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List of Publications by Year in Descending Order

123 papers	7,527 citations	45 h-index	85 g-index
129 ext. papers	8,065 ext. citations	9.4 avg, IF	6.06 L-index

#	Paper	IF	Citations
123	The Molecular Basis for Life in Extreme Environments. *Annual Review of Biophysics*, **2021**, 50, 343-372	21.1	9
122	Using biochemistry and biophysics to extinguish androgen receptor signaling in prostate cancer. *Journal of Biological Chemistry*, **2021**, 296, 100240	5.4	6
121	Self-Masked Aldehyde Inhibitors: A Novel Strategy for Inhibiting Cysteine Proteases. *Journal of Medicinal Chemistry*, **2021**, 64, 11267-11287	8.3	3
120	Membrane Proteins Have Distinct Fast Internal Motion and Residual Conformational Entropy. *Angewandte Chemie*, **2020**, 132, 11201-11207	3.6	3
119	Membrane Proteins Have Distinct Fast Internal Motion and Residual Conformational Entropy. *Angewandte Chemie - International Edition*, **2020**, 59, 11108-11114	16.4	9
118	Protein conformational entropy is not slaved to water. *Scientific Reports*, **2020**, 10, 17587	4.9	1
117	Extending the Detection Limit in Fragment Screening of Proteins Using Reverse Micelle Encapsulation. *ACS Chemical Biology*, **2019**, 14, 2224-2232	4.9	5
116	Site-Resolved and Quantitative Characterization of Very Weak Protein-Ligand Interactions. *ACS Chemical Biology*, **2019**, 14, 1398-1402	4.9	3
115	Reverse Micelle Encapsulation of Proteins for NMR Spectroscopy. *Methods in Enzymology*, **2019**, 615, 43-75	1.7	7
114	Characterizing Protein Hydration Dynamics Using Solution NMR Spectroscopy. *Methods in Enzymology*, **2019**, 615, 77-101	1.7	10
113	Water loading driven size, shape, and composition of cetyltrimethylammonium/hexanol/pentane reverse micelles. *Journal of Colloid and Interface Science*, **2019**, 540, 207-217	9.3	10
112	Characterization of Internal Protein Dynamics and Conformational Entropy by NMR Relaxation. *Methods in Enzymology*, **2019**, 615, 237-284	1.7	13
111	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	11.5	36
110	Measuring Entropy in Molecular Recognition by Proteins. *Annual Review of Biophysics*, **2018**, 47, 41-61	21.1	45
109	Improving yields of deuterated, methyl labeled protein by growing in HO. *Journal of Biomolecular NMR*, **2018**, 71, 263-273	3	11
108	Practical aspects of high-pressure NMR spectroscopy and its applications in protein biophysics and structural biology. *Methods*, **2018**, 148, 67-80	4.6	23
107	Solution NMR investigation of the response of the lactose repressor core domain dimer to hydrostatic pressure. *Biophysical Chemistry*, **2017**, 231, 39-44	3.5	6

106	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	11.5	7
105	Entropy in molecular recognition by proteins. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 6563-6568	11.5	96
104	On the ability of molecular dynamics force fields to recapitulate NMR derived protein side chain order parameters. *Protein Science*, **2016**, 25, 1156-60	6.3	20
103	Characterization of Cetyltrimethylammonium Bromide/Hexanol Reverse Micelles by Experimentally Benchmarked Molecular Dynamics Simulations. *Langmuir*, **2016**, 32, 1674-84	4	20
102	Optimized expression and purification of biophysical quantities of Lac repressor and Lac repressor regulatory domain. *Protein Expression and Purification*, **2016**, 123, 75-82	2	4
101	The unusual internal motion of the villin headpiece subdomain. *Protein Science*, **2016**, 25, 423-32	6.3	4
100	Accurate determination of rates from non-uniformly sampled relaxation data. *Journal of Biomolecular NMR*, **2016**, 65, 157-170	3	13
99	Design Principles for SuCESsFul Biosensors: Specific Fluorophore/Analyte Binding and Minimization of Fluorophore/Scaffold Interactions. *Journal of Molecular Biology*, **2016**, 428, 4228-4241	6.5	8
98	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	11.5	4
97	A sharp thermal transition of fast aromatic-ring dynamics in ubiquitin. *Angewandte Chemie - International Edition*, **2015**, 54, 102-7	16.4	22
96	On the relationship between NMR-derived amide order parameters and protein backbone entropy changes. *Proteins: Structure, Function and Bioinformatics*, **2015**, 83, 922-30	4.2	46
95	Biophysics: Enzymes surf the heat wave. *Nature*, **2015**, 517, 149-50	50.4	4
94	A Sharp Thermal Transition of Fast Aromatic-Ring Dynamics in Ubiquitin. *Angewandte Chemie*, **2015**, 127, 104-109	3.6	
93	Defining the Apoptotic Trigger: THE INTERACTION OF CYTOCHROME c AND CARDIOLIPIN. *Journal of Biological Chemistry*, **2015**, 290, 30879-87	5.4	48
92	Reverse micelles as a platform for dynamic nuclear polarization in solution NMR of proteins. *Journal of the American Chemical Society*, **2014**, 136, 2800-7	16.4	18
91	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, 3465-74	16.4	45
90	Measurement and control of pH in the aqueous interior of reverse micelles. *Journal of Physical Chemistry B*, **2014**, 118, 2020-31	3.4	26
89	Dynamic and thermodynamic response of the Ras protein Cdc42Hs upon association with the effector domain of PAK3. *Journal of Molecular Biology*, **2014**, 426, 3520-38	6.5	7

88	Banding of NMR-derived methyl order parameters: implications for protein dynamics. *Proteins: Structure, Function and Bioinformatics*, **2014**, 82, 2106-17	4.2	12
87	High-resolution NMR spectroscopy of encapsulated proteins dissolved in low-viscosity fluids. *Journal of Magnetic Resonance*, **2014**, 241, 137-47	3	34
86	Role of cavities and hydration in the pressure unfolding of T4 lysozyme. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 13846-51	11.5	58
85	Partial alignment and measurement of residual dipolar couplings of proteins under high hydrostatic pressure. *Journal of Biomolecular NMR*, **2013**, 56, 353-7	3	12
84	Elementary tetrahelical protein design for diverse oxidoreductase functions. *Nature Chemical Biology*, **2013**, 9, 826-833	11.7	104
83	Microscopic insights into the NMR relaxation-based protein conformational entropy meter. *Journal of the American Chemical Society*, **2013**, 135, 15092-100	16.4	105
82	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	8.1	133
81	A surprising role for conformational entropy in protein function. *Topics in Current Chemistry*, **2013**, 337, 69-94		26
80	A 13C labeling strategy reveals a range of aromatic side chain motion in calmodulin. *Journal of the American Chemical Society*, **2013**, 135, 9560-3	16.4	38
79	Al NMR: a novel NMR data processing program optimized for sparse sampling. *Journal of Biomolecular NMR*, **2012**, 52, 79-89	3	7
78	The dynamical response of hen egg white lysozyme to the binding of a carbohydrate ligand. *Protein Science*, **2012**, 21, 1066-73	6.3	24
77	Coupled motion in proteins revealed by pressure perturbation. *Journal of the American Chemical Society*, **2012**, 134, 8543-50	16.4	83
76	Site-resolved measurement of water-protein interactions by solution NMR. *Nature Structural and Molecular Biology*, **2011**, 18, 245-9	17.6	178
75	Modification of encapsulation pressure of reverse micelles in liquid ethane. *Journal of Magnetic Resonance*, **2011**, 212, 229-33	3	11
74	Optimized linear prediction for radial sampled multidimensional NMR experiments. *Journal of Magnetic Resonance*, **2011**, 212, 240-4	3	
73	Optimization of NMR spectroscopy of encapsulated proteins dissolved in low viscosity fluids. *Journal of Biomolecular NMR*, **2011**, 50, 421-30	3	18
72	Mapping the hydration dynamics of ubiquitin. *Journal of the American Chemical Society*, **2011**, 133, 12326-9	16.4	96
71	The role of conformational entropy in molecular recognition by calmodulin. *Nature Chemical Biology*, **2010**, 6, 352-8	11.7	209

70	A method for solution NMR structural studies of large integral membrane proteins: reverse micelle encapsulation. *Biochimica Et Biophysica Acta - Biomembranes*, **2010**, 1798, 150-60	3.8	26
69	Reverse micelle encapsulation of membrane-anchored proteins for solution NMR studies. *Structure*, **2010**, 18, 9-16	5.2	41
68	SEnD NMR: sensitivity enhanced n-dimensional NMR. *Journal of Magnetic Resonance*, **2010**, 202, 250-8	3	2
67	Reverse micelles in integral membrane protein structural biology by solution NMR spectroscopy. *Structure*, **2009**, 17, 345-51	5.2	33
66	AMORE-HX: a multidimensional optimization of radial enhanced NMR-sampled hydrogen exchange. *Journal of Biomolecular NMR*, **2009**, 45, 233-9	3	7
65	Fast structural dynamics in reduced and oxidized cytochrome c. *Protein Science*, **2009**, 18, 670-4	6.3	14
64	Re-evaluation of the model-free analysis of fast internal motion in proteins using NMR relaxation. *Journal of Physical Chemistry B*, **2008**, 112, 12095-103	3.4	20
63	Optimized angle selection for radial sampled NMR experiments. *Journal of Magnetic Resonance*, **2008**, 195, 169-78	3	6
62	Conformational entropy in molecular recognition by proteins. *FASEB Journal*, **2008**, 22, 528.3	0.9	
61	NMR Structure of a Disulfide-Crosslinked Ib3 Cytoplasmic Domain Heterodimer. *Blood*, **2008**, 112, 2866-2866	2.2	
60	Temperature dependence of fast dynamics in proteins. *Biophysical Journal*, **2007**, 92, L43-5	2.9	35
59	Phasing arbitrarily sampled multidimensional NMR data. *Journal of Magnetic Resonance*, **2007**, 187, 363-70	3	5
58	Conformational entropy in molecular recognition by proteins. *Nature*, **2007**, 448, 325-9	50.4	526
57	Characterization of the fast dynamics of protein amino acid side chains using NMR relaxation in solution. *Chemical Reviews*, **2006**, 106, 1672-99	68.1	270
56	Cold denaturation of encapsulated ubiquitin. *Journal of the American Chemical Society*, **2006**, 128, 10652-3	16.4	37
55	Magnetic susceptibility-induced alignment of proteins in reverse micelles. *Journal of the American Chemical Society*, **2006**, 128, 15930-1	16.4	14
54	Conformational dynamics of calmodulin in complex with the calmodulin-dependent kinase kinase alpha calmodulin-binding domain. *Biochemistry*, **2006**, 45, 8732-41	3.2	27
53	Characterization of the backbone and side chain dynamics of the CaM-CaMKIp complex reveals microscopic contributions to protein conformational entropy. *Biochemistry*, **2006**, 45, 9841-8	3.2	26

52	High-resolution NMR studies of encapsulated proteins in liquid ethane. *Journal of the American Chemical Society*, **2005**, 127, 10176-7	16.4	32
51	Changes in calmodulin main-chain dynamics upon ligand binding revealed by cross-correlated NMR relaxation measurements. *Journal of the American Chemical Society*, **2005**, 127, 828-9	16.4	37
50	Backbone and side chain dynamics of mutant calmodulin-peptide complexes. *Biochemistry*, **2005**, 44, 12627-39	3.2	27
49	New reverse micelle surfactant systems optimized for high-resolution NMR spectroscopy of encapsulated proteins. *Langmuir*, **2005**, 21, 10632-7	4	24
48	Self contained high pressure cell, apparatus and procedure for the preparation of encapsulated proteins dissolved in low viscosity fluids for NMR spectroscopy. *Review of Scientific Instruments*, **2005**, 76, 1-7	1.7	132
47	NMR spectroscopy of proteins encapsulated in a positively charged surfactant. *Journal of Magnetic Resonance*, **2005**, 175, 158-62	3	31
46	Novel surfactant mixtures for NMR spectroscopy of encapsulated proteins dissolved in low-viscosity fluids. *Protein Science*, **2005**, 14, 2919-21	6.3	27
45	Direct access to the cooperative substructure of proteins and the protein ensemble via cold denaturation. *Nature Structural and Molecular Biology*, **2004**, 11, 352-7	17.6	125
44	Forced folding and structural analysis of metastable proteins. *Journal of the American Chemical Society*, **2004**, 126, 9498-9	16.4	64
43	Improved side-chain prediction accuracy using an ab initio potential energy function and a very large rotamer library. *Protein Science*, **2004**, 13, 735-51	6.3	75
42	Preparation, characterization, and NMR spectroscopy of encapsulated proteins dissolved in low viscosity fluids. *Journal of Biomolecular NMR*, **2003**, 25, 313-23	3	28
41	Backbone and side-chain heteronuclear resonance assignments and hyperfine NMR shifts in horse cytochrome c. *Protein Science*, **2003**, 12, 2104-8	6.3	25
40	Dynamics and entropy of a calmodulin-peptide complex studied by NMR and molecular dynamics. *Biochemistry*, **2003**, 42, 562-70	3.2	59
39	A simple and effective NMR cell for studies of encapsulated proteins dissolved in low viscosity solvents. *Journal of Biomolecular NMR*, **2002**, 23, 311-6	3	23
38	A direct test of the reductionist approach to structural studies of calmodulin activity: relevance of peptide models of target proteins. *Journal of Biological Chemistry*, **2002**, 277, 16351-4	5.4	43
37	NMR Spectroscopy of Encapsulated Proteins Dissolved in Low Viscosity Fluids **2002**, 121-160		4
36	Temperature dependence of the internal dynamics of a calmodulin-peptide complex. *Biochemistry*, **2002**, 41, 13814-25	3.2	83
35	High-resolution nuclear magnetic resonance of encapsulated proteins dissolved in low viscosity fluids. *Methods in Enzymology*, **2001**, 339, 54-70	1.7	15

34	Microscopic origins of entropy, heat capacity and the glass transition in proteins. *Nature*, **2001**, 411, 501-4	30.4	273
33	On the dynamic origins of allosteric activation. *Science*, **2001**, 293, 1395	33.3	19
32	Main chain and side chain dynamics of a heme protein: 15N and 2H NMR relaxation studies of R. capsulatus ferrocytochrome c2. *Biochemistry*, **2001**, 40, 6559-69	3.2	40
31	Validation of protein structure from preparations of encapsulated proteins dissolved in low viscosity fluids. *Journal of the American Chemical Society*, **2001**, 123, 2691-2	16.4	68
30	Hydrophobic modulation of heme properties in heme protein maquettes. *Biochemistry*, **2001**, 40, 10550-61	3.2	41
29	Dynamics of a de novo designed three-helix bundle protein studied by 15N, 13C, and 2H NMR relaxation methods. *Biochemistry*, **2001**, 40, 9560-9	3.2	42
28	Main chain and side chain dynamics of oxidized flavodoxin from Cyanobacterium anabaena. *Biochemistry*, **2001**, 40, 14744-53	3.2	35
27	Dynamic activation of protein function: a view emerging from NMR spectroscopy. *Nature Structural Biology*, **2001**, 8, 926-31		253
26	Redistribution and loss of side chain entropy upon formation of a calmodulin-peptide complex. *Nature Structural Biology*, **2000**, 7, 72-7		255
25	Optimal Use of Cryogenic Probe Technology in NMR Studies of Proteins. *Journal of the American Chemical Society*, **2000**, 122, 4823-4824	16.4	74
24	Assessing potential bias in the determination of rotational correlation times of proteins by NMR relaxation. *Journal of Biomolecular NMR*, **1999**, 13, 101-12	3	64
23	Preparation of encapsulated proteins dissolved in low viscosity fluids. *Journal of Biomolecular NMR*, **1999**, 14, 75-8	3	30
22	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	16.4	97
21	Sequence-specific resonance assignments for a designed four-alpha-helix bundle protein. *Journal of Biomolecular NMR*, **1998**, 11, 227-8	3	12
20	Local stability and dynamics of apocytochrome b562 examined by the dependence of hydrogen exchange on hydrostatic pressure. *Biochemistry*, **1998**, 37, 9877-83	3.2	111
19	Local dynamics and stability of apocytochrome b562 examined by hydrogen exchange. *Biochemistry* , **1998**, 37, 3687-98	3.2	89
18	The Reorganization Energy of Cytochrome c Revisited. *Journal of Physical Chemistry B*, **1997**, 101, 825-836	3.4	213
17	Improved labeling strategy for 13C relaxation measurements of methyl groups in proteins. *Journal of Biomolecular NMR*, **1997**, 9, 437-40	3	52

16	Solution structure of horse heart ferricytochrome c and detection of redox-related structural changes by high-resolution 1H NMR. *Biochemistry*, **1996**, 35, 12275-86	3.2	123
15	High-Resolution Triple-Resonance NMR Spectroscopy of a Novel Calmodulin Peptide Complex at Kilobar Pressures. *Journal of the American Chemical Society*, **1996**, 118, 11329-11330	16.4	58
14	Internal dynamics of human ubiquitin revealed by 13C-relaxation studies of randomly fractionally labeled protein. *Biochemistry*, **1996**, 35, 6116-25	3.2	153
13	Molecular recognition by calmodulin: pressure-induced reorganization of a novel calmodulin-peptide complex. *Biochemistry*, **1996**, 35, 1599-605	3.2	13
12	Insights into the local residual entropy of proteins provided by NMR relaxation. *Protein Science*, **1996**, 5, 2647-50	6.3	202
11	Design and synthesis of multi-haem proteins. *Nature*, **1994**, 368, 425-32	50.4	535
10	Calmodulin interacts with amphiphilic peptides composed of all D-amino acids. *Nature*, **1994**, 368, 651-3	50.4	61
9	Solution structure of apocytochrome b562. *Nature Structural and Molecular Biology*, **1994**, 1, 30-5	17.6	109
8	Structural water in oxidized and reduced horse heart cytochrome c. *Nature Structural and Molecular Biology*, **1994**, 1, 378-82	17.6	53
7	Fast internal main-chain dynamics of human ubiquitin. *Biochemistry*, **1992**, 31, 3645-52	3.2	167
6	Assignment of the backbone 1H and 15N NMR resonances of bacteriophage T4 lysozyme. *Biochemistry*, **1990**, 29, 6341-62	3.2	87
5	Structural characterization of the interactions between calmodulin and skeletal muscle myosin light chain kinase: effect of peptide (576-594)G binding on the Ca2+-binding domains. *Biochemistry*, **1989**, 28, 4011-20	3.2	43
4	Proton resonance assignments of horse ferricytochrome c. *Biochemistry*, **1989**, 28, 195-203	3.2	125
3	Proton resonance assignments of horse ferrocytochrome c. *Biochemistry*, **1989**, 28, 186-94	3.2	103
2	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	16.4	122
1	Two-dimensional 1H NMR studies of cytochrome c: hydrogen exchange in the N-terminal helix. *Biochemistry*, **1986**, 25, 1107-14	3.2	122