

GFT NMR, a New Approach To Rapidly Obtain Precise H Information

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Citation Report

#	ARTICLE	IF	CITATIONS
2	Multiple quadrature detection in reduced dimensionality experiments. <i>Journal of Biomolecular NMR</i> , 2003, 26, 157-166.	1.6	68
3	Optimized set of two-dimensional experiments for fast sequential assignment, secondary structure determination, and backbone fold validation of ¹³ C/ ¹⁵ N-labelled proteins. <i>Journal of Biomolecular NMR</i> , 2003, 27, 57-67.	1.6	37
4	New methods for fast multidimensional NMR. <i>Journal of Biomolecular NMR</i> , 2003, 27, 101-114.	1.6	179
5	Reconstruction of the three-dimensional NMR spectrum of a protein from a set of plane projections. <i>Journal of Biomolecular NMR</i> , 2003, 27, 383-387.	1.6	58
6	New high-throughput NMR. <i>Targets</i> , 2003, 2, 39-40.	0.3	1
7	NMR assignment of protein side chains using residue-correlated labeling and NOE spectra. <i>Journal of Magnetic Resonance</i> , 2003, 165, 237-247.	1.2	2
8	High-throughput backbone resonance assignment of small ¹³ C, ¹⁵ N-labeled proteins by a triple-resonance experiment with four sequential connectivity pathways using chemical shift-dependent, apparent (1H, ¹³ C): HNCACB-coded HAHB. <i>Journal of Magnetic Resonance</i> , 2003, 165, 315-319.	1.2	1
9	Structural biology, ligand binding, metabomics—the changing face of high-field, high-resolution NMR spectroscopy. <i>Computational and Theoretical Chemistry</i> , 2003, 666-667, 499-505.	1.5	2
10	Hadamard NMR spectroscopy. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2003, 42, 95-122.	3.9	193
12	Principles and Features of Single-Scan Two-Dimensional NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2003, 125, 9204-9217.	6.6	236
13	Single-Scan NMR Spectroscopy at Arbitrary Dimensions. <i>Journal of the American Chemical Society</i> , 2003, 125, 11385-11396.	6.6	77
14	Projection-Reconstruction of Three-Dimensional NMR Spectra. <i>Journal of the American Chemical Society</i> , 2003, 125, 13958-13959.	6.6	170
15	High-throughput screening of structural proteomics targets using NMR. <i>FEBS Letters</i> , 2003, 552, 207-213.	1.3	33
16	Covariance nuclear magnetic resonance spectroscopy. <i>Journal of Chemical Physics</i> , 2004, 120, 5253-5260.	1.2	232
17	Automation of NMR structure determination of proteins. <i>Current Opinion in Structural Biology</i> , 2004, 14, 547-553.	2.6	55
18	The NMR solution structure of the 30S ribosomal protein S27e encoded in gene RS27_ARCFU of <i>Archaeoglobus fulgidis</i> reveals a novel protein fold. <i>Protein Science</i> , 2004, 13, 1407-1416.	3.1	12
19	GFT NMR Experiments for Polypeptide Backbone and ¹³ C ² Chemical Shift Assignment. <i>Journal of Biomolecular NMR</i> , 2004, 28, 117-130.	1.6	38
20	Triple Resonance MAS NMR with (¹³ C, ¹⁵ N) Labeled Molecules: Reduced Dimensionality Data Acquisition Via ¹³ C- ¹⁵ N Heteronuclear Two-Spin Coherence Transfer Pathways. <i>Journal of Biomolecular NMR</i> , 2004, 28, 185-190.	1.6	4

#	ARTICLE	IF	CITATIONS
21	Fast reconstruction of four-dimensional NMR spectra from plane projections. <i>Journal of Biomolecular NMR</i> , 2004, 28, 391-395.	1.6	44
22	Combined frequency- and time-domain NMR spectroscopy. Application to fast protein resonance assignment. <i>Journal of Biomolecular NMR</i> , 2004, 29, 57-64.	1.6	24
23	(3,2)D GFT-NMR experiments for fast data collection from proteins. <i>Journal of Biomolecular NMR</i> , 2004, 29, 467-476.	1.6	20
24	DEPT spectral editing in HCONH-type experiments. Application to fast protein backbone and side chain assignment. <i>Journal of Magnetic Resonance</i> , 2004, 167, 178-184.	1.2	10
25	A generalized approach to automated NMR peak list editing: application to reduced dimensionality triple resonance spectra. <i>Journal of Magnetic Resonance</i> , 2004, 170, 263-277.	1.2	38
26	The DQ-HN{CACB} and DQ-HN(CO){CACB} sequences with evolution of double quantum $C\hat{I}\pm\hat{I}^2$ coherences. <i>Journal of Magnetic Resonance</i> , 2004, 171, 186-191.	1.2	4
27	The set of triple-resonance sequences with a multiple quantum coherence evolution period. <i>Journal of Magnetic Resonance</i> , 2004, 171, 338-344.	1.2	3
28	Addressing the overlap problem in the quantitative analysis of two dimensional NMR spectra: Application to ^{15}N relaxation measurements. <i>Journal of Biomolecular NMR</i> , 2004, 30, 347-352.	1.6	14
29	High-throughput NMR spectroscopy. <i>Analytical and Bioanalytical Chemistry</i> , 2004, 378, 1403-1404.	1.9	24
30	Speeding Up Biomolecular NMR Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2004, 43, 782-786.	7.2	11
32	The radon transform: A new scheme for fast multidimensional NMR. <i>Concepts in Magnetic Resonance</i> , 2004, 22A, 4-11.	1.3	61
33	Distant echoes of the accordion: Reduced dimensionality, GFT-NMR, and projection-reconstruction of multidimensional spectra. <i>Concepts in Magnetic Resonance</i> , 2004, 23A, 63-75.	1.3	54
34	Ultra-high resolution 3D NMR spectra from limited-size data sets. <i>Journal of Magnetic Resonance</i> , 2004, 169, 215-224.	1.2	21
35	Accelerated acquisition of high resolution triple-resonance spectra using non-uniform sampling and maximum entropy reconstruction. <i>Journal of Magnetic Resonance</i> , 2004, 170, 15-21.	1.2	217
36	Ultrafast 2D NMR spectroscopy using a continuous spatial encoding of the spin interactions. <i>Journal of Magnetic Resonance</i> , 2004, 171, 163-170.	1.2	82
37	Coherence transfer in proteins. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2004, 44, 97-137.	3.9	59
38	Automated structure determination of proteins by NMR spectroscopy. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2004, 44, 33-96.	3.9	98
39	A fast method for the measurement of long spin lattice relaxation times by single scan inversion recovery experiment. <i>Chemical Physics Letters</i> , 2004, 383, 99-103.	1.2	22

#	ARTICLE	IF	CITATIONS
40	Three-dimensional solution NMR spectroscopy of complex structures and mixtures. <i>Analyst</i> , The, 2004, 129, 687.	1.7	22
41	G-matrix Fourier transform NMR spectroscopy for complete protein resonance assignment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 9642-9647.	3.3	125
42	Generalized Reconstruction of n-D NMR Spectra from Multiple Projections: Application to the 5-D HACACONH Spectrum of Protein G B1 Domain. <i>Journal of the American Chemical Society</i> , 2004, 126, 1000-1001.	6.6	57
43	Automated Analysis of Protein NMR Assignments and Structures. <i>Chemical Reviews</i> , 2004, 104, 3541-3556.	23.0	90
44	New approaches for NMR screening in drug discovery. <i>Drug Discovery Today: Technologies</i> , 2004, 1, 277-283.	4.0	31
45	Sub-second 2D NMR Spectroscopy at Sub-millimolar Concentrations. <i>Journal of the American Chemical Society</i> , 2004, 126, 11756-11757.	6.6	15
46	Protein folding studied by real-time NMR spectroscopy. <i>Methods</i> , 2004, 34, 65-74.	1.9	54
47	Resolving ambiguities in two-dimensional NMR spectra: the \tilde{T} experiment. <i>Journal of Magnetic Resonance</i> , 2005, 172, 329-332.	1.2	18
48	3D NMR spectroscopy for resonance assignment and structure elucidation of proteins under MAS: novel pulse schemes and sensitivity considerations. <i>Journal of Magnetic Resonance</i> , 2005, 173, 64-74.	1.2	61
49	AutoLink: Automated sequential resonance assignment of biopolymers from NMR data by relative-hypothesis-prioritization-based simulated logic. <i>Journal of Magnetic Resonance</i> , 2005, 174, 133-151.	1.2	80
50	Rapid assignment of protein side chain resonances using projection reconstruction of (4,3)D HC(CCO)NH and intra-HC(C)NH experiments. <i>Journal of Magnetic Resonance</i> , 2005, 175, 170-176.	1.2	17
51	Signal identification in NMR spectra with coupled evolution periods. <i>Journal of Magnetic Resonance</i> , 2005, 176, 47-53.	1.2	28
52	Fast ^1H - ^{13}C correlation data for use in automatic structure confirmation of small organic compounds. <i>Magnetic Resonance in Chemistry</i> , 2005, 43, 124-131.	1.1	7
53	Resolving overlap in two-dimensional NMR spectra: nuclear Overhauser effects in a polysaccharide. <i>Magnetic Resonance in Chemistry</i> , 2005, 43, 791-794.	1.1	15
54	Reduced data acquisition time in multi-dimensional NMR spectroscopy using multiple-coil probes. <i>Journal of Magnetic Resonance</i> , 2005, 173, 134-139.	1.2	21
55	High-throughput analysis of protein NMR spectra. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2005, 46, 109-129.	3.9	33
56	High-resolution aliphatic side-chain assignments in 3D HCcoNH experiments with joint ^1H - ^{13}C evolution and non-uniform sampling. <i>Journal of Biomolecular NMR</i> , 2005, 32, 55-60.	1.6	29
57	SOFAST-HMQC Experiments for Recording Two-dimensional Deteronuclear Correlation Spectra of Proteins within a Few Seconds. <i>Journal of Biomolecular NMR</i> , 2005, 33, 199-211.	1.6	603

#	ARTICLE	IF	CITATIONS
58	GFT NMR based resonance assignment for the 21 kDa human protein UFC1. Journal of Biomolecular NMR, 2005, 32, 261-261.	1.6	14
59	NMR structure of protein yqbG from Bacillus subtilis reveals a novel $\hat{1}\pm$ -helical protein fold. Proteins: Structure, Function and Bioinformatics, 2005, 62, 288-291.	1.5	3
61	NMR Spectroscopy and Protein Structure Determination: Applications to Drug Discovery and Development. Current Pharmaceutical Biotechnology, 2005, 6, 105-120.	0.9	57
62	Rapid NMR Data Collection. Methods in Enzymology, 2005, 394, 78-108.	0.4	86
63	Automated projection spectroscopy (APSY). Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10876-10881.	3.3	232
64	NMR data collection and analysis protocol for high-throughput protein structure determination. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10487-10492.	3.3	108
65	Multiway Decomposition of NMR Spectra with Coupled Evolution Periods. Journal of the American Chemical Society, 2005, 127, 13486-13487.	6.6	74
66	High-Resolution Iterative Frequency Identification for NMR as a General Strategy for Multidimensional Data Collection. Journal of the American Chemical Society, 2005, 127, 12528-12536.	6.6	118
67	Multidimensional NMR Spectroscopy for Protein Characterization and Assignment inside Cells. Journal of the American Chemical Society, 2005, 127, 10848-10849.	6.6	42
68	Probing Structure and Functional Dynamics of (Large) Proteins with Aromatic Rings: \hat{A} L-GFT-TROSY (4,3)DHCCH NMR Spectroscopy. Journal of the American Chemical Society, 2005, 127, 14578-14579.	6.6	32
69	NUCLEAR MAGNETIC RESONANCE SPECTROSCOPY APPLICATIONS Pharmaceutical. , 2005, , 321-332.		1
71	Nonuniform Sampling in Biomolecular NMR. , 2008, , 1305-1311.		4
72	Nuclear Magnetic Resonance-Based Screening Methods for Drug Discovery. , 2006, 316, 227-289.		5
73	Polar Fourier transforms of radially sampled NMR data. Journal of Magnetic Resonance, 2006, 182, 84-95.	1.2	51
74	Multidimensional HRMAS NMR: a platform for in vivo studies using intact bacterial cells. Analyst, The, 2006, 131, 777.	1.7	40
75	Enhanced Covariance Spectroscopy from Minimal Datasets. Journal of the American Chemical Society, 2006, 128, 15564-15565.	6.6	34
76	Targeted Acquisition for Real-Time NMR Spectroscopy. Journal of the American Chemical Society, 2006, 128, 13421-13426.	6.6	70
77	Hyperdimensional NMR Spectroscopy. Journal of the American Chemical Society, 2006, 128, 6020-6021.	6.6	55

#	ARTICLE	IF	CITATIONS
79	High-Resolution Protein Structure Determination by NMR. Annual Reports on NMR Spectroscopy, 2006, 59, 235-273.	0.7	5
80	Modern High Resolution NMR for the Study of Structure, Dynamics and Interactions of Biological Macromolecules. Zeitschrift Fur Physikalische Chemie, 2006, 220, 567-613.	1.4	14
81	NMR structure of protein PA2021 from Pseudomonas aeruginosa. Proteins: Structure, Function and Bioinformatics, 2006, 65, 767-770.	1.5	1
82	Hadamard frequency-encoded SOFAST-HMQC for ultrafast two-dimensional protein NMR. Journal of Magnetic Resonance, 2006, 178, 334-339.	1.2	34
83	Two-dimensional Fourier transform of arbitrarily sampled NMR data sets. Journal of Magnetic Resonance, 2006, 179, 323-328.	1.2	135
84	Spectral reconstruction methods in fast NMR: Reduced dimensionality, random sampling and maximum entropy. Journal of Magnetic Resonance, 2006, 182, 96-105.	1.2	92
85	Rapid Determination of Protein Solubility and Stability Conditions for NMR Studies Using Incomplete Factorial Design. Journal of Biomolecular NMR, 2006, 34, 137-151.	1.6	15
86	PR-CALC: A Program for the Reconstruction of NMR Spectra from Projections. Journal of Biomolecular NMR, 2006, 34, 179-195.	1.6	19
87	Random sampling of evolution time space and Fourier transform processing. Journal of Biomolecular NMR, 2006, 36, 157-168.	1.6	101
88	Simultaneous \hat{I}_x/\hat{I}_y spin-state selection for ^{13}C and ^{15}N from a time-shared HSQC-IPAP experiment. Journal of Biomolecular NMR, 2006, 37, 65-77.	1.6	17
89	Three-dimensional correlated accordion NMR spectroscopy of proteins. Journal of Magnetic Resonance, 2006, 180, 203-209.	1.2	1
90	Application du traitement par entropie maximale aux données RMN multidimensionnelles; cas de l'échantillonnage partiel. Comptes Rendus Chimie, 2006, 9, 364-373.	0.2	13
91	Solution NMR in structural genomics. Current Opinion in Structural Biology, 2006, 16, 611-617.	2.6	43
92	Deterministic and statistical methods for reconstructing multidimensional NMR spectra. Magnetic Resonance in Chemistry, 2006, 44, 197-209.	1.1	35
93	Automated structure verification based on ^1H NMR prediction. Magnetic Resonance in Chemistry, 2006, 44, 524-538.	1.1	27
94	Principles and applications of GFT projection NMR spectroscopy. Magnetic Resonance in Chemistry, 2006, 44, S51-S60.	1.1	51
95	Fast multidimensional NMR spectroscopy by spin-state selective off-resonance decoupling (SITAR). Magnetic Resonance in Chemistry, 2006, 44, S196-S205.	1.1	10
96	Robust and versatile interpretation of spectra with coupled evolution periods using multi-way decomposition. Magnetic Resonance in Chemistry, 2006, 44, S185-S195.	1.1	21

#	ARTICLE	IF	CITATIONS
97	How Far Can the Sensitivity of NMR Be Increased?. Annual Reports on NMR Spectroscopy, 2006, 58, 155-175.	0.7	44
98	Ultrafast-based projection-reconstruction three-dimensional nuclear magnetic resonance spectroscopy. Journal of Chemical Physics, 2007, 127, 034507.	1.2	20
99	NMR Shows Hydrophobic Interactions Replace Glycine Packing in the Triple Helix at a Natural Break in the (Gly-X-Y) Repeat. Journal of Biological Chemistry, 2007, 282, 22699-22706.	1.6	30
100	Fast Minimization by Iterative Thresholding for Multidimensional NMR Spectroscopy. Eurasip Journal on Advances in Signal Processing, 2007, 2007, .	1.0	56
101	LARGER PROTEINS AND MOLECULAR INTERACTIONS. , 2007, , 725-780.		12
102	Ultrahigh-Resolution ^1H - ^{13}C HSQC Spectra of Metabolite Mixtures Using Nonlinear Sampling and Forward Maximum Entropy Reconstruction. Journal of the American Chemical Society, 2007, 129, 5108-5116.	6.6	131
103	Resolution-Enhanced 4D $^{15}\text{N}/^{13}\text{C}$ NOESY Protein NMR Spectroscopy by Application of the Covariance Transform. Journal of the American Chemical Society, 2007, 129, 14126-14127.	6.6	26
104	Coherence pathway selection by cogwheel phase cycling in liquid-state NMR. Concepts in Magnetic Resonance Part A: Bridging Education and Research, 2007, 30A, 81-99.	0.2	10
105	Three-dimensional NMR Spectroscopy of organic molecules by random sampling of evolution time space and multidimensional Fourier transformation. Magnetic Resonance in Chemistry, 2007, 45, 171-174.	1.1	13
106	Two-dimensional spectroscopy with parallel acquisition of ^1H and ^{19}F correlations. Magnetic Resonance in Chemistry, 2007, 45, 378-380.	1.1	36
107	SPEED: single-point evaluation of the evolution dimension. Magnetic Resonance in Chemistry, 2007, 45, 711-713.	1.1	25
108	Reconstruction of a solid-state high-resolution heteronuclear J-resolved 2D spectrum from 1D experiments. Chemical Physics Letters, 2007, 442, 474-477.	1.2	1
109	Sampling of the NMR time domain along concentric rings. Journal of Magnetic Resonance, 2007, 184, 207-221.	1.2	48
110	2D separated-local-field spectra from projections of 1D experiments. Journal of Magnetic Resonance, 2007, 184, 330-336.	1.2	8
111	Nonuniform sampling and maximum entropy reconstruction applied to the accurate measurement of residual dipolar couplings. Journal of Magnetic Resonance, 2007, 186, 201-211.	1.2	19
112	NMR data processing using iterative thresholding and minimum l_1 -norm reconstruction. Journal of Magnetic Resonance, 2007, 188, 295-300.	1.2	128
113	Lineshapes and artifacts in Multidimensional Fourier Transform of arbitrary sampled NMR data sets. Journal of Magnetic Resonance, 2007, 188, 344-356.	1.2	70
114	NMR structure of protein yjbR from Escherichia coli reveals a double-wing DNA binding motif. Proteins: Structure, Function and Bioinformatics, 2007, 67, 501-504.	1.5	11

#	ARTICLE	IF	CITATIONS
116	An automated tool for maximum entropy reconstruction of biomolecular NMR spectra. <i>Nature Methods</i> , 2007, 4, 467-468.	9.0	64
117	Physical methods and techniques : NMR spectroscopy. <i>Annual Reports on the Progress of Chemistry Section B</i> , 2007, 103, 331.	0.8	1
118	High-precision frequency measurements: indispensable tools at the core of the molecular-level analysis of complex systems. <i>Analytical and Bioanalytical Chemistry</i> , 2007, 389, 1311-1327.	1.9	267
119	J-Spectroscopy in the presence of residual dipolar couplings: determination of one-bond coupling constants and scalable resolution. <i>Journal of Biomolecular NMR</i> , 2007, 37, 231-243.	1.6	45
120	HIFI-C: a robust and fast method for determining NMR couplings from adaptive 3D to 2D projections. <i>Journal of Biomolecular NMR</i> , 2007, 38, 341-351.	1.6	13
121	Four-dimensional heteronuclear correlation experiments for chemical shift assignment of solid proteins. <i>Journal of Biomolecular NMR</i> , 2007, 39, 107-131.	1.6	94
122	Covariance NMR in higher dimensions: application to 4D NOESY spectroscopy of proteins. <i>Journal of Biomolecular NMR</i> , 2007, 39, 165-175.	1.6	32
123	Spatially encoded strategies in the execution of biomolecular-oriented 3D NMR experiments. <i>Journal of Biomolecular NMR</i> , 2007, 39, 291-301.	1.6	10
124	Rapid measurement of $3J(\text{HN}\hat{=}^{\text{H}}\text{I}\pm)$ and $3J(\text{N}\hat{=}^{\text{H}}\text{I}^2)$ coupling constants in polypeptides. <i>Journal of Biomolecular NMR</i> , 2007, 39, 259-263.	1.6	29
125	Forty years of Progress in Nuclear Magnetic Resonance Spectroscopy. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2007, 50, 179-198.	3.9	35
126	Protein assignments without peak lists using higher-order spectra. <i>Journal of Magnetic Resonance</i> , 2007, 189, 173-181.	1.2	22
127	Randomization improves sparse sampling in multidimensional NMR. <i>Journal of Magnetic Resonance</i> , 2008, 193, 317-320.	1.2	49
128	Optimized angle selection for radial sampled NMR experiments. <i>Journal of Magnetic Resonance</i> , 2008, 195, 169-178.	1.2	6
129	Protein chaperones Q8ZP25_SALTY from <i>Salmonella</i> and HYAE_ECOLI from <i>Escherichia coli</i> exhibit thioredoxin-like structures despite lack of canonical thioredoxin active site sequence motif. <i>Journal of Structural and Functional Genomics</i> , 2008, 9, 41-49.	1.2	12
130	Projected $[1\text{H}, 15\text{N}]\text{-HMQC-}[1\text{H}, 1\text{H}]\text{-NOESY}$ for large molecular systems: application to a 121 kDa protein-DNA complex. <i>Journal of Biomolecular NMR</i> , 2008, 40, 175-181.	1.6	4
131	GFT projection NMR based resonance assignment of membrane proteins: application to subunit c of <i>E. coli</i> F1FO ATP synthase in LPPG micelles. <i>Journal of Biomolecular NMR</i> , 2008, 40, 157-163.	1.6	19
132	High-resolution pyrimidine- and ribose-specific 4D HCCH-COSY spectra of RNA using the filter diagonalization method. <i>Journal of Biomolecular NMR</i> , 2008, 41, 209-219.	1.6	3
133	Identification of C-terminal neighbours of amino acid residues without an aliphatic ^{13}C as an aid to NMR assignments in proteins. <i>Journal of Biomolecular NMR</i> , 2008, 41, 191-197.	1.6	24

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134	Assignment of protein NMR spectra based on projections, multi-way decomposition and a fast correlation approach. <i>Journal of Biomolecular NMR</i> , 2008, 42, 87-97.	1.6	21
135	APSY-NMR with proteins: practical aspects and backbone assignment. <i>Journal of Biomolecular NMR</i> , 2008, 42, 179-195.	1.6	55
136	Automatic assignment of protein backbone resonances by direct spectrum inspection in targeted acquisition of NMR data. <i>Journal of Biomolecular NMR</i> , 2008, 42, 77-86.	1.6	5
137	Chemical shift based editing of CH ₃ groups in fractionally ¹³ C-labelled proteins using GFT (3, 2)D CT-HCCH-COSY: stereospecific assignments of CH ₃ groups of Val and Leu residues. <i>Journal of Biomolecular NMR</i> , 2008, 42, 149-154.	1.6	14
138	High resolution 4-D spectroscopy with sparse concentric shell sampling and FFT-CLEAN. <i>Journal of Biomolecular NMR</i> , 2008, 42, 225-239.	1.6	79
139	NMR structure of protein Cgl2762 from <i>Corynebacterium glutamicum</i> implicated in DNA transposition reveals a helix-turn-helix motif attached to a flexibly disordered leucine zipper. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 1650-1654.	1.5	1
140	NMR structure of the peptidyl transferase domain from <i>Pseudomonas syringae</i> expands the structural coverage of the hydrolysis domains of class 1 peptide chain release factors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1027-1031.	1.5	8
141	Maximum entropy spectral reconstruction of nonuniformly sampled data. <i>Concepts in Magnetic Resonance Part A: Bridging Education and Research</i> , 2008, 32A, 436-448.	0.2	65
142	Structure-based profiling of metabolites and isotopomers by NMR. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2008, 52, 69-117.	3.9	209
143	Hyperdimensional NMR spectroscopy. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2008, 52, 22-30.	3.9	39
144	Fast (4,3)D GFT-TS NMR for NOESY of small to medium-sized proteins. <i>Journal of Magnetic Resonance</i> , 2008, 190, 142-148.	1.2	5
145	Fast multi-dimensional NMR by minimal sampling. <i>Journal of Magnetic Resonance</i> , 2008, 191, 164-168.	1.2	20
146	An alternative approach for recording of multidimensional NMR data based on frequency dependent folding mechanism. <i>Journal of Magnetic Resonance</i> , 2008, 191, 291-303.	1.2	7
147	Automated NMR Assignment of Protein Side Chain Resonances Using Automated Projection Spectroscopy (APSY). <i>Journal of the American Chemical Society</i> , 2008, 130, 12073-12079.	6.6	28
148	Characterization of Conformational and Dynamic Properties of Natively Unfolded Human and Mouse I κ B-Synuclein Ensembles by NMR: Implication for Aggregation. <i>Journal of Molecular Biology</i> , 2008, 378, 1104-1115.	2.0	112
149	¹³ C-Sialic Acid Labeling of Glycans on Glycoproteins Using ST6Gal-I. <i>Journal of the American Chemical Society</i> , 2008, 130, 11864-11865.	6.6	25
150	Structural proteomics by NMR spectroscopy. <i>Expert Review of Proteomics</i> , 2008, 5, 589-601.	1.3	42
151	Z-matrix formalism for quantitative noise assessment of covariance nuclear magnetic resonance spectra. <i>Journal of Chemical Physics</i> , 2008, 129, 104511.	1.2	21

#	ARTICLE	IF	CITATIONS
153	On NMR-based Structural Proteomics. , 2008, , 307-329.		0
155	Using NMR-Detected Backbone Amide ¹ H Exchange to Assess Macromolecular Crowding Effects on Globular-Protein Stability. <i>Methods in Enzymology</i> , 2009, 466, 1-18.	0.4	28
157	Recent Advances in Solution NMR: Fast Methods and Heteronuclear Direct Detection. <i>ChemPhysChem</i> , 2009, 10, 1356-1368.	1.0	90
158	Clean Absorption-Mode NMR Data Acquisition. <i>Angewandte Chemie - International Edition</i> , 2009, 48, 1479-1483.	7.2	6
159	Narrow peaks and high dimensionalities: Exploiting the advantages of random sampling. <i>Journal of Magnetic Resonance</i> , 2009, 197, 219-228.	1.2	75
160	Unique opportunities for NMR methods in structural genomics. <i>Journal of Structural and Functional Genomics</i> , 2009, 10, 101-106.	1.2	25
161	Clean absorption mode NMR data acquisition based on time-proportional phase incrementation. <i>Journal of Structural and Functional Genomics</i> , 2009, 10, 227-232.	1.2	5
162	Analytical solution to the coupled evolution of multidimensional NMR data. <i>Journal of Biomolecular NMR</i> , 2009, 44, 13-23.	1.6	12
163	Highly automated protein backbone resonance assignment within a few hours: the «BATCH» strategy and software package. <i>Journal of Biomolecular NMR</i> , 2009, 44, 43-57.	1.6	20
164	CSSI-PRO: a method for secondary structure type editing, assignment and estimation in proteins using linear combination of backbone chemical shifts. <i>Journal of Biomolecular NMR</i> , 2009, 44, 185-194.	1.6	7
165	FM reconstruction of non-uniformly sampled protein NMR data at higher dimensions and optimization by distillation. <i>Journal of Biomolecular NMR</i> , 2009, 45, 283-294.	1.6	69
166	Aliasing in reduced dimensionality NMR spectra: (3,2)D HNHA and (4,2)D HN(COCA)NH experiments as examples. <i>Journal of Biomolecular NMR</i> , 2009, 45, 351-356.	1.6	15
167	Fast-pulsing longitudinal relaxation optimized techniques: Enriching the toolbox of fast biomolecular NMR spectroscopy. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2009, 55, 238-265.	3.9	78
168	Enhanced spectral resolution by high-dimensional NMR using the filter diagonalization method and «hidden»-dimensions. <i>Journal of Magnetic Resonance</i> , 2009, 196, 12-22.	1.2	5
169	Optimized sampling patterns for multidimensional T2 experiments. <i>Journal of Magnetic Resonance</i> , 2009, 197, 63-70.	1.2	5
170	Nonuniform sampling and spectral aliasing. <i>Journal of Magnetic Resonance</i> , 2009, 199, 88-93.	1.2	76
171	Spectroscopy by Integration of Frequency and Time Domain Information for Fast Acquisition of High-Resolution Dark Spectra. <i>Journal of the American Chemical Society</i> , 2009, 131, 4648-4656.	6.6	95
172	Speeding Up ¹³ C Direct Detection Biomolecular NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2009, 131, 15339-15345.	6.6	88

#	ARTICLE	IF	CITATIONS
173	Principles and Progress in Ultrafast Multidimensional Nuclear Magnetic Resonance. Annual Review of Physical Chemistry, 2009, 60, 429-448.	4.8	73
175	Single-scan 2D NMR correlations by multiple coherence transfers. Journal of Magnetic Resonance, 2010, 203, 311-315.	1.2	5
176	Gridding and fast Fourier transformation on non-uniformly sparse sampled multidimensional NMR data. Journal of Magnetic Resonance, 2010, 204, 165-168.	1.2	21
177	Iterative algorithm of discrete Fourier transform for processing randomly sampled NMR data sets. Journal of Biomolecular NMR, 2010, 47, 65-77.	1.6	82
178	High-resolution methyl edited GFT NMR experiments for protein resonance assignments and structure determination. Journal of Biomolecular NMR, 2010, 48, 137-145.	1.6	7
179	Strategy for complete NMR assignment of disordered proteins with highly repetitive sequences based on resolution-enhanced 5D experiments. Journal of Biomolecular NMR, 2010, 48, 169-177.	1.6	99
180	Automated protein resonance assignments of magic angle spinning solid-state NMR spectra of \hat{I}^{21} immunoglobulin binding domain of protein G (GB1). Journal of Biomolecular NMR, 2010, 48, 123-128.	1.6	27
181	GFT projection NMR spectroscopy for proteins in the solid state. Journal of Biomolecular NMR, 2010, 48, 213-223.	1.6	26
182	Time-shared NMR experiments. Concepts in Magnetic Resonance Part A: Bridging Education and Research, 2010, 36A, 1-23.	0.2	33
183	Exclusively Heteronuclear NMR Experiments to Obtain Structural and Dynamic Information on Proteins. ChemPhysChem, 2010, 11, 689-695.	1.0	36
185	Rapid Three-dimensional MAS NMR Spectroscopy at Critical Sensitivity. Angewandte Chemie - International Edition, 2010, 49, 9215-9218.	7.2	35
186	Toward multipurpose NMR experiments. Magnetic Resonance in Chemistry, 2010, 48, 1-8.	1.1	7
187	Fast multidimensional localized parallel NMR spectroscopy for the analysis of samples. Magnetic Resonance in Chemistry, 2010, 48, 749-752.	1.1	11
188	Targeted projection NMR spectroscopy for unambiguous metabolic profiling of complex mixtures. Magnetic Resonance in Chemistry, 2010, 48, 727-733.	1.1	17
189	Biomolecular NMR data analysis. Progress in Nuclear Magnetic Resonance Spectroscopy, 2010, 56, 329-345.	3.9	11
190	Radial sampling for fast NMR: Concepts and practices over three decades. Progress in Nuclear Magnetic Resonance Spectroscopy, 2010, 57, 381-419.	3.9	82
191	Random sampling in multidimensional NMR spectroscopy. Progress in Nuclear Magnetic Resonance Spectroscopy, 2010, 57, 420-434.	3.9	97
192	A practical implementation of cross-spectrum in protein backbone resonance assignment. Journal of Magnetic Resonance, 2010, 203, 208-212.	1.2	8

#	ARTICLE	IF	CITATIONS
193	Fast acquisition of high resolution 4-D amideâ€“amide NOESY with diagonal suppression, sparse sampling and FFT-CLEAN. <i>Journal of Magnetic Resonance</i> , 2010, 204, 173-178.	1.2	22
194	Solution NMR structures of proteins VPA0419 from <i>Vibrio parahaemolyticus</i> and yiiS from <i>Shigella flexneri</i> provide structural coverage for protein domain family PFAM 04175. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 779-784.	1.5	0
195	Concepts in Projection-Reconstruction. <i>Topics in Current Chemistry</i> , 2010, 316, 1-20.	4.0	15
196	Derivation of Peptide and Protein Structure using NMR Spectroscopy. , 2010, , 279-325.		6
197	Applications of Non-Uniform Sampling and Processing. <i>Topics in Current Chemistry</i> , 2011, 316, 125-148.	4.0	119
198	Data Sampling in Multidimensional NMR: Fundamentals and Strategies. <i>Topics in Current Chemistry</i> , 2011, 316, 49-77.	4.0	41
199	Automated Projection Spectroscopy and Its Applications. <i>Topics in Current Chemistry</i> , 2011, 316, 21-47.	4.0	17
200	Protein Crowding Tunes Protein Stability. <i>Journal of the American Chemical Society</i> , 2011, 133, 7116-7120.	6.6	255
202	NMR Studies of Metalloproteins. <i>Topics in Current Chemistry</i> , 2011, 326, 69-98.	4.0	9
203	Generalized Fourier Transform for Non-Uniform Sampled Data. <i>Topics in Current Chemistry</i> , 2011, 316, 79-124.	4.0	27
204	Binding Site Identification and Structure Determination of Proteinâ€“Ligand Complexes by NMR. <i>Methods in Enzymology</i> , 2011, 493, 241-275.	0.4	58
205	Membrane Proteins Structure and Dynamics by Nuclear Magnetic Resonance. , 2011, 1, 2175-2187.		1
207	Improved Technologies Now Routinely Provide Protein NMR Structures Useful for Molecular Replacement. <i>Structure</i> , 2011, 19, 757-766.	1.6	34
208	Parallel receivers and sparse sampling in multidimensional NMR. <i>Journal of Magnetic Resonance</i> , 2011, 213, 1-13.	1.2	28
209	Theory of mirrored time domain sampling for NMR spectroscopy. <i>Journal of Magnetic Resonance</i> , 2011, 213, 46-57.	1.2	2
210	Methods of reconstruction of spectra in multidimensional NMR spectroscopy. <i>Russian Journal of Physical Chemistry B</i> , 2011, 5, 554-570.	0.2	1
211	A novel strategy for NMR resonance assignment and protein structure determination. <i>Journal of Biomolecular NMR</i> , 2011, 49, 27-38.	1.6	46
212	Knowledge-based nonuniform sampling in multidimensional NMR. <i>Journal of Biomolecular NMR</i> , 2011, 50, 247-262.	1.6	30

#	ARTICLE	IF	CITATIONS
213	AUTOBA: Automation of backbone assignment from HN(C)N suite of experiments. Journal of Biomolecular NMR, 2011, 50, 285-297.	1.6	8
214	(¹⁵ N-ε±ε% ¹³ C ²) edited (4, 3)D ¹ H(CC)CONH TOCSY and (4, 3)D ¹ NOESY HNC0 experiments for unambiguous side chain and NOE assignments of proteins with high shift degeneracy. Magnetic Resonance in Chemistry, 2011, 49, 693-699.	1.1	7
216	Compressed sensing and the reconstruction of ultrafast 2D NMR data: Principles and biomolecular applications. Journal of Magnetic Resonance, 2011, 209, 352-358.	1.2	56
217	A Geometric Arrangement Algorithm for Structure Determination of Symmetric Protein Homo-Oligomers from NOEs and RDCs. Journal of Computational Biology, 2011, 18, 1507-1523.	0.8	6
218	Random phase detection in multidimensional NMR. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 16640-16644.	3.3	18
219	4D solid-state NMR for protein structure determination. Physical Chemistry Chemical Physics, 2012, 14, 5239.	1.3	42
220	A Time-Saving Strategy for MAS NMR Spectroscopy by Combining Nonuniform Sampling and Paramagnetic Relaxation Assisted Condensed Data Collection. Journal of Physical Chemistry B, 2012, 116, 13585-13596.	1.2	36
221	NMR in Infection Research. , 2012, , 985-1007.		0
222	Automated protein backbone assignment using the projection-decomposition approach. Journal of Biomolecular NMR, 2012, 54, 43-51.	1.6	5
223	PACSY, a relational database management system for protein structure and chemical shift analysis. Journal of Biomolecular NMR, 2012, 54, 169-179.	1.6	33
224	GFT projection NMR for efficient ¹ H/ ¹³ C sugar spin system identification in nucleic acids. Journal of Biomolecular NMR, 2012, 54, 337-342.	1.6	4
225	Direct Sequential Hit Strategy for Unambiguous and Accurate Backbone Assignment of ¹³ C/ ¹⁵ N Labeled Proteins. The National Academy of Sciences, India, 2012, 35, 389-399.	0.8	5
226	Reduced Dimensionality (4,3)D- ¹ H- ¹³ C NH for Rapid Assignment of ¹ H- ¹³ C ¹⁵ N HSQC Peaks in Proteins: An Analytical Tool for Protein Folding, Proteomics, and Drug Discovery Programs. Analytical Chemistry, 2012, 84, 10404-10410.	3.2	6
227	Advances in Nuclear Magnetic Resonance for Drug Discovery. Methods in Molecular Biology, 2012, 910, 195-266.	0.4	12
228	Enhanced Sensitivity by Nonuniform Sampling Enables Multidimensional MAS NMR Spectroscopy of Protein Assemblies. Journal of Physical Chemistry B, 2012, 116, 7416-7427.	1.2	89
229	Low concentration of a Gd-chelate increases the signal-to-noise ratio in fast pulsing BEST experiments. Journal of Magnetic Resonance, 2012, 224, 32-37.	1.2	4
230	HyperSPASM NMR: A new approach to single-shot 2D correlations on DNP-enhanced samples. Journal of Magnetic Resonance, 2012, 225, 115-119.	1.2	13
232	The Handbook of Metabolomics. Methods in Pharmacology and Toxicology, 2012, , .	0.1	22

#	ARTICLE	IF	CITATIONS
233	Principles of NMR for Applications in Metabolomics. <i>Methods in Pharmacology and Toxicology</i> , 2012, , 127-197.	0.1	5
234	Novel Sampling Approaches in Higher Dimensional NMR. <i>Topics in Current Chemistry</i> , 2012, , .	4.0	30
235	Bioinformatics and Drug Discovery. <i>Methods in Molecular Biology</i> , 2012, , .	0.4	17
236	Increasing the Sensitivity of Magnetic Resonance Spectroscopy and Imaging. <i>Analytical Chemistry</i> , 2012, 84, 9-16.	3.2	49
237	Sparse sampling methods in multidimensional NMR. <i>Physical Chemistry Chemical Physics</i> , 2012, 14, 10835-10843.	1.3	77
238	Recent progress in NMR spectroscopy: Toward the study of intrinsically disordered proteins of increasing size and complexity. <i>IUBMB Life</i> , 2012, 64, 473-481.	1.5	53
239	4D Non-uniformly sampled HCBCACON and 1 J(NC $\hat{\pm}$)-selective HCBCANCO experiments for the sequential assignment and chemical shift analysis of intrinsically disordered proteins. <i>Journal of Biomolecular NMR</i> , 2012, 53, 139-148.	1.6	40
240	MQD $\hat{\pm}$ Multiplex $\hat{\pm}$ Quadrature Detection in Multi $\hat{\pm}$ Dimensional NMR. <i>ChemPhysChem</i> , 2012, 13, 342-346.	1.0	7
241	AI NMR: a novel NMR data processing program optimized for sparse sampling. <i>Journal of Biomolecular NMR</i> , 2012, 52, 79-89.	1.6	7
242	Sugar-to-base correlation in nucleic acids with a 5D APSY-HCNCH or two 3D APSY-HCN experiments. <i>Journal of Biomolecular NMR</i> , 2012, 52, 141-150.	1.6	8
243	Efficient sequential assignments in proteins with reduced dimensionality 3D HN(CA)NH. <i>Journal of Biomolecular NMR</i> , 2012, 52, 115-126.	1.6	14
244	Comparison of various sampling schemes and accumulation profiles in covariance spectroscopy with exponentially decaying 2D signals. <i>Analyst</i> , The, 2013, 138, 2411.	1.7	13
245	Formalism for hypercomplex multidimensional NMR employing partial-component subsampling. <i>Journal of Magnetic Resonance</i> , 2013, 227, 20-24.	1.2	18
246	Magic Angle Spinning NMR Studies of Protein Assemblies: Recent Advances in Methodology and Applications. <i>Annual Reports on NMR Spectroscopy</i> , 2013, , 293-357.	0.7	4
247	Solution NMR structure of CD1104B from pathogenic <i>Clostridium difficile</i> reveals a distinct $\hat{\pm}$ -helical architecture and provides first structural representative of protein domain family PF14203. <i>Journal of Structural and Functional Genomics</i> , 2013, 14, 155-160.	1.2	2
248	Rapid and Accurate Measurement of the Frequency $\hat{\pm}$ Frequency Correlation Function. <i>Journal of Physical Chemistry A</i> , 2013, 117, 5891-5898.	1.1	21
249	NASR: An Effective Approach for Simultaneous Noise and Artifact Suppression in NMR Spectroscopy. <i>Analytical Chemistry</i> , 2013, 85, 2523-2528.	3.2	15
250	Applications of Projection NMR Techniques. <i>Annual Reports on NMR Spectroscopy</i> , 2013, 78, 55-102.	0.7	1

#	ARTICLE	IF	CITATIONS
251	4D experiments measured with APSY for automated backbone resonance assignments of large proteins. <i>Journal of Biomolecular NMR</i> , 2013, 56, 149-154.	1.6	2
252	High-Dimensional NMR Spectra for Structural Studies of Biomolecules. <i>ChemPhysChem</i> , 2013, 14, 3015-3025.	1.0	31
253	Efficient protocol for backbone and side-chain assignments of large, intrinsically disordered proteins: transient secondary structure analysis of 49.2 kDa microtubule associated protein 2c. <i>Journal of Biomolecular NMR</i> , 2013, 56, 291-301.	1.6	38
254	High-Quality NMR Structure of Human Anti-Apoptotic Protein Domain Mcl-1(171-327) for Cancer Drug Design. <i>PLoS ONE</i> , 2014, 9, e96521.	1.1	24
255	Spatially Selective Heteronuclear Multiple-Quantum Coherence Spectroscopy for Biomolecular NMR Studies. <i>ChemPhysChem</i> , 2014, 15, 1872-1879.	1.0	6
256	A six-dimensional alpha proton detection-based APSY experiment for backbone assignment of intrinsically disordered proteins. <i>Journal of Biomolecular NMR</i> , 2014, 60, 231-240.	1.6	17
257	Communication: Ultrafast homonuclear correlation spectroscopy with diagonal suppression. <i>Journal of Chemical Physics</i> , 2014, 140, 231103.	1.2	8
258	Reducing acquisition times in multidimensional NMR with a time-optimized Fourier encoding algorithm. <i>Journal of Chemical Physics</i> , 2014, 141, 194201.	1.2	17
259	Fast multidimensional NMR spectroscopy for sparse spectra. <i>NMR in Biomedicine</i> , 2014, 27, 640-655.	1.6	5
260	Practical aspects of NMR signal assignment in larger and challenging proteins. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2014, 78, 47-75.	3.9	54
261	Automated NMR resonance assignment strategy for RNA via the phosphodiester backbone based on high-dimensional through-bond APSY experiments. <i>Journal of Biomolecular NMR</i> , 2014, 59, 87-93.	1.6	16
262	Multidimensional Approaches to NMR-Based Metabolomics. <i>Analytical Chemistry</i> , 2014, 86, 47-57.	3.2	112
263	A fast NMR method for resonance assignments: application to metabolomics. <i>Journal of Biomolecular NMR</i> , 2014, 58, 165-173.	1.6	41
264	Development and application of aromatic [¹³ C, ¹ H] SOFAST-HMQC NMR experiment for nucleic acids. <i>Journal of Biomolecular NMR</i> , 2014, 60, 77-83.	1.6	34
265	Nonuniform sampling and non-Fourier signal processing methods in multidimensional NMR. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2014, 83, 21-41.	3.9	197
266	Bayesian reconstruction of projection reconstruction NMR (PR-NMR). <i>Computers in Biology and Medicine</i> , 2014, 54, 89-99.	3.9	1
267	Enhancing the resolution of multi-dimensional heteronuclear NMR spectra of intrinsically disordered proteins by homonuclear broadband decoupling. <i>Chemical Communications</i> , 2014, 50, 1488-1490.	2.2	45
269	Sensitivity gains, linearity, and spectral reproducibility in nonuniformly sampled multidimensional MAS NMR spectra of high dynamic range. <i>Journal of Biomolecular NMR</i> , 2014, 59, 57-73.	1.6	31

#	ARTICLE	IF	CITATIONS
270	Automated robust and accurate assignment of protein resonances for solid state NMR. Journal of Biomolecular NMR, 2014, 59, 119-134.	1.6	15
271	Strategy for automated NMR resonance assignment of RNA: application to 48-nucleotide K10. Journal of Biomolecular NMR, 2014, 59, 231-240.	1.6	13
272	Perspectives in magnetic resonance: NMR in the post-FFT era. Journal of Magnetic Resonance, 2014, 241, 60-73.	1.2	122
273	Toward optimal-resolution NMR of intrinsically disordered proteins. Journal of Magnetic Resonance, 2014, 241, 41-52.	1.2	29
274	Six- and seven-dimensional experiments by combination of sparse random sampling and projection spectroscopy dedicated for backbone resonance assignment of intrinsically disordered proteins. Journal of Biomolecular NMR, 2015, 63, 283-290.	1.6	17
275	Simultaneous acquisition of three NMR spectra in a single experiment for rapid resonance assignments in metabolomics. Journal of Chemical Sciences, 2015, 127, 1091-1097.	0.7	8
276	Fast acquisition of multidimensional NMR spectra of solids and mesophases using alternative sampling methods. Magnetic Resonance in Chemistry, 2015, 53, 927-939.	1.1	11
278	Non-Uniform Sampling and UNIO Automation for Efficient Protein NMR Structure Determination. Chemistry - A European Journal, 2015, 21, 12363-12369.	1.7	3
279	Facing and Overcoming Sensitivity Challenges in Biomolecular NMR Spectroscopy. Angewandte Chemie - International Edition, 2015, 54, 9162-9185.	7.2	258
280	Non-uniform sampling: post-Fourier era of NMR data collection and processing. Magnetic Resonance in Chemistry, 2015, 53, 921-926.	1.1	107
281	The relations between metabolic variations and genetic evolution of different species. Analytical Biochemistry, 2015, 477, 105-114.	1.1	15
282	Pure shift NMR. Progress in Nuclear Magnetic Resonance Spectroscopy, 2015, 86-87, 1-20.	3.9	268
283	Solid-State Covariance NMR Spectroscopy. Annual Reports on NMR Spectroscopy, 2015, , 77-113.	0.7	6
284	Applications of high dimensionality experiments to biomolecular NMR. Progress in Nuclear Magnetic Resonance Spectroscopy, 2015, 90-91, 49-73.	3.9	33
285	NMRFAM-SDF: a protein structure determination framework. Journal of Biomolecular NMR, 2015, 62, 481-495.	1.6	4
286	Magic angle spinning NMR of viruses. Progress in Nuclear Magnetic Resonance Spectroscopy, 2015, 86-87, 21-40.	3.9	23
287	Magic Angle Spinning NMR Spectroscopy: A Versatile Technique for Structural and Dynamic Analysis of Solid-Phase Systems. Analytical Chemistry, 2015, 87, 5458-5469.	3.2	86
288	Nonuniform sampling of hypercomplex multidimensional NMR experiments: Dimensionality, quadrature phase and randomization. Journal of Magnetic Resonance, 2015, 254, 121-130.	1.2	18

#	ARTICLE	IF	CITATIONS
289	Development of a method for reconstruction of crowded NMR spectra from undersampled time-domain data. <i>Journal of Biomolecular NMR</i> , 2015, 62, 31-41.	1.6	3
290	Enhanced biosynthetically directed fractional carbon-13 enrichment of proteins for backbone NMR assignments. <i>Protein Expression and Purification</i> , 2015, 115, 1-10.	0.6	5
291	NMR Methods for the Study of Intrinsically Disordered Proteins Structure, Dynamics, and Interactions: General Overview and Practical Guidelines. <i>Advances in Experimental Medicine and Biology</i> , 2015, 870, 49-122.	0.8	69
292	ADAPT-NMR 3.0: utilization of BEST-type triple-resonance NMR experiments to accelerate the process of data collection and assignment. <i>Journal of Biomolecular NMR</i> , 2015, 62, 247-252.	1.6	0
293	Computational de novo design of a four-helix bundle protein. <i>Protein Science</i> , 2015, 24, 434-445.	3.1	24
294	Reduced dimensionality (3,2)D NMR experiments and their automated analysis: implications to high-throughput structural studies on proteins. <i>Magnetic Resonance in Chemistry</i> , 2015, 53, 79-87.	1.1	0
295	Nuclear Magnetic Resonance Spectroscopy Applications Pharmaceutical. , 2016, , 304-304.		0
296	Design of structurally distinct proteins using strategies inspired by evolution. <i>Science</i> , 2016, 352, 687-690.	6.0	132
297	Absolute Minimal Sampling in High-Dimensional NMR Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 14169-14172.	7.2	19
298	Absolut minimales Sampling in der hochdimensionalen NMR-Spektroskopie. <i>Angewandte Chemie</i> , 2016, 128, 14376-14379.	1.6	5
299	Non-Uniform Sampling Ultrahigh Resolution TOCSY NMR: Analysis of Complex Mixtures at Microgram Levels. <i>ChemPhysChem</i> , 2016, 17, 2304-2308.	1.0	26
300	Lorentzian sparsity based spectroscopic reconstruction for fast high-dimensional magnetic resonance spectroscopy. <i>Physics in Medicine and Biology</i> , 2016, 61, 215-226.	1.6	2
301	Multidimensional J-driven NMR correlations by single-scan offset-encoded recoupling. <i>Journal of Magnetic Resonance</i> , 2016, 265, 33-44.	1.2	3
302	F 1 F 2-selective NMR spectroscopy. <i>Journal of Biomolecular NMR</i> , 2017, 68, 41-52.	1.6	11
303	Interpolating and extrapolating with hmsIST: seeking a tmax for optimal sensitivity, resolution and frequency accuracy. <i>Journal of Biomolecular NMR</i> , 2017, 68, 139-154.	1.6	24
304	Acceleration of protein backbone NMR assignment by combinatorial labeling: application to a small molecule binding study. <i>Biopolymers</i> , 2017, 107, e23013.	1.2	9
305	Sparse multidimensional iterative lineshape-enhanced (SMILE) reconstruction of both non-uniformly sampled and conventional NMR data. <i>Journal of Biomolecular NMR</i> , 2017, 68, 101-118.	1.6	238
306	A fast approach to 3D HSQC-based spectroscopy based on a Fourier phase encoding of pre-targeted resonances. <i>Journal of Magnetic Resonance</i> , 2017, 274, 95-102.	1.2	3

#	ARTICLE	IF	CITATIONS
307	An irregular sampler. Concepts in Magnetic Resonance Part A: Bridging Education and Research, 2017, 46A, .	0.2	1
308	Compressed sensing: Reconstruction of non-uniformly sampled multidimensional NMR data. Concepts in Magnetic Resonance Part A: Bridging Education and Research, 2017, 46A, .	0.2	20
309	Sensitivity-Enhanced Four-Dimensional Amide-Amide Correlation NMR Experiments for Sequential Assignment of Proline-Rich Disordered Proteins. Journal of the American Chemical Society, 2018, 140, 3518-3522.	6.6	13
310	¹³ C APSY-NMR for sequential assignment of intrinsically disordered proteins. Journal of Biomolecular NMR, 2018, 70, 167-175.	1.6	16
311	(3, 2)D ¹ H, ¹³ C BIRD _r , X-HSQC-TOCSY for NMR structure elucidation of mixtures: application to complex carbohydrates. Journal of Biomolecular NMR, 2018, 70, 115-122.	1.6	10
312	Advances in NMR Data Acquisition and Processing for Protein Structure Determination. , 2018, , 63-90.		0
313	An efficient combination of BEST and NUS methods in multidimensional NMR spectroscopy for high throughput analysis of proteins. RSC Advances, 2018, 8, 17616-17621.	1.7	10
314	Non-Uniform and Absolute Minimal Sampling for High-Throughput Multidimensional NMR Applications. Chemistry - A European Journal, 2018, 24, 11535-11544.	1.7	14
315	Accelerating NMR-Based Structural Studies of Proteins by Combining Amino Acid Selective Unlabeling and Fast NMR Methods. Magnetochemistry, 2018, 4, 2.	1.0	1
316	Emerging solution NMR methods to illuminate the structural and dynamic properties of proteins. Current Opinion in Structural Biology, 2019, 58, 294-304.	2.6	26
317	A suite of solid-state NMR experiments to utilize orphaned magnetization for assignment of proteins using parallel high and low gamma detection. Journal of Magnetic Resonance, 2019, 305, 219-231.	1.2	18
318	Reduced dimensionality hyphenated NMR experiments for the structure determination of compounds in mixtures. Faraday Discussions, 2019, 218, 191-201.	1.6	3
319	Improving the sensitivity of FT-NMR spectroscopy by apodization weighted sampling. Journal of Biomolecular NMR, 2019, 73, 155-165.	1.6	29
320	SpinStudioJ: A cross-platform NMR data acquisition and processing workbench based on a plugin architecture. Magnetic Resonance in Chemistry, 2019, 57, 380-389.	1.1	1
321	Longitudinal Relaxation Optimization Enhances ¹ H-Detected HSQC in Solid-State NMR Spectroscopy on Challenging Biological Systems. Chemistry - A European Journal, 2019, 25, 4115-4122.	1.7	6
322	Polarization calibration of wide-field-of-view interference polarization imaging spectrometer. Journal of Quantitative Spectroscopy and Radiative Transfer, 2019, 224, 44-54.	1.1	2
323	Artificial intelligence enhanced two-dimensional nanoscale nuclear magnetic resonance spectroscopy. Npj Quantum Information, 2020, 6, .	2.8	8
324	Emerging Techniques in Fast Multidimensional NMR. , 2006, , 129-145.		3

#	ARTICLE	IF	CITATIONS
325	Assigning Backbone NMR Resonances for Full Length Tau Isoforms: Efficient Compromise between Manual Assignments and Reduced Dimensionality. PLoS ONE, 2012, 7, e34679.	1.1	31
326	NMR Structure of Lipoprotein YxeF from Bacillus subtilis Reveals a Calycin Fold and Distant Homology with the Lipocalin Blc from Escherichia coli. PLoS ONE, 2012, 7, e37404.	1.1	6
327	Rapid Measurement of Pseudocontact Shifts in Paramagnetic Proteins by GFT NMR Spectroscopy. The Open Magnetic Resonance Journal, 2008, 1, 16-28.	0.5	13
328	A Method to Selectively Observe a Desired Linear Combination of Chemical Shifts in GFT Projection NMR Spectroscopy. The Open Magnetic Resonance Journal, 2008, 1, 95-103.	0.5	2
329	What's the big deal about big data?. Big Data & Information Analytics, 2015, 1, 31-79.	1.3	5
330	Real-time Acquisition of Three Dimensional NMR Spectra by Non-uniform Sampling and Maximum Entropy Processing. Bulletin of the Korean Chemical Society, 2008, 29, 2017-2022.	1.0	3
331	あさひ...fNMRā, 'çYæ™, é-“āsæ, -ā@šā™ā, <æ-1æ³. Journal of the Spectroscopical Society of Japan, 2004, 53, 259-261.	0.6	0
332	Derivation of Peptide and Protein Structure using NMR Spectroscopy. , 2010, , 14-49.		0
333	New methods for NMR spectral analysis. Journal of Analytical Science and Technology, 2011, 2, A88-A93.	1.0	0
336	Solid-state covariance NMR spectroscopy: An update. Annual Reports on NMR Spectroscopy, 2020, 100, 153-201.	0.7	0
337	Principles and Application of Projected Multidimensional NMR Spectroscopy â€” G-matrix Fourier Transform NMR. , 2006, , 147-162.		1
338	Advances in protein NMR provided by the NIGMS Protein Structure Initiative: impact on drug discovery. Current Opinion in Drug Discovery & Development, 2010, 13, 335-49.	1.9	7
339	Structural Genomics by NMR Spectroscopy. , 2007, , 1-11.		0