Peter E Wright

List of Publications by Year
in descending order

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341 papers	47,694 citations	1457 107 h-index	1895 208 g-index
364 all docs	364 docs citations	364 times ranked	31397 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

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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

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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

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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

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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

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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

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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

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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

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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

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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
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