Lewis E Kay

List of Publications by Year
in descending order

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233	31,325	5268	4548
papers	citations	83 h-index	171 g-index

253	253	253	15555
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Pure absorption gradient enhanced heteronuclear single quantum correlation spectroscopy with improved sensitivity. Journal of the American Chemical Society, 1992, 114, 10663-10665.	13.7	2,456
2	Backbone Dynamics of a Free and a Phosphopeptide-Complexed Src Homology 2 Domain Studied by 15N NMR Relaxation. Biochemistry, 1994, 33, 5984-6003.	2.5	2,136
3	Backbone dynamics of proteins as studied by nitrogen-15 inverse detected heteronuclear NMR spectroscopy: application to staphylococcal nuclease. Biochemistry, 1989, 28, 8972-8979.	2.5	1,856
4	Intrinsic dynamics of an enzyme underlies catalysis. Nature, 2005, 438, 117-121.	27.8	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. Biochemistry, 1990, 29, 4659-4667.	2.5	926
6	New Tools Provide New Insights in NMR Studies of Protein Dynamics. Science, 2006, 312, 224-228.	12.6	720
7	Cross-Correlated Relaxation Enhanced1Hâ^'13C NMR Spectroscopy of Methyl Groups in Very High Molecular Weight Proteins and Protein Complexes. Journal of the American Chemical Society, 2003, 125, 10420-10428.	13.7	550
8	Spectral density function mapping using 15N relaxation data exclusively. Journal of Biomolecular NMR, 1995, 6, 153-162.	2.8	494
9	Quantitative dynamics and binding studies of the 20S proteasome by NMR. Nature, 2007, 445, 618-622.	27.8	472
10	Folding of an intrinsically disordered protein by phosphorylation as a regulatory switch. Nature, 2015, 519, 106-109.	27.8	471
11	Isotope labeling strategies for the study of high-molecular-weight proteins by solution NMR spectroscopy. Nature Protocols, 2006, 1, 749-754.	12.0	469
12	A robust and cost-effective method for the production of Val, Leu, Ile (delta 1) methyl-protonated 15N-, 13C-, 2H-labeled proteins. Journal of Biomolecular NMR, 1999, 13, 369-374.	2.8	461
13	Slow Dynamics in Folded and Unfolded States of an SH3 Domain. Journal of the American Chemical Society, 2001, 123, 11341-11352.	13.7	454
14	Low-populated folding intermediates of Fyn SH3 characterized by relaxation dispersion NMR. Nature, 2004, 430, 586-590.	27.8	445
15	Studying â€œInvisibleâ€•Excited Protein States in Slow Exchange with a Major State Conformation. Journal of the American Chemical Society, 2012, 134, 8148-8161.	13.7	430
16	A heteronuclear correlation experiment for simultaneous determination of 15N longitudinal decay and chemical exchange rates of systems in slow equilibrium. Journal of Biomolecular NMR, 1994, 4, 727-734.	2.8	417
17	NMR spectroscopy brings invisible protein states into focus. Nature Chemical Biology, 2009, 5, 808-814.	8.0	403
18	Structural and hydrodynamic properties of an intrinsically disordered region of a germ cell-specific protein on phase separation. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E8194-E8203.	7.1	381

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19	Studying excited states of proteins by NMR spectroscopy. Nature Structural Biology, 2001, 8, 932-935.	9.7	366
20	Structure of an Intermediate State in Protein Folding and Aggregation. Science, 2012, 336, 362-366.	12.6	339
21	Protein dynamics and conformational disorder in molecular recognition. Journal of Molecular Recognition, 2010, 23, 105-116.	2.1	337
22	Measurement of Slow (Î¼sâ^'ms) Time Scale Dynamics in Protein Side Chains by15N Relaxation Dispersion NMR Spectroscopy:Â Application to Asn and Gln Residues in a Cavity Mutant of T4 Lysozyme. Journal of the American Chemical Society, 2001, 123, 967-975.	13.7	298
23	Observing biological dynamics at atomic resolution using NMR. Trends in Biochemical Sciences, 2009, 34, 601-611.	7.5	295
24	A Transient and Low-Populated Protein-Folding Intermediate at Atomic Resolution. Science, 2010, 329, 1312-1316.	12.6	282
25	Structural and Dynamic Analysis of Residual Dipolar Coupling Data for Proteins. Journal of the American Chemical Society, 2001, 123, 1416-1424.	13.7	277
26	Solution structure of a minor and transiently formed state of a T4 lysozyme mutant. Nature, 2011, 477, 111-114.	27.8	265
27	Latent and active p53 are identical in conformation. Nature Structural Biology, 2001, 8, 756-760.	9.7	261
28	Protein dynamics from NMR. Nature Structural Biology, 1998, 5, 513-517.	9.7	254
29	Production and Incorporation of15N,13C,2H (1H-Î´1 Methyl) Isoleucine into Proteins for Multidimensional NMR Studies. Journal of the American Chemical Society, 1997, 119, 7599-7600.	13.7	248
30	Nuclear Magnetic Resonance Spectroscopy of High-Molecular-Weight Proteins. Annual Review of Biochemistry, 2004, 73, 107-146.	11.1	247
31	Global Folds of Highly Deuterated, Methyl-Protonated Proteins by Multidimensional NMR. Biochemistry, 1997, 36, 1389-1401.	2.5	244
32	Probing Invisible, Low-Populated States of Protein Molecules by Relaxation Dispersion NMR Spectroscopy: An Application to Protein Folding. Accounts of Chemical Research, 2008, 41, 442-451.	15.6	241
33	Unraveling the Mechanism of Protein Disaggregation Through a ClpB-DnaK Interaction. Science, 2013, 339, 1080-1083.	12.6	240
34	Phospho-dependent phase separation of FMRP and CAPRIN1 recapitulates regulation of translation and deadenylation. Science, 2019, 365, 825-829.	12.6	240
35	NMR paves the way for atomic level descriptions of sparsely populated, transiently formed biomolecular conformers. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 12867-12874.	7.1	230
36	Four-Dimensional NMR Spectroscopy of a 723-Residue Protein:Â Chemical Shift Assignments and Secondary Structure of Malate Synthase G. Journal of the American Chemical Society, 2002, 124, 10025-10035.	13.7	225

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37	An Isotope Labeling Strategy for Methyl TROSY Spectroscopy. Journal of Biomolecular NMR, 2004, 28, 165-172.	2.8	221
38	Dynamic Regulation of Archaeal Proteasome Gate Opening As Studied by TROSY NMR. Science, 2010, 328, 98-102.	12.6	221
39	Probing Slow Dynamics in High Molecular Weight Proteins by Methyl-TROSY NMR Spectroscopy:Â Application to a 723-Residue Enzyme. Journal of the American Chemical Society, 2004, 126, 3964-3973.	13.7	210
40	Three-dimensional triple-resonance NMR spectroscopy of isotopically enriched proteins. Journal of Magnetic Resonance, 1990, 89, 496-514.	0.5	205
41	Bringing Dynamic Molecular Machines into Focus by Methyl-TROSY NMR. Annual Review of Biochemistry, 2014, 83, 291-315.	11.1	200
42	An Improved ¹⁵N Relaxation Dispersion Experiment for the Measurement of Millisecond Time-Scale Dynamics in Proteins. Journal of Physical Chemistry B, 2008, 112, 5898-5904.	2.6	196
43	Quantitative NMR spectroscopy of supramolecular complexes: Dynamic side pores in ClpP are important for product release. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 16678-16683.	7.1	195
44	Comparison of different modes of two-dimensional reverse-correlation NMR for the study of proteins. Journal of Magnetic Resonance, 1990, 86, 304-318.	0.5	191
45	Oncogenic and RASopathy-associated K-RAS mutations relieve membrane-dependent occlusion of the effector-binding site. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6625-6630.	7.1	191
46	Methyl TROSY: explanation and experimental verification. Magnetic Resonance in Chemistry, 2003, 41, 843-852.	1.9	190
47	Structures of invisible, excited protein states by relaxation dispersion NMR spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 11766-11771.	7.1	186
48	Distribution of molecular size within an unfolded state ensemble using small-angle X-ray scattering and pulse field gradient NMR techniques. Journal of Molecular Biology, 2002, 316, 101-112.	4.2	181
49	Methyl Groups as Probes of Structure and Dynamics in NMR Studies of High-Molecular-Weight Proteins. ChemBioChem, 2005, 6, 1567-1577.	2.6	175
50	Measurement of bond vector orientations in invisible excited states of proteins. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 18473-18477.	7.1	172
51	Probing Slow Time Scale Dynamics at Methyl-Containing Side Chains in Proteins by Relaxation Dispersion NMR Measurements:Â Application to Methionine Residues in a Cavity Mutant of T4 Lysozyme. Journal of the American Chemical Society, 2001, 123, 4556-4566.	13.7	170
52	Reconstructing NMR Spectra of â€œInvisibleâ€•Excited Protein States Using HSQC and HMQC Experiments. Journal of the American Chemical Society, 2002, 124, 12352-12360.	13.7	169
53	Solution NMR of supramolecular complexes: providing new insights into function. Nature Methods, 2007, 4, 697-703.	19.0	163
54	Fractional 13C enrichment of isolated carbons using [1-13C]- or [2-13C]-glucose facilitates the accurate measurement of dynamics at backbone CÎ± and side-chain methyl positions in proteins. Journal of Biomolecular NMR, 2007, 38, 199-212.	2.8	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. FEBS Letters, 1994, 350, 87-90.	2.8	156
56	Probing Chemical Shifts of Invisible States of Proteins with Relaxation Dispersion NMR Spectroscopy: How Well Can We Do?. Journal of the American Chemical Society, 2008, 130, 2667-2675.	13.7	155
57	Architecture of the high mobility group nucleosomal protein 2-nucleosome complex as revealed by methyl-based NMR. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 12283-12288.	7.1	155
58	Pulsed-field gradient-enhanced three-dimensional NMR experiment for correlating 13C.alpha./.beta., 13C', and 1H.alpha. chemical shifts in uniformly carbon-13-labeled proteins dissolved in water. Journal of the American Chemical Society, 1993, 115, 2055-2057.	13.7	152
59	TROSY Triple-Resonance Four-Dimensional NMR Spectroscopy of a 46 ns Tumbling Protein. Journal of the American Chemical Society, 1999, 121, 2571-2575.	13.7	148
60	Direct demonstration of an intramolecular SH2â€”phosphotyrosine interaction in the Crk protein. Nature, 1995, 374, 477-479.	27.8	132
61	Improved 1HN-detected triple resonance TROSY-based experiments. Journal of Biomolecular NMR, 1999, 13, 3-10.	2.8	132
62	An NMR Experiment for the Accurate Measurement of Heteronuclear Spin-Lock Relaxation Rates. Journal of the American Chemical Society, 2002, 124, 10743-10753.	13.7	130
63	Proteasome allostery as a population shift between interchanging conformers. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E3454-62.	7.1	128
64	Probing conformational dynamics in biomolecules via chemical exchange saturation transfer: a primer. Journal of Biomolecular NMR, 2017, 67, 243-271.	2.8	123
65	Title is missing!. Journal of Biomolecular NMR, 1999, 14, 333-343.	2.8	122
66	Off-Resonance R1ĪNMR Studies of Exchange Dynamics in Proteins with Low Spin-Lock Fields:Â An Application to a Fyn SH3 Domain. Journal of the American Chemical Society, 2005, 127, 713-721.	13.7	122
67	Structure of a AAA+ unfoldase in the process of unfolding substrate. ELife, 2017, 6, .	6.0	119
68	An NMR View of Protein Dynamics in Health and Disease. Annual Review of Biophysics, 2019, 48, 297-319.	10.0	113
69	Structure of a Numb PTB domainâ€“peptide complex suggests a basis for diverse binding specificity. Nature Structural Biology, 1998, 5, 1075-1083.	9.7	112
70	A single-quantum methyl 13C-relaxation dispersion experiment with improved sensitivity. Journal of Biomolecular NMR, 2007, 38, 79-88.	2.8	112
71	Using relaxation dispersion NMR spectroscopy to determine structures of excited, invisible protein states. Journal of Biomolecular NMR, 2008, 41, 113-120.	2.8	112
72	Measurement of histidine pK _a values and tautomer populations in invisible protein states. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E1705-12.	7.1	111

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73	Multidimensional NMR Methods for Protein Structure Determination. IUBMB Life, 2001, 52, 291-302.	3.4	110
74	Slow Internal Dynamics in Proteins:Â 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.	13.7	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.	7.1	106
76	NMR spectroscopy captures the essential role of dynamics in regulating biomolecular function. Cell, 2021, 184, 577-595.	28.9	103
77	New Views of Functionally Dynamic Proteins by Solution NMR Spectroscopy. Journal of Molecular Biology, 2016, 428, 323-331.	4.2	102
78	A Multidimensional NMR Experiment for Measurement of the Protein Dihedral Angle Ï^ Based on Cross-Correlated Relaxation between1HÎ±â^'13CÎ±Dipolar and13Câ€˜ (Carbonyl) Chemical Shift Anisotropy Mechanisms. Journal of the American Chemical Society, 1997, 119, 11938-11940.	13.7	100
79	Multiple-Quantum Relaxation Dispersion NMR Spectroscopy Probing Millisecond Time-Scale Dynamics in Proteins:â€‰ Theory and Application. Journal of the American Chemical Society, 2004, 126, 7320-7329.	13.7	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.	4.2	97
81	A processive rotary mechanism couples substrate unfolding and proteolysis in the ClpXP degradation machinery. ELife, 2020, 9, .	6.0	94
82	Flexibility and Ligand Exchange in a Buried Cavity Mutant of T4 Lysozyme Studied by Multinuclear NMRâ€. Biochemistry, 2000, 39, 12614-12622.	2.5	92
83	Thermal fluctuations of immature SOD1 lead to separate folding and misfolding pathways. ELife, 2015, 4, e07296.	6.0	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.	13.7	88
85	An NMR Experiment for Measuring Methylâ^'Methyl NOEs in13C-Labeled Proteins with High Resolution. Journal of the American Chemical Society, 1998, 120, 7617-7625.	13.7	86
86	An (H)C(CO)NH-TOCSY pulse scheme for sequential assignment of protonated methyl groups in otherwise deuterated 15N, 13C-labeled proteins. Journal of Biomolecular NMR, 1996, 8, 351-356.	2.8	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.	2.6	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.	7.1	85
89	Analysis of deuterium relaxation-derived methyl axis order parameters and correlation with local structure. Journal of Biomolecular NMR, 1999, 13, 181-185.	2.8	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.	7.1	84

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91	Solution NMR spectroscopy of supra-molecular systems, why bother? A methyl-TROSY view. Journal of Magnetic Resonance, 2011, 210, 159-170.	2.1	80
92	Dramatic acceleration of protein folding by stabilization of a nonnative backbone conformation. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 7954-7959.	7.1	79
93	ClpB N-terminal domain plays a regulatory role in protein disaggregation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E6872-81.	7.1	79
94	A 2D 13C-CEST experiment for studying slowly exchanging protein systems using methyl probes: an application to protein folding. Journal of Biomolecular NMR, 2012, 53, 303-310.	2.8	76
95	Triple-resonance NOESY-based experiments with improved spectral resolution: applications to structural characterization of unfolded, partially folded and folded proteins. Journal of Biomolecular NMR, 1997, 9, 181-200.	2.8	75
96	Sequential assignment of proline-rich regions in proteins: application to modular binding domain complexes. Journal of Biomolecular NMR, 2000, 16, 253-259.	2.8	74
97	A Dynamic molecular basis for malfunction in disease mutants of p97/VCP. ELife, 2016, 5, .	6.0	74
98	Unveiling invisible protein states with NMR spectroscopy. Current Opinion in Structural Biology, 2020, 60, 39-49.	5.7	73
99	Measurement of Methyl2H Quadrupolar Couplings in Oriented Proteins. How Uniform Is the Quadrupolar Coupling Constant?. Journal of the American Chemical Society, 1999, 121, 10608-10613.	13.7	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. Journal of the American Chemical Society, 2011, 133, 9063-9068.	13.7	72
101	Promiscuous binding by Hsp70 results in conformational heterogeneity and fuzzy chaperone-substrate ensembles. ELife, 2017, 6, .	6.0	72
102	Conserved conformational selection mechanism of Hsp70 chaperone-substrate interactions. ELife, 2018, 7, .	6.0	71
103	Accurate Measurement of Alpha Proton Chemical Shifts of Excited Protein States by Relaxation Dispersion NMR Spectroscopy. Journal of the American Chemical Society, 2009, 131, 1915-1926.	13.7	68
104	A simple strategy for 13C,1H labeling at the Ile-Î³2 methyl position in highly deuterated proteins. Journal of Biomolecular NMR, 2010, 48, 129-135.	2.8	68
105	Methyl group dynamics from relaxation of double quantum filtered NMR signals. Application to deoxycholate. Journal of the American Chemical Society, 1987, 109, 3829-3835.	13.7	66
106	Ï‡1 Torsion Angle Dynamics in Proteins from Dipolar Couplings. Journal of the American Chemical Society, 2001, 123, 6892-6903.	13.7	65
107	Measurement of carbonyl chemical shifts of excited protein states by relaxation dispersion NMR spectroscopy: comparison between uniformly and selectively 13C labeled samples. Journal of Biomolecular NMR, 2008, 42, 35-47.	2.8	65
108	Measurement of Proton Chemical Shifts in Invisible States of Slowly Exchanging Protein Systems by Chemical Exchange Saturation Transfer. Journal of Physical Chemistry B, 2012, 116, 14311-14317.	2.6	64

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109	¹³CHD₂ Methyl Group Probes of Millisecond Time Scale Exchange in Proteins by ¹H Relaxation Dispersion: An Application to Proteasome Gating Residue Dynamics. Journal of the American Chemical Society, 2010, 132, 10992-10995.	13.7	60
110	Visualizing Side Chains of Invisible Protein Conformers by Solution NMR. Journal of Molecular Biology, 2014, 426, 763-774.	4.2	59
111	Structure and Dynamics of a CheY-Binding Domain of the Chemotaxis Kinase CheA Determined by Nuclear Magnetic Resonance Spectroscopyâ€,â€¡. Biochemistry, 1996, 35, 5633-5640.	2.5	58
112	Probing Structure in Invisible Protein States with Anisotropic NMR Chemical Shifts. Journal of the American Chemical Society, 2008, 130, 2734-2735.	13.7	58
113	Atomic resolution mechanism of ligand binding to a solvent inaccessible cavity in T4 lysozyme. PLoS Computational Biology, 2018, 14, e1006180.	3.2	58
114	Relaxation Rates of Degenerate1H Transitions in Methyl Groups of Proteins as Reporters of Side-Chain Dynamics. Journal of the American Chemical Society, 2006, 128, 7299-7308.	13.7	57
115	Reversible inhibition of the ClpP protease via an N-terminal conformational switch. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E6447-E6456.	7.1	56
116	Quantifying Millisecond Exchange Dynamics in Proteins by CPMG Relaxation Dispersion NMR Using Side-Chain ¹H Probes. Journal of the American Chemical Society, 2012, 134, 3178-3189.	13.7	55
117	Unfolding the mechanism of the AAA+ unfoldase VAT by a combined cryo-EM, solution NMR study. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4190-9.	7.1	55
118	An HNCO-based Pulse Scheme for the Measurement of 13CÎ±-1HÎ± One-bond Dipolar couplings in 15N, 13C Labeled Proteins. Journal of Biomolecular NMR, 1998, 12, 325-332.	2.8	54
119	Stabilization of amyloidogenic immunoglobulin light chains by small molecules. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 8360-8369.	7.1	52
120	Increasing the Exchange Time-Scale That Can Be Probed by CPMG Relaxation Dispersion NMR. Journal of Physical Chemistry B, 2011, 115, 14891-14900.	2.6	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. Journal of Biomolecular NMR, 2001, 21, 31-40.	2.8	50
122	A 4D TROSY-based pulse scheme for correlating 1HNi,15Ni,13Calphai,13C'i-1 chemical shifts in high molecular weight, 15N,13C, 2H labeled proteins. Journal of Biomolecular NMR, 1999, 15, 309-313.	2.8	49
123	NMR Experiments for Studies of Dilute and Condensed Protein Phases: Application to the Phase-Separating Protein CAPRIN1. Journal of the American Chemical Society, 2020, 142, 2471-2489.	13.7	49
124	Effects of maturation on the conformational free-energy landscape of SOD1. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E2546-E2555.	7.1	48
125	Probing the free energy landscapes of ALS disease mutants of SOD1 by NMR spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E6939-E6945.	7.1	47
126	An allosteric switch regulates Mycobacterium tuberculosis ClpP1P2 protease function as established by cryo-EM and methyl-TROSY NMR. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 5895-5906.	7.1	47

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127	Isotope labeling methods for studies of excited protein states by relaxation dispersion NMR spectroscopy. Nature Protocols, 2009, 4, 1641-1648.	12.0	46
128	Probing Slow Chemical Exchange at Carbonyl Sites in Proteins by Chemical Exchange Saturation Transfer NMR Spectroscopy. Angewandte Chemie - International Edition, 2013, 52, 4156-4159.	13.8	45
129	Role of domain interactions in the aggregation of full-length immunoglobulin light chains. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 854-863.	7.1	45
130	The RNF168 paralog RNF169 defines a new class of ubiquitylated histone reader involved in the response to DNA damage. ELife, 2017, 6, .	6.0	44
131	A Sensitive Pulse Scheme for Measuring the Backbone Dihedral Angle psi Based on Cross-correlation Between (13)C (alpha)- (1)Halpha Dipolar and Carbonyl Chemical Shift Anisotropy Relaxation Interactions. Journal of Biomolecular NMR, 1998, 11, 213-220.	2.8	43
132	1Hâ^'13C Dipoleâ^'Dipole Cross-Correlated Spin Relaxation As a Probe of Dynamics in Unfolded Proteins:â€‰ Application to the DrkN SH3 Domain. Journal of the American Chemical Society, 1999, 121, 3555-3556.	13.7	42
133	Investigating the Dynamics of Destabilized Nucleosomes Using Methyl-TROSY NMR. Journal of the American Chemical Society, 2018, 140, 4774-4777.	13.7	42
134	Measuring hydrogen exchange rates in invisible protein excited states. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 8820-8825.	7.1	41
135	Measuring 13CÎ² chemical shifts of invisible excited states in proteins by relaxation dispersion NMR spectroscopy. Journal of Biomolecular NMR, 2009, 44, 139-155.	2.8	40
136	Assignment of Ile, Leu, and Val Methyl Correlations in Supra-Molecular Systems: An Application to Aspartate Transcarbamoylase. Journal of the American Chemical Society, 2009, 131, 16534-16543.	13.7	40
137	Enhancing the Sensitivity of CPMG Relaxation Dispersion to Conformational Exchange Processes by Multipleâ€Quantum Spectroscopy. Angewandte Chemie - International Edition, 2016, 55, 11490-11494.	13.8	40
138	Interaction hot spots for phase separation revealed by NMR studies of a CAPRIN1 condensed phase. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	40
139	Optimal methyl labeling for studies of supra-molecular systems. Journal of Biomolecular NMR, 2010, 47, 163-169.	2.8	39
140	A methyl-TROSY approach for NMR studies of high-molecular-weight DNA with application to the nucleosome core particle. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 12836-12846.	7.1	38
141	Assessment of molecular structure using frame-independent orientational restraints derived from residual dipolar couplings. Journal of Biomolecular NMR, 2000, 18, 239-252.	2.8	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. Journal of the American Chemical Society, 2011, 133, 10974-10982.	13.7	37
143	Polyubiquitin-Photoactivatable Crosslinking Reagents for Mapping Ubiquitin Interactome Identify Rpn1 as a Proteasome Ubiquitin-Associating Subunit. Cell Chemical Biology, 2017, 24, 443-457.e6.	5.2	37
144	Alternate Binding Modes for a Ubiquitinâ€“SH3 Domain Interaction Studied by NMR Spectroscopy. Journal of Molecular Biology, 2009, 386, 391-405.	4.2	36

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145	Separating Dipolar and Chemical Exchange Magnetization Transfer Processes in ¹Hâ€CEST. Angewandte Chemie - International Edition, 2017, 56, 6122-6125.	13.8	35
146	Dramatic Decrease in CEST Measurement Times Using Multiâ€Site Excitation. ChemPhysChem, 2018, 19, 1707-1710.	2.1	35
147	Pulse schemes for the measurement of 3JC'C gamma and 3JNC gamma scalar couplings in 15N,13C uniformly labeled proteins. Journal of Biomolecular NMR, 1997, 9, 409-422.	2.8	34
148	Quantifying Two-Bond ¹HNâ^'¹³CO and One-Bond ¹H^{Î±}â^'¹³C^{Î±} Dipolar Couplings of Invisible Protein States by Spin-State Selective Relaxation Dispersion NMR Spectroscopy. Journal of the American Chemical Society, 2008, 130, 8397-8405.	13.7	34
149	Atomistic picture of conformational exchange in a T4 lysozyme cavity mutant: an experiment-guided molecular dynamics study. Chemical Science, 2016, 7, 3602-3613.	7.4	34
150	Measurement of Methyl Axis Orientations in Invisible, Excited States of Proteins by Relaxation Dispersion NMR Spectroscopy. Journal of the American Chemical Society, 2009, 131, 11939-11948.	13.7	33
151	Exploiting conformational plasticity in the AAA+ protein VCP/p97 to modify function. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E6822-E6829.	7.1	33
152	Separating Degenerate1H Transitions in Methyl Group Probes for Single-Quantum1H-CPMG Relaxation Dispersion NMR Spectroscopy. Journal of the American Chemical Society, 2007, 129, 9514-9521.	13.7	32
153	An R1Ï•expression for a spin in chemical exchange between two sites with unequal transverse relaxation rates. Journal of Biomolecular NMR, 2013, 55, 211-218.	2.8	32
154	Probing Conformational Exchange in Weakly Interacting, Slowly Exchanging Protein Systems via Off-Resonance R_{1Ï} Experiments: Application to Studies of Protein Phase Separation. Journal of the American Chemical Society, 2018, 140, 2115-2126.	13.7	32
155	Solution NMR Spectroscopy Provides an Avenue for the Study of Functionally Dynamic Molecular Machines: The Example of Protein Disaggregation. Journal of the American Chemical Society, 2016, 138, 1466-1477.	13.7	31
156	A Methylâ€TROSYâ€Based ¹H Relaxation Dispersion Experiment for Studies of Conformational Exchange in High Molecular Weight Proteins. Angewandte Chemie - International Edition, 2019, 58, 6250-6254.	13.8	31
157	Cooperative subunit dynamics modulate p97 function. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 158-167.	7.1	31
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