David E Wemmer

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Regulation of the transcriptional activator NtrC1: structural studies of the regulatory and AAA+ ATPase domains. Genes and Development, 2003, 17, 2552-2563.	5.9	181
2	Crystal structure of an activated response regulator bound to its target. Nature Structural Biology, 2001, 8, 52-56.	9.7	134
3	Understanding the impact of ionic liquid pretreatment on eucalyptus. Biofuels, 2010, 1, 33-46.	2.4	129
4	Helix propagation in trifluoroethanol solutions. Biopolymers, 1992, 32, 1695-1702.	2.4	107
5	NMR Characterization of Hairpin Polyamide Complexes with the Minor Groove of DNA. Journal of the American Chemical Society, 1997, 119, 7909-7916.	13.7	96
6	Molecular Imaging of Cancer Cells Using a Bacteriophageâ€Based ¹²⁹ Xe NMR Biosensor. Angewandte Chemie - International Edition, 2013, 52, 4849-4853.	13.8	93
7	Alpha helix capping in synthetic model peptides by reciprocal side chain-main chain interactions: Evidence for an N terminal "capping box― Proteins: Structure, Function and Bioinformatics, 1994, 18, 1-7.	2.6	91
8	Fragmentation of Lignin Samples with Commercial Pd/C under Ambient Pressure of Hydrogen. ACS Catalysis, 2016, 6, 7385-7392.	11.2	86
9	Solidâ€state NMR studies of the prion protein H1 fragment. Protein Science, 1996, 5, 1655-1661.	7.6	84
10	Optimization of Xenon Biosensors for Detection of Protein Interactions. ChemBioChem, 2006, 7, 65-73.	2.6	81
11	Solution structure of the DNAâ€binding domain of the heat shock transcription factor determined by multidimensional heteronuclear magnetic resonance spectroscopy. Protein Science, 1994, 3, 1806-1821.	7.6	77
12	PHO13 deletion-induced transcriptional activation prevents sedoheptulose accumulation during xylose metabolism in engineered Saccharomyces cerevisiae. Metabolic Engineering, 2016, 34, 88-96.	7.0	74
13	A Template for Stabilization of a Peptide α-Helix: Synthesis and Evaluation of Conformational Effects by Circular Dichroism and NMR. Journal of the American Chemical Society, 1997, 119, 6461-6472.	13.7	72
14	ATP Ground- and Transition States of Bacterial Enhancer Binding AAA+ ATPases Support Complex Formation with Their Target Protein, If 54. Structure, 2007, 15, 429-440.	3.3	64
15	Ligands recognizing the minor groove of DNA: Development and applications. Biopolymers, 1999, 52, 197-211.	2.4	60
16	Cellulose Deficiency Is Enhanced on Hyper Accumulation of Sucrose by a H ⁺ -Coupled Sucrose Symporter. Plant Physiology, 2016, 171, 110-124.	4.8	57
17	An Experimental and Theoretical Investigation of the Chemical Shielding Tensors of13Cαof Alanine, Valine, and Leucine Residues in Solid Peptides and in Proteins in Solution. Journal of the American Chemical Society, 2001, 123, 10362-10369.	13.7	54
18	Structure and Regulatory Mechanism of Aquifex aeolicus NtrC4: Variability and Evolution in Bacterial Transcriptional Regulation. Journal of Molecular Biology, 2008, 384, 1058-1075.	4.2	54

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19	Yeast heat shock transcription factor Nâ€ŧerminal activation domains are unstructured as probed by heteronuclear NMR spectroscopy. Protein Science, 1996, 5, 262-269.	7.6	52
20	Rotaxane-mediated suppression and activation of cucurbit[6]uril for molecular detection by ¹²⁹ Xe hyperCEST NMR. Chemical Communications, 2016, 52, 3119-3122.	4.1	47
21	Structural Changes Associated with Transthyretin Misfolding and Amyloid Formation Revealed by Solution and Solid-State NMR. Biochemistry, 2016, 55, 1941-1944.	2.5	38
22	Rotaxane probes for protease detection by ¹²⁹ Xe hyperCEST NMR. Chemical Communications, 2017, 53, 1076-1079.	4.1	38
23	Beryllofluoride Binding Mimics Phosphorylation of Aspartate in Response Regulators. Journal of Bacteriology, 2005, 187, 8229-8230.	2.2	37
24	Structural Basis of DNA Recognition by the Alternative Sigma-factor, σ54. Journal of Molecular Biology, 2007, 369, 1070-1078.	4.2	37
25	Identification of MEDIATOR16 as the <i>Arabidopsis</i> COBRA suppressor MONGOOSE1. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 16048-16053.	7.1	37
26	The Arabidopsis COBRA Protein Facilitates Cellulose Crystallization at the Plasma Membrane. Journal of Biological Chemistry, 2014, 289, 34911-34920.	3.4	35
27	Studies of DNA dumbbells. II. Construction and characterization of DNA dumbbells with a 16 base-pair duplex stem and Tn end loops (n = 2, 3, 4, 6, 8, 10, 14). Biopolymers, 1992, 32, 865-879.	2.4	34
28	Receiver Domains Control the Active-State Stoichiometry of Aquifex aeolicus If 54 Activator NtrC4, as Revealed by Electrospray Ionization Mass Spectrometry. Journal of Molecular Biology, 2009, 393, 634-643.	4.2	34
29	Extending the recognition site of designed minor groove binding molecules. Nature Structural and Molecular Biology, 1996, 3, 321-324.	8.2	32
30	The C-terminal RpoN Domain of σ54 Forms an Unpredicted Helix-Turn-Helix Motif Similar to Domains of σ70*. Journal of Biological Chemistry, 2005, 280, 41530-41536.	3.4	31
31	Molecular Sensing Using Hyperpolarized Xenon NMR Spectroscopy. Israel Journal of Chemistry, 2014, 54, 104-112.	2.3	29
32	Backbone dynamics of sequence specific recognition and binding by the yeast <i>Pho4</i> bHLH domain probed by NMR. Protein Science, 2000, 9, 2354-2365.	7.6	28
33	NMR Characterization of the Aliphatic β/β Pairing for Recognition of A·T/T·A Base Pairs in the Minor Groove of DNA. Journal of the American Chemical Society, 1999, 121, 2956-2964.	13.7	26
34	Solid-State NMR Studies Reveal Native-like β-Sheet Structures in Transthyretin Amyloid. Biochemistry, 2016, 55, 5272-5278.	2.5	25
35	Targeted Molecular Imaging of Cancer Cells Using MS2-Based ¹²⁹ Xe NMR. Bioconjugate Chemistry, 2016, 27, 1796-1801.	3.6	23
36	Directly Functionalized Cucurbit[7]uril as a Biosensor for the Selective Detection of Protein Interactions by ¹²⁹ Xe hyperCESTâ€NMR. Chemistry - A European Journal, 2019, 25, 6108-6112.	3.3	22

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37	Structure of the RNA Polymerase Core-Binding Domain of σ54 Reveals a Likely Conformational Fracture Point. Journal of Molecular Biology, 2009, 390, 70-82.	4.2	21
38	Structure and Dynamics of Distamycin A with d(CGCAAATTGGC):d(GCCAATTTGCG) at Low Drug: DNA Ratios. Journal of Biomolecular Structure and Dynamics, 1990, 8, 81-97.	3.5	19
39	Rotaxane Probes for the Detection of Hydrogen Peroxide by ¹²⁹ Xe HyperCEST NMR Spectroscopy. Angewandte Chemie - International Edition, 2019, 58, 9948-9953.	13.8	19
40	Investigation of DOTA–Metal Chelation Effects on the Chemical Shift of ¹²⁹ Xe. ChemPhysChem, 2015, 16, 3573-3577.	2.1	17
41	Grassroots Efforts To Quantify and Improve the Academic Climate of an R1 STEM Department: Using Evidence-Based Discussions To Foster Community. Journal of Chemical Education, 2019, 96, 2149-2157.	2.3	17
42	Structural Mechanism of GAF-Regulated σ54 Activators from Aquifex aeolicus. Journal of Molecular Biology, 2013, 425, 156-170.	4.2	16
43	1H resonance assignments, secondary structure and general topology of single-chain monellin in solution as determined by1H 2D-NMR. Journal of Biomolecular NMR, 1992, 2, 557-572.	2.8	15
44	Solution structure of a core peptide derived from scyllatoxin. Proteins: Structure, Function and Bioinformatics, 1994, 18, 205-215.	2.6	15
45	DNA Recognition by a σ54 Transcriptional Activator from Aquifex aeolicus. Journal of Molecular Biology, 2014, 426, 3553-3568.	4.2	13
46	A saturation-mutagenesis analysis of the interplay between stability and activation in Ras. ELife, 2022, 11, .	6.0	13
47	Deletion of a single amino acid changes the folding of an apamin hybrid sequence peptide to that of endothelin. Biopolymers, 1997, 41, 451-460.	2.4	12
48	¹²⁹ Xe NMR Relaxation-Based Macromolecular Sensing. Journal of the American Chemical Society, 2016, 138, 9747-9750.	13.7	11
49	Thermodynamics of the helix-coil transition: Binding of S15 and a hybrid sequence, disulfide stabilized peptide to the S-protein. Proteins: Structure, Function and Bioinformatics, 2001, 42, 523-530.	2.6	10
50	A facile method for expression and purification of 15 N isotope-labeled human Alzheimer's β-amyloid peptides from E. coli for NMR-based structural analysis. Protein Expression and Purification, 2015, 116, 82-89.	1.3	8
51	Nondisruptive Dissolution of Hyperpolarized 129 Xe into Viscous Aqueous and Organic Liquid Crystalline Environments. Angewandte Chemie - International Edition, 2016, 55, 4666-4670.	13.8	8
52	Structure of the Michaelis Complex of an Efficient Antibody Acyl Transferase Determined by Transferred Nuclear Overhauser Enhancement Spectroscopy. Journal of the American Chemical Society, 1998, 120, 7395-7396.	13.7	6
53	The energetics of structural change in maltose-binding protein. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 12529-12530.	7.1	6
54	Role of the σ54 Activator Interacting Domain in Bacterial Transcription Initiation. Journal of Molecular Biology, 2016, 428, 4669-4685.	4.2	6

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55	Rotaxane Probes for the Detection of Hydrogen Peroxide by 129 Xe HyperCEST NMR Spectroscopy. Angewandte Chemie, 2019, 131, 10053-10058.	2.0	5
56	Unconstrained peptoid tetramer exhibits a predominant conformation in aqueous solution. Biopolymers, 2019, 110, e23267.	2.4	5
57	Frontispiece: Nondisruptive Dissolution of Hyperpolarized ¹²⁹ Xe into Viscous Aqueous and Organic Liquid Crystalline Environments. Angewandte Chemie - International Edition, 2016, 55, .	13.8	1
58	Rebuttal: Conformational Changes of SpoOF along the Phosphotransfer Pathway. Journal of Bacteriology, 2005, 187, 8228-8228.	2.2	0
59	The Rut Pathway for Pyrimidine Degradation: Novel Chemistry and Toxicity Problems. Journal of Bacteriology, 2011, 193, 326-326.	2.2	0
60	SnapShot: Biomolecular NMR. Cell, 2016, 166, 1600.	28.9	0