

Lewis E Kay

List of Publications by Year in descending order

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233
papers

31,325
citations

5248

83
h-index

4535

171
g-index

253
all docs

253
docs citations

253
times ranked

15555
citing authors

#	ARTICLE	IF	CITATIONS
1	Pure absorption gradient enhanced heteronuclear single quantum correlation spectroscopy with improved sensitivity. <i>Journal of the American Chemical Society</i> , 1992, 114, 10663-10665.	6.6	2,456
2	Backbone Dynamics of a Free and a Phosphopeptide-Complexed Src Homology 2 Domain Studied by ¹⁵ N NMR Relaxation. <i>Biochemistry</i> , 1994, 33, 5984-6003.	1.2	2,136
3	Backbone dynamics of proteins as studied by nitrogen-15 inverse detected heteronuclear NMR spectroscopy: application to staphylococcal nuclease. <i>Biochemistry</i> , 1989, 28, 8972-8979.	1.2	1,856
4	Intrinsic dynamics of an enzyme underlies catalysis. <i>Nature</i> , 2005, 438, 117-121.	13.7	1,018
5	A novel approach for sequential assignment of proton, carbon-13, and nitrogen-15 spectra of larger proteins: heteronuclear triple-resonance three-dimensional NMR spectroscopy. Application to calmodulin. <i>Biochemistry</i> , 1990, 29, 4659-4667.	1.2	926
6	New Tools Provide New Insights in NMR Studies of Protein Dynamics. <i>Science</i> , 2006, 312, 224-228.	6.0	720
7	Cross-Correlated Relaxation Enhanced ¹ H- ¹³ C NMR Spectroscopy of Methyl Groups in Very High Molecular Weight Proteins and Protein Complexes. <i>Journal of the American Chemical Society</i> , 2003, 125, 10420-10428.	6.6	550
8	Spectral density function mapping using ¹⁵ N relaxation data exclusively. <i>Journal of Biomolecular NMR</i> , 1995, 6, 153-162.	1.6	494
9	Quantitative dynamics and binding studies of the 20S proteasome by NMR. <i>Nature</i> , 2007, 445, 618-622.	13.7	472
10	Folding of an intrinsically disordered protein by phosphorylation as a regulatory switch. <i>Nature</i> , 2015, 519, 106-109.	13.7	471
11	Isotope labeling strategies for the study of high-molecular-weight proteins by solution NMR spectroscopy. <i>Nature Protocols</i> , 2006, 1, 749-754.	5.5	469
12	A robust and cost-effective method for the production of Val, Leu, Ile (delta 1) methyl-protonated ¹⁵ N-, ¹³ C-, ² H-labeled proteins. <i>Journal of Biomolecular NMR</i> , 1999, 13, 369-374.	1.6	461
13	Slow Dynamics in Folded and Unfolded States of an SH3 Domain. <i>Journal of the American Chemical Society</i> , 2001, 123, 11341-11352.	6.6	454
14	Low-populated folding intermediates of Fyn SH3 characterized by relaxation dispersion NMR. <i>Nature</i> , 2004, 430, 586-590.	13.7	445
15	Studying "Invisible" Excited Protein States in Slow Exchange with a Major State Conformation. <i>Journal of the American Chemical Society</i> , 2012, 134, 8148-8161.	6.6	430
16	A heteronuclear correlation experiment for simultaneous determination of ¹⁵ N longitudinal decay and chemical exchange rates of systems in slow equilibrium. <i>Journal of Biomolecular NMR</i> , 1994, 4, 727-734.	1.6	417
17	NMR spectroscopy brings invisible protein states into focus. <i>Nature Chemical Biology</i> , 2009, 5, 808-814.	3.9	403
18	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.	3.3	381

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19	Studying excited states of proteins by NMR spectroscopy. <i>Nature Structural Biology</i> , 2001, 8, 932-935.	9.7	366
20	Structure of an Intermediate State in Protein Folding and Aggregation. <i>Science</i> , 2012, 336, 362-366.	6.0	339
21	Protein dynamics and conformational disorder in molecular recognition. <i>Journal of Molecular Recognition</i> , 2010, 23, 105-116.	1.1	337
22	Measurement of Slow (μ s) Time Scale Dynamics in Protein Side Chains by 15 N Relaxation Dispersion NMR Spectroscopy: Application to Asn and Gln Residues in a Cavity Mutant of T4 Lysozyme. <i>Journal of the American Chemical Society</i> , 2001, 123, 967-975.	6.6	298
23	Observing biological dynamics at atomic resolution using NMR. <i>Trends in Biochemical Sciences</i> , 2009, 34, 601-611.	3.7	295
24	A Transient and Low-Populated Protein-Folding Intermediate at Atomic Resolution. <i>Science</i> , 2010, 329, 1312-1316.	6.0	282
25	Structural and Dynamic Analysis of Residual Dipolar Coupling Data for Proteins. <i>Journal of the American Chemical Society</i> , 2001, 123, 1416-1424.	6.6	277
26	Solution structure of a minor and transiently formed state of a T4 lysozyme mutant. <i>Nature</i> , 2011, 477, 111-114.	13.7	265
27	Latent and active p53 are identical in conformation. <i>Nature Structural Biology</i> , 2001, 8, 756-760.	9.7	261
28	Protein dynamics from NMR. <i>Nature Structural Biology</i> , 1998, 5, 513-517.	9.7	254
29	Production and Incorporation of 15 N, 13 C, 2 H (1 H- 1 H Methyl) Isoleucine into Proteins for Multidimensional NMR Studies. <i>Journal of the American Chemical Society</i> , 1997, 119, 7599-7600.	6.6	248
30	Nuclear Magnetic Resonance Spectroscopy of High-Molecular-Weight Proteins. <i>Annual Review of Biochemistry</i> , 2004, 73, 107-146.	5.0	247
31	Global Folds of Highly Deuterated, Methyl-Protonated Proteins by Multidimensional NMR. <i>Biochemistry</i> , 1997, 36, 1389-1401.	1.2	244
32	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, 442-451.	7.6	241
33	Unraveling the Mechanism of Protein Disaggregation Through a ClpB-DnaK Interaction. <i>Science</i> , 2013, 339, 1080-1083.	6.0	240
34	Phospho-dependent phase separation of FMRP and CAPRIN1 recapitulates regulation of translation and deadenylation. <i>Science</i> , 2019, 365, 825-829.	6.0	240
35	NMR paves the way for atomic level descriptions of sparsely populated, transiently formed biomolecular conformers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 12867-12874.	3.3	230
36	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, 10025-10035.	6.6	225

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37	An Isotope Labeling Strategy for Methyl TROSY Spectroscopy. <i>Journal of Biomolecular NMR</i> , 2004, 28, 165-172.	1.6	221
38	Dynamic Regulation of Archaeal Proteasome Gate Opening As Studied by TROSY NMR. <i>Science</i> , 2010, 328, 98-102.	6.0	221
39	Probing Slow Dynamics in High Molecular Weight Proteins by Methyl-TROSY NMR Spectroscopy: Application to a 723-Residue Enzyme. <i>Journal of the American Chemical Society</i> , 2004, 126, 3964-3973.	6.6	210
40	Three-dimensional triple-resonance NMR spectroscopy of isotopically enriched proteins. <i>Journal of Magnetic Resonance</i> , 1990, 89, 496-514.	0.5	205
41	Bringing Dynamic Molecular Machines into Focus by Methyl-TROSY NMR. <i>Annual Review of Biochemistry</i> , 2014, 83, 291-315.	5.0	200
42	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, 5898-5904.	1.2	196
43	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, 16678-16683.	3.3	195
44	Comparison of different modes of two-dimensional reverse-correlation NMR for the study of proteins. <i>Journal of Magnetic Resonance</i> , 1990, 86, 304-318.	0.5	191
45	Oncogenic and RASopathy-associated K-RAS mutations relieve membrane-dependent occlusion of the effector-binding site. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6625-6630.	3.3	191
46	Methyl TROSY: explanation and experimental verification. <i>Magnetic Resonance in Chemistry</i> , 2003, 41, 843-852.	1.1	190
47	Structures of invisible, excited protein states by relaxation dispersion NMR spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 11766-11771.	3.3	186
48	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, 101-112.	2.0	181
49	Methyl Groups as Probes of Structure and Dynamics in NMR Studies of High-Molecular-Weight Proteins. <i>ChemBioChem</i> , 2005, 6, 1567-1577.	1.3	175
50	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, 18473-18477.	3.3	172
51	Probing Slow Time Scale Dynamics at Methyl-Containing Side Chains in Proteins by Relaxation Dispersion NMR Measurements: Application to Methionine Residues in a Cavity Mutant of T4 Lysozyme. <i>Journal of the American Chemical Society</i> , 2001, 123, 4556-4566.	6.6	170
52	Reconstructing NMR Spectra of "Invisible" Excited Protein States Using HSQC and HMQC Experiments. <i>Journal of the American Chemical Society</i> , 2002, 124, 12352-12360.	6.6	169
53	Solution NMR of supramolecular complexes: providing new insights into function. <i>Nature Methods</i> , 2007, 4, 697-703.	9.0	163
54	Fractional ¹³ C enrichment of isolated carbons using [1- ¹³ C]- or [2- ¹³ C]-glucose facilitates the accurate measurement of dynamics at backbone C α and side-chain methyl positions in proteins. <i>Journal of Biomolecular NMR</i> , 2007, 38, 199-212.	1.6	160

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55	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.	1.3	156
56	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, 2667-2675.	6.6	155
57	Architecture of the high mobility group nucleosomal protein 2-nucleosome complex as revealed by methyl-based NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 12283-12288.	3.3	155
58	Pulsed-field gradient-enhanced three-dimensional NMR experiment for correlating ¹³ C.alpha./beta., ¹³ C', and ¹ H.alpha. chemical shifts in uniformly carbon-13-labeled proteins dissolved in water. <i>Journal of the American Chemical Society</i> , 1993, 115, 2055-2057.	6.6	152
59	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.	6.6	148
60	Direct demonstration of an intramolecular SH2â€”phosphotyrosine interaction in the Crk protein. <i>Nature</i> , 1995, 374, 477-479.	13.7	132
61	Improved ¹ HN-detected triple resonance TROSY-based experiments. <i>Journal of Biomolecular NMR</i> , 1999, 13, 3-10.	1.6	132
62	An NMR Experiment for the Accurate Measurement of Heteronuclear Spin-Lock Relaxation Rates. <i>Journal of the American Chemical Society</i> , 2002, 124, 10743-10753.	6.6	130
63	Proteasome allostery as a population shift between interchanging conformers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E3454-62.	3.3	128
64	Probing conformational dynamics in biomolecules via chemical exchange saturation transfer: a primer. <i>Journal of Biomolecular NMR</i> , 2017, 67, 243-271.	1.6	123
65	Title is missing!. <i>Journal of Biomolecular NMR</i> , 1999, 14, 333-343.	1.6	122
66	Off-Resonance R1NMR Studies of Exchange Dynamics in Proteins with Low Spin-Lock Fields:Â An Application to a Fyn SH3 Domain. <i>Journal of the American Chemical Society</i> , 2005, 127, 713-721.	6.6	122
67	Structure of a AAA+ unfoldase in the process of unfolding substrate. <i>ELife</i> , 2017, 6, .	2.8	119
68	An NMR View of Protein Dynamics in Health and Disease. <i>Annual Review of Biophysics</i> , 2019, 48, 297-319.	4.5	113
69	Structure of a Numb PTB domainâ€”peptide complex suggests a basis for diverse binding specificity. <i>Nature Structural Biology</i> , 1998, 5, 1075-1083.	9.7	112
70	A single-quantum methyl ¹³ C-relaxation dispersion experiment with improved sensitivity. <i>Journal of Biomolecular NMR</i> , 2007, 38, 79-88.	1.6	112
71	Using relaxation dispersion NMR spectroscopy to determine structures of excited, invisible protein states. <i>Journal of Biomolecular NMR</i> , 2008, 41, 113-120.	1.6	112
72	Measurement of histidine pK _a values and tautomer populations in invisible protein states. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1705-12.	3.3	111

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73	Multidimensional NMR Methods for Protein Structure Determination. IUBMB Life, 2001, 52, 291-302.	1.5	110
74	Slow Internal Dynamics in Proteins: Application of NMR Relaxation Dispersion Spectroscopy to Methyl Groups in a Cavity Mutant of T4 Lysozyme. Journal of the American Chemical Society, 2002, 124, 1443-1451.	6.6	110
75	Tracing an allosteric pathway regulating the activity of the HslV protease. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2140-2145.	3.3	106
76	NMR spectroscopy captures the essential role of dynamics in regulating biomolecular function. Cell, 2021, 184, 577-595.	13.5	103
77	New Views of Functionally Dynamic Proteins by Solution NMR Spectroscopy. Journal of Molecular Biology, 2016, 428, 323-331.	2.0	102
78	A Multidimensional NMR Experiment for Measurement of the Protein Dihedral Angle γ Based on Cross-Correlated Relaxation between ^1H - ^{13}C Dipolar and ^{13}C (Carbonyl) Chemical Shift Anisotropy Mechanisms. Journal of the American Chemical Society, 1997, 119, 11938-11940.	6.6	100
79	Multiple-Quantum Relaxation Dispersion NMR Spectroscopy Probing Millisecond Time-Scale Dynamics in Proteins: Theory and Application. Journal of the American Chemical Society, 2004, 126, 7320-7329.	6.6	100
80	Quantitative NMR Studies of High Molecular Weight Proteins: Application to Domain Orientation and Ligand Binding in the 723 Residue Enzyme Malate Synthase G. Journal of Molecular Biology, 2003, 327, 1121-1133.	2.0	97
81	A processive rotary mechanism couples substrate unfolding and proteolysis in the ClpXP degradation machinery. ELife, 2020, 9, .	2.8	94
82	Flexibility and Ligand Exchange in a Buried Cavity Mutant of T4 Lysozyme Studied by Multinuclear NMR. Biochemistry, 2000, 39, 12614-12622.	1.2	92
83	Thermal fluctuations of immature SOD1 lead to separate folding and misfolding pathways. ELife, 2015, 4, e07296.	2.8	91
84	Determination of Isoleucine Side-Chain Conformations in Ground and Excited States of Proteins from Chemical Shifts. Journal of the American Chemical Society, 2010, 132, 7589-7591.	6.6	88
85	An NMR Experiment for Measuring Methyl-Methyl NOEs in ^{13}C -Labeled Proteins with High Resolution. Journal of the American Chemical Society, 1998, 120, 7617-7625.	6.6	86
86	An (H)C(CO)NH-TOCSY pulse scheme for sequential assignment of protonated methyl groups in otherwise deuterated ^{15}N , ^{13}C -labeled proteins. Journal of Biomolecular NMR, 1996, 8, 351-356.	1.6	85
87	An Optimized Relaxation-Based Coherence Transfer NMR Experiment for the Measurement of Side-Chain Order in Methyl-Protonated, Highly Deuterated Proteins. Journal of Physical Chemistry B, 2011, 115, 14878-14884.	1.2	85
88	Mapping the conformation of a client protein through the Hsp70 functional cycle. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10395-10400.	3.3	85
89	Analysis of deuterium relaxation-derived methyl axis order parameters and correlation with local structure. Journal of Biomolecular NMR, 1999, 13, 181-185.	1.6	84
90	Hsp70 biases the folding pathways of client proteins. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2794-801.	3.3	84

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91	Solution NMR spectroscopy of supra-molecular systems, why bother? A methyl-TROSY view. <i>Journal of Magnetic Resonance</i> , 2011, 210, 159-170.	1.2	80
92	Dramatic acceleration of protein folding by stabilization of a nonnative backbone conformation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7954-7959.	3.3	79
93	ClpB N-terminal domain plays a regulatory role in protein disaggregation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E6872-81.	3.3	79
94	A 2D ¹³ C-CEST experiment for studying slowly exchanging protein systems using methyl probes: an application to protein folding. <i>Journal of Biomolecular NMR</i> , 2012, 53, 303-310.	1.6	76
95	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.	1.6	75
96	Sequential assignment of proline-rich regions in proteins: application to modular binding domain complexes. <i>Journal of Biomolecular NMR</i> , 2000, 16, 253-259.	1.6	74
97	A Dynamic molecular basis for malfunction in disease mutants of p97/VCP. <i>ELife</i> , 2016, 5, .	2.8	74
98	Unveiling invisible protein states with NMR spectroscopy. <i>Current Opinion in Structural Biology</i> , 2020, 60, 39-49.	2.6	73
99	Measurement of Methyl ² H Quadrupolar Couplings in Oriented Proteins. How Uniform Is the Quadrupolar Coupling Constant?. <i>Journal of the American Chemical Society</i> , 1999, 121, 10608-10613.	6.6	72
100	Site-Directed Methyl Group Labeling as an NMR Probe of Structure and Dynamics in Supramolecular Protein Systems: Applications to the Proteasome and to the ClpP Protease. <i>Journal of the American Chemical Society</i> , 2011, 133, 9063-9068.	6.6	72
101	Promiscuous binding by Hsp70 results in conformational heterogeneity and fuzzy chaperone-substrate ensembles. <i>ELife</i> , 2017, 6, .	2.8	72
102	Conserved conformational selection mechanism of Hsp70 chaperone-substrate interactions. <i>ELife</i> , 2018, 7, .	2.8	71
103	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, 1915-1926.	6.6	68
104	A simple strategy for ¹³ C, ¹ H labeling at the Ile- ^β 2 methyl position in highly deuterated proteins. <i>Journal of Biomolecular NMR</i> , 2010, 48, 129-135.	1.6	68
105	Methyl group dynamics from relaxation of double quantum filtered NMR signals. Application to deoxycholate. <i>Journal of the American Chemical Society</i> , 1987, 109, 3829-3835.	6.6	66
106	¹ H Torsion Angle Dynamics in Proteins from Dipolar Couplings. <i>Journal of the American Chemical Society</i> , 2001, 123, 6892-6903.	6.6	65
107	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.	1.6	65
108	Measurement of Proton Chemical Shifts in Invisible States of Slowly Exchanging Protein Systems by Chemical Exchange Saturation Transfer. <i>Journal of Physical Chemistry B</i> , 2012, 116, 14311-14317.	1.2	64

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109	¹³ CHD ₂ Methyl Group Probes of Millisecond Time Scale Exchange in Proteins by ¹ H Relaxation Dispersion: An Application to Proteasome Gating Residue Dynamics. <i>Journal of the American Chemical Society</i> , 2010, 132, 10992-10995.	6.6	60
110	Visualizing Side Chains of Invisible Protein Conformers by Solution NMR. <i>Journal of Molecular Biology</i> , 2014, 426, 763-774.	2.0	59
111	Structure and Dynamics of a CheY-Binding Domain of the Chemotaxis Kinase CheA Determined by Nuclear Magnetic Resonance Spectroscopy. <i>Biochemistry</i> , 1996, 35, 5633-5640.	1.2	58
112	Probing Structure in Invisible Protein States with Anisotropic NMR Chemical Shifts. <i>Journal of the American Chemical Society</i> , 2008, 130, 2734-2735.	6.6	58
113	Atomic resolution mechanism of ligand binding to a solvent inaccessible cavity in T4 lysozyme. <i>PLoS Computational Biology</i> , 2018, 14, e1006180.	1.5	58
114	Relaxation Rates of Degenerate ¹ H Transitions in Methyl Groups of Proteins as Reporters of Side-Chain Dynamics. <i>Journal of the American Chemical Society</i> , 2006, 128, 7299-7308.	6.6	57
115	Reversible inhibition of the ClpP protease via an N-terminal conformational switch. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E6447-E6456.	3.3	56
116	Quantifying Millisecond Exchange Dynamics in Proteins by CPMG Relaxation Dispersion NMR Using Side-Chain ¹ H Probes. <i>Journal of the American Chemical Society</i> , 2012, 134, 3178-3189.	6.6	55
117	Unfolding the mechanism of the AAA+ unfoldase VAT by a combined cryo-EM, solution NMR study. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4190-9.	3.3	55
118	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, 325-332.	1.6	54
119	Stabilization of amyloidogenic immunoglobulin light chains by small molecules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 8360-8369.	3.3	52
120	Increasing the Exchange Time-Scale That Can Be Probed by CPMG Relaxation Dispersion NMR. <i>Journal of Physical Chemistry B</i> , 2011, 115, 14891-14900.	1.2	51
121	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.	1.6	50
122	A 4D TROSY-based pulse scheme for correlating ¹ H _{Ni} , ¹⁵ N _i , ¹³ C _α , ¹³ C _{i-1} chemical shifts in high molecular weight, ¹⁵ N, ¹³ C, ² H labeled proteins. <i>Journal of Biomolecular NMR</i> , 1999, 15, 309-313.	1.6	49
123	NMR Experiments for Studies of Dilute and Condensed Protein Phases: Application to the Phase-Separating Protein CAPRIN1. <i>Journal of the American Chemical Society</i> , 2020, 142, 2471-2489.	6.6	49
124	Effects of maturation on the conformational free-energy landscape of SOD1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2546-E2555.	3.3	48
125	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.	3.3	47
126	An allosteric switch regulates <i>Mycobacterium tuberculosis</i> ClpP1P2 protease function as established by cryo-EM and methyl-TROSY NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5895-5906.	3.3	47

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127	Isotope labeling methods for studies of excited protein states by relaxation dispersion NMR spectroscopy. <i>Nature Protocols</i> , 2009, 4, 1641-1648.	5.5	46
128	Probing Slow Chemical Exchange at Carbonyl Sites in Proteins by Chemical Exchange Saturation Transfer NMR Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 4156-4159.	7.2	45
129	Role of domain interactions in the aggregation of full-length immunoglobulin light chains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 854-863.	3.3	45
130	The RNF168 paralog RNF169 defines a new class of ubiquitylated histone reader involved in the response to DNA damage. <i>ELife</i> , 2017, 6, .	2.8	44
131	A Sensitive Pulse Scheme for Measuring the Backbone Dihedral Angle ψ Based on Cross-correlation Between $(^{13}\text{C}(\alpha)-^1\text{H})$ Dipolar and Carbonyl Chemical Shift Anisotropy Relaxation Interactions. <i>Journal of Biomolecular NMR</i> , 1998, 11, 213-220.	1.6	43
132	^1H - ^{13}C Dipole-Dipole Cross-Correlated Spin Relaxation As a Probe of Dynamics in Unfolded Proteins: Application to the DrkN SH3 Domain. <i>Journal of the American Chemical Society</i> , 1999, 121, 3555-3556.	6.6	42
133	Investigating the Dynamics of Destabilized Nucleosomes Using Methyl-TROSY NMR. <i>Journal of the American Chemical Society</i> , 2018, 140, 4774-4777.	6.6	42
134	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, 8820-8825.	3.3	41
135	Measuring ^{13}C chemical shifts of invisible excited states in proteins by relaxation dispersion NMR spectroscopy. <i>Journal of Biomolecular NMR</i> , 2009, 44, 139-155.	1.6	40
136	Assignment of Ile, Leu, and Val Methyl Correlations in Supra-Molecular Systems: An Application to Aspartate Transcarbamoylase. <i>Journal of the American Chemical Society</i> , 2009, 131, 16534-16543.	6.6	40
137	Enhancing the Sensitivity of CPMG Relaxation Dispersion to Conformational Exchange Processes by Multiple-Quantum Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 11490-11494.	7.2	40
138	Interaction hot spots for phase separation revealed by NMR studies of a CAPRIN1 condensed phase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	40
139	Optimal methyl labeling for studies of supra-molecular systems. <i>Journal of Biomolecular NMR</i> , 2010, 47, 163-169.	1.6	39
140	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.	3.3	38
141	Assessment of molecular structure using frame-independent orientational restraints derived from residual dipolar couplings. <i>Journal of Biomolecular NMR</i> , 2000, 18, 239-252.	1.6	37
142	Nonnative Interactions in the FF Domain Folding Pathway from an Atomic Resolution Structure of a Sparsely Populated Intermediate: An NMR Relaxation Dispersion Study. <i>Journal of the American Chemical Society</i> , 2011, 133, 10974-10982.	6.6	37
143	Polyubiquitin-Photoactivatable Crosslinking Reagents for Mapping Ubiquitin Interactome Identify Rpn1 as a Proteasome Ubiquitin-Associating Subunit. <i>Cell Chemical Biology</i> , 2017, 24, 443-457.e6.	2.5	37
144	Alternate Binding Modes for a Ubiquitin-SH3 Domain Interaction Studied by NMR Spectroscopy. <i>Journal of Molecular Biology</i> , 2009, 386, 391-405.	2.0	36

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