Frank Delaglio

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7786056/publications.pdf

Version: 2024-02-01

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	NMRPipe: A multidimensional spectral processing system based on UNIX pipes. Journal of Biomolecular NMR, 1995, 6, 277-93.	2.8	14,090
2	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
3	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
4	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
5	Measurement ofJand Dipolar Couplings from Simplified Two-Dimensional NMR Spectra. Journal of Magnetic Resonance, 1998, 131, 373-378.	2.1	931
6	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
7	[2] Measurement of homo- and heteronuclear J couplings from quantitative J correlation. Methods in Enzymology, 1994, 239, 79-105.	1.0	373
8	NMRbox: A Resource for Biomolecular NMR Computation. Biophysical Journal, 2017, 112, 1529-1534.	0.5	336
9	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
10	Protein Structure Determination Using Molecular Fragment Replacement and NMR Dipolar Couplings. Journal of the American Chemical Society, 2000, 122, 2142-2143.	13.7	250
11	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
12	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
13	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
14	Measurement of15N-13C J couplings in staphylococcal nuclease. Journal of Biomolecular NMR, 1991, 1, 439-446.	2.8	95
15	Complete Relative Stereochemistry of Multiple Stereocenters Using Only Residual Dipolar Couplings. Journal of the American Chemical Society, 2004, 126, 5008-5017.	13.7	84
16	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
17	Enabling adoption of 2D-NMR for the higher order structure assessment of monoclonal antibody therapeutics. MAbs, 2019, 11, 94-105.	5.2	67
18	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

#	Article	IF	Citations
19	Measurement of Homonuclear Proton Couplings from Regular 2D COSY Spectra. Journal of Magnetic Resonance, 2001, 149, 276-281.	2.1	63
20	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
21	Measurement of one-bond 15N-13C' dipolar couplings in medium sized proteins. Journal of Biomolecular NMR, 2000, 18, 101-105.	2.8	56
22	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
23	Solution structure of Î³S-crystallin by molecular fragment replacement NMR. Protein Science, 2005, 14, 3101-3114.	7.6	41
24	The utility of residual dipolar couplings in detecting motion in carbohydrates: application to sucrose. Carbohydrate Research, 2005, 340, 863-874.	2.3	38
25	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
26	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
27	Nonuniform sampling in multidimensional NMR for improving spectral sensitivity. Methods, 2018, 138-139, 62-68.	3.8	23
28	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
29	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
30	A practical implementation of de-Pake-ing via weighted Fourier transformation. PeerJ, 2013, 1, e30.	2.0	13
31	Non-Uniform Sampling for All: More NMR Spectral Quality, Less Measurement Time. American Pharmaceutical Review, 2017, 20, .	0.0	13
32	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
33	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
34	Principal Component Analysis of 1D 1H Diffusion Edited NMR Spectra of Protein Therapeutics. Journal of Pharmaceutical Sciences, 2021, 110, 3385-3394.	3.3	11
35	Practical Guidelines for 13C-Based NMR Metabolomics. Methods in Molecular Biology, 2019, 2037, 69-95.	0.9	10
36	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

#	Article	IF	Citations
37	A practical implementation of cross-spectrum in protein backbone resonance assignment. Journal of Magnetic Resonance, 2010, 203, 208-212.	2.1	8
38	Reducing the measurement time of exact NOEs by non-uniform sampling. Journal of Biomolecular NMR, 2020, 74, 717-739.	2.8	7
39	NUScon: a community-driven platform for quantitative evaluation of nonuniform sampling in NMR. Magnetic Resonance, 2021, 2, 843-861.	1.9	7
40	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
41	Interlaboratory Studies Using the NISTmAb to Advance Biopharmaceutical Structural Analytics. Frontiers in Molecular Biosciences, 2022, 9, .	3.5	5
42	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
43	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