solution Structure of a Transient Photoreceptor Intermediate: ^1H - ^{25}N Photoactive Yellow Protein. <i>Structure</i> , 2005, 13, 953-962.	1.6	71

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55	Nuclear Magnetic Resonance Solution Structure of the Arc Repressor Using Relaxation Matrix Calculations. <i>Journal of Molecular Biology</i> , 1994, 236, 328-341.	2.0	69
56	Solution Structure of Dimeric Mnt Repressor (1-76). <i>Biochemistry</i> , 1994, 33, 15036-15045.	1.2	67
57	Conformational changes in phospholipase A2 upon binding to micellar interfaces in the absence and presence of competitive inhibitors. A proton and nitrogen-15 NMR study. <i>Biochemistry</i> , 1992, 31, 10024-10030.	1.2	66
58	Solution Structure of the Sequence-specific HMG Box of the Lymphocyte Transcriptional Activator Sox-4. <i>Journal of Biological Chemistry</i> , 1995, 270, 30516-30524.	1.6	65
59	Structural Properties of the Promiscuous VP16 Activation Domain. <i>Biochemistry</i> , 2005, 44, 827-839.	1.2	63
60	Improved HSQC experiments for the observation of exchange broadened signals. <i>Journal of Biomolecular NMR</i> , 1996, 8, 223-8.	1.6	62
61	Crystal structure and collagen-binding site of immune inhibitory receptor LAIR-1: unexpected implications for collagen binding by platelet receptor GPIIb/IIIa. <i>Blood</i> , 2010, 115, 1364-1373.	0.6	62
62	Time- and ensemble-averaged direct NOE restraints. <i>Journal of Biomolecular NMR</i> , 1994, 4, 143-9.	1.6	60
63	Microsecond time scale dynamics in the RXR DNA-binding domain from a combination of spin-echo and off-resonance rotating frame relaxation measurements. <i>Journal of Biomolecular NMR</i> , 1999, 13, 275-288.	1.6	59
64	Function and Interactions of ERCC1-XPF in DNA Damage Response. <i>Molecules</i> , 2018, 23, 3205.	1.7	59
65	Critical Scaffolding Regions of the Tumor Suppressor Axin1 Are Natively Unfolded. <i>Journal of Molecular Biology</i> , 2011, 405, 773-786.	2.0	58
66	A novel μ -conopeptide, CnIIIc, exerts potent and preferential inhibition of Na ^v 1.2/1.4 channels and blocks neuronal nicotinic acetylcholine receptors. <i>British Journal of Pharmacology</i> , 2012, 166, 1654-1668.	2.7	55
67	Spatial arrangement of the three α helices in the solution conformation of E. coli lac repressor DNA-binding domain. <i>FEBS Letters</i> , 1984, 174, 243-247.	1.3	54
68	Time-saving methods for heteronuclear multidimensional NMR of (¹³ C, ¹⁵ N) doubly labeled proteins. <i>Journal of Biomolecular NMR</i> , 1994, 4, 201-13.	1.6	54
69	The solution structure of serine protease PB92 from <i>Bacillus alcalophilus</i> presents a rigid fold with a flexible substrate-binding site. <i>Structure</i> , 1997, 5, 521-532.	1.6	53
70	Mobilities of the Inner Three Core Residues and the Man(α 6) Branch of the Glycan at Asn78 of the α -Subunit of Human Chorionic Gonadotropin Are Restricted by the Protein. <i>Biochemistry</i> , 1998, 37, 1933-1940.	1.2	51
71	Hinge-helix formation and DNA bending in various lac repressor-operator complexes. <i>EMBO Journal</i> , 1999, 18, 6472-6480.	3.5	51
72	Interactions of Kid-Kis toxin-antitoxin complexes with the parD operator-promoter region of plasmid R1 are piloted by the Kis antitoxin and tuned by the stoichiometry of Kid-Kis oligomers. <i>Nucleic Acids Research</i> , 2007, 35, 1737-1749.	6.5	51

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73	MONTY: a Monte Carlo approach to protein-DNA recognition. <i>Journal of Molecular Biology</i> , 1994, 235, 318-324.	2.0	49
74	¹ H, ¹³ C, and ¹⁵ N resonance assignments and secondary structure analysis of the HU protein from <i>Bacillus stearothermophilus</i> using two- and three-dimensional double- and triple-resonance heteronuclear magnetic resonance spectroscopy. <i>Biochemistry</i> , 1994, 33, 14858-14870.	1.2	49
75	The tetramerization domain of the Mnt repressor consists of two right-handed coiled coils. <i>Nature Structural Biology</i> , 1999, 6, 755-759.	9.7	49
76	Sulforaphane inhibits pancreatic cancer through disrupting Hsp90α-p50Cdc37 complex and direct interactions with amino acids residues of Hsp90. <i>Journal of Nutritional Biochemistry</i> , 2012, 23, 1617-1626.	1.9	49
77	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
78	Determination of protein structures from nuclear magnetic resonance data using a restrained molecular dynamics approach: The lac repressor DNA binding domain. <i>Biochimie</i> , 1985, 67, 707-715.	1.3	48
79	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
80	Specificity and Affinity of Lac Repressor for the Auxiliary Operators O2 and O3 Are Explained by the Structures of Their Protein-DNA Complexes. <i>Journal of Molecular Biology</i> , 2009, 390, 478-489.	2.0	46
81	Solution structure of the α-subunit of human chorionic gonadotropin. <i>FEBS Journal</i> , 1999, 260, 490-498.	0.2	45
82	Mutations in the glucocorticoid receptor DNA-binding domain mimic an allosteric effect of DNA 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 2000, 301, 947-958.	2.0	45
83	Effects of the N-Linked Glycans on the 3D Structure of the Free α-Subunit of Human Chorionic Gonadotropin. <i>Biochemistry</i> , 2000, 39, 6012-6021.	1.2	43
84	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
85	Structure, stability, and IgE binding of the peach allergen <i>Pru p 7</i> . <i>Biopolymers</i> , 2014, 102, 416-425.	1.2	43
86	An EPR study of the photodissociation reactions of oxidised cytochrome c oxidase-nitric oxide complexes. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 1983, 724, 176-183.	0.5	42
87	Symmetry and Asymmetry of the RING-RING Dimer of Rad18. <i>Journal of Molecular Biology</i> , 2011, 410, 424-435.	2.0	41
88	Computer-assisted assignment of 2D ¹ H NMR spectra of proteins: Basic algorithms and application to phoratoxin B. <i>Journal of Biomolecular NMR</i> , 1991, 1, 23-47.	1.6	40
89	Identification of the ribosome binding sites of translation initiation factor IF3 by multidimensional heteronuclear NMR spectroscopy. <i>Rna</i> , 1999, 5, 82-92.	1.6	40
90	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

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91	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
92	Solution Structure of the Immunodominant Region of Protein G of Bovine Respiratory Syncytial Virus. <i>Biochemistry</i> , 1996, 35, 14684-14688.	1.2	38
93	Measurement of (15)N- (1)H coupling constants in uniformly (15)N-labeled proteins: Application to the photoactive yellow protein. <i>Journal of Biomolecular NMR</i> , 1997, 10, 301-306.	1.6	38
94	E2 ^c -Cbl Recognition Is Necessary but not Sufficient for Ubiquitination Activity. <i>Journal of Molecular Biology</i> , 2009, 385, 507-519.	2.0	37
95	Homonuclear three-dimensional proton NMR spectroscopy of pike parvalbumin. Comparison of short- and medium-range NOEs from 2D and 3D NMR. <i>Journal of the American Chemical Society</i> , 1990, 112, 5024-5030.	6.6	36
96	LexA repressor and iron uptake regulator from <i>Escherichia coli</i> : new members of the CAP-like DNA binding domain superfamily. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 1449-1453.	1.0	36
97	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
98	An Altered-specificity Ubiquitin-conjugating Enzyme/Ubiquitin-Protein Ligase Pair. <i>Journal of Molecular Biology</i> , 2004, 337, 157-165.	2.0	35
99	Observation of intersubunit NOEs in a dimeric P22 Mnt repressor mutant by a time-shared [15N, 13C] double half-filter technique. <i>Journal of Biomolecular NMR</i> , 1993, 3, 709.	1.6	34
100	A model for the LexA repressor DNA complex. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 21, 226-236.	1.5	34
101	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
102	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
103	Millisecond to Microsecond Time Scale Dynamics of the Retinoid X and Retinoic Acid Receptor DNA-Binding Domains and Dimeric Complex Formation. <i>Biochemistry</i> , 1999, 38, 1951-1956.	1.2	33
104	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
105	<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
106	A Natural Product Switch for a Dynamic Protein Interface. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 6443-6448.	7.2	32
107	Solution Structure of the Ubiquitin-conjugating Enzyme UbcH5B. <i>Journal of Molecular Biology</i> , 2004, 344, 513-526.	2.0	31
108	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

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109	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
110	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
111	Two-dimensional NMR studies on des-pentapeptide-insulin. Proton resonance assignments and secondary structure analysis. <i>FEBS Journal</i> , 1990, 191, 147-153.	0.2	29
112	Porcine pancreatic phospholipase A2: sequence-specific proton and nitrogen-15 NMR assignments and secondary structure. <i>Biochemistry</i> , 1991, 30, 3135-3146.	1.2	29
113	¹ H, ¹³ C and ¹⁵ N NMR backbone assignments of the 269-residue serine protease PB92 from <i>Bacillus alcalophilus</i> . <i>Journal of Biomolecular NMR</i> , 1994, 4, 123-8.	1.6	29
114	Monte Carlo docking of protein-DNA complexes: incorporation of DNA flexibility and experimental data. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 761-768.	1.0	29
115	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
116	Structural Dynamics in the Activation of Epac. <i>Journal of Biological Chemistry</i> , 2008, 283, 6501-6508.	1.6	29
117	Assignment of the ¹ H-NMR spectrum of a lac repressor headpiece-operator complex in H ₂ O and identification of NOEs. Consequences for protein-DNA interaction. <i>FEBS Journal</i> , 1990, 194, 629-637.	0.2	28
118	Solution Structure of the C-terminal Domain of TFIIF 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
119	High-level expression of biologically active glycoprotein hormones in <i>Pichia pastoris</i> strains—selection of strain GS115, and not X-33, for the production of biologically active N-glycosylated ¹⁵ N-labeled phCG. <i>Glycoconjugate Journal</i> , 2008, 25, 245-257.	1.4	28
120	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
121	<i>E. coli</i> MG1655 modulates its phospholipid composition through the cell cycle. <i>FEBS Letters</i> , 2015, 589, 2726-2730.	1.3	28
122	The cytochrome c oxidase-azide-nitric oxide complex as a model for the oxygen-binding site. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 1984, 765, 196-209.	0.5	27
123	Rapid acquisition of three-dimensional triple-resonance experiments using pulsed field gradient techniques. <i>Journal of Biomolecular NMR</i> , 1992, 2, 395-400.	1.6	27
124	Gradient-enhanced 3D NOESY-HMQC spectroscopy. <i>Journal of Biomolecular NMR</i> , 1992, 2, 301-305.	1.6	27
125	Structure and dynamics of the DNA binding protein HU from <i>Bacillus stearothermophilus</i> by NMR spectroscopy. , 1996, 40, 553-559.		27
126	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

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127	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
128	The solution structure of a monomeric insulin. A two-dimensional ¹ H-NMR study of des-(B26-B30)-insulin in combination with distance geometry and restrained molecular dynamics. <i>FEBS Journal</i> , 1991, 202, 447-458.	0.2	25
129	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
130	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
131	Glycosylation of Conotoxins. <i>Marine Drugs</i> , 2013, 11, 623-642.	2.2	25
132	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
133	Applications of two-dimensional ¹ H nuclear magnetic resonance methods in photochemically induced dynamic nuclear polarisation spectroscopy. <i>Faraday Discussions of the Chemical Society</i> , 1984, 78, 245.	2.2	24
134	Title is missing!. <i>Journal of Biomolecular NMR</i> , 1998, 11, 265-277.	1.6	24
135	Identification of the Single-stranded DNA Binding Surface of the Transcriptional Coactivator PC4 by NMR. <i>Journal of Biological Chemistry</i> , 1999, 274, 3693-3699.	1.6	24
136	SAMPLEX: Automatic mapping of perturbed and unperturbed regions of proteins and complexes. <i>BMC Bioinformatics</i> , 2010, 11, 51.	1.2	24
137	Structural Dynamics of Bacterial Translation Initiation Factor IF2. <i>Journal of Biological Chemistry</i> , 2012, 287, 10922-10932.	1.6	24
138	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
139	Two-dimensional ¹ H-NMR studies of phospholipase-A2-inhibitor complexes bound to a micellar lipid-water interface. <i>FEBS Journal</i> , 1991, 199, 601-607.	0.2	23
140	Rapid protein fold determination using secondary chemical shifts and cross-hydrogen bond ¹⁵ N- ¹³ C' scalar couplings (3hbJNC'). <i>Journal of Biomolecular NMR</i> , 2001, 21, 221-233.	1.6	23
141	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
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