

# G Marius Clore

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9004611/publications.pdf>

Version: 2024-02-01

571  
papers

67,188  
citations

640

123  
h-index

890

242  
g-index

592  
all docs

592  
docs citations

592  
times ranked

31996  
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystallography & NMR System: A New Software Suite for Macromolecular Structure Determination. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 905-921.	2.5	14,711
2	The Xplor-NIH NMR molecular structure determination package. <i>Journal of Magnetic Resonance</i> , 2003, 160, 65-73.	1.2	2,165
3	Solution structure of a calmodulin-target peptide complex by multidimensional NMR. <i>Science</i> , 1992, 256, 632-638.	6.0	1,381
4	Deviations from the simple two-parameter model-free approach to the interpretation of nitrogen-15 nuclear magnetic relaxation of proteins. <i>Journal of the American Chemical Society</i> , 1990, 112, 4989-4991.	6.6	1,021
5	Overcoming the overlap problem in the assignment of proton NMR spectra of larger proteins by use of three-dimensional heteronuclear proton-nitrogen-15 Hartmann-Hahn-multiple quantum coherence and nuclear Overhauser-multiple quantum coherence spectroscopy: application to interleukin 1.β. <i>Biochemistry</i> , 1989, 28, 6150-6156.	1.2	970
6	A novel, highly stable fold of the immunoglobulin binding domain of streptococcal protein G. <i>Science</i> , 1991, 253, 657-661.	6.0	792
7	Determination of three-dimensional structures of proteins from interproton distance data by hybrid distance geometry-dynamical simulated annealing calculations. <i>FEBS Letters</i> , 1988, 229, 317-324.	1.3	756
8	Using Xplor-NIH for NMR molecular structure determination. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2006, 48, 47-62.	3.9	700
9	Theory, Practice, and Applications of Paramagnetic Relaxation Enhancement for the Characterization of Transient Low-Population States of Biological Macromolecules and Their Complexes. <i>Chemical Reviews</i> , 2009, 109, 4108-4139.	23.0	692
10	Determination of the three-dimensional solution structure of the C-terminal domain of cellobiohydrolase I from <i>Trichoderma reesei</i> . A study using nuclear magnetic resonance and hybrid distance geometry-dynamical simulated annealing. <i>Biochemistry</i> , 1989, 28, 7241-7257.	1.2	542
11	Analysis of the backbone dynamics of interleukin-1.β. using two-dimensional inverse detected heteronuclear nitrogen-15-proton NMR spectroscopy. <i>Biochemistry</i> , 1990, 29, 7387-7401.	1.2	524
12	Determination of three-dimensional structures of proteins from interproton distance data by dynamical simulated annealing from a random array of atoms Circumventing problems associated with folding. <i>FEBS Letters</i> , 1988, 239, 129-136.	1.3	517
13	Determination of three-dimensional structures of proteins by simulated annealing with interproton distance restraints. Application to crambin, potato carboxypeptidase inhibitor and barley serine proteinase inhibitor 2. <i>Protein Engineering, Design and Selection</i> , 1988, 2, 27-38.	1.0	513
14	Molecular basis of human 46X,Y sex reversal revealed from the three-dimensional solution structure of the human SRY-DNA complex. <i>Cell</i> , 1995, 81, 705-714.	13.5	496
15	Three-dimensional structure of interleukin 8 in solution. <i>Biochemistry</i> , 1990, 29, 1689-1696.	1.2	482
16	NMR structure of a specific DNA complex of Zn-containing DNA binding domain of GATA-1. <i>Science</i> , 1993, 261, 438-446.	6.0	477
17	Structures of larger proteins in solution: three- and four-dimensional heteronuclear NMR spectroscopy. <i>Science</i> , 1991, 252, 1390-1399.	6.0	470
18	Use of dipolar <sup>1</sup> H- <sup>15</sup> N and <sup>1</sup> H- <sup>13</sup> C couplings in the structure determination of magnetically oriented macromolecules in solution. <i>Nature Structural Biology</i> , 1997, 4, 732-738.	9.7	456

#	ARTICLE	IF	CITATIONS
19	Visualization of transient encounter complexes in protein-protein association. <i>Nature</i> , 2006, 444, 383-386.	13.7	397
20	Open-to-closed transition in apo maltose-binding protein observed by paramagnetic NMR. <i>Nature</i> , 2007, 449, 1078-1082.	13.7	390
21	Three-dimensional solution structure of the 44kDa ectodomain of SIV gp41. <i>EMBO Journal</i> , 1998, 17, 4572-4584.	3.5	386
22	Atomic-resolution dynamics on the surface of amyloid- $\beta^2$ protofibrils probed by solution NMR. <i>Nature</i> , 2011, 480, 268-272.	13.7	374
23	A Robust Method for Determining the Magnitude of the Fully Asymmetric Alignment Tensor of Oriented Macromolecules in the Absence of Structural Information. <i>Journal of Magnetic Resonance</i> , 1998, 133, 216-221.	1.2	368
24	Crystal structure of interleukin 8: symbiosis of NMR and crystallography.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1991, 88, 502-506.	3.3	353
25	Detecting transient intermediates in macromolecular binding by paramagnetic NMR. <i>Nature</i> , 2006, 440, 1227-1230.	13.7	349
26	Sequence-specific determination of protein and peptide concentrations by absorbance at 205 nm. <i>Protein Science</i> , 2013, 22, 851-858.	3.1	342
27	Three-dimensional structure of proteins determined by molecular dynamics with interproton distance restraints: application to crambin.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1986, 83, 3801-3805.	3.3	339
28	The solution structure of HIV-1 Nef reveals an unexpected fold and permits delineation of the binding surface for the SH3 domain of Hck tyrosine protein kinase. <i>Nature Structural and Molecular Biology</i> , 1996, 3, 340-345.	3.6	337
29	The solution structure of an HMG-I(Y)-DNA complex defines a new architectural minor groove binding motif. <i>Nature Structural Biology</i> , 1997, 4, 657-665.	9.7	337
30	Determination of Three-Dimensional Structures of Proteins and Nucleic Acids in Solution by Nuclear Magnetic Resonance Spectroscopy. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 1989, 24, 479-564.	2.3	330
31	Measurement of Residual Dipolar Couplings of Macromolecules Aligned in the Nematic Phase of a Colloidal Suspension of Rod-Shaped Viruses. <i>Journal of the American Chemical Society</i> , 1998, 120, 10571-10572.	6.6	324
32	Four-dimensional heteronuclear triple-resonance NMR spectroscopy of interleukin-1 beta in solution. <i>Science</i> , 1990, 249, 411-414.	6.0	322
33	Solution Structure of the DNA Binding Domain of HIV-1 Integrase. <i>Biochemistry</i> , 1995, 34, 9826-9833.	1.2	321
34	Solution structure of the N-terminal zinc binding domain of HIV-1 integrase. <i>Nature Structural Biology</i> , 1997, 4, 567-577.	9.7	320
35	Ensemble Approach for NMR Structure Refinement against $^1\text{H}$ Paramagnetic Relaxation Enhancement Data Arising from a Flexible Paramagnetic Group Attached to a Macromolecule. <i>Journal of the American Chemical Society</i> , 2004, 126, 5879-5896.	6.6	317
36	High-resolution structure of the oligomerization domain of p53 by multidimensional NMR. <i>Science</i> , 1994, 265, 386-391.	6.0	311

#	ARTICLE	IF	CITATIONS
37	Direct Structure Refinement against Residual Dipolar Couplings in the Presence of Rhombicity of Unknown Magnitude. <i>Journal of Magnetic Resonance</i> , 1998, 131, 159-162.	1.2	303
38	Intercalation, DNA Kinking, and the Control of Transcription. <i>Science</i> , 1996, 271, 778-784.	6.0	297
39	The solution conformation of the antibacterial peptide cecropin A: a nuclear magnetic resonance and dynamical simulated annealing study. <i>Biochemistry</i> , 1988, 27, 7620-7629.	1.2	296
40	Application of molecular dynamics with interproton distance restraints to three-dimensional protein structure determination. <i>Journal of Molecular Biology</i> , 1986, 191, 523-551.	2.0	288
41	Three-dimensional structure of potato carboxypeptidase inhibitor in solution. A study using nuclear magnetic resonance, distance geometry, and restrained molecular dynamics. <i>Biochemistry</i> , 1987, 26, 8012-8023.	1.2	279
42	Three-dimensional NMR spectroscopy of a protein in solution. <i>Nature</i> , 1988, 332, 374-376.	13.7	258
43	Solution conformation of a heptadecapeptide comprising the DNA binding helix F of the cyclic AMP receptor protein of <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1985, 186, 435-455.	2.0	256
44	[11] Multidimensional heteronuclear nuclear magnetic resonance of proteins. <i>Methods in Enzymology</i> , 1994, 239, 349-363.	0.4	250
45	Demonstration of positionally disordered water within a protein hydrophobic cavity by NMR. <i>Science</i> , 1995, 267, 1813-1817.	6.0	250
46	Solution structure of cyanovirin-N, a potent HIV-inactivating protein. <i>Nature Structural Biology</i> , 1998, 5, 571-578.	9.7	249
47	R-factor, FreeR, and Complete Cross-Validation for Dipolar Coupling Refinement of NMR Structures. <i>Journal of the American Chemical Society</i> , 1999, 121, 9008-9012.	6.6	245
48	The three-dimensional structure of $\hat{1}\pm$ 1-purothionin in solution: combined use of nuclear magnetic resonance, distance geometry and restrained molecular dynamics. <i>EMBO Journal</i> , 1986, 5, 2729-2735.	3.5	241
49	Practical aspects of $^1\text{H}$ transverse paramagnetic relaxation enhancement measurements on macromolecules. <i>Journal of Magnetic Resonance</i> , 2007, 184, 185-195.	1.2	239
50	Determining the structures of large proteins and protein complexes by NMR. <i>Trends in Biotechnology</i> , 1998, 16, 22-34.	4.9	238
51	Improving the Packing and Accuracy of NMR Structures with a Pseudopotential for the Radius of Gyration. <i>Journal of the American Chemical Society</i> , 1999, 121, 2337-2338.	6.6	237
52	A common sense approach to peak picking in two-, three-, and four-dimensional spectra using automatic computer analysis of contour diagrams. <i>Journal of Magnetic Resonance</i> , 1991, 95, 214-220.	0.5	233
53	MINOR GROOVE-BINDING ARCHITECTURAL PROTEINS: Structure, Function, and DNA Recognition. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 1998, 27, 105-131.	18.3	233
54	Applications of three- and four-dimensional heteronuclear NMR spectroscopy to protein structure determination. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 1991, 23, 43-92.	3.9	232

#	ARTICLE	IF	CITATIONS
55	High-resolution solution structure of the beta chemokine hMIP-1 beta by multidimensional NMR. <i>Science</i> , 1994, 263, 1762-1767.	6.0	232
56	New methods of structure refinement for macromolecular structure determination by NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 5891-5898.	3.3	231
57	Solution structure of human thioredoxin in a mixed disulfide intermediate complex with its target peptide from the transcription factor NF $\kappa$ B. <i>Structure</i> , 1995, 3, 289-297.	1.6	228
58	Refined solution structure of the oligomerization domain of the tumour suppressor p53. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 321-333.	3.6	218
59	Identification by NMR of the Binding Surface for the Histidine-Containing Phosphocarrier Protein HPr on the N-Terminal Domain of Enzyme I of the <i>Escherichia coli</i> Phosphotransferase System. <i>Biochemistry</i> , 1997, 36, 4393-4398.	1.2	212
60	The Impact of Direct Refinement against $^{13}\text{C}$ and $^{13}\text{C}$ Chemical Shifts on Protein Structure Determination by NMR. <i>Journal of Magnetic Resonance Series B</i> , 1995, 106, 92-96.	1.6	203
61	A Palindromic Regulatory Site within Vertebrate GATA-1 Promoters Requires Both Zinc Fingers of the GATA-1 DNA-Binding Domain for High-Affinity Interaction. <i>Molecular and Cellular Biology</i> , 1996, 16, 2238-2247.	1.1	203
62	Elucidating transient macromolecular interactions using paramagnetic relaxation enhancement. <i>Current Opinion in Structural Biology</i> , 2007, 17, 603-616.	2.6	201
63	Assignment of the side-chain proton and carbon-13 resonances of interleukin-1.beta. using double- and triple-resonance heteronuclear three-dimensional NMR spectroscopy. <i>Biochemistry</i> , 1990, 29, 8172-8184.	1.2	200
64	The solution structure of a specific GAGA factor-DNA complex reveals a modular binding mode. <i>Nature Structural Biology</i> , 1997, 4, 122-132.	9.7	198
65	Improving the quality of NMR and crystallographic protein structures by means of a conformational database potential derived from structure databases. <i>Protein Science</i> , 1996, 5, 1067-1080.	3.1	197
66	Solution structure of the 40,000 Mr phosphoryl transfer complex between the N-terminal domain of enzyme I and HPr. <i>Nature Structural Biology</i> , 1999, 6, 166-173.	9.7	194
67	How Much Backbone Motion in Ubiquitin Is Required To Account for Dipolar Coupling Data Measured in Multiple Alignment Media as Assessed by Independent Cross-Validation?. <i>Journal of the American Chemical Society</i> , 2004, 126, 2923-2938.	6.6	194
68	Visualizing transient dark states by NMR spectroscopy. <i>Quarterly Reviews of Biophysics</i> , 2015, 48, 35-116.	2.4	194
69	$^1\text{H}$ - $^1\text{H}$ correlation via isotropic mixing of $^{13}\text{C}$ magnetization, a new three-dimensional approach for assigning $^1\text{H}$ and $^{13}\text{C}$ spectra of $^{13}\text{C}$ -enriched proteins. <i>Journal of Magnetic Resonance</i> , 1990, 88, 425-431.	0.5	190
70	Complete resonance assignment for the polypeptide backbone of interleukin 1.beta. using three-dimensional heteronuclear NMR spectroscopy. <i>Biochemistry</i> , 1990, 29, 3542-3556.	1.2	189
71	High-resolution three-dimensional structure of interleukin 1.beta. in solution by three- and four-dimensional nuclear magnetic resonance spectroscopy. <i>Biochemistry</i> , 1991, 30, 2315-2323.	1.2	189
72	Accurate and rapid docking of protein-protein complexes on the basis of intermolecular nuclear Overhauser enhancement data and dipolar couplings by rigid body minimization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 9021-9025.	3.3	186

#	ARTICLE	IF	CITATIONS
73	Solution structure of the constant region of nuclear envelope protein LAP2 reveals two LEM-domain structures: one binds BAF and the other binds DNA. <i>EMBO Journal</i> , 2001, 20, 4399-4407.	3.5	186
74	Improvements and Extensions in the Conformational Database Potential for the Refinement of NMR and X-ray Structures of Proteins and Nucleic Acids. <i>Journal of Magnetic Resonance</i> , 1997, 125, 171-177.	1.2	185
75	Four-dimensional carbon-13/carbon-13-edited nuclear Overhauser enhancement spectroscopy of a protein in solution: application to interleukin 1.beta.. <i>Biochemistry</i> , 1991, 30, 12-18.	1.2	182
76	Kinetics of Amyloid I <sup>2</sup> Monomer-to-Oligomer Exchange by NMR Relaxation. <i>Journal of the American Chemical Society</i> , 2010, 132, 9948-9951.	6.6	179
77	Kinetics of folding of the all-beta sheet protein interleukin-1 beta. <i>Science</i> , 1993, 260, 1110-1113.	6.0	178
78	A 500 ps molecular dynamics simulation study of interleukin-1I <sup>2</sup> in water. <i>Journal of Molecular Biology</i> , 1992, 226, 239-250.	2.0	177
79	Increased Resolution and Improved Spectral Quality in Four-Dimensional 13C/13C-Separated HMQC-NOESY-HMQC Spectra Using Pulsed Field Gradients. <i>Journal of Magnetic Resonance Series B</i> , 1993, 101, 210-213.	1.6	177
80	An efficient and cost-effective isotope labeling protocol for proteins expressed in Escherichia coli. <i>Journal of Biomolecular NMR</i> , 1998, 11, 97-102.	1.6	176
81	Defining long range order in NMR structure determination from the dependence of heteronuclear relaxation times on rotational diffusion anisotropy. <i>Nature Structural Biology</i> , 1997, 4, 443-449.	9.7	174
82	Solution structure of recombinant hirudin and the Lys-47 .fwdarw. Glu mutants: a nuclear magnetic resonance and hybrid distance geometry-dynamical simulated annealing study. <i>Biochemistry</i> , 1989, 28, 2601-2617.	1.2	173
83	A powerful method of sequential proton resonance assignment in proteins using relayed15N-1H multiple quantum coherence spectroscopy. <i>FEBS Letters</i> , 1989, 243, 93-98.	1.3	173
84	Identification of a binding site for the human immunodeficiency virus type 1 nucleocapsid protein.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993, 90, 5219-5223.	3.3	172
85	Solvent isotope effect and protein stability. <i>Nature Structural Biology</i> , 1995, 2, 852-855.	9.7	172
86	NMR structural and kinetic characterization of a homeodomain diffusing and hopping on nonspecific DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15062-15067.	3.3	172
87	Internal Coordinates for Molecular Dynamics and Minimization in Structure Determination and Refinement. <i>Journal of Magnetic Resonance</i> , 2001, 152, 288-302.	1.2	170
88	Three-Dimensional Solution Structure of Human Interleukin-4 by Multidimensional Heteronuclear Magnetic Resonance Spectroscopy. <i>Science</i> , 1992, 256, 1673-1677.	6.0	169
89	Autoprocessing of HIV-1 protease is tightly coupled to protein folding. <i>Nature Structural Biology</i> , 1999, 6, 868-875.	9.7	168
90	Xplorâ€NIH for molecular structure determination from NMR and other data sources. <i>Protein Science</i> , 2018, 27, 26-40.	3.1	167

#	ARTICLE	IF	CITATIONS
91	Solution Structure of the 30 kDa N-Terminal Domain of Enzyme I of the Escherichia coli Phosphoenolpyruvate: Sugar Phosphotransferase System by Multidimensional NMR. <i>Biochemistry</i> , 1997, 36, 2517-2530.	1.2	165
92	Correlation between $^3\text{HJNC}\tilde{\text{e}}$ and Hydrogen Bond Length in Proteins. <i>Journal of the American Chemical Society</i> , 1999, 121, 6275-6279.	6.6	165
93	Detection of nuclear Overhauser effects between degenerate amide proton resonances by heteronuclear three-dimensional NMR spectroscopy. <i>Journal of the American Chemical Society</i> , 1990, 112, 9020-9022.	6.6	164
94	Theory and applications of the transferred nuclear overhauser effect to the study of the conformations of small ligands bound to proteins. <i>Journal of Magnetic Resonance</i> , 1982, 48, 402-417.	0.5	162
95	Structural comparisons among the short-chain helical cytokines. <i>Structure</i> , 1994, 2, 159-173.	1.6	162
96	Crystal structure of cyanovirin-N, a potent HIV-inactivating protein, shows unexpected domain swapping. <i>Journal of Molecular Biology</i> , 1999, 288, 403-412.	2.0	160
97	The solution structure of human thioredoxin complexed with its target from Ref-1 reveals peptide chain reversal. <i>Structure</i> , 1996, 4, 613-620.	1.6	157
98	Exploring the Limits of Precision and Accuracy of Protein Structures Determined by Nuclear Magnetic Resonance Spectroscopy. <i>Journal of Molecular Biology</i> , 1993, 231, 82-102.	2.0	156
99	Assessing the quality of solution nuclear magnetic resonance structures by complete cross-validation. <i>Science</i> , 1993, 261, 328-331.	6.0	155
100	Determination of three-dimensional structures of proteins in solution by nuclear magnetic resonance spectroscopy. <i>Protein Engineering, Design and Selection</i> , 1987, 1, 275-288.	1.0	153
101	Identification and localization of bound internal water in the solution structure of interleukin 1. beta. by heteronuclear three-dimensional proton rotating-frame Overhauser nitrogen-15-proton multiple quantum coherence NMR spectroscopy. <i>Biochemistry</i> , 1990, 29, 5671-5676.	1.2	153
102	Structure refinement of oligonucleotides by molecular dynamics with nuclear overhauser effect interproton distance restraints: Application to $5\text{\AA}^2$ d(C-G-T-A-C-G) <sub>2</sub> . <i>Journal of Molecular Biology</i> , 1986, 188, 455-475.	2.0	152
103	High-resolution three-dimensional structure of reduced recombinant human thioredoxin in solution. <i>Biochemistry</i> , 1991, 30, 2685-2698.	1.2	151
104	Structure and dynamics of KH domains from FBP bound to single-stranded DNA. <i>Nature</i> , 2002, 415, 1051-1056.	13.7	150
105	The high-resolution three-dimensional solution structures of the oxidized and reduced states of human thioredoxin. <i>Structure</i> , 1994, 2, 503-522.	1.6	149
106	Molecular Basis for Synergistic Transcriptional Activation by Oct1 and Sox2 Revealed from the Solution Structure of the 42-kDa Oct1-Sox2-Hoxb1-DNA Ternary Transcription Factor Complex. <i>Journal of Biological Chemistry</i> , 2004, 279, 1449-1457.	1.6	147
107	The high-resolution, three-dimensional solution structure of human interleukin-4 determined by multidimensional heteronuclear magnetic resonance spectroscopy. <i>Biochemistry</i> , 1993, 32, 6744-6762.	1.2	143
108	Determination of the three-dimensional solution structure of the antihypertensive and antiviral protein BDS-I from the sea anemone <i>Anemonia sulcata</i> : a study using nuclear magnetic resonance and hybrid distance geometry-dynamical simulated annealing. <i>Biochemistry</i> , 1989, 28, 2188-2198.	1.2	142

#	ARTICLE	IF	CITATIONS
109	Two-, Three-, and Four-Dimensional NMR Methods for Obtaining Larger and More Precise Three-Dimensional Structures of Proteins in Solution. Annual Review of Biophysics and Biophysical Chemistry, 1991, 20, 29-63.	12.2	142
110	Evaluation of Cross-Correlation Effects and Measurement of One-Bond Couplings in Proteins with Short Transverse Relaxation Times. Journal of Magnetic Resonance, 2000, 143, 184-196.	1.2	142
111	Design of an expression system for detecting folded protein domains and mapping macromolecular interactions by NMR. Protein Science, 1997, 6, 2359-2364.	3.1	142
112	High-resolution three-dimensional structure of a single zinc finger from a human enhancer binding protein in solution. Biochemistry, 1990, 29, 9324-9334.	1.2	139
113	Structural and dynamic characterization of the urea denatured state of the immunoglobulin binding domain of streptococcal protein G by multidimensional heteronuclear NMR spectroscopy. Protein Science, 1995, 4, 2605-2615.	3.1	136
114	NMR structure determination of proteins and protein complexes larger than 20 kDa. Current Opinion in Chemical Biology, 1998, 2, 564-570.	2.8	134
115	Amplitudes of Protein Backbone Dynamics and Correlated Motions in a Small $\hat{I}^{\pm}/\hat{I}^2$ Protein: Correspondence of Dipolar Coupling and Heteronuclear Relaxation Measurements. Biochemistry, 2004, 43, 10678-10691.	1.2	134
116	The Impact of Direct Refinement against Three-Bond $\text{HN-C}^{\alpha}\text{H}$ Coupling Constants on Protein Structure Determination by NMR. Journal of Magnetic Resonance Series B, 1994, 104, 99-103.	1.6	133
117	A common sense approach to peak picking in two-, three-, and four-dimensional spectra using automatic computer analysis of contour diagrams. Journal of Magnetic Resonance, 2011, 213, 357-363.	1.2	133
118	Four p53 DNA-binding domain peptides bind natural p53-response elements and bend the DNA.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 8591-8595.	3.3	132
119	Structural Basis for SRY-dependent 46-X,Y Sex Reversal: Modulation of DNA Bending by a Naturally Occurring Point Mutation. Journal of Molecular Biology, 2001, 312, 481-499.	2.0	132
120	Fast folding of a prototypic polypeptide: The immunoglobulin binding domain of streptococcal protein G. Protein Science, 1994, 3, 1945-1952.	3.1	131
121	A small single-"finger" peptide from the erythroid transcription factor GATA-1 binds specifically to DNA as a zinc or iron complex.. Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 1676-1680.	3.3	130
122	Three-dimensional structures of $\hat{I}^{\pm}$ and $\hat{I}^2$ chemokines. FASEB Journal, 1995, 9, 57-62.	0.2	130
123	Molecular basis of sequence-specific single-stranded DNA recognition by KH domains: solution structure of a complex between hnRNP K KH3 and single-stranded DNA. EMBO Journal, 2002, 21, 3476-3485.	3.5	128
124	Long Distance Measurements up to 160Å... in the GroEL Tetradecamer Using Q-band DEER EPR Spectroscopy. Angewandte Chemie - International Edition, 2016, 55, 15905-15909.	7.2	128
125	The single Cys2-His2 zinc finger domain of the GAGA protein flanked by basic residues is sufficient for high-affinity specific DNA binding.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 2822-2826.	3.3	127
126	Disordered water within a hydrophobic protein cavity visualized by x-ray crystallography. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 103-108.	3.3	126



#	ARTICLE	IF	CITATIONS
127	Design of a Novel Peptide Inhibitor of HIV Fusion That Disrupts the Internal Trimeric Coiled-coil of gp41. <i>Journal of Biological Chemistry</i> , 2002, 277, 14238-14245.	1.6	125
128	Docking of Protein-Protein Complexes on the Basis of Highly Ambiguous Intermolecular Distance Restraints Derived from $^{1}H/^{15}N$ Chemical Shift Mapping and Backbone $^{15}N$ - $^1H$ Residual Dipolar Couplings Using Conjoined Rigid Body/Torsion Angle Dynamics. <i>Journal of the American Chemical Society</i> , 2003, 125, 2902-2912.	6.6	125
129	Relationship between electrostatics and redox function in human thioredoxin: characterization of pH titration shifts using two-dimensional homo- and heteronuclear NMR. <i>Biochemistry</i> , 1992, 31, 3442-3452.	1.2	124
130	The solution structure of the human ETS1-DNA complex reveals a novel mode of binding and true side chain intercalation. <i>Cell</i> , 1995, 83, 761-771.	13.5	124
131	Visualizing transient events in amino-terminal autoprocessing of HIV-1 protease. <i>Nature</i> , 2008, 455, 693-696.	13.7	123
132	The Impact of Direct Refinement against Proton Chemical Shifts on Protein Structure Determination by NMR. <i>Journal of Magnetic Resonance Series B</i> , 1995, 107, 293-297.	1.6	119
133	Solution Structure of the 128 kDa Enzyme I Dimer from <i>Escherichia coli</i> and Its 146 kDa Complex with HPr Using Residual Dipolar Couplings and Small- and Wide-Angle X-ray Scattering. <i>Journal of the American Chemical Society</i> , 2010, 132, 13026-13045.	6.6	118
134	Structure and Dynamics of Full-Length HIV-1 Capsid Protein in Solution. <i>Journal of the American Chemical Society</i> , 2013, 135, 16133-16147.	6.6	114
135	Solution structure of the cellular factor BAF responsible for protecting retroviral DNA from autointegration. <i>Nature Structural Biology</i> , 1998, 5, 903-909.	9.7	113
136	Water suppression in two-dimensional spin-locked NMR experiments using a novel phase-cycling procedure. <i>Journal of the American Chemical Society</i> , 1987, 109, 6511-6513.	6.6	112
137	Transient, Sparsely Populated Compact States of Apo and Calcium-Loaded Calmodulin Probed by Paramagnetic Relaxation Enhancement: Interplay of Conformational Selection and Induced Fit. <i>Journal of the American Chemical Society</i> , 2011, 133, 18966-18974.	6.6	112
138	A proton nuclear magnetic resonance study of the antihypertensive and antiviral protein BDS-I from the sea anemone <i>Anemonia sulcata</i> : sequential and stereospecific resonance assignment and secondary structure. <i>Biochemistry</i> , 1989, 28, 2178-2187.	1.2	110
139	The VMD-XPLOR Visualization Package for NMR Structure Refinement. <i>Journal of Magnetic Resonance</i> , 2001, 149, 239-244.	1.2	110
140	Theory of the time dependent transferred nuclear Overhauser effect: Applications to structural analysis of ligand-protein complexes in solution. <i>Journal of Magnetic Resonance</i> , 1983, 53, 423-442.	0.5	109
141	Three-dimensional solution structure of the E3-binding domain of the dihydrolipoamide succinyltransferase core from the 2-oxoglutarate dehydrogenase multienzyme complex of <i>Escherichia coli</i> . <i>Biochemistry</i> , 1992, 31, 3463-3471.	1.2	109
142	$^1H$ -Nmr stereospecific assignments by conformational data-base searches. <i>Biopolymers</i> , 1990, 29, 813-822.	1.2	108
143	Impact of Residual Dipolar Couplings on the Accuracy of NMR Structures Determined from a Minimal Number of NOE Restraints. <i>Journal of the American Chemical Society</i> , 1999, 121, 6513-6514.	6.6	108
144	Concordance of Residual Dipolar Couplings, Backbone Order Parameters and Crystallographic B-factors for a Small $\beta$ -sheet Protein: A Unified Picture of High Probability, Fast Atomic Motions in Proteins. <i>Journal of Molecular Biology</i> , 2006, 355, 879-886.	2.0	108

#	ARTICLE	IF	CITATIONS
145	Structures of larger proteins, protein-ligand and protein-DNA complexes by multidimensional heteronuclear NMR. <i>Protein Science</i> , 1994, 3, 372-390.	3.1	107
146	Replica exchange simulations of transient encounter complexes in protein-protein association. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 12855-12860.	3.3	107
147	Stereospecific assignment of $\beta^2$ -methylene protons in larger proteins using 3D <sup>15</sup> N-separated Hartmann-Hahn and <sup>13</sup> C-separated rotating frame Overhauser spectroscopy. <i>Journal of Biomolecular NMR</i> , 1991, 1, 13-22.	1.6	106
148	The pKa values of two histidine residues in human haemoglobin, the Bohr effect, and the dipole moments of $\alpha$ -helices. <i>Journal of Molecular Biology</i> , 1985, 183, 491-498.	2.0	103
149	Mapping the Topology and Determination of a Low-Resolution Three-Dimensional Structure of the Calmodulin-Melittin Complex by Chemical Cross-Linking and High-Resolution FTICRMS: A Direct Demonstration of Multiple Binding Modes. <i>Biochemistry</i> , 2004, 43, 4703-4715.	1.2	103
150	Characterization of the low-temperature intermediates of the reaction of fully reduced soluble cytochrome oxidase with oxygen by electron-paramagnetic-resonance and optical spectroscopy. <i>Biochemical Journal</i> , 1980, 185, 139-154.	1.7	102
151	Identification of the Contact Surface of a Streptococcal Protein G Domain Complexed with a Human Fc Fragment. <i>Journal of Molecular Biology</i> , 1993, 233, 331-335.	2.0	102
152	1.67-Å X-ray structure of the B2 immunoglobulin-binding domain of streptococcal protein G and comparison to the NMR structure of the B1 domain. <i>Biochemistry</i> , 1992, 31, 10449-10457.	1.2	101
153	A Physical Picture of Atomic Motions within the Dickerson DNA Dodecamer in Solution Derived from Joint Ensemble Refinement against NMR and Large-Angle X-ray Scattering Data. <i>Biochemistry</i> , 2007, 46, 1152-1166.	1.2	99
154	Probing exchange kinetics and atomic resolution dynamics in high-molecular-weight complexes using dark-state exchange saturation transfer NMR spectroscopy. <i>Nature Protocols</i> , 2012, 7, 1523-1533.	5.5	98
155	The conformations of hirudin in solution: a study using nuclear magnetic resonance, distance geometry and restrained molecular dynamics. <i>EMBO Journal</i> , 1987, 6, 529-537.	3.5	97
156	Ionization Equilibria for Side-Chain Carboxyl Groups in Oxidized and Reduced Human Thioredoxin and in the Complex with Its Target Peptide from the Transcription Factor NF- $\kappa$ B. <i>Biochemistry</i> , 1996, 35, 7-13.	1.2	97
157	Heteronuclear NMR Spectroscopy for Lysine NH <sub>3</sub> Groups in Proteins: A Unique Effect of Water Exchange on <sup>15</sup> N Transverse Relaxation. <i>Journal of the American Chemical Society</i> , 2007, 129, 2971-2980.	6.6	97
158	Refolding proteins by gel filtration chromatography. <i>FEBS Letters</i> , 1994, 345, 125-130.	1.3	95
159	Covalent Trimers of the Internal N-terminal Trimeric Coiled-coil of gp41 and Antibodies Directed against Them Are Potent Inhibitors of HIV Envelope-mediated Cell Fusion. <i>Journal of Biological Chemistry</i> , 2003, 278, 20278-20285.	1.6	94
160	Solution structure of human growth hormone releasing factor. <i>Journal of Molecular Biology</i> , 1986, 191, 553-561.	2.0	93
161	Solution structure of the MEF2A-DNA complex: structural basis for the modulation of DNA bending and specificity by MADS-box transcription factors. <i>EMBO Journal</i> , 2000, 19, 2615-2628.	3.5	93
162	Solution structure of the phosphoryl transfer complex between the signal transducing proteins HPr and IIAGlucose of the <i>Escherichia coli</i> phosphoenolpyruvate:sugar phosphotransferase system. <i>EMBO Journal</i> , 2000, 19, 5635-5649.	3.5	93

#	ARTICLE	IF	CITATIONS
163	Mapping the binding surface of interleukin-8 complexed with an N-terminal fragment of the Type 1 human interleukin-8 receptor. <i>FEBS Letters</i> , 1994, 338, 93-97.	1.3	92
164	Sources of and Solutions to Problems in the Refinement of Protein NMR Structures against Torsion Angle Potentials of Mean Force. <i>Journal of Magnetic Resonance</i> , 2000, 146, 249-254.	1.2	91
165	Intrinsic unfoldase/foldase activity of the chaperonin GroEL directly demonstrated using multinuclear relaxation-based NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8817-8823.	3.3	91
166	Stereochemistry of binding of the tetrapeptide acetyl-Pro-Ala-Pro-Tyr-NH <sub>2</sub> to porcine pancreatic elastase. <i>Journal of Molecular Biology</i> , 1986, 190, 259-267.	2.0	89
167	Direct Observation of Enhanced Translocation of a Homeodomain between DNA Cognate Sites by NMR Exchange Spectroscopy. <i>Journal of the American Chemical Society</i> , 2006, 128, 404-405.	6.6	89
168	Design and Properties of NCCG-gp41, a Chimeric gp41 Molecule with Nanomolar HIV Fusion Inhibitory Activity. <i>Journal of Biological Chemistry</i> , 2001, 276, 29485-29489.	1.6	88
169	Studies on the solution conformation of human thioredoxin using heteronuclear nitrogen-15-proton nuclear magnetic resonance spectroscopy. <i>Biochemistry</i> , 1990, 29, 1566-1572.	1.2	87
170	Determination of the Secondary Structure of Interleukin-8 by Nuclear Magnetic Resonance Spectroscopy. <i>Journal of Biological Chemistry</i> , 1989, 264, 18907-18911.	1.6	86
171	Global jumping and domain-specific intersegment transfer between DNA cognate sites of the multidomain transcription factor Oct-1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 13871-13876.	3.3	85
172	The polypeptide fold of the globular domain of histone H5 in solution. A study using nuclear magnetic resonance, distance geometry and restrained molecular dynamics.. <i>EMBO Journal</i> , 1987, 6, 1833-1842.	3.5	83
173	Analysis of the backbone dynamics of the ribonuclease H domain of the human immunodeficiency virus reverse transcriptase using nitrogen-15 relaxation measurements. <i>Biochemistry</i> , 1992, 31, 9150-9157.	1.2	83
174	Determination of the Relative Orientation of the Two Halves of the Domain-Swapped Dimer of Cyanovirin-N in Solution Using Dipolar Couplings and Rigid Body Minimization. <i>Journal of the American Chemical Society</i> , 2000, 122, 6009-6016.	6.6	83
175	Three-dimensional structure of acyl carrier protein in solution determined by nuclear magnetic resonance and the combined use of dynamical simulated annealing and distance geometry. <i>FEBS Journal</i> , 1988, 175, 9-15.	0.2	82
176	Completely Automated, Highly Error-Tolerant Macromolecular Structure Determination from Multidimensional Nuclear Overhauser Enhancement Spectra and Chemical Shift Assignments. <i>Journal of the American Chemical Society</i> , 2004, 126, 6258-6273.	6.6	82
177	Three-dimensional structure of phoratoxin in solution: combined use of nuclear magnetic resonance, distance geometry, and restrained molecular dynamics. <i>Biochemistry</i> , 1987, 26, 1732-1745.	1.2	81
178	Structural characterization of a 39-residue synthetic peptide containing the two zinc binding domains from the HIV-1 p7 nucleocapsid protein by CD and NMR spectroscopy. <i>FEBS Letters</i> , 1991, 292, 25-30.	1.3	81
179	Refinement of the solution structure of the DNA decamer 5'-d(CTGGATCCAG) <sub>2</sub> : combined use of nuclear magnetic resonance and restrained molecular dynamics. <i>Biochemistry</i> , 1987, 26, 3734-3744.	1.2	80
180	Visualization of Transient Ultra-Weak Protein Self-Association in Solution Using Paramagnetic Relaxation Enhancement. <i>Journal of the American Chemical Society</i> , 2008, 130, 4048-4056.	6.6	80

#	ARTICLE	IF	CITATIONS
181	Mechanistic details of a protein-protein association pathway revealed by paramagnetic relaxation enhancement titration measurements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 1379-1384.	3.3	80
182	A 1 H-NMR study of the solution conformation of secretin resonance assignment and secondary structure. <i>FEBS Letters</i> , 1987, 215, 88-94.	1.3	77
183	$\pi$ 1 Rotamer Populations and Angles of Mobile Surface Side Chains Are Accurately Predicted by a Torsion Angle Database Potential of Mean Force. <i>Journal of the American Chemical Society</i> , 2002, 124, 2866-2867.	6.6	76
184	Improving the Accuracy of NMR Structures of RNA by Means of Conformational Database Potentials of Mean Force as Assessed by Complete Dipolar Coupling Cross-Validation. <i>Journal of the American Chemical Society</i> , 2003, 125, 1518-1525.	6.6	76
185	Characterization of Nonspecific Protein-DNA Interactions by $^1\text{H}$ Paramagnetic Relaxation Enhancement. <i>Journal of the American Chemical Society</i> , 2004, 126, 12800-12808.	6.6	76
186	Probing the transient dark state of substrate binding to GroEL by relaxation-based solution NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11361-11366.	3.3	76
187	Combining experimental information from crystal and solution studies: joint X-ray and NMR refinement. <i>Science</i> , 1992, 257, 961-964.	6.0	75
188	Solution NMR Structure of the Barrier-to-Autointegration Factor-Emerin Complex. <i>Journal of Biological Chemistry</i> , 2007, 282, 14525-14535.	1.6	75
189	Solution of a Protein Crystal Structure with a Model Obtained from NMR Interproton Distance Restraints. <i>Science</i> , 1987, 235, 1049-1053.	6.0	74
190	Refinement of the solution structure of the DNA hexamer 5'd(GCATGC) <sub>2</sub> : combined use of nuclear magnetic resonance and restrained molecular dynamics. <i>Biochemistry</i> , 1987, 26, 3718-3733.	1.2	74
191	Determination of the secondary structure and molecular topology of interleukin-1 $\beta$ . by use of two- and three-dimensional heteronuclear nitrogen-15-proton NMR spectroscopy. <i>Biochemistry</i> , 1990, 29, 4668-4682.	1.2	73
192	Investigation of the backbone dynamics of the $\text{igg}$ binding domain of streptococcal protein g by heteronuclear two-dimensional $^1\text{H}$ - $^{15}\text{N}$ nuclear magnetic resonance spectroscopy. <i>Protein Science</i> , 1994, 3, 15-21.	3.1	73
193	Role of Electrostatic Interactions in Transient Encounter Complexes in Protein-Protein Association Investigated by Paramagnetic Relaxation Enhancement. <i>Journal of the American Chemical Society</i> , 2007, 129, 12954-12955.	6.6	73
194	Practical Aspects of Paramagnetic Relaxation Enhancement in Biological Macromolecules. <i>Methods in Enzymology</i> , 2015, 564, 485-497.	0.4	73
195	A novel class of winged helix-turn-helix protein: the DNA binding domain of Mu transposase. <i>Structure</i> , 1994, 2, 1041-1048.	1.6	72
196	Structures of Protein Complexes by Multidimensional Heteronuclear Magnetic Resonance Spectroscopy. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 1995, 30, 351-385.	2.3	72
197	EDTA-Derivatized Deoxythymidine as a Tool for Rapid Determination of Protein Binding Polarity to DNA by Intermolecular Paramagnetic Relaxation Enhancement. <i>Journal of the American Chemical Society</i> , 2003, 125, 6634-6635.	6.6	72
198	The N-terminal fingers of chicken GATA-2 and GATA-3 are independent sequence-specific DNA binding domains. <i>EMBO Journal</i> , 1997, 16, 2874-2882.	3.5	71

#	ARTICLE	IF	CITATIONS
199	Relaxation-Optimized NMR Spectroscopy of Methylene Groups in Proteins and Nucleic Acids. <i>Journal of the American Chemical Society</i> , 2004, 126, 10560-10570.	6.6	71
200	Proton nuclear magnetic resonance studies on cyclic nucleotide binding to the Escherichia coli adenosine cyclic 3',5'-phosphate receptor protein. <i>Biochemistry</i> , 1982, 21, 4040-4048.	1.2	70
201	Analysis of the Backbone Dynamics of Interleukin-8 by 15N Relaxation Measurements. <i>Journal of Molecular Biology</i> , 1993, 230, 364-372.	2.0	70
202	Identification of N-terminal helix capping boxes by means of 13C chemical shifts. <i>Journal of Biomolecular NMR</i> , 1994, 4, 455-8.	1.6	70
203	Direct Refinement against Proton-Proton Dipolar Couplings in NMR Structure Determination of Macromolecules. <i>Journal of Magnetic Resonance</i> , 2000, 142, 393-396.	1.2	70
204	Structure of the Plasmodium 6-cysteine s48/45 domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 6692-6697.	3.3	69
205	Solution conformations of human growth hormone releasing factor: comparison of the restrained molecular dynamics and distance geometry methods for a system without long-range distance data. <i>Protein Engineering, Design and Selection</i> , 1987, 1, 399-406.	1.0	68
206	Reversible steps in the bacteriorhodopsin photocycle.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1992, 89, 3610-3614.	3.3	67
207	HIV-I protease: Maturation, enzyme specificity, and drug resistance. <i>Advances in Pharmacology</i> , 2000, 49, 111-146.	1.2	67
208	Solution Structure of the Monovalent Lectin Microvirin in Complex with Man <sub>1</sub> (1 $\alpha$ 2)Man Provides a Basis for Anti-HIV Activity with Low Toxicity. <i>Journal of Biological Chemistry</i> , 2011, 286, 20788-20796.	1.6	67
209	Characterization of the intermediates in the reaction of mixed-valence state soluble cytochrome oxidase with oxygen at low temperatures by optical and electron-paramagnetic-resonance spectroscopy. <i>Biochemical Journal</i> , 1980, 185, 155-167.	1.7	66
210	High-resolution structure of Ascaris trypsin inhibitor in solution: direct evidence for a pH-induced conformational transition in the reactive site. <i>Structure</i> , 1994, 2, 669-678.	1.6	66
211	The solution structure of a fungal AREA protein-DNA complex: an alternative binding mode for the basic carboxyl tail of GATA factors 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1998, 277, 605-620.	2.0	66
212	Nucleotide sequence of the dihydrofolate reductase gene of methotrexate-resistant Lactobacillus casei. <i>Gene</i> , 1985, 35, 217-222.	1.0	65
213	Exploring sparsely populated states of macromolecules by diamagnetic and paramagnetic NMR relaxation. <i>Protein Science</i> , 2011, 20, 229-246.	3.1	65
214	Stereochemistry of ATP and GTP bound to fish haemoglobins. <i>Journal of Molecular Biology</i> , 1984, 178, 731-742.	2.0	64
215	The solution structure of a RNA pentadecamer comprising the anticodon loop and stem of yeast tRNAPhe. A 500 MHz 1H-n.m.r. study. <i>Biochemical Journal</i> , 1984, 221, 737-751.	1.7	64
216	Probing the three-dimensional structures of DNA and RNA oligonucleotides in solution by nuclear Overhauser enhancement measurements. <i>FEBS Letters</i> , 1985, 179, 187-198.	1.3	64

#	ARTICLE	IF	CITATIONS
217	Rewighted atomic densities to represent ensembles of NMR structures. <i>Journal of Biomolecular NMR</i> , 2002, 23, 221-225.	1.6	64
218	Visualizing lowly-populated regions of the free energy landscape of macromolecular complexes by paramagnetic relaxation enhancement. <i>Molecular BioSystems</i> , 2008, 4, 1058.	2.9	64
219	Comparison of the solution and X-ray structures of barley serine proteinase inhibitor 2. <i>Protein Engineering, Design and Selection</i> , 1987, 1, 313-318.	1.0	63
220	High-resolution solution structure of the double Cys2His2 zinc finger from the human enhancer binding protein MBP-1. <i>Biochemistry</i> , 1992, 31, 3907-3917.	1.2	63
221	Correction of the NMR structure of the ETS1/DNA complex. <i>Journal of Biomolecular NMR</i> , 1997, 10, 317-328.	1.6	63
222	Improving the Accuracy of NMR Structures of DNA by Means of a Database Potential of Mean Force Describing Base-Base Positional Interactions. <i>Journal of the American Chemical Society</i> , 2001, 123, 3903-3918.	6.6	63
223	Unraveling the structure and dynamics of the human DNAJB6b chaperone by NMR reveals insights into Hsp40-mediated proteostasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 21529-21538.	3.3	62
224	Architectural Accommodation in the Complex of Four p53 DNA Binding Domain Peptides with the p21/waf1/cip1 DNA Response Element. <i>Journal of Biological Chemistry</i> , 1997, 272, 14830-14841.	1.6	61
225	Solution Structure of the Phosphoryl Transfer Complex between the Cytoplasmic A Domain of the Mannitol Transporter IIMannitol and HPr of the Escherichia coli Phosphotransferase System. <i>Journal of Biological Chemistry</i> , 2002, 277, 42289-42298.	1.6	61
226	Using Conjoined Rigid Body/Torsion Angle Simulated Annealing to Determine the Relative Orientation of Covalently Linked Protein Domains from Dipolar Couplings. <i>Journal of Magnetic Resonance</i> , 2002, 154, 329-335.	1.2	61
227	Solution Structure of the Phosphoryl Transfer Complex between the Signal-transducing Protein IIGlucose and the Cytoplasmic Domain of the Glucose Transporter IICGlucose of the Escherichia coli Glucose Phosphotransferase System. <i>Journal of Biological Chemistry</i> , 2003, 278, 25191-25206.	1.6	61
228	Probing initial transient oligomerization events facilitating Huntingtin fibril nucleation at atomic resolution by relaxation-based NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 3562-3571.	3.3	61
229	Encounter complexes and dimensionality reduction in protein-protein association. <i>ELife</i> , 2014, 3, e01370.	2.8	61
230	Analysis of the relative contributions of the nuclear Overhauser interproton distance restraints and the empirical energy function in the calculation of oligonucleotide structures using restrained molecular dynamics. <i>Biochemistry</i> , 1989, 28, 5978-5984.	1.2	60
231	NMR Spectroscopic Analysis of the DNA Conformation Induced by the Human Testis Determining Factor SRY. <i>Biochemistry</i> , 1995, 34, 11998-12004.	1.2	60
232	Comparison of the solution nuclear magnetic resonance and crystal structures of interleukin-8. <i>Journal of Molecular Biology</i> , 1991, 217, 611-620.	2.0	59
233	Proton, nitrogen-15, carbon-13, carbon-13 monoxide assignments of human interleukin-4 using three-dimensional double- and triple-resonance heteronuclear magnetic resonance spectroscopy. <i>Biochemistry</i> , 1992, 31, 4334-4346.	1.2	59
234	Determining the Magnitude of the Fully Asymmetric Diffusion Tensor from Heteronuclear Relaxation Data in the Absence of Structural Information. <i>Journal of the American Chemical Society</i> , 1998, 120, 4889-4890.	6.6	59

#	ARTICLE	IF	CITATIONS
235	Conformational Changes in HIV-1 gp41 in the Course of HIV-1 Envelope Glycoprotein-Mediated Fusion and Inactivation. <i>Biochemistry</i> , 2005, 44, 12471-12479.	1.2	59
236	Global Dynamics and Exchange Kinetics of a Protein on the Surface of Nanoparticles Revealed by Relaxation-Based Solution NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2016, 138, 5789-5792.	6.6	59
237	Determination of the secondary structure of interleukin-8 by nuclear magnetic resonance spectroscopy. <i>Journal of Biological Chemistry</i> , 1989, 264, 18907-11.	1.6	59
238	The determination of the three-dimensional structure of barley serine proteinase inhibitor 2 by nuclear magnetic resonance, distance geometry and restrained molecular dynamics. <i>Protein Engineering, Design and Selection</i> , 1987, 1, 305-311.	1.0	58
239	Practical aspects of proton-carbon-carbon-proton three-dimensional correlation spectroscopy of <sup>13</sup> C-labeled proteins. <i>Journal of Magnetic Resonance</i> , 1990, 87, 620-627.	0.5	58
240	Preparation of Uniformly Isotope-labeled DNA Oligonucleotides for NMR Spectroscopy. <i>Journal of Biological Chemistry</i> , 1998, 273, 2374-2378.	1.6	58
241	Crystal Structures of the HIV-1 Inhibitory Cyanobacterial Protein MVL Free and Bound to Man3GlcNAc2. <i>Journal of Biological Chemistry</i> , 2005, 280, 29269-29276.	1.6	58
242	Mapping the Binding of the N-terminal Extracellular Tail of the CXCR4 Receptor to Stromal Cell-derived Factor-1. <i>Journal of Molecular Biology</i> , 2005, 345, 651-658.	2.0	58
243	Smooth statistical torsion angle potential derived from a large conformational database via adaptive kernel density estimation improves the quality of NMR protein structures. <i>Protein Science</i> , 2012, 21, 1824-1836.	3.1	58
244	Theoretical aspects of specific and non-specific equilibrium binding of proteins to DNA as studied by the nitrocellulose filter binding assay. <i>Journal of Molecular Biology</i> , 1982, 155, 447-466.	2.0	57
245	Multinuclear NMR characterization of two coexisting conformational states of the <i>Lactobacillus casei</i> dihydrofolate reductase-trimethoprim-NADP complex. <i>Biochemistry</i> , 1984, 23, 4733-4742.	1.2	56
246	An investigation into the solution structures of two self-complementary DNA oligomers, 5'-d(C-G-T-A-C-G) and 5'-d(A-C-G-C-G-C-G-T), by means of nuclear-Overhauser-enhancement measurements. <i>Biochemical Journal</i> , 1984, 221, 723-726.	1.7	56
247	A rigid disulfide-linked nitroxide side chain simplifies the quantitative analysis of PRE data. <i>Journal of Biomolecular NMR</i> , 2011, 51, 105-114.	1.6	56
248	Internal mobility in a double-stranded B DNA hexamer and undecamer. <i>FEBS Letters</i> , 1984, 172, 219-225.	1.3	55
249	Point mutations of human interleukin-1 with decreased receptor binding affinity. <i>FEBS Letters</i> , 1986, 209, 295-298.	1.3	55
250	The influence of stereospecific assignments on the determination of three-dimensional structures of proteins by nuclear magnetic resonance spectroscopy. <i>FEBS Letters</i> , 1989, 243, 223-233.	1.3	55
251	Localization of bound water in the solution structure of a complex of the erythroid transcription factor GATA-1 with DNA. <i>Structure</i> , 1994, 2, 89-94.	1.6	55
252	Rapid Identification of Medium- to Large-Scale Interdomain Motion in Modular Proteins Using Dipolar Couplings. <i>Journal of the American Chemical Society</i> , 2001, 123, 8634-8635.	6.6	55

#	ARTICLE	IF	CITATIONS
253	Using small angle solution scattering data in Xplor-NIH structure calculations. Progress in Nuclear Magnetic Resonance Spectroscopy, 2014, 80, 1-11.	3.9	55
254	Purification and characterization of the RNase H domain of HIV-1 reverse transcriptase expressed in recombinant Escherichia coli. FEBS Letters, 1990, 270, 76-80.	1.3	54
255	Comparison of the solution nuclear magnetic resonance and X-ray crystal structures of human recombinant interleukin-1 $\beta$ . Journal of Molecular Biology, 1991, 221, 47-53.	2.0	54
256	Solution NMR Structure of the 48-kDa IIAMannose-HPr Complex of the Escherichia coli Mannose Phosphotransferase System. Journal of Biological Chemistry, 2005, 280, 20775-20784.	1.6	54
257	The 1-1 hard pulse: A simple and effective method of water resonance suppression in FT 1H NMR. Journal of Magnetic Resonance, 1983, 54, 170-173.	0.5	53
258	The three-dimensional structure of alpha1-purothionin in solution: combined use of nuclear magnetic resonance, distance geometry and restrained molecular dynamics. EMBO Journal, 1986, 5, 2729-35.	3.5	53
259	Conformation of NAD <sup>+</sup> bound to yeast and horse liver alcohol dehydrogenase in solution. Journal of Molecular Biology, 1982, 157, 155-160.	2.0	51
260	Automated sequence- and stereo-specific assignment of methyl-labeled proteins by paramagnetic relaxation and methyl $\beta$ -methyl nuclear overhauser enhancement spectroscopy. Journal of Biomolecular NMR, 2011, 51, 319-328.	1.6	51
261	Structure, dynamics and biophysics of the cytoplasmic protein $\alpha$ -protein complexes of the bacterial phosphoenolpyruvate: sugar phosphotransferase system. Trends in Biochemical Sciences, 2013, 38, 515-530.	3.7	51
262	Antibody elicited against the gp41 N-heptad repeat (NHR) coiled-coil can neutralize HIV-1 with modest potency but non-neutralizing antibodies also bind to NHR mimetics. Virology, 2008, 377, 170-183.	1.1	50
263	Determination of the positions of bound water molecules in the solution structure of reduced human thioredoxin by heteronuclear three-dimensional nuclear magnetic resonance spectroscopy. Journal of Molecular Biology, 1991, 220, 209-216.	2.0	49
264	Localization of bound water in the solution structure of the immunoglobulin binding domain of streptococcal protein G. Journal of Molecular Biology, 1992, 223, 853-856.	2.0	49
265	Rapid screening for structural integrity of expressed proteins by heteronuclear NMR spectroscopy. Protein Science, 1996, 5, 174-177.	3.1	49
266	The extracellular domain of immunodeficiency virus gp41 protein: Expression in Escherichia coli, purification, and crystallization. Protein Science, 1997, 6, 1653-1660.	3.1	49
267	A simple and robust protocol for high-yield expression of perdeuterated proteins in Escherichia coli grown in shaker flasks. Journal of Biomolecular NMR, 2016, 66, 85-91.	1.6	49
268	Determination of the Secondary Structure and Folding Topology of an RNA Binding Domain of Mammalian hnRNP A1 Protein Using Three-Dimensional Heteronuclear Magnetic Resonance Spectroscopy. Biochemistry, 1994, 33, 2852-2858.	1.2	48
269	Conformation and dynamics of the Gag polyprotein of the human immunodeficiency virus 1 studied by NMR spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3374-3379.	3.3	48
270	Refinement of the solution structure of the DNA dodecamer 5'd(CGCGPATTCGCG)2 containing a stable purine-thymine base pair: combined use of nuclear magnetic resonance and restrained molecular dynamics. Biochemistry, 1988, 27, 4185-4197.	1.2	47



#	ARTICLE	IF	CITATIONS
271	Thermodynamics of Unfolding of the All .beta.-Sheet Protein Interleukin-1.beta.. Biochemistry, 1994, 33, 9327-9332.	1.2	47
272	Use of NMR to Detect Water Within Nonpolar Protein Cavities. Science, 1995, 270, 1847-1849.	6.0	47
273	Proton nuclear magnetic resonance study of hirudin: resonance assignment and secondary structure. Biochemistry, 1987, 26, 333-338.	1.2	46
274	Long-range <sup>15</sup> N- <sup>1</sup> H correlation as an aid to sequential proton resonance assignment of proteins Application to the DNA-binding protein inner from phage Mu. FEBS Letters, 1988, 238, 17-21.	1.3	46
275	Theoretical and computational advances in biomolecular NMR spectroscopy. Current Opinion in Structural Biology, 2002, 12, 146-153.	2.6	46
276	Structure of calmodulin-target peptide complexes. Current Opinion in Structural Biology, 1993, 3, 838-845.	2.6	45
277	Characterizing Methyl-Bearing Side Chain Contacts and Dynamics Mediating Amyloid $\beta^2$ Protofibril Interactions Using <sup>13</sup> C <sup>13</sup> C-methyl- $\beta$ -DEPT and Lifetime Line Broadening. Angewandte Chemie - International Edition, 2014, 53, 10345-10349.	7.2	45
278	A comparison of the restrained molecular dynamics and distance geometry methods for determining three-dimensional structures of proteins on the basis of interproton distances. FEBS Letters, 1987, 213, 269-277.	1.3	44
279	Structural Basis of HIV-1 Neutralization by Affinity Matured Fabs Directed against the Internal Trimeric Coiled-Coil of gp41. PLoS Pathogens, 2010, 6, e1001182.	2.1	44
280	Nuclear magnetic resonance study of the solution structure of $\beta$ 1-purothionin. Journal of Molecular Biology, 1987, 193, 571-578.	2.0	43
281	Experimental support for the "hydrophobic zipper" hypothesis. Science, 1994, 263, 536-536.	6.0	43
282	Solution structure of the Mu end DNA-binding $\beta$ subdomain of phage Mu transposase: modular DNA recognition by two tethered domains. EMBO Journal, 1997, 16, 7532-7541.	3.5	43
283	NMR-Driven Discovery of Benzoylanthranilic Acid Inhibitors of Far Upstream Element Binding Protein Binding to the Human Oncogene c-myc Promoter. Journal of Medicinal Chemistry, 2004, 47, 4851-4857.	2.9	43
284	TROSY-Based <i>i</i> -z-Exchange Spectroscopy: Application to the Determination of the Activation Energy for Intermolecular Protein Translocation between Specific Sites on Different DNA Molecules. Journal of the American Chemical Society, 2007, 129, 13232-13237.	6.6	43
285	Hybrid Approaches to Structural Characterization of Conformational Ensembles of Complex Macromolecular Systems Combining NMR Residual Dipolar Couplings and Solution X-ray Scattering. Chemical Reviews, 2016, 116, 6305-6322.	23.0	43
286	Refinement of the solution structure of the B DNA hexamer 5 $\beta$ d(C-G-T-A-C-G) <sub>2</sub> on the basis of inter-proton distance data. Journal of Molecular Biology, 1985, 185, 219-226.	2.0	42
287	Comparison of four independently determined structures of human recombinant interleukin $\beta$ 4. Nature Structural and Molecular Biology, 1994, 1, 301-310.	3.6	42
288	Monomer $\beta$ -trimer equilibrium of the ectodomain of SIV gp41: Insight into the mechanism of peptide inhibition of HIV infection. Protein Science, 1999, 8, 1904-1907.	3.1	41

#	ARTICLE	IF	CITATIONS
289	A nuclear-Overhauser-enhancement study of the solution structure of a double-stranded DNA undecamer comprising a portion of the specific target site for the cyclic-AMP-receptor protein in the gal operon. Sequential resonance assignment. FEBS Journal, 1984, 141, 119-129.	0.2	40
290	The binding of the cyclic AMP receptor protein to synthetic DNA sites containing permutations in the consensus sequence TGTGA. Biochemical Journal, 1987, 246, 227-232.	1.7	40
291	Purification and characterization of the DNA-binding protein Ner of bacteriophage Mu. Gene, 1988, 65, 259-268.	1.0	40
292	Solution structure of the His 12 → Cys mutant of the N-terminal zinc binding domain of HIV-1 integrase complexed to cadmium. Protein Science, 1998, 7, 2669-2674.	3.1	40
293	The solution structure of the Leu22 → Val mutant AREA DNA binding domain complexed with a TGATAG core element defines a role for hydrophobic packing in the determination of specificity 1 Edited by P. E. Wright. Journal of Molecular Biology, 1998, 277, 621-634.	2.0	40
294	Interplay between conformational selection and induced fit in multidomain protein-ligand binding probed by paramagnetic relaxation enhancement. Biophysical Chemistry, 2014, 186, 3-12.	1.5	40
295	Recombinant-derived interleukin-1 $\beta$ stabilized against specific deamidation. Protein Engineering, Design and Selection, 1987, 1, 413-417.	1.0	39
296	Three-dimensional triple-resonance NMR of $^{13}\text{C}/^{15}\text{N}$ -enriched proteins using constant-time evolution. Journal of Magnetic Resonance, 1991, 94, 209-213.	0.5	39
297	An Efficient Triple-Resonance Experiment for Proton-Directed Sequential Backbone Assignment of Medium-Sized Proteins. Journal of Magnetic Resonance Series B, 1994, 105, 196-198.	1.6	39
298	A Novel Membrane Anchor Function for the N-terminal Amphipathic Sequence of the Signal-transducing Protein IIAGlucose of the Escherichia coli Phosphotransferase System. Journal of Biological Chemistry, 2000, 275, 39811-39814.	1.6	39
299	Water in the Polar and Nonpolar Cavities of the Protein Interleukin-1 $\beta$ . Journal of Physical Chemistry B, 2010, 114, 16290-16297.	1.2	39
300	Structure-Independent Analysis of the Breadth of the Positional Distribution of Disordered Groups in Macromolecules from Order Parameters for Long, Variable-Length Vectors Using NMR Paramagnetic Relaxation Enhancement. Journal of the American Chemical Society, 2010, 132, 13346-13356.	6.6	39
301	Analysis of an enzyme-substrate complex by x-ray crystallography and transferred nuclear overhauser enhancement measurements: porcine pancreatic elastase and a hexapeptide. Biochemistry, 1988, 27, 725-730.	1.2	38
302	Determination of Three-Bond $^1\text{H}$ - $^{31}\text{P}$ Couplings in Nucleic Acids and Protein-Nucleic Acid Complexes by Quantitative Correlation Spectroscopy. Journal of Magnetic Resonance, 1998, 134, 164-167.	1.2	38
303	Contrast-Matched Small-Angle X-ray Scattering from a Heavy-Atom-Labeled Protein in Structure Determination: Application to a Lead-Substituted Calmodulin-Peptide Complex. Journal of the American Chemical Society, 2012, 134, 14686-14689.	6.6	38
304	Dependence of Distance Distributions Derived from Double Electron-Electron Resonance Pulsed EPR Spectroscopy on Pulse Sequence Time. Angewandte Chemie - International Edition, 2015, 54, 5336-5339.	7.2	38
305	Proton, carbon-13, and phosphorus-31 nuclear magnetic resonance studies of the dihydrofolate reductase-NADP-folate complex: characterization of three coexisting conformational states. Biochemistry, 1982, 21, 5831-5838.	1.2	37
306	Determination of the backbone conformation of secretin by restrained molecular dynamics on the basis of interproton distance data. FEBS Journal, 1988, 171, 479-484.	0.2	37

#	ARTICLE	IF	CITATIONS
307	Relationships Between the Precision of High-Resolution Protein NMR Structures, Solution-Order Parameters, and Crystallographic B Factors. <i>Journal of Magnetic Resonance Series B</i> , 1993, 101, 325-327.	1.6	37
308	The oligomerization domain of p53: Crystal structure of the trigonal form. <i>FEBS Letters</i> , 1996, 399, 166-170.	1.3	37
309	Determination of the secondary structure and global topology of the 44 kDa ectodomain of gp41 of the simian immunodeficiency virus by multidimensional nuclear magnetic resonance spectroscopy. <i>Journal of Molecular Biology</i> , 1997, 271, 819-826.	2.0	37
310	A Monoclonal Fab Derived from a Human Nonimmune Phage Library Reveals a New Epitope on gp41 and Neutralizes Diverse Human Immunodeficiency Virus Type 1 Strains. <i>Journal of Virology</i> , 2007, 81, 12946-12953.	1.5	37
311	Combined Use of Residual Dipolar Couplings and Solution X-ray Scattering To Rapidly Probe Rigid-Body Conformational Transitions in a Non-phosphorylatable Active-Site Mutant of the 128 kDa Enzyme I Dimer. <i>Journal of the American Chemical Society</i> , 2011, 133, 424-427.	6.6	37
312	Intra- and intermolecular translocation of the bi-domain transcription factor Oct1 characterized by liquid crystal and paramagnetic NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E169-76.	3.3	37
313	Nuclear magnetic resonance study of the globular domain of chicken histone H5: resonance assignment and secondary structure.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1986, 83, 7628-7632.	3.3	36
314	Protein structure determination in solution by two-dimensional and three-dimensional nuclear magnetic resonance spectroscopy. <i>Analytical Chemistry</i> , 1990, 62, 2-15.	3.2	36
315	Improving NMR Structures of RNA. <i>Structure</i> , 2016, 24, 806-815.	1.6	36
316	Structure of the ribotrinucleoside diphosphate codon UpUpC bound to tRNAPhe from yeast. <i>Journal of Molecular Biology</i> , 1984, 174, 163-173.	2.0	35
317	Determination of the secondary structure of the DNA binding protein Ner from phage .mu. using proton homonuclear and nitrogen-15-proton heteronuclear NMR spectroscopy. <i>Biochemistry</i> , 1989, 28, 5081-5089.	1.2	35
318	Secondary structure of the ribonuclease H domain of the human immunodeficiency virus reverse transcriptase in solution using three-dimensional double and triple resonance heteronuclear magnetic resonance spectroscopy. <i>Journal of Molecular Biology</i> , 1991, 221, 1081-1090.	2.0	35
319	Symmetry and asymmetry in the function of Escherichia coli integration host factor: implications for target identification by DNA-binding proteins. <i>Current Biology</i> , 1994, 4, 477-487.	1.8	35
320	<sup>1</sup> H-NMR Studies on Nucleotide Binding to the Sarcoplasmic Reticulum Ca <sup>2+</sup> ATPase. <i>FEBS Journal</i> , 2005, 128, 113-117.	0.2	35
321	Binding kinetics and substrate selectivity in HIV-1 protease-Gag interactions probed at atomic resolution by chemical exchange NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9855-E9862.	3.3	35
322	An unusual conformation of NAD <sup>+</sup> bound to sorbitoldehydrogenase?. <i>Journal of Molecular Biology</i> , 1984, 172, 559-572.	2.0	34
323	A <sup>1</sup> H-NMR study of human interleukin-1beta. Sequence-specific assignment of aromatic residues using site-directed mutant proteins. <i>FEBS Journal</i> , 1986, 161, 37-43.	0.2	34
324	Exploring translocation of proteins on DNA by NMR. <i>Journal of Biomolecular NMR</i> , 2011, 51, 209-219.	1.6	34

#	ARTICLE	IF	CITATIONS
325	Chaperonin GroEL accelerates protofibril formation and decorates fibrils of the Het-s prion protein. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 9104-9109.	3.3	34
326	Interaction of Huntingtin Exon-1 Peptides with Lipid-Based Micellar Nanoparticles Probed by Solution NMR and Q-Band Pulsed EPR. Journal of the American Chemical Society, 2018, 140, 6199-6202.	6.6	34
327	<sup>19</sup> F-n.m.r. studies of 3- <sup>5</sup> -difluoromethotrexate binding to Lactobacillus casei dihydrofolate reductase. Molecular motion and coenzyme-induced conformational changes. Biochemical Journal, 1984, 217, 659-666.	1.7	33
328	Probing the sequence-specific interaction of the cyclic AMP receptor protein with DNA by site-directed mutagenesis. Biochemical Journal, 1987, 242, 645-653.	1.7	33
329	Large interdomain rearrangement triggered by suppression of micro- to millisecond dynamics in bacterial Enzyme I. Nature Communications, 2015, 6, 5960.	5.8	33
330	Protein NMR: Boundless opportunities. Journal of Magnetic Resonance, 2019, 306, 187-191.	1.2	33
331	Kinetic and structural studies on the intermediates formed in the reactions of 5'-adenosine monophosphate and 5'-guanosine monophosphate with cis-dichlorodiammineplatinum(II) using proton and platinum-195 magnetic resonance spectroscopy. Journal of the American Chemical Society, 1982, 104, 1369-1375.	6.6	32
332	The structure of the double-stranded RNA pentamer 5'(CACAG) . 5'(CUGUG) determined by nuclear Overhauser enhancement measurements: Interproton distance determination and structure refinement on the basis of X-ray coordinates. FEBS Journal, 1985, 151, 153-165.	0.2	32
333	Solution structure of the $\beta^3$ subdomain of the Mu end DNA-binding domain of phage Mu transposase. Journal of Molecular Biology, 1997, 273, 19-25.	2.0	32
334	A simple and reliable approach to docking protein-protein complexes from very sparse NOE-derived intermolecular distance restraints. Journal of Biomolecular NMR, 2006, 36, 37-44.	1.6	32
335	The mechanism of reaction of fully reduced membrane-bound cytochrome oxidase with oxygen at 176K. Biochemical Journal, 1978, 173, 799-810.	1.7	31
336	Conformational selection of syn -cAMP upon binding to the cAMP receptor protein. FEBS Letters, 1981, 136, 160-164.	1.3	31
337	Visualization of cAMP receptor protein-induced DNA kinking by electron microscopy. Journal of Molecular Biology, 1984, 179, 751-757.	2.0	31
338	A simple method for delineating well-defined and variable regions in protein structures determined from interproton distance data. FEBS Letters, 1987, 219, 11-16.	1.3	31
339	Sequential resonance assignment and secondary structure determination of the Ascaris trypsin inhibitor, a member of a novel class of proteinase inhibitors. Biochemistry, 1990, 29, 183-189.	1.2	31
340	Three-dimensional Solution Structure of the Cytoplasmic B Domain of the Mannitol Transporter IIMannitol of the Escherichia coli Phosphotransferase System. Journal of Biological Chemistry, 2004, 279, 39115-39121.	1.6	31
341	Backbone dynamics of the oligomerization domain of p53 determined from <sup>15</sup> N NMR relaxation measurements. Protein Science, 1995, 4, 855-862.	3.1	31
342	TiO <sub>2</sub> Nanoparticles Catalyze Oxidation of Huntingtin Exon 1-Derived Peptides Impeding Aggregation: A Quantitative NMR Study of Binding and Kinetics. Journal of the American Chemical Society, 2019, 141, 94-97.	6.6	31

#	ARTICLE	IF	CITATIONS
343	Modeling the three-dimensional structure of the monocyte chemoattractant and activating protein MCAF/MCP-1 on the basis of the solution structure of interleukin-8. <i>Protein Engineering, Design and Selection</i> , 1991, 4, 263-269.	1.0	30
344	Analysis of hydrophobicity in the $\beta$ and $\beta^2$ chemokine families and its relevance to dimerization. <i>Protein Science</i> , 1994, 3, 2064-2072.	3.1	30
345	A Potential Involving Multiple Proton Chemical-Shift Restraints for Nonstereospecifically Assigned Methyl and Methylene Protons. <i>Journal of Magnetic Resonance Series B</i> , 1996, 112, 79-81.	1.6	30
346	Impact of Phosphorylation on Structure and Thermodynamics of the Interaction between the N-terminal Domain of Enzyme I and the Histidine Phosphocarrier Protein of the Bacterial Phosphotransferase System. <i>Journal of Biological Chemistry</i> , 2008, 283, 18980-18989.	1.6	30
347	A $^1\text{H}$ n.m.r. study of the role of the glutamate moiety in the binding of methotrexate to <i>Lactobacillus casei</i> dihydrofolate reductase. <i>British Journal of Pharmacology</i> , 1984, 81, 309-315.	2.7	29
348	Core mutants of the immunoglobulin binding domain of streptococcal protein G: Stability and structural integrity. <i>FEBS Letters</i> , 1996, 398, 312-316.	1.3	29
349	Differential Inhibition of HIV-1 and SIV Envelope-Mediated Cell Fusion by C34 Peptides Derived from the C-Terminal Heptad Repeat of gp41 from Diverse Strains of HIV-1, HIV-2, and SIV. <i>Journal of Medicinal Chemistry</i> , 2005, 48, 3036-3044.	2.9	29
350	A Pseudopotential for Improving the Packing of Ellipsoidal Protein Structures Determined from NMR Data. <i>Journal of Physical Chemistry B</i> , 2008, 112, 6070-6073.	1.2	29
351	Sequestering of the Prehairpin Intermediate of gp41 by Peptide N36 Mut(e,g) Potentiates the Human Immunodeficiency Virus Type 1 Neutralizing Activity of Monoclonal Antibodies Directed against the N-Terminal Helical Repeat of gp41. <i>Journal of Virology</i> , 2008, 82, 10032-10041.	1.5	29
352	Probing the mechanism of inhibition of amyloid- $\beta$ (1-42)-induced neurotoxicity by the chaperonin GroEL. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11924-E11932.	3.3	29
353	Isotope-Filtered 2D HOHAHA Spectroscopy of a Peptide-Protein Complex Using Heteronuclear Hartmann-Hahn Dephasing. <i>Journal of Magnetic Resonance Series A</i> , 1994, 106, 269-273.	1.6	28
354	Biophysical Characterization of gp41 Aggregates Suggests a Model for the Molecular Mechanism of HIV-associated Neurological Damage and Dementia. <i>Journal of Biological Chemistry</i> , 2000, 275, 19877-19882.	1.6	28
355	Conformational Selection and Substrate Binding Regulate the Monomer/Dimer Equilibrium of the C-terminal domain of Escherichia coli Enzyme I. <i>Journal of Biological Chemistry</i> , 2012, 287, 26989-26998.	1.6	28
356	The Length of the Calmodulin Linker Determines the Extent of Transient Interdomain Association and Target Affinity. <i>Journal of the American Chemical Society</i> , 2013, 135, 9648-9651.	6.6	28
357	Dynamic equilibrium between closed and partially closed states of the bacterial Enzyme I unveiled by solution NMR and X-ray scattering. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11565-11570.	3.3	28
358	Long Distance Measurements up to 160 Å in the GroEL Tetradecamer Using Q-Band DEER EPR Spectroscopy. <i>Angewandte Chemie</i> , 2016, 128, 16137-16141.	1.6	28
359	Time-resolved DEER EPR and solid-state NMR afford kinetic and structural elucidation of substrate binding to $\text{Ca}^{2+}$ -ligated calmodulin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	28
360	Refinement of the solution structure of the ribonucleotide 5'r(GCAUGC) <sub>2</sub> : combined use of nuclear magnetic resonance and restrained molecular dynamics. <i>Biochemistry</i> , 1988, 27, 1735-1743.	1.2	27

#	ARTICLE	IF	CITATIONS
361	Mutations in the cyclic AMP binding site of the cyclic AMP receptor protein of <i>Escherichia coli</i> . <i>Biochemical Journal</i> , 1988, 253, 801-807.	1.7	27
362	A Common Interface on Histidine-containing Phosphocarrier Protein for Interaction with Its Partner Proteins. <i>Journal of Biological Chemistry</i> , 2000, 275, 16401-16403.	1.6	27
363	Characterization and HIV-1 Fusion Inhibitory Properties of Monoclonal Fabs Obtained From a Human Non-immune Phage Library Selected Against Diverse Epitopes of the Ectodomain of HIV-1 gp41. <i>Journal of Molecular Biology</i> , 2005, 353, 945-951.	2.0	27
364	Solution Structure of a Post-transition State Analog of the Phosphotransfer Reaction between the A and B Cytoplasmic Domains of the Mannitol Transporter IIMannitol of the <i>Escherichia coli</i> Phosphotransferase System. <i>Journal of Biological Chemistry</i> , 2006, 281, 8939-8949.	1.6	27
365	Solution NMR Structures of Productive and Non-productive Complexes between the A and B Domains of the Cytoplasmic Subunit of the Mannose Transporter of the <i>Escherichia coli</i> Phosphotransferase System. <i>Journal of Biological Chemistry</i> , 2008, 283, 11024-11037.	1.6	27
366	Using the Experimentally Determined Components of the Overall Rotational Diffusion Tensor To Restrain Molecular Shape and Size in NMR Structure Determination of Globular Proteins and Protein-Protein Complexes. <i>Journal of the American Chemical Society</i> , 2009, 131, 9522-9531.	6.6	27
367	Interplay between Minor and Major Groove-binding Transcription Factors Sox2 and Oct1 in Translocation on DNA Studied by Paramagnetic and Diamagnetic NMR. <i>Journal of Biological Chemistry</i> , 2012, 287, 14349-14363.	1.6	27
368	A two-dimensional NMR study of the solution structure of a DNA dodecamer comprising the consensus sequence for the specific DNA-binding sites of the glucocorticoid receptor protein. <i>FEBS Journal</i> , 1984, 145, 629-636.	0.2	26
369	A proton nuclear magnetic resonance assignment and secondary structure determination of recombinant human thioredoxin. <i>Biochemistry</i> , 1989, 28, 7088-7097.	1.2	26
370	Determination of the secondary structure and folding topology of human interleukin-4 using three-dimensional heteronuclear magnetic resonance spectroscopy. <i>Biochemistry</i> , 1992, 31, 4347-4353.	1.2	26
371	Structural Basis for Enzyme I Inhibition by $\alpha$ -Ketoglutarate. <i>ACS Chemical Biology</i> , 2013, 8, 1232-1240.	1.6	26
372	The Energetics of a Three-State Protein Folding System Probed by High-Pressure Relaxation Dispersion NMR Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 11157-11161.	7.2	26
373	Conformation of the DNA undecamer 5'-d(A-A-G-T-G-T-G-A-T-A-T) bound to the single-stranded DNA binding protein of <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1986, 187, 119-124.	2.0	25
374	Low resolution structure of interleukin-1 $\beta$ in solution derived from $^1\text{H}$ - $^{15}\text{N}$ heteronuclear three-dimensional nuclear magnetic resonance spectroscopy. <i>Journal of Molecular Biology</i> , 1990, 214, 811-817.	2.0	25
375	Transient HIV-1 Gag-protease interactions revealed by paramagnetic NMR suggest origins of compensatory drug resistance mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12456-12461.	3.3	25
376	Confinement and Stabilization of Fyn SH3 Folding Intermediate Mimetics within the Cavity of the Chaperonin GroEL Demonstrated by Relaxation-Based NMR. <i>Biochemistry</i> , 2017, 56, 903-906.	1.2	25
377	N-terminal-methionylated interleukin-1 $\beta$ has reduced receptor-binding affinity. <i>FEBS Letters</i> , 1987, 215, 160-164.	1.3	24
378	Computer-aided sequential assignment of protein $^1\text{H}$ NMR spectra. <i>Journal of Magnetic Resonance</i> , 1988, 80, 119-127.	0.5	24

#	ARTICLE	IF	CITATIONS
379	Practical and theoretical aspects of three-dimensional homonuclear Hartmann-Hahn-nuclear overhauser enhancement spectroscopy of proteins. <i>Journal of Magnetic Resonance</i> , 1989, 83, 450-472.	0.5	24
380	Preparation, characterization and application of interleukin-1beta mutant proteins with surface-accessible cysteine residues. <i>FEBS Journal</i> , 1989, 179, 565-571.	0.2	24
381	Peptides from Second Extracellular Loop of C-C Chemokine Receptor Type 5 (CCR5) Inhibit Diverse Strains of HIV-1. <i>Journal of Biological Chemistry</i> , 2012, 287, 15076-15086.	1.6	24
382	The mechanism of reaction of ferricyanide-pretreated mixed-valence-state membrane-bound cytochrome oxidase with oxygen at 173 K. <i>Biochemical Journal</i> , 1978, 173, 811-820.	1.7	23
383	Proton nuclear magnetic resonance study of the histidine residues of the Escherichia coli adenosine cyclic 3',5'-phosphate receptor protein. pH titration behavior, deuterium exchange, and partial assignments. <i>Biochemistry</i> , 1982, 21, 4048-4053.	1.2	23
384	Three-dimensional homonuclear Hartmann-Hahn-nuclear overhauser enhancement spectroscopy in H <sub>2</sub> O and its application to proteins. <i>Journal of Magnetic Resonance</i> , 1989, 81, 212-216.	0.5	23
385	<sup>1</sup> H and <sup>15</sup> N resonance assignments and secondary structure of the human thioredoxin C62A, C69A, C73A mutant. <i>Journal of Biomolecular NMR</i> , 1992, 2, 431-445.	1.6	23
386	Synergistic Inhibition of HIV-1 Envelope-Mediated Membrane Fusion by Inhibitors Targeting the N and C-Terminal Heptad Repeats of gp41. <i>Journal of Molecular Biology</i> , 2006, 364, 283-289.	2.0	23
387	Coupling between internal dynamics and rotational diffusion in the presence of exchange between discrete molecular conformations. <i>Journal of Chemical Physics</i> , 2012, 136, 034108.	1.2	23
388	An S/T motif controls reversible oligomerization of the Hsp40 chaperone DNAJB6b through subtle reorganization of a $\beta^2$ sheet backbone. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30441-30450.	3.3	23
389	Quantitative Interpretation of Solvent Paramagnetic Relaxation for Probing Protein-Cosolute Interactions. <i>Journal of the American Chemical Society</i> , 2020, 142, 8281-8290.	6.6	23
390	NMR structures of proteins and protein complexes beyond 20,000 M(r). <i>Nature Structural Biology</i> , 1997, 4 Suppl, 849-53.	9.7	23
391	<sup>1</sup> H-NMR studies on nucleotide binding to the catalytic sites of bovine mitochondrial F <sub>1</sub> -ATPase. <i>FEBS Letters</i> , 1988, 242, 178-182.	1.3	22
392	The wing of the enhancer-binding domain of Mu phage transposase is flexible and is essential for efficient transposition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 1146-1150.	3.3	22
393	3D NMR Experiments for Measuring <sup>15</sup> N Relaxation Data of Large Proteins: Application to the 44 kDa Ectodomain of SIV gp41. <i>Journal of Magnetic Resonance</i> , 1998, 135, 368-372.	1.2	22
394	Tautomeric state and pK <sub>a</sub> of the phosphorylated active site histidine in the N-terminal domain of enzyme I of the Escherichia coli phosphoenolpyruvate: Sugar phosphotransferase system. <i>Protein Science</i> , 1998, 7, 789-793.	3.1	22
395	Temperature-Dependent Intermediates in HIV-1 Envelope Glycoprotein-Mediated Fusion Revealed by Inhibitors that Target N- and C-Terminal Helical Regions of HIV-1 gp41. <i>Biochemistry</i> , 2004, 43, 8230-8233.	1.2	22
396	Intramolecular domain-domain association/dissociation and phosphoryl transfer in the mannitol transporter of Escherichia coli are not coupled. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 3153-3158.	3.3	22

#	ARTICLE	IF	CITATIONS
397	Affinity maturation by targeted diversification of the CDR-H2 loop of a monoclonal Fab derived from a synthetic naïve human antibody library and directed against the internal trimeric coiled-coil of gp41 yields a set of Fabs with improved HIV-1 neutralization potency and breadth. <i>Virology</i> , 2009, 393, 112-119.	1.1	22
398	Targeting a Dark Excited State of HIV-1 Nucleocapsid by Antiretroviral Thioesters Revealed by NMR Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 2687-2691.	7.2	22
399	Spin-State Selective Carbon-Detected HNC0 with TROSY Optimization in All Dimensions and Double Echo Antiecho Sensitivity Enhancement in Both Indirect Dimensions. <i>Journal of the American Chemical Society</i> , 2007, 129, 5484-5491.	6.6	21
400	<sup>13</sup> C NMR evidence for three slowly interconverting conformations of the dihydrofolate reductase-NADP <sup>+</sup> -folate complex. <i>Biochemical and Biophysical Research Communications</i> , 1981, 101, 1139-1144.	1.0	20
401	Glucose-6-phosphate dehydrogenase. A transferred nuclear Overhauser enhancement study of NADP <sup>+</sup> conformations in enzyme-coenzyme binary complexes. <i>FEBS Journal</i> , 1984, 145, 365-371.	0.2	20
402	Determination of ligand conformation in macromolecular complexes using the transferred nuclear overhauser effect. <i>Biochemical Pharmacology</i> , 1990, 40, 115-119.	2.0	20
403	Automated error-tolerant macromolecular structure determination from multidimensional nuclear Overhauser enhancement spectra and chemical shift assignments: improved robustness and performance of the PASD algorithm. <i>Journal of Biomolecular NMR</i> , 2008, 41, 221-239.	1.6	20
404	Investigation of the Structure and Dynamics of the Capsid "Spacer Peptide...1" Nucleocapsid Fragment of the HIV-1 Gag Polyprotein by Solution NMR Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 1025-1028.	7.2	20
405	Abrogation of prenucleation, transient oligomerization of the Huntingtin exon 1 protein by human profilin I. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5844-5852.	3.3	20
406	Structural Basis of the Association of HIV-1 Matrix Protein with DNA. <i>PLoS ONE</i> , 2010, 5, e15675.	1.1	20
407	Interproton distance measurements in solution for a double-stranded DNA undecamer comprising a portion of the specific target site for the cyclic AMP receptor protein in the gal operon. <i>FEBS Letters</i> , 1984, 175, 117-123.	1.3	19
408	Slow conformational dynamics at the metal coordination site of a zinc finger. <i>Journal of the American Chemical Society</i> , 1991, 113, 4350-4351.	6.6	19
409	Structures of larger proteins, protein-ligand and protein-DNA complexes by multi-dimensional heteronuclear NMR. <i>Progress in Biophysics and Molecular Biology</i> , 1994, 62, 153-184.	1.4	19
410	Submillisecond Freezing Permits Cryoprotectant-Free EPR Double Electron-Electron Resonance Spectroscopy. <i>ChemPhysChem</i> , 2020, 21, 1224-1229.	1.0	19
411	The kinetics and thermodynamics of the reaction of solid-state fully reduced membrane-bound cytochrome oxidase with carbon monoxide as studied by dual-wavelength multichannel spectroscopy and flash photolysis. <i>Biochemical Journal</i> , 1978, 175, 709-725.	1.7	18
412	Is human thioredoxin monomeric or dimeric?. <i>Protein Science</i> , 1999, 8, 426-429.	3.1	18
413	Seeing the invisible by paramagnetic and diamagnetic NMR. <i>Biochemical Society Transactions</i> , 2013, 41, 1343-1354.	1.6	18
414	Exchange saturation transfer and associated NMR techniques for studies of protein interactions involving high-molecular-weight systems. <i>Journal of Biomolecular NMR</i> , 2019, 73, 461-469.	1.6	18



#	ARTICLE	IF	CITATIONS
415	Spatial domain organization in the HIV-1 reverse transcriptase p66 homodimer precursor probed by double electron-electron resonance EPR. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17809-17816.	3.3	18
416	Specific DNA binding to a major histocompatibility complex enhancer sequence by a synthetic 57-residue double zinc finger peptide from a human enhancer binding protein.. Journal of Biological Chemistry, 1991, 266, 7306-7311.	1.6	18
417	An investigation into the solution structure of the single-stranded DNA undecamer 5'd AAGTGTGATAT by means of nuclear Overhauser enhancement measurements. European Biophysics Journal, 1984, 11, 95-102.	1.2	17
418	Complexes of Neutralizing and Non-Neutralizing Affinity Matured Fabs with a Mimetic of the Internal Trimeric Coiled-Coil of HIV-1 gp41. PLoS ONE, 2013, 8, e78187.	1.1	17
419	A NMR experiment for simultaneous correlations of valine and leucine/isoleucine methyls with carbonyl chemical shifts in proteins. Journal of Biomolecular NMR, 2014, 58, 1-8.	1.6	17
420	Decorrelating Kinetic and Relaxation Parameters in Exchange Saturation Transfer NMR: A Case Study of N-Terminal Huntingtin Peptides Binding to Unilamellar Lipid Vesicles. Journal of Physical Chemistry B, 2018, 122, 11271-11278.	1.2	17
421	NMR methods for exploring "dark" states in ligand binding and protein-protein interactions. Progress in Nuclear Magnetic Resonance Spectroscopy, 2022, 128, 1-24.	3.9	17
422	The polypeptide fold of the globular domain of histone H5 in solution. A study using nuclear magnetic resonance, distance geometry and restrained molecular dynamics. EMBO Journal, 1987, 6, 1833-42.	3.5	17
423	Characterization of the electronic properties and geometric environment of the iron atom in the "myoglobin hydrogen-peroxide" Complex by soret-excited resonance raman spectroscopy. Inorganica Chimica Acta, 1980, 46, 77-84.	1.2	16
424	Specific DNA binding of the cyclic AMP receptor protein to a synthetic oligodeoxyribonucleotide. FEBS Letters, 1983, 159, 102-106.	1.3	16
425	Comparison of histidine proton magnetic resonances of human carbonmonoxyhaemoglobin in different buffers. Journal of Molecular Biology, 1985, 186, 471-473.	2.0	16
426	A proton nuclear magnetic resonance study of the conformation of bovine anaphylatoxin C5a in solution. FEBS Letters, 1988, 238, 289-294.	1.3	16
427	Direct Use of <sup>15</sup> N Relaxation Rates as Experimental Restraints on Molecular Shape and Orientation for Docking of Protein~Protein Complexes. Journal of the American Chemical Society, 2010, 132, 5987-5989.	6.6	16
428	Impact of Protein/Protein Interactions on Global Intermolecular Translocation Rates of the Transcription Factors Sox2 and Oct1 between DNA Cognate Sites Analyzed by z-Exchange NMR Spectroscopy. Journal of Biological Chemistry, 2012, 287, 26962-26970.	1.6	16
429	Quantitative Resolution of Monomer~Dimer Populations by Inversion Modulated DEER EPR Spectroscopy. ChemPhysChem, 2016, 17, 2987-2991.	1.0	16
430	Quantitative Characterization of Configurational Space Sampled by HIV-1 Nucleocapsid Using Solution NMR, X-ray Scattering and Protein Engineering. ChemPhysChem, 2016, 17, 1548-1552.	1.0	16
431	Probing transient excited states of the bacterial cell division regulator MinE by relaxation dispersion NMR spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25446-25455.	3.3	16
432	A three-dimensional potential of mean force to improve backbone and sidechain hydrogen bond geometry in Xplor~NIH protein structure determination. Protein Science, 2020, 29, 100-110.	3.1	16

#	ARTICLE	IF	CITATIONS
433	Specific DNA binding to a major histocompatibility complex enhancer sequence by a synthetic 57-residue double zinc finger peptide from a human enhancer binding protein. <i>Journal of Biological Chemistry</i> , 1991, 266, 7306-11.	1.6	16
434	DNA binding of cAMP receptor protein and its N-terminal core stabilizes the double helix and is modulated by the allosteric effector cAMP. <i>FEBS Letters</i> , 1982, 139, 37-40.	1.3	15
435	A nuclear Overhauser enhancement study on the imino proton resonances of a DNA pentadecamer comprising the specific target site of the cyclic AMP receptor protein in the ara BAD operon. <i>FEBS Letters</i> , 1984, 165, 216-222.	1.3	15
436	Overproduction of the cyclic AMP receptor protein of <i>Escherichia coli</i> and expression of the engineered C-terminal DNA-binding domain. <i>Biochemical Journal</i> , 1986, 236, 643-649.	1.7	15
437	Site directed mutants of human interleukin-1 $\alpha$ : A 1 H-NMR and receptor binding study. <i>FEBS Letters</i> , 1988, 231, 135-138.	1.3	15
438	A short recollection on the paper entitled "A common sense approach to peak picking in two-, three-, and four-dimensional spectra using automatic computer analysis of contour diagrams" by D.S. Garrett, R. Powers, A.M. Gronenborn, and G.M. Clore [ <i>J. Magn. Reson.</i> 95 (1991) 214-220]. <i>Journal of Magnetic Resonance</i> , 2011, 213, 364-365.	1.2	15
439	An efficient protocol for incorporation of an unnatural amino acid in perdeuterated recombinant proteins using glucose-based media. <i>Journal of Biomolecular NMR</i> , 2012, 52, 191-195.	1.6	15
440	Dissecting intrinsic chaperonin activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 7-8.	3.3	14
441	Sensitivity improvement for correlations involving arginine side-chain N $\mu$ /H $\mu$ resonances in multi-dimensional NMR experiments using broadband 15N 180 $^\circ$ pulses. <i>Journal of Biomolecular NMR</i> , 2006, 36, 251-257.	1.6	14
442	Low-temperature kinetics of the reactions of fully reduced membrane-bound cytochrome oxidase with oxygen in the Soret, $\beta$ and near-infrared regions. <i>Biochemical Journal</i> , 1979, 177, 613-621.	1.7	13
443	The kinetics of the reactions of low spin ferric haem undecapeptide with hydrogen peroxide. <i>Inorganica Chimica Acta</i> , 1981, 56, 143-148.	1.2	13
444	Determination of the conformations of cyclic nucleotides bound to the N-terminal core of the cyclic AMP receptor protein of <i>Escherichia coli</i> by 1H-NMR. <i>FEBS Letters</i> , 1982, 145, 197-202.	1.3	13
445	A 3D triple-resonance NMR technique for qualitative measurement of carbonyl-H $\beta$ J couplings in isotopically enriched proteins. <i>Journal of Magnetic Resonance</i> , 1992, 96, 215-221.	0.5	13
446	A systematic case study on using NMR models for molecular replacement: p53 tetramerization domain revisited. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1535-1540.	2.5	13
447	Accurate Orientation of the Functional Groups of Asparagine and Glutamine Side Chains Using One- and Two-Bond Dipolar Couplings. <i>Journal of the American Chemical Society</i> , 2001, 123, 8642-8643.	6.6	13
448	No Interaction of Barrier-to-Autointegration Factor (BAF) with HIV-1 MA, Cone-Rod Homeobox (Crx) or MAN1-C in Absence of DNA. <i>PLoS ONE</i> , 2011, 6, e25123.	1.1	13
449	Atomic view of cosolute-induced protein denaturation probed by NMR solvent paramagnetic relaxation enhancement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	13
450	Sequence-dependent structural variations in two right-handed alternating pyrimidine-purine DNA oligomers in solution determined by nuclear Overhauser enhancement measurements. <i>EMBO Journal</i> , 1983, 2, 2109-15.	3.5	13

#	ARTICLE	IF	CITATIONS
451	Yeast tRNA <sup>Asp</sup> : codon and wobble codon-anticodon interactions. A transferred nuclear Overhauser enhancement study. <i>FEBS Journal</i> , 1984, 145, 359-364.	0.2	12
452	The solution structure of the Mu Ner protein reveals a helix-turn-helix DNA recognition motif. <i>Structure</i> , 1995, 3, 1087-1095.	1.6	12
453	Accurate Determination of Leucine and Valine Side-chain Conformations using U-[ <sup>15</sup> N/ <sup>13</sup> C/ <sup>2</sup> H]/[ <sup>1</sup> H-(methine/methyl)-Leu/Val] Isotope Labeling, NOE Pattern Recognition, and Methine C <sup>13</sup> â€“H <sup>13</sup> /C <sup>12</sup> â€“H <sup>12</sup> Residual Dipolar Couplings: Application to the 34-kDa Enzyme IIACHitobiose. <i>Journal of Biomolecular NMR</i> , 2005, 33, 105-121.	1.6	12
454	Solution Structure of the IIACHitobiose-HPr Complex of the N,Nâ€™ <sup>2</sup> -Diacetylchitobiose Branch of the Escherichia coli Phosphotransferase System. <i>Journal of Biological Chemistry</i> , 2012, 287, 23819-23829.	1.6	12
455	The conformations of hirudin in solution: a study using nuclear magnetic resonance, distance geometry and restrained molecular dynamics. <i>EMBO Journal</i> , 1987, 6, 529-37.	3.5	12
456	Reaction of Mixed Valence State Cytochrome Oxidase with Oxygen in Plant Mitochondria. <i>Plant Physiology</i> , 1981, 68, 229-235.	2.3	11
457	The C34 Peptide Fusion Inhibitor Binds to the Six-Helix Bundle Core Domain of HIV-1 gp41 by Displacement of the C-Terminal Helical Repeat Region. <i>Biochemistry</i> , 2015, 54, 6796-6805.	1.2	11
458	Mutations Proximal to Sites of Autoproteolysis and the Î±-Helix That Co-evolve under Drug Pressure Modulate the Autoprocessing and Vitality of HIV-1 Protease. <i>Biochemistry</i> , 2015, 54, 5414-5424.	1.2	11
459	Probing the Binding Modes of a Multidomain Protein to Lipid-based Nanoparticles by Relaxation-based NMR. <i>Journal of Physical Chemistry Letters</i> , 2017, 8, 2535-2540.	2.1	11
460	Extensive Sampling of the Cavity of the GroEL Nanomachine by Protein Substrates Probed by Paramagnetic Relaxation Enhancement. <i>Journal of Physical Chemistry Letters</i> , 2018, 9, 3368-3371.	2.1	11
461	Microsecond Backbone Motions Modulate the Oligomerization of the DNAJB6 Chaperone. <i>Angewandte Chemie - International Edition</i> , 2022, 61, .	7.2	11
462	Characterization of the intermediates in the reaction of membrane-bound mixed-valence-state cytochrome oxidase with oxygen at low temperatures by optical spectroscopy in the visible region. <i>Biochemical Journal</i> , 1980, 187, 617-622.	1.7	10
463	How accurately can interproton distances in macromolecules really be determined by full relaxation matrix analysis of nuclear overhauser enhancement data?. <i>Journal of Magnetic Resonance</i> , 1989, 84, 398-409.	0.5	10
464	Where is NMR taking us?. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994, 19, 273-276.	1.5	10
465	Visualization of the Phosphorylated Active Site Loop of the Cytoplasmic B Domain of the Mannitol Transporter IIMannitol of the Escherichia coli Phosphotransferase System by NMR Spectroscopy and Residual Dipolar Couplings. <i>Journal of Molecular Biology</i> , 2005, 353, 1129-1136.	2.0	10
466	Optimized NMR Experiments for the Isolation of I = 1/2 Manifold Transitions in Methyl Groups of Proteins. <i>ChemPhysChem</i> , 2020, 21, 13-19.	1.0	10
467	Magicâ€™Pulse Driven Separation of Degenerate 1 H Transitions in Methyl Groups of Proteins: Application to Studies of Methyl Axis Dynamics. <i>ChemPhysChem</i> , 2020, 21, 1087-1091.	1.0	10
468	Site-directed mutants of the cAMP receptor protein-DNA binding of five mutant proteins. <i>Protein Engineering, Design and Selection</i> , 1987, 1, 201-203.	1.0	9

#	ARTICLE	IF	CITATIONS
469	Histidine proton resonances of carbonmonoxyhaemoglobins A and Cowtown in chloride-free buffer. <i>Journal of Molecular Biology</i> , 1987, 195, 453-455.	2.0	9
470	DNA Binding Specificity of the Mu Ner Protein. <i>Biochemistry</i> , 1995, 34, 2946-2955.	1.2	9
471	Molecular determinants of mammalian sex. <i>Trends in Biochemical Sciences</i> , 1996, 21, 302-308.	3.7	9
472	Solution Structure of Enzyme II A Chitobiose from the N,N <sup>ε</sup> -Diacetylchitobiose Branch of the <i>Escherichia coli</i> Phosphotransferase System. <i>Journal of Biological Chemistry</i> , 2005, 280, 11770-11780.	1.6	9
473	Using multiple quantum coherence to increase the <sup>15</sup> N resolution in a three-dimensional TROSY HNCO experiment for accurate PRE and RDC measurements. <i>Journal of Magnetic Resonance</i> , 2009, 200, 173-177.	1.2	9
474	Optimized selection of slow-relaxing <sup>13</sup> C transitions in methyl groups of proteins: application to relaxation dispersion. <i>Journal of Biomolecular NMR</i> , 2020, 74, 673-680.	1.6	9
475	Kinetics of Fast Tetramerization of the Huntingtin Exon 1 Protein Probed by Concentration-Dependent On-Resonance <sup>1</sup> H Measurements. <i>Journal of Physical Chemistry Letters</i> , 2020, 11, 5643-5648.	2.1	9
476	Chapter 2. Low- $\gamma$ ; Nuclei Detection Experiments for Biomolecular NMR. <i>RSC Biomolecular Sciences</i> , 0, , 25-52.	0.4	9
477	Large Chaperone Complexes Through the Lens of Nuclear Magnetic Resonance Spectroscopy. <i>Annual Review of Biophysics</i> , 2022, 51, 223-246.	4.5	9
478	Quantitative NMR analysis of the kinetics of prenucleation oligomerization and aggregation of pathogenic huntingtin exon-1 protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	9
479	Application of the z-COSY technique with a modified pulse sequence to measurement of coupling constants in macromolecules. <i>Journal of Magnetic Resonance</i> , 1987, 75, 534-539.	0.5	8
480	Solution Structure of the II A Chitobiose-II B Chitobiose Complex of the N,N <sup>ε</sup> -Diacetylchitobiose Branch of the <i>Escherichia coli</i> Phosphotransferase System. <i>Journal of Biological Chemistry</i> , 2010, 285, 4173-4184.	1.6	8
481	Impact of <sup>15</sup> N <sup>2</sup> / <sub>R</sub> / <sub>1</sub> Relaxation Restraints on Molecular Size, Shape, and Bond Vector Orientation for NMR Protein Structure Determination with Sparse Distance Restraints. <i>Journal of the American Chemical Society</i> , 2011, 133, 6154-6157.	6.6	8
482	Probing Conformational States of the Finger and Thumb Subdomains of HIV-1 Reverse Transcriptase Using Double Electron <sup>ε</sup> Electron Resonance Electron Paramagnetic Resonance Spectroscopy. <i>Biochemistry</i> , 2018, 57, 489-493.	1.2	8
483	A simple protocol for expression of isotope-labeled proteins in <i>Escherichia coli</i> grown in shaker flasks at high cell density. <i>Journal of Biomolecular NMR</i> , 2019, 73, 743-748.	1.6	8
484	Quantitative Agreement between Conformational Substates of Holo Calcium-Loaded Calmodulin Detected by Double Electron <sup>ε</sup> Electron Resonance EPR and Predicted by Molecular Dynamics Simulations. <i>Journal of the American Chemical Society</i> , 2022, 144, 12043-12051.	6.6	8
485	A temperature-induced absorption band centred in the region of 666 nm related to the configuration of the active site in frozen cytochrome oxidase. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 1979, 545, 483-495.	0.5	7
486	The kinetics of the reaction of aquo Fe(III) myoglobin with hydrogen peroxide at pH 8. <i>Inorganica Chimica Acta</i> , 1980, 46, 139-146.	1.2	7

#	ARTICLE	IF	CITATIONS
487	Transfer-of-saturation NMR studies of protein-ligand complexes. Three-site exchange. Journal of Magnetic Resonance, 1981, 45, 151-161.	0.5	7
488	Generating Accurate Contact Maps of Transient Long-Range Interactions in Intrinsically Disordered Proteins by Paramagnetic Relaxation Enhancement. Biophysical Journal, 2013, 104, 1635-1636.	0.2	7
489	Binding of HIV-1 gp41-Directed Neutralizing and Non-Neutralizing Fragment Antibody Binding Domain (Fab) and Single Chain Variable Fragment (ScFv) Antibodies to the Ectodomain of gp41 in the Pre-Hairpin and Six-Helix Bundle Conformations. PLoS ONE, 2014, 9, e104683.	1.1	7
490	Probing the Rate-Limiting Step for Intramolecular Transfer of a Transcription Factor between Specific Sites on the Same DNA Molecule by <sup>15</sup> N-Exchange NMR Spectroscopy. Journal of the American Chemical Society, 2014, 136, 14369-14372.	6.6	7
491	Towards interpretation of intermolecular paramagnetic relaxation enhancement outside the fast exchange limit. Journal of Biomolecular NMR, 2016, 66, 1-7.	1.6	7
492	Probing the Interaction of Huntingtin Exon <sup>1</sup> Polypeptides with the Chaperonin Nanomachine GroEL. ChemBioChem, 2021, 22, 1985-1991.	1.3	7
493	The solution structure of a B-DNA undecamer comprising a portion of the specific target site for the cAMP receptor protein in the gal operon. Refinement on the basis of interproton distance data. EMBO Journal, 1985, 4, 829-35.	3.5	7
494	Refinement of the solution structure of the RNA-DNA hybrid 5 <sup>2</sup> -[r(GCA)d(TGC)] <sub>2</sub> Combined use of nuclear magnetic resonance and restrained molecular dynamics. FEBS Letters, 1988, 236, 62-70.	1.3	6
495	Quantitative Exchange NMR-Based Analysis of Huntingtin <sup>1</sup> SH3 Interactions Suggests an Allosteric Mechanism of Inhibition of Huntingtin Aggregation. Journal of the American Chemical Society, 2021, 143, 9672-9681.	6.6	6
496	<sup>1</sup> H-NMR studies on nucleotide binding to the sarcoplasmic reticulum Ca <sup>2+</sup> ATPase. Determination of the conformations of bound nucleotides by the measurement of proton-proton transferred nuclear Overhauser enhancements. FEBS Journal, 1982, 128, 113-17.	0.2	6
497	CO binding to mitochondrial mixed valence state cytochrome oxidase at low temperatures. Biochimica Et Biophysica Acta - Bioenergetics, 1980, 590, 34-49.	0.5	5
498	Modulation of specific binding of Lactobacillus casei dihydrofolate reductase to DNA by folinic acid. FEBS Letters, 1981, 133, 92-94.	1.3	5
499	A re-evaluation of the low-temperature kinetics of the reaction of fully reduced mitochondrial cytochrome oxidase with carbon monoxide and the spectral characterization of species IC in the soret and visible regions. Biochimica Et Biophysica Acta - Bioenergetics, 1981, 634, 129-139.	0.5	5
500	A two-dimensional nuclear overhauser enhancement experiment using semiselective soft pulses, and its applications to proteins. Journal of Magnetic Resonance, 1988, 78, 371-375.	0.5	5
501	XIPP: multi-dimensional NMR analysis software. Journal of Biomolecular NMR, 2020, 74, 9-25.	1.6	5
502	<sup>T</sup> <sub>m</sub> filtering by <sup>1</sup> H-methyl labeling in a deuterated protein for pulsed double electron <sup>1</sup> electron resonance EPR. Chemical Communications, 2020, 56, 10890-10893.	2.2	5
503	Probing Side-Chain Dynamics in Proteins by NMR Relaxation of Isolated <sup>13</sup> C Magnetization Modes in <sup>13</sup> CH <sub>3</sub> Methyl Groups. Journal of Physical Chemistry B, 2021, 125, 3343-3352.	1.2	5
504	Characterization of the DNA binding region recognized by dihydrofolate reductase from lactobacillus casei.. Journal of Biological Chemistry, 1983, 258, 11256-11259.	1.6	5

#	ARTICLE	IF	CITATIONS
505	Visualization of Sparsely-populated Lower-order Oligomeric States of Human Mitochondrial Hsp60 by Cryo-electron Microscopy. <i>Journal of Molecular Biology</i> , 2021, 433, 167322.	2.0	5
506	NMR and X-ray analysis of the three-dimensional structure of interleukin-8. <i>Cytokines</i> , 1992, 4, 18-40.	1.5	5
507	Characterization of the DNA binding region recognized by dihydrofolate reductase from <i>lactobacillus casei</i> . <i>Journal of Biological Chemistry</i> , 1983, 258, 11256-9.	1.6	5
508	NMR spectroscopy, excited states and relevance to problems in cell biology – transient pre-nucleation tetramerization of huntingtin and insights into Huntington's disease. <i>Journal of Cell Science</i> , 2022, 135, .	1.2	5
509	Cooperative non-specific DNA binding of the N-terminal core of the cyclic AMP receptor protein of <i>Escherichia coli</i> and its modulation by cyclic AMP. <i>FEBS Letters</i> , 1983, 164, 57-62.	1.3	4
510	A nuclear magnetic resonance study of the ribotrinucleoside diphosphate UpUpC. <i>Nucleic Acids Research</i> , 1983, 11, 5691-5699.	6.5	4
511	Interference between transverse cross-correlated relaxation and longitudinal relaxation affects apparent J-coupling and transverse cross-correlated relaxation. <i>Chemical Physics Letters</i> , 2006, 423, 123-125.	1.2	4
512	<sup>13</sup> C-detected HN(CA)C and HMCPC experiments using a single methyl-reprotonated sample for unambiguous methyl resonance assignment. <i>Journal of Biomolecular NMR</i> , 2006, 36, 259-266.	1.6	4
513	Inhibition of HIV Maturation via Selective Unfolding and Cross-Linking of Gag Polyprotein by a Mercaptobenzamide Acetylator. <i>Journal of the American Chemical Society</i> , 2019, 141, 8327-8338.	6.6	4
514	Determining methyl sidechain conformations in a CS-ROSETTA model using methyl <sup>1</sup> H- <sup>13</sup> C residual dipolar couplings. <i>Journal of Biomolecular NMR</i> , 2020, 74, 111-118.	1.6	4
515	A simple and cost-effective protocol for high-yield expression of deuterated and selectively isoleucine/leucine/valine methyl protonated proteins in <i>Escherichia coli</i> grown in shaker flasks. <i>Journal of Biomolecular NMR</i> , 2021, 75, 83-87.	1.6	4
516	The measurement of relaxation rates of degenerate <sup>1</sup> H transitions in methyl groups of proteins using acute angle radiofrequency pulses. <i>Journal of Magnetic Resonance</i> , 2021, 330, 107034.	1.2	4
517	Determination of Structures of Larger Proteins in Solution by Three- and Four-dimensional Heteronuclear Magnetic Resonance Spectroscopy. , 1993, , 1-32.		4
518	Interpretation of NMR Data in Terms of Protein Structure. , 1991, , 375-389.		4
519	Secondary structure of the ribonuclease H domain of the human immunodeficiency virus reverse transcriptase in solution using three-dimensional double and triple resonance heteronuclear magnetic resonance spectroscopy. <i>Journal of Molecular Biology</i> , 1991, 221, 1081-1090.	2.0	4
520	Chapter 9. Characterising RNA Dynamics using NMR Residual Dipolar Couplings. <i>RSC Biomolecular Sciences</i> , 0, , 184-215.	0.4	4
521	Automatic phasing of pure phase absorption two-dimensional NMR spectra. <i>Journal of Magnetic Resonance</i> , 1988, 79, 154-157.	0.5	3
522	Rapid screening for structural integrity of expressed proteins by heteronuclear NMR spectroscopy. <i>Protein Science</i> , 1996, 5, 981-981.	3.1	3

#	ARTICLE	IF	CITATIONS
523	NMR in Structural and Cell Biology. , 2016, , 98-107.		3
524	Disassembly/reassembly strategy for the production of highly pure GroEL, a tetradecameric supramolecular machine, suitable for quantitative NMR, EPR and mutational studies. Protein Expression and Purification, 2018, 142, 8-15.	0.6	3
525	Probing the Interaction between HIV-1 Protease and the Homodimeric p66/p66 <sup>TM</sup> Reverse Transcriptase Precursor by Double Electron-Electron Resonance EPR Spectroscopy. ChemBioChem, 2020, 21, 3051-3055.	1.3	3
526	Studies of the Reaction of Cytochrome c Oxidase with Oxygen at Low Temperature.. Acta Chemica Scandinavica, 1979, 33b, 615-618.	0.7	3
527	<i>Response</i> : Similarity of Protein G and Ubiquitin. Science, 1991, 254, 581-581.	6.0	3
528	Protection against nuclease cleavage of pBR322 DNA by the cAMP receptor protein of Escherichia coli. Journal of Molecular Biology, 1983, 166, 93-98.	2.0	2
529	The P53 Tumor Suppressor Protein. , 1995, , 407-418.		2
530	Targeting a Dark Excited State of HIV-1 Nucleocapsid by Antiretroviral Thioesters Revealed by NMR Spectroscopy. Angewandte Chemie, 2018, 130, 2717-2721.	1.6	2
531	Determining Structures of Large Proteins and Protein Complexes by NMR. , 2002, , 3-26.		2
532	A computer analysis of cyanide stimulated oxygen uptake inChlorella protothecoides. FEBS Letters, 1977, 79, 353-356.	1.3	1
533	Numerical solution of the Hodgkin-Huxley equations in a moving coordinate system. Simulation of nerve impulse transmission over long distances. Journal of Computational Physics, 1981, 40, 318-326.	1.9	1
534	Cooperative DNA binding by lambda integration protein - a key component of specificity. FEBS Journal, 1986, 161, 727-731.	0.2	1
535	Analysis of the backbone dynamics of interleukin-1 .beta. using two-dimensional inverse detected heteronuclear nitrogen-15-proton NMR spectroscopy [Erratum to document cited in CA113(9):76266p]. Biochemistry, 1991, 30, 312-312.	1.2	1
536	High-resolution structure of a double zinc finger from the human enhancer binding protein MPB-1 in solution. The Protein Journal, 1992, 11, 408-409.	1.1	1
537	Chapter 6. Paramagnetic NMR Spectroscopy and Lowly Populated States. RSC Biomolecular Sciences, 0, , 130-150.	0.4	1
538	Chapter 8. Residual Dipolar Couplings as a Tool for the Study of Protein Conformation and Conformational Flexibility. RSC Biomolecular Sciences, 0, , 166-183.	0.4	1
539	Reply to Marchenko et al.: Flux analysis of GroEL-assisted protein folding/unfolding. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E6833-E6834.	3.3	1
540	Editorial overview " Biophysical methods: "Seeing is believing"™. Current Opinion in Structural Biology, 2021, 70, iii-v.	2.6	1

#	ARTICLE	IF	CITATIONS
541	Comparison of the NMR and X-Ray Structures of Hirudin. , 1991, , 57-65.		1
542	Dynamics of SOX2 Interactions with DNA. , 2016, , 25-41.		1
543	Improving the quality of NMR and crystallographic protein structures by means of a conformational database potential derived from structure databases. Acta Crystallographica Section A: Foundations and Advances, 1996, 52, C564-C564.	0.3	1
544	Spectroscopic evidence for an oxygen bridge between the iron atom of cytochrome a3 and CuB in the class C group of compounds formed in the reaction of mixed valence state cytochrome oxidase with oxygen. Inorganica Chimica Acta, 1981, 55, L47-L49.	1.2	0
545	Synthesis and <sup>1</sup> H-NMR Studies of DNA-RNA Hybrids for Structural Analysis. Nucleosides & Nucleotides, 1988, 7, 733-736.	0.5	0
546	Commentary on the article: Purification and characterization of the Ner repressor of bacteriophage Mu (1989) FEBS Lett. 244, 369-375 G. Kukulj, P.P. Tolias and M.S. DuBow. FEBS Letters, 1989, 251, 282-282.	1.3	0
547	MPSA short communications. The Protein Journal, 1994, 13, 431-512.	1.1	0
548	GAGA: Structural Basis for Single Cys2His2 Zinc Finger-DNA Interaction. , 2005, , 20-25.		0
549	Kinetics of Amyloid-Beta Monomer to Oligomer Exchange by NMR Relaxation. Biophysical Journal, 2011, 100, 531a.	0.2	0
550	Chapter 5. NMR Studies of Disordered but Functional Proteins. RSC Biomolecular Sciences, 0, , 111-129.	0.4	0
551	Chapter 13. Recent Developments in Biomolecular Solid-State NMR. RSC Biomolecular Sciences, 0, , 318-334.	0.4	0
552	Chapter 12. NMR of Membrane Proteins. RSC Biomolecular Sciences, 0, , 271-317.	0.4	0
553	Structure Determination of Large Macromolecular Complexes Using NMR. , 2017, , 316-318.		0
554	Reaction of Cytochrome c Oxidase with Oxygen. , 1982, , 267-269.		0
555	The Solution Structures of RNA Fragments Determined by Nuclear Overhauser Enhancement Measurements. , 1986, , 137-149.		0
556	Determination of 3D-Structures of Macromolecules by Restrained Molecular Dynamics on the Basis of Interproton Distances. Springer Series in Biophysics, 1987, , 108-112.	0.4	0
557	Analysis of Backbone Dynamics of Interleukin-1 $\beta$ . , 1991, , 227-231.		0
558	Analysis of backbone dynamics of interleukin-1 $\beta$ . , 1991, , 53-56.		0



#	ARTICLE	IF	CITATIONS
559	Identification of a binding site for the human immunodeficiency virus type 1 nucleocapsid protein. , 1994, , 956-957.		0
560	Three- and Four-Dimensional Heteronuclear NMR. , 1995, , 493-503.		0
561	Structures of Multimeric Proteins by NMR. , 1996, , 237-242.		0
562	Determination of Structures of Larger Proteins in Solution by Three- and Four-Dimensional Heteronuclear Magnetic Resonance Spectroscopy <sup>11</sup> An earlier version of this chapter appeared in Science 252, 1390â€“1399 (1991). , 1996, , 181-204.		0
563	Understanding SRY-Related 46X,Y Sex Reversal at the Atomic Level. Nucleic Acids and Molecular Biology, 1997, , 265-273.	0.2	0
564	Determining Structures of Protein/DNA Complexes by NMR. , 1998, , 1-13.		0
565	Effects of mutations on tetramer formation of tumor suppressor protein p53. , 1999, , 303-305.		0
566	Microsecond Backbone Motions Modulate the Oligomerization of the DNAJB6 Chaperone. Angewandte Chemie, 0, , .	1.6	0
567	Chapter 3. Making the Most of Chemical Shifts. RSC Biomolecular Sciences, 0, , 53-83.	0.4	0
568	Chapter 4. Protein Structure Determination using Sparse NMR Data. RSC Biomolecular Sciences, 0, , 84-110.	0.4	0
569	Chapter 7. NMR Relaxation Dispersion Studies of Large Enzymes in Solution. RSC Biomolecular Sciences, 0, , 151-165.	0.4	0
570	Chapter 10. Non-Canonical Ligand-Binding Events as Detected by NMR. RSC Biomolecular Sciences, 0, , 216-253.	0.4	0
571	Chapter 11. Recent Advances in Biomolecular NMR for Drug Discovery. RSC Biomolecular Sciences, 0, , 254-270.	0.4	0