David E Wemmer

List of Publications by Year
in descending order

60	2,474	159585	197818
papers	citations	30 h-index	49 g-index

64	64	64	2952
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A saturation-mutagenesis analysis of the interplay between stability and activation in Ras. ELife, 2022, 11, .	6.0	13
2	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
3	Rotaxane Probes for the Detection of Hydrogen Peroxide by ¹²⁹Xe HyperCEST NMR Spectroscopy. Angewandte Chemie - International Edition, 2019, 58, 9948-9953.	13.8	19
4	Rotaxane Probes for the Detection of Hydrogen Peroxide by 129 Xe HyperCEST NMR Spectroscopy. Angewandte Chemie, 2019, 131, 10053-10058.	2.0	5
5	Unconstrained peptoid tetramer exhibits a predominant conformation in aqueous solution. Biopolymers, 2019, 110, e23267.	2.4	5
6	Directly Functionalized Cucurbit[7]uril as a Biosensor for the Selective Detection of Protein Interactions by ¹²⁹Xe hyperCESTâ€...NMR. Chemistry - A European Journal, 2019, 25, 6108-6112.	3.3	22
7	Rotaxane probes for protease detection by ¹²⁹Xe hyperCEST NMR. Chemical Communications, 2017, 53, 1076-1079.	4.1	38
8	Frontispiece: Nondisruptive Dissolution of Hyperpolarized ¹²⁹Xe into Viscous Aqueous and Organic Liquid Crystalline Environments. Angewandte Chemie - International Edition, 2016, 55, .	13.8	1
9	Cellulose Deficiency Is Enhanced on Hyper Accumulation of Sucrose by a H⁺-Coupled Sucrose Symporter. Plant Physiology, 2016, 171, 110-124.	4.8	57
10	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
11	Role of the Ïƒ54 Activator Interacting Domain in Bacterial Transcription Initiation. Journal of Molecular Biology, 2016, 428, 4669-4685.	4.2	6
12	Solid-State NMR Studies Reveal Native-like Î²-Sheet Structures in Transthyretin Amyloid. Biochemistry, 2016, 55, 5272-5278.	2.5	25
13	SnapShot: Biomolecular NMR. Cell, 2016, 166, 1600.	28.9	0
14	Targeted Molecular Imaging of Cancer Cells Using MS2-Based ¹²⁹Xe NMR. Bioconjugate Chemistry, 2016, 27, 1796-1801.	3.6	23
15	¹²⁹Xe NMR Relaxation-Based Macromolecular Sensing. Journal of the American Chemical Society, 2016, 138, 9747-9750.	13.7	11
16	Fragmentation of Lignin Samples with Commercial Pd/C under Ambient Pressure of Hydrogen. ACS Catalysis, 2016, 6, 7385-7392.	11.2	86
17	Rotaxane-mediated suppression and activation of cucurbit[6]uril for molecular detection by ¹²⁹Xe hyperCEST NMR. Chemical Communications, 2016, 52, 3119-3122.	4.1	47
18	Structural Changes Associated with Transthyretin Misfolding and Amyloid Formation Revealed by Solution and Solid-State NMR. Biochemistry, 2016, 55, 1941-1944.	2.5	38

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19	PHO13 deletion-induced transcriptional activation prevents sedoheptulose accumulation during xylose metabolism in engineered Saccharomyces cerevisiae. Metabolic Engineering, 2016, 34, 88-96.	7.0	74
20	Investigation of DOTAâ€“Metal Chelation Effects on the Chemical Shift of ¹²⁹Xe. ChemPhysChem, 2015, 16, 3573-3577.	2.1	17
21	Identification of MEDIATOR16 as the Arabidopsis COBRA suppressor MONGOOSE1. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 16048-16053.	7.1	37
22	A facile method for expression and purification of 15 N isotope-labeled human Alzheimerâ€™s Î²-amyloid peptides from E. coli for NMR-based structural analysis. Protein Expression and Purification, 2015, 116, 82-89.	1.3	8
23	Molecular Sensing Using Hyperpolarized Xenon NMR Spectroscopy. Israel Journal of Chemistry, 2014, 54, 104-112.	2.3	29
24	The Arabidopsis COBRA Protein Facilitates Cellulose Crystallization at the Plasma Membrane. Journal of Biological Chemistry, 2014, 289, 34911-34920.	3.4	35
25	DNA Recognition by a Ïƒ54 Transcriptional Activator from Aquifex aeolicus. Journal of Molecular Biology, 2014, 426, 3553-3568.	4.2	13
26	Structural Mechanism of GAF-Regulated Ïƒ54 Activators from Aquifex aeolicus. Journal of Molecular Biology, 2013, 425, 156-170.	4.2	16
27	Molecular Imaging of Cancer Cells Using a Bacteriophageâ€Based ¹²⁹Xe NMR Biosensor. Angewandte Chemie - International Edition, 2013, 52, 4849-4853.	13.8	93
28	The Rut Pathway for Pyrimidine Degradation: Novel Chemistry and Toxicity Problems. Journal of Bacteriology, 2011, 193, 326-326.	2.2	0
29	Understanding the impact of ionic liquid pretreatment on eucalyptus. Biofuels, 2010, 1, 33-46.	2.4	129
30	Structure of the RNA Polymerase Core-Binding Domain of Ïƒ54 Reveals a Likely Conformational Fracture Point. Journal of Molecular Biology, 2009, 390, 70-82.	4.2	21
31	Receiver Domains Control the Active-State Stoichiometry of Aquifex aeolicus Ïƒ54 Activator NtrC4, as Revealed by Electrospray Ionization Mass Spectrometry. Journal of Molecular Biology, 2009, 393, 634-643.	4.2	34
32	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
33	Structural Basis of DNA Recognition by the Alternative Sigma-factor, Ïƒ54. Journal of Molecular Biology, 2007, 369, 1070-1078.	4.2	37
34	ATP Ground- and Transition States of Bacterial Enhancer Binding AAA+ ATPases Support Complex Formation with Their Target Protein, Ïƒ54. Structure, 2007, 15, 429-440.	3.3	64
35	Optimization of Xenon Biosensors for Detection of Protein Interactions. ChemBioChem, 2006, 7, 65-73.	2.6	81
36	Rebuttal: Conformational Changes of Spo0F along the Phosphotransfer Pathway. Journal of Bacteriology, 2005, 187, 8228-8228.	2.2	0

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37	Beryllofluoride Binding Mimics Phosphorylation of Aspartate in Response Regulators. Journal of Bacteriology, 2005, 187, 8229-8230.	2.2	37
38	The C-terminal RpoN Domain of Ïƒ54 Forms an Unpredicted Helix-Turn-Helix Motif Similar to Domains of Ïƒ70*. Journal of Biological Chemistry, 2005, 280, 41530-41536.	3.4	31
39	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
40	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
41	An Experimental and Theoretical Investigation of the Chemical Shielding Tensors of13CÎ±of 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
42	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
43	Crystal structure of an activated response regulator bound to its target. Nature Structural Biology, 2001, 8, 52-56.	9.7	134
44	Backbone dynamics of sequence specific recognition and binding by the yeast Pho4 bHLH domain probed by NMR. Protein Science, 2000, 9, 2354-2365.	7.6	28
45	Ligands recognizing the minor groove of DNA: Development and applications. Biopolymers, 1999, 52, 197-211.	2.4	60
46	NMR Characterization of the Aliphatic Î²/Î² Pairing for Recognition of AÂ·T/TÂ·A Base Pairs in the Minor Groove of DNA. Journal of the American Chemical Society, 1999, 121, 2956-2964.	13.7	26
47	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
48	A Template for Stabilization of a Peptide Î±-Helix:Â Synthesis and Evaluation of Conformational Effects by Circular Dichroism and NMR. Journal of the American Chemical Society, 1997, 119, 6461-6472.	13.7	72
49	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
50	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
51	Yeast heat shock transcription factor Nâ€terminal activation domains are unstructured as probed by heteronuclear NMR spectroscopy. Protein Science, 1996, 5, 262-269.	7.6	52
52	Solidâ€state NMR studies of the prion protein H1 fragment. Protein Science, 1996, 5, 1655-1661.	7.6	84
53	Extending the recognition site of designed minor groove binding molecules. Nature Structural and Molecular Biology, 1996, 3, 321-324.	8.2	32
54	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

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55	Alpha helix capping in synthetic model peptides by reciprocal side chain-main chain interactions: Evidence for an N terminal â€œcapping boxâ€• Proteins: Structure, Function and Bioinformatics, 1994, 18, 1-7.	2.6	91
56	Solution structure of a core peptide derived from scyllatoxin. Proteins: Structure, Function and Bioinformatics, 1994, 18, 205-215.	2.6	15
57	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
58	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
59	Helix propagation in trifluoroethanol solutions. Biopolymers, 1992, 32, 1695-1702.	2.4	107
60	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