

Hans Robert Kalbitzer

List of Publications by Year in descending order

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177
papers

5,421
citations

76326

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110387

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all docs

183
docs citations

183
times ranked

5067
citing authors

#	ARTICLE	IF	CITATIONS
1	Substrate-assisted catalysis as a mechanism for GTP hydrolysis of p21ras and other GTP-binding proteins. <i>Nature Structural Biology</i> , 1995, 2, 36-44.	9.7	259
2	Conformational Transitions in p21ras and in Its Complexes with the Effector Protein Raf-RBD and the GTPase Activating Protein GAP. <i>Biochemistry</i> , 1996, 35, 10308-10320.	2.5	227
3	Combined chemical shift changes and amino acid specific chemical shift mapping of protein-protein interactions. <i>Journal of Biomolecular NMR</i> , 2007, 39, 275-289.	2.8	200
4	Human Immunodeficiency Virus Type 1 Nef Protein Is Incorporated into Virus Particles and Specifically Cleaved by the Viral Proteinase. <i>Virology</i> , 1996, 219, 228-236.	2.4	190
5	Thermodynamic and Kinetic Characterization of the Interaction between the Ras Binding Domain of AF6 and Members of the Ras Subfamily. <i>Journal of Biological Chemistry</i> , 1999, 274, 13556-13562.	3.4	126
6	Conformational States of Human Rat Sarcoma (Ras) Protein Complexed with Its Natural Ligand GTP and Their Role for Effector Interaction and GTP Hydrolysis. <i>Journal of Biological Chemistry</i> , 2010, 285, 39768-39778.	3.4	120
7	Nucleotide-binding characteristics of human guanylate-binding protein 1 (hGBP1) and identification of the third GTP-binding motif 1. Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1999, 292, 321-332.	4.2	114
8	Structure of the Ras-binding domain of RalGEF and implications for Ras binding and signalling. <i>Nature Structural Biology</i> , 1997, 4, 694-699.	9.7	111
9	Structure of the anchor-domain of myristoylated and non-myristoylated HIV-1 Nef protein 1. Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1999, 289, 123-138.	4.2	107
10	NMR structure of inactivation gates from mammalian voltage-dependent potassium channels. <i>Nature</i> , 1997, 385, 272-275.	27.8	104
11	Automated structure determination of proteins by NMR spectroscopy. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2004, 44, 33-96.	7.5	98
12	Stabilizing a Weak Binding State for Effectors in the Human Ras Protein by Cyclen Complexes. <i>Angewandte Chemie - International Edition</i> , 2010, 49, 3830-3833.	13.8	97
13	Fundamental Link between Folding States and Functional States of Proteins. <i>Journal of the American Chemical Society</i> , 2009, 131, 16714-16719.	13.7	90
14	Three-dimensional structures and properties of a transforming and a nontransforming glycine-12 mutant of p21H-ras. <i>Biochemistry</i> , 1993, 32, 8411-8420.	2.5	88
15	Conformational States of Ras Complexed with the GTP Analogue GppNHp or GppCH2p: Implications for the Interaction with Effector Proteins. <i>Biochemistry</i> , 2005, 44, 2225-2236.	2.5	85
16	Human Immunodeficiency Virus Type 1 Nef protein modulates the lipid composition of virions and host cell membrane microdomains. <i>Retrovirology</i> , 2007, 4, 70.	2.0	70
17	Characterisation of the metal-ion-GDP complex at the active sites of transforming and nontransforming p21 proteins by observation of the 17O-Mn superhyperfine coupling and by kinetic methods. <i>FEBS Journal</i> , 1987, 162, 49-55.	0.2	69
18	The Recombinant Dehydrin-Like Desiccation Stress Protein from the Resurrection Plant <i>Craterostigma plantagineum</i> Displays No Defined Three-Dimensional Structure in Its Native State. <i>Biological Chemistry Hoppe-Seyler</i> , 1996, 377, 555-562.	1.4	67

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19	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. <i>Biophysical Chemistry</i> , 2002, 96, 129-140.	2.8	65
20	Control of K+ channel gating by protein phosphorylation: structural switches of the inactivation gate. <i>Nature Structural Biology</i> , 1999, 6, 146-150.	9.7	64
21	Role of Entropy in Protein Thermostability: Folding Kinetics of a Hyperthermophilic Cold Shock Protein at High Temperatures Using ¹⁹ F NMR. <i>Biochemistry</i> , 2002, 41, 11670-11680.	2.5	64
22	Perturbation of the conformational equilibria in Ras by selective mutations as studied by ³¹ P NMR spectroscopy. <i>FEBS Letters</i> , 2004, 578, 305-310.	2.8	64
23	A bacterial toxin catalyzing tyrosine glycosylation of Rho and deamidation of Gq and Gi proteins. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1273-1280.	8.2	61
24	Intrinsic Allosteric Inhibition of Signaling Proteins by Targeting Rare Interaction States Detected by High-Pressure NMR Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 14242-14246.	13.8	60
25	Indirect Referencing of ³¹ P and ¹⁹ F NMR Spectra. <i>Journal of Magnetic Resonance Series B</i> , 1996, 113, 177-178.	1.6	58
26	Metal-Bis(2-picoly)amine Complexes as State-1(T) Inhibitors of Activated Ras Protein. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 10647-10651.	13.8	58
27	Automated assignment of NOESY NMR spectra using a knowledge based method (KNOWNOE). <i>Journal of Biomolecular NMR</i> , 2002, 23, 271-287.	2.8	53
28	Solution Structure of the Ras Binding Domain of the Protein Kinase Byr2 from <i>Schizosaccharomyces pombe</i> . <i>Structure</i> , 2001, 9, 1029-1041.	3.3	52
29	Formation of Fenestrae in Murine Liver Sinusoids Depends on Plasmalemma Vesicle-Associated Protein and Is Required for Lipoprotein Passage. <i>PLoS ONE</i> , 2014, 9, e115005.	2.5	52
30	RFAC, a program for automated NMR R-factor estimation. <i>Journal of Biomolecular NMR</i> , 2000, 17, 137-151.	2.8	50
31	Slow conformational dynamics of the guanine nucleotide-binding protein Ras complexed with the GTP analogue GTPγS. <i>FEBS Journal</i> , 2007, 274, 1419-1433.	4.7	50
32	Relax, a Flexible Program for the Back Calculation of NOESY Spectra Based on Complete-Relaxation-Matrix Formalism. <i>Journal of Magnetic Resonance</i> , 1997, 124, 177-188.	2.1	47
33	High-sensitivity sapphire cells for high pressure NMR spectroscopy on proteins. <i>Journal of Magnetic Resonance</i> , 2003, 161, 127-131.	2.1	47
34	A novel mechanism for the modulation of the Ras-effector interaction by small molecules. <i>Biochemical and Biophysical Research Communications</i> , 2005, 334, 709-713.	2.1	47
35	Structure of the Metal-Water Complex in Ras-GDP Studied by High-Field EPR Spectroscopy and ³¹ P NMR Spectroscopy. <i>Biochemistry</i> , 2001, 40, 1884-1889.	2.5	46
36	Infrequent cavity-forming fluctuations in HPr from <i>Staphylococcus carnosus</i> revealed by pressure- and temperature-dependent tyrosine ring flips. <i>Protein Science</i> , 2009, 13, 3104-3114.	7.6	45

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37	Stability and proteolytic domains of Nef protein from human immunodeficiency virus (HIV) type 1. FEBS Journal, 1994, 221, 811-819.	0.2	44
38	Observation of intermediate states of the human prion protein by high pressure NMR spectroscopy. BMC Structural Biology, 2006, 6, 16.	2.3	44
39	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
40	The solution structure of the histidine-containing protein (HPr) from Staphylococcus aureus as determined by two-dimensional ¹ H-NMR spectroscopy. FEBS Journal, 1993, 216, 205-214.	0.2	43
41	Conformational States of the Nuclear GTP-Binding Protein Ran and Its Complexes with the Exchange Factor RCC1 and the Effector Protein RanBP1. Biochemistry, 1999, 38, 11250-11260.	2.5	43
42	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
43	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
44	The lipoprotein subfraction profile: heritability and identification of quantitative trait loci. Journal of Lipid Research, 2008, 49, 715-723.	4.2	41
45	Improved Binding of Raf to Ras-GDP Is Correlated with Biological Activity. Journal of Biological Chemistry, 2009, 284, 31893-31902.	3.4	41
46	Pressure-induced local unfolding of the Ras binding domain of RaIGDS. Nature Structural Biology, 2000, 7, 547-550.	9.7	39
47	NMR-Spectroscopic Mapping of an Engineered Cavity in the I14A Mutant of HPr from <i>Staphylococcus carnosus</i> Using Xenon. Journal of the American Chemical Society, 2003, 125, 8726-8727.	13.7	37
48	Structure of the Leech Protein Saratin and Characterization of Its Binding to Collagen. Journal of Molecular Biology, 2008, 381, 913-927.	4.2	36
49	NMR Structure and Functional Characteristics of the Hydrophilic N Terminus of the Potassium Channel β -Subunit Kv _{2.1} . Journal of Biological Chemistry, 1999, 274, 35521-35525.	3.4	35
50	Pulsed Pressure Perturbations, an Extra Dimension in NMR Spectroscopy of Proteins. Journal of the American Chemical Society, 2011, 133, 13646-13651.	13.7	35
51	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
52	Stem cell metabolic and spectroscopic profiling. Trends in Biotechnology, 2013, 31, 204-213.	9.3	34
53	Oligomerization of the Nef protein from human immunodeficiency virus (HIV) type 1. FEBS Journal, 1993, 214, 451-457.	0.2	33
54	Glucosylation of Ras by <i>Clostridium sordellii</i> Lethal Toxin: Consequences for Effector Loop Conformations Observed by NMR Spectroscopy. Biochemistry, 2003, 42, 11951-11959.	2.5	33

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55	Large-Scale Candidate Gene Analysis of HDL Particle Features. PLoS ONE, 2011, 6, e14529.	2.5	32
56	The Structure of the EF-Tu . GDP . Me ²⁺ Complex. FEBS Journal, 1982, 124, 109-115.	0.2	31
57	Ceramic cells for high pressure NMR spectroscopy of proteins. Journal of Magnetic Resonance, 2010, 204, 196-199.	2.1	31
58	Distinct Conformational States of the Alzheimer β -Amyloid Peptide Can Be Detected by High-Pressure NMR Spectroscopy. Angewandte Chemie - International Edition, 2013, 52, 8943-8947.	13.8	30
59	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
60	Solution structure of human proinsulin C-peptide. FEBS Journal, 2005, 272, 4284-4293.	4.7	29
61	Mobility of the N-Terminal Segment of Rabbit Skeletal Muscle F-Actin Detected by ¹ H and ¹⁹ F Nuclear Magnetic Resonance Spectroscopy. Biochemistry, 1996, 35, 12686-12693.	2.5	28
62	Genetic associations with lipoprotein subfractions provide information on their biological nature. Human Molecular Genetics, 2012, 21, 1433-1443.	2.9	28
63	Pressure Dependence of ¹⁵ N Chemical Shifts in Model Peptides Ac-Gly-Gly-X-Ala-NH ₂ . Materials, 2012, 5, 1774-1786.	2.9	27
64	Computer Assisted Assignment of ¹³ C or ¹⁵ N Edited 3D-NOESY- ² D HSQC Spectra Using Back Calculated and Experimental Spectra. Journal of Magnetic Resonance, 1999, 137, 39-45.	2.1	26
65	Ca ²⁺ -dependent Conformational Changes in a C-terminal Cytosolic Domain of Polycystin-2. Journal of Biological Chemistry, 2009, 284, 24372-24383.	3.4	26
66	Rabbit skeletal muscle myosin unfolded carboxyl-terminus and its role in molecular assembly. FEBS Letters, 1991, 281, 23-26.	2.8	25
67	Physiological buffers for NMR spectroscopy. Journal of Biomolecular NMR, 1995, 5, 321-2.	2.8	25
68	Reversible monomer-oligomer transition in human prion protein. Prion, 2008, 2, 118-122.	1.8	25
69	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
70	A new high sensitivity ¹⁹ F probe for labeling cysteine groups of proteins. NMR in Biomedicine, 1992, 5, 347-350.	2.8	24
71	The Structural Isomerisation of Human-Muscle Adenylate Kinase as Studied by ¹ H-Nuclear Magnetic Resonance. FEBS Journal, 1982, 126, 531-536.	0.2	23
72	The Chemical Shift Baseline for High-Pressure NMR Spectra of Proteins. Angewandte Chemie - International Edition, 2016, 55, 8757-8760.	13.8	23

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73	Observation of Slow Dynamic Exchange Processes in Ras Protein Crystals by ³¹ P Solid State NMR Spectroscopy. <i>Journal of Molecular Biology</i> , 2002, 323, 899-907.	4.2	22
74	High-Resolution Structure of the Histidine-Containing Phosphocarrier Protein (HPr) from <i>Staphylococcus aureus</i> and Characterization of Its Interaction with the Bifunctional HPr Kinase/Phosphorylase. <i>Journal of Bacteriology</i> , 2004, 186, 5906-5918.	2.2	22
75	Solid-state ³¹ P NMR Spectroscopy of Microcrystals of the Ras Protein and its Effector Loop Mutants: Comparison Between Crystalline and Solution State. <i>Journal of Molecular Biology</i> , 2004, 342, 1033-1040.	4.2	22
76	Electron-paramagnetic-resonance studies of manganese(II) complexes with elongation factor Tu from <i>Bacillus stearothermophilus</i> . Observation of a GTP hydrolysis intermediate state complex. <i>FEBS Journal</i> , 1984, 141, 591-597.	0.2	21
77	Species-specific Differences in the Intermediate States of Human and Syrian Hamster Prion Protein Detected by High Pressure NMR Spectroscopy. <i>Journal of Biological Chemistry</i> , 2007, 282, 22689-22698.	3.4	21
78	Zinc(II)cyclen peptide conjugates interacting with the weak effector binding state of Ras. <i>Inorganica Chimica Acta</i> , 2011, 365, 38-48.	2.4	21
79	¹ H NMR spectroscopy quantifies visibility of lipoproteins, subclasses, and lipids at varied temperatures and pressures. <i>Journal of Lipid Research</i> , 2019, 60, 1516-1534.	4.2	21
80	Proton nuclear magnetic resonance studies on the structure and mechanism of the HPr protein of <i>Staphylococcus aureus</i> . <i>Biochemistry</i> , 1981, 20, 1599-1605.	2.5	20
81	Expression, purification and biochemical characterisation of the human immunodeficiency virus 1 nef gene product. <i>FEBS Journal</i> , 1992, 205, 1115-1121.	0.2	20
82	Cu ²⁺ -cyclen as Probe to Identify Conformational States in Guanine Nucleotide Binding Proteins. <i>Journal of the American Chemical Society</i> , 2011, 133, 2048-2051.	13.7	20
83	Relationship between Nonlinear Pressure-Induced Chemical Shift Changes and Thermodynamic Parameters. <i>Journal of Physical Chemistry B</i> , 2014, 118, 5681-5690.	2.6	20
84	Two-dimensional proton NMR studies on HPr protein from <i>Staphylococcus aureus</i> : complete sequential assignments and secondary structure. <i>Biochemistry</i> , 1991, 30, 11186-11192.	2.5	19
85	High-temperature solution NMR structure of TmCsp. <i>Protein Science</i> , 2004, 13, 342-350.	7.6	18
86	High Pressure NMR Methods for Characterizing Functional Substates of Proteins. <i>Sub-Cellular Biochemistry</i> , 2015, 72, 179-197.	2.4	17
87	Equilibria between conformational states of the Ras oncogene protein revealed by high pressure crystallography. <i>Chemical Science</i> , 2022, 13, 2001-2010.	7.4	17
88	On the Analysis of Competitive Binding of Various Ligands to Cooperative and Independent Binding Sites of Macromolecules. <i>Zeitschrift Fur Naturforschung - Section C Journal of Biosciences</i> , 1979, 34, 757-769.	1.4	16
89	Synthesis, characterization and application of two nucleoside triphosphate analogues, GTP ^γ and GTP ^β . <i>FEBS Journal</i> , 2002, 269, 3270-3278.	0.2	16
90	Solution Structures of the Inactive and BeF ₃ -activated Response Regulator CheY2. <i>Journal of Molecular Biology</i> , 2004, 338, 287-297.	4.2	16

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91	Mapping of protein structural ensembles by chemical shifts. <i>Journal of Biomolecular NMR</i> , 2010, 48, 71-83.	2.8	16
92	¹ H-Nuclear Magnetic Resonance Spectroscopy of Glioblastoma Cancer Stem Cells. <i>Stem Cells and Development</i> , 2011, 20, 2189-2195.	2.1	16
93	Elucidating the Mode of Action of a Typical Ras State 1(T) Inhibitor. <i>Biochemistry</i> , 2014, 53, 3867-3878.	2.5	16
94	The effect of phosphorylation of the histidyl residue in the tetrapeptide Gly-Gly-His-Ala. Changes of chemical shift and pK values in ¹ H- and ³¹ P-NMR spectra. <i>Magnetic Resonance in Chemistry</i> , 1981, 17, 88-91.	0.7	15
95	Mechanism of the Activation of Proteinase Inhibitor Synthesis by Systemin Involves β^2 -Sheet Structure, a Specific DNA-Binding Protein Domain. <i>Journal of Structural Biology</i> , 1995, 115, 30-36.	2.8	15
96	Polyamine Spider Toxins and Mammalian N-Methyl-d-Aspartate Receptors. Structural Basis for Channel Blocking and Binding of Argiotoxin636. <i>FEBS Journal</i> , 1996, 240, 416-426.	0.2	15
97	Solution structure of the matrix attachment region-binding domain of chicken MeCP2. <i>FEBS Journal</i> , 2003, 270, 3263-3270.	0.2	15
98	A restraint molecular dynamics and simulated annealing approach for protein homology modeling utilizing mean angles. <i>BMC Bioinformatics</i> , 2005, 6, 91.	2.6	15
99	Solution Structure of the Ran-binding Domain 2 of RanBP2 and its Interaction with the C Terminus of Ran. <i>Journal of Molecular Biology</i> , 2005, 348, 711-725.	4.2	15
100	Intrinsic disorder in the common N-terminus of human adenovirus 5 E1B-55K and its related E1BN proteins indicated by studies on E1B-93R. <i>Virology</i> , 2011, 418, 133-143.	2.4	15
101	³¹ P NMR spectra of thiophosphate analogues of guanosine nucleotides. <i>FEBS Letters</i> , 1980, 121, 211-214.	2.8	14
102	Conformational states of human H-Ras detected by high-field EPR, ENDOR, and ³¹ P NMR spectroscopy. <i>Magnetic Resonance in Chemistry</i> , 2005, 43, S74-S83.	1.9	14
103	PSCD Domains of Pleuralin-1 from the Diatom <i>Cylindrotheca fusiformis</i> : NMR Structures and Interactions with Other Biosilica-Associated Proteins. <i>Structure</i> , 2016, 24, 1178-1191.	3.3	14
104	Pressure-dependent electronic structure calculations using integral equation-based solvation models. <i>Biophysical Chemistry</i> , 2020, 257, 106258.	2.8	14
105	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. <i>Biochemistry</i> , 1991, 30, 8083-8091.	2.5	13
106	Determination of Mean and Standard Deviation of Dihedral Angles. <i>Biochemical and Biophysical Research Communications</i> , 1999, 257, 348-350.	2.1	13
107	Interaction of CheY2 and CheY2 ^{EP} with the cognate CheA kinase in the chemosensory signaling chain of <i>Sinorhizobium meliloti</i> . <i>Molecular Microbiology</i> , 2008, 69, 1373-1384.	2.5	13
108	Inhibition of amyloid A β aggregation by high pressures or specific d-enantiomeric peptides. <i>Chemical Communications</i> , 2018, 54, 3294-3297.	4.1	13

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109	Complete ^1H Nuclear Magnetic Resonance Assignments and Structural Characterization of a Fusion Protein of the β -Amylase Inhibitor Tendamistat with the Activation Domain of the Human Immunodeficiency Virus Type 1 Tat Protein. <i>Journal of Molecular Biology</i> , 1995, 250, 672-688.	4.2	12
110	High-pressure NMR study of the complex of a GTPase Rap1A with its effector RalGDS. <i>FEBS Letters</i> , 2001, 506, 180-184.	2.8	12
111	Improved simulation of NOESY spectra by RELAX-JT2 including effects of J-coupling, transverse relaxation and chemical shift anisotropy. <i>Journal of Biomolecular NMR</i> , 2004, 30, 121-131.	2.8	12
112	The pressure and temperature perturbation approach reveals a whole variety of conformational substates of amyloidogenic hIAPP monitored by 2D NMR spectroscopy. <i>Biophysical Chemistry</i> , 2019, 254, 106239.	2.8	12
113	Use of Global Symmetries in Automated Signal Class Recognition by a Bayesian Method. <i>Journal of Magnetic Resonance</i> , 1997, 129, 165-172.	2.1	11
114	AUREMOL-RFAC-3D, combination of R-factors and their use for automated quality assessment of protein solution structures. <i>Journal of Biomolecular NMR</i> , 2006, 37, 15-30.	2.8	11
115	Pressure dependence of backbone chemical shifts in the model peptides Ac-Gly-Gly-Xxx-Ala-NH ₂ . <i>Journal of Biomolecular NMR</i> , 2016, 65, 65-77.	2.8	11
116	SHORT COMMUNICATION: Biochemical analysis of cervical mucus by nuclear magnetic resonance spectroscopy*. <i>Human Reproduction</i> , 1992, 7, 915-917.	0.9	10
117	Physiological Conditions and Practicality for Protein Nuclear Magnetic Resonance Spectroscopy: Experimental Methodologies and Theoretical Background. <i>Methods in Enzymology</i> , 2001, 339, 3-19.	1.0	10
118	Solution structure of the active-centre mutant I14A of the histidine-containing phosphocarrier protein from <i>Staphylococcus carnosus</i> . <i>FEBS Journal</i> , 2004, 271, 4815-4824.	0.2	10
119	State 1(T) Inhibitors of Activated Ras. <i>The Enzymes</i> , 2013, 33 Pt A, 69-94.	1.7	10
120	^{31}P nuclear magnetic resonance spectroscopy of the phosphorylated tetrapeptide Gly β ;Gly β ;Asp β ;Ala. <i>Magnetic Resonance in Chemistry</i> , 1988, 26, 260-263.	1.9	9
121	Mobile segments in rabbit skeletal muscle F-actin detected by ^1H nuclear magnetic resonance spectroscopy. <i>FEBS Letters</i> , 1994, 351, 405-410.	2.8	9
122	Structural studies of histidine-containing phosphocarrier protein from <i>Enterococcus faecalis</i> . <i>FEBS Journal</i> , 1998, 252, 51-58.	0.2	9
123	Molecular Alignment of Proteins in Bicellar Solutions: Quantitative Evaluation of Effects Induced in 2D COSY Spectra. <i>Biochemical and Biophysical Research Communications</i> , 2000, 272, 694-698.	2.1	9
124	Synthesis and NMR spectroscopy of peptides containing either phosphorylated or phosphonylated <i>cis</i> - or <i>trans</i> -4-hydroxyproline. <i>Chemical Biology and Drug Design</i> , 1997, 49, 163-173.	1.1	9
125	NMR Spectroscopy of Macrophages Loaded with Native, Oxidized or Enzymatically Degraded Lipoproteins. <i>PLoS ONE</i> , 2013, 8, e56360.	2.5	9
126	Conformational States of the Small G Protein Arf-1 in Complex with the Guanine Nucleotide Exchange Factor ARNO-Sec7. <i>Journal of Biological Chemistry</i> , 2004, 279, 17004-17012.	3.4	8

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127	Singular spectrum analysis for an automated solvent artifact removal and baseline correction of 1D NMR spectra. <i>Journal of Magnetic Resonance</i> , 2011, 210, 177-183.	2.1	8
128	Structural transitions in full-length human prion protein detected by xenon as probe and spin labeling of the N-terminal domain. <i>Scientific Reports</i> , 2016, 6, 28419.	3.3	8
129	Pressure dependence of side chain ¹³ C chemical shifts in model peptides Ac-Gly-Gly-Xxx-Ala-NH ₂ . <i>Journal of Biomolecular NMR</i> , 2017, 69, 53-67.	2.8	8
130	High resolution proton magnetic resonance spectroscopy of human cervical mucus. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2002, 28, 827-840.	2.8	7
131	PERMOL: restraint-based protein homology modeling using DYANA or CNS. <i>Bioinformatics</i> , 2005, 21, 2110-2111.	4.1	7
132	Automated solvent artifact removal and base plane correction of multidimensional NMR protein spectra by AUREMOL-SSA. <i>Journal of Biomolecular NMR</i> , 2010, 47, 101-111.	2.8	7
133	Limiting factors of the translation machinery. <i>Journal of Biotechnology</i> , 2010, 150, 44-50.	3.8	7
134	High pressure ³¹ P NMR spectroscopy on guanine nucleotides. <i>Journal of Biomolecular NMR</i> , 2017, 67, 1-13.	2.8	7
135	NMR Spectroscopic Study of Noble Gas Binding into the Engineered Cavity of HPr(I14A) from <i>Staphylococcus carnosus</i> . <i>Journal of Physical Chemistry B</i> , 2005, 109, 17795-17798.	2.6	6
136	Rapid assignment of solution ³¹ P NMR spectra of large proteins by solid-state spectroscopy. <i>Biochemical and Biophysical Research Communications</i> , 2006, 346, 301-305.	2.1	6
137	Solid-phase synthesis of α - and methylphosphonopeptides. <i>International Journal of Peptide and Protein Research</i> , 1996, 47, 245-253.	0.1	6
138	Conformational Substates of Amyloidogenic hIAPP Revealed by High Pressure NMR Spectroscopy. <i>ChemistrySelect</i> , 2016, 1, 3239-3243.	1.5	6
139	Automated Protein NMR Structure Determination in Solution. <i>Methods in Molecular Biology</i> , 2010, 673, 95-127.	0.9	6
140	Structure determination of polypeptides and proteins by two-dimensional nuclear magnetic resonance spectroscopy. <i>Physica B: Condensed Matter</i> , 1990, 164, 180-192.	2.7	5
141	A general method for the unbiased improvement of solution NMR structures by the use of related X-ray data, the AUREMOL-ISIC algorithm. <i>BMC Structural Biology</i> , 2006, 6, 14.	2.3	5
142	NMR-assignments of a cytosolic domain of the C-terminus of polycystin-2. <i>Biomolecular NMR Assignments</i> , 2009, 3, 141-144.	0.8	5
143	RNA secondary structure and in vitro translation efficiency. <i>Protein Expression and Purification</i> , 2012, 82, 26-31.	1.3	5
144	Pressure response of amide one-bond J-couplings in model peptides and proteins. <i>Journal of Biomolecular NMR</i> , 2014, 60, 45-50.	2.8	5

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145	Stereospecific assignment of the asparagine and glutamine sidechain amide protons in proteins from chemical shift analysis. <i>Journal of Biomolecular NMR</i> , 2017, 67, 157-164.	2.8	5
146	Solid-State ³¹ P NMR Spectroscopy of Precipitated Guanine Nucleotide-Binding Protein Ras in Complexes with Its Effector Molecules Raf Kinase and RalGDS. <i>Journal of Physical Chemistry B</i> , 2007, 111, 2752-2757.	2.6	4
147	Novel Metal-Organic Frameworks Incorporating [Cp [∞] 2Mo2P4S] (Cp [∞] = 1-tBu-3,4-Me2C5H2), P4S3 and Cu2I2 Building Blocks. <i>European Journal of Inorganic Chemistry</i> , 2011, 2011, 785-793.	2.0	4
148	Chemical shift assignments of the canecystatin-1 from <i>Saccharum officinarum</i> . <i>Biomolecular NMR Assignments</i> , 2013, 7, 163-165.	0.8	4
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