Peter E Wright

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/3050365/publications.pdf

Version: 2024-02-01

341 papers	47,694 citations	1713 107 h-index	2196 208 g-index
364 all docs	364 docs citations	364 times ranked	35267 citing authors

#	Article	IF	Citations
1	Intrinsically unstructured proteins and their functions. Nature Reviews Molecular Cell Biology, 2005, 6, 197-208.	16.1	3,403
2	Intrinsically unstructured proteins: re-assessing the protein structure-function paradigm. Journal of Molecular Biology, 1999, 293, 321-331.	2.0	2,668
3	Intrinsically disordered proteins in cellular signalling and regulation. Nature Reviews Molecular Cell Biology, 2015, 16, 18-29.	16.1	1,849
4	The role of dynamic conformational ensembles in biomolecular recognition. Nature Chemical Biology, 2009, 5, 789-796.	3.9	1,649
5	Classification of Intrinsically Disordered Regions and Proteins. Chemical Reviews, 2014, 114, 6589-6631.	23.0	1,618
6	Zinc finger proteins: new insights into structural and functional diversity. Current Opinion in Structural Biology, 2001, 11, 39-46.	2.6	1,240
7	Coupling of folding and binding for unstructured proteins. Current Opinion in Structural Biology, 2002, 12, 54-60.	2.6	1,223
8	Mechanism of coupled folding and binding of an intrinsically disordered protein. Nature, 2007, 447, 1021-1025.	13.7	984
9	Linking folding and binding. Current Opinion in Structural Biology, 2009, 19, 31-38.	2.6	932
10	The Dynamic Energy Landscape of Dihydrofolate Reductase Catalysis. Science, 2006, 313, 1638-1642.	6.0	877
11	Solution Structure of the KIX Domain of CBP Bound to the Transactivation Domain of CREB: A Model for Activator:Coactivator Interactions. Cell, 1997, 91, 741-752.	13.5	705
12	Folding of immunogenic peptide fragments of proteins in water solution. Journal of Molecular Biology, 1988, 201, 161-200.	2.0	685
13	Intramolecular motions of a zinc finger DNA-binding domain from Xfin characterized by proton-detected natural abundance carbon-13 heteronuclear NMR spectroscopy. Journal of the American Chemical Society, 1991, 113, 4371-4380.	6.6	616
14	Unfolded Proteins and Protein Folding Studied by NMR. Chemical Reviews, 2004, 104, 3607-3622.	23.0	596
15	Structural basis for DNA bending by the architectural transcription factor LEF-1. Nature, 1995, 376, 791-795.	13.7	582
16	Sequence-Dependent Correction of Random Coil NMR Chemical Shifts. Journal of the American Chemical Society, 2001, 123, 2970-2978.	6.6	562
17	Conformation of peptide fragments of proteins in aqueous solution: implications for initiation of protein folding. Biochemistry, 1988, 27, 7167-7175.	1.2	505
18	Folding of immunogenic peptide fragments of proteins in water solution. Journal of Molecular Biology, 1988, 201, 201-217.	2.0	477

#	Article	IF	Citations
19	â€˜Random coilâ€™ 1H chemical shifts obtained as a function of temperature and trifluoroethanol concentration for the peptide series GGXGG. Journal of Biomolecular NMR, 1995, 5, 14-24.	1.6	476
20	Structure, Dynamics, and Catalytic Function of Dihydrofolate Reductase. Annual Review of Biophysics and Biomolecular Structure, 2004, 33, 119-140.	18.3	444
21	An NMR Perspective on Enzyme Dynamics. Chemical Reviews, 2006, 106, 3055-3079.	23.0	424
22	Mutual synergistic folding in recruitment of CBP/p300 by p160 nuclear receptor coactivators. Nature, 2002, 415, 549-553.	13.7	423
23	A Dynamic Knockout Reveals That Conformational Fluctuations Influence the Chemical Step of Enzyme Catalysis. Science, 2011, 332, 234-238.	6.0	414
24	Folding of peptide fragments comprising the complete sequence of proteins. Journal of Molecular Biology, 1992, 226, 795-817.	2.0	385
25	Structural basis for Hif-1Â/CBP recognition in the cellular hypoxic response. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 5271-5276.	3.3	376
26	Recommendations for the presentation of NMR structures of proteins and nucleic acids. IUPAC-IUBMB-IUPAB Inter-Union Task Group on the Standardization of Data Bases of Protein and Nucleic Acid Structures Determined by NMR Spectroscopy. Journal of Biomolecular NMR, 1998, 12, 1-23.	1.6	347
27	Structural and dynamic characterization of partially folded states of apomyoglobin and implications for protein folding. Nature Structural Biology, 1998, 18, 148-155.	9.7	344
28	Recognition of the mRNA AU-rich element by the zinc finger domain of TIS11d. Nature Structural and Molecular Biology, 2004, 11, 257-264.	3.6	320
29	Modulation of allostery by protein intrinsic disorder. Nature, 2013, 498, 390-394.	13.7	295
30	Suppression of the effects of cross-correlation between dipolar and anisotropic chemical shift relaxation mechanisms in the measurement of spin-spin relaxation rates. Molecular Physics, 1992, 75, 699-711.	0.8	287
31	PRAK Is Essential for ras-Induced Senescence and Tumor Suppression. Cell, 2007, 128, 295-308.	13.5	286
32	High-resolution solution structures of oxidized and reduced Escherichia coli thioredoxin. Structure, 1994, 2, 853-868.	1.6	281
33	Random coil chemical shifts in acidic 8 M urea: implementation of random coil shift data in NMRView. Journal of Biomolecular NMR, 2000, 18, 43-48.	1.6	272
34	The role of hydrophobic interactions in initiation and propagation of protein folding. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 13057-13061.	3.3	266
35	Role of Intrinsic Protein Disorder in the Function and Interactions of the Transcriptional Coactivators CREB-binding Protein (CBP) and p300. Journal of Biological Chemistry, 2016, 291, 6714-6722.	1.6	251
36	The immunodominant site of a synthetic immunogen has a conformational preference in water for a type-II reverse turn. Nature, 1985, 318, 480-483.	13.7	246

#	Article	IF	Citations
37	Backbone Dynamics in Dihydrofolate Reductase Complexes:Â Role of Loop Flexibility in the Catalytic Mechanismâ€. Biochemistry, 2001, 40, 9846-9859.	1.2	246
38	Is Apomyoglobin a Molten Globule? Structural Characterization by NMR. Journal of Molecular Biology, 1996, 263, 531-538.	2.0	242
39	Electrostatic calculations of side-chain pKa values in myoglobin and comparison with NMR data for histidines. Biochemistry, 1993, 32, 8045-8056.	1.2	237
40	Backbone dynamics of the Bacillus subtilis glucose permease IIA domain determined from nitrogen-15 NMR relaxation measurements. Biochemistry, 1992, 31, 4394-4406.	1.2	233
41	Peptide conformation and protein folding. Current Opinion in Structural Biology, 1993, 3, 60-65.	2.6	232
42	Assemblages: Functional units formed by cellular phase separation. Journal of Cell Biology, 2014, 206, 579-588.	2.3	227
43	Folding of peptide fragments comprising the complete sequence of proteins. Journal of Molecular Biology, 1992, 226, 819-835.	2.0	226
44	Conformational propensities of intrinsically disordered proteins influence the mechanism of binding and folding. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 9614-9619.	3.3	222
45	Recommendations for the presentation of NMR structures of proteins and nucleic acids. Journal of Molecular Biology, 1998, 280, 933-952.	2.0	217
46	NMR Structural and Dynamic Characterization of the Acid-Unfolded State of Apomyoglobin Provides Insights into the Early Events in Protein Foldingâ€,â€¡. Biochemistry, 2001, 40, 3561-3571.	1.2	212
47	Peptide models of protein folding initiation sites. 1. Secondary structure formation by peptides corresponding to the G- and H-helixes of myoglobin. Biochemistry, 1993, 32, 6337-6347.	1.2	209
48	Insights into the structure and dynamics of unfolded proteins from nuclear magnetic resonance. Advances in Protein Chemistry, 2002, 62, 311-340.	4.4	208
49	Cooperative regulation of p53 by modulation of ternary complex formation with CBP/p300 and HDM2. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 6591-6596.	3.3	197
50	pE-DB: a database of structural ensembles of intrinsically disordered and of unfolded proteins. Nucleic Acids Research, 2014, 42, D326-D335.	6.5	195
51	Graded enhancement of p53 binding to CREB-binding protein (CBP) by multisite phosphorylation. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 19290-19295.	3.3	188
52	Equilibrium NMR studies of unfolded and partially folded proteins. Nature Structural Biology, 1998, 5, 499-503.	9.7	187
53	Solution structure of the first three zinc fingers of TFIIIA bound to the cognate DNA sequence: determinants of affinity and sequence specificity. Journal of Molecular Biology, 1997, 273, 183-206.	2.0	182
54	Solution Structure of the KIX Domain of CBP Bound to the Transactivation Domain of c-Myb. Journal of Molecular Biology, 2004, 337, 521-534.	2.0	181

#	Article	IF	Citations
55	Three-dimensional solution structure of the reduced form of Escherichia coli thioredoxin determined by nuclear magnetic resonance spectroscopy. Biochemistry, 1990, 29, 4129-4136.	1.2	177
56	How Do Proteins Interact?. Science, 2008, 320, 1429-1430.	6.0	174
57	Local Structural Plasticity of the Prion Protein. Analysis of NMR Relaxation Dynamicsâ€. Biochemistry, 2001, 40, 2743-2753.	1.2	171
58	Cooperativity in Transcription Factor Binding to the Coactivator CREB-binding Protein (CBP). Journal of Biological Chemistry, 2002, 277, 43168-43174.	1.6	166
59	Structural Basis for Cooperative Transcription Factor Binding to the CBP Coactivator. Journal of Molecular Biology, 2006, 355, 1005-1013.	2.0	166
60	Structural Characterization of Unfolded States of Apomyoglobin using Residual Dipolar Couplings. Journal of Molecular Biology, 2004, 340, 1131-1142.	2.0	165
61	Proton NMR studies of the solution conformations of an analog of the C-peptide of ribonuclease A. Biochemistry, 1989, 28, 7059-7064.	1.2	162
62	Dynamics of the Dihydrofolate Reductase-Folate Complex: Catalytic Sites and Regions Known To Undergo Conformational Change Exhibit Diverse Dynamical Features. Biochemistry, 1995, 34, 11037-11048.	1.2	162
63	Structure of the Escherichia coli Quorum Sensing Protein SdiA: Activation of the Folding Switch by Acyl Homoserine Lactones. Journal of Molecular Biology, 2006, 355, 262-273.	2.0	162
64	Structure of the p53 Transactivation Domain in Complex with the Nuclear Receptor Coactivator Binding Domain of CREB Binding Protein. Biochemistry, 2010, 49, 9964-9971.	1.2	162
65	Functional advantages of dynamic protein disorder. FEBS Letters, 2015, 589, 2433-2440.	1.3	162
66	Analysis of an Activator:Coactivator Complex Reveals an Essential Role for Secondary Structure in Transcriptional Activation. Molecular Cell, 1998, 2, 353-359.	4.5	155
67	Divergent evolution of protein conformational dynamics in dihydrofolate reductase. Nature Structural and Molecular Biology, 2013, 20, 1243-1249.	3.6	153
68	Stabilization of a type VI turn in a family of linear peptides in water solution. Journal of Molecular Biology, 1994, 243, 736-753.	2.0	152
69	Defining the role of active-site loop fluctuations in dihydrofolate reductase catalysis. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 5032-5037.	3.3	152
70	Dynamics of a flexible loop in dihydrofolate reductase from Escherichia coli and its implication for catalysis. Biochemistry, 1994, 33, 439-442.	1.2	150
71	Comparison of backbone and tryptophan side-chain dynamics of reduced and oxidized Escherichia coli thioredoxin using nitrogen-15 NMR relaxation measurements. Biochemistry, 1993, 32, 426-435.	1.2	148
72	Nuclear Magnetic Resonance Methods for Elucidation of Structure and Dynamics in Disordered States. Methods in Enzymology, 2001, 339, 258-270.	0.4	148

#	Article	IF	Citations
73	Structural basis for recruitment of CBP/p300 coactivators by STAT1 and STAT2 transactivation domains. EMBO Journal, 2009, 28, 948-958.	3.5	147
74	INSIGHTS INTO PROTEIN FOLDING FROM NMR. Annual Review of Physical Chemistry, 1996, 47, 369-395.	4.8	144
75	Structure of the PHD Zinc Finger from Human Williams-Beuren Syndrome Transcription Factor. Journal of Molecular Biology, 2000, 304, 723-729.	2.0	142
76	Integrated description of protein dynamics from room-temperature X-ray crystallography and NMR. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E445-54.	3.3	142
77	Mapping of the binding interfaces of the proteins of the bacterial phosphotransferase system, HPr and IIAglc. Biochemistry, 1993, 32, 32-37.	1.2	141
78	Solution structure and acetyl-lysine binding activity of the GCN5 bromodomain. Journal of Molecular Biology, 2000, 304, 355-370.	2.0	141
79	Mapping Long-range Contacts in a Highly Unfolded Protein. Journal of Molecular Biology, 2002, 322, 655-662.	2.0	140
80	Hypersensitive termination of the hypoxic response by a disordered protein switch. Nature, 2017, 543, 447-451.	13.7	140
81	Recommendations for the presentation of NMR structures of proteins and nucleic acids. IUPAC-IUBMB-IUPAB inter-union task group on the standardization of data bases of protein and nucleic acid structures determined by NMR spectroscopy. FEBS Journal, 1998, 256, 1-15.	0.2	137
82	Conformational preferences in the Ser133 -phosphorylated and non-phosphorylated forms of the kinase inducible transactivation domain of CREB. FEBS Letters, 1998, 430, 317-322.	1.3	137
83	DNA-induced Î±-helix capping in conserved linker sequences is a determinant of binding affinity in Cys2-His2 zinc fingers. Journal of Molecular Biology, 2000, 295, 719-727.	2.0	137
84	Chemical shift dispersion and secondary structure prediction in unfolded and partly folded proteins. FEBS Letters, 1997, 419, 285-289.	1.3	135
85	Roles of Phosphorylation and Helix Propensity in the Binding of the KIX Domain of CREB-binding Protein by Constitutive (c-Myb) and Inducible (CREB) Activators. Journal of Biological Chemistry, 2002, 277, 42241-42248.	1.6	134
86	Millisecond timescale fluctuations in dihydrofolate reductase are exquisitely sensitive to the bound ligands. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 1373-1378.	3.3	133
87	NMR Order Parameters of Biomolecules: A New Analytical Representation and Application to the Gaussian Axial Fluctuation Model. Journal of the American Chemical Society, 1994, 116, 8426-8427.	6.6	131
88	Molecular Hinges in Protein Folding:Â the Urea-Denatured State of Apomyoglobinâ€. Biochemistry, 2002, 41, 12681-12686.	1.2	130
89	Automated identification of functional dynamic contact networks from X-ray crystallography. Nature Methods, 2013, 10, 896-902.	9.0	130
90	Role of Secondary Structure in Discrimination between Constitutive and Inducible Activators. Molecular and Cellular Biology, 1999, 19, 5601-5607.	1.1	127

#	Article	IF	Citations
91	Quantitative Analysis of Multisite Proteinâ€“Ligand Interactions by NMR: Binding of Intrinsically Disordered p53 Transactivation Subdomains with the TAZ2 Domain of CBP. Journal of the American Chemical Society, 2012, 134, 3792-3803.	6.6	123
92	Solution Structure of the Cysteine-rich Domain of the Escherichia coli Chaperone Protein DnaJ. Journal of Molecular Biology, 2000, 300, 805-818.	2.0	121
93	Solution structure of the TAZ2 (CH3) domain of the transcriptional adaptor protein CBP. Journal of Molecular Biology, 2000, 303, 243-253.	2.0	121
94	Native and Non-native Secondary Structure and Dynamics in the pH 4 Intermediate of Apomyoglobinâ€. Biochemistry, 2000, 39, 2894-2901.	1.2	121
95	Solution Structure of the Hdm2 C2H2C4 RING, a Domain Critical for Ubiquitination of p53. Journal of Molecular Biology, 2006, 363, 433-450.	2.0	120
96	Conformational Changes in the Active Site Loops of Dihydrofolate Reductase during the Catalytic Cycleâ€. Biochemistry, 2004, 43, 16046-16055.	1.2	119
97	Structural basis for subversion of cellular control mechanisms by the adenoviral E1A oncoprotein. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 13260-13265.	3.3	119
98	Three-dimensional structure of a type VI turn in a linear peptide in water solution Evidence for stacking of aromatic rings as a major stabilizing factor. Journal of Molecular Biology, 1994, 243, 754-766.	2.0	118
99	Analysis of the RelA:CBP/p300 Interaction Reveals Its Involvement in NF-Î¹B-Driven Transcription. PLoS Biology, 2013, 11, e1001647.	2.6	118
100	Mechanisms of Transthyretin Inhibition of Î²-Amyloid AggregationIn Vitro. Journal of Neuroscience, 2013, 33, 19423-19433.	1.7	118
101	Absence of a stable intermediate on the folding pathway of protein A. Protein Science, 1997, 6, 1449-1457.	3.1	117
102	Domain packing and dynamics in the DNA complex of the N-terminal zinc fingers of TFIIIA. Nature Structural Biology, 1997, 4, 605-608.	9.7	116
103	High-resolution solution structure of reduced French bean plastocyanin and comparison with the crystal structure of poplar plastocyanin. Journal of Molecular Biology, 1991, 221, 533-555.	2.0	114
104	SANE (Structure Assisted NOE Evaluation): an automated model-based approach for NOE assignment. Journal of Biomolecular NMR, 2001, 19, 321-329.	1.6	113
105	Comparison of protein solution structures refined by molecular dynamics simulation in vacuum, with a generalized Born model, and with explicit water. Journal of Biomolecular NMR, 2002, 22, 317-331.	1.6	112
106	Identification of Native and Non-native Structure in Kinetic Folding Intermediates of Apomyoglobin. Journal of Molecular Biology, 2006, 355, 139-156.	2.0	112
107	[13] Use of chemical shifts and coupling constants in nuclear magnetic resonance structural studies on peptides and proteins. Methods in Enzymology, 1994, 239, 392-416.	0.4	111
108	Finding Our Way in the Dark Proteome. Journal of the American Chemical Society, 2016, 138, 9730-9742.	6.6	111

#	Article	IF	Citations
109	Chemical shift as a probe of molecular interfaces: NMR studies of DNA binding by the three amino-terminal zinc finger domains from transcription factor IIIA. Journal of Biomolecular NMR, 1998, 12, 51-71.	1.6	110
110	Peptide models of protein folding initiation sites. 3. The G-H helical hairpin of myoglobin. Biochemistry, 1993, 32, 6356-6364.	1.2	109
111	Mapping the Interactions of the p53 Transactivation Domain with the KIX Domain of CBP. Biochemistry, 2009, 48, 2115-2124.	1.2	109
112	Specific interaction of the first three zinc fingers of TFIIIA with the internal control region of the Xenopus 5 S RNA gene. Journal of Molecular Biology, 1992, 223, 857-871.	2.0	106
113	Modeling transient collapsed states of an unfolded protein to provide insights into early folding events. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6278-6283.	3.3	105
114	Expanding the Paradigm: Intrinsically Disordered Proteins and Allosteric Regulation. Journal of Molecular Biology, 2018, 430, 2309-2320.	2.0	105
115	NMR Characterization of the Metallo-Î²-lactamase from Bacteroides fragilis and Its Interaction with a Tight-Binding Inhibitor:â€‰ Role of an Active-Site Loop. Biochemistry, 1999, 38, 14507-14514.	1.2	104
116	Characterization of a folding intermediate of apoplastocyanin trapped by proline isomerization. Biochemistry, 1993, 32, 12299-12310.	1.2	103
117	Solution Structure of Carbonmonoxy Myoglobin Determined from Nuclear Magnetic Resonance Distance and Chemical Shift Constraints. Journal of Molecular Biology, 1994, 244, 183-197.	2.0	103
118	Assignment of the proton NMR spectrum of reduced and oxidized thioredoxin: sequence-specific assignments, secondary structure, and global fold. Biochemistry, 1989, 28, 7074-7087.	1.2	102
119	Molecular basis for recognition of methylated and specific DNA sequences by the zinc finger protein Kaiso. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 15229-15234.	3.3	101
120	Functional role of a mobile loop of Escherichia coli dihydrofolate reductase in transition-state stabilization. Biochemistry, 1992, 31, 7826-7833.	1.2	100
121	Monomeric Complex of Human Orphan Estrogen Related Receptor-2 with DNA: A Pseudo-dimer Interface Mediates Extended Half-site Recognition. Journal of Molecular Biology, 2003, 327, 819-832.	2.0	97
122	Interaction of the TAZ1 Domain of the CREB-Binding Protein with the Activation Domain of CITED2. Journal of Biological Chemistry, 2004, 279, 3042-3049.	1.6	97
123	Antigenic peptides. FASEB Journal, 1995, 9, 37-42.	0.2	96
124	Conservation of folding pathways in evolutionarily distant globin sequences. Nature Structural Biology, 2000, 7, 679-686.	9.7	95
125	Recognition of the disordered p53 transactivation domain by the transcriptional adapter zinc finger domains of CREB-binding protein. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1853-62.	3.3	94
126	Quenchâ€flow experiments combined with mass spectrometry show apomyoglobin folds through an obligatory intermediate. Protein Science, 1999, 8, 45-49.	3.1	93

#	Article	IF	Citations
127	Long-range regulation of p53 DNA binding by its intrinsically disordered N-terminal transactivation domain. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11302-E11310.	3.3	93
128	Peptide models of protein folding initiation sites. 2. The G-H turn region of myoglobin acts as a helix stop signal. Biochemistry, 1993, 32, 6348-6355.	1.2	92
129	Structure of the Wilms Tumor Suppressor Protein Zinc Finger Domain Bound to DNA. Journal of Molecular Biology, 2007, 372, 1227-1245.	2.0	91
130	Assignment of resonances in the 1H nuclear magnetic resonance spectrum of the carbon monoxide complex of sperm whale myoglobin by phase-sensitive two-dimensional techniques. Journal of Molecular Biology, 1987, 194, 313-327.	2.0	90
131	Elucidation of the Protein Folding Landscape by NMR. Methods in Enzymology, 2005, 394, 299-321.	0.4	90
132	The Apomyoglobin Folding Pathway Revisited: Structural Heterogeneity in the Kinetic Burst Phase Intermediate. Journal of Molecular Biology, 2002, 322, 483-489.	2.0	89
133	Hierarchical folding mechanism of apomyoglobin revealed by ultra-fast H/D exchange coupled with 2D NMR. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 13859-13864.	3.3	89
134	NMR Relaxation Study of the Complex Formed Between CBP and the Activation Domain of the Nuclear Hormone Receptor Coactivator ACTR^{â€}. Biochemistry, 2008, 47, 1299-1308.	1.2	86
135	Improved low pH bicelle system for orienting macromolecules over a wide temperature range. Journal of Biomolecular NMR, 1999, 13, 387-391.	1.6	84
136	NMR study of the interaction of plastocyanin with chromium(III) analogues of inorganic electron transfer reagents. Biochimica Et Biophysica Acta - Bioenergetics, 1980, 591, 162-176.	0.5	83
137	Complete assignment of the 1H nuclear magnetic resonance spectrum of French bean plastocyanin. Journal of Molecular Biology, 1988, 202, 603-622.	2.0	83
138	Folding propensities of peptide fragments of myoglobin. Protein Science, 1997, 6, 706-716.	3.1	82
139	High Pressure NMR Reveals that Apomyoglobin is an Equilibrium Mixture from the Native to the Unfolded. Journal of Molecular Biology, 2002, 320, 311-319.	2.0	81
140	ZZ Domain of CBP: an Unusual Zinc Finger Fold in a Protein Interaction Module. Journal of Molecular Biology, 2004, 343, 1081-1093.	2.0	81
141	Effect of H helix destabilizing mutations on the kinetic and equilibrium folding of apomyoglobin 1 1Edited by F. Cohen. Journal of Molecular Biology, 1999, 285, 269-282.	2.0	79
142	Structural and dynamic characterization of an unfolded state of poplar apo-plastocyanin formed under nondenaturing conditions. Protein Science, 2001, 10, 1056-1066.	3.1	79
143	A Distal Mutation Perturbs Dynamic Amino Acid Networks in Dihydrofolate Reductase. Biochemistry, 2013, 52, 4605-4619.	1.2	77
144	CBP/p300 TAZ1 Domain Forms a Structured Scaffold for Ligand Binding,. Biochemistry, 2005, 44, 490-497.	1.2	76

#	Article	IF	Citations
145	NMR solution structure of the inserted domain of human leukocyte function associated antigen-1. Journal of Molecular Biology, 2000, 295, 1251-1264.	2.0	74
146	Effect of Cofactor Binding and Loop Conformation on Side Chain Methyl Dynamics in Dihydrofolate Reductase. Biochemistry, 2004, 43, 374-383.	1.2	73
147	Computational methods for determining protein structures from NMR data. Biochemical Pharmacology, 1990, 40, 15-22.	2.0	72
148	Induced Fit and â€œLock and Keyâ€•Recognition of 5S RNA by Zinc Fingers of Transcription Factor IIIA. Journal of Molecular Biology, 2006, 357, 275-291.	2.0	72
149	Solution structure of Escherichia coli glutaredoxin-2 shows similarity to mammalian glutathione-S-transferases. Journal of Molecular Biology, 2001, 310, 907-918.	2.0	71
150	Fast and accurate fitting of relaxation dispersion data using the flexible software package GLOVE. Journal of Biomolecular NMR, 2013, 56, 275-283.	1.6	71
151	Measurement of protein unfolding/refolding kinetics and structural characterization of hidden intermediates by NMR relaxation dispersion. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 9078-9083.	3.3	70
152	Structural analyses of CREB-CBP transcriptional activator-coactivator complexes by NMR spectroscopy: implications for mapping the boundaries of structural domains. Journal of Molecular Biology, 1999, 287, 859-865.	2.0	68
153	Changes in the Apomyoglobin Folding Pathway Caused by Mutation of the Distal Histidine Residue. Biochemistry, 2000, 39, 11227-11237.	1.2	68
154	Complete assignment of the 1H nuclear magnetic resonance spectrum of French bean plastocyanin. Journal of Molecular Biology, 1988, 202, 623-636.	2.0	67
155	Relative Contributions of the Zinc Fingers of Transcription Factor IIIA to the Energetics of DNA Binding. Journal of Molecular Biology, 1994, 244, 23-25.	2.0	66
156	DNA-induced conformational changes are the basis for cooperative dimerization by the DNA binding domain of the retinoid X receptor. Journal of Molecular Biology, 1998, 284, 533-539.	2.0	66
157	Packing, specificity, and mutability at the binding interface between the p160 coactivator and CREB-binding protein. Protein Science, 2004, 13, 203-210.	3.1	66
158	Localized Structural Fluctuations Promote Amyloidogenic Conformations in Transthyretin. Journal of Molecular Biology, 2013, 425, 977-988.	2.0	65
159	Assignment of heme and distal amino acid resonances in the 1H-NMR spectra of the carbon monoxide and oxygen complexes of sperm whale myoglobin. BBA - Proteins and Proteomics, 1985, 832, 175-185.	2.1	62
160	Probing Protein/Protein Interactions with Mass Spectrometry and Isotopic Labeling:Â Analysis of the p21/Cdk2 Complex. Journal of the American Chemical Society, 1996, 118, 5320-5321.	6.6	62
161	The LEF-1 High-Mobility Group Domain Undergoes a Disorder-to-Order Transition upon Formation of a Complex with Cognate DNAâ€. Biochemistry, 2004, 43, 8725-8734.	1.2	62
162	Enhanced picture of protein-folding intermediates using organic solvents in H/D exchange and quench-flow experiments. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4765-4770.	3.3	62

#	Article	IF	Citations
163	Measurement of relaxation time constants for methyl groups by proton-detected heteronuclear NMR spectroscopy. Chemical Physics Letters, 1991, 185, 41-46.	1.2	61
164	NMR evidence for multiple conformations in a highly helical model peptide. Biochemistry, 1993, 32, 13089-13097.	1.2	61
165	The High-Risk HPV16 E7 Oncoprotein Mediates Interaction between the Transcriptional Coactivator CBP and the Retinoblastoma Protein pRb. Journal of Molecular Biology, 2014, 426, 4030-4048.	2.0	61
166	Model-free Analysis of Protein Dynamics: Assessment of Accuracy and Model Selection Protocols Based on Molecular Dynamics Simulation. Journal of Biomolecular NMR, 2004, 29, 243-257.	1.6	60
167	NMR illuminates intrinsic disorder. Current Opinion in Structural Biology, 2021, 70, 44-52.	2.6	60
168	Dynamics of the Metallo-Î²-Lactamase from Bacteroides fragilis in the Presence and Absence of a Tight-Binding Inhibitor. Biochemistry, 2000, 39, 13356-13364.	1.2	59
169	The Proof by 13C-NMR Spectroscopy of the Predominance of the C5 Pathway over the Shemin Pathway in Chlorophyll Biosynthesis in Higher Plants and of the Formation of the Methyl Ester Group of Chlorophyll from Glycine. FEBS Journal, 1983, 130, 509-516.	0.2	58
170	Probing protein structure using biochemical and biophysical methods. Journal of Chromatography A, 1997, 777, 23-30.	1.8	58
171	High-resolution solution structure of the retinoid X receptor DNA-binding domain. Journal of Molecular Biology, 1998, 281, 271-284.	2.0	58
172	Alternative Splicing of Wilms' Tumor Suppressor Protein Modulates DNA Binding Activity through Isoform-Specific DNA-Induced Conformational Changesâ€. Biochemistry, 2000, 39, 5341-5348.	1.2	58
173	Localization of Sites of Interaction between p23 and Hsp90 in Solution. Journal of Biological Chemistry, 2006, 281, 14457-14464.	1.6	58
174	NMR and molecular dynamics studies of the hydration of a zinc finger-DNA complex 1 1Edited by M. F. Summers. Journal of Molecular Biology, 2000, 302, 1101-1117.	2.0	57
175	Accurate scoring of non-uniform sampling schemes for quantitative NMR. Journal of Magnetic Resonance, 2014, 246, 31-35.	1.2	57
176	Polypeptide backbone resonance assignments and secondary structure of Bacillus subtilis enzyme IIIglc determined by two-dimensional and three-dimensional heteronuclear NMR spectroscopy. Biochemistry, 1991, 30, 6896-6907.	1.2	56
177	Role of a solvent-exposed tryptophan in the recognition and binding of antibiotic substrates for a metallo-Î²-lactamase. Protein Science, 2003, 12, 1368-1375.	3.1	56
178	Role of the CBP catalytic core in intramolecular SUMOylation and control of histone H3 acetylation. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E5335-E5342.	3.3	56
179	Assignment of the aliphatic proton and carbon-13 resonances of the Bacillus subtilis glucose permease IIA domain using double- and triple-resonance heteronuclear three-dimensional NMR spectroscopy. Biochemistry, 1992, 31, 4413-4425.	1.2	55
180	Sequence Determinants of a Protein Folding Pathway. Journal of Molecular Biology, 2005, 351, 383-392.	2.0	54

#	Article	IF	Citations
181	Populating the equilibrium molten globule state of apomyoglobin under conditions suitable for structural characterization by NMR. FEBS Letters, 1997, 417, 92-96.	1.3	53
182	The Intrinsically Disordered RNR Inhibitor Sml1 Is a Dynamic Dimer. Biochemistry, 2008, 47, 13428-13437.	1.2	53
183	Conformational Relaxation following Hydride Transfer Plays a Limiting Role in Dihydrofolate Reductase Catalysisâ€. Biochemistry, 2008, 47, 9227-9233.	1.2	53
184	Prion Proteins with Pathogenic and Protective Mutations Show Similar Structure and Dynamics. Biochemistry, 2009, 48, 8120-8128.	1.2	53
185	A modified strategy for identification of1H spin systems in proteins. Biopolymers, 1987, 26, 973-977.	1.2	52
186	Improved resolution in three-dimensional constant-time triple resonance NMR spectroscopy of proteins. Journal of Biomolecular NMR, 1992, 2, 103-108.	1.6	52
187	Tailoring Relaxation Dispersion Experiments for Fast-Associating Protein Complexes. Journal of the American Chemical Society, 2007, 129, 13406-13407.	6.6	52
188	Role of the B Helix in Early Folding Events in Apomyoglobin: Evidence from Site-directed Mutagenesis for Native-like Long Range Interactions. Journal of Molecular Biology, 2003, 334, 293-307.	2.0	51
189	Evidence for two interconverting protein isomers in the methotrexate complex of dihydrofolate reductase from Escherichia coli. Biochemistry, 1991, 30, 2184-2191.	1.2	50
190	Conformation of a T cell stimulating peptide in aqueous solution. FEBS Letters, 1989, 250, 400-404.	1.3	49
191	1H and 15N resonance assignments and secondary structure of the carbon monoxide complex of sperm whale myoglobin. Journal of Biomolecular NMR, 1994, 4, 491-504.	1.6	49
192	Electron transfer reagent binding sites on plastocyanin. Nature, 1980, 283, 682-683.	13.7	48
193	Prediction of the Rotational Tumbling Time for Proteins with Disordered Segments. Journal of the American Chemical Society, 2009, 131, 6814-6821.	6.6	48
194	Perspective: the essential role of NMR in the discovery and characterization of intrinsically disordered proteins. Journal of Biomolecular NMR, 2019, 73, 651-659.	1.6	48
195	Low resolution solution structure of theBacillus subtilisglucose permease IIA domain derived from heteronuclear three-dimensional NMR spectroscopy. FEBS Letters, 1992, 296, 148-152.	1.3	47
196	Interaction of the RNA binding Fingers ofXenopusTranscription Factor IIIA with Specific Regions of 5 S Ribosomal RNA. Journal of Molecular Biology, 1995, 248, 44-57.	2.0	47
197	Conformational and Dynamic Characterization of the Molten Globule State of an Apomyoglobin Mutant with an Altered Folding Pathwayâ€. Biochemistry, 2001, 40, 14459-14467.	1.2	45
198	Cofactor-Mediated Conformational Dynamics Promote Product Release From Escherichia coli Dihydrofolate Reductase via an Allosteric Pathway. Journal of the American Chemical Society, 2015, 137, 9459-9468.	6.6	45

#	Article	IF	Citations
199	Contribution of Increased Length and Intact Capping Sequences to the Conformational Preference for Helix in a 31-Residue Peptide from the C Terminus of Myohemerythrin. Biochemistry, 1997, 36, 5234-5244.	1.2	44
200	Potential bias in NMR relaxation data introduced by peak intensity analysis and curve fitting methods. Journal of Biomolecular NMR, 2001, 21, 1-9.	1.6	44
201	How Does Your Protein Fold? Elucidating the Apomyoglobin Folding Pathway. Accounts of Chemical Research, 2017, 50, 105-111.	7.6	44
202	Assessment of zinc finger orientations by residual dipolar coupling constants. Journal of Biomolecular NMR, 2000, 16, 9-21.	1.6	43
203	Anisotropic rotational diffusion in model-free analysis for a ternary DHFR complex. , 2001, 19, 209-230.		43
204	Inherent flexibility in a potent inhibitor of blood coagulation, recombinant nematode anticoagulant protein c2. FEBS Journal, 1999, 265, 539-548.	0.2	42
205	Inhibition of DNA Binding by Human Estrogen-Related Receptor 2 and Estrogen Receptor Î± with Minor Groove Binding Polyamidesâ€. Biochemistry, 2005, 44, 4196-4203.	1.2	42
206	Kinetics and mechanisms of the oxidation of myoglobin by Fe(III) and Cu(II) complexes. BBA - Proteins and Proteomics, 1987, 912, 384-397.	2.1	41
207	The CBP/p300 TAZ1 domain in its native state is not a binding partner of MDM2. Biochemical Journal, 2004, 381, 685-691.	1.7	41
208	Proton NMR studies of human C3a anaphylatoxin in solution: sequential resonance assignments, secondary structure, and global fold. Biochemistry, 1988, 27, 9139-9148.	1.2	39
209	Relationship between1H and13C NMR chemical shifts and the secondary and tertiary structure of a zinc finger peptide. Journal of Biomolecular NMR, 1992, 2, 307-322.	1.6	39
210	Conformational studies of peroxidaseâ€“substrate complexes. Structure of the indolepropionic acidâ€“horseradish peroxidase complex. Journal of the Chemical Society Chemical Communications, 1975, .	2.0	38
211	Diagnostic chemical shift markers for loop conformation and substrate and cofactor binding in dihydrofolate reductase complexes. Protein Science, 2009, 12, 2230-2238.	3.1	38
212	Partial proton NMR assignments of the Escherichia coli dihydrofolate reductase complex with folate: evidence for a unique conformation of bound folate. Biochemistry, 1990, 29, 9667-9677.	1.2	35
213	Differential Side Chain Hydration in a Linear Peptide Containing a Type VI Turn. Journal of the American Chemical Society, 1994, 116, 12051-12052.	6.6	35
214	Electron transfer from cytochrome b5 to iron and copper complexes. Biochemistry, 1987, 26, 7102-7107.	1.2	34
215	Conformational dynamics of a membrane protein chaperone enables spatially regulated substrate capture and release. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1615-24.	3.3	33
216	Role of Backbone Dynamics in Modulating the Interactions of Disordered Ligands with the TAZ1 Domain of the CREB-Binding Protein. Biochemistry, 2019, 58, 1354-1362.	1.2	33

#	Article	IF	Citations
217	A phosphorylation-dependent switch in the disordered p53 transactivation domain regulates DNA binding. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	33
218	Leu628 of the KIX domain of CBP is a key residue for the interaction with the MLL transactivation domain. FEBS Letters, 2010, 584, 4500-4504.	1.3	32
219	NMR Spectroscopic Studies of the DNA-binding Domain of the Monomer-binding Nuclear Orphan Receptor, Human Estrogen Related Receptor-2. Journal of Biological Chemistry, 1997, 272, 18038-18043.	1.6	31
220	An allosteric peptide inhibitor of HIF-1Î± regulates hypoxia-induced retinal neovascularization. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 28297-28306.	3.3	31
221	Assignment of proton, nitrogen-15, and carbon-13 resonances, identification of elements of secondary structure and determination of the global fold of the DNA-binding domain of GAL4. Biochemistry, 1993, 32, 2144-2153.	1.2	30
222	Association between the first two immunoglobulin-like domains of the neural cell adhesion molecule N-CAM. FEBS Letters, 1999, 451, 162-168.	1.3	30
223	Overexpression of post-translationally modified peptides in Escherichia coli by co-expression with modifying enzymes. Protein Expression and Purification, 2008, 57, 108-115.	0.6	30
224	NMR Measurements Reveal the Structural Basis of Transthyretin Destabilization by Pathogenic Mutations. Biochemistry, 2018, 57, 4421-4430.	1.2	30
225	Folding of a Î²-sheet Protein Monitored by Real-time NMR Spectroscopy. Journal of Molecular Biology, 2003, 328, 1161-1171.	2.0	29
226	Kinetic analysis of the multistep aggregation pathway of human transthyretin. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E6201-E6208.	3.3	29
227	[6] Multiple-quantum nuclear magnetic resonance. Methods in Enzymology, 1989, 176, 114-134.	0.4	28
228	Zinc is required for folding and binding of a single zinc finger to DNA. FEBS Letters, 1991, 279, 289-294.	1.3	28
229	1H, 15N and 13C resonance assignments, secondary structure, and the conformation of substrate in the binary folate complex of Escherichia coli dihydrofolate reductase. Journal of Biomolecular NMR, 1994, 4, 349-366.	1.6	28
230	1H-NMR studies of ferric soybean leghemoglobin Assignment of hyperfine shifted resonances of complexes with cyanide, nicotinate, pyridine and azide. Biochimica Et Biophysica Acta (BBA) - Protein Structure, 1980, 625, 202-220.	1.7	27
231	Defining the Structural Basis for Allosteric Product Release from E. coli Dihydrofolate Reductase Using NMR Relaxation Dispersion. Journal of the American Chemical Society, 2017, 139, 11233-11240.	6.6	27
232	Structural Basis for Interaction of the Tandem Zinc Finger Domains of Human Muscleblind with Cognate RNA from Human Cardiac Troponin T. Biochemistry, 2017, 56, 4154-4168.	1.2	27
233	Measurement of heme accessibility in soybean ferric leghemoglobin a and its complexes by proton magnetic relaxation. Biochemistry, 1981, 20, 587-594.	1.2	26
234	The Kinetic and Equilibrium Molten Globule Intermediates of Apoleghemoglobin Differ in Structure. Journal of Molecular Biology, 2008, 378, 715-725.	2.0	26

#	Article	IF	Citations
235	Slow Dynamics of Tryptophanâ€“Water Networks in Proteins. Journal of the American Chemical Society, 2018, 140, 675-682.	6.6	26
236	Differences in amino acid composition and heme electronic structure of the multiple monomeric hemoglobin components of Glycera dibranchiata. BBA - Proteins and Proteomics, 1985, 832, 357-364.	2.1	25
237	Sequence requirements for stabilization of a peptide reverse turn in water solution. Proline is not essential for stability. FEBS Journal, 1998, 255, 462-471.	0.2	25
238	Solution structure of the third immunoglobulin domain of the neural cell adhesion molecule N-CAM: can solution studies define the mechanism of homophilic binding?. Journal of Molecular Biology, 2001, 311, 161-172.	2.0	25
239	Solid-State NMR Studies Reveal Native-like Î²-Sheet Structures in Transthyretin Amyloid. Biochemistry, 2016, 55, 5272-5278.	1.2	25
240	Complete assignment of the 1 H NMR spectrum of a synthetic zinc finger from Xfin Sequential resonance assignments and secondary structure. FEBS Letters, 1989, 254, 159-164.	1.3	24
241	Molecular basis for proton-dependent anion binding by soybean leghaemoglobin a. Nature, 1979, 280, 87-88.	13.7	23
242	The zinc finger motif Conservation of chemical shifts and correlation with structure. FEBS Letters, 1992, 309, 29-32.	1.3	23
243	Amide proton hydrogen exchange rates for sperm whale myoglobin obtained from ¹⁵Nâ€¹H NMR spectra. Protein Science, 2000, 9, 186-193.	3.1	23
244	PCR-based gene synthesis and protein NMR spectroscopy. Structure, 1997, 5, 1407-1412.	1.6	22
245	How Do Intrinsically Disordered Viral Proteins Hijack the Cell?. Biochemistry, 2018, 57, 4045-4046.	1.2	22
246	Multivalency enables unidirectional switch-like competition between intrinsically disordered proteins. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	22
247	Heme orientation in the major monomeric hemoglobins of Glycera dibranchiata. BBA - Proteins and Proteomics, 1985, 832, 365-372.	2.1	21
248	Antigen-antibody interactions: An NMR approach. Biochemical Pharmacology, 1990, 40, 83-88.	2.0	21
249	Embryonic Neural Inducing Factor Churchill Is not a DNA-binding Zinc Finger Protein: Solution Structure Reveals a Solvent-exposed Î²-Sheet and Zinc Binuclear Cluster. Journal of Molecular Biology, 2007, 371, 1274-1289.	2.0	21
250	A two-dimensional NMR method for assignment of imidazole ring proton resonances of histidine residues in proteins. Biochemical and Biophysical Research Communications, 1982, 106, 559-565.	1.0	20
251	Complete assignment of lysine resonances in 1 H NMR spectra of proteins as probes of surface structure and dynamics. FEBS Letters, 1987, 222, 109-114.	1.3	20
252	Structural determinants of Cys2 His2 zinc fingers. FEBS Letters, 1992, 296, 11-15.	1.3	20

#	Article	IF	Citations
253	Distributed torsion angle grid search in high dimensions: a systematic approach to NMR structure determination. Journal of Biomolecular NMR, 1998, 11, 241-263.	1.6	20
254	Determination of Feâ˜Ligand Bond Lengths and the Feâ˜Nâ˜O Bond Angles in Soybean Ferrous and Ferric NitrosylleghemoglobinaUsing Multiple-Scattering XAFS Analysesâ€. Biochemistry, 1999, 38, 16491-16499.	1.2	20
255	Structure of the Nuclear Factor ALY:â€‰ Insights into Post-Transcriptional Regulatory and mRNA Nuclear Export Processes. Biochemistry, 2003, 42, 7348-7357.	1.2	20
256	According to current textbooks, a well-defined three-dimensional structure is a prerequisite for the function of a protein. Is this correct?. IUBMB Life, 2006, 58, 107-109.	1.5	20
257	Combinatorial regulation of a signal-dependent activator by phosphorylation and acetylation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17116-17121.	3.3	20
258	Structural Characterization of Interactions between the Double-Stranded RNA-Binding Zinc Finger Protein JAZ and Nucleic Acids. Biochemistry, 2014, 53, 1495-1510.	1.2	20
259	Fluorotryptophan Incorporation Modulates the Structure and Stability of Transthyretin in a Site-Specific Manner. Biochemistry, 2017, 56, 5570-5581.	1.2	20
260	What can two-dimensional NMR tell us about proteins?. Trends in Biochemical Sciences, 1989, 14, 255-260.	3.7	19
261	Identification of a minimal domain of 5 S ribosomal RNA sufficient for high affinity interactions with the RNA-specific zinc fingers of transcription factor IIIA 1 1Edited by D. E. Draper. Journal of Molecular Biology, 1999, 291, 549-560.	2.0	19
262	NMR Solution Structure of the Peptide Fragment 1â˜30, Derived from Unprocessed Mouse Doppel Protein, in DHPC Micellesâ€. Biochemistry, 2006, 45, 159-166.	1.2	19
263	NMR Characterization of Information Flow and Allosteric Communities in the MAP Kinase p38Î³. Scientific Reports, 2016, 6, 28655.	1.6	19
264	CHÂ·Â·Â·O Hydrogen Bonds Mediate Highly Specific Recognition of Methylated CpG Sites by the Zinc Finger Protein Kaiso. Biochemistry, 2018, 57, 2109-2120.	1.2	19
265	Kinetics and mechanisms of reduction of Cu(II) and Fe(III) complexes by soybean leghemoglobin Î±. BBA - Proteins and Proteomics, 1991, 1079, 182-196.	2.1	18
266	Solution Structure of the N-terminal Zinc Fingers of the Xenopus laevis double-stranded RNA-binding Protein ZFa. Journal of Molecular Biology, 2005, 351, 718-730.	2.0	18
267	Mapping the interactions of adenoviral E1A proteins with the p160 nuclear receptor coactivator binding domain of CBP. Protein Science, 2016, 25, 2256-2267.	3.1	18
268	Structural basis for cooperative regulation of KIX-mediated transcription pathways by the HTLV-1 HBZ activation domain. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 10040-10045.	3.3	18
269	Simplification of 1H NMR spectra of proteins by one-dimensional multiple quantum filtration. Biochemical and Biophysical Research Communications, 1985, 131, 1094-1102.	1.0	17
270	Proton NMR studies of plastocyanin: assignment of aromatic and methyl group resonances from two-dimensional spectra. Biochemistry, 1986, 25, 2364-2374.	1.2	17

#	Article	IF	Citations
271	NMR studies of the heme pocket conformations of monomeric hemoglobins from Glycera dibranchiata. Implications for ligand binding. FEBS Journal, 1987, 166, 399-408.	0.2	17
272	Hydrogen Exchange in the Carbon Monoxide Complex of Soybean Leghemoglobin. FEBS Journal, 1996, 237, 212-220.	0.2	17
273	A NOESY-HSQC simulation program, SPIRIT. Journal of Biomolecular NMR, 1998, 11, 17-29.	1.6	17
274	Energetic Frustration of Apomyoglobin Folding: Role of the B Helix. Journal of Molecular Biology, 2010, 396, 1319-1328.	2.0	17
275	Kaiso uses all three zinc fingers and adjacent sequence motifs for high affinity binding to sequenceâ€specific and methylâ€CpG DNA targets. FEBS Letters, 2012, 586, 734-739.	1.3	17
276	Structural characterization of partially folded intermediates of apomyoglobin H64F. Protein Science, 2008, 17, 313-321.	3.1	16
277	Consequences of Stabilizing the Natively Disordered F Helix for the Folding Pathway of Apomyoglobin. Journal of Molecular Biology, 2011, 411, 248-263.	2.0	16
278	Side-Chain Conformational Heterogeneity of Intermediates in the Escherichia coli Dihydrofolate Reductase Catalytic Cycle. Biochemistry, 2013, 52, 3464-3477.	1.2	16
279	Probing the Non-Native H Helix Translocation in Apomyoglobin Folding Intermediates. Biochemistry, 2014, 53, 3767-3780.	1.2	16
280	Conformational disorder of the distal leucine in monomericGlycerahemoglobins and implications for oxygen binding. FEBS Letters, 1985, 187, 219-223.	1.3	15
281	NMR studies of the conformations of leghemoglobins from soybean and lupin. FEBS Journal, 1988, 178, 419-435.	0.2	15
282	Immunogenic peptides corresponding to the dominant antigenic region alanine-597 to cysteine-619 in the transmembrane protein of simian immunodeficiency virus have a propensity to fold in aqueous solution. Biochemistry, 1992, 31, 1458-1463.	1.2	15
283	NMR Assignments and Secondary Structure of the Retinoid X Receptor alpha DNA-binding Domain. Evidence for the Novel C-terminal Helix. FEBS Journal, 1994, 224, 639-650.	0.2	15
284	Identification of the regions involved in DNA binding by the mouse PEBP2Î± protein. FEBS Letters, 2000, 470, 125-130.	1.3	15
285	Assigment of heme and distal amino acid resonances in the proton NMR spectra of the oxyen and carbon monoxide complexes of soybean leghemoglobin. BBA - Proteins and Proteomics, 1983, 744, 281-290.	2.1	14
286	Changes in structure and dynamics of the Fv fragment of a catalytic antibody upon binding of inhibitor. Protein Science, 2003, 12, 1386-1394.	3.1	14
287	Identification of endogenous ligands bound to bacterially expressed human andE. colidihydrofolate reductase by 2D NMR. FEBS Letters, 2011, 585, 3528-3532.	1.3	14
288	Thermodynamic Stability and Aggregation Kinetics of EF Helix and EF Loop Variants of Transthyretin. Biochemistry, 2021, 60, 756-764.	1.2	14

#	Article	IF	Citations
289	Conformational influences in copper co-ordination compounds. Part V. Crystal and molecular structure of {1,2-bis-[(2-aminobenzylidene)-amino]propanato(2â€“)}copper(II). Journal of the Chemical Society Dalton Transactions, 1973, , 1508-1512.	1.1	13
290	E.s.r. and optical spectral properties of copper(II) complexes with Schiff-base ligands derived from o-aminobenzaldehyde. Journal of the Chemical Society Dalton Transactions, 1975, , 867.	1.1	13
291	NMR studies of oxyleghemoglobin. BBA - Proteins and Proteomics, 1983, 749, 281-288.	2.1	12
292	Gene synthesis, high-level expression and assignment of backbone15N and13C resonances of soybean leghemoglobin. FEBS Letters, 1996, 399, 283-289.	1.3	12
293	Assessment of major and minor groove DNA interactions by the zinc fingers of Xenopus transcription factor IIIA. Nucleic Acids Research, 1996, 24, 2567-2574.	6.5	12
294	The CH2 domain of CBP/p300 is a novel zinc finger. FEBS Letters, 2013, 587, 2506-2511.	1.3	12
295	1H resonance assignments and secondary structure of the carbon monoxide complex of soybean leghemoglobin determined by homonuclear two-dimensional and three-dimensional NMR spectroscopy. FEBS Journal, 1994, 219, 611-626.	0.2	10
296	1H NMR studies of heme pocket conformation in zinc-substituted leghemoglobin, a diamagnetic analog of deoxyleghemoglobin. Journal of Inorganic Biochemistry, 1986, 28, 303-309.	1.5	9
297	Multi-probe relaxation dispersion measurements increase sensitivity to protein dynamics. Physical Chemistry Chemical Physics, 2016, 18, 5789-5798.	1.3	9
298	Characterization of the High-Affinity Fuzzy Complex between the Disordered Domain of the E7 Oncoprotein from High-Risk HPV and the TAZ2 Domain of CBP. Biochemistry, 2021, 60, 3887-3898.	1.2	9
299	1H resonances of proximal histidine in CO complexes of hemoglobins provide a sensitive probe of coordination geometry. FEBS Letters, 1987, 213, 289-292.	1.3	8
300	Structural consequences of heme isomerism in monomeric hemoglobins from Glycera dibranchiata. FEBS Journal, 1987, 166, 409-414.	0.2	8
301	Side Chain Conformational Averaging in Human Dihydrofolate Reductase. Biochemistry, 2014, 53, 1134-1145.	1.2	8
302	Mispacking of the Phe87 Side Chain Reduces the Kinetic Stability of Human Transthyretin. Biochemistry, 2018, 57, 6919-6922.	1.2	8
303	A Disorder-to-Order Transition Activates an ATP-Independent Membrane Protein Chaperone. Journal of Molecular Biology, 2020, 432, 166708.	2.0	8
304	Differences in the heme environment of soybean leghemoglobin components shown by 1H-NMR spectroscopy. BBA - Proteins and Proteomics, 1982, 700, 171-177.	2.1	7
305	Assignment of 1H, 13C and 15N resonances of the I-domain of human leukocyte function associated antigen-1. Journal of Biomolecular NMR, 2000, 16, 271-272.	1.6	7
306	Structural Basis for Graded Inhibition of CREB:DNA Interactions by Multisite Phosphorylation. Biochemistry, 2018, 57, 6964-6972.	1.2	7

#	Article	IF	Citations
307	Comparison of backbone dynamics of the p50 dimerization domain of NFÎºB in the homodimeric transcription factor NFÎºB1 and in its heterodimeric complex with RelA (p65). Protein Science, 2019, 28, 2064-2072.	3.1	7
308	A Dynamic Switch in Inactive p38Î³ Leads to an Excited State on the Pathway to an Active Kinase. Biochemistry, 2019, 58, 5160-5172.	1.2	7
309	A Conformational Switch in the Zinc Finger Protein Kaiso Mediates Differential Readout of Specific and Methylated DNA Sequences. Biochemistry, 2020, 59, 1909-1926.	1.2	7
310	THE H-HELIX OF MYOGLOBIN AS A POTENTIAL INDEPENDENT PROTEIN FOLDING DOMAIN. , 1990, , 283-293.		7
311	The identification of metalâ€binding ligand residues in metalloproteins using nuclear magnetic resonance spectroscopy. Protein Science, 1998, 7, 2476-2479.	3.1	6
312	Assignment of a 15 kDa protein complex formed between the p160 coactivator ACTR and CREB binding protein. Journal of Biomolecular NMR, 2002, 22, 377-378.	1.6	6
313	The molecular basis of allostery in a facilitated dissociation process. Structure, 2021, 29, 1327-1338.e5.	1.6	6
314	1H, 13C and 15N NMR backbone assignments of 25.5 kDa metallo-beta-lactamase from Bacteroides fragilis. Journal of Biomolecular NMR, 1998, 12, 201-202.	1.6	5
315	Characterization of monomeric and dimeric B domain of Staphylococcal protein A. Chemical Biology and Drug Design, 1999, 54, 344-352.	1.2	5
316	A transthyretin monomer intermediate undergoes local unfolding and transient interaction with oligomers in a kinetically concerted aggregation pathway. Journal of Biological Chemistry, 2022, 298, 102162.	1.6	5
317	High-resolution solution structure ofBacillus subtilis IIAglc. , 1998, 31, 258-270.		4
318	Backbone resonance assignments for the Fv fragment of the catalytic antibody NPN43C9 with bound p-nitrophenol. Journal of Biomolecular NMR, 1999, 15, 83-84.	1.6	4
319	Structure and Function of the CBP/p300 TAZ Domains. , 2005, , 114-120.		4
320	RNA Binding by the KTS Splice Variants of Wilmsâ€™ Tumor Suppressor Protein WT1. Biochemistry, 2020, 59, 3889-3901.	1.2	4
321	Modeling of Hidden Structures Using Sparse Chemical Shift Data from NMR Relaxation Dispersion. Biophysical Journal, 2021, 120, 296-305.	0.2	4
322	Role of Active Site Loop Dynamics in Mediating Ligand Release from E. coli Dihydrofolate Reductase. Biochemistry, 2021, 60, 2663-2671.	1.2	4
323	Interactions of a Long Noncoding RNA with Domains of NF-ÎºB and IÎºBÎ±: Implications for the Inhibition of Non-Signal-Related Phosphorylation. Biochemistry, 2022, 61, 367-376.	1.2	4
324	Assignment of 1H, 13C, and 15N resonances of reduced Escherichia coli glutaredoxin 2. Journal of Biomolecular NMR, 1999, 14, 197-198.	1.6	3

#	Article	IF	Citations
325	Backbone H(N), N, Calpha, C' and Cbeta assignments of the 19 kDa DHFR/NADPH complex at 9 degrees C and pH 7.6. Journal of Biomolecular NMR, 2000, 16, 349-350.	1.6	3
326	Tight complexes from disordered proteins. Nature, 2018, 555, 37-38.	13.7	3
327	Determining Binding Kinetics of Intrinsically Disordered Proteins by NMR Spectroscopy. Methods in Molecular Biology, 2020, 2141, 663-681.	0.4	3
328	Introduction:â€‰ Biological Nuclear Magnetic Resonance. Chemical Reviews, 2004, 104, 3517-3518.	23.0	2
329	Biophysical methods Editorial overview. Current Opinion in Structural Biology, 1993, 3, 723-724.	2.6	1
330	Biophysical methods Faster and bigger. Current Opinion in Structural Biology, 1996, 6, 583-584.	2.6	1
331	Unfolded Proteins and Protein Folding Studied by NMR. ChemInform, 2004, 35, no.	0.1	1
332	Editorial from the Editor-in-Chief. Journal of Molecular Biology, 2009, 385, 1-2.	2.0	1
333	NMR Structural Studies of Flexible Molecules. , 1996, , 245-249.		1
334	Structural Biology â€“ Painting the Mechanistic Landscape of Biomolecules. Journal of Molecular Biology, 2022, 434, 167566.	2.0	1
335	Structural and dynamic studies of DNA recognition by NF-ÎºB p50 RHR homodimer using methyl NMR spectroscopy. Nucleic Acids Research, 0, , .	6.5	1
336	Measurement of intrinsic exchange rates of amide protons in a 15N-labeled peptide. Journal of Biomolecular NMR, 1996, 7, 341.	1.6	0
337	S03A3 Metastable structure detected by relaxation dispersion NMR spectroscopy(Visualising) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.0	0
338	3P040 Mapping the Interactions of the Intrinsically Disordered p53 Transactivation Subdomains with the TAZ2 Domain of CBP by NMR(Protein: Structure & Function,The 48th Annual Meeting of the) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2	0.0	0
339	Structural Basis for Cooperative Transcription Factor Binding to the CBP Coactivator. FASEB Journal, 2012, 26, lb266.	0.2	0
340	Functional Interactions of Intrinsically Disordered Proteins in Signaling Networks. FASEB Journal, 2013, 27, 459.3.	0.2	0
341	Client Specificity of an ATPâ€independent Chaperone is Regulated by a Temperature Sensitive Switch. FASEB Journal, 2022, 36, .	0.2	0