

Mikael Akke

List of Publications by Year in descending order

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108
papers

7,653
citations

61984

43
h-index

53230

85
g-index

132
all docs

132
docs citations

132
times ranked

5910
citing authors

#	ARTICLE	IF	CITATIONS
1	Backbone Dynamics of Escherichia coli Ribonuclease H: Correlations with Structure and Function in an Active Enzyme. <i>Journal of Molecular Biology</i> , 1995, 246, 144-163.	4.2	948
2	Enzyme Dynamics During Catalysis. <i>Science</i> , 2002, 295, 1520-1523.	12.6	688
3	NMR order parameters and free energy: an analytical approach and its application to cooperative calcium(2+) binding by calbindin D9k. <i>Journal of the American Chemical Society</i> , 1993, 115, 9832-9833.	13.7	347
4	Monitoring Macromolecular Motions on Microsecond to Millisecond Time Scales by R_1/ρ_1 Constant Relaxation Time NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 1996, 118, 911-912.	13.7	273
5	Backbone dynamics of calcium-loaded calbindin D9k studied by two-dimensional proton-detected nitrogen-15 NMR spectroscopy. <i>Biochemistry</i> , 1992, 31, 4856-4866.	2.5	210
6	Protein Flexibility and Conformational Entropy in Ligand Design Targeting the Carbohydrate Recognition Domain of Galectin-3. <i>Journal of the American Chemical Society</i> , 2010, 132, 14577-14589.	13.7	209
7	Dynamics of Ribonuclease H: Temperature Dependence of Motions on Multiple Time Scales. <i>Biochemistry</i> , 1996, 35, 16009-16023.	2.5	195
8	Effects of ion binding on the backbone dynamics of calbindin D9k determined by nitrogen-15 NMR relaxation. <i>Biochemistry</i> , 1993, 32, 9832-9844.	2.5	184
9	The structure of calyculin reveals a novel homodimeric fold for S100 Ca ²⁺ -binding proteins. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 790-796.	8.2	180
10	Practical Aspects of Two-Dimensional Proton-Detected ¹⁵ N Spin Relaxation Measurements. <i>Journal of Magnetic Resonance Series B</i> , 1993, 102, 253-264.	1.6	162
11	Fractional ¹³ C enrichment of isolated carbons using [1- ¹³ C]- or [2- ¹³ C]-glucose facilitates the accurate measurement of dynamics at backbone C α and side-chain methyl positions in proteins. <i>Journal of Biomolecular NMR</i> , 2007, 38, 199-212.	2.8	160
12	Signal transduction versus buffering activity in Ca ²⁺ -binding proteins. <i>Nature Structural and Molecular Biology</i> , 1994, 1, 239-245.	8.2	152
13	Structural dynamics in the C-terminal domain of calmodulin at low calcium levels 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1999, 293, 883-899.	4.2	148
14	From snapshot to movie: phi analysis of protein folding transition states taken one step further. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 14854-14859.	7.1	145
15	The Carbohydrate-Binding Site in Galectin-3 Is Preorganized To Recognize a Sugarlike Framework of Oxygens: Ultra-High-Resolution Structures and Water Dynamics. <i>Biochemistry</i> , 2012, 51, 296-306.	2.5	137
16	Backbone dynamics and energetics of a Calmodulin domain mutant exchanging between closed and open conformations. <i>Journal of Molecular Biology</i> , 1999, 289, 603-617.	4.2	122
17	NMR methods for characterizing microsecond to millisecond dynamics in recognition and catalysis. <i>Current Opinion in Structural Biology</i> , 2002, 12, 642-647.	5.7	120
18	The Ribosomal Stalk Binds to Translation Factors IF2, EF-Tu, EF-G and RF3 via a Conserved Region of the L12 C-terminal Domain. <i>Journal of Molecular Biology</i> , 2007, 365, 468-479.	4.2	114

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19	Calbindin D28k Exhibits Properties Characteristic of a Ca ²⁺ Sensor. <i>Journal of Biological Chemistry</i> , 2002, 277, 16662-16672.	3.4	113
20	High-resolution Solution Structure of Calcium-loaded Calbindin D9k. <i>Journal of Molecular Biology</i> , 1993, 231, 711-734.	4.2	112
21	Pervasive conformational fluctuations on microsecond time scales in a fibronectin type III domain. <i>Nature Structural Biology</i> , 1998, 5, 55-59.	9.7	105
22	Protein stability and electrostatic interactions between solvent exposed charged side chains. <i>Proteins: Structure, Function and Bioinformatics</i> , 1990, 8, 23-29.	2.6	98
23	Interplay between Conformational Entropy and Solvation Entropy in Protein-Ligand Binding. <i>Journal of the American Chemical Society</i> , 2019, 141, 2012-2026.	13.7	89
24	Dynamics of the Transition between Open and Closed Conformations in a Calmodulin C-Terminal Domain Mutant. <i>Structure</i> , 2001, 9, 185-195.	3.3	88
25	Biosynthetic ¹³ C Labeling of Aromatic Side Chains in Proteins for NMR Relaxation Measurements. <i>Journal of the American Chemical Society</i> , 2006, 128, 2506-2507.	13.7	76
26	Systematic Tuning of Fluoro-galectin-3 Interactions Provides Thiodigalactoside Derivatives with Single-Digit nM Affinity and High Selectivity. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 1164-1175.	6.4	76
27	Molecular basis for co-operativity in Ca ²⁺ binding to calbindin D9k. <i>Journal of Molecular Biology</i> , 1991, 220, 173-189.	4.2	75
28	Conformational entropy changes upon lactose binding to the carbohydrate recognition domain of galectin-3. <i>Journal of Biomolecular NMR</i> , 2009, 45, 157-169.	2.8	75
29	Transient structural distortion of metal-free Cu/Zn superoxide dismutase triggers aberrant oligomerization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 18273-18278.	7.1	74
30	Conformation and Dynamics of Ribosomal Stalk Protein L12 in Solution and on the Ribosome. <i>Biochemistry</i> , 2004, 43, 5930-5936.	2.5	71
31	Base dynamics in a UUCG tetraloop RNA hairpin characterized by ¹⁵ N spin relaxation: correlations with structure and stability. <i>Rna</i> , 1997, 3, 702-9.	3.5	70
32	Solution Structure of (Cd ²⁺) ₁ -calbindin D9k Reveals Details of the Stepwise Structural Changes along the Apo → (Ca ²⁺) ₁ → (Ca ²⁺) ₂ Binding Pathway. <i>Journal of Molecular Biology</i> , 1995, 252, 102-121.	4.2	68
33	Nuclear magnetic resonance studies of the internal dynamics in apo, (Cd ²⁺) ₁ and (Ca ²⁺) ₂ Calbindin D9k. <i>Journal of Molecular Biology</i> , 1992, 227, 1100-1117.	4.2	67
34	Characterization of Chemical Exchange Using Residual Dipolar Coupling. <i>Journal of the American Chemical Society</i> , 2007, 129, 13396-13397.	13.7	67
35	Structure and Dynamics of Ribosomal Protein L12: An Ensemble Model Based on SAXS and NMR Relaxation. <i>Biophysical Journal</i> , 2010, 98, 2374-2382.	0.5	67
36	Conformational dynamics and thermodynamics of protein-ligand binding studied by NMR relaxation. <i>Biochemical Society Transactions</i> , 2012, 40, 419-423.	3.4	60

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37	Functional Dynamics of Human FKBP12 Revealed by Methyl ¹³ C Rotating Frame Relaxation Dispersion NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2006, 128, 5718-5727.	13.7	58
38	Local Cooperativity in an Amyloidogenic State of Human Lysozyme Observed at Atomic Resolution. <i>Journal of the American Chemical Society</i> , 2010, 132, 15580-15588.	13.7	55
39	Three-dimensional solution structure of calcium-loaded porcine calbindin D9k determined by nuclear magnetic resonance spectroscopy. <i>Biochemistry</i> , 1992, 31, 1011-1020.	2.5	54
40	Computational design of a leucine-rich repeat protein with a predefined geometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17875-17880.	7.1	53
41	Ring Flips Revisited: ¹³ C Relaxation Dispersion Measurements of Aromatic Side Chain Dynamics and Activation Barriers in Basic Pancreatic Trypsin Inhibitor. <i>Biochemistry</i> , 2014, 53, 4519-4525.	2.5	52
42	Conserved S/T Residues of the Human Chaperone DNAJB6 Are Required for Effective Inhibition of A ^β 242 Amyloid Fibril Formation. <i>Biochemistry</i> , 2018, 57, 4891-4902.	2.5	52
43	Intramolecular Dynamics of Low Molecular Weight Protein Tyrosine Phosphatase in Monomer-Dimer Equilibrium Studied by NMR: A Model for Changes in Dynamics upon Target Binding. <i>Journal of Molecular Biology</i> , 2002, 322, 137-152.	4.2	49
44	Correlated dynamics of consecutive residues reveal transient and cooperative unfolding of secondary structure in proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 16984-16989.	7.1	47
45	Sequence and Context Dependence of EF-Hand Loop Dynamics. An ¹⁵ N Relaxation Study of a Calcium-Binding Site Mutant of Calbindin D9k. <i>Biochemistry</i> , 1998, 37, 2586-2595.	2.5	41
46	May the driving force be with you—whatever it is. , 2000, 7, 11-13.		41
47	Conformational exchange of aromatic side chains characterized by L-optimized TROSY-selected ¹³ C CPMG relaxation dispersion. <i>Journal of Biomolecular NMR</i> , 2012, 54, 9-14.	2.8	40
48	Carbonyl ¹³ C transverse relaxation measurements to sample protein backbone dynamics. <i>Magnetic Resonance in Chemistry</i> , 2003, 41, 853-865.	1.9	39
49	Combined Use of NMR Relaxation Measurements and Hydrodynamic Calculations To Study Protein Association. Evidence for Tetramers of Low Molecular Weight Protein Tyrosine Phosphatase in Solution. <i>Journal of the American Chemical Society</i> , 2003, 125, 916-923.	13.7	38
50	Starting-Condition Dependence of Order Parameters Derived from Molecular Dynamics Simulations. <i>Journal of Chemical Theory and Computation</i> , 2010, 6, 2176-2190.	5.3	38
51	Multiple-Timescale Dynamics of Side-Chain Carboxyl and Carbonyl Groups in Proteins by ¹³ C Nuclear Spin Relaxation. <i>Journal of the American Chemical Society</i> , 2008, 130, 15805-15807.	13.7	37
52	Ultrastructural evidence for self-replication of Alzheimer-associated A ^β 242 amyloid along the sides of fibrils. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 11265-11273.	7.1	37
53	A De Novo Designed Coiled-Coil Peptide with a Reversible pH-Induced Oligomerization Switch. <i>Structure</i> , 2016, 24, 946-955.	3.3	36
54	Differential Responses of the Backbone and Side-Chain Conformational Dynamics in FKBP12 upon Binding the Transition-State Analog FK506: Implications for Transition-State Stabilization and Target Protein Recognition. <i>Journal of Molecular Biology</i> , 2009, 387, 233-244.	4.2	35

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55	Compact oleic acid in HAMLET. FEBS Letters, 2005, 579, 6095-6100.	2.8	34
56	Off-resonance rotating-frame amide proton spin relaxation experiments measuring microsecond chemical exchange in proteins. Journal of Biomolecular NMR, 2005, 32, 163-173.	2.8	33
57	Elucidation of Hydrogen Bonding Patterns in Ligand-Free, Lactose- and Glycerol-Bound Galectin-3C by Neutron Crystallography to Guide Drug Design. Journal of Medicinal Chemistry, 2018, 61, 4412-4420.	6.4	32
58	Dynamic allosteric communication pathway directing differential activation of the glucocorticoid receptor. Science Advances, 2020, 6, eabb5277.	10.3	32
59	Conformational Entropies and Order Parameters: Convergence, Reproducibility, and Transferability. Journal of Chemical Theory and Computation, 2014, 10, 432-438.	5.3	31
60	Site-Specific Protonation Kinetics of Acidic Side Chains in Proteins Determined by pH-Dependent Carboxyl ¹³ C NMR Relaxation. Journal of the American Chemical Society, 2015, 137, 3093-3101.	13.7	31
61	Slow Aromatic Ring Flips Detected Despite Near-Degenerate NMR Frequencies of the Exchanging Nuclei. Journal of Physical Chemistry B, 2013, 117, 9241-9247.	2.6	30
62	Heteronuclear-Correlation NMR Spectroscopy with Simultaneous Isotope Filtration, Quadrature Detection, and Sensitivity Enhancement Using z Rotations. Journal of Magnetic Resonance Series B, 1994, 104, 298-302.	1.6	27
63	¹³ C relaxation experiments for aromatic side chains employing longitudinal- and transverse-relaxation optimized NMR spectroscopy. Journal of Biomolecular NMR, 2012, 53, 181-190.	2.8	26
64	Molecular insights into substrate recognition and catalytic mechanism of the chaperone and FKBP peptidyl-prolyl isomerase SlyD. BMC Biology, 2016, 14, 82.	3.8	26
65	¹⁵ N NMR assignments and chemical shift analysis of uniformly labeled ¹⁵ N calbindin D9k in the apo, (Cd ²⁺) ₁ and (Ca ²⁺) ₂ states. FEBS Letters, 1992, 303, 136-140.	2.8	25
66	Structural Characterization of the Ribosomal P1A [~] P2B Protein Dimer by Small-Angle X-ray Scattering and NMR Spectroscopy. Biochemistry, 2007, 46, 1988-1998.	2.5	25
67	Specific ¹² C ¹³ C ¹⁵ N ² D ₂ ¹² C ¹³ C ¹⁵ N ³ D ₂ S ¹³ C ¹⁵ N ^μ HD Isotopomer Labeling of Methionine To Characterize Protein Dynamics by ¹ H and ¹³ C NMR Relaxation Dispersion. Journal of the American Chemical Society, 2012, 134, 18562-18565.	13.7	25
68	Cu/Zn Superoxide Dismutase Forms Amyloid Fibrils under Near-Physiological Quiescent Conditions: The Roles of Disulfide Bonds and Effects of Denaturant. ACS Chemical Neuroscience, 2017, 8, 2019-2026.	3.5	25
69	Off-resonance rotating-frame relaxation dispersion experiment for ¹³ C in aromatic side chains using L-optimized TROSY-selection. Journal of Biomolecular NMR, 2014, 59, 23-29.	2.8	24
70	Structural model of dodecameric heat-shock protein Hsp21: Flexible N-terminal arms interact with client proteins while C-terminal tails maintain the dodecamer and chaperone activity. Journal of Biological Chemistry, 2017, 292, 8103-8121.	3.4	24
71	Quantitative Analysis of Conformational Exchange Contributions to ¹ H ¹⁵ N Multiple-Quantum Relaxation Using Field-Dependent Measurements. Time Scale and Structural Characterization of Exchange in a Calmodulin C-Terminal Domain Mutant. Journal of the American Chemical Society, 2004, 126, 928-935.	13.7	23
72	Unfolding and inactivation of cutinases by AOT and guanidine hydrochloride. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2005, 1748, 74-83.	2.3	23

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73	Microsecond Protein Dynamics Measured by ^{13}C Rotating-Frame Spin Relaxation. <i>ChemBioChem</i> , 2005, 6, 1685-1692.	2.6	23
74	Structural Analysis of a Complex between Small Ubiquitin-like Modifier 1 (SUMO1) and the ZZ Domain of CREB-binding Protein (CBP/p300) Reveals a New Interaction Surface on SUMO. <i>Journal of Biological Chemistry</i> , 2016, 291, 12658-12672.	3.4	23
75	The inverted chevron plot measured by NMR relaxation reveals a native-like unfolding intermediate in acyl-CoA binding protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6877-6882.	7.1	22
76	The Dynameomics Entropy Dictionary: A Large-Scale Assessment of Conformational Entropy across Protein Fold Space. <i>Journal of Physical Chemistry B</i> , 2017, 121, 3933-3945.	2.6	21
77	A statistical analysis of NMR spectrometer noise. <i>Journal of Magnetic Resonance</i> , 2003, 162, 176-188.	2.1	20
78	Local Unfolding and Aggregation Mechanisms of SOD1: A Monte Carlo Exploration. <i>Journal of Physical Chemistry B</i> , 2013, 117, 9194-9202.	2.6	20
79	Stability and Local Unfolding of SOD1 in the Presence of Protein Crowders. <i>Journal of Physical Chemistry B</i> , 2019, 123, 1920-1930.	2.6	20
80	Protein conformational exchange measured by ^1H $R_1\rho$ -relaxation dispersion of methyl groups. <i>Journal of Biomolecular NMR</i> , 2013, 57, 47-55.	2.8	19
81	Entropy-Entropy Compensation between the Protein, Ligand, and Solvent Degrees of Freedom Fine-Tunes Affinity in Ligand Binding to Galectin-3C. <i>Jacs Au</i> , 2021, 1, 484-500.	7.9	17
82	Transient Aggregation and Stable Dimerization Induced by Introducing an Alzheimer Sequence into a Water-Soluble Protein. <i>Biochemistry</i> , 2004, 43, 12964-12978.	2.5	16
83	Conformational Entropy of FK506 Binding to FKBP12 Determined by Nuclear Magnetic Resonance Relaxation and Molecular Dynamics Simulations. <i>Biochemistry</i> , 2018, 57, 1451-1461.	2.5	16
84	Protein loop compaction and the origin of the effect of arginine and glutamic acid mixtures on solubility, stability and transient oligomerization of proteins. <i>European Biophysics Journal</i> , 2011, 40, 1327-1338.	2.2	15
85	Designing interactions by control of protein-ligand complex conformation: tuning arginine-arene interaction geometry for enhanced electrostatic protein-ligand interactions. <i>Chemical Science</i> , 2018, 9, 1014-1021.	7.4	15
86	100% complete assignment of non-labile ^1H , ^{13}C , and ^{15}N signals for calcium-loaded calbindin D9k P43G. <i>Biomolecular NMR Assignments</i> , 2011, 5, 79-84.	0.8	14
87	pKa Values for the Unfolded State under Native Conditions Explain the pH-Dependent Stability of PGB1. <i>Biophysical Journal</i> , 2010, 99, 3365-3373.	0.5	13
88	Dynamics of Aromatic Side Chains in the Active Site of FKBP12. <i>Biochemistry</i> , 2017, 56, 334-343.	2.5	13
89	An open and shut case., 2001, 8, 910-912.		12
90	Accurate Backbone ^{13}C and ^{15}N Chemical Shift Tensors in Galectin-3 Determined by MAS NMR and QM/MM: Details of Structure and Environment Matter. <i>ChemPhysChem</i> , 2020, 21, 1436-1443.	2.1	10

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91	Structural Insights into the Calcium-Mediated Allosteric Transition in the C-Terminal Domain of Calmodulin from Nuclear Magnetic Resonance Measurements. <i>Biochemistry</i> , 2016, 55, 19-28.	2.5	9
92	Chemical Shifts of the Carbohydrate Binding Domain of Galectin-3 from Magic Angle Spinning NMR and Hybrid Quantum Mechanics/Molecular Mechanics Calculations. <i>Journal of Physical Chemistry B</i> , 2018, 122, 2931-2939.	2.6	9
93	Minute Additions of DMSO Affect Protein Dynamics Measurements by NMR Relaxation Experiments through Significant Changes in Solvent Viscosity. <i>ChemPhysChem</i> , 2019, 20, 326-332.	2.1	9
94	Rapid NMR Relaxation Measurements Using Optimal Nonuniform Sampling of Multidimensional Accordion Data Analyzed by a Sparse Reconstruction Method. <i>Journal of Physical Chemistry A</i> , 2019, 123, 5718-5723.	2.5	9
95	Structural characterization of the microbial enzyme urocanate reductase mediating imidazole propionate production. <i>Nature Communications</i> , 2021, 12, 1347.	12.8	9
96	Transition-State Compressibility and Activation Volume of Transient Protein Conformational Fluctuations. <i>Jacs Au</i> , 2021, 1, 833-842.	7.9	9
97	Out of hot water. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 912-913.	8.2	8
98	¹⁵ N NMR assignments of (Cd ²⁺) ₂ -calbindin D9k and comparison with (Ca ²⁺) ₂ -calbindin D9k. Cadmium as a substitute for calcium in calcium-binding proteins. <i>Magnetic Resonance in Chemistry</i> , 1993, 31, S128-S132.	1.9	6
99	Revealing Well-Defined Soluble States during Amyloid Fibril Formation by Multilinear Analysis of NMR Diffusion Data. <i>Journal of the American Chemical Society</i> , 2019, 141, 18649-18652.	13.7	6
100	Ca ²⁺ Binding in Proteins of the Calmodulin Superfamily: Cooperativity, Electrostatic Contributions and Molecular Mechanisms. <i>Novartis Foundation Symposium</i> , 1991, 161, 222-236.	1.1	6
101	Mapping the energy landscape of protein-ligand binding via linear free energy relationships determined by protein NMR relaxation dispersion. <i>RSC Chemical Biology</i> , 2021, 2, 259-265.	4.1	5
102	Letter to the Editor: Sequential ¹ H, ¹⁵ N and ¹³ C NMR Assignment of Human Calbindin D28k. <i>Journal of Biomolecular NMR</i> , 2004, 28, 305-306.	2.8	3
103	Backbone ¹ H, ¹³ C, and ¹⁵ N resonance assignments of the ligand binding domain of the human wildtype glucocorticoid receptor and the F602S mutant variant. <i>Biomolecular NMR Assignments</i> , 2018, 12, 263-268.	0.8	3
104	¹ H R ₁ ρ relaxation dispersion experiments in aromatic side chains. <i>Journal of Biomolecular NMR</i> , 2021, 75, 383-392.	2.8	3
105	Rotamer Jumps, Proton Exchange, and Amine Inversion Dynamics of Dimethylated Lysine Residues in Proteins Resolved by pH-Dependent ¹ H and ¹³ C NMR Relaxation Dispersion. <i>Journal of Physical Chemistry B</i> , 2019, 123, 9742-9750.	2.6	1
106	Adsorption of unfolded Cu/Zn superoxide dismutase onto hydrophobic surfaces catalyzes its formation of amyloid fibrils. <i>Protein Engineering, Design and Selection</i> , 2019, 32, 77-85.	2.1	1
107	Backbone ¹ H, ¹³ C, and ¹⁵ N resonance assignments of BoMan26A, a ¹ β-mannanase of the glycoside hydrolase family 26 from the human gut bacterium <i>Bacteroides ovatus</i> . <i>Biomolecular NMR Assignments</i> , 2019, 13, 213-218.	0.8	1
108	Rapid measurement of heteronuclear transverse relaxation rates using non-uniformly sampled ¹ H and ¹³ C NMR accordion experiments. <i>Magnetic Resonance</i> , 2021, 2, 571-587.		1