Dominique P Frueh

List of Publications by Year
in descending order

47 papers	1,911 citations	279798 23 h-index	254184 43 g-index
54 all docs	54 docs citations	54 times ranked	2328 citing authors

#	Article	IF	Citations
1	Global protein dynamics as communication sensors in peptide synthetase domains. Science Advances, 2022, 8, .	10.3	5
2	NMR as a readout to monitor and restore the integrity of complex chemoenzymatic reactions. Journal of Magnetic Resonance, 2022, 342, 107265.	2.1	0
3	Conserved allosteric ensembles in disordered proteins using TROSY/anti-TROSY R2-filtered spectroscopy. Biophysical Journal, 2021, 120, 2498-2510.	0.5	4
4	Using delayed decoupling to attenuate residual signals in editing filters. Magnetic Resonance, 2021, 2, 475-487.	1.9	4
5	Minimizing Pervasive Artifacts in 4D Covariance Maps for Protein Side Chain NMR Assignments. Journal of Physical Chemistry A, 2021, 125, 8313-8323.	2.5	2
6	Structural Dynamics Couple Substrate Recognition with Allosteric Domain Communication in Nonribosomal Peptide Synthetases. FASEB Journal, 2019, 33, 468.4.	0.5	0
7	Covariance NMR Processing and Analysis for Protein Assignment. Methods in Molecular Biology, 2018, 1688, 353-373.	0.9	10
8	Molecular Cross‐Talk between Nonribosomal Peptide Synthetase Carrier Proteins and Unstructured Linker Regions. ChemBioChem, 2017, 18, 629-632.	2.6	8
9	Molecular impact of covalent modifications on nonribosomal peptide synthetase carrier protein communication. Journal of Biological Chemistry, 2017, 292, 10002-10013.	3.4	12
10	Covariance nuclear magnetic resonance methods for obtaining protein assignments and novel correlations. Concepts in Magnetic Resonance Part A: Bridging Education and Research, 2017, 46A, .	0.5	3
11	Assignment of methyl NMR resonances of a 52 kDa protein with residue-specific 4D correlation maps. Journal of Biomolecular NMR, 2015, 62, 281-290.	2.8	16
12	A Nuclear Magnetic Resonance Method for Probing Molecular Influences of Substrate Loading in Nonribosomal Peptide Synthetase Carrier Proteins. Biochemistry, 2015, 54, 1154-1156.	2.5	14
13	Solution Structure of a Nonribosomal Peptide Synthetase Carrier Protein Loaded with Its Substrate Reveals Transient, Well-Defined Contacts. Journal of the American Chemical Society, 2015, 137, 12100-12109.	13.7	37
14	Effortless assignment with 4D covariance sequential correlation maps. Journal of Magnetic Resonance, 2015, 260, 83-88.	2.1	10
15	A 3D time-shared NOESY experiment designed to provide optimal resolution for accurate assignment of NMR distance restraints in large proteins. Journal of Biomolecular NMR, 2014, 60, 265-274.	2.8	13
16	SARA: a software environment for the analysis of relaxation data acquired with accordion spectroscopy. Journal of Biomolecular NMR, 2014, 58, 83-99.	2.8	5
17	Practical aspects of NMR signal assignment in larger and challenging proteins. Progress in Nuclear Magnetic Resonance Spectroscopy, 2014, 78, 47-75.	7.5	54
18	Facilitated Assignment of Large Protein NMR Signals with Covariance Sequential Spectra Using Spectral Derivatives. Journal of the American Chemical Society, 2014, 136, 13106-13109.	13.7	15

#	Article	IF	Citations
19	NMR methods for structural studies of large monomeric and multimeric proteins. Current Opinion in Structural Biology, 2013, 23, 734-739.	5.7	66
20	Multiple Substrate and Domain Binding in Non-Ribosomal Peptide Synthetases. Biophysical Journal, 2013, 104, 180a.	0.5	0
21	Hidden in Plain Sight: Subtle Effects of the 8-Oxoguanine Lesion on the Structure, Dynamics, and Thermodynamics of a 15-Base Pair Oligodeoxynucleotide Duplex. Biochemistry, 2011, 50, 8463-8477.	2.5	31
22	Global dynamic conformational changes in the suppressor domain of IP$_3$ receptor by stepwise binding of the two lobes of calmodulin. FASEB Journal, 2011, 25, 840-850.	0.5	15
23	Transient Domain Interactions in Non‐Ribosomal Peptide Synthetases. FASEB Journal, 2011, 25, .	0.5	0
24	CACA-TOCSY with alternate 13C–12C labeling: a 13Cα direct detection experiment for mainchain resonance assignment, dihedral angle information, and amino acid type identification. Journal of Biomolecular NMR, 2010, 47, 55-63.	2.8	23
25	Nitrogen-detected CAN and CON experiments as alternative experiments for main chain NMR resonance assignments. Journal of Biomolecular NMR, 2010, 47, 271-282.	2.8	34
26	High-Resolution 3D CANCA NMR Experiments for Complete Mainchain Assignments Using C^{α} Direct Detection. Journal of the American Chemical Society, 2010, 132, 2945-2951.	13.7	25
27	Neutralizing Positive Charges at the Surface of a Protein Lowers Its Rate of Amide Hydrogen Exchange without Altering Its Structure or Increasing Its Thermostability. Journal of the American Chemical Society, 2010, 132, 17411-17425.	13.7	29
28	FM reconstruction of non-uniformly sampled protein NMR data at higher dimensions and optimization by distillation. Journal of Biomolecular NMR, 2009, 45, 283-294.	2.8	69
29	Time-shared HSQC-NOESY for accurate distance constraints measured at high-field in 15N-13C-ILV methyl labeled proteins. Journal of Biomolecular NMR, 2009, 45, 311-318.	2.8	14
30	A Double TROSY hNCAnH Experiment for Efficient Assignment of Large and Challenging Proteins. Journal of the American Chemical Society, 2009, 131, 12880-12881.	13.7	23
31	A nuclear receptor-like pathway regulating multidrug resistance in fungi. Nature, 2008, 452, 604-609.	27.8	294
32	Structural basis for the selectivity of the external thioesterase of the surfactin synthetase. Nature, 2008, 454, 907-911.	27.8	112
33	Dynamic thiolation–thioesterase structure of a non-ribosomal peptide synthetase. Nature, 2008, 454, 903-906.	27.8	151
34	In situ observation of protein phosphorylation by high-resolution NMR spectroscopy. Nature Structural and Molecular Biology, 2008, 15, 321-329.	8.2	153
35	Fourier synthesis techniques for NMR spectroscopy in inhomogeneous fields. Journal of Chemical Physics, 2008, 128, 214503.	3.0	8
36	Effects of Redox Potential and Ca2+ on the Inositol 1,4,5-Trisphosphate Receptor L3-1 Loop Region. Journal of Biological Chemistry, 2008, 283, 25567-25575.	3.4	39

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37	NMR Methods for Studying Protein–Protein Interactions Involved in Translation Initiation. Methods in Enzymology, 2007, 430, 283-331.	1.0	48
38	Non-uniformly Sampled Double-TROSY hNcaNH Experiments for NMR Sequential Assignments of Large Proteins. Journal of the American Chemical Society, 2006, 128, 5757-5763.	13.7	63
39	Mapping of the Auto-inhibitory Interactions of Protein Kinase R by Nuclear Magnetic Resonance. Journal of Molecular Biology, 2006, 364, 352-363.	4.2	35
40	Determination of all NOes in 1H–13C–Me-ILV-U–2H–15N Proteins with Two Time-Shared Experiments. Journal of Biomolecular NMR, 2006, 34, 31-40.	2.8	36
41	Fast Assignment of 15N-HSQC Peaks using High-Resolution 3D HNcocaNH Experiments with Non-Uniform Sampling. Journal of Biomolecular NMR, 2005, 33, 43-50.	2.8	59
42	Unambiguous Assignment of NMR Protein Backbone Signals with a Time-shared Triple-resonance Experiment. Journal of Biomolecular NMR, 2005, 33, 187-196.	2.8	31
43	Sensitivity enhancement in NMR of macromolecules by application of optimal control theory. Journal of Biomolecular NMR, 2005, 32, 23-30.	2.8	35
44	Triple Quantum Decoherence under Multiple Refocusing: Slow Correlated Chemical Shift Modulations of C^2 and N Nuclei in Proteins. Journal of Biomolecular NMR, 2004, 28, 263-272.	2.8	27
45	Evidence of Slow Motions by Cross-Correlated Chemical Shift Modulation in Deuterated and Protonated Proteins. Journal of Biomolecular NMR, 2004, 28, 173-177.	2.8	8
46	Accelerated acquisition of high resolution triple-resonance spectra using non-uniform sampling and maximum entropy reconstruction. Journal of Magnetic Resonance, 2004, 170, 15-21.	2.1	217
47	Internal motions in proteins and interference effects in nuclear magnetic resonance. Progress in Nuclear Magnetic Resonance Spectroscopy, 2002, 41, 305-324.	7.5	52