D Flemming Hansen

List of Publications by Year
in descending order

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74 papers	3,377 citations	136740 32 h-index	149479 56 g-index
75 all docs	75 docs citations	75 times ranked	2764 citing authors

#	Article	IF	Citations
1	Structural mass spectrometry decodes domain interaction and dynamics of the full-length Human Histone Deacetylase 2. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2022, 1870, 140759.	1.1	0
2	Towards autonomous analysis of chemical exchange saturation transfer experiments using deep neural networks. Journal of Biomolecular NMR, 2022, 76, 75-86.	1.6	7
3	FID-Net: A versatile deep neural network architecture for NMR spectral reconstruction and virtual decoupling. Journal of Biomolecular NMR, 2021, 75, 179-191.	1.6	32
4	Methodological advancements for characterising protein side chains by NMR spectroscopy. Current Opinion in Structural Biology, 2021, 70, 61-69.	2.6	8
5	Aromatic side-chain flips orchestrate the conformational sampling of functional loops in human histone deacetylase 8. Chemical Science, 2021, 12, 9318-9327.	3.7	5
6	Virtual Homonuclear Decoupling in Direct Detection Nuclear Magnetic Resonance Experiments Using Deep Neural Networks. Journal of the American Chemical Society, 2021, 143, 16935-16942.	6.6	17
7	Post-translational insertion of boron in proteins to probe and modulate function. Nature Chemical Biology, 2021, 17, 1245-1261.	3.9	15
8	A distal regulatory region of a class I human histone deacetylase. Nature Communications, 2020, 11, 3841.	5.8	25
9	Multiquantum Chemical Exchange Saturation Transfer NMR to Quantify Symmetrical Exchange: Application to Rotational Dynamics of the Guanidinium Group in Arginine Side Chains. Journal of Physical Chemistry Letters, 2020, 11, 5649-5654.	2.1	16
10	Mechanism of Crosstalk between the LSD1 Demethylase and HDAC1 Deacetylase in the CoREST Complex. Cell Reports, 2020, 30, 2699-2711.e8.	2.9	74
11	Potent non-hydroxamate inhibitors of histone deacetylase-8: Role and scope of an isoindolin-2-yl linker with an Î±-amino amide as the zinc-binding unit. Bioorganic and Medicinal Chemistry Letters, 2020, 30, 126926.	1.0	10
12	Arginine Sideâ€Chain Hydrogen Exchange: Quantifying Arginine Sideâ€Chain Interactions in Solution. ChemPhysChem, 2019, 20, 252-259.	1.0	8
13	Using Deep Neural Networks to Reconstruct Non-uniformly Sampled NMR Spectra. Journal of Biomolecular NMR, 2019, 73, 577-585.	1.6	62
14	Interaction Between the a3 Region of Factor VIII and the TILâ€™Eâ€™ Domains of the von Willebrand Factor. Biophysical Journal, 2019, 117, 479-489.	0.2	9
15	Determining isoleucine side-chain rotamer-sampling in proteins from ¹³C chemical shift. Chemical Communications, 2019, 55, 14107-14110.	2.2	10
16	A Chemical Biology Approach to Understanding Molecular Recognition of Lipidâ€…II by Nisin(1â€“12): Synthesis and NMR Ensemble Analysis of Nisin(1â€“12) and Analogues. Chemistry - A European Journal, 2019, 25, 14572-14582.	1.7	16
17	Molecular Recognition of Lipid II by Lantibiotics: Synthesis and Conformational Studies of Analogues of Nisin and Mutacin Rings A and B. Journal of Organic Chemistry, 2019, 84, 11493-11512.	1.7	26
18	Characterising side chains in large proteins by protonless 13C-detected NMR spectroscopy. Nature Communications, 2019, 10, 1747.	5.8	26

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19	Importance of the Force Field Choice in Capturing Functionally Relevant Dynamics in the von Willebrand Factor. Journal of Physical Chemistry Letters, 2019, 10, 1928-1934.	2.1	32
20	Intra-residue methylâ€“methyl correlations for valine and leucine residues in large proteins from a 3D-HMBC-HMQC experiment. Journal of Biomolecular NMR, 2019, 73, 749-757.	1.6	14
21	CPMG Experiments for Protein Minor Conformer Structure Determination. Methods in Molecular Biology, 2018, 1688, 223-242.	0.4	11
22	Measurement of 15 N longitudinal relaxation rates in 15 NH 4 + spin systems to characterise rotational correlation times and chemical exchange. Journal of Magnetic Resonance, 2017, 279, 91-98.	1.2	4
23	Determining rotational dynamics of the guanidino group of arginine side chains in proteins by carbon-detected NMR. Chemical Communications, 2017, 53, 10062-10065.	2.2	15
24	A 13C-detected 15N double-quantum NMR experiment to probe arginine side-chain guanidinium 15NÎ· chemical shifts. Journal of Biomolecular NMR, 2017, 69, 123-132.	1.6	23
25	Characterizing Active Site Conformational Heterogeneity along the Trajectory of an Enzymatic Phosphoryl Transfer Reaction. Angewandte Chemie, 2016, 128, 11705-11709.	1.6	0
26	Excited States of Nucleic Acids Probed by Proton Relaxation Dispersion NMR Spectroscopy. Angewandte Chemie, 2016, 128, 12187-12191.	1.6	8
27	Excited States of Nucleic Acids Probed by Proton Relaxation Dispersion NMR Spectroscopy. Angewandte Chemie - International Edition, 2016, 55, 12008-12012.	7.2	48
28	Characterizing Active Site Conformational Heterogeneity along the Trajectory of an Enzymatic Phosphoryl Transfer Reaction. Angewandte Chemie - International Edition, 2016, 55, 11533-11537.	7.2	16
29	Visualizing the Molecular Recognition Trajectory of an Intrinsically Disordered Protein Using Multinuclear Relaxation Dispersion NMR. Journal of the American Chemical Society, 2015, 137, 1220-1229.	6.6	128
30	Relaxation Dispersion NMR Spectroscopy. Biological Magnetic Resonance, 2015, , 75-132.	0.4	11
31	Using ¹⁵Nâ€Ammonium to Characterise and Map Potassium Binding Sites in Proteins by NMR Spectroscopy. ChemBioChem, 2014, 15, 543-548.	1.3	22
32	Heteronuclear transverse and longitudinal relaxation in AX4 spin systems: Application to 15N relaxations in 15NH4+. Journal of Magnetic Resonance, 2014, 246, 136-148.	1.2	6
33	Solution structure of the major factor VIII binding region on von Willebrand factor. Blood, 2014, 123, 4143-4151.	0.6	41
34	Probing Arginine Sideâ€Chains and Their Dynamics with Carbonâ€Detected NMR Spectroscopy: Application to the 42â€…kDa Human Histone Deacetylaseâ€…8 at High pH. Angewandte Chemie - International Edition, 2013, 52, 3145-3147.	7.2	34
35	Loop Interactions and Dynamics Tune the Enzymatic Activity of the Human Histone Deacetylase 8. Journal of the American Chemical Society, 2013, 135, 17862-17868.	6.6	35
36	Accurate Structure and Dynamics of the Metal-Site of Paramagnetic Metalloproteins from NMR Parameters Using Natural Bond Orbitals. Journal of the American Chemical Society, 2012, 134, 4670-4682.	6.6	17

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37	Probing Dynamic Conformations of the High-Molecular-Weight Î±B-Crystallin Heat Shock Protein Ensemble by NMR Spectroscopy. Journal of the American Chemical Society, 2012, 134, 15343-15350.	6.6	63
38	Determining Valine Side-Chain Rotamer Conformations in Proteins from Methyl ¹³C Chemical Shifts: Application to the 360 kDa Half-Proteasome. Journal of the American Chemical Society, 2011, 133, 8272-8281.	6.6	51
39	Divided-Evolution-Based Pulse Scheme for Quantifying Exchange Processes in Proteins: Powerful Complement to Relaxation Dispersion Experiments. Journal of the American Chemical Society, 2011, 133, 1935-1945.	6.6	15
40	Solution structure of a minor and transiently formed state of a T4 lysozyme mutant. Nature, 2011, 477, 111-114.	13.7	265
41	Measuring 1HN temperature coefficients in invisible protein states by relaxation dispersion NMR spectroscopy. Journal of Biomolecular NMR, 2011, 50, 13-18.	1.6	12
42	Measurement of signs of chemical shift differences between ground and excited protein states: a comparison between H(S/M)QC and R 1Ï•methods. Journal of Biomolecular NMR, 2010, 46, 205-216.	1.6	22
43	A simple method for measuring signs of 1HN chemical shift differences between ground and excited protein states. Journal of Biomolecular NMR, 2010, 47, 135-141.	1.6	26
44	Determination of Isoleucine Side-Chain Conformations in Ground and Excited States of Proteins from Chemical Shifts. Journal of the American Chemical Society, 2010, 132, 7589-7591.	6.6	88
45	Determination of Leu Side-Chain Conformations in Excited Protein States by NMR Relaxation Dispersion. Journal of the American Chemical Society, 2010, 132, 42-43.	6.6	72
46	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.	6.6	60
47	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.	1.6	41
48	Isotope labeling methods for studies of excited protein states by relaxation dispersion NMR spectroscopy. Nature Protocols, 2009, 4, 1641-1648.	5.5	46
49	Selective Characterization of Microsecond Motions in Proteins by NMR Relaxation. Journal of the American Chemical Society, 2009, 131, 16257-16265.	6.6	54
50	Measuring the Signs of ¹H^{Î±} Chemical Shift Differences Between Ground and Excited Protein States by Off-Resonance Spin-Lock R_{1Ï} NMR Spectroscopy. Journal of the American Chemical Society, 2009, 131, 10832-10833.	6.6	27
51	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.	6.6	68
52	Measurement of Methyl Group Motional Parameters of Invisible, Excited Protein States by NMR Spectroscopy. Journal of the American Chemical Society, 2009, 131, 12745-12754.	6.6	30
53	Measurement of Methyl Axis Orientations in Invisible, Excited States of Proteins by Relaxation Dispersion NMR Spectroscopy. Journal of the American Chemical Society, 2009, 131, 11939-11948.	6.6	33
54	Binding Kinetics of Histone Chaperone Chz1 and Variant Histone H2A.Z-H2B by Relaxation Dispersion NMR Spectroscopy. Journal of Molecular Biology, 2009, 387, 1-9.	2.0	22

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55	Using relaxation dispersion NMR spectroscopy to determine structures of excited, invisible protein states. Journal of Biomolecular NMR, 2008, 41, 113-120.	1.6	112
56	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.	1.6	65
57	NMR structure of chaperone Chz1 complexed with histones H2A.Z-H2B. Nature Structural and Molecular Biology, 2008, 15, 868-869.	3.6	87
58	Characterization of Conformational Exchange of a Histidine Side Chain: Protonation, Rotamerization, and Tautomerization of His61 in Plastocyanin from Anabaena variabilis. Journal of the American Chemical Society, 2008, 130, 8460-8470.	6.6	51
59	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.	1.2	196
60	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.	6.6	34
61	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.	6.6	155
62	Probing Structure in Invisible Protein States with Anisotropic NMR Chemical Shifts. Journal of the American Chemical Society, 2008, 130, 2734-2735.	6.6	58
63	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.	3.3	186
64	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.	3.3	172
65	An Exchange-Free Measure of ¹⁵N Transverse Relaxation:â€‰ An NMR Spectroscopy Application to the Study of a Folding Intermediate with Pervasive Chemical Exchange. Journal of the American Chemical Society, 2007, 129, 11468-11479.	6.6	66
66	Improved magnetization alignment schemes for spin-lock relaxation experiments. Journal of Biomolecular NMR, 2007, 37, 245-255.	1.6	35
67	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.	1.6	160
68	Reinvestigation of the method used to map the electronic structure of blue copper proteins by NMR relaxation. Journal of Biological Inorganic Chemistry, 2006, 11, 277-285.	1.1	12
69	On the use of pseudocontact shifts in the structure determination of metalloproteins. Magnetic Resonance in Chemistry, 2006, 44, 294-301.	1.1	21
70	Determination of the geometric structure of the metal site in a blue copper protein by paramagnetic NMR. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 1738-1743.	3.3	34
71	Mapping the Electronic Structure of the Blue Copper Site in Plastocyanin by NMR Relaxation. Journal of the American Chemical Society, 2004, 126, 1247-1252.	6.6	20
72	Implications of using approximate Blochâ€“McConnell equations in NMR analyses of chemically exchanging systems: application to the electron self-exchange of plastocyanin. Journal of Magnetic Resonance, 2003, 163, 215-227.	1.2	30

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73	Detection of Short-Lived Transient Proteinâ^'Protein Interactions by Intermolecular Nuclear Paramagnetic Relaxation:Â Plastocyanin fromAnabaenavariabilis. Journal of the American Chemical Society, 2003, 125, 6858-6859.	6.6	27
74	A General Method for Determining the Electron Self-Exchange Rates of Blue Copper Proteins by Longitudinal NMR Relaxation. Journal of the American Chemical Society, 2002, 124, 4093-4096.	6.6	22