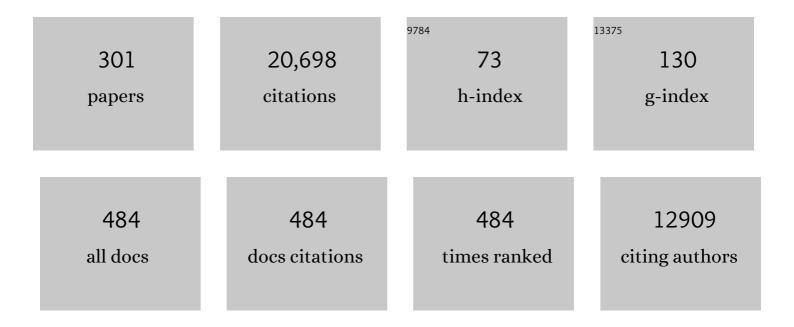
Gottfried Otting

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Clean TOCSY for proton spin system identification in macromolecules. Journal of the American Chemical Society, 1988, 110, 7870-7872.	13.7	1,191
2	Protein hydration in aqueous solution. Science, 1991, 254, 974-980.	12.6	795
3	Homeodomain-DNA recognition. Cell, 1994, 78, 211-223.	28.9	770
4	Alignment of Biological Macromolecules in Novel Nonionic Liquid Crystalline Media for NMR Experiments. Journal of the American Chemical Society, 2000, 122, 7793-7797.	13.7	600
5	Stereospecific nuclear magnetic resonance assignments of the methyl groups of valine and leucine in the DNA-binding domain of the 434 repressor by biosynthetically directed fractional carbon-13 labeling. Biochemistry, 1989, 28, 7510-7516.	2.5	597
6	The structure of the Antennapedia homeodomain determined by NMR spectroscopy in solution: Comparison with prokaryotic repressors. Cell, 1989, 59, 573-580.	28.9	513
7	Protein NMR Using Paramagnetic lons. Annual Review of Biophysics, 2010, 39, 387-405.	10.0	354
8	Heteronuclear filters in two-dimensional [¹ H, ¹ H]-NMR spectroscopy: combined use with isotope labelling for studies of macromolecular conformation and intermolecular interactions. Quarterly Reviews of Biophysics, 1990, 23, 39-96.	5.7	350
9	Proton exchange rates from amino acid side chains— implications for image contrast. Magnetic Resonance in Medicine, 1996, 35, 30-42.	3.0	309
10	Studies of protein hydration in aqueous solution by direct NMR observation of individual protein-bound water molecules. Journal of the American Chemical Society, 1989, 111, 1871-1875.	13.7	308
11	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
12	NMR structure of the death domain of the p75 neurotrophin receptor. EMBO Journal, 1997, 16, 4999-5005.	7.8	269
13	NMR Structure Determination of Proteinâ^Ligand Complexes by Lanthanide Labeling. Accounts of Chemical Research, 2007, 40, 206-212.	15.6	267
14	Hydration of Proteins. Journal of Molecular Biology, 1993, 231, 1040-1048.	4.2	235
15	The structure of the homeodomain and its functional implications. Trends in Genetics, 1990, 6, 323-329.	6.7	229
16	NMR observation of individual molecules of hydration water bound to DNA duplexes: direct evidence for a spine of hydration water present in aqueous solution. Nucleic Acids Research, 1992, 20, 6549-6553.	14.5	221
17	Dynamics of Protein and Peptide Hydration. Journal of the American Chemical Society, 2004, 126, 102-114.	13.7	215
18	Saposin fold revealed by the NMR structure of NK-lysin. Nature Structural Biology, 1997, 4, 793-795.	9.7	214

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19	NMR studies of water bound to biological molecules. Progress in Nuclear Magnetic Resonance Spectroscopy, 1997, 31, 259-285.	7.5	204
20	Identification of Protein Surfaces by NMR Measurements with a Paramagnetic Gd(III) Chelate. Journal of the American Chemical Society, 2002, 124, 372-373.	13.7	201
21	Disulfide bond isomerization in BPTI and BPTI(G36S): An NMR study of correlated mobility in proteins. Biochemistry, 1993, 32, 3571-3582.	2.5	173
22	Prospects for lanthanides in structural biology by NMR. Journal of Biomolecular NMR, 2008, 42, 1-9.	2.8	172
23	Numbat: an interactive software tool for fitting Δχ-tensors to molecular coordinates using pseudocontact shifts. Journal of Biomolecular NMR, 2008, 41, 179-189.	2.8	168
24	Paramagnetic labelling of proteins and oligonucleotides for NMR. Journal of Biomolecular NMR, 2010, 46, 101-112.	2.8	157
25	Origin of τ2 and τ2 ridges in 2D NMR spectra and procedures for suppression. Journal of Magnetic Resonance, 1986, 66, 187-193.	0.5	152
26	The Death-domain Fold of the ASC PYRIN Domain, Presenting a Basis for PYRIN/PYRIN Recognition. Journal of Molecular Biology, 2003, 332, 1155-1163.	4.2	143
27	Nanometer-Scale Distance Measurements in Proteins Using Gd ³⁺ Spin Labeling. Journal of the American Chemical Society, 2010, 132, 9040-9048.	13.7	143
28	Main protease mutants of SARS-CoV-2 variants remain susceptible to nirmatrelvir. Bioorganic and Medicinal Chemistry Letters, 2022, 62, 128629.	2.2	131
29	Structure determination of the Antp(C39 → S) homeodomain from nuclear magnetic resonance data in solution using a novel strategy for the structure calculation with the programs DIANA, CALIBA, HABAS and GLOMSA. Journal of Molecular Biology, 1991, 217, 531-540.	4.2	130
30	Lanthanide Labeling Offers Fast NMR Approach to 3D Structure Determinations of Proteinâ^'Protein Complexes. Journal of the American Chemical Society, 2006, 128, 3696-3702.	13.7	125
31	Pseudocontact shifts in biomolecular NMR using paramagnetic metal tags. Progress in Nuclear Magnetic Resonance Spectroscopy, 2017, 98-99, 20-49.	7.5	125
32	Determination of the three-dimensional structure of theAntennapedia homeodomain fromDrosophila in solution by1H nuclear magnetic resonance spectroscopy. Journal of Molecular Biology, 1990, 214, 183-197.	4.2	122
33	NMR structure of Escherichia coli glutaredoxin 3-glutathione mixed disulfide complex: implications for the enzymatic mechanism 1 1Edited by P. E. Wright. Journal of Molecular Biology, 1999, 286, 541-552.	4.2	121
34	Binding of Low Molecular Weight Inhibitors Promotes Large Conformational Changes in the Dengue Virus NS2B-NS3 Protease: Fold Analysis by Pseudocontact Shifts. Journal of the American Chemical Society, 2011, 133, 19205-19215.	13.7	119
35	NMR spectroscopy of hydroxyl protons in aqueous solutions of peptides and proteins. Journal of Biomolecular NMR, 1992, 2, 447-465.	2.8	117
36	A Dipicolinic Acid Tag for Rigid Lanthanide Tagging of Proteins and Paramagnetic NMR Spectroscopy. Journal of the American Chemical Society, 2008, 130, 10486-10487.	13.7	117

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37	Solvent suppression using a spin lock in 2D and 3D NMR spectroscopy with H2O solutions. Journal of Magnetic Resonance, 1989, 85, 608-613.	0.5	115
38	Solution structure of the DNA-binding domain and model for the complex of multifunctiona hexameric arginine represser with DNA. Nature Structural Biology, 1997, 4, 819-826.	9.7	115
39	Protein Hydration Viewed by High-Resolution NMR Spectroscopy: Implications for Magnetic Resonance Image Contrast. Accounts of Chemical Research, 1995, 28, 171-177.	15.6	114
40	Protein hydration studied with homonuclear 3D1H NMR experiments. Journal of Biomolecular NMR, 1991, 1, 209-215.	2.8	113
41	Precise vicinal coupling constants3JHNα in proteins from nonlinear fits of J-modulated [15N,1H]-COSY experiments. Journal of Biomolecular NMR, 1992, 2, 257-274.	2.8	112
42	Organic solvents identify specific ligand binding sites on protein surfaces. Nature Biotechnology, 1997, 15, 264-268.	17.5	108
43	Spin-state selection filters for the measurement of heteronuclear one-bond coupling constants. Journal of Biomolecular NMR, 1998, 12, 435-441.	2.8	107
44	Proton exchange with internal water molecules in the protein BPTI in aqueous solution. Journal of the American Chemical Society, 1991, 113, 4363-4364.	13.7	106
45	Hydrophobic Interactions in a Cyanobacterial Plastocyaninâ^'Cytochrome f Complex. Journal of the American Chemical Society, 2001, 123, 10444-10453.	13.7	106
46	Protein Structure Determination from Pseudocontact Shifts Using ROSETTA. Journal of Molecular Biology, 2012, 416, 668-677.	4.2	106
47	DOTA-Amide Lanthanide Tag for Reliable Generation of Pseudocontact Shifts in Protein NMR Spectra. Bioconjugate Chemistry, 2011, 22, 2118-2125.	3.6	104
48	Gadolinium Tagging for High-Precision Measurements of 6 nm Distances in Protein Assemblies by EPR. Journal of the American Chemical Society, 2011, 133, 10418-10421.	13.7	104
49	Molecular electroporation: a unifying concept for the description of membrane pore formation by antibacterial peptides, exemplified with NKâ€lysin. FEBS Letters, 1999, 462, 155-158.	2.8	103
50	Structure Determination of Proteinâ^'Ligand Complexes by Transferred Paramagnetic Shifts. Journal of the American Chemical Society, 2006, 128, 12910-12916.	13.7	102
51	Specificity of Urea Binding to Proteins. Journal of the American Chemical Society, 1994, 116, 9670-9674.	13.7	101
52	Support of1H NMR assignments in proteins by biosynthetically directed fractional13C-labeling. Journal of Biomolecular NMR, 1992, 2, 323-334.	2.8	99
53	Thioredoxin Fold as Homodimerization Module in the Putative Chaperone ERp29. Structure, 2001, 9, 457-471.	3.3	97
54	Lanthanide-Binding Peptides for NMR Measurements of Residual Dipolar Couplings and Paramagnetic Effects from Multiple Angles. Journal of the American Chemical Society, 2008, 130, 1681-1687.	13.7	96

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55	NMR detection of hydration water in the intermolecular interface of a protein-DNA complex. Journal of the American Chemical Society, 1993, 115, 1189-1190.	13.7	95
56	NMR identification of hydrophobic cavities with ow water occupancies in protein structures using small gas molecules. Nature Structural and Molecular Biology, 1997, 4, 396-404.	8.2	95
57	Backbone Assignment of Fully Protonated Solid Proteins by ¹ H Detection and Ultrafast Magicâ€Angleâ€Spinning NMR Spectroscopy. Angewandte Chemie - International Edition, 2012, 51, 10756-10759.	13.8	95
58	A fluorescence quenching assay to discriminate between specific and nonspecific inhibitors of dengue virus protease. Analytical Biochemistry, 2009, 395, 195-204.	2.4	92
59	Multipleâ€6ite Labeling of Proteins with Unnatural Amino Acids. Angewandte Chemie - International Edition, 2012, 51, 2243-2246.	13.8	89
60	Optimization of an Escherichia coli system for cell-free synthesis of selectively 15N-labelled proteins for rapid analysis by NMR spectroscopy. FEBS Journal, 2004, 271, 4084-4093.	0.2	87
61	Rapid pulse length determination in high-resolution NMR. Journal of Magnetic Resonance, 2005, 176, 115-119.	2.1	86
62	Mutations in the COCH gene are a frequent cause of autosomal dominant progressive cochleo-vestibular dysfunction, but not of Meniere's disease. European Journal of Human Genetics, 2003, 11, 744-748.	2.8	85
63	Fast Structure-Based Assignment of15N HSQC Spectra of Selectively15N-Labeled Paramagnetic Proteins. Journal of the American Chemical Society, 2004, 126, 2963-2970.	13.7	83
64	New nuclear magnetic resonance experiment for measurements of the vicinal coupling constants 3JHN.alpha. in proteins. Journal of the American Chemical Society, 1990, 112, 3663-3665.	13.7	82
65	Site-Specific Labelling of Proteins with a Rigid Lanthanide-Binding Tag. ChemBioChem, 2006, 7, 1599-1604.	2.6	82
66	Lanthanide Tags for Site-Specific Ligation to an Unnatural Amino Acid and Generation of Pseudocontact Shifts in Proteins. Bioconjugate Chemistry, 2013, 24, 260-268.	3.6	81
67	Nuclear Magnetic Resonance Spectroscopy of a DNA Complex with the Uniformly 13C-Labeled Antennapedia Homeodomain and Structure Determination of the DNA-bound Homeodomain. Journal of Molecular Biology, 1993, 234, 1070-1083.	4.2	80
68	Water molecules in DNA recognition II: a molecular dynamics view of the structure and hydration of the trp operator 1 1Edited by B. Honig. Journal of Molecular Biology, 1998, 282, 859-873.	4.2	80
69	Protein engineering with unnatural amino acids. Current Opinion in Structural Biology, 2013, 23, 581-587.	5.7	80
70	Site-specific Labelling with a Metal Chelator for Protein-structure Refinement. Journal of Biomolecular NMR, 2004, 29, 351-361.	2.8	78
71	Flaviviral Protease Inhibitors Identified by Fragment-Based Library Docking into a Structure Generated by Molecular Dynamics. Journal of Medicinal Chemistry, 2009, 52, 4860-4868.	6.4	77
72	Improving a Natural Enzyme Activity through Incorporation of Unnatural Amino Acids. Journal of the American Chemical Society, 2011, 133, 326-333.	13.7	77

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73	Three-Dimensional Protein Fold Determination from Backbone Amide Pseudocontact Shifts Generated by Lanthanide Tags at Multiple Sites. Structure, 2013, 21, 883-890.	3.3	77
74	Efficient purging scheme for proton-detected heteronuclear two-dimensional NMR. Journal of Magnetic Resonance, 1988, 76, 569-574.	0.5	76
75	NMR Analysis of the Dynamic Exchange of the NS2B Cofactor between Open and Closed Conformations of the West Nile Virus NS2B-NS3 Protease. PLoS Neglected Tropical Diseases, 2009, 3, e561.	3.0	75
76	Spectroscopic selection of distance measurements in a protein dimer with mixed nitroxide and Gd3+ spin labels. Physical Chemistry Chemical Physics, 2012, 14, 4355.	2.8	73
77	Nanometer-Range Distance Measurement in a Protein Using Mn ²⁺ Tags. Journal of Physical Chemistry Letters, 2012, 3, 157-160.	4.6	72
78	Memory T Cell RNA Rearrangement Programmed by Heterogeneous Nuclear Ribonucleoprotein hnRNPLL. Immunity, 2008, 29, 863-875.	14.3	71
79	Discovery of a Non-Peptidic Inhibitor of West Nile Virus NS3 Protease by High-Throughput Docking. PLoS Neglected Tropical Diseases, 2009, 3, e356.	3.0	71
80	Experimental NMR techniques for studies of protein-ligand interactions. Current Opinion in Structural Biology, 1993, 3, 760-768.	5.7	69
81	NMR analysis of in vitro-synthesized proteins without purification: a high-throughput approach. FEBS Letters, 2002, 524, 159-162.	2.8	69
82	Cell-Free Transcription/Translation from PCR-Amplified DNA for High-Throughput NMR Studies. Angewandte Chemie - International Edition, 2007, 46, 3356-3358.	13.8	69
83	Protein conformation by EPR spectroscopy using gadolinium tags clicked to genetically encoded p-azido- <scp>l</scp> -phenylalanine. Chemical Communications, 2015, 51, 15898-15901.	4.1	67
84	An α/β-HSQC-α/β Experiment for Spin-State Selective Editing of IS Cross Peaks. Journal of Magnetic Resonance, 1998, 133, 364-367.	2.1	66
85	In Vivo Protein Cyclization Promoted by a Circularly Permuted Synechocystis sp. PCC6803 DnaB Mini-intein. Journal of Biological Chemistry, 2002, 277, 7790-7798.	3.4	66
86	15N-Labelled proteins by cell-free protein synthesis FEBS Journal, 2006, 273, 4154-4159.	4.7	66
87	Translational incorporation of L-3,4-dihydroxyphenylalanine into proteins. FEBS Journal, 2005, 272, 3162-3171.	4.7	64
88	Hydration of DNA in aqueous solution: NMR evidence for a kinetic destabilization of the minor groove hydration of d-(TTAA)2versus d-(AATT)2segments. Nucleic Acids Research, 1994, 22, 2249-2254.	14.5	63
89	Direct NMR observation of the Cys-14 thiol proton of reducedEscherichia coliglutaredoxin-3 supports the presence of an active site thiol-thiolate hydrogen bond. FEBS Letters, 1999, 449, 196-200.	2.8	63
90	NMR structure of the N-terminal domain of E. coli DnaB helicase: implications for structure rearrangements in the helicase hexamer. Structure, 1999, 7, 681-690.	3.3	62

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91	Crystal and Solution Structures of the Helicase-binding Domain of Escherichia coli Primase. Journal of Biological Chemistry, 2005, 280, 11495-11504.	3.4	62
92	<i>De Novo</i> Discovery of Nonstandard Macrocyclic Peptides as Noncompetitive Inhibitors of the Zika Virus NS2B-NS3 Protease. ACS Medicinal Chemistry Letters, 2019, 10, 168-174.	2.8	62
93	Protein structure and interactions by combined use of sequential NMR assignments and isotope labeling. Journal of the American Chemical Society, 1987, 109, 1090-1092.	13.7	61
94	Glutaredoxin-3 from Escherichia coli. Journal of Biological Chemistry, 1996, 271, 6736-6745.	3.4	61
95	Role of Charged and Hydrophobic Residues in the Oligomerization of the PYRIN Domain of ASC. Biochemistry, 2005, 44, 575-583.	2.5	61
96	Protein hydration in aqueous solution. Faraday Discussions, 1992, 93, 35-45.	3.2	60
97	1H-Detected INEPT-INADEQUATE at Natural 13C Abundance. Journal of Magnetic Resonance Series A, 1995, 113, 128-130.	1.6	60
98	Pathway of chymotrypsin evolution suggested by the structure of the FMN-binding protein from Desulfovibrio vulgaris (Miyazaki F). Nature Structural Biology, 1997, 4, 975-979.	9.7	60
99	NMR structure of the LCCL domain and implications for DFNA9 deafness disorder. EMBO Journal, 2001, 20, 5347-5353.	7.8	60
100	Cell-Free Protein Synthesis for Analysis by NMR Spectroscopy. Methods in Molecular Biology, 2008, 426, 257-268.	0.9	60
101	Sequence-Specific and Stereospecific Assignment of Methyl Groups Using Paramagnetic Lanthanides. Journal of the American Chemical Society, 2007, 129, 13749-13757.	13.7	59
102	Gd3+ Spin Labeling for Measuring Distances in Biomacromolecules. Methods in Enzymology, 2015, 563, 415-457.	1.0	59
103	How reliable are pseudocontact shifts induced in proteins and ligands by mobile paramagnetic metal tags? A modelling study. Journal of Biomolecular NMR, 2013, 56, 203-216.	2.8	58
104	Editing of 2D 1H NMR spectra using X half-filters. combined use with residue-selective 15N labeling of proteins. Journal of Magnetic Resonance, 1986, 70, 500-505.	0.5	57
105	POMA: A Complete Mathematica Implementation of the NMR Product-Operator Formalism. Journal of Magnetic Resonance Series A, 1993, 101, 103-105.	1.6	57
106	Lipid membrane binding of NK-lysin. FEBS Letters, 1998, 425, 341-344.	2.8	57
107	Solution Structure of a Naturally-Occurring Zincâ~'Peptide Complex Demonstrates that the N-Terminal Zinc-Binding Module of the Lasp-1 LIM Domain Is an Independent Folding Unitâ€,‡. Biochemistry, 1996, 35, 12723-12732.	2.5	56
108	Weak Alignment of Paramagnetic Proteins Warrants Correction for Residual CSA Effects in Measurements of Pseudocontact Shifts. Journal of the American Chemical Society, 2005, 127, 17190-17191.	13.7	56

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109	Efficient χ-tensor determination and NH assignment of paramagnetic proteins. Journal of Biomolecular NMR, 2006, 35, 79-87.	2.8	56
110	[Ln(DPA) ₃] ^{3â^'} Is a Convenient Paramagnetic Shift Reagent for Protein NMR Studies. Journal of the American Chemical Society, 2009, 131, 10352-10353.	13.7	56
111	NMR structure determination reveals that the homeodomain is connected through a flexible linker to the main body in the Drosophila Antennapedia protein Proceedings of the National Academy of Sciences of the United States of America, 1992, 89, 10738-10742.	7.1	55
112	Polypeptide hydration in mixed solvents at low temperatures. Journal of the American Chemical Society, 1992, 114, 7093-7095.	13.7	55
113	Warum Pentose- und nicht Hexose-Nucleinsären??. Teil VI. â€ ⁻ Homo-DNS':1H-,13C-,31P- und15N-NMR-spektroskopische Untersuchung von ddGlc(A-A-A-A-A-T-T-T-T) in wäsriger Lösung. Helvetica Chimica Acta, 1993, 76, 2701-2756.	1.6	55
114	Amino-acid Type Identification in 15N-HSQC Spectra by Combinatorial Selective 15N-labelling. Journal of Biomolecular NMR, 2006, 34, 13-21.	2.8	55
115	Gadolinium(III) Spin Labels for High‣ensitivity Distance Measurements in Transmembrane Helices. Angewandte Chemie - International Edition, 2013, 52, 11831-11834.	13.8	54
116	The unstructured C-terminus of the τ subunit of Escherichia coli DNA polymerase III holoenzyme is the site of interaction with the α subunit. Nucleic Acids Research, 2007, 35, 2813-2824.	14.5	53
117	Sensitive NMR Approach for Determining the Binding Mode of Tightly Binding Ligand Molecules to Protein Targets. Journal of the American Chemical Society, 2016, 138, 4539-4546.	13.7	53
118	NMR Structure of Citrobacter freundii AmpD, Comparison with Bacteriophage T7 Lysozyme and Homology with PGRP Domains. Journal of Molecular Biology, 2003, 327, 833-842.	4.2	52
119	W-band orientation selective DEER measurements on a Gd3+/nitroxide mixed-labeled protein dimer with a dual mode cavity. Journal of Magnetic Resonance, 2013, 227, 66-71.	2.1	52
120	Bound or Free: Interaction of the C-Terminal Domain ofEscherichia coliSingle-Stranded DNA-Binding Protein (SSB) with the Tetrameric Core of SSB. Biochemistry, 2014, 53, 1925-1934.	2.5	52
121	Thiol–ene reaction: a versatile tool in site-specific labelling of proteins with chemically inert tags for paramagnetic NMR. Chemical Communications, 2012, 48, 2704.	4.1	51
122	3â€Mercaptoâ€2,6â€Pyridinedicarboxylic Acid: A Small Lanthanideâ€Binding Tag for Protein Studies by NMR Spectroscopy. Chemistry - A European Journal, 2010, 16, 3827-3832.	3.3	50
123	Binding mode of the activityâ€modulating Câ€ŧerminal segment of <scp>NS</scp> 2B to <scp>NS</scp> 3 in the dengue virus <scp>NS</scp> 2B– <scp>NS</scp> 3 protease. FEBS Journal, 2014, 281, 1517-1533.	4.7	50
124	Improved Spectral Resolution in 1H NMR Spectroscopy by Homonuclear Semiselective Shaped Pulse Decoupling during Acquisition. Journal of the American Chemical Society, 1994, 116, 8847-8848.	13.7	49
125	High-yield cell-free protein synthesis for site-specific incorporation of unnatural amino acids at two sites. Biochemical and Biophysical Research Communications, 2012, 418, 652-656.	2.1	49
126	NMR studies of ligand binding. Current Opinion in Structural Biology, 2018, 48, 16-22.	5.7	48

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127	Determination of the Nuclear Magnetic Resonance Structure of the DNA-binding Domain of the P22 c2 Repressor (1 to 76) in Solution and Comparison with the DNA-binding Domain of the 434 Repressor. Journal of Molecular Biology, 1994, 235, 1003-1020.	4.2	47
128	Water molecules in DNA recognition I: hydration lifetimes of trp operator DNA in solution measured by NMR spectroscopy 1 1Edited by B. Honig. Journal of Molecular Biology, 1998, 282, 847-858.	4.2	47
129	Modulation of the distance dependence of paramagnetic relaxation enhancements by CSA×DSA cross-correlation. Journal of Magnetic Resonance, 2004, 171, 233-243.	2.1	46
130	The dengue virus NS2B–NS3 protease retains the closed conformation in the complex with BPTI. FEBS Letters, 2014, 588, 2206-2211.	2.8	46
131	Biocompatible Macrocyclization between Cysteine and 2-Cyanopyridine Generates Stable Peptide Inhibitors. Organic Letters, 2019, 21, 4709-4712.	4.6	46
132	Solution conformations of a linked construct of the Zika virus NS2B-NS3 protease. Antiviral Research, 2017, 142, 141-147.	4.1	45
133	Selective Distance Measurements Using Triple Spin Labeling with Gd ³⁺ , Mn ²⁺ , and a Nitroxide. Journal of Physical Chemistry Letters, 2017, 8, 5277-5282.	4.6	45
134	A Probehead with Switchable Quality Factor. Suppression of Radiation Damping. Journal of Magnetic Resonance Series B, 1995, 106, 199-201.	1.6	44
135	Engineering of a bis-chelator motif into a protein α-helix for rigid lanthanide binding and paramagnetic NMR spectroscopy. Chemical Communications, 2011, 47, 7368.	4.1	44
136	NMR structure of oxidized glutaredoxin 3 from Escherichia coli. Journal of Molecular Biology, 2000, 303, 423-432.	4.2	43
137	Determination of scalar coupling constants by inverse Fourier transformation of in-phase multiplets. Journal of Magnetic Resonance, 1992, 99, 552-560.	0.5	42
138	Stabilization of Native Protein Fold by Intein-Mediated Covalent Cyclization. Journal of Molecular Biology, 2005, 346, 1095-1108.	4.2	42
139	NMR Structure of the WIF Domain of the Human Wnt-Inhibitory Factor-1. Journal of Molecular Biology, 2006, 357, 942-950.	4.2	42
140	A New Gd ³⁺ Spin Label for Gd ³⁺ –Gd ³⁺ Distance Measurements in Proteins Produces Narrow Distance Distributions. Journal of Physical Chemistry Letters, 2015, 6, 5016-5021.	4.6	42
141	NMR experiments for the sign determination of homonuclear scalar and residual dipolar couplings. Journal of Biomolecular NMR, 2000, 16, 343-346.	2.8	41
142	Selective excitation of intense solvent signals in the presence of radiation damping. Journal of Biomolecular NMR, 1995, 5, 420-6.	2.8	39
143	Solution structure of Domains IVa and V of the Ï,, subunit of Escherichia coli DNA polymerase III and interaction with the α subunit. Nucleic Acids Research, 2007, 35, 2825-2832.	14.5	39
144	RIDME distance measurements using Gd(<scp>iii</scp>) tags with a narrow central transition. Physical Chemistry Chemical Physics, 2016, 18, 19037-19049.	2.8	39

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145	Suppression of isotope scrambling in cell-free protein synthesis by broadband inhibition of PLP enymes for selective 15N-labelling and production of perdeuterated proteins in H2O. Journal of Biomolecular NMR, 2011, 50, 35-42.	2.8	37
146	Compact, hydrophilic, lanthanide-binding tags for paramagnetic NMR spectroscopy. Chemical Science, 2015, 6, 2614-2624.	7.4	37
147	Mosquito-Derived Anophelin Sulfoproteins Are Potent Antithrombotics. ACS Central Science, 2018, 4, 468-476.	11.3	37
148	Structure of the RTP-DNA complex and the mechanism of polar replication fork arrest. Nature Structural Biology, 2001, 8, 206-210.	9.7	36
149	Intramolecular binding mode of the C-terminus of <i>Escherichia coli</i> single-stranded DNA binding protein determined by nuclear magnetic resonance spectroscopy. Nucleic Acids Research, 2014, 42, 2750-2757.	14.5	36
150	Altered conformational sampling along an evolutionary trajectory changes the catalytic activity of an enzyme. Nature Communications, 2020, 11, 5945.	12.8	36
151	Paramagnetic Chemical Probes for Studying Biological Macromolecules. Chemical Reviews, 2022, 122, 9571-9642.	47.7	36
152	Cell-free synthesis of 15 N-labeled proteins for NMR studies. IUBMB Life, 2005, 57, 615-622.	3.4	35
153	NMR study of complexes between low molecular mass inhibitors and the West Nile virus NS2B–NS3 protease. FEBS Journal, 2009, 276, 4244-4255.	4.7	35
154	1H And 13C NMR chemical shifts of the diastereotopic methyl groups of valyl and leucyl residues in peptides and proteins. Tetrahedron, 1990, 46, 3287-3296.	1.9	34
155	Isolation and structure of a new galactolipid from oat seeds. Lipids, 1998, 33, 355-363.	1.7	34
156	Proofreading exonuclease on a tether: the complex between the E. coli DNA polymerase III subunits α, Îμ, Î, and β reveals a highly flexible arrangement of the proofreading domain. Nucleic Acids Research, 2013, 41, 5354-5367.	14.5	34
157	3D Structure Determination of an Unstable Transient Enzyme Intermediate by Paramagnetic NMR Spectroscopy. Angewandte Chemie - International Edition, 2016, 55, 13744-13748.	13.8	34
158	Heteronuclear correlation experiments for the determination of one-bond coupling constants. Journal of Biomolecular NMR, 1998, 11, 445-450.	2.8	33
159	Strategies for Measurements of Pseudocontact Shifts in Protein NMR Spectroscopy. ChemPhysChem, 2007, 8, 2309-2313.	2.1	33
160	Generation of Pseudocontact Shifts in Protein NMR Spectra with a Genetically Encoded Cobalt(II)â€Binding Amino Acid. Angewandte Chemie - International Edition, 2011, 50, 692-694.	13.8	33
161	Site-Specific Incorporation of Selenocysteine by Genetic Encoding as a Photocaged Unnatural Amino Acid. Bioconjugate Chemistry, 2018, 29, 2257-2264.	3.6	33
162	Paramagpy: software for fitting magnetic susceptibility tensors using paramagnetic effects measured in NMR spectra. Magnetic Resonance, 2020, 1, 1-12.	1.9	33

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