A Joshua Wand

List of Publications by Year
in descending order

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125 papers	8,550 citations	50244 46 h-index	46771 89 g-index
129 all docs	129 docs citations	129 times ranked	5779 citing authors

#	Article	IF	Citations
1	A fine balance of hydrophobic-electrostatic communication pathways in a pH-switching protein. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	3
2	Using biochemistry and biophysics to extinguish androgen receptor signaling in prostate cancer. Journal of Biological Chemistry, 2021, 296, 100240.	1.6	17
3	The Molecular Basis for Life in Extreme Environments. Annual Review of Biophysics, 2021, 50, 343-372.	4.5	31
4	Self-Masked Aldehyde Inhibitors: A Novel Strategy for Inhibiting Cysteine Proteases. Journal of Medicinal Chemistry, 2021, 64, 11267-11287.	2.9	19
5	Protein conformational entropy is not slaved to water. Scientific Reports, 2020, 10, 17587.	1.6	8
6	Membrane Proteins Have Distinct Fast Internal Motion and Residual Conformational Entropy. Angewandte Chemie, 2020, 132, 11201-11207.	1.6	3
7	Membrane Proteins Have Distinct Fast Internal Motion and Residual Conformational Entropy. Angewandte Chemie - International Edition, 2020, 59, 11108-11114.	7.2	21
8	Site-Resolved and Quantitative Characterization of Very Weak Proteinâ€"Ligand Interactions. ACS Chemical Biology, 2019, 14, 1398-1402.	1.6	5
9	Extending the Detection Limit in Fragment Screening of Proteins Using Reverse Micelle Encapsulation. ACS Chemical Biology, 2019, 14, 2224-2232.	1.6	7
10	Reverse Micelle Encapsulation of Proteins for NMR Spectroscopy. Methods in Enzymology, 2019, 615, 43-75.	0.4	9
11	Characterizing Protein Hydration Dynamics Using Solution NMR Spectroscopy. Methods in Enzymology, 2019, 615, 77-101.	0.4	12
12	Water loading driven size, shape, and composition of cetyltrimethylammonium/hexanol/pentane reverse micelles. Journal of Colloid and Interface Science, 2019, 540, 207-217.	5.0	14
13	Characterization of Internal Protein Dynamics and Conformational Entropy by NMR Relaxation. Methods in Enzymology, 2019, 615, 237-284.	0.4	19
14	Dynamic activation and regulation of the mitogen-activated protein kinase p38. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4655-4660.	3.3	52
15	Measuring Entropy in Molecular Recognition by Proteins. Annual Review of Biophysics, 2018, 47, 41-61.	4.5	77
16	Improving yields of deuterated, methyl labeled protein by growing in H2O. Journal of Biomolecular NMR, 2018, 71, 263-273.	1.6	20
17	Practical aspects of high-pressure NMR spectroscopy and its applications in protein biophysics and structural biology. Methods, 2018, 148, 67-80.	1.9	34
18	Conformational Entropy. , 2018, , 1-4.		0

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19	Solution NMR investigation of the response of the lactose repressor core domain dimer to hydrostatic pressure. Biophysical Chemistry, 2017, 231, 39-44.	1.5	11
20	Bringing disorder and dynamics in protein allostery into focus. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 4278-4280.	3.3	11
21	Entropy in molecular recognition by proteins. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 6563-6568.	3.3	139
22	Optimized expression and purification of biophysical quantities of Lac repressor and Lac repressor regulatory domain. Protein Expression and Purification, 2016, 123, 75-82.	0.6	8
23	The unusual internal motion of the villin headpiece subdomain. Protein Science, 2016, 25, 423-432.	3.1	5
24	Accurate determination of rates from non-uniformly sampled relaxation data. Journal of Biomolecular NMR, 2016, 65, 157-170.	1.6	15
25	Design Principles for SuCESsFul Biosensors: Specific Fluorophore/Analyte Binding and Minimization of Fluorophore/Scaffold Interactions. Journal of Molecular Biology, 2016, 428, 4228-4241.	2.0	11
26	On the ability of molecular dynamics force fields to recapitulate <scp>NMR</scp> derived protein side chain order parameters. Protein Science, 2016, 25, 1156-1160.	3.1	21
27	Characterization of Cetyltrimethylammonium Bromide/Hexanol Reverse Micelles by Experimentally Benchmarked Molecular Dynamics Simulations. Langmuir, 2016, 32, 1674-1684.	1.6	23
28	Frontispiece: A Sharp Thermal Transition of Fast Aromaticâ€Ring Dynamics in Ubiquitin. Angewandte Chemie - International Edition, 2015, 54, .	7.2	0
29	Defining the Apoptotic Trigger. Journal of Biological Chemistry, 2015, 290, 30879-30887.	1.6	53
30	Reply to Kitahara and Mulder: An ensemble view of protein stability best explains pressure effects in a T4 lysozyme cavity mutant. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E924-E924.	3.3	4
31	A Sharp Thermal Transition of Fast Aromatic-Ring Dynamics in Ubiquitin. Angewandte Chemie - International Edition, 2015, 54, 102-107.	7.2	31
32	On the relationship between NMR-derived amide order parameters and protein backbone entropy changes. Proteins: Structure, Function and Bioinformatics, 2015, 83, 922-930.	1.5	60
33	Enzymes surf the heat wave. Nature, 2015, 517, 149-150.	13.7	6
34	Role of cavities and hydration in the pressure unfolding of T ₄ lysozyme. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13846-13851.	3.3	71
35	Reverse Micelles As a Platform for Dynamic Nuclear Polarization in Solution NMR of Proteins. Journal of the American Chemical Society, 2014, 136, 2800-2807.	6.6	22
36	Optimized Reverse Micelle Surfactant System for High-Resolution NMR Spectroscopy of Encapsulated Proteins and Nucleic Acids Dissolved in Low Viscosity Fluids. Journal of the American Chemical Society, 2014, 136, 3465-3474.	6.6	50

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37	Measurement and Control of pH in the Aqueous Interior of Reverse Micelles. Journal of Physical Chemistry B, 2014, 118, 2020-2031.	1.2	33
38	Dynamic and Thermodynamic Response of the Ras Protein Cdc42Hs upon Association with the Effector Domain of PAK3. Journal of Molecular Biology, 2014, 426, 3520-3538.	2.0	10
39	Banding 2of NMR-derived methyl order parameters: Implications for protein dynamics. Proteins: Structure, Function and Bioinformatics, 2014, 82, 2106-2117.	1.5	18
40	High-resolution NMR spectroscopy of encapsulated proteins dissolved in low-viscosity fluids. Journal of Magnetic Resonance, 2014, 241, 137-147.	1.2	36
41	Partial alignment and measurement of residual dipolar couplings of proteins under high hydrostatic pressure. Journal of Biomolecular NMR, 2013, 56, 353-357.	1.6	14
42	Elementary tetrahelical protein design for diverse oxidoreductase functions. Nature Chemical Biology, 2013, 9, 826-833.	3.9	125
43	Microscopic Insights into the NMR Relaxation-Based Protein Conformational Entropy Meter. Journal of the American Chemical Society, 2013, 135, 15092-15100.	6.6	123
44	The dark energy of proteins comes to light: conformational entropy and its role in protein function revealed by NMR relaxation. Current Opinion in Structural Biology, 2013, 23, 75-81.	2.6	155
45	A Surprising Role for Conformational Entropy in Protein Function. Topics in Current Chemistry, 2013, 337, 69-94.	4.0	29
46	A ¹³C Labeling Strategy Reveals a Range of Aromatic Side Chain Motion in Calmodulin. Journal of the American Chemical Society, 2013, 135, 9560-9563.	6.6	49
47	The dynamical response of hen egg white lysozyme to the binding of a carbohydrate ligand. Protein Science, 2012, 21, 1066-1073.	3.1	30
48	Coupled Motion in Proteins Revealed by Pressure Perturbation. Journal of the American Chemical Society, 2012, 134, 8543-8550.	6.6	99
49	AI NMR: a novel NMR data processing program optimized for sparse sampling. Journal of Biomolecular NMR, 2012, 52, 79-89.	1.6	7
50	Mapping the Hydration Dynamics of Ubiquitin. Journal of the American Chemical Society, 2011, 133, 12326-12329.	6.6	103
51	Site-resolved measurement of water-protein interactions by solution NMR. Nature Structural and Molecular Biology, 2011, 18, 245-249.	3.6	212
52	Modification of encapsulation pressure of reverse micelles in liquid ethane. Journal of Magnetic Resonance, 2011, 212, 229-233.	1.2	12
53	Optimized linear prediction for radial sampled multidimensional NMR experiments. Journal of Magnetic Resonance, 2011, 212, 240-244.	1.2	0
54	Optimization of NMR spectroscopy of encapsulated proteins dissolved in low viscosity fluids. Journal of Biomolecular NMR, 2011, 50, 421-30.	1.6	20

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55	Reverse Micelle Encapsulation of Membrane-Anchored Proteins for Solution NMR Studies. Structure, 2010, 18, 9-16.	1.6	48
56	SEnD NMR: Sensitivity Enhanced n-Dimensional NMR. Journal of Magnetic Resonance, 2010, 202, 250-258.	1.2	2
57	The role of conformational entropy in molecular recognition by calmodulin. Nature Chemical Biology, 2010, 6, 352-358.	3.9	237
58	A method for solution NMR structural studies of large integral membrane proteins: Reverse micelle encapsulation. Biochimica Et Biophysica Acta - Biomembranes, 2010, 1798, 150-160.	1.4	27
59	Reverse Micelles in Integral Membrane Protein Structural Biology by Solution NMR Spectroscopy. Structure, 2009, 17, 345-351.	1.6	37
60	AMORE-HX: a multidimensional optimization of radial enhanced NMR-sampled hydrogen exchange. Journal of Biomolecular NMR, 2009, 45, 233-239.	1.6	8
61	Fast structural dynamics in reduced and oxidized cytochrome c. Protein Science, 2009, 18, 670-674.	3.1	14
62	Optimized angle selection for radial sampled NMR experiments. Journal of Magnetic Resonance, 2008, 195, 169-178.	1.2	6
63	Re-Evaluation of the Model-Free Analysis of Fast Internal Motion in Proteins Using NMR Relaxation. Journal of Physical Chemistry B, 2008, 112, 12095-12103.	1.2	23
64	Conformational entropy in molecular recognition by proteins. FASEB Journal, 2008, 22, 528.3.	0.2	0
65	NMR Structure of a Disulfide-Crosslinked Î±IIbÎ²3 Cytoplasmic Domain Heterodimer. Blood, 2008, 112, 2866-2866.	0.6	0
66	Temperature Dependence of Fast Dynamics in Proteins. Biophysical Journal, 2007, 92, L43-L45.	0.2	38
67	Phasing arbitrarily sampled multidimensional NMR data. Journal of Magnetic Resonance, 2007, 187, 363-370.	1.2	5
68	Conformational entropy in molecular recognition by proteins. Nature, 2007, 448, 325-329.	13.7	604
69	Characterization of the Fast Dynamics of Protein Amino Acid Side Chains Using NMR Relaxation in Solution. Chemical Reviews, 2006, 106, 1672-1699.	23.0	300
70	Cold Denaturation of Encapsulated Ubiquitin. Journal of the American Chemical Society, 2006, 128, 10652-10653.	6.6	38
71	Magnetic Susceptibility-Induced Alignment of Proteins in Reverse Micelles. Journal of the American Chemical Society, 2006, 128, 15930-15931.	6.6	14
72	Conformational Dynamics of Calmodulin in Complex with the Calmodulin-Dependent Kinase Kinase Î± Calmodulin-Binding Domain. Biochemistry, 2006, 45, 8732-8741.	1.2	28

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73	Characterization of the Backbone and Side Chain Dynamics of the CaMâˆ’CaMKIp Complex Reveals Microscopic Contributions to Protein Conformational Entropyâ€. Biochemistry, 2006, 45, 9841-9848.	1.2	28
74	NMR spectroscopy of proteins encapsulated in a positively charged surfactant. Journal of Magnetic Resonance, 2005, 175, 158-162.	1.2	32
75	Novel surfactant mixtures for NMR spectroscopy of encapsulated proteins dissolved in low-viscosity fluids. Protein Science, 2005, 14, 2919-2921.	3.1	27
76	High-Resolution NMR Studies of Encapsulated Proteins in Liquid Ethane. Journal of the American Chemical Society, 2005, 127, 10176-10177.	6.6	33
77	Changes in Calmodulin Main-Chain Dynamics upon Ligand Binding Revealed by Cross-Correlated NMR Relaxation Measurements. Journal of the American Chemical Society, 2005, 127, 828-829.	6.6	40
78	Backbone and Side Chain Dynamics of Mutant Calmodulinâˆ’Peptide Complexes. Biochemistry, 2005, 44, 12627-12639.	1.2	29
79	New Reverse Micelle Surfactant Systems Optimized for High-Resolution NMR Spectroscopy of Encapsulated Proteins. Langmuir, 2005, 21, 10632-10637.	1.6	24
80	Self-contained high-pressure cell, apparatus, and procedure for the preparation of encapsulated proteins dissolved in low viscosity fluids for nuclear magnetic resonance spectroscopy. Review of Scientific Instruments, 2005, 76, 094101.	0.6	172
81	Direct access to the cooperative substructure of proteins and the protein ensemble via cold denaturation. Nature Structural and Molecular Biology, 2004, 11, 352-357.	3.6	134
82	Forced Folding and Structural Analysis of Metastable Proteins. Journal of the American Chemical Society, 2004, 126, 9498-9499.	6.6	65
83	Improved side-chain prediction accuracy using an ab initio potential energy function and a very large rotamer library. Protein Science, 2004, 13, 735-751.	3.1	85
84	Preparation, characterization, and NMR spectroscopy of encapsulated proteins dissolved in low viscosity fluids. Journal of Biomolecular NMR, 2003, 25, 313-323.	1.6	30
85	Backbone and side-chain heteronuclear resonance assignments and hyperfine NMR shifts in horse cytochromec. Protein Science, 2003, 12, 2104-2108.	3.1	25
86	Dynamics and Entropy of a Calmodulinâˆ’Peptide Complex Studied by NMR and Molecular Dynamicsâ€. Biochemistry, 2003, 42, 562-570.	1.2	61
87	A Direct Test of the Reductionist Approach to Structural Studies of Calmodulin Activity. Journal of Biological Chemistry, 2002, 277, 16351-16354.	1.6	43
88	NMR Spectroscopy of Encapsulated Proteins Dissolved in Low Viscosity Fluids. , 2002, , 121-160.		4
89	Temperature Dependence of the Internal Dynamics of a Calmodulinâˆ’Peptide Complex. Biochemistry, 2002, 41, 13814-13825.	1.2	88
90	A simple and effective NMR cell for studies of encapsulated proteins dissolved in low viscosity solvents. Journal of Biomolecular NMR, 2002, 23, 311-316.	1.6	24

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91	Main Chain and Side Chain Dynamics of a Heme Protein:Â15N and2H NMR Relaxation Studies ofR.capsulatusFerrocytochromec2â€. Biochemistry, 2001, 40, 6559-6569.	1.2	42
92	Validation of Protein Structure from Preparations of Encapsulated Proteins Dissolved in Low Viscosity Fluids. Journal of the American Chemical Society, 2001, 123, 2691-2692.	6.6	72
93	Hydrophobic Modulation of Heme Properties in Heme Protein Maquettesâ€. Biochemistry, 2001, 40, 10550-10561.	1.2	42
94	Dynamics of a De Novo Designed Three-Helix Bundle Protein Studied by15N,13C, and2H NMR Relaxation Methodsâ€. Biochemistry, 2001, 40, 9560-9569.	1.2	44
95	Main Chain and Side Chain Dynamics of Oxidized Flavodoxin fromCyanobacterium anabaenaâ€. Biochemistry, 2001, 40, 14744-14753.	1.2	38
96	Dynamic activation of protein function: a view emerging from NMR spectroscopy. Nature Structural Biology, 2001, 8, 926-931.	9.7	277
97	High-Resolution Nuclear Magnetic Resonance of Encapsulated Proteins Dissolved in Low Viscosity Fluids. Methods in Enzymology, 2001, 339, 54-70.	0.4	19
98	Microscopic origins of entropy, heat capacity and the glass transition in proteins. Nature, 2001, 411, 501-504.	13.7	292
99	On the Dynamic Origins of Allosteric Activation. Science, 2001, 293, 1395a-1395.	6.0	23
100	Redistribution and loss of side chain entropy upon formation of a calmodulin-peptide complex. Nature Structural Biology, 2000, 7, 72-77.	9.7	282
101	Optimal Use of Cryogenic Probe Technology in NMR Studies of Proteins. Journal of the American Chemical Society, 2000, 122, 4823-4824.	6.6	78
102	Assessing potential bias in the determination of rotational correlation times of proteins by NMR relaxation. , 1999, 13, 101-112.		69
103	Preparation of encapsulated proteins dissolved in low viscosity fluids. Journal of Biomolecular NMR, 1999, 14, 75-78.	1.6	32
104	Comparison of 2H and 13C NMR Relaxation Techniques for the Study of Protein Methyl Group Dynamics in Solution. Journal of the American Chemical Society, 1999, 121, 2891-2902.	6.6	111
105	Sequence-specific resonance assignments for a designed four-alpha-helix bundle protein. Journal of Biomolecular NMR, 1998, 11, 227-228.	1.6	12
106	Local Stability and Dynamics of Apocytochrome b562 Examined by the Dependence of Hydrogen Exchange on Hydrostatic Pressure,. Biochemistry, 1998, 37, 9877-9883.	1.2	116
107	Local Dynamics and Stability of Apocytochrome b562 Examined by Hydrogen Exchange. Biochemistry, 1998, 37, 3687-3698.	1.2	93
108	The Reorganization Energy of Cytochrome c Revisited. Journal of Physical Chemistry B, 1997, 101, 825-836.	1.2	220

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109	Improved labeling strategy for 13C relaxation measurements of methyl groups in proteins. Journal of Biomolecular NMR, 1997, 9, 437-440.	1.6	55
110	Solution Structure of Horse Heart Ferricytochromecand Detection of Redox-Related Structural Changes by High-Resolution1H NMRâ€,â€¡. Biochemistry, 1996, 35, 12275-12286.	1.2	135
111	High-Resolution Triple-Resonance NMR Spectroscopy of a Novel CalmodulinÂ·Peptide Complex at Kilobar Pressures. Journal of the American Chemical Society, 1996, 118, 11329-11330.	6.6	62
112	Internal Dynamics of Human Ubiquitin Revealed by 13C-Relaxation Studies of Randomly Fractionally Labeled Protein. Biochemistry, 1996, 35, 6116-6125.	1.2	157
113	Molecular Recognition by Calmodulin:â€‰ Pressure-Induced Reorganization of a Novel Calmodulinâ˜Peptide Complex. Biochemistry, 1996, 35, 1599-1605.	1.2	14
114	Insights into the local residual entropy of proteins provided by NMR relaxation. Protein Science, 1996, 5, 2647-2650.	3.1	225
115	Design and synthesis of multi-haem proteins. Nature, 1994, 368, 425-432.	13.7	592
116	Calmodulin interacts with amphiphilic peptides composed of all D-amino acids. Nature, 1994, 368, 651-653.	13.7	70
117	Solution structure of apocytochrome b562. Nature Structural and Molecular Biology, 1994, 1, 30-35.	3.6	119
118	Structural water in oxidized and reduced horse heart cytochrome c. Nature Structural and Molecular Biology, 1994, 1, 378-382.	3.6	58
119	Fast internal main-chain dynamics of human ubiquitin. Biochemistry, 1992, 31, 3645-3652.	1.2	177
120	Assignment of the backbone proton and nitrogen-15 NMR resonances of bacteriophage T4 lysozyme. Biochemistry, 1990, 29, 6341-6362.	1.2	92
121	Structural characterization of the interactions between calmodulin and skeletal muscle myosin light chain kinase: effect of peptide (576-594)G binding on the calcium-binding domains. Biochemistry, 1989, 28, 4011-4020.	1.2	48
122	Proton resonance assignments of horse ferricytochrome c. Biochemistry, 1989, 28, 195-203.	1.2	130
123	Proton resonance assignments of horse ferrocytochrome c. Biochemistry, 1989, 28, 186-194.	1.2	133
124	Model-independent and model-dependent analysis of the global and internal dynamics of cyclosporin A. Journal of the American Chemical Society, 1989, 111, 4571-4578.	6.6	137
125	Two-dimensional proton NMR studies of cytochrome c: hydrogen exchange in the N-terminal helix. Biochemistry, 1986, 25, 1107-1114.	1.2	142