Frank Delaglio

List of Publications by Year
in descending order

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43 papers	25,343 citations	218677 26 h-index	254184 43 g-index
45 all docs	45 docs citations	45 times ranked	21324 citing authors

#	Article	IF	Citations
1	Interlaboratory Studies Using the NISTmAb to Advance Biopharmaceutical Structural Analytics. Frontiers in Molecular Biosciences, 2022, 9, .	3.5	5
2	A simple approach for reconstruction of non-uniformly sampled pseudo-3D NMR data for accurate measurement of spin relaxation parameters. Journal of Biomolecular NMR, 2021, 75, 213-219.	2.8	1
3	Principal Component Analysis of 1D 1H Diffusion Edited NMR Spectra of Protein Therapeutics. Journal of Pharmaceutical Sciences, 2021, 110, 3385-3394.	3.3	11
4	NUScon: a community-driven platform for quantitative evaluation of nonuniform sampling in NMR. Magnetic Resonance, 2021, 2, 843-861.	1.9	7
5	The NMR Spectral Measurement Database: A System for Organizing and Accessing NMR Spectra of Therapeutic Proteins. Journal of Research of the National Institute of Standards and Technology, 2021, 126, .	1.2	1
6	Principal component analysis for automated classification of 2D spectra and interferograms of protein therapeutics: influence of noise, reconstruction details, and data preparation. Journal of Biomolecular NMR, 2020, 74, 643-656.	2.8	12
7	Reducing the measurement time of exact NOEs by non-uniform sampling. Journal of Biomolecular NMR, 2020, 74, 717-739.	2.8	7
8	Assessment of the Higherâ€Order Structure of Formulated Monoclonal Antibody Therapeutics by 2D Methyl Correlated NMR and Principal Component Analysis. Current Protocols in Protein Science, 2020, 100, e105.	2.8	9
9	Chemometric outlier classification of 2D-NMR spectra to enable higher order structure characterization of protein therapeutics. Chemometrics and Intelligent Laboratory Systems, 2020, 199, 103973.	3.5	6
10	Comparative Analysis of One-Dimensional Protein Fingerprint by Line Shape Enhancement and Two-Dimensional ¹H,¹³C Methyl NMR Methods for Characterization of the Higher Order Structure of IgG1 Monoclonal Antibodies. Analytical Chemistry, 2020, 92, 6366-6373.	6.5	12
11	Best Practices in Utilization of 2D-NMR Spectral Data as the Input for Chemometric Analysis in Biopharmaceutical Applications. Journal of Chemical Information and Modeling, 2020, 60, 2339-2355.	5.4	18
12	Enabling adoption of 2D-NMR for the higher order structure assessment of monoclonal antibody therapeutics. MAbs, 2019, 11, 94-105.	5.2	67
13	Practical Guidelines for 13C-Based NMR Metabolomics. Methods in Molecular Biology, 2019, 2037, 69-95.	0.9	10
14	Nonuniform sampling in multidimensional NMR for improving spectral sensitivity. Methods, 2018, 138-139, 62-68.	3.8	23
15	Selective suppression of excipient signals in 2D 1Hâ€“13C methyl spectra of biopharmaceutical products. Journal of Biomolecular NMR, 2018, 72, 149-161.	2.8	18
16	NMRbox: A Resource for Biomolecular NMR Computation. Biophysical Journal, 2017, 112, 1529-1534.	0.5	336
17	Multivariate Analysis of Two-Dimensional ¹H, ¹³C Methyl NMR Spectra of Monoclonal Antibody Therapeutics To Facilitate Assessment of Higher Order Structure. Analytical Chemistry, 2017, 89, 11839-11845.	6.5	63
18	Sparse multidimensional iterative lineshape-enhanced (SMILE) reconstruction of both non-uniformly sampled and conventional NMR data. Journal of Biomolecular NMR, 2017, 68, 101-118.	2.8	238

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19	Non-Uniform Sampling for All: More NMR Spectral Quality, Less Measurement Time. American Pharmaceutical Review, 2017, 20, .	0.0	13
20	A practical implementation of de-Pake-ing via weighted Fourier transformation. PeerJ, 2013, 1, e30.	2.0	13
21	A practical implementation of cross-spectrum in protein backbone resonance assignment. Journal of Magnetic Resonance, 2010, 203, 208-212.	2.1	8
22	TALOS+: a hybrid method for predicting protein backbone torsion angles from NMR chemical shifts. Journal of Biomolecular NMR, 2009, 44, 213-223.	2.8	2,305
23	Consistent blind protein structure generation from NMR chemical shift data. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 4685-4690.	7.1	776
24	Local and global structure of the monomeric subunit of the potassium channel KcsA probed by NMR. Biochimica Et Biophysica Acta - Biomembranes, 2007, 1768, 3260-3270.	2.6	33
25	The utility of residual dipolar couplings in detecting motion in carbohydrates: application to sucrose. Carbohydrate Research, 2005, 340, 863-874.	2.3	38
26	Solution structure of Î³S-crystallin by molecular fragment replacement NMR. Protein Science, 2005, 14, 3101-3114.	7.6	41
27	Molecular Fragment Replacement Approach to Protein Structure Determination by Chemical Shift and Dipolar Homology Database Mining. Methods in Enzymology, 2005, 394, 42-78.	1.0	49
28	Complete Relative Stereochemistry of Multiple Stereocenters Using Only Residual Dipolar Couplings. Journal of the American Chemical Society, 2004, 126, 5008-5017.	13.7	84
29	Overall structure and sugar dynamics of a DNA dodecamer from homo- and heteronuclear dipolar couplings and 31P chemical shift anisotropy. Journal of Biomolecular NMR, 2003, 26, 297-315.	2.8	129
30	Evaluation of Backbone Proton Positions and Dynamics in a Small Protein by Liquid Crystal NMR Spectroscopy. Journal of the American Chemical Society, 2003, 125, 9179-9191.	13.7	278
31	Direct observation of dipolar couplings between distant protons in weakly aligned nucleic acids. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 11333-11338.	7.1	34
32	A structural model for Alzheimer's Î²-amyloid fibrils based on experimental constraints from solid state NMR. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16742-16747.	7.1	1,757
33	Measurement of Homonuclear Proton Couplings from Regular 2D COSY Spectra. Journal of Magnetic Resonance, 2001, 149, 276-281.	2.1	63
34	Measurement of one-bond 15N-13C' dipolar couplings in medium sized proteins. Journal of Biomolecular NMR, 2000, 18, 101-105.	2.8	56
35	Protein Structure Determination Using Molecular Fragment Replacement and NMR Dipolar Couplings. Journal of the American Chemical Society, 2000, 122, 2142-2143.	13.7	250
36	Protein backbone angle restraints from searching a database for chemical shift and sequence homology. Journal of Biomolecular NMR, 1999, 13, 289-302.	2.8	2,825

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37	Measurement ofJand Dipolar Couplings from Simplified Two-Dimensional NMR Spectra. Journal of Magnetic Resonance, 1998, 131, 373-378.	2.1	931
38	Measurement of Dipolar Couplings for Methylene and Methyl Sites in Weakly Oriented Macromolecules and Their Use in Structure Determination. Journal of Magnetic Resonance, 1998, 134, 365-369.	2.1	118
39	NMRPipe: A multidimensional spectral processing system based on UNIX pipes. Journal of Biomolecular NMR, 1995, 6, 277-93.	2.8	14,090
40	[2] Measurement of homo- and heteronuclear J couplings from quantitative J correlation. Methods in Enzymology, 1994, 239, 79-105.	1.0	373
41	The use of 1JC?H? coupling constants as a probe for protein backbone conformation. Journal of Biomolecular NMR, 1993, 3, 67-80.	2.8	65
42	An empirical correlation between 1JC.alpha.H.alpha. and protein backbone conformation. Journal of the American Chemical Society, 1992, 114, 9674-9675.	13.7	68
43	Measurement of15N-13C J couplings in staphylococcal nuclease. Journal of Biomolecular NMR, 1991, 1, 439-446.	2.8	95