Hans Robert Kalbitzer

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Equilibria between conformational states of the Ras oncogene protein revealed by high pressure crystallography. Chemical Science, 2022, 13, 2001-2010.	7.4	17
2	Pressure-dependent electronic structure calculations using integral equation-based solvation models. Biophysical Chemistry, 2020, 257, 106258.	2.8	14
3	RNA and DNA Binding Epitopes of the Cold Shock Protein TmCsp from the Hyperthermophile Thermotoga maritima. Protein Journal, 2020, 39, 487-500.	1.6	4
4	Pressure dependence of side chain 1H and 15N-chemical shifts in the model peptides Ac-Gly-Gly-Xxx-Ala-NH2. Journal of Biomolecular NMR, 2020, 74, 381-399.	2.8	1
5	Complete sequential assignment and secondary structure prediction of the cannulae forming protein CanA from the hyperthermophilic archaeon Pyrodictium abyssi. Biomolecular NMR Assignments, 2020, 14, 141-146.	0.8	3
6	1H NMR spectroscopy quantifies visibility of lipoproteins, subclasses, and lipids at varied temperatures and pressures. Journal of Lipid Research, 2019, 60, 1516-1534.	4.2	21
7	The pressure and temperature perturbation approach reveals a whole variety of conformational substates of amyloidogenic hIAPP monitored by 2D NMR spectroscopy. Biophysical Chemistry, 2019, 254, 106239.	2.8	12
8	High pressure response of 1H NMR chemical shifts of purine nucleotides. Biophysical Chemistry, 2019, 254, 106261.	2.8	1
9	Inhibition of amyloid Aβ aggregation by high pressures or specific <scp>d</scp> -enantiomeric peptides. Chemical Communications, 2018, 54, 3294-3297.	4.1	13
10	Stereospecific assignment of the asparagine and glutamine sidechain amide protons in proteins from chemical shift analysis. Journal of Biomolecular NMR, 2017, 67, 157-164.	2.8	5
11	High pressure 31P NMR spectroscopy on guanine nucleotides. Journal of Biomolecular NMR, 2017, 67, 1-13.	2.8	7
12	Pressure response of 31 P chemical shifts of adenine nucleotides. Biophysical Chemistry, 2017, 231, 50-54.	2.8	4
13	Pressure dependence of side chain 13C chemical shifts in model peptides Ac-Gly-Gly-Xxx-Ala-NH2. Journal of Biomolecular NMR, 2017, 69, 53-67.	2.8	8
14	Die Basislinie der chemischen Verschiebung in Hochdruckâ€NMRâ€ S pektren von Proteinen. Angewandte Chemie, 2016, 128, 8900-8904.	2.0	3
15	The Chemical Shift Baseline for Highâ€Pressure NMR Spectra of Proteins. Angewandte Chemie - International Edition, 2016, 55, 8757-8760.	13.8	23
16	Pressure dependence of backbone chemical shifts in the model peptides Ac-Gly-Gly-Xxx-Ala-NH2. Journal of Biomolecular NMR, 2016, 65, 65-77.	2.8	11
17	Conformational Substates of Amyloidogenic hIAPP Revealed by High Pressure NMR Spectroscopy. ChemistrySelect, 2016, 1, 3239-3243.	1.5	6
18	PSCD Domains of Pleuralin-1 from the Diatom Cylindrotheca fusiformis : NMR Structures and Interactions with Other Biosilica-Associated Proteins. Structure, 2016, 24, 1178-1191.	3.3	14

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19	Structural transitions in full-length human prion protein detected by xenon as probe and spin labeling of the N-terminal domain. Scientific Reports, 2016, 6, 28419.	3.3	8
20	Cosolvent and Crowding Effects on the Temperature and Pressure Dependent Conformational Dynamics and Stability of Globular Actin. Journal of Physical Chemistry B, 2016, 120, 6575-6586.	2.6	25
21	High Pressure NMR Methods for Characterizing Functional Substates of Proteins. Sub-Cellular Biochemistry, 2015, 72, 179-197.	2.4	17
22	Human Cytomegalovirus Major Immediate Early 1 Protein Targets Host Chromosomes by Docking to the Acidic Pocket on the Nucleosome Surface. Journal of Virology, 2014, 88, 1228-1248.	3.4	35
23	Formation of Fenestrae in Murine Liver Sinusoids Depends on Plasmalemma Vesicle-Associated Protein and Is Required for Lipoprotein Passage. PLoS ONE, 2014, 9, e115005.	2.5	52
24	Relationship between Nonlinear Pressure-Induced Chemical Shift Changes and Thermodynamic Parameters. Journal of Physical Chemistry B, 2014, 118, 5681-5690.	2.6	20
25	Elucidating the Mode of Action of a Typical Ras State 1(T) Inhibitor. Biochemistry, 2014, 53, 3867-3878.	2.5	16
26	Pressure response of amide one-bond J-couplings in model peptides and proteins. Journal of Biomolecular NMR, 2014, 60, 45-50.	2.8	5
27	Chemical shift assignments of the canecystatin-1 from Saccharum officinarum. Biomolecular NMR Assignments, 2013, 7, 163-165.	0.8	4
28	State 1(T) Inhibitors of Activated Ras. The Enzymes, 2013, 33 Pt A, 69-94.	1.7	10
29	1.2Ââ"« X-ray Structure of the Renal Potassium Channel Kv1.3 T1 Domain. Protein Journal, 2013, 32, 533-542.	1.6	3
30	Intrinsic Allosteric Inhibition of Signaling Proteins by Targeting Rare Interaction States Detected by Highâ€Pressure NMR Spectroscopy. Angewandte Chemie - International Edition, 2013, 52, 14242-14246.	13.8	60
31	A bacterial toxin catalyzing tyrosine glycosylation of Rho and deamidation of Gq and Gi proteins. Nature Structural and Molecular Biology, 2013, 20, 1273-1280.	8.2	61
32	Stem cell metabolic and spectroscopic profiling. Trends in Biotechnology, 2013, 31, 204-213.	9.3	34
33	Enhanced in vitro translation at reduced temperatures using a cold-shock RNA motif. Biotechnology Letters, 2013, 35, 389-395.	2.2	4
34	Distinct Conformational States of the Alzheimer βâ€Amyloid Peptide Can Be Detected by Highâ€Pressure NMR Spectroscopy. Angewandte Chemie - International Edition, 2013, 52, 8943-8947.	13.8	30
35	NMR Spectroscopy of Macrophages Loaded with Native, Oxidized or Enzymatically Degraded Lipoproteins. PLoS ONE, 2013, 8, e56360.	2.5	9
36	Pressure Dependence of 15N Chemical Shifts in Model Peptides Ac-Gly-Gly-X-Ala-NH2. Materials, 2012, 5, 1774-1786.	2.9	27

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37	A Singleâ€Cell NMR Membrane Transport Assay. ChemBioChem, 2012, 13, 2501-2504.	2.6	3
38	RNA secondary structure and in vitro translation efficiency. Protein Expression and Purification, 2012, 82, 26-31.	1.3	5
39	Metal–Bis(2â€picolyl)amine Complexes as Stateâ€1(T) Inhibitors of Activated Ras Protein. Angewandte Chemie - International Edition, 2012, 51, 10647-10651.	13.8	58
40	Genetic associations with lipoprotein subfractions provide information on their biological nature. Human Molecular Genetics, 2012, 21, 1433-1443.	2.9	28
41	Pulsed Pressure Perturbations, an Extra Dimension in NMR Spectroscopy of Proteins. Journal of the American Chemical Society, 2011, 133, 13646-13651.	13.7	35
42	Synthesis of New Water-Soluble Cholesterol Derivatives. Synthetic Communications, 2011, 41, 2876-2887.	2.1	3
43	Cu2+-cyclen as Probe to Identify Conformational States in Guanine Nucleotide Binding Proteins. Journal of the American Chemical Society, 2011, 133, 2048-2051.	13.7	20
44	Large-Scale Candidate Gene Analysis of HDL Particle Features. PLoS ONE, 2011, 6, e14529.	2.5	32
45	Intrinsic disorder in the common N-terminus of human adenovirus 5 E1B-55K and its related E1BN proteins indicated by studies on E1B-93R. Virology, 2011, 418, 133-143.	2.4	15
46	¹ H-Nuclear Magnetic Resonance Spectroscopy of Glioblastoma Cancer Stem Cells. Stem Cells and Development, 2011, 20, 2189-2195.	2.1	16
47	Novel Metal-Organic Frameworks Incorporating [Cp°2Mo2P4S] (Cp° = 1-tBu-3,4-Me2C5H2), P4S3 and Cu2l2 Building Blocks. European Journal of Inorganic Chemistry, 2011, 2011, 785-793.	2.0	4
48	Zinc(II)cyclen–peptide conjugates interacting with the weak effector binding state of Ras. Inorganica Chimica Acta, 2011, 365, 38-48.	2.4	21
49	Singular spectrum analysis for an automated solvent artifact removal and baseline correction of 1D NMR spectra. Journal of Magnetic Resonance, 2011, 210, 177-183.	2.1	8
50	Ceramic cells for high pressure NMR spectroscopy of proteins. Journal of Magnetic Resonance, 2010, 204, 196-199.	2.1	31
51	Automated solvent artifact removal and base plane correction of multidimensional NMR protein spectra by AUREMOL-SSA. Journal of Biomolecular NMR, 2010, 47, 101-111.	2.8	7
52	Mapping of protein structural ensembles by chemical shifts. Journal of Biomolecular NMR, 2010, 48, 71-83.	2.8	16
53	Stabilizing a Weak Binding State for Effectors in the Human Ras Protein by Cyclen Complexes. Angewandte Chemie - International Edition, 2010, 49, 3830-3833.	13.8	97
54	Limiting factors of the translation machinery. Journal of Biotechnology, 2010, 150, 44-50.	3.8	7

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55	The interaction of ammonia and xenon with the imidazole glycerol phosphate synthase from <i>Thermotoga maritima</i> as detected by NMR spectroscopy. Protein Science, 2010, 19, 1774-1782.	7.6	2
56	Conformational States of Human Rat Sarcoma (Ras) Protein Complexed with Its Natural Ligand GTP and Their Role for Effector Interaction and GTP Hydrolysis. Journal of Biological Chemistry, 2010, 285, 39768-39778.	3.4	120
57	Automated Protein NMR Structure Determination in Solution. Methods in Molecular Biology, 2010, 673, 95-127.	0.9	6
58	Improved Binding of Raf to Ras·GDP Is Correlated with Biological Activity. Journal of Biological Chemistry, 2009, 284, 31893-31902.	3.4	41
59	Ca2+-dependent Conformational Changes in a C-terminal Cytosolic Domain of Polycystin-2. Journal of Biological Chemistry, 2009, 284, 24372-24383.	3.4	26
60	Chemical shift optimization in multidimensional NMR spectra by AUREMOL-SHIFTOPT. Journal of Biomolecular NMR, 2009, 43, 197-210.	2.8	2
61	Protein structure calculation with data imputation: the use of substitute restraints. Journal of Biomolecular NMR, 2009, 45, 397-411.	2.8	2
62	NMR-assignments of a cytosolic domain of the C-terminus of polycystin-2. Biomolecular NMR Assignments, 2009, 3, 141-144.	0.8	5
63	NMR assignments of oxidised thioredoxin from Plasmodium falciparum. Biomolecular NMR Assignments, 2009, 3, 159-161.	0.8	3
64	NMR assignments of a 48ÂkDa tetramer of the T1 domain of the mammalian voltage gated potassium channel Kv1.4. Biomolecular NMR Assignments, 2009, 3, 167-170.	0.8	2
65	Crystallization and preliminary X-ray diffraction studies of the tetramerization domain derived from the human potassium channel Kv1.3. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 688-691.	0.7	1
66	Fundamental Link between Folding States and Functional States of Proteins. Journal of the American Chemical Society, 2009, 131, 16714-16719.	13.7	90
67	Infrequent cavity-forming fluctuations in HPr from Staphylococcus carnosus revealed by pressure- and temperature-dependent tyrosine ring flips. Protein Science, 2009, 13, 3104-3114.	7.6	45
68	Interaction of CheY2 and CheY2â€P with the cognate CheA kinase in the chemosensoryâ€signalling chain of <i>Sinorhizobium meliloti</i> . Molecular Microbiology, 2008, 69, 1373-1384.	2.5	13
69	Structure of the Leech Protein Saratin and Characterization of Its Binding to Collagen. Journal of Molecular Biology, 2008, 381, 913-927.	4.2	36
70	Reversible monomer-oligomer transition in human prion protein. Prion, 2008, 2, 118-122.	1.8	25
71	The lipoprotein subfraction profile: heritability and identification of quantitative trait loci. Journal of Lipid Research, 2008, 49, 715-723.	4.2	41
72	Species-specific Differences in the Intermediate States of Human and Syrian Hamster Prion Protein Detected by High Pressure NMR Spectroscopy. Journal of Biological Chemistry, 2007, 282, 22689-22698.	3.4	21

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73	Solid-State31P NMR Spectroscopy of Precipitated Guanine Nucleotide-Binding Protein Ras in Complexes with Its Effector Molecules Raf Kinase and RalGDS. Journal of Physical Chemistry B, 2007, 111, 2752-2757.	2.6	4
74	Human Immunodeficiency Virus Type 1 Nef protein modulates the lipid composition of virions and host cell membrane microdomains. Retrovirology, 2007, 4, 70.	2.0	70
75	Elucidation of Protein–Protein and Protein–Ligand Interactions by NMR Spectroscopy. , 2007, , 189-229.		0
76	Slow conformational dynamics of the guanine nucleotide-binding protein Ras complexed with the GTP analogue GTPÎ ³ S. FEBS Journal, 2007, 274, 1419-1433.	4.7	50
77	Combined chemical shift changes and amino acid specific chemical shift mapping of protein–protein interactions. Journal of Biomolecular NMR, 2007, 39, 275-289.	2.8	200
78	Rapid assignment of solution 31P NMR spectra of large proteins by solid-state spectroscopy. Biochemical and Biophysical Research Communications, 2006, 346, 301-305.	2.1	6
79	A general method for the unbiased improvement of solution NMR structures by the use of related X-ray data, the AUREMOL-ISIC algorithm. BMC Structural Biology, 2006, 6, 14.	2.3	5
80	Observation of intermediate states of the human prion protein by high pressure NMR spectroscopy. BMC Structural Biology, 2006, 6, 16.	2.3	44
81	AUREMOL-RFAC-3D, combination of R-factors and their use for automated quality assessment of protein solution structures. Journal of Biomolecular NMR, 2006, 37, 15-30.	2.8	11
82	Solution structure of human proinsulin C-peptide. FEBS Journal, 2005, 272, 4284-4293.	4.7	29
83	A restraint molecular dynamics and simulated annealing approach for protein homology modeling utilizing mean angles. BMC Bioinformatics, 2005, 6, 91.	2.6	15
84	Conformational states of human H-Ras detected by high-field EPR, ENDOR, and31P NMR spectroscopy. Magnetic Resonance in Chemistry, 2005, 43, S74-S83.	1.9	14
85	1H, 13C, andÂ15NÂSequence-specific Resonance Assignment and Secondary Structure ofÂPlasmodium falciparumÂThioredoxin. Journal of Biomolecular NMR, 2005, 32, 340-340.	2.8	3
86	Sequential Backbone Assignment of Peroxisome Proliferator-Activated Receptor-Î ³ Ligand Binding Domain. Journal of Biomolecular NMR, 2005, 32, 259-259.	2.8	3
87	PERMOL: restraint-based protein homology modeling using DYANA or CNS. Bioinformatics, 2005, 21, 2110-2111.	4.1	7
88	NMR Spectroscopic Study of Noble Gas Binding into the Engineered Cavity of HPr(I14A) from Staphylococcus carnosus. Journal of Physical Chemistry B, 2005, 109, 17795-17798.	2.6	6
89	Solution Structure of the Ran-binding Domain 2 of RanBP2 and its Interaction with the C Terminus of Ran. Journal of Molecular Biology, 2005, 348, 711-725.	4.2	15
90	A novel mechanism for the modulation of the Ras-effector interaction by small molecules. Biochemical and Biophysical Research Communications, 2005, 334, 709-713.	2.1	47

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91	Conformational States of Ras Complexed with the GTP Analogue GppNHp or GppCH2p:  Implications for the Interaction with Effector Proteins. Biochemistry, 2005, 44, 2225-2236.	2.5	85
92	High-Resolution Structure of the Histidine-Containing Phosphocarrier Protein (HPr) from Staphylococcus aureus and Characterization of Its Interaction with the Bifunctional HPr Kinase/Phosphorylase. Journal of Bacteriology, 2004, 186, 5906-5918.	2.2	22
93	The central domain of the matrix protein of HIV-1: influence on protein structure and virus infectivity. Biological Chemistry, 2004, 385, 303-13.	2.5	3
94	Conformational States of the Small G Protein Arf-1 in Complex with the Guanine Nucleotide Exchange Factor ARNO-Sec7. Journal of Biological Chemistry, 2004, 279, 17004-17012.	3.4	8
95	Solution structure of the active-centre mutant I14A of the histidine-containing phosphocarrier protein from Staphylococcus carnosus. FEBS Journal, 2004, 271, 4815-4824.	0.2	10
96	Improved simulation of NOESY spectra by RELAX-JT2 including effects of J-coupling, transverse relaxation and chemical shift anisotropy. Journal of Biomolecular NMR, 2004, 30, 121-131.	2.8	12
97	Automated structure determination of proteins by NMR spectroscopy. Progress in Nuclear Magnetic Resonance Spectroscopy, 2004, 44, 33-96.	7.5	98
98	High-temperature solution NMR structure of TmCsp. Protein Science, 2004, 13, 342-350.	7.6	18
99	Perturbation of the conformational equilibria in Ras by selective mutations as studied by31P NMR spectroscopy. FEBS Letters, 2004, 578, 305-310.	2.8	64
100	Solution Structures of the Inactive and BeF3-activated Response Regulator CheY2. Journal of Molecular Biology, 2004, 338, 287-297.	4.2	16
101	Solid-state 31P NMR Spectroscopy of Microcrystals of the Ras Protein and its Effector Loop Mutants: Comparison Between Crystalline and Solution State. Journal of Molecular Biology, 2004, 342, 1033-1040.	4.2	22
102	High-sensitivity sapphire cells for high pressure NMR spectroscopy on proteins. Journal of Magnetic Resonance, 2003, 161, 127-131.	2.1	47
103	Solution structure of the matrix attachment region-binding domain of chicken MeCP2. FEBS Journal, 2003, 270, 3263-3270.	0.2	15
104	NMR-Spectroscopic Mapping of an Engineered Cavity in the I14A Mutant of HPr fromStaphylococcuscarnosusUsing Xenon. Journal of the American Chemical Society, 2003, 125, 8726-8727.	13.7	37
105	Glucosylation of Ras byClostridium sordelliiLethal Toxin:Â Consequences for Effector Loop Conformations Observed by NMR Spectroscopyâ€. Biochemistry, 2003, 42, 11951-11959.	2.5	33
106	Structure Determination and Ligand Interactions of the PDZ2b Domain of PTP-Bas (hPTP1E): Splicing-induced Modulation of Ligand Specificity. Journal of Molecular Biology, 2003, 334, 143-155.	4.2	29
107	Role of Entropy in Protein Thermostability:Â Folding Kinetics of a Hyperthermophilic Cold Shock Protein at High Temperatures Using19F NMRâ€. Biochemistry, 2002, 41, 11670-11680.	2.5	64
108	Myosin II from rabbit skeletal muscle andDictyostelium discoideumand its interaction with F-actin studied by1H NMR spectroscopy. FEBS Letters, 2002, 521, 121-126.	2.8	2

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109	Observation of Slow Dynamic Exchange Processes in Ras Protein Crystals by 31P Solid State NMR Spectroscopy. Journal of Molecular Biology, 2002, 323, 899-907.	4.2	22
110	Synthesis, characterization and application of two nucleoside triphosphate analogues, GTPγNH2 and GTPγF. FEBS Journal, 2002, 269, 3270-3278.	0.2	16
111	High resolution proton magnetic resonance spectroscopy of human cervical mucus. Journal of Pharmaceutical and Biomedical Analysis, 2002, 28, 827-840.	2.8	7
112	1H-NMR parameters of common amino acid residues measured in aqueous solutions of the linear tetrapeptides Gly-Gly-X-Ala at pressures between 0.1 and 200 MPa. Biophysical Chemistry, 2002, 96, 129-140.	2.8	65
113	Sequence-specific resonance assignment of the second Ran-binding domain of human RanBP2. Journal of Biomolecular NMR, 2002, 22, 185-186.	2.8	2
114	Automated assignment of NOESY NMR spectra using a knowledge based method (KNOWNOE). Journal of Biomolecular NMR, 2002, 23, 271-287.	2.8	53
115	High-pressure NMR study of the complex of a GTPase Rap1A with its effector RalGDS. FEBS Letters, 2001, 506, 180-184.	2.8	12
116	Structure of the Metalâ^`Water Complex in Ras·GDP Studied by High-Field EPR Spectroscopy and 31P NMR Spectroscopy. Biochemistry, 2001, 40, 1884-1889.	2.5	46
117	1H, 13C and 15N sequence-specific resonance assignment of the PSCD4 domain of diatom cell wall protein pleuralin-1 [etter]. Journal of Biomolecular NMR, 2001, 20, 191-192.	2.8	2
118	Sequential assignment and secondary structure of the 14 kDa chemotactic protein CheY2 from Sinorhizobium meliloti. Journal of Biomolecular NMR, 2001, 19, 287-288.	2.8	2
119	Sequential assignment and secondary structure of saratin, an inhibitor of von Willebrand factor-dependent platelet adhesion to collagen. Journal of Biomolecular NMR, 2001, 21, 77-78.	2.8	3
120	Overcoming the problems associated with poor spectra quality of the protein kinase Byr2 using residual dipolar couplings. Protein Science, 2001, 10, 1260-1263.	7.6	2
121	Solution Structure of the Ras Binding Domain of the Protein Kinase Byr2 from Schizosaccharomyces pombe. Structure, 2001, 9, 1029-1041.	3.3	52
122	Physiological Conditions and Practicality for Protein Nuclear Magnetic Resonance Spectroscopy: Experimental Methodologies and Theoretical Background. Methods in Enzymology, 2001, 339, 3-19.	1.0	10
123	Pressure-induced local unfolding of the Ras binding domain of RalGDS. Nature Structural Biology, 2000, 7, 547-550.	9.7	39
124	RFAC, a program for automated NMR R-factor estimation. Journal of Biomolecular NMR, 2000, 17, 137-151.	2.8	50
125	Sequence-specific 1H, 13C, and 15N assignments of the MAR-binding domain of chicken MeCP2/ARBP. Journal of Biomolecular NMR, 2000, 17, 175-176.	2.8	2
126	Molecular Alignment of Proteins in Bicellar Solutions: Quantitative Evaluation of Effects Induced in 2D COSY Spectra. Biochemical and Biophysical Research Communications, 2000, 272, 694-698.	2.1	9

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127	¹⁵ N and ¹ H NMR study of histidine containing protein (hpr) from <i>staphylococcus carnosus</i> at high pressure. Protein Science, 2000, 9, 693-703.	7.6	42
128	Thermodynamic and Kinetic Characterization of the Interaction between the Ras Binding Domain of AF6 and Members of the Ras Subfamily. Journal of Biological Chemistry, 1999, 274, 13556-13562.	3.4	126
129	NMR Structure and Functional Characteristics of the Hydrophilic N Terminus of the Potassium Channel β-Subunit Kvβ1.1. Journal of Biological Chemistry, 1999, 274, 35521-35525.	3.4	35
130	Control of K+ channel gating by protein phosphorylation: structural switches of the inactivation gate. Nature Structural Biology, 1999, 6, 146-150.	9.7	64
131	Computer Assisted Assignment of13C or15N Edited 3D-NOESY–HSQC Spectra Using Back Calculated and Experimental Spectra. Journal of Magnetic Resonance, 1999, 137, 39-45.	2.1	26
132	Conformational States of the Nuclear GTP-Binding Protein Ran and Its Complexes with the Exchange Factor RCC1 and the Effector Protein RanBP1â€. Biochemistry, 1999, 38, 11250-11260.	2.5	43
133	Structure of the anchor-domain of myristoylated and non-myristoylated HIV-1 Nef protein 1 1Edited by A. R. Fersht. Journal of Molecular Biology, 1999, 289, 123-138.	4.2	107
134	Nucleotide-binding characteristics of human guanylate-binding protein 1 (hGBP1) and identification of the third GTP-binding motif 1 1Edited by P. E. Wright. Journal of Molecular Biology, 1999, 292, 321-332.	4.2	114
135	Determination of Mean and Standard Deviation of Dihedral Angles. Biochemical and Biophysical Research Communications, 1999, 257, 348-350.	2.1	13
136	Structural studies of histidine-containing phosphocarrier protein from Enterococcus faecalis. FEBS Journal, 1998, 252, 51-58.	0.2	9
137	Structure of the Ras-binding domain of RalGEF and implications for Ras binding and signalling. Nature Structural Biology, 1997, 4, 694-699.	9.7	111
138	NMR structure of inactivation gates from mammalian voltage-dependent potassium channels. Nature, 1997, 385, 272-275.	27.8	104
139	Relax, a Flexible Program for the Back Calculation of NOESY Spectra Based on Complete-Relaxation-Matrix Formalism. Journal of Magnetic Resonance, 1997, 124, 177-188.	2.1	47
140	Use of Global Symmetries in Automated Signal Class Recognition by a Bayesian Method. Journal of Magnetic Resonance, 1997, 129, 165-172.	2.1	11
141	Synthesis and NMR spectroscopy of peptides containing either phosphorylated or phosphonylated <i>cis</i> ―or <i>trans</i> â€4â€hydroxy‣â€proline. Chemical Biology and Drug Design, 1997, 49, 163-173.	1.1	9
142	Conformational Transitions in p21rasand in Its Complexes with the Effector Protein Raf-RBD and the GTPase Activating Protein GAPâ€. Biochemistry, 1996, 35, 10308-10320.	2.5	227
143	Mobility of the N-Terminal Segment of Rabbit Skeletal Muscle F-Actin Detected by1H and19F Nuclear Magnetic Resonance Spectroscopy. Biochemistry, 1996, 35, 12686-12693.	2.5	28
144	Human Immunodeficiency Virus Type 1 Nef Protein Is Incorporated into Virus Particles and Specifically Cleaved by the Viral Proteinase. Virology, 1996, 219, 228-236.	2.4	190

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145	Polyamine Spider Toxins and Mammalian N-Methyl-d-Aspartate Receptors. Structural Basis for Channel Blocking and Binding of Argiotoxin636. FEBS Journal, 1996, 240, 416-426.	0.2	15
146	Indirect Referencing of31P and19F NMR Spectra. Journal of Magnetic Resonance Series B, 1996, 113, 177-178.	1.6	58
147	The Recombinant Dehydrin-Like Desiccation Stress Protein from the Resurrection PlantCraterostigma plantagineumDisplays No Defined Three-Dimensional Structure in Its Native State. Biological Chemistry Hoppe-Seyler, 1996, 377, 555-562.	1.4	67
148	Solidâ€phase synthesis of H―and methylphosphonopeptides. International Journal of Peptide and Protein Research, 1996, 47, 245-253.	0.1	6
149	Expression, Purification and Characterization of the Enzyme II Mannitol-Specific Domain from Staphylococcus carnosus and Determination of the Active-Site Cysteine Residue. FEBS Journal, 1995, 233, 116-122.	0.2	1
150	A general Bayesian method for an automated signal class recognition in 2D NMR spectra combined with a multivariate discriminant analysis. Journal of Biomolecular NMR, 1995, 5, 287-96.	2.8	42
151	Physiological buffers for NMR spectroscopy. Journal of Biomolecular NMR, 1995, 5, 321-2.	2.8	25
152	Substrate-assisted catalysis as a mechanism for GTP hydrolysis of p21ras and other GTP-binding proteins. Nature Structural Biology, 1995, 2, 36-44.	9.7	259
153	Complete1H Nuclear Magnetic Resonance Assignments and Structural Characterization of a Fusion Protein of the α-Amylase Inhibitor Tendamistat with the Activation Domain of the Human Immunodeficiency Virus Type 1 Tat Protein. Journal of Molecular Biology, 1995, 250, 672-688.	4.2	12
154	Mechanism of the Activation of Proteinase Inhibitor Synthesis by Systemin Involves β-Sheet Structure, a Specific DNA-Binding Protein Domain. Journal of Structural Biology, 1995, 115, 30-36.	2.8	15
155	Stability and proteolytic domains of Nef protein from human immunodeficiency virus (HIV) type 1. FEBS Journal, 1994, 221, 811-819.	0.2	44
156	Mobile segments in rabbit skeletal muscle F-actin detected by1H nuclear magnetic resonance spectroscopy. FEBS Letters, 1994, 351, 405-410.	2.8	9
157	¹ H and ³¹ P NMR spectroscopy of phosphorylated model peptides. International Journal of Peptide and Protein Research, 1994, 44, 193-198.	0.1	44
158	Oligomerization of the Nef protein from human immunodeficiency virus (HIV) type 1. FEBS Journal, 1993, 214, 451-457.	0.2	33
159	The solution structure of the histidine-containing protein (HPr) from Staphylococcus aureus as determined by two-dimensional 1H-NMR spectroscopy. FEBS Journal, 1993, 216, 205-214.	0.2	43
160	Three-dimensional structures and properties of a transforming and a nontransforming glycine-12 mutant of p21H-ras. Biochemistry, 1993, 32, 8411-8420.	2.5	88
161	SHORT COMMUNICATION: Biochemical analysis of cervical mucus by nuclear magnetic resonance spectroscopy*. Human Reproduction, 1992, 7, 915-917.	0.9	10
162	High protein mobility in skinned rabbit muscle fibres observed by 1 H NMR spectroscopy. FEBS Letters, 1992, 298, 226-228.	2.8	2

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163	Expression, purification and biochemical characterisation of the human immunodificiency virus 1 nef gene product. FEBS Journal, 1992, 205, 1115-1121.	0.2	20
164	A new high sensitivity19F probe for labeling cysteine groups of proteins. NMR in Biomedicine, 1992, 5, 347-350.	2.8	24
165	C-terminal structure and mobility of rabbit skeletal muscle light meromyosin as studied by one- and two-dimensional proton NMR spectroscopy and x-ray small-angle scattering. Biochemistry, 1991, 30, 8083-8091.	2.5	13
166	Two-dimensional proton NMR studies on HPr protein from Staphylococcus aureus: complete sequential assignments and secondary structure. Biochemistry, 1991, 30, 11186-11192.	2.5	19
167	Rabbit skeletal muscle myosin unfolded carboxyl-terminus and its role in molecular assembly. FEBS Letters, 1991, 281, 23-26.	2.8	25
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