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	Structural basis of protein substrate processing by human mitochondrial high-temperature requirement A2 protease. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2203172119.	7.1	6
2	Towards autonomous analysis of chemical exchange saturation transfer experiments using deep neural networks. Journal of Biomolecular NMR, 2022, 76, 75-86.	2.8	7
3	Revisiting dipolar relaxation of a homonuclear spin pair in the presence of a radio frequency field: a tutorial. Journal of Magnetic Resonance Open, 2022, , 100065.	1.1	0
4	Allovalency observed by transferred NOE: interactions of sulfated tyrosine residues in the Nâ€terminal segment of CCR5 with the CCL5 chemokine. FEBS Journal, 2021, 288, 1648-1663.	4.7	7
5	NMR spectroscopy captures the essential role of dynamics in regulating biomolecular function. Cell, 2021, 184, 577-595.	28.9	103
6	Oligomeric assembly regulating mitochondrial HtrA2 function as examined by methyl-TROSY NMR. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	28
7	Global multi-method analysis of interaction parameters for reversibly self-associating macromolecules at high concentrations. Scientific Reports, 2021, 11, 5741.	3.3	7
8	A life writ large: Chris Dobson 1949â€“2019. Journal of Magnetic Resonance, 2021, 326, 106947.	2.1	0
9	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
10	Competing stress-dependent oligomerization pathways regulate self-assembly of the periplasmic protease-chaperone DegP. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	11
11	Dissecting the role of interprotomer cooperativity in the activation of oligomeric high-temperature requirement A2 protein. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2111257118.	7.1	11
12	The A39G FF domain folds on a volcano-shaped free energy surface via separate pathways. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	10
13	Opening of a cryptic pocket in Î²-lactamase increases penicillinase activity. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	17
14	Probing allosteric interactions in homo-oligomeric molecular machines using solution NMR spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	7
15	Unveiling invisible protein states with NMR spectroscopy. Current Opinion in Structural Biology, 2020, 60, 39-49.	5.7	73
16	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
17	An intrinsically disordered motif regulates the interaction between the p47 adaptor and the p97 AAA+ ATPase. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 26226-26236.	7.1	19
18	A pH-Dependent Conformational Switch Controls N. meningitidis ClpP Protease Function. Journal of the American Chemical Society, 2020, 142, 20519-20523.	13.7	12

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19	Analyzing multi-step ligand binding reactions for oligomeric proteins by NMR: Theoretical and computational considerations. Journal of Magnetic Resonance, 2020, 318, 106802.	2.1	4
20	Probing Cooperativity of Nâ€Terminal Domain Orientations in the p97 Molecular Machine: Synergy Between NMR Spectroscopy and Cryoâ€EM. Angewandte Chemie, 2020, 132, 22609-22612.	2.0	1
21	Probing Cooperativity of Nâ€Terminal Domain Orientations in the p97 Molecular Machine: Synergy Between NMR Spectroscopy and Cryoâ€EM. Angewandte Chemie - International Edition, 2020, 59, 22423-22426.	13.8	4
22	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
23	Structural basis for the stabilization of amyloidogenic immunoglobulin light chains by hydantoins. Bioorganic and Medicinal Chemistry Letters, 2020, 30, 127356.	2.2	15
24	Exploring long-range cooperativity in the 20S proteasome core particle from Thermoplasma acidophilum using methyl-TROSYâ€“based NMR. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 5298-5309.	7.1	16
25	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
26	Confronting the Invisible: Assignment of Protein ¹H^N Chemical Shifts in Cases of Extreme Broadening. Journal of Physical Chemistry Letters, 2020, 11, 3384-3389.	4.6	7
27	The methyl 13C-edited/13C-filtered transferred NOE for studying protein interactions with short linear motifs. Journal of Biomolecular NMR, 2020, 74, 681-693.	2.8	7
28	A processive rotary mechanism couples substrate unfolding and proteolysis in the ClpXP degradation machinery. ELife, 2020, 9, .	6.0	94
29	The evolution of solution state NMR pulse sequences through the â€˜eyesâ€™ of triple-resonance spectroscopy. Journal of Magnetic Resonance, 2019, 306, 48-54.	2.1	1
30	A Methylâ€TROSYâ€Based ¹H Relaxation Dispersion Experiment for Studies of Conformational Exchange in High Molecular Weight Proteins. Angewandte Chemie, 2019, 131, 6316-6320.	2.0	2
31	The Role of Protein Thermodynamics and Primary Structure in Fibrillogenesis of Variable Domains from Immunoglobulin Light Chains. Journal of the American Chemical Society, 2019, 141, 13562-13571.	13.7	24
32	Revisiting 1HN CPMG relaxation dispersion experiments: a simple modification can eliminate large artifacts. Journal of Biomolecular NMR, 2019, 73, 641-650.	2.8	12
33	Phospho-dependent phase separation of FMRP and CAPRIN1 recapitulates regulation of translation and deadenylation. Science, 2019, 365, 825-829.	12.6	240
34	An NMR View of Protein Dynamics in Health and Disease. Annual Review of Biophysics, 2019, 48, 297-319.	10.0	113
35	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
36	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

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37	Artifacts can emerge in spectra recorded with even the simplest of pulse schemes: an HMQC case study. Journal of Biomolecular NMR, 2019, 73, 423-427.	2.8	6
38	ClpP protease activation results from the reorganization of the electrostatic interaction networks at the entrance pores. Communications Biology, 2019, 2, 410.	4.4	20
39	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
40	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
41	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
42	Dramatic Decrease in CEST Measurement Times Using Multiâ€Site Excitation. ChemPhysChem, 2018, 19, 1707-1710.	2.1	35
43	A new class of CEST experiment based on selecting different magnetization components at the start and end of the CEST relaxation element: an application to 1H CEST. Journal of Biomolecular NMR, 2018, 70, 93-102.	2.8	10
44	Probing Conformational Exchange in Weakly Interacting, Slowly Exchanging Protein Systems via Off-Resonance R_{1ρ} Experiments: Application to Studies of Protein Phase Separation. Journal of the American Chemical Society, 2018, 140, 2115-2126.	13.7	32
45	Exploring methods to expedite the recording of CEST datasets using selective pulse excitation. Journal of Magnetic Resonance, 2018, 292, 1-7.	2.1	16
46	Investigating the Dynamics of Destabilized Nucleosomes Using Methyl-TROSY NMR. Journal of the American Chemical Society, 2018, 140, 4774-4777.	13.7	42
47	A methyl 1H double quantum CPMG experiment to study protein conformational exchange. Journal of Biomolecular NMR, 2018, 72, 79-91.	2.8	16
48	Measuring Diffusion Constants of Invisible Protein Conformers by Tripleâ€Quantum ¹H CPMG Relaxation Dispersion. Angewandte Chemie - International Edition, 2018, 57, 16777-16780.	13.8	17
49	Measuring Diffusion Constants of Invisible Protein Conformers by Tripleâ€Quantum 1 H CPMG Relaxation Dispersion. Angewandte Chemie, 2018, 130, 17019-17022.	2.0	5
50	Measuring Solvent Hydrogen Exchange Rates by Multifrequency Excitation ¹⁵N CEST: Application to Protein Phase Separation. Journal of Physical Chemistry B, 2018, 122, 11206-11217.	2.6	19
51	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
52	Conserved conformational selection mechanism of Hsp70 chaperone-substrate interactions. ELife, 2018, 7, .	6.0	71
53	Advanced isotopic labeling for the NMR investigation of challenging proteins and nucleic acids. Journal of Biomolecular NMR, 2018, 71, 115-117.	2.8	15
54	Cotranslocational processing of the protein substrate calmodulin by an AAA+ unfoldase occurs via unfolding and refolding intermediates. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E4786-E4795.	7.1	12

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55	Atomic resolution mechanism of ligand binding to a solvent inaccessible cavity in T4 lysozyme. PLoS Computational Biology, 2018, 14, e1006180.	3.2	58
56	Self-Assembly of Human Profilin-1 Detected by Carrâ€“Purcellâ€“Meiboomâ€“Gill Nuclear Magnetic Resonance (CPMG NMR) Spectroscopy. Biochemistry, 2017, 56, 692-703.	2.5	23
57	Interplay of buried histidine protonation and protein stability in prion misfolding. Scientific Reports, 2017, 7, 882.	3.3	17
58	Longitudinal relaxation optimized amide 1H-CEST experiments for studying slow chemical exchange processes in fully protonated proteins. Journal of Biomolecular NMR, 2017, 67, 295-307.	2.8	16
59	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
60	Selected topics in solution-phase biomolecular NMR spectroscopy. Journal of Magnetic Resonance, 2017, 278, 141.	2.1	0
61	Probing conformational dynamics in biomolecules via chemical exchange saturation transfer: a primer. Journal of Biomolecular NMR, 2017, 67, 243-271.	2.8	123
62	Simultaneous NMR characterisation of multiple minima in the free energy landscape of an RNA UUCG tetraloop. Physical Chemistry Chemical Physics, 2017, 19, 2797-2804.	2.8	18
63	Separating Dipolar and Chemical Exchange Magnetization Transfer Processes in ¹Hâ€CEST. Angewandte Chemie - International Edition, 2017, 56, 6122-6125.	13.8	35
64	Probing the cooperativity of Thermoplasma acidophilum proteasome core particle gating by NMR spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9846-E9854.	7.1	22
65	Biophysics in Canada. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 1479-1482.	2.3	0
66	Conformational heterogeneity in the Hsp70 chaperoneâ€substrate ensemble identified from analysis of NMRâ€detected titration data. Protein Science, 2017, 26, 2207-2220.	7.6	19
67	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
68	An enhanced sensitivity methyl 1H triple-quantum pulse scheme for measuring diffusion constants of macromolecules. Journal of Biomolecular NMR, 2017, 68, 249-255.	2.8	9
69	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
70	Separating Dipolar and Chemical Exchange Magnetization Transfer Processes in ¹Hâ€CEST. Angewandte Chemie, 2017, 129, 6218-6221.	2.0	2
71	Probing slow timescale dynamics in proteins using methyl 1H CEST. Journal of Biomolecular NMR, 2017, 68, 215-224.	2.8	22
72	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

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73	Structure of a AAA+ unfoldase in the process of unfolding substrate. ELife, 2017, 6, .	6.0	119
74	Promiscuous binding by Hsp70 results in conformational heterogeneity and fuzzy chaperone-substrate ensembles. ELife, 2017, 6, .	6.0	72
75	Enhancing the Sensitivity of CPMG Relaxation Dispersion to Conformational Exchange Processes by Multipleâ€Quantum Spectroscopy. Angewandte Chemie, 2016, 128, 11662-11666.	2.0	7
76	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
77	Evaluating the influence of initial magnetization conditions on extracted exchange parameters in NMR relaxation experiments: applications to CPMG and CEST. Journal of Biomolecular NMR, 2016, 65, 143-156.	2.8	6
78	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
79	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
80	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
81	A magnet moment silenced: A tribute to my friend and mentor Alex D. Bain. Concepts in Magnetic Resonance Part A: Bridging Education and Research, 2016, 45A, e21420.	0.5	0
82	Mechanism of Amyloidogenesis of a Bacterial AAA+ Chaperone. Structure, 2016, 24, 1095-1109.	3.3	12
83	Quantitative measurement of exchange dynamics in proteins via 13C relaxation dispersion of 13CHD2-labeled samples. Journal of Biomolecular NMR, 2016, 65, 59-64.	2.8	10
84	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
85	Concurrent Increases and Decreases in Local Stability and Conformational Heterogeneity in Cu, Zn Superoxide Dismutase Variants Revealed by Temperature-Dependence of Amide Chemical Shifts. Biochemistry, 2016, 55, 1346-1361.	2.5	26
86	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
87	New Views of Functionally Dynamic Proteins by Solution NMR Spectroscopy. Journal of Molecular Biology, 2016, 428, 323-331.	4.2	102
88	Evolution of magnetization due to asymmetric dimerization: theoretical considerations and application to aberrant oligomers formed by apoSOD1^{2SH}. Physical Chemistry Chemical Physics, 2016, 18, 5720-5728.	2.8	8
89	A Dynamic molecular basis for malfunction in disease mutants of p97/VCP. ELife, 2016, 5, .	6.0	74
90	Probing Invisible, Excited Protein States by Nonâ€Uniformly Sampled Pseudoâ€4D CEST Spectroscopy. Angewandte Chemie - International Edition, 2015, 54, 10507-10511.	13.8	25

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91	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
92	13CHD2â€“CEST NMR spectroscopy provides an avenue for studies of conformational exchange in high molecular weight proteins. Journal of Biomolecular NMR, 2015, 63, 187-199.	2.8	30
93	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
94	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
95	Folding of an intrinsically disordered protein by phosphorylation as a regulatory switch. Nature, 2015, 519, 106-109.	27.8	471
96	Thermal fluctuations of immature SOD1 lead to separate folding and misfolding pathways. ELife, 2015, 4, e07296.	6.0	91
97	Triple resonance-based 13CÎ± and 13CÎ² CEST experiments for studies of ms timescale dynamics in proteins. Journal of Biomolecular NMR, 2014, 60, 203-208.	2.8	28
98	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
99	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
100	Visualizing Side Chains of Invisible Protein Conformers by Solution NMR. Journal of Molecular Biology, 2014, 426, 763-774.	4.2	59
101	A Similar In Vitro and In Cell Lysate Folding Intermediate for the FF Domain. Journal of Molecular Biology, 2014, 426, 3214-3220.	4.2	14
102	Bringing Dynamic Molecular Machines into Focus by Methyl-TROSY NMR. Annual Review of Biochemistry, 2014, 83, 291-315.	11.1	200
103	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
104	Probing slowly exchanging protein systems via 13CÎ±-CEST: monitoring folding of the Im7 protein. Journal of Biomolecular NMR, 2013, 55, 279-289.	2.8	24
105	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
106	Unraveling the Mechanism of Protein Disaggregation Through a ClpB-DnaK Interaction. Science, 2013, 339, 1080-1083.	12.6	240
107	A Computational Study of the Effects of ¹³Câ€“¹³C Scalar Couplings on ¹³C CEST NMR Spectra: Towards Studies on a Uniformly ¹³Câ€Labeled Protein. ChemBioChem, 2013, 14, 1709-1713.	2.6	19
108	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

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109	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
110	FV-162 Is a Novel Orally Bioavailable Proteasome Inhibitor With Improved Pharmacokinetics That Displays Preclinical Efficacy In Vitro and In Vivo. Blood, 2013, 122, 1988-1988.	1.4	0
111	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
112	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
113	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
114	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
115	Structure of an Intermediate State in Protein Folding and Aggregation. Science, 2012, 336, 362-366.	12.6	339
116	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
117	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
118	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
119	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
120	NMR studies of protein structure and dynamics â€“ A look backwards and forwards. Journal of Magnetic Resonance, 2011, 213, 492-494.	2.1	16
121	Solution structure of a minor and transiently formed state of a T4 lysozyme mutant. Nature, 2011, 477, 111-114.	27.8	265
122	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
123	Solution NMR spectroscopy of supra-molecular systems, why bother? A methyl-TROSY view. Journal of Magnetic Resonance, 2011, 210, 159-170.	2.1	80
124	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
125	Protein dynamics and conformational disorder in molecular recognition. Journal of Molecular Recognition, 2010, 23, 105-116.	2.1	337
126	Optimal methyl labeling for studies of supra-molecular systems. Journal of Biomolecular NMR, 2010, 47, 163-169.	2.8	39

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127	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
128	Dynamic Regulation of Archaeal Proteasome Gate Opening As Studied by TROSY NMR. Science, 2010, 328, 98-102.	12.6	221
129	A Transient and Low-Populated Protein-Folding Intermediate at Atomic Resolution. Science, 2010, 329, 1312-1316.	12.6	282
130	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
131	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
132	Observing biological dynamics at atomic resolution using NMR. Trends in Biochemical Sciences, 2009, 34, 601-611.	7.5	295
133	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
134	NMR spectroscopy brings invisible protein states into focus. Nature Chemical Biology, 2009, 5, 808-814.	8.0	403
135	Isotope labeling methods for studies of excited protein states by relaxation dispersion NMR spectroscopy. Nature Protocols, 2009, 4, 1641-1648.	12.0	46
136	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
137	Measurement of Methyl Group Motional Parameters of Invisible, Excited Protein States by NMR Spectroscopy. Journal of the American Chemical Society, 2009, 131, 12745-12754.	13.7	30
138	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
139	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
140	Alternate Binding Modes for a Ubiquitinâ€“SH3 Domain Interaction Studied by NMR Spectroscopy. Journal of Molecular Biology, 2009, 386, 391-405.	4.2	36
141	Using relaxation dispersion NMR spectroscopy to determine structures of excited, invisible protein states. Journal of Biomolecular NMR, 2008, 41, 113-120.	2.8	112
142	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
143	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
144	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

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145	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
146	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
147	Probing Structure in Invisible Protein States with Anisotropic NMR Chemical Shifts. Journal of the American Chemical Society, 2008, 130, 2734-2735.	13.7	58
148	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
149	A Novel Non-Competitive Chemical Proteasome Inhibitor Displays Preclinical Activity in Myeloma and Leukemia.. Blood, 2008, 112, 1711-1711.	1.4	0
150	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
151	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
152	Solution NMR of supramolecular complexes: providing new insights into function. Nature Methods, 2007, 4, 697-703.	19.0	163
153	Quantitative dynamics and binding studies of the 20S proteasome by NMR. Nature, 2007, 445, 618-622.	27.8	472
154	A single-quantum methyl 13C-relaxation dispersion experiment with improved sensitivity. Journal of Biomolecular NMR, 2007, 38, 79-88.	2.8	112
155	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
156	New Tools Provide New Insights in NMR Studies of Protein Dynamics. Science, 2006, 312, 224-228.	12.6	720
157	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
158	Isotope labeling strategies for the study of high-molecular-weight proteins by solution NMR spectroscopy. Nature Protocols, 2006, 1, 749-754.	12.0	469
159	Intrinsic dynamics of an enzyme underlies catalysis. Nature, 2005, 438, 117-121.	27.8	1,018
160	Methyl Groups as Probes of Structure and Dynamics in NMR Studies of High-Molecular-Weight Proteins. ChemBioChem, 2005, 6, 1567-1577.	2.6	175
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