

Kurt WÃ¼thrich

List of Publications by Year in descending order

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docs citations

201
times ranked

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citing authors

#	ARTICLE	IF	CITATIONS
1	GPCR large-amplitude dynamics by ¹⁹ F-NMR of aprepitant bound to the neurokinin 1 receptor. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2122682119.	7.1	16
2	Dual-acting antitumor agents targeting the A2A adenosine receptor and histone deacetylases: Design and synthesis of 4-(furan-2-yl)-1H-pyrazolo[3,4-d]pyrimidin-6-amine derivatives. European Journal of Medicinal Chemistry, 2022, 236, 114326.	5.5	5
3	G Protein-coupled Receptor (GPCR) Reconstitution and Labeling for Solution Nuclear Magnetic Resonance (NMR) Studies of the Structural Basis of Transmembrane Signaling. Molecules, 2022, 27, 2658.	3.8	8
4	OCRE Domains of Splicing Factors RBM5 and RBM10: Tyrosine Ringâ€˜Flip Frequencies Determined by Integrated Use of 1 H NMR Spectroscopy and Molecular Dynamics Simulations. ChemBioChem, 2021, 22, 565-570.	2.6	4
5	A2A Adenosine Receptor Partial Agonism Related to Structural Rearrangements in an Activation Microswitch. Structure, 2021, 29, 170-176.e3.	3.3	30
6	Design and preparation of the class B G proteinâ€˜coupled receptors GLPâ€˜1R and GCGR for ¹⁹ Fâ€˜NMR studies in solution. FEBS Journal, 2021, 288, 4053-4063.	4.7	9
7	SARS Coronavirus Unique Domain: Three-Domain Molecular Architecture in Solution and RNA Binding. , 2021, , 155-173.		0
8	Structural plasticity of the cellular prion protein and implications in health and disease. , 2021, , 127-132.		0
9	GPCR drug discovery: integrating solution NMR data with crystal and cryo-EM structures. , 2021, , 197-220.		1
10	Sequence-Specific Resonance Assignment of Soluble Nonglobular Proteins by 7D APSY-NMR Spectroscopy. , 2021, , 72-77.		0
11	Nuclear Magnetic Resonance Structure of a Novel Globular Domain in RBM10 Containing OCRE, the Octamer Repeat Sequence Motif. , 2021, , 105-111.		0
12	Biased Signaling Pathways in Î² ₂ -Adrenergic Receptor Characterized by ¹⁹ F-NMR. , 2021, , 179-183.		0
13	Allosteric Coupling of Drug Binding and Intracellular Signaling in the A2A Adenosine Receptor. , 2021, , 184-196.		0
14	Richard R. Ernst (1933â€˜2021) â€˜ A life of NMR, classical music and Tibetan art. Journal of Magnetic Resonance, 2021, 331, 107047.	2.1	0
15	Brownian motion, spin diffusion and protein structure determination in solution. Journal of Magnetic Resonance, 2021, 331, 107031.	2.1	5
16	Tumor Immunotherapy Using A2A Adenosine Receptor Antagonists. Pharmaceuticals, 2020, 13, 237.	3.8	23
17	Biased Signaling of the G-Protein-Coupled Receptor Î²2AR Is Governed by Conformational Exchange Kinetics. Structure, 2020, 28, 371-377.e3.	3.3	36
18	Disulfideâ€˜Containing Detergents (DCDs) for the Structural Biology of Membrane Proteins. Chemistry - A European Journal, 2019, 25, 11635-11640.	3.3	5

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19	Human substance P receptor binding mode of the antagonist drug aprepitant by NMR and crystallography. Nature Communications, 2019, 10, 638.	12.8	43
20	GPCR drug discovery: integrating solution NMR data with crystal and cryo-EM structures. Nature Reviews Drug Discovery, 2019, 18, 59-82.	46.4	179
21	Splicing Site Recognition by Synergy of Three Domains in Splicing Factor RBM10. Biochemistry, 2018, 57, 1563-1567.	2.5	8
22	Allosteric Coupling of Drug Binding and Intracellular Signaling in the A2A Adenosine Receptor. Cell, 2018, 172, 68-80.e12.	28.9	173
23	A _{2A} adenosine receptor functional states characterized by ¹⁹F-NMR. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 12733-12738.	7.1	96
24	Molecular interactions connecting the function of the serine-arginine-rich protein SRSF1 to protein phosphatase 1. Journal of Biological Chemistry, 2018, 293, 16751-16760.	3.4	21
25	Extrinsic Tryptophans as NMR Probes of Allosteric Coupling in Membrane Proteins: Application to the A_{2A} Adenosine Receptor. Journal of the American Chemical Society, 2018, 140, 8228-8235.	13.7	41
26	Globally Monitoring Allosteric Coupling in the A_{2A} Adenosine Receptor by NMR in Solution. FASEB Journal, 2018, 32, 533.99.	0.5	0
27	Solvent-accessibility of discrete residue positions in the polypeptide hormone glucagon by 19F-NMR observation of 4-fluorophenylalanine. Journal of Biomolecular NMR, 2017, 68, 1-6.	2.8	8
28	Prion protein <i>Î</i> ² 2â€“ <i>Î</i> [±] 2 loop conformational landscape. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 9617-9622.	7.1	26
29	Protease resistance of infectious prions is suppressed by removal of a single atom in the cellular prion protein. PLoS ONE, 2017, 12, e0170503.	2.5	7
30	<scp>NMR</scp> reveals structural rearrangements associated to substrate insertion in nucleotide-adding enzymes. Protein Science, 2016, 25, 917-925.	7.6	1
31	<scp>NMR</scp> in structural genomics to increase structural coverage of the protein universe. FEBS Journal, 2016, 283, 3870-3881.	4.7	5
32	UHM-ULM interactions in the RBM39-U2AF65 splicing-factor complex. Acta Crystallographica Section D: Structural Biology, 2016, 72, 497-511.	2.3	36
33	Dynamic Local Polymorphisms in the Gbx1 Homeodomain Induced by DNA Binding. Structure, 2016, 24, 1372-1379.	3.3	2
34	Ring current shifts in 19F-NMR of membrane proteins. Journal of Biomolecular NMR, 2016, 65, 1-5.	2.8	27
35	Î² -Adrenergic Receptor Conformational Response to Fusion Protein in the Third Intracellular Loop. Structure, 2016, 24, 2190-2197.	3.3	43
36	Directional Phosphorylation and Nuclear Transport of the Splicing Factor SRSF1 Is Regulated by an RNA Recognition Motif. Journal of Molecular Biology, 2016, 428, 2430-2445.	4.2	27

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37	The acidic domain is a unique structural feature of the splicing factor SYNCRIP. Protein Science, 2016, 25, 1545-1550.	7.6	9
38	Dlx5 Homeodomain:DNA Complex: Structure, Binding and Effect of Mutations Related to Split Hand and Foot Malformation Syndrome. Journal of Molecular Biology, 2016, 428, 1130-1141.	4.2	10
39	Nuclear Magnetic Resonance Structure of a Novel Globular Domain in RBM10 Containing OCRE, the Octamer Repeat Sequence Motif. Structure, 2016, 24, 158-164.	3.3	18
40	Inâ€Membrane Chemical Modification (IMCM) for Siteâ€Specific Chromophore Labeling of GPCRs. Angewandte Chemie - International Edition, 2015, 54, 15246-15249.	13.8	23
41	Cofactorâ€induced reversible folding of <scp>F</scp>lavodoxinâ€4 from <scp><i>L</i></scp><i>actobacillus acidophilus</i>. Protein Science, 2015, 24, 1600-1608.	7.6	2
42	Nonâ€Uniform Sampling and Jâ€UNIO Automation for Efficient Protein NMR Structure Determination. Chemistry - A European Journal, 2015, 21, 12363-12369.	3.3	3
43	APSY-NMR for protein backbone assignment in high-throughput structural biology. Journal of Biomolecular NMR, 2015, 61, 47-53.	2.8	22
44	NMR structure determination of the protein NP_344798.1 as the first representative of Pfam PF06042. Journal of Biomolecular NMR, 2015, 61, 83-87.	2.8	4
45	Single-molecule view of basal activity and activation mechanisms of the G protein-coupled receptor Î²₂ AR. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14254-14259.	7.1	87
46	NMR structure and dynamics of the agonist dynorphin peptide bound to the human kappa opioid receptor. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11852-11857.	7.1	80
47	J-UNIO protocol used for NMR structure determination of the 206-residue protein NP_346487.1 from Streptococcus pneumoniae TIGR4. Journal of Biomolecular NMR, 2015, 61, 65-72.	2.8	2
48	Micro-scale NMR Experiments for Monitoring the Optimization of Membrane Protein Solutions for Structural Biology. Bio-protocol, 2015, 5, .	0.4	1
49	Walter Jakob Gehring: A master of developmental biology. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 12574-12575.	7.1	2
50	Solutionâ€NMR Characterization of Outerâ€Membrane Protein A from <i>E. coli</i> in Lipid Bilayer Nanodiscs and Detergent Micelles. ChemBioChem, 2014, 15, 995-1000.	2.6	39
51	NMR Polypeptide Backbone Conformation of the E.Âcoli Outer Membrane Protein W. Structure, 2014, 22, 1204-1209.	3.3	30
52	NMR Structures of Î±-Proteobacterial ATPase-Regulating Î¶-Subunits. Journal of Molecular Biology, 2014, 426, 2547-2553.	4.2	18
53	Structural representative of the protein family PF14466 has a new fold and establishes links with the C2 and PLAT domains from the widely distant Pfams PF00168 and PF01477. Protein Science, 2013, 22, 1000-1007.	7.6	5
54	NMRâ€profiles of protein solutions. Biopolymers, 2013, 99, 825-831.	2.4	17

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55	Fluorine-19 NMR of integral membrane proteins illustrated with studies of GPCRs. Current Opinion in Structural Biology, 2013, 23, 740-747.	5.7	81
56	Structural plasticity of the cellular prion protein and implications in health and disease. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 8549-8554.	7.1	35
57	$\hat{\Gamma}^2$ -Adrenergic Receptor Activation by Agonists Studied with ^{19}F -NMR Spectroscopy. Angewandte Chemie - International Edition, 2013, 52, 10762-10765.	13.8	71
58	The GPCR Network: a large-scale collaboration to determine human GPCR structure and function. Nature Reviews Drug Discovery, 2013, 12, 25-34.	46.4	252
59	$\hat{\Gamma}^2$ -Adrenergic Receptor Solutions for Structural Biology Analyzed with Microscale NMR Diffusion Measurements. Angewandte Chemie - International Edition, 2013, 52, 331-335.	13.8	21
60	Thermodynamic Stability of Psychrophilic and Mesophilic Pheromones of the Protozoan Ciliate Euplotes. Biology, 2013, 2, 142-150.	2.8	14
61	The J-UNIO protocol for automated protein structure determination by NMR in solution. Journal of Biomolecular NMR, 2012, 53, 341-354.	2.8	57
62	Micro-coil NMR to monitor optimization of the reconstitution conditions for the integral membrane protein OmpW in detergent micelles. Journal of Biomolecular NMR, 2012, 54, 129-133.	2.8	11
63	Translational Diffusion Measurements by Microcoil NMR in Aqueous Solutions of the Fos-10 Detergent-Solubilized Membrane Protein OmpX. Journal of Physical Chemistry B, 2012, 116, 6775-6780.	2.6	10
64	Coding genes and molecular structures of the diffusible signalling proteins (pheromones) of the polar ciliate, Euplotes nobilii. Marine Genomics, 2012, 8, 9-13.	1.1	11
65	Biased Signaling Pathways in $\hat{\Gamma}^2$ -Adrenergic Receptor Characterized by ^{19}F -NMR. Science, 2012, 335, 1106-1110.	12.6	618
66	Dynamic Conformational Equilibria in the Physiological Function of the Bombyx mori Pheromone-Binding Protein. Journal of Molecular Biology, 2011, 408, 922-931.	4.2	29
67	Translational Diffusion of Macromolecular Assemblies Measured Using Transverse-Relaxation-Optimized Pulsed Field Gradient NMR. Journal of the American Chemical Society, 2011, 133, 16354-16357.	13.7	28
68	Celebrating its 20th anniversary in 2011, the Journal of Biomolecular NMR looks forward to the second decade of the 21st century. Journal of Biomolecular NMR, 2011, 49, 1-2.	2.8	2
69	NMR structure of the <i>Bordetella bronchiseptica</i> protein NP_888769.1 establishes a new phage-related protein family PF13554. Protein Science, 2011, 20, 1137-1144.	7.6	5
70	Nuclear magnetic resonance spectroscopy with the stringent substrate rhodanese bound to the single-ring variant SR1 of the <i>E. coli</i> chaperonin GroEL. Protein Science, 2011, 20, 1380-1386.	7.6	20
71	Antarctic and Arctic populations of the ciliate <i>Euplotes nobilii</i> show common pheromone-mediated cell-cell signaling and cross-mating. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3181-3186.	7.1	40
72	NMR structure of the protein NP_247299.1: comparison with the crystal structure. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1367-1380.	0.7	13

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73	Comparison of NMR and crystal structures for the proteins TM1112 and TM1367. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1381-1392.	0.7	14
74	NMR in a crystallography-based high-throughput protein structure-determination environment. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1365-1366.	0.7	7
75	Comparison of NMR and crystal structures highlights conformational isomerism in protein active sites. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1393-1405.	0.7	18
76	The JCSG high-throughput structural biology pipeline. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1137-1142.	0.7	99
77	The water-born protein pheromones of the polar protozoan ciliate, Euplotes nobilii: Coding genes and molecular structures. Polar Science, 2010, 4, 237-244.	1.2	4
78	Prion Protein-Detergent Micelle Interactions Studied by NMR in Solution. Journal of Biological Chemistry, 2009, 284, 22713-22721.	3.4	29
79	Nuclear Magnetic Resonance Structure of the Nucleic Acid-Binding Domain of Severe Acute Respiratory Syndrome Coronavirus Nonstructural Protein 3. Journal of Virology, 2009, 83, 12998-13008.	3.4	63
80	Nuclear Magnetic Resonance Structure Shows that the Severe Acute Respiratory Syndrome Coronavirus-Unique Domain Contains a Macrodomain Fold. Journal of Virology, 2009, 83, 1823-1836.	3.4	50
81	Molecular cold-adaptation: Comparative analysis of two homologous families of psychrophilic and mesophilic signal proteins of the protozoan ciliate, <i>Euplotes</i>. IUBMB Life, 2009, 61, 838-845.	3.4	30
82	Molecular cold-adaptation: Comparative analysis of two homologous families of psychrophilic and mesophilic signal proteins of the protozoan ciliate, Euplotes. IUBMB Life, 2009, 61, spcone-spcone.	3.4	0
83	NMR Characterization of Membrane Proteinâ€™Detergent Micelle Solutions by Use of Microcoil Equipment. Journal of the American Chemical Society, 2009, 131, 18450-18456.	13.7	27
84	Automated sequence-specific protein NMR assignment using the memetic algorithm MATCH. Journal of Biomolecular NMR, 2008, 41, 127-138.	2.8	111
85	Automated amino acid side-chain NMR assignment of proteins using 13C- and 15N-resolved 3D [1H,1H]-NOESY. Journal of Biomolecular NMR, 2008, 42, 23-33.	2.8	66
86	APSY-NMR with proteins: practical aspects and backbone assignment. Journal of Biomolecular NMR, 2008, 42, 179-195.	2.8	55
87	Solution NMR structure determination of proteins revisited. Journal of Biomolecular NMR, 2008, 42, 155-158.	2.8	100
88	NMR assignment of the nonstructural protein nsp3(1066â€“1181) from SARS-CoV. Biomolecular NMR Assignments, 2008, 2, 135-138.	0.8	4
89	Interactions with Hydrophobic Clusters in the Ureaâ€Unfolded Membrane Protein OmpX. Angewandte Chemie - International Edition, 2008, 47, 977-981.	13.8	21
90	Microscale NMR Screening of New Detergents for Membrane Protein Structural Biology. Journal of the American Chemical Society, 2008, 130, 7357-7363.	13.7	49

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91	Proteomics Analysis Unravels the Functional Repertoire of Coronavirus Nonstructural Protein 3. <i>Journal of Virology</i> , 2008, 82, 5279-5294.	3.4	167
92	A key molecular switch specifies species barriers in prion disease. <i>FASEB Journal</i> , 2008, 22, 173.2.	0.5	0
93	Nuclear Magnetic Resonance Structure of the N-Terminal Domain of Nonstructural Protein 3 from the Severe Acute Respiratory Syndrome Coronavirus. <i>Journal of Virology</i> , 2007, 81, 12049-12060.	3.4	75
94	Cold-adaptation in Sea-water-borne Signal Proteins: Sequence and NMR Structure of the Pheromone En-6 from the Antarctic Ciliate <i>Euplotes nobilii</i> . <i>Journal of Molecular Biology</i> , 2007, 372, 277-286.	4.2	24
95	Sequence-Specific Resonance Assignment of Soluble Nonglobular Proteins by 7D APSY-NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2007, 129, 10823-10828.	13.7	71
96	NMR structure of a KlbA intein precursor from <i>Methanococcus jannaschii</i> . <i>Protein Science</i> , 2007, 16, 1316-1328.	7.6	44
97	Cold-adapted signal proteins: NMR structures of pheromones from the antarctic ciliate <i>Euplotes nobilii</i> . <i>IUBMB Life</i> , 2007, 59, 578-585.	3.4	17
98	NMR assignment of a KlbA intein precursor from <i>Methanococcus jannaschii</i> . <i>Biomolecular NMR Assignments</i> , 2007, 1, 19-21.	0.8	2
99	NMR assignment of the domain 513-651 from the SARS-CoV nonstructural protein nsp3. <i>Biomolecular NMR Assignments</i> , 2007, 1, 191-194.	0.8	4
100	Effective rotational correlation times of proteins from NMR relaxation interference. <i>Journal of Magnetic Resonance</i> , 2006, 178, 72-76.	2.1	238
101	Solution structure of Asl1650, an acyl carrier protein from <i>Anabaena</i> sp. PCC 7120 with a variant phosphopantetheinylation-site sequence. <i>Protein Science</i> , 2006, 15, 1030-1041.	7.6	19
102	Automated Resonance Assignment of Proteins: 6 DAPSY-NMR. <i>Journal of Biomolecular NMR</i> , 2006, 35, 27-37.	2.8	80
103	Towards miniaturization of a structural genomics pipeline using micro-expression and microcoil NMR. <i>Journal of Structural and Functional Genomics</i> , 2006, 6, 259-267.	1.2	32
104	Proton-proton Overhauser NMR spectroscopy with polypeptide chains in large structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15445-15450.	7.1	30
105	NMR structure of the conserved hypothetical protein TM0487 from <i>Thermotoga maritima</i> : Implications for 216 homologous DUF59 proteins. <i>Protein Science</i> , 2005, 14, 2880-2886.	7.6	14
106	Managing the solvent water polarization to obtain improved NMR spectra of large molecular structures. <i>Journal of Biomolecular NMR</i> , 2005, 32, 61-70.	2.8	46
107	Direct NMR observation of a substrate protein bound to the chaperonin GroEL. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 12748-12753.	7.1	114
108	Automated projection spectroscopy (APSY). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 10876-10881.	7.1	232

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109	NMR screening and crystal quality of bacterially expressed prokaryotic and eukaryotic proteins in a structural genomics pipeline. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1901-1905.	7.1	81
110	Automated NMR structure determination and disulfide bond identification of the myotoxin crostamine from <i>Crotalus durissus terrificus</i> . Toxicon, 2005, 46, 759-767.	1.6	84
111	Letter to the Editor: ¹ H-, ¹³ C- and ¹⁵ N-NMR Assignment of the Conserved Hypothetical Protein TM0487 from <i>Thermotoga Maritima</i> . Journal of Biomolecular NMR, 2004, 29, 453-454.	2.8	4
112	Uniform and Residue-specific ¹⁵ N-labeling of Proteins on a Highly Deuterated Background. Journal of Biomolecular NMR, 2004, 29, 289-297.	2.8	70
113	Letter to the Editor: NMR Structure Determination of the Hypothetical Protein TM1290 from <i>Thermotoga Maritima</i> using Automated NOESY Analysis. Journal of Biomolecular NMR, 2004, 29, 403-406.	2.8	19
114	NMR for structural proteomics of <i>Thermotoga maritima</i> : Screening and structure determination. Journal of Structural and Functional Genomics, 2004, 5, 205-215.	1.2	31
115	Nonrandom Structure in the Urea-Unfolded <i>Escherichia coli</i> Outer Membrane Protein X (OmpX). Biochemistry, 2004, 43, 860-869.	2.5	49
116	NMR Structure of the Integral Membrane Protein OmpX. Journal of Molecular Biology, 2004, 336, 1211-1221.	4.2	173
117	NMR assignment of the conserved hypothetical protein TM1290 of <i>Thermotoga maritima</i> . Journal of Biomolecular NMR, 2003, 25, 167-168.	2.8	15
118	NMR-Untersuchungen von Struktur und Funktion biologischer Makromoleküle (Nobel-Vortrag). Angewandte Chemie, 2003, 115, 3462-3486.	2.0	36
119	NMR Studies of Structure and Function of Biological Macromolecules (Nobel Lecture). Angewandte Chemie - International Edition, 2003, 42, 3340-3363.	13.8	215
120	NMR solution structure determination of membrane proteins reconstituted in detergent micelles. FEBS Letters, 2003, 555, 144-150.	2.8	93
121	Lipid-protein interactions in DHPC micelles containing the integral membrane protein OmpX investigated by NMR spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 13533-13537.	7.1	125
122	TROSY-NMR reveals interaction between ERp57 and the tip of the calreticulin P-domain. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 1954-1959.	7.1	269
123	Solution NMR Techniques for Large Molecular and Supramolecular Structures. Journal of the American Chemical Society, 2002, 124, 12144-12153.	13.7	141
124	Protein NMR Structure Determination with Automated NOE Assignment Using the New Software CANDID and the Torsion Angle Dynamics Algorithm DYANA. Journal of Molecular Biology, 2002, 319, 209-227.	4.2	1,408
125	NMR analysis of a 900K GroEL-GroES complex. Nature, 2002, 418, 207-211.	27.8	394
126	A Structurally Deviant Member of the <i>Euplotes raikovi</i> Pheromone Family: Er-23. Journal of Eukaryotic Microbiology, 2002, 49, 86-92.	1.7	23

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127	Side chain NMR assignments in the membrane protein OmpX reconstituted in DHPC micelles. Journal of Biomolecular NMR, 2002, 23, 289-301.	2.8	51
128	Protein NMR structure determination with automated NOE-identification in the NOESY spectra using the new software ATNOS. Journal of Biomolecular NMR, 2002, 24, 171-189.	2.8	448
129	NMR structure of the Euplotes raikovi pheromone Er -23 and identification of its five disulfide bonds 1 Edited by M. F. Summers. Journal of Molecular Biology, 2001, 313, 923-931.	4.2	33
130	Solution NMR studies of the integral membrane proteins OmpX and OmpA from Escherichia coli. FEBS Letters, 2001, 504, 173-178.	2.8	123
131	NMR structure of the pheromone Er-22 from Euplotes raikovi. Journal of Biomolecular NMR, 2001, 19, 75-78.	2.8	18
132	The way to NMR structures of proteins. , 2001, 8, 923-925.		139
133	[15N,1H]/[13C,1H]-TROSY for simultaneous detection of backbone 15N-1H, aromatic 13C-1H and side-chain 15N-1H2 correlations in large proteins. Journal of Biomolecular NMR, 2000, 17, 195-202.	2.8	35
134	[13C]-constant-time [15N,1H]-TROSY-HNCA for sequential assignments of large proteins. Journal of Biomolecular NMR, 1999, 14, 85-88.	2.8	56
135	Improved sensitivity and coherence selection for [15N,1H]-TROSY elements in triple resonance experiments. Journal of Biomolecular NMR, 1999, 15, 181-184.	2.8	94
136	TROSY-type Triple-Resonance Experiments for Sequential NMR Assignments of Large Proteins. Journal of the American Chemical Society, 1999, 121, 844-848.	13.7	315
137	Single Transition-to-single Transition Polarization Transfer (ST2-PT) in [15N,1H]-TROSY. Journal of Biomolecular NMR, 1998, 12, 345-348.	2.8	246
138	Automated Peak Picking and Peak Integration in Macromolecular NMR Spectra Using AUTOPSY. Journal of Magnetic Resonance, 1998, 135, 288-297.	2.1	121
139	Transverse Relaxation-Optimized Spectroscopy (TROSY) for NMR Studies of Aromatic Spin Systems in 13C-Labeled Proteins. Journal of the American Chemical Society, 1998, 120, 6394-6400.	13.7	288
140	NMR characterization of the full-length recombinant murine prion protein, m PrP(23-231). FEBS Letters, 1997, 413, 282-288.	2.8	659
141	GARANT-a general algorithm for resonance assignment of multidimensional nuclear magnetic resonance spectra. Journal of Computational Chemistry, 1997, 18, 139-149.	3.3	129
142	Hydration and DNA Recognition by Homeodomains. Cell, 1996, 85, 1057-1065.	28.9	112
143	MOLMOL: A program for display and analysis of macromolecular structures. Journal of Molecular Graphics, 1996, 14, 51-55.	1.1	6,760
144	Automated sequence-specific NMR assignment of homologous proteins using the program GARANT. Journal of Biomolecular NMR, 1996, 7, 207-13.	2.8	117

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145	Three-dimensional 1H-TOCSY-relayed ct-[13C,1H]-HMQC for aromatic spin system identification in uniformly 13C-labeled proteins. Journal of Biomolecular NMR, 1996, 7, 99-106.	2.8	40
146	The NMR solution structure of the pheromone Erâ€11 from the ciliated protozoan <i>Euplotes raikovi</i>. Protein Science, 1996, 5, 1512-1522.	7.6	30
147	NMR structure of the mouse prion protein domain PrP(121â€231). Nature, 1996, 382, 180-182.	27.8	1,201
148	Statistical Basis for the Use of13CÎ±Chemical Shifts in Protein Structure Determination. Journal of Magnetic Resonance Series B, 1995, 109, 229-233.	1.6	103
149	Structure comparison of the pheromones E<i>r</i>â€1, E<i>r</i>â€10, and E<i>r</i>â€2 from <i>Euplotes raikovi</i>. Protein Science, 1994, 3, 1537-1546.	7.6	48
150	Destabilization of the complete protein secondary structure on binding to the chaperone GroEL. Nature, 1994, 368, 261-265.	27.8	157
151	NMR assignments as a basis for structural characterization of denatured states of globular proteins. Current Opinion in Structural Biology, 1994, 4, 93-99.	5.7	91
152	Determination of the Nuclear Magnetic Resonance Solution Structure of an Antennapedia Homeodomain-DNA Complex. Journal of Molecular Biology, 1993, 234, 1084-1097.	4.2	278
153	Determination of the nuclear magnetic resonance solution structure of the DNA-binding domain (residues 1 to 69) of the 434 repressor and comparison with the X-ray crystal structure. Journal of Molecular Biology, 1992, 223, 743-767.	4.2	70
154	Processing of multi-dimensional NMR data with the new software PROSA. Journal of Biomolecular NMR, 1992, 2, 619-629.	2.8	281
155	Structure of human cyclophilin and its binding site for cyclosporin A determined by X-ray crystallography and NMR spectroscopy. Nature, 1991, 353, 276-279.	27.8	281
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