

Lewis E Kay

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#	Paper	IF	Citations
178	Backbone dynamics of a free and phosphopeptide-complexed Src homology 2 domain studied by ¹⁵ N NMR relaxation. <i>Biochemistry</i> , 1994 , 33, 5984-6003	3.2	1979
177	Backbone dynamics of proteins as studied by ¹⁵ N inverse detected heteronuclear NMR spectroscopy: application to staphylococcal nuclease. <i>Biochemistry</i> , 1989 , 28, 8972-9	3.2	1694
176	Deviations from the simple two-parameter model-free approach to the interpretation of nitrogen-15 nuclear magnetic relaxation of proteins. <i>Journal of the American Chemical Society</i> , 1990 , 112, 4989-4991	16.4	937
175	Intrinsic dynamics of an enzyme underlies catalysis. <i>Nature</i> , 2005 , 438, 117-21	50.4	925
174	Backbone dynamics of calmodulin studied by ¹⁵ N relaxation using inverse detected two-dimensional NMR spectroscopy: the central helix is flexible. <i>Biochemistry</i> , 1992 , 31, 5269-78	3.2	884
173	A novel approach for sequential assignment of ¹ H, ¹³ C, and ¹⁵ N spectra of proteins: heteronuclear triple-resonance three-dimensional NMR spectroscopy. Application to calmodulin. <i>Biochemistry</i> , 1990 , 29, 4659-67	3.2	837
172	New tools provide new insights in NMR studies of protein dynamics. <i>Science</i> , 2006 , 312, 224-8	33.3	638
171	Backbone ¹ H and ¹⁵ N resonance assignments of the N-terminal SH3 domain of drk in folded and unfolded states using enhanced-sensitivity pulsed field gradient NMR techniques. <i>Journal of Biomolecular NMR</i> , 1994 , 4, 845-58	3	617
170	Three-dimensional heteronuclear NMR of nitrogen-15 labeled proteins. <i>Journal of the American Chemical Society</i> , 1989 , 111, 1515-1517	16.4	543
169	Methods for Measurement of Intermolecular NOEs by Multinuclear NMR Spectroscopy: Application to a Bacteriophage λ -N-Peptide/boxBRNA Complex. <i>Journal of the American Chemical Society</i> , 1997 , 119, 6711-6721	16.4	529
168	The use of ² H, ¹³ C, ¹⁵ N multidimensional NMR to study the structure and dynamics of proteins. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 1998 , 27, 357-406		511
167	A Suite of Triple Resonance NMR Experiments for the Backbone Assignment of ¹⁵ N, ¹³ C, ² H Labeled Proteins with High Sensitivity. <i>Journal of the American Chemical Society</i> , 1994 , 116, 11655-11666	16.4	481
166	Spectral density function mapping using ¹⁵ N relaxation data exclusively. <i>Journal of Biomolecular NMR</i> , 1995 , 6, 153-62	3	454
165	A robust and cost-effective method for the production of Val, Leu, Ile (δ 1) methyl-protonated ¹⁵ N-, ¹³ C-, ² H-labeled proteins. <i>Journal of Biomolecular NMR</i> , 1999 , 13, 369-74	3	420
164	Quantitative dynamics and binding studies of the 20S proteasome by NMR. <i>Nature</i> , 2007 , 445, 618-22	50.4	415
163	Low-populated folding intermediates of Fyn SH3 characterized by relaxation dispersion NMR. <i>Nature</i> , 2004 , 430, 586-90	50.4	410
162	Slow dynamics in folded and unfolded states of an SH3 domain. <i>Journal of the American Chemical Society</i> , 2001 , 123, 11341-52	16.4	408

161	NMR spectroscopy brings invisible protein states into focus. <i>Nature Chemical Biology</i> , 2009 , 5, 808-14	11.7	342
160	Studying excited states of proteins by NMR spectroscopy. <i>Nature Structural Biology</i> , 2001 , 8, 932-5		332
159	Studying "invisible" excited protein states in slow exchange with a major state conformation. <i>Journal of the American Chemical Society</i> , 2012 , 134, 8148-61	16.4	321
158	Structure of an intermediate state in protein folding and aggregation. <i>Science</i> , 2012 , 336, 362-6	33.3	292
157	Solution structure and dynamics of the outer membrane enzyme PagP by NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 13560-5	11.5	282
156	Ile, Leu, and Val methyl assignments of the 723-residue malate synthase G using a new labeling strategy and novel NMR methods. <i>Journal of the American Chemical Society</i> , 2003 , 125, 13868-78	16.4	279
155	Protein dynamics and conformational disorder in molecular recognition. <i>Journal of Molecular Recognition</i> , 2010 , 23, 105-16	2.6	277
154	Selective methyl group protonation of perdeuterated proteins. <i>Journal of Molecular Biology</i> , 1996 , 263, 627-36	6.5	272
153	Measurement of ² H T1 and T1.ρ. Relaxation Times in Uniformly ¹³ C-Labeled and Fractionally ² H-Labeled Proteins in Solution. <i>Journal of the American Chemical Society</i> , 1995 , 117, 11536-11544	16.4	263
152	Dynamics of methyl groups in proteins as studied by proton-detected ¹³ C NMR spectroscopy. Application to the leucine residues of staphylococcal nuclease. <i>Biochemistry</i> , 1992 , 31, 5253-63	3.2	259
151	Observing biological dynamics at atomic resolution using NMR. <i>Trends in Biochemical Sciences</i> , 2009 , 34, 601-11	10.3	256
150	Global folds of highly deuterated, methyl-protonated proteins by multidimensional NMR. <i>Biochemistry</i> , 1997 , 36, 1389-401	3.2	231
149	NMR structure of the bacteriophage lambda N peptide/boxB RNA complex: recognition of a GNRA fold by an arginine-rich motif. <i>Cell</i> , 1998 , 93, 289-99	56.2	229
148	NMR studies of protein structure and dynamics. <i>Journal of Magnetic Resonance</i> , 2005 , 173, 193-207	3	229
147	Structural and hydrodynamic properties of an intrinsically disordered region of a germ cell-specific protein on phase separation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E8194-E8203	11.5	227
146	Latent and active p53 are identical in conformation. <i>Nature Structural Biology</i> , 2001 , 8, 756-60		227
145	Production and Incorporation of ¹⁵ N, ¹³ C, ² H (¹ H-β Methyl) Isoleucine into Proteins for Multidimensional NMR Studies. <i>Journal of the American Chemical Society</i> , 1997 , 119, 7599-7600	16.4	221
144	Nuclear magnetic resonance spectroscopy of high-molecular-weight proteins. <i>Annual Review of Biochemistry</i> , 2004 , 73, 107-46	29.1	218

143	Solution Structure of a Cellulose-Binding Domain from <i>Cellulomonas fimi</i> by Nuclear Magnetic Resonance Spectroscopy. <i>Biochemistry</i> , 1995 , 34, 6993-7009	3.2	217
142	Probing invisible, low-populated States of protein molecules by relaxation dispersion NMR spectroscopy: an application to protein folding. <i>Accounts of Chemical Research</i> , 2008 , 41, 442-51	24.3	212
141	Four-dimensional NMR spectroscopy of a 723-residue protein: chemical shift assignments and secondary structure of malate synthase g. <i>Journal of the American Chemical Society</i> , 2002 , 124, 10025-35	16.4	205
140	An isotope labeling strategy for methyl TROSY spectroscopy. <i>Journal of Biomolecular NMR</i> , 2004 , 28, 165-72	3	192
139	Solution structure of a TBP-TAF(II)230 complex: protein mimicry of the minor groove surface of the TATA box unwound by TBP. <i>Cell</i> , 1998 , 94, 573-83	56.2	191
138	New developments in isotope labeling strategies for protein solution NMR spectroscopy. <i>Current Opinion in Structural Biology</i> , 2000 , 10, 585-92	8.1	190
137	Orienting domains in proteins using dipolar couplings measured by liquid-state NMR: differences in solution and crystal forms of maltodextrin binding protein loaded with beta-cyclodextrin. <i>Journal of Molecular Biology</i> , 2000 , 295, 1265-73	6.5	181
136	Quantitative NMR spectroscopy of supramolecular complexes: dynamic side pores in ClpP are important for product release. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 16678-83	11.5	175
135	NMR Experiments for the Measurement of Carbon Relaxation Properties in Highly Enriched, Uniformly ¹³ C, ¹⁵ N-Labeled Proteins: Application to ¹³ C.alpha. Carbons. <i>Journal of the American Chemical Society</i> , 1994 , 116, 8266-8278	16.4	167
134	Four-dimensional ¹³ C/ ¹³ C-edited nuclear Overhauser enhancement spectroscopy of a protein in solution: application to interleukin 1 beta. <i>Biochemistry</i> , 1991 , 30, 12-8	3.2	167
133	An HNCA Pulse Scheme for the Backbone Assignment of ¹⁵ N, ¹³ C, ² H-Labeled Proteins: Application to a 37-kDa Trp Repressor-DNA Complex. <i>Journal of the American Chemical Society</i> , 1994 , 116, 6464-6465	16.4	163
132	Bringing dynamic molecular machines into focus by methyl-TROSY NMR. <i>Annual Review of Biochemistry</i> , 2014 , 83, 291-315	29.1	162
131	Distribution of molecular size within an unfolded state ensemble using small-angle X-ray scattering and pulse field gradient NMR techniques. <i>Journal of Molecular Biology</i> , 2002 , 316, 101-12	6.5	158
130	Reconstructing NMR spectra of "invisible" excited protein states using HSQC and HMQC experiments. <i>Journal of the American Chemical Society</i> , 2002 , 124, 12352-60	16.4	155
129	Measurement of bond vector orientations in invisible excited states of proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 18473-7	11.5	154
128	Solution NMR spectroscopy beyond 25 kDa. <i>Current Opinion in Structural Biology</i> , 1997 , 7, 722-31	8.1	153
127	Methyl TROSY: explanation and experimental verification. <i>Magnetic Resonance in Chemistry</i> , 2003 , 41, 843-852	2.1	153
126	NOE data demonstrating a compact unfolded state for an SH3 domain under non-denaturing conditions. <i>Journal of Molecular Biology</i> , 1999 , 289, 619-38	6.5	149

125	Characterization of the backbone dynamics of folded and denatured states of an SH3 domain. <i>Biochemistry</i> , 1997 , 36, 2390-402	3.2	148
124	Global folds of proteins with low densities of NOEs using residual dipolar couplings: application to the 370-residue maltodextrin-binding protein. <i>Journal of Molecular Biology</i> , 2000 , 300, 197-212	6.5	147
123	Fractional ¹³ C enrichment of isolated carbons using [1- ¹³ C]- or [2- ¹³ C]-glucose facilitates the accurate measurement of dynamics at backbone α and side-chain methyl positions in proteins. <i>Journal of Biomolecular NMR</i> , 2007 , 38, 199-212	3	145
122	A pulsed field gradient isotope-filtered 3D ¹³ C HMQC-NOESY experiment for extracting intermolecular NOE contacts in molecular complexes. <i>FEBS Letters</i> , 1994 , 350, 87-90	3.8	145
121	An improved ¹⁵ N relaxation dispersion experiment for the measurement of millisecond time-scale dynamics in proteins. <i>Journal of Physical Chemistry B</i> , 2008 , 112, 5898-904	3.4	144
120	Probing chemical shifts of invisible states of proteins with relaxation dispersion NMR spectroscopy: how well can we do?. <i>Journal of the American Chemical Society</i> , 2008 , 130, 2667-75	16.4	142
119	TROSY Triple-Resonance Four-Dimensional NMR Spectroscopy of a 46 ns Tumbling Protein. <i>Journal of the American Chemical Society</i> , 1999 , 121, 2571-2575	16.4	139
118	Solution NMR of supramolecular complexes: providing new insights into function. <i>Nature Methods</i> , 2007 , 4, 697-703	21.6	138
117	Contributions to protein entropy and heat capacity from bond vector motions measured by NMR spin relaxation. <i>Journal of Molecular Biology</i> , 1997 , 272, 790-804	6.5	134
116	Methyl groups as probes of supra-molecular structure, dynamics and function. <i>Journal of Biomolecular NMR</i> , 2010 , 46, 75-87	3	133
115	Direct demonstration of an intramolecular SH2-phosphotyrosine interaction in the Crk protein. <i>Nature</i> , 1995 , 374, 477-9	50.4	128
114	Assignment of ¹⁵ N, ¹³ C- ¹³ C, and HN Resonances in an ¹⁵ N, ¹³ C, ² H Labeled 64 kDa Trp Repressor-Operator Complex Using Triple-Resonance NMR Spectroscopy and ² H-Decoupling. <i>Journal of the American Chemical Society</i> , 1996 , 118, 6570-6579	16.4	127
113	Pulsed field gradient multi-dimensional NMR methods for the study of protein structure and dynamics in solution. <i>Progress in Biophysics and Molecular Biology</i> , 1995 , 63, 277-99	4.7	126
112	Backbone and methyl dynamics of the regulatory domain of troponin C: anisotropic rotational diffusion and contribution of conformational entropy to calcium affinity. <i>Journal of Molecular Biology</i> , 1998 , 278, 667-86	6.5	118
111	Three-dimensional triple-resonance NMR spectroscopy of isotopically enriched proteins. <i>Journal of Magnetic Resonance</i> , 1990 , 89, 496-514		118
110	Deuterium spin probes of side-chain dynamics in proteins. 2. Spectral density mapping and identification of nanosecond time-scale side-chain motions. <i>Journal of the American Chemical Society</i> , 2002 , 124, 6449-60	16.4	115
109	Ligand-induced structural changes to maltodextrin-binding protein as studied by solution NMR spectroscopy. <i>Journal of Molecular Biology</i> , 2001 , 309, 961-74	6.5	114
108	The NMR structure of the 38 kDa U1A protein - PIE RNA complex reveals the basis of cooperativity in regulation of polyadenylation by human U1A protein. <i>Nature Structural Biology</i> , 2000 , 7, 329-35		110

107	A study of protein side-chain dynamics from new 2H auto-correlation and 13C cross-correlation NMR experiments: application to the N-terminal SH3 domain from drk. <i>Journal of Molecular Biology</i> , 1998 , 276, 939-54	6.5	108
106	TROSY-based HNC0 pulse sequences for the measurement of 1HN-15N, 15N-13CO, 1HN-13CO, 13CO-13C and 1HN-13C dipolar couplings in 15N, 13C, 2H-labeled proteins. <i>Journal of Biomolecular NMR</i> , 1999 , 14, 333-343	3	100
105	Probing side-chain dynamics in the proteasome by relaxation violated coherence transfer NMR spectroscopy. <i>Journal of the American Chemical Society</i> , 2007 , 129, 1743-50	16.4	97
104	A single-quantum methyl 13C-relaxation dispersion experiment with improved sensitivity. <i>Journal of Biomolecular NMR</i> , 2007 , 38, 79-88	3	96
103	Using relaxation dispersion NMR spectroscopy to determine structures of excited, invisible protein states. <i>Journal of Biomolecular NMR</i> , 2008 , 41, 113-20	3	95
102	Multidimensional NMR methods for protein structure determination. <i>IUBMB Life</i> , 2001 , 52, 291-302	4.7	95
101	Studies on the solution conformation of human thioredoxin using heteronuclear 15N-1H nuclear magnetic resonance spectroscopy. <i>Biochemistry</i> , 1990 , 29, 1566-72	3.2	86
100	An (H)C(CO)NH-TOCSY pulse scheme for sequential assignment of protonated methyl groups in otherwise deuterated (15)N, (13)C-labeled proteins. <i>Journal of Biomolecular NMR</i> , 1996 , 8, 351-6	3	85
99	Independent ligand-induced folding of the RNA-binding domain and two functionally distinct antitermination regions in the phage lambda N protein. <i>Molecular Cell</i> , 1998 , 1, 265-75	17.6	84
98	Multiple-site exchange in proteins studied with a suite of six NMR relaxation dispersion experiments: an application to the folding of a Fyn SH3 domain mutant. <i>Journal of the American Chemical Society</i> , 2005 , 127, 15602-11	16.4	84
97	Probing conformational dynamics in biomolecules via chemical exchange saturation transfer: a primer. <i>Journal of Biomolecular NMR</i> , 2017 , 67, 243-271	3	78
96	Structure and dynamics of bacteriophage IKe major coat protein in MPG micelles by solution NMR. <i>Biochemistry</i> , 1996 , 35, 5145-57	3.2	75
95	Identification of a collapsed intermediate with non-native long-range interactions on the folding pathway of a pair of Fyn SH3 domain mutants by NMR relaxation dispersion spectroscopy. <i>Journal of Molecular Biology</i> , 2006 , 363, 958-76	6.5	73
94	A "three-pronged" binding mechanism for the SAP/SH2D1A SH2 domain: structural basis and relevance to the XLP syndrome. <i>EMBO Journal</i> , 2002 , 21, 314-23	13	73
93	Triple-resonance NOESY-based experiments with improved spectral resolution: applications to structural characterization of unfolded, partially folded and folded proteins. <i>Journal of Biomolecular NMR</i> , 1997 , 9, 181-200	3	69
92	Thermal fluctuations of immature SOD1 lead to separate folding and misfolding pathways. <i>ELife</i> , 2015 , 4, e07296	8.9	67
91	Accurate measurement of alpha proton chemical shifts of excited protein states by relaxation dispersion NMR spectroscopy. <i>Journal of the American Chemical Society</i> , 2009 , 131, 1915-26	16.4	65
90	Measurement of carbonyl chemical shifts of excited protein states by relaxation dispersion NMR spectroscopy: comparison between uniformly and selectively (13)C labeled samples. <i>Journal of Biomolecular NMR</i> , 2008 , 42, 35-47	3	62

89	An NMR View of Protein Dynamics in Health and Disease. <i>Annual Review of Biophysics</i> , 2019 , 48, 297-319	21.1	60
88	Field gradient techniques in NMR spectroscopy. <i>Current Opinion in Structural Biology</i> , 1995 , 5, 674-81	8.1	60
87	Determination of Leu side-chain conformations in excited protein states by NMR relaxation dispersion. <i>Journal of the American Chemical Society</i> , 2010 , 132, 42-3	16.4	59
86	Comprehensive NOE characterization of a partially folded large fragment of staphylococcal nuclease Delta131Delta, using NMR methods with improved resolution. <i>Journal of Molecular Biology</i> , 1997 , 272, 9-20	6.5	56
85	Probing structure in invisible protein states with anisotropic NMR chemical shifts. <i>Journal of the American Chemical Society</i> , 2008 , 130, 2734-5	16.4	56
84	Functional dynamics of human FKBP12 revealed by methyl ¹³ C rotating frame relaxation dispersion NMR spectroscopy. <i>Journal of the American Chemical Society</i> , 2006 , 128, 5718-27	16.4	55
83	The effects of mutations on motions of side-chains in protein L studied by ² H NMR dynamics and scalar couplings. <i>Journal of Molecular Biology</i> , 2003 , 329, 551-63	6.5	54
82	The folding pathway of an FF domain: characterization of an on-pathway intermediate state under folding conditions by (¹⁵ N, (¹³ C(alpha) and (¹³ C-methyl relaxation dispersion and (¹ H/(² H)-exchange NMR spectroscopy. <i>Journal of Molecular Biology</i> , 2007 , 372, 497-512	6.5	51
81	An HNCQ-based Pulse Scheme for the Measurement of ¹³ C- ¹ H One-bond Dipolar couplings in ¹⁵ N, ¹³ C Labeled Proteins. <i>Journal of Biomolecular NMR</i> , 1998 , 12, 325-32	3	50
80	Visualizing side chains of invisible protein conformers by solution NMR. <i>Journal of Molecular Biology</i> , 2014 , 426, 763-74	6.5	48
79	Determining valine side-chain rotamer conformations in proteins from methyl ¹³ C chemical shifts: application to the 360 kDa half-proteasome. <i>Journal of the American Chemical Society</i> , 2011 , 133, 8272-81	16.4	47
78	Nuclear magnetic resonance methods for high molecular weight proteins: a study involving a complex of maltose binding protein and beta-cyclodextrin. <i>Methods in Enzymology</i> , 2001 , 339, 174-203	1.7	47
77	Phi-value analysis of a three-state protein folding pathway by NMR relaxation dispersion spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 15717-22	11.5	46
76	Direct structure refinement of high molecular weight proteins against residual dipolar couplings and carbonyl chemical shift changes upon alignment: an application to maltose binding protein. <i>Journal of Biomolecular NMR</i> , 2001 , 21, 31-40	3	46
75	Side chain assignments of Ile delta 1 methyl groups in high molecular weight proteins: an application to a 46 ns tumbling molecule. <i>Journal of the American Chemical Society</i> , 2003 , 125, 5701-6	16.4	45
74	Isotope labeling methods for studies of excited protein states by relaxation dispersion NMR spectroscopy. <i>Nature Protocols</i> , 2009 , 4, 1641-8	18.8	44
73	A 4D TROSY-based pulse scheme for correlating ¹ H ^{Ni} , ¹⁵ N ⁱ , ¹³ C ^{alpha} _i , ¹³ C ^Q _i chemical shifts in high molecular weight, ¹⁵ N, ¹³ C, ² H labeled proteins. <i>Journal of Biomolecular NMR</i> , 1999 , 15, 309-13	3	44
72	Side chain dynamics in unfolded protein states: an NMR based ² H spin relaxation study of delta131delta. <i>Journal of the American Chemical Society</i> , 2003 , 125, 1748-58	16.4	43

71	Conformational instability of the MARK3 UBA domain compromises ubiquitin recognition and promotes interaction with the adjacent kinase domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 14336-41	11.5	39
70	Measuring ¹³ Cβ chemical shifts of invisible excited states in proteins by relaxation dispersion NMR spectroscopy. <i>Journal of Biomolecular NMR</i> , 2009 , 44, 139-55	3	38
69	Measuring hydrogen exchange rates in invisible protein excited states. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 8820-5	11.5	37
68	Abp1p and Fyn SH3 domains fold through similar low-populated intermediate states. <i>Biochemistry</i> , 2006 , 45, 10175-83	3.2	37
67	Heteronuclear 3D NMR and isotopic labeling of calmodulin. Towards the complete assignment of the ¹ H NMR spectrum. <i>Biochemical Pharmacology</i> , 1990 , 40, 153-60	6	37
66	Probing the free energy landscapes of ALS disease mutants of SOD1 by NMR spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E6939-E6945	11.5	35
65	CPMG relaxation dispersion NMR experiments measuring glycine ¹ H α and ¹³ C α chemical shifts in the invisible excited states of proteins. <i>Journal of Biomolecular NMR</i> , 2009 , 45, 45-55	3	34
64	NMR studies of tandem WW domains of Nedd4 in complex with a PY motif-containing region of the epithelial sodium channel. <i>Biochemistry and Cell Biology</i> , 1998 , 76, 341-350	3.6	34
63	Probing slow chemical exchange at carbonyl sites in proteins by chemical exchange saturation transfer NMR spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2013 , 52, 4156-9	16.4	33
62	Stereospecific assignment of the NH ₂ resonances from the primary amides of asparagine and glutamine side chains in isotopically labeled proteins. <i>Journal of Biomolecular NMR</i> , 1997 , 9, 306-12	3	29
61	Practical aspects of 3D heteronuclear NMR of proteins. <i>Journal of Magnetic Resonance</i> , 1989 , 84, 72-84		29
60	Probing the free energy landscape of the fast-folding gpW protein by relaxation dispersion NMR. <i>Journal of the American Chemical Society</i> , 2014 , 136, 7444-51	16.4	28
59	A comparative CEST NMR study of slow conformational dynamics of small GTPases complexed with GTP and GTP analogues. <i>Angewandte Chemie - International Edition</i> , 2013 , 52, 10771-4	16.4	28
58	Side-chain interactions in the folding pathway of a Fyn SH3 domain mutant studied by relaxation dispersion NMR spectroscopy. <i>Biochemistry</i> , 2005 , 44, 15430-6	3.2	28
57	Significantly Improved Resolution for NOE Correlations from Valine and Isoleucine (Cβ) Methyl Groups in ¹⁵ N, ¹³ C- and ¹⁵ N, ¹³ C, ² H-Labeled Proteins. <i>Journal of the American Chemical Society</i> , 1998 , 120, 4825-4831	16.4	28
56	An R(1) expression for a spin in chemical exchange between two sites with unequal transverse relaxation rates. <i>Journal of Biomolecular NMR</i> , 2013 , 55, 211-8	3	27
55	Solution structure and dynamics of integral membrane proteins by NMR: a case study involving the enzyme PagP. <i>Methods in Enzymology</i> , 2005 , 394, 335-50	1.7	27
54	Assignment of ¹ H(N), ¹⁵ N, ¹³ C(α), ¹³ CO and ¹³ C(β) resonances in a 67 kDa p53 dimer using 4D-TROSY NMR spectroscopy. <i>Journal of Biomolecular NMR</i> , 2000 , 18, 173-6	3	27

53	(13)CHD2-CEST NMR spectroscopy provides an avenue for studies of conformational exchange in high molecular weight proteins. <i>Journal of Biomolecular NMR</i> , 2015 , 63, 187-99	3	26
52	Measurement of methyl group motional parameters of invisible, excited protein states by NMR spectroscopy. <i>Journal of the American Chemical Society</i> , 2009 , 131, 12745-54	16.4	26
51	Measurement of (13)C(alpha)-(13)C(beta) dipolar couplings in (15)N,(13)C,(2)H-labeled proteins: application to domain orientation in maltose binding protein. <i>Journal of the American Chemical Society</i> , 2001 , 123, 2858-64	16.4	25
50	Solution NMR Spectroscopy Provides an Avenue for the Study of Functionally Dynamic Molecular Machines: The Example of Protein Disaggregation. <i>Journal of the American Chemical Society</i> , 2016 , 138, 1466-77	16.4	24
49	Probing Conformational Exchange in Weakly Interacting, Slowly Exchanging Protein Systems via Off-Resonance R Experiments: Application to Studies of Protein Phase Separation. <i>Journal of the American Chemical Society</i> , 2018 , 140, 2115-2126	16.4	22
48	Probing Invisible, Excited Protein States by Non-Uniformly Sampled Pseudo-4D CEST Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2015 , 54, 10507-11	16.4	22
47	Unusual helix-containing greek keys in development-specific Ca(2+)-binding protein S. 1H, 15N, and 13C assignments and secondary structure determined with the use of multidimensional double and triple resonance heteronuclear NMR spectroscopy. <i>Biochemistry</i> , 1994 , 33, 2409-21	3.2	22
46	Probing non-specific interactions of Ca ²⁺ -calmodulin in E. coli lysate. <i>Journal of Biomolecular NMR</i> , 2013 , 55, 239-47	3	21
45	Measurement of signs of chemical shift differences between ground and excited protein states: a comparison between H(S/M)QC and R1rho methods. <i>Journal of Biomolecular NMR</i> , 2010 , 46, 205-16	3	20
44	Practical aspects of proton-carbon-carbon-proton three-dimensional correlation spectroscopy of 13C-labeled proteins. <i>Journal of Magnetic Resonance</i> , 1990 , 87, 620-627		20
43	Subunit-specific backbone NMR assignments of a 64 kDa trp repressor/DNA complex: a role for N-terminal residues in tandem binding. <i>Journal of Biomolecular NMR</i> , 1998 , 11, 307-18	3	19
42	Probing residual interactions in unfolded protein states using NMR spin relaxation techniques: an application to delta131delta. <i>Journal of the American Chemical Society</i> , 2003 , 125, 11988-92	16.4	19
41	A Methyl-TROSY-Based H Relaxation Dispersion Experiment for Studies of Conformational Exchange in High Molecular Weight Proteins. <i>Angewandte Chemie - International Edition</i> , 2019 , 58, 6250-6254	16.4	18
40	A methyl-TROSY approach for NMR studies of high-molecular-weight DNA with application to the nucleosome core particle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 12836-12846	11.5	18
39	Strong coupling effects during X-pulse CPMG experiments recorded on heteronuclear ABX spin systems: artifacts and a simple solution. <i>Journal of Biomolecular NMR</i> , 2007 , 38, 41-6	3	18
38	Multidimensional triple resonance NMR spectroscopy of isotopically uniformly enriched proteins: a powerful new strategy for structure determination. <i>Novartis Foundation Symposium</i> , 1991 , 161, 108-19; discussion 119-35		18
37	Folding of the four-helix bundle FF domain from a compact on-pathway intermediate state is governed predominantly by water motion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 19268-73	11.5	15
36	New methods for the measurement of NH?C?H coupling constants in 15N-labeled proteins. <i>Journal of Magnetic Resonance</i> , 1990 , 86, 110-126		15

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