Kurt WÃ¼thrich

List of Publications by Year
in descending order

195 papers	32,163 citations	9786 73 h-index	3915 177 g-index
201 all docs	201 docs citations	201 times ranked	17934 citing authors

#	Article	IF	Citations
1	MOLMOL: A program for display and analysis of macromolecular structures. Journal of Molecular Graphics, 1996, 14, 51-55.	1.1	6,760
2	NMR with Proteins and Nucleic Acids. Europhysics News, 1986, 17, 11-13.	0.3	4,189
3	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
4	NMR structure of the mouse prion protein domain PrP(121â€“231). Nature, 1996, 382, 180-182.	27.8	1,201
5	Polypeptide secondary structure determination by nuclear magnetic resonance observation of short proton-proton distances. Journal of Molecular Biology, 1984, 180, 715-740.	4.2	771
6	NMR characterization of the full-length recombinant murine prion protein, m PrP(23-231). FEBS Letters, 1997, 413, 282-288.	2.8	659
7	Protein structures in solution by nuclear magnetic resonance and distance geometry. Journal of Molecular Biology, 1987, 196, 611-639.	4.2	646
8	Biased Signaling Pathways in Î² ₂ -Adrenergic Receptor Characterized by ¹⁹ F-NMR. Science, 2012, 335, 1106-1110.	12.6	618
9	Sequential resonance assignments in protein 1H nuclear magnetic resonance spectra. Journal of Molecular Biology, 1982, 155, 321-346.	4.2	608
10	Solution conformation of proteinase inhibitor IIA from bull seminal plasma by 1H nuclear magnetic resonance and distance geometry. Journal of Molecular Biology, 1985, 182, 295-315.	4.2	599
11	Sequential resonance assignments in protein 1H nuclear magnetic resonance spectra. Journal of Molecular Biology, 1982, 155, 347-366.	4.2	583
12	Sequential resonance assignments as a basis for determination of spatial protein structures by high resolution proton nuclear magnetic resonance. Journal of Molecular Biology, 1982, 155, 311-319.	4.2	568
13	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
14	NMR analysis of a 900K GroELâ€“GroES complex. Nature, 2002, 418, 207-211.	27.8	394
15	An evaluation of the combined use of nuclear magnetic resonance and distance geometry for the determination of protein conformations in solution. Journal of Molecular Biology, 1985, 182, 281-294.	4.2	383
16	Three-dimensional structure of rabbit liver [Cd7]metallothionein-2a in aqueous solution determined by nuclear magnetic resonance. Journal of Molecular Biology, 1988, 201, 637-657.	4.2	315
17	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
18	Transverse Relaxation-Optimized Spectroscopy (TROSY) for NMR Studies of Aromatic Spin Systems in13C-Labeled Proteins. Journal of the American Chemical Society, 1998, 120, 6394-6400.	13.7	288

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19	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
20	Processing of multi-dimensional NMR data with the new software PROSA. Journal of Biomolecular NMR, 1992, 2, 619-629.	2.8	281
21	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
22	Systematic Application of Two-Dimensional 1H Nuclear-Magnetic-Resonance Techniques for Studies of Proteins. 2. Combined Use of Correlated Spectroscopy and Nuclear Overhauser Spectroscopy for Sequential Assignments of Backbone Resonances and Elucidation of Polypeptide Secondary Structures. FEBS Journal, 1981, 114, 375-384.	0.2	274
23	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
24	Combined use of proton-proton overhauser enhancements and a distance geometry algorithm for determination of polypeptide conformations. Application to micelle-bound glucagon. Biochimica Et Biophysica Acta (BBA) - Protein Structure, 1981, 667, 377-396.	1.7	259
25	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
26	Single Transition-to-single Transition Polarization Transfer (ST2-PT) in [15N,1H]-TROSY. Journal of Biomolecular NMR, 1998, 12, 345-348.	2.8	246
27	Effective rotational correlation times of proteins from NMR relaxation interference. Journal of Magnetic Resonance, 2006, 178, 72-76.	2.1	238
28	Determination of the complete three-dimensional structure of the Î±-amylase inhibitor tendamistat in aqueous solution by nuclear magnetic resonance and distance geometry. Journal of Molecular Biology, 1988, 204, 675-724.	4.2	232
29	Automated projection spectroscopy (APSY). Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10876-10881.	7.1	232
30	NMR Studies of Structure and Function of Biological Macromolecules (Nobel Lecture). Angewandte Chemie - International Edition, 2003, 42, 3340-3363.	13.8	215
31	Conformation of [Cd7]-metallothionein-2 from rat liver in aqueous solution determined by nuclear magnetic resonance spectroscopy. Journal of Molecular Biology, 1988, 203, 251-268.	4.2	204
32	Studies by 1H nuclear magnetic resonance and distance geometry of the solution conformation of the Î±-amylase inhibitor Tendamistat. Journal of Molecular Biology, 1986, 189, 377-382.	4.2	194
33	GPCR drug discovery: integrating solution NMR data with crystal and cryo-EM structures. Nature Reviews Drug Discovery, 2019, 18, 59-82.	46.4	179
34	Sequential resonance assignments in protein 1H nuclear magnetic resonance spectra. Journal of Molecular Biology, 1982, 155, 367-388.	4.2	177
35	Individual assignments of amide proton resonances in the proton NMR spectrum of the basic pancreatic trypsin inhibitor. Biochimica Et Biophysica Acta (BBA) - Protein Structure, 1979, 577, 177-194.	1.7	174
36	NMR Structure of the Integral Membrane Protein OmpX. Journal of Molecular Biology, 2004, 336, 1211-1221.	4.2	173

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37	Allosteric Coupling of Drug Binding and Intracellular Signaling in the A2A Adenosine Receptor. Cell, 2018, 172, 68-80.e12.	28.9	173
38	Secondary structure of the Î±-amylase polypeptide inhibitor Tendamistat from Streptomyces tendae determined in solution by 1H nuclear magnetic resonance. Journal of Molecular Biology, 1985, 183, 503-507.	4.2	170
39	Proteomics Analysis Unravels the Functional Repertoire of Coronavirus Nonstructural Protein 3. Journal of Virology, 2008, 82, 5279-5294.	3.4	167
40	Comparison of the high-resolution structures of the Î±-amylase inhibitor tendamistat determined by nuclear magnetic resonance in solution and by X-ray diffraction in single crystals. Journal of Molecular Biology, 1989, 206, 677-687.	4.2	157
41	Destabilization of the complete protein secondary structure on binding to the chaperone GroEL. Nature, 1994, 368, 261-265.	27.8	157
42	Polypeptide fold in the two metal clusters of metallothionein-2 by nuclear magnetic resonance in solution. Journal of Molecular Biology, 1986, 187, 125-129.	4.2	146
43	Solution NMR Techniques for Large Molecular and Supramolecular Structures. Journal of the American Chemical Society, 2002, 124, 12144-12153.	13.7	141
44	The way to NMR structures of proteins. , 2001, 8, 923-925.		139
45	Internal motion in globular proteins. Trends in Biochemical Sciences, 1978, 3, 227-230.	7.5	130
46	GARANT-a general algorithm for resonance assignment of multidimensional nuclear magnetic resonance spectra. Journal of Computational Chemistry, 1997, 18, 139-149.	3.3	129
47	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
48	Solution NMR studies of the integral membrane proteins OmpX and OmpA fromEscherichia coli. FEBS Letters, 2001, 504, 173-178.	2.8	123
49	Automated Peak Picking and Peak Integration in Macromolecular NMR Spectra Using AUTOPSY. Journal of Magnetic Resonance, 1998, 135, 288-297.	2.1	121
50	Systematic Application of Two-Dimensional 1H Nuclear-Magnetic-Resonance Techniques for Studies of Proteins. 1. Combined Use of Spin-Echo-Correlated Spectroscopy and J-Resolved Spectroscopy for the Identification of Complete Spin Systems of Non-labile Protons in Amino-Acid Residues. FEBS Journal, 1981, 114, 365-374.	0.2	118
51	Automated sequence-specific NMR assignment of homologous proteins using the program GARANT. Journal of Biomolecular NMR, 1996, 7, 207-13.	2.8	117
52	Direct NMR observation of a substrate protein bound to the chaperonin GroEL. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 12748-12753.	7.1	114
53	Hydration and DNA Recognition by Homeodomains. Cell, 1996, 85, 1057-1065.	28.9	112
54	Automated sequence-specific protein NMR assignment using the memetic algorithm MATCH. Journal of Biomolecular NMR, 2008, 41, 127-138.	2.8	111

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55	Dynamic model of globular protein conformations based on NMR studies in solution. Nature, 1978, 275, 247-248.	27.8	103
56	Ring current effects in the conformation dependent NMR chemical shifts of aliphatic protons in the basic pancreatic trypsin inhibitor. Biochimica Et Biophysica Acta (BBA) - Protein Structure, 1979, 576, 409-423.	1.7	103
57	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
58	Solution NMR structure determination of proteins revisited. Journal of Biomolecular NMR, 2008, 42, 155-158.	2.8	100
59	The JCSG high-throughput structural biology pipeline. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1137-1142.	0.7	99
60	Secondary structure in the solution conformation of the proteinase inhibitor IIA from bull seminal plasma by nuclear magnetic resonance. Journal of Molecular Biology, 1984, 173, 341-359.	4.2	96
61	A _{2A} adenosine receptor functional states characterized by ¹⁹ F-NMR. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 12733-12738.	7.1	96
62	Structural study of the heme crevice in cytochrome based on individual assignments of the 1H-NMR lines of the heme group and selected amino acid residues. Biochimica Et Biophysica Acta (BBA) - Protein Structure, 1980, 621, 204-217.	1.7	95
63	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
64	NMR solution structure determination of membrane proteins reconstituted in detergent micelles. FEBS Letters, 2003, 555, 144-150.	2.8	93
65	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
66	Sequence-specific resonance assignments in the 1H nuclear-magnetic-resonance spectrum of the Lac repressor DNA-binding domain 1-51 from Escherichia coli by two-dimensional spectroscopy. FEBS Journal, 1983, 137, 279-292.	0.2	87
67	Single-molecule view of basal activity and activation mechanisms of the G protein-coupled receptor Î² ₂ AR. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14254-14259.	7.1	87
68	Automated NMR structure determination and disulfide bond identification of the myotoxin crotamine from Crotalus durissus terrificus. Toxicon, 2005, 46, 759-767.	1.6	84
69	Assignment of the 1H nuclear magnetic resonance spectrum of the proteinase inhibitor IIA from bull seminal plasma by two-dimensional nuclear magnetic resonance at 500 MHz. Journal of Molecular Biology, 1983, 166, 641-665.	4.2	82
70	Dynamics of the aromatic amino acid residues in the globular conformation of the basic pancreatic trypsin inhibitor (BPTI). Biophysics of Structure and Mechanism, 1976, 2, 159-180.	1.9	81
71	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
72	Fluorine-19 NMR of integral membrane proteins illustrated with studies of GPCRs. Current Opinion in Structural Biology, 2013, 23, 740-747.	5.7	81

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73	Automated Resonance Assignment of Proteins: 6 DAPSY-NMR. Journal of Biomolecular NMR, 2006, 35, 27-37.	2.8	80
74	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
75	Nuclear Magnetic Resonance Structure of the N-Terminal Domain of Nonstructural Protein 3 from the Severe Acute Respiratory Syndrome Coronavirus. Journal of Virology, 2007, 81, 12049-12060.	3.4	75
76	Assignment of the 1H nuclear magnetic resonance spectrum of the trypsin inhibitor E from Dendroaspis polylepis polylepis. Journal of Molecular Biology, 1982, 159, 323-351.	4.2	73
77	Sequence-Specific Resonance Assignment of Soluble Nonglobular Proteins by 7D APSY-NMR Spectroscopy. Journal of the American Chemical Society, 2007, 129, 10823-10828.	13.7	71
78	Î²₂â€Adrenergic Receptor Activation by Agonists Studied with ¹⁹Fâ€…NMR Spectroscopy. Angewandte Chemie - International Edition, 2013, 52, 10762-10765.	13.8	71
79	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
80	Uniform and Residue-specific15N-labeling of Proteins on a Highly Deuterated Background. Journal of Biomolecular NMR, 2004, 29, 289-297.	2.8	70
81	Melittin bound to dodecylphosphocholine micelles 1H-NMR assignments and global conformational features. Biochimica Et Biophysica Acta - Biomembranes, 1981, 647, 95-111.	2.6	67
82	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
83	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
84	Sequence-specific 1H-NMR assignments in rabbit-liver metallothionein-2. FEBS Journal, 1986, 157, 275-289.	0.2	59
85	Metal co-ordination in rat liver metallothionein-2 prepared with or without reconstitution of the metal clusters, and comparison with rabbit liver metallothionein-2. Journal of Molecular Biology, 1987, 196, 711-719.	4.2	58
86	The J-UNIO protocol for automated protein structure determination by NMR in solution. Journal of Biomolecular NMR, 2012, 53, 341-354.	2.8	57
87	[13C]-constant-time [15N,1H]-TROSY-HNCA for sequential assignments of large proteins. Journal of Biomolecular NMR, 1999, 14, 85-88.	2.8	56
88	113Cd-1H spin-spin couplings in homonuclear 1H correlated spectroscopy of metallothionein. Identification of the cysteine 1H spin systems. FEBS Journal, 1984, 143, 659-667.	0.2	55
89	APSY-NMR with proteins: practical aspects and backbone assignment. Journal of Biomolecular NMR, 2008, 42, 179-195.	2.8	55
90	Reinvestigation of the aromatic side-chains in the basic pancreatic trypsin inhibitor by heteronuclear two-dimensional nuclear magnetic resonance. Journal of Molecular Biology, 1987, 196, 227-231.	4.2	53

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91	Side chain NMR assignments in the membrane protein OmpX reconstituted in DHPC micelles. Journal of Biomolecular NMR, 2002, 23, 289-301.	2.8	51
92	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
93	Nonrandom Structure in the Urea-Unfolded Escherichia coli Outer Membrane Protein X (OmpX). Biochemistry, 2004, 43, 860-869.	2.5	49
94	Microscale NMR Screening of New Detergents for Membrane Protein Structural Biology. Journal of the American Chemical Society, 2008, 130, 7357-7363.	13.7	49
95	Structure comparison of the pheromones Erâ€1, Erâ€10, and Erâ€2 from Euplotes raikovi. Protein Science, 1994, 3, 1537-1546.	7.6	48
96	Managing the solvent water polarization to obtain improved NMR spectra of large molecular structures. Journal of Biomolecular NMR, 2005, 32, 61-70.	2.8	46
97	Solution of the phase problem in the X-ray diffraction method for proteins with the nuclear magnetic resonance solution structure as initial model. Journal of Molecular Biology, 1989, 206, 669-676.	4.2	45
98	NMR structure of a KlbA intein precursor fromMethanococcus jannaschii. Protein Science, 2007, 16, 1316-1328.	7.6	44
99	Î² 2 -Adrenergic Receptor Conformational Response to Fusion Protein in the Third Intracellular Loop. Structure, 2016, 24, 2190-2197.	3.3	43
100	Human substance P receptor binding mode of the antagonist drug aprepitant by NMR and crystallography. Nature Communications, 2019, 10, 638.	12.8	43
101	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
102	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
103	Antarctic and Arctic populations of the ciliate Euplotes nobilii 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
104	Solutionâ€NMR Characterization of Outerâ€Membrane Protein A from E. coli in Lipid Bilayer Nanodiscs and Detergent Micelles. ChemBioChem, 2014, 15, 995-1000.	2.6	39
105	NMR-Untersuchungen von Struktur und Funktion biologischer MakromolekÃ¼le (Nobel-Vortrag). Angewandte Chemie, 2003, 115, 3462-3486.	2.0	36
106	UHMâ€“ULM interactions in the RBM39â€“U2AF65 splicing-factor complex. Acta Crystallographica Section D: Structural Biology, 2016, 72, 497-511.	2.3	36
107	Biased Signaling of the G-Protein-Coupled Receptor Î²2AR Is Governed by Conformational Exchange Kinetics. Structure, 2020, 28, 371-377.e3.	3.3	36
108	Sequential Individual Resonance Assignments in the 1H Nuclear-Magnetic-Resonance Spectrum of Cardiotoxin VII 2 from Naja mossambica mossambica. FEBS Journal, 1983, 130, 497-508.	0.2	35

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109	[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
110	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
111	NMR structure of the Euplotes raikovi pheromone E r -23 and identification of its five disulfide bonds 1 1Edited by M. F. Summers. Journal of Molecular Biology, 2001, 313, 923-931.	4.2	33
112	Towards miniaturization of a structural genomics pipeline using micro-expression and microcoil NMR. Journal of Structural and Functional Genomics, 2006, 6, 259-267.	1.2	32
113	NMR for structural proteomics of Thermotoga maritima: Screening and structure determination. Journal of Structural and Functional Genomics, 2004, 5, 205-215.	1.2	31
114	The NMR solution structure of the pheromone Erâ€•1 1 from the ciliated protozoan Euplotes raikovi. Protein Science, 1996, 5, 1512-1522.	7.6	30
115	Proton-proton Overhauser NMR spectroscopy with polypeptide chains in large structures. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15445-15450.	7.1	30
116	Molecular coldâ€adaptation: Comparative analysis of two homologous families of psychrophilic and mesophilic signal proteins of the protozoan ciliate, Euplotes. IUBMB Life, 2009, 61, 838-845.	3.4	30
117	NMR Polypeptide Backbone Conformation of the E.Âcoli Outer Membrane Protein W. Structure, 2014, 22, 1204-1209.	3.3	30
118	A2A Adenosine Receptor Partial Agonism Related to Structural Rearrangements in an Activation Microswitch. Structure, 2021, 29, 170-176.e3.	3.3	30
119	Prion Protein-Detergent Micelle Interactions Studied by NMR in Solution. Journal of Biological Chemistry, 2009, 284, 22713-22721.	3.4	29
120	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
121	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
122	NMR Characterization of Membrane Proteinâˆ'Detergent Micelle Solutions by Use of Microcoil Equipment. Journal of the American Chemical Society, 2009, 131, 18450-18456.	13.7	27
123	Ring current shifts in 19F-NMR of membrane proteins. Journal of Biomolecular NMR, 2016, 65, 1-5.	2.8	27
124	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
125	Prion protein Î² 2â€“ Î± 2 loop conformational landscape. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 9617-9622.	7.1	26
126	Cold-adaptation in Sea-water-borne Signal Proteins: Sequence and NMR Structure of the Pheromone En-6 from the Antarctic Ciliate Euplotes nobilii. Journal of Molecular Biology, 2007, 372, 277-286.	4.2	24

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127	A Structurally Deviant Member of the Euplotes raikovi Pheromone Family: Er-23. Journal of Eukaryotic Microbiology, 2002, 49, 86-92.	1.7	23
128	Inâ€Membrane Chemical Modification (IMCM) for Siteâ€Specific Chromophore Labeling of GPCRs. Angewandte Chemie - International Edition, 2015, 54, 15246-15249.	13.8	23
129	Tumor Immunotherapy Using A2A Adenosine Receptor Antagonists. Pharmaceuticals, 2020, 13, 237.	3.8	23
130	APSY-NMR for protein backbone assignment in high-throughput structural biology. Journal of Biomolecular NMR, 2015, 61, 47-53.	2.8	22
131	Interactions with Hydrophobic Clusters in the Ureaâ€Unfolded Membrane Protein OmpX. Angewandte Chemie - International Edition, 2008, 47, 977-981.	13.8	21
132	Î²₂â€Adrenergic Receptor Solutions for Structural Biology Analyzed with Microscale NMR Diffusion Measurements. Angewandte Chemie - International Edition, 2013, 52, 331-335.	13.8	21
133	Molecular interactions connecting the function of the serine-arginineâ€"rich protein SRSF1 to protein phosphatase 1. Journal of Biological Chemistry, 2018, 293, 16751-16760.	3.4	21
134	Nuclear magnetic resonance spectroscopy with the stringent substrate rhodanese bound to the singleâ€ring variant SR1 of the E. coli chaperonin GroEL. Protein Science, 2011, 20, 1380-1386.	7.6	20
135	Letter to the Editor: NMR Structure Determination of the Hypothetical Protein TM1290 from Thermotoga Maritima using Automated NOESY Analysis. Journal of Biomolecular NMR, 2004, 29, 403-406.	2.8	19
136	Solution structure of Asl1650, an acyl carrier protein fromAnabaenasp. PCC 7120 with a variant phosphopantetheinylation-site sequence. Protein Science, 2006, 15, 1030-1041.	7.6	19
137	NMR structure of the pheromone Er-22 from Euplotes raikovi. Journal of Biomolecular NMR, 2001, 19, 75-78.	2.8	18
138	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
139	NMR Structures of Î±-Proteobacterial ATPase-Regulating Î¶-Subunits. Journal of Molecular Biology, 2014, 426, 2547-2553.	4.2	18
140	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
141	Coldâ€adapted signal proteins: NMR structures of pheromones from the antarctic ciliate Euplotes nobilii. IUBMB Life, 2007, 59, 578-585.	3.4	17
142	NMRâ€profiles of protein solutions. Biopolymers, 2013, 99, 825-831.	2.4	17
143	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
144	NMR assignment of the conserved hypothetical protein TM1290 of Thermotoga maritima. Journal of Biomolecular NMR, 2003, 25, 167-168.	2.8	15

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145	Characterization of the proteinase inhibitor IIA from bull seminal plasma by 1H nuclear magnetic resonance. Journal of Molecular Biology, 1983, 166, 631-640.	4.2	14
146	NMR structure of the conserved hypothetical protein TM0487 fromThermotoga maritima: Implications for 216 homologous DUF59 proteins. Protein Science, 2005, 14, 2880-2886.	7.6	14
147	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
148	Thermodynamic Stability of Psychrophilic and Mesophilic Pheromones of the Protozoan Ciliate Euplotes. Biology, 2013, 2, 142-150.	2.8	14
149	Sequence-specific 1H-NMR assignments in rat-liver metallothionein-2. FEBS Journal, 1987, 167, 457-466.	0.2	13
150	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
151	Preliminary structural comparison of the proteinase isoinhibitors IIA and IIB from bull seminal plasma based on individual assignments of the 1H nuclear magnetic resonance spectra by two-dimensional nuclear magnetic resonance at 500 MHz. Journal of Molecular Biology, 1983, 166, 669-676.	4.2	11
152	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
153	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
154	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
155	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
156	The acidic domain is a unique structural feature of the splicing factor SYNCRIP. Protein Science, 2016, 25, 1545-1550.	7.6	9
157	Design and preparation of the class B G proteinâ€coupled receptors GLPâ€1R and GCGR for ¹⁹Fâ€NMR studies in solution. FEBS Journal, 2021, 288, 4053-4063.	4.7	9
158	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
159	Splicing Site Recognition by Synergy of Three Domains in Splicing Factor RBM10. Biochemistry, 2018, 57, 1563-1567.	2.5	8
160	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
161	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
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