Tairan Yuwen

List of Publications by Year
in descending order

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150 papers	21,661 citations	15504 65 h-index	9345 143 g-index
152 all docs	152 docs citations	152 times ranked	11518 citing authors

#	Article	IF	Citations
1	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
2	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
3	Intrinsic dynamics of an enzyme underlies catalysis. Nature, 2005, 438, 117-121.	27.8	1,018
4	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
5	New Tools Provide New Insights in NMR Studies of Protein Dynamics. Science, 2006, 312, 224-228.	12.6	720
6	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
7	Quantitative dynamics and binding studies of the 20S proteasome by NMR. Nature, 2007, 445, 618-622.	27.8	472
8	Folding of an intrinsically disordered protein by phosphorylation as a regulatory switch. Nature, 2015, 519, 106-109.	27.8	471
9	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
10	Slow Dynamics in Folded and Unfolded States of an SH3 Domain. Journal of the American Chemical Society, 2001, 123, 11341-11352.	13.7	454
11	Low-populated folding intermediates of Fyn SH3 characterized by relaxation dispersion NMR. Nature, 2004, 430, 586-590.	27.8	445
12	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
13	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
14	NMR spectroscopy brings invisible protein states into focus. Nature Chemical Biology, 2009, 5, 808-814.	8.0	403
15	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
16	Studying excited states of proteins by NMR spectroscopy. Nature Structural Biology, 2001, 8, 932-935.	9.7	366
17	Structure of an Intermediate State in Protein Folding and Aggregation. Science, 2012, 336, 362-366.	12.6	339
18	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

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19	Observing biological dynamics at atomic resolution using NMR. Trends in Biochemical Sciences, 2009, 34, 601-611.	7.5	295
20	A Transient and Low-Populated Protein-Folding Intermediate at Atomic Resolution. Science, 2010, 329, 1312-1316.	12.6	282
21	Solution structure of a minor and transiently formed state of a T4 lysozyme mutant. Nature, 2011, 477, 111-114.	27.8	265
22	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
23	Nuclear Magnetic Resonance Spectroscopy of High-Molecular-Weight Proteins. Annual Review of Biochemistry, 2004, 73, 107-146.	11.1	247
24	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
25	An Isotope Labeling Strategy for Methyl TROSY Spectroscopy. Journal of Biomolecular NMR, 2004, 28, 165-172.	2.8	221
26	Dynamic Regulation of Archaeal Proteasome Gate Opening As Studied by TROSY NMR. Science, 2010, 328, 98-102.	12.6	221
27	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
28	Bringing Dynamic Molecular Machines into Focus by Methyl-TROSY NMR. Annual Review of Biochemistry, 2014, 83, 291-315.	11.1	200
29	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
30	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
31	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
32	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
33	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
34	Methyl Groups as Probes of Structure and Dynamics in NMR Studies of High-Molecular-Weight Proteins. ChemBioChem, 2005, 6, 1567-1577.	2.6	175
35	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
36	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

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37	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
38	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
39	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
40	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
41	Improved 1HN-detected triple resonance TROSY-based experiments. Journal of Biomolecular NMR, 1999, 13, 3-10.	2.8	132
42	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
43	Probing conformational dynamics in biomolecules via chemical exchange saturation transfer: a primer. Journal of Biomolecular NMR, 2017, 67, 243-271.	2.8	123
44	Off-Resonance R1ÏNMR 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
45	An NMR View of Protein Dynamics in Health and Disease. Annual Review of Biophysics, 2019, 48, 297-319.	10.0	113
46	A single-quantum methyl 13C-relaxation dispersion experiment with improved sensitivity. Journal of Biomolecular NMR, 2007, 38, 79-88.	2.8	112
47	Using relaxation dispersion NMR spectroscopy to determine structures of excited, invisible protein states. Journal of Biomolecular NMR, 2008, 41, 113-120.	2.8	112
48	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
49	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
50	NMR spectroscopy captures the essential role of dynamics in regulating biomolecular function. Cell, 2021, 184, 577-595.	28.9	103
51	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
52	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
53	Double- and Zero-Quantum NMR Relaxation Dispersion Experiments Sampling Millisecond Time Scale Dynamics in Proteins. Journal of the American Chemical Society, 2004, 126, 1886-1891.	13.7	91
54	Thermal fluctuations of immature SOD1 lead to separate folding and misfolding pathways. ELife, 2015, 4, e07296.	6.0	91

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55	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
56	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
57	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
58	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
59	Slow conformational exchange and overall rocking motion in ubiquitin protein crystals. Nature Communications, 2017, 8, 145.	12.8	78
60	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
61	A Dynamic molecular basis for malfunction in disease mutants of p97/VCP. ELife, 2016, 5, .	6.0	74
62	Unveiling invisible protein states with NMR spectroscopy. Current Opinion in Structural Biology, 2020, 60, 39-49.	5.7	73
63	Promiscuous binding by Hsp70 results in conformational heterogeneity and fuzzy chaperone-substrate ensembles. ELife, 2017, 6, .	6.0	72
64	Conserved conformational selection mechanism of Hsp70 chaperone-substrate interactions. ELife, 2018, 7, .	6.0	71
65	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
66	Observing the overall rocking motion of a protein in a crystal. Nature Communications, 2015, 6, 8361.	12.8	67
67	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
68	Ï‡1 Torsion Angle Dynamics in Proteins from Dipolar Couplings. Journal of the American Chemical Society, 2001, 123, 6892-6903.	13.7	65
69	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
70	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
71	Microsecond Time-Scale Conformational Exchange in Proteins: Using Long Molecular Dynamics Trajectory To Simulate NMR Relaxation Dispersion Data. Journal of the American Chemical Society, 2012, 134, 2555-2562.	13.7	64
72	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

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73	Comparison of 13CH3, 13CH2D, and 13CHD2 methyl labeling strategies in proteins. Journal of Biomolecular NMR, 2005, 33, 25-41.	2.8	59
74	Visualizing Side Chains of Invisible Protein Conformers by Solution NMR. Journal of Molecular Biology, 2014, 426, 763-774.	4.2	59
75	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
76	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
77	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
78	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
79	Selective Characterization of Microsecond Motions in Proteins by NMR Relaxation. Journal of the American Chemical Society, 2009, 131, 16257-16265.	13.7	54
80	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
81	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
82	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
83	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
84	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
85	Isotope labeling methods for studies of excited protein states by relaxation dispersion NMR spectroscopy. Nature Protocols, 2009, 4, 1641-1648.	12.0	46
86	Role of Electrostatic Interactions in Binding of Peptides and Intrinsically Disordered Proteins to Their Folded Targets. 1. NMR and MD Characterization of the Complex between the c-Crk N-SH3 Domain and the Peptide Sos. Biochemistry, 2014, 53, 6473-6495.	2.5	46
87	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
88	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
89	Investigating the Dynamics of Destabilized Nucleosomes Using Methyl-TROSY NMR. Journal of the American Chemical Society, 2018, 140, 4774-4777.	13.7	42
90	CPMG relaxation dispersion NMR experiments measuring glycine 1HÎ± and 13CÎ± chemical shifts in the â€˜invisibleâ€™ excited states of proteins. Journal of Biomolecular NMR, 2009, 45, 45-55.	2.8	41

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91	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
92	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
93	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
94	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
95	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
96	Optimal methyl labeling for studies of supra-molecular systems. Journal of Biomolecular NMR, 2010, 47, 163-169.	2.8	39
97	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
98	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
99	Alternate Binding Modes for a Ubiquitinâ€“SH3 Domain Interaction Studied by NMR Spectroscopy. Journal of Molecular Biology, 2009, 386, 391-405.	4.2	36
100	Complementarity of ensemble and single-molecule measures of protein motion: A relaxation dispersion NMR study of an enzyme complex. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 11910-11915.	7.1	35
101	Separating Dipolar and Chemical Exchange Magnetization Transfer Processes in ¹Hâ€CEST. Angewandte Chemie - International Edition, 2017, 56, 6122-6125.	13.8	35
102	Dramatic Decrease in CEST Measurement Times Using Multiâ€Site Excitation. ChemPhysChem, 2018, 19, 1707-1710.	2.1	35
103	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
104	CP-HISQC: a better version of HSQC experiment for intrinsically disordered proteins under physiological conditions. Journal of Biomolecular NMR, 2014, 58, 175-192.	2.8	34
105	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
106	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
107	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
108	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

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109	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
110	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
111	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
112	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
113	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
114	Estimates of methyl 13C and 1H CSA values (??) in proteins from cross-correlated spin relaxation. Journal of Biomolecular NMR, 2004, 30, 397-406.	2.8	26
115	Probing Invisible, Excited Protein States by Nonâ€Uniformly Sampled Pseudoâ€4D CEST Spectroscopy. Angewandte Chemie - International Edition, 2015, 54, 10507-10511.	13.8	25
116	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
117	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
118	Probing slow timescale dynamics in proteins using methyl 1H CEST. Journal of Biomolecular NMR, 2017, 68, 215-224.	2.8	22
119	Proton-decoupled CPMG: A better experiment for measuring 15N R2 relaxation in disordered proteins. Journal of Magnetic Resonance, 2014, 241, 155-169.	2.1	21
120	Domain cooperativity in multidomain proteins: what can we learn from molecular alignment in anisotropic media?. Journal of Biomolecular NMR, 2011, 51, 131-150.	2.8	19
121	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
122	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
123	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
124	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
125	Role of Electrostatic Interactions in Binding of Peptides and Intrinsically Disordered Proteins to Their Folded Targets: 2. The Model of Encounter Complex Involving the Double Mutant of the c-Crk N-SH3 Domain and Peptide Sos. Biochemistry, 2016, 55, 1784-1800.	2.5	16
126	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

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127	Exploring methods to expedite the recording of CEST datasets using selective pulse excitation. Journal of Magnetic Resonance, 2018, 292, 1-7.	2.1	16
128	A methyl 1H double quantum CPMG experiment to study protein conformational exchange. Journal of Biomolecular NMR, 2018, 72, 79-91.	2.8	16
129	Cross-correlated spin relaxation effects in methyl 1H CPMG-based relaxation dispersion experiments: Complications and a simple solution. Journal of Biomolecular NMR, 2005, 31, 337-342.	2.8	15
130	Chemical shift prediction of RNA imino groups: application toward characterizing RNA excited states. Nature Communications, 2021, 12, 1595.	12.8	15
131	A New Spin Probe of Protein Dynamics:Â Nitrogen Relaxation in15Nâ^'2H Amide Groups. Journal of the American Chemical Society, 2005, 127, 3220-3229.	13.7	12
132	Revisiting 1HN CPMG relaxation dispersion experiments: a simple modification can eliminate large artifacts. Journal of Biomolecular NMR, 2019, 73, 641-650.	2.8	12
133	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
134	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
135	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
136	An application of pulse-gradient double-quantum spin echoes to diffusion measurements on molecules with scalar-coupled spins. Journal of Magnetic Resonance, 1986, 67, 103-113.	0.5	7
137	Enhancing the Sensitivity of CPMG Relaxation Dispersion to Conformational Exchange Processes by Multipleâ€Quantum Spectroscopy. Angewandte Chemie, 2016, 128, 11662-11666.	2.0	7
138	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
139	Towards autonomous analysis of chemical exchange saturation transfer experiments using deep neural networks. Journal of Biomolecular NMR, 2022, 76, 75-86.	2.8	7
140	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
141	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
142	Dipolar dynamic frequency shifts in multiple-quantum spectra of methyl groups in proteins: correlation with side-chain motion. Magnetic Resonance in Chemistry, 2006, 44, S122-S129.	1.9	5
143	Measuring Diffusion Constants of Invisible Protein Conformers by Tripleâ€Quantum 1 H CPMG Relaxation Dispersion. Angewandte Chemie, 2018, 130, 17019-17022.	2.0	5
144	Removal of 2H-decoupling sidebands in 13CHD2 13C-CEST profiles. Journal of Biomolecular NMR, 2021, 75, 133-142.	2.8	3

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145	Separating Dipolar and Chemical Exchange Magnetization Transfer Processes in ¹Hâ€CEST. Angewandte Chemie, 2017, 129, 6218-6221.	2.0	2
146	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
147	Molecular Insight into the Extracellular Chaperone Serum Albumin in Modifying the Folding Free Energy Landscape of Client Proteins. Journal of Physical Chemistry Letters, 2022, 13, 2711-2717.	4.6	2
148	Understanding and solving abnormal peak splitting in 3D HCCH-TOCSY and HCC(CO)NH-TOCSY. Journal of Biomolecular NMR, 2020, 74, 213-221.	2.8	1
149	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
150	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