Peter Wright

List of Articles by Year in descending order

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388 peer-reviewed articles	43,913 peer-reviewed citations	1492 103 peer-reviewed h-index	75848 6.47 score
430 documents	55498 doc citations	1440 113 h-index	53166 citing authors

#	Article	IF	Citations
1	Initiation of transthyretin aggregation at neutral pH by fluid agitation. Proceedings of the National Academy of Sciences of the United States of America, 2025, 122, .	5.2	6
2	Switchable client specificity in a dual functional chaperone coordinates light-harvesting complex biogenesis. Science Advances, 2025, 11, .	8.1	1
3	Mechanism of inhibition of acid-mediated transthyretin aggregation by designed peptides. Journal of Biological Chemistry, 2025, 301, 110594.	1.3	2
4	Probing the Dissociation Pathway of a Kinetically Labile Transthyretin Mutant. Journal of the American Chemical Society, 2024, 146, 532-542.	11.7	13
5	Conformational Dynamics of an Amyloidogenic Intermediate of Transthyretin: Implications for Structural Remodeling and Amyloid Formation. Journal of Molecular Biology, 2024, 436, 168673.	2.9	10
6	Mispacking of the F87 sidechain drives aggregation-promoting conformational fluctuations in the subunit interfaces of the transthyretin tetramer. Protein Science, 2024, 33, .	3.5	2
7	Role of conformational dynamics in pathogenic protein aggregation. Current Opinion in Chemical Biology, 2023, 73, 102280.	4.6	23
8	From Immunogenic Peptides to Intrinsically Disordered Proteins. Israel Journal of Chemistry, 2023, 63, .	1.3	2
9	The smallest functional antibody fragment: Ultralong CDR H3 antibody knob regions potently neutralize SARS-CoV-2. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	5.2	23
10	Glutamine-rich regions of the disordered CREB transactivation domain mediate dynamic intra- and intermolecular interactions. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	5.2	18
11	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, .	5.2	38
12	Interactions of a Long Noncoding RNA with Domains of NF-κB and IκBα: Implications for the Inhibition of Non-Signal-Related Phosphorylation. Biochemistry, 2022, 61, 367-376.	1.5	10
13	Client Specificity of an ATP-independent Chaperone is Regulated by a Temperature Sensitive Switch. FASEB Journal, 2022, 36, .	2.3	0
14	Structural biology - Painting the mechanistic landscape of biomolecules. Current Research in Structural Biology, 2022, 4, iv.	2.4	3
15	Structural and dynamic studies of DNA recognition by NF-κB p50 RHR homodimer using methyl NMR spectroscopy. Nucleic Acids Research, 2022, 50, 7147-7160.	10.7	5
16	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.	1.3	13
17	Transient On- and Off-Pathway Protein Folding Intermediate States Characterized with NMR Relaxation Dispersion. Journal of Physical Chemistry B, 2022, 126, 9539-9548.	2.0	6
18	Mapping Interactions of the Intrinsically Disordered C-Terminal Regions of Tetrameric p53 by Segmental Isotope Labeling and NMR. Biochemistry, 2022, 61, 2709-2719.	1.5	15

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19	Modeling of Hidden Structures Using Sparse Chemical Shift Data from NMR Relaxation Dispersion. Biophysical Journal, 2021, 120, 296-305.	1.5	5
20	Thermodynamic Stability and Aggregation Kinetics of EF Helix and EF Loop Variants of Transthyretin. Biochemistry, 2021, 60, 756-764.	1.5	29
21	Role of Active Site Loop Dynamics in Mediating Ligand Release from E. coli Dihydrofolate Reductase. Biochemistry, 2021, 60, 2663-2671.	1.5	14
22	The molecular basis of allostery in a facilitated dissociation process. Structure, 2021, 29, 1327-1338.e5.	2.4	18
23	NMR illuminates intrinsic disorder. Current Opinion in Structural Biology, 2021, 70, 44-52.	4.6	104
24	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, .	5.2	82
25	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.	1.5	13
26	A Disorder-to-Order Transition Activates an ATP-Independent Membrane Protein Chaperone. Journal of Molecular Biology, 2020, 432, 166708.	2.9	10
27	An allosteric peptide inhibitor of HIF-1α regulates hypoxia-induced retinal neovascularization. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 28297-28306.	5.2	55
28	RNA Binding by the KTS Splice Variants of Wilms' Tumor Suppressor Protein WT1. Biochemistry, 2020, 59, 3889-3901.	1.5	7
29	A Conformational Switch in the Zinc Finger Protein Kaiso Mediates Differential Readout of Specific and Methylated DNA Sequences. Biochemistry, 2020, 59, 1909-1926.	1.5	16
30	Comparison of backbone dynamics of the p50 dimerization domain of NFκB in the homodimeric transcription factor NFκB1 and in its heterodimeric complex with RelA (p65). Protein Science, 2019, 28, 2064-2072.	3.5	8
31	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	54
32	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.	1.5	47
33	A Dynamic Switch in Inactive p38γ Leads to an Excited State on the Pathway to an Active Kinase. Biochemistry, 2019, 58, 5160-5172.	1.5	12
34	Expanding the Paradigm: Intrinsically Disordered Proteins and Allosteric Regulation. Journal of Molecular Biology, 2018, 430, 2309-2320.	2.9	141
35	Slow Dynamics of Tryptophan–Water Networks in Proteins. Journal of the American Chemical Society, 2018, 140, 675-682.	11.7	32
36	CH···O Hydrogen Bonds Mediate Highly Specific Recognition of Methylated CpG Sites by the Zinc Finger Protein Kaiso. Biochemistry, 2018, 57, 2109-2120.	1.5	31

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37	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, .	5.2	139
38	Mispacking of the Phe87 Side Chain Reduces the Kinetic Stability of Human Transthyretin. Biochemistry, 2018, 57, 6919-6922.	1.5	16
39	Structural Basis for Graded Inhibition of CREB:DNA Interactions by Multisite Phosphorylation. Biochemistry, 2018, 57, 6964-6972.	1.5	13
40	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.	5.2	20
41	NMR Measurements Reveal the Structural Basis of Transthyretin Destabilization by Pathogenic Mutations. Biochemistry, 2018, 57, 4421-4430.	1.5	45
42	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, .	5.2	44
43	Hypersensitive termination of the hypoxic response by a disordered protein switch. Nature, 2017, 543, 447-451.	30.7	178
44	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, .	5.2	70
45	How Does Your Protein Fold? Elucidating the Apomyoglobin Folding Pathway. Accounts of Chemical Research, 2017, 50, 105-111.	11.6	55
46	Fluorotryptophan Incorporation Modulates the Structure and Stability of Transthyretin in a Site-Specific Manner. Biochemistry, 2017, 56, 5570-5581.	1.5	28
47	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.	11.7	31
48	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.	1.5	35
49	NMR Characterization of Information Flow and Allosteric Communities in the MAP Kinase p38γ. Scientific Reports, 2016, 6, .	2.7	24
50	Solid-State NMR Studies Reveal Native-like β-Sheet Structures in Transthyretin Amyloid. Biochemistry, 2016, 55, 5272-5278.	1.5	28
51	Mapping the interactions of adenoviral E1A proteins with the p160 nuclear receptor coactivator binding domain of CBP. Protein Science, 2016, 25, 2256-2267.	3.5	19
52	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, .	5.2	116
53	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.	1.3	336
54	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, .	5.2	38

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55	Multi-probe relaxation dispersion measurements increase sensitivity to protein dynamics. Physical Chemistry Chemical Physics, 2016, 18, 5789-5798.	2.0	12
56	Functional advantages of dynamic protein disorder. FEBS Letters, 2015, 589, 2433-2440.	1.8	187
57	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.	11.7	48
58	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.	5.2	264
59	pE-DB: a database of structural ensembles of intrinsically disordered and of unfolded proteins. Nucleic Acids Research, 2014, 42, D326-D335.	10.7	211
60	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.	5.2	27
61	Assemblages: Functional units formed by cellular phase separation. Journal of Cell Biology, 2014, 206, 579-588.	3.6	257
62	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, .	5.2	174
63	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.	2.9	85
64	Side Chain Conformational Averaging in Human Dihydrofolate Reductase. Biochemistry, 2014, 53, 1134-1145.	1.5	10
65	Probing the Non-Native H Helix Translocation in Apomyoglobin Folding Intermediates. Biochemistry, 2014, 53, 3767-3780.	1.5	18
66	Accurate scoring of non-uniform sampling schemes for quantitative NMR. Journal of Magnetic Resonance, 2014, 246, 31-35.	1.6	64
67	Classification of Intrinsically Disordered Regions and Proteins. Chemical Reviews, 2014, 114, 6589-6631.	42.5	2,199
68	Structural Characterization of Interactions between the Double-Stranded RNA-Binding Zinc Finger Protein JAZ and Nucleic Acids. Biochemistry, 2014, 53, 1495-1510.	1.5	28
69	Intrinsically disordered proteins in cellular signalling and regulation. Nature Reviews Molecular Cell Biology, 2014, 16, 18-29.	69.0	2,494
70	Automated identification of functional dynamic contact networks from X-ray crystallography. Nature Methods, 2013, 10, 896-902.	13.1	146
71	Fast and accurate fitting of relaxation dispersion data using the flexible software package GLOVE. Journal of Biomolecular NMR, 2013, 56, 275-283.	1.6	80
72	The CH2 domain of CBP/p300 is a novel zinc finger. FEBS Letters, 2013, 587, 2506-2511.	1.8	13

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73	Divergent evolution of protein conformational dynamics in dihydrofolate reductase. Nature Structural and Molecular Biology, 2013, 20, 1243-1249.	5.8	186
74	Localized Structural Fluctuations Promote Amyloidogenic Conformations in Transthyretin. Journal of Molecular Biology, 2013, 425, 977-988.	2.9	79
75	A Distal Mutation Perturbs Dynamic Amino Acid Networks in Dihydrofolate Reductase. Biochemistry, 2013, 52, 4605-4619.	1.5	84
76	Modulation of allostery by protein intrinsic disorder. Nature, 2013, 498, 390-394.	30.7	317
77	Side-Chain Conformational Heterogeneity of Intermediates in the Escherichia coli Dihydrofolate Reductase Catalytic Cycle. Biochemistry, 2013, 52, 3464-3477.	1.5	19
78	Analysis of the RelA:CBP/p300 Interaction Reveals Its Involvement in NF-κB-Driven Transcription. PLoS Biology, 2013, 11, e1001647.	3.1	156
79	Mechanisms of Transthyretin Inhibition of β-Amyloid AggregationIn Vitro. Journal of Neuroscience, 2013, 33, 19423-19433.	2.3	143
80	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.	5.2	124
81	Quantitative Analysis of Multisite Protein–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.	11.7	136
82	Kaiso uses all three zinc fingers and adjacent sequence motifs for high affinity binding to sequence-specific and methyl-CpG DNA targets. FEBS Letters, 2012, 586, 734-739.	1.8	22
83	Consequences of Stabilizing the Natively Disordered F Helix for the Folding Pathway of Apomyoglobin. Journal of Molecular Biology, 2011, 411, 248-263.	2.9	16
84	Identification of endogenous ligands bound to bacterially expressed human andE. colidihydrofolate reductase by 2D NMR. FEBS Letters, 2011, 585, 3528-3532.	1.8	15
85	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.	5.2	74
86	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.	1.8	35
87	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.	5.2	211
88	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.	5.2	139
89	Structure of the p53 Transactivation Domain in Complex with the Nuclear Receptor Coactivator Binding Domain of CREB Binding Protein. Biochemistry, 2010, 49, 9964-9971.	1.5	183
90	Energetic Frustration of Apomyoglobin Folding: Role of the B Helix. Journal of Molecular Biology, 2010, 396, 1319-1328.	2.9	17

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91	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.	5.2	213
92	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.	5.2	128
93	Linking folding and binding. Current Opinion in Structural Biology, 2009, 19, 31-38.	4.6	1,003
94	Diagnostic chemical shift markers for loop conformation and substrate and cofactor binding in dihydrofolate reductase complexes. Protein Science, 2009, 12, 2230-2238.	3.5	37
95	Mapping the Interactions of the p53 Transactivation Domain with the KIX Domain of CBP. Biochemistry, 2009, 48, 2115-2124.	1.5	116
96	Prion Proteins with Pathogenic and Protective Mutations Show Similar Structure and Dynamics. Biochemistry, 2009, 48, 8120-8128.	1.5	55
97	Structural basis for recruitment of CBP/p300 coactivators by STAT1 and STAT2 transactivation domains. EMBO Journal, 2009, 28, 948-958.	5.1	177
98	Prediction of the Rotational Tumbling Time for Proteins with Disordered Segments. Journal of the American Chemical Society, 2009, 131, 6814-6821.	11.7	55
99	Structural characterization of partially folded intermediates of apomyoglobin H64F. Protein Science, 2008, 17, 313-321.	3.5	16
100	The Kinetic and Equilibrium Molten Globule Intermediates of Apoleghemoglobin Differ in Structure. Journal of Molecular Biology, 2008, 378, 715-725.	2.9	27
101	Overexpression of post-translationally modified peptides in Escherichia coli by co-expression with modifying enzymes. Protein Expression and Purification, 2008, 57, 108-115.	1.1	37
102	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.	5.2	90
103	NMR Relaxation Study of the Complex Formed Between CBP and the Activation Domain of the Nuclear Hormone Receptor Coactivator ACTR†. Biochemistry, 2008, 47, 1299-1308.	1.5	92
104	The Intrinsically Disordered RNR Inhibitor Sml1 Is a Dynamic Dimer. Biochemistry, 2008, 47, 13428-13437.	1.5	57
105	Conformational Relaxation following Hydride Transfer Plays a Limiting Role in Dihydrofolate Reductase Catalysis. Biochemistry, 2008, 47, 9227-9233.	1.5	57
106	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.	5.2	106
107	PRAK Is Essential for ras-Induced Senescence and Tumor Suppression. Cell, 2007, 128, 295-308.	23.4	303
108	Embryonic Neural Inducing Factor Churchill Is not a DNA-binding Zinc Finger Protein: Solution Structure Reveals a Solvent-exposed β-Sheet and Zinc Binuclear Cluster. Journal of Molecular Biology, 2007, 371, 1274-1289.	2.9	24

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109	Structure of the Wilms Tumor Suppressor Protein Zinc Finger Domain Bound to DNA. Journal of Molecular Biology, 2007, 372, 1227-1245.	2.9	96
110	Tailoring Relaxation Dispersion Experiments for Fast-Associating Protein Complexes. Journal of the American Chemical Society, 2007, 129, 13406-13407.	11.7	56
111	Mechanism of coupled folding and binding of an intrinsically disordered protein. Nature, 2007, 447, 1021-1025.	30.7	1,038
112	An NMR Perspective on Enzyme Dynamics. Chemical Reviews, 2006, 106, 3055-3079.	42.5	458
113	NMR Solution Structure of the Peptide Fragment 1−30, Derived from Unprocessed Mouse Doppel Protein, in DHPC Micelles†. Biochemistry, 2006, 45, 159-166.	1.5	19
114	Structural Basis for Cooperative Transcription Factor Binding to the CBP Coactivator. Journal of Molecular Biology, 2006, 355, 1005-1013.	2.9	183
115	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.	2.9	171
116	Identification of Native and Non-native Structure in Kinetic Folding Intermediates of Apomyoglobin. Journal of Molecular Biology, 2006, 355, 139-156.	2.9	114
117	Induced Fit and “Lock and Key” Recognition of 5S RNA by Zinc Fingers of Transcription Factor IIIA. Journal of Molecular Biology, 2006, 357, 275-291.	2.9	81
118	Solution Structure of the Hdm2 C2H2C4 RING, a Domain Critical for Ubiquitination of p53. Journal of Molecular Biology, 2006, 363, 433-450.	2.9	121
119	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.	2.1	20
120	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.	5.2	319
121	Localization of Sites of Interaction between p23 and Hsp90 in Solution. Journal of Biological Chemistry, 2006, 281, 14457-14464.	1.3	63
122	Intrinsically unstructured proteins and their functions. Nature Reviews Molecular Cell Biology, 2005, 6, 197-208.	69.0	3,738
123	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.	5.2	170
124	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.	5.2	63
125	Inhibition of DNA Binding by Human Estrogen-Related Receptor 2 and Estrogen Receptor α with Minor Groove Binding Polyamides†. Biochemistry, 2005, 44, 4196-4203.	1.5	43
126	CBP/p300 TAZ1 Domain Forms a Structured Scaffold for Ligand Binding,. Biochemistry, 2005, 44, 490-497.	1.5	89

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127	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.	2.9	19
128	Sequence Determinants of a Protein Folding Pathway. Journal of Molecular Biology, 2005, 351, 383-392.	2.9	55
129	Interaction of the TAZ1 Domain of the CREB-Binding Protein with the Activation Domain of CITED2. Journal of Biological Chemistry, 2004, 279, 3042-3049.	1.3	110
130	Recognition of the mRNA AU-rich element by the zinc finger domain of TIS11d. Nature Structural and Molecular Biology, 2004, 11, 257-264.	5.8	347
131	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
132	The LEF-1 High-Mobility Group Domain Undergoes a Disorder-to-Order Transition upon Formation of a Complex with Cognate DNA†. Biochemistry, 2004, 43, 8725-8734.	1.5	67
133	Effect of Cofactor Binding and Loop Conformation on Side Chain Methyl Dynamics in Dihydrofolate Reductase. Biochemistry, 2004, 43, 374-383.	1.5	74
134	Conformational Changes in the Active Site Loops of Dihydrofolate Reductase during the Catalytic Cycle†. Biochemistry, 2004, 43, 16046-16055.	1.5	127
135	Unfolded Proteins and Protein Folding Studied by NMR. Chemical Reviews, 2004, 104, 3607-3622.	42.5	633
136	Packing, specificity, and mutability at the binding interface between the p160 coactivator and CREB-binding protein. Protein Science, 2004, 13, 203-210.	3.5	70
137	Solution Structure of the KIX Domain of CBP Bound to the Transactivation Domain of c-Myb. Journal of Molecular Biology, 2004, 337, 521-534.	2.9	198
138	Structural Characterization of Unfolded States of Apomyoglobin using Residual Dipolar Couplings. Journal of Molecular Biology, 2004, 340, 1131-1142.	2.9	165
139	ZZ Domain of CBP: an Unusual Zinc Finger Fold in a Protein Interaction Module. Journal of Molecular Biology, 2004, 343, 1081-1093.	2.9	93
140	Structure, Dynamics, and Catalytic Function of Dihydrofolate Reductase. Annual Review of Biophysics and Biomolecular Structure, 2004, 33, 119-140.	17.4	496
141	The CBP/p300 TAZ1 domain in its native state is not a binding partner of MDM2. Biochemical Journal, 2004, 381, 685-691.	2.3	42
142	Changes in structure and dynamics of the Fv fragment of a catalytic antibody upon binding of inhibitor. Protein Science, 2003, 12, 1386-1394.	3.5	17
143	Role of a solvent-exposed tryptophan in the recognition and binding of antibiotic substrates for a metallo-β-lactamase. Protein Science, 2003, 12, 1368-1375.	3.5	57
144	Structure of the Nuclear Factor ALY: Insights into Post-Transcriptional Regulatory and mRNA Nuclear Export Processes. Biochemistry, 2003, 42, 7348-7357.	1.5	20

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145	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.	2.9	51
146	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.	2.9	105
147	Folding of a β-sheet Protein Monitored by Real-time NMR Spectroscopy. Journal of Molecular Biology, 2003, 328, 1161-1171.	2.9	29
148	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.	1.3	143
149	Structural basis for Hif-1 /CBP recognition in the cellular hypoxic response. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 5271-5276.	5.2	409
150	Solution NMR spectroscopy of [α-15N]lysine-labeled rhodopsin: The single peak observed in both conventional and TROSY-type HSQC spectra is ascribed to Lys-339 in the carboxyl-terminal peptide sequence. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 3452-3457.	5.2	62
151	Molecular Hinges in Protein Folding: the Urea-Denatured State of Apomyoglobin†. Biochemistry, 2002, 41, 12681-12686.	1.5	133
152	Insights into the structure and dynamics of unfolded proteins from nuclear magnetic resonance. Advances in Protein Chemistry, 2002, , 311-340.	5.3	217
153	The Apomyoglobin Folding Pathway Revisited: Structural Heterogeneity in the Kinetic Burst Phase Intermediate. Journal of Molecular Biology, 2002, 322, 483-489.	2.9	91
154	Cooperativity in Transcription Factor Binding to the Coactivator CREB-binding Protein (CBP). Journal of Biological Chemistry, 2002, 277, 43168-43174.	1.3	178
155	High Pressure NMR Reveals that Apomyoglobin is an Equilibrium Mixture from the Native to the Unfolded. Journal of Molecular Biology, 2002, 320, 311-319.	2.9	87
156	Mapping Long-range Contacts in a Highly Unfolded Protein. Journal of Molecular Biology, 2002, 322, 655-662.	2.9	142
157	Coupling of folding and binding for unstructured proteins. Current Opinion in Structural Biology, 2002, 12, 54-60.	4.6	1,288
158	Mutual synergistic folding in recruitment of CBP/p300 by p160 nuclear receptor coactivators. Nature, 2002, 415, 549-553.	30.7	451
159	Title is missing!. Journal of Biomolecular NMR, 2002, 22, 317-331.	1.6	113
160	Title is missing!. Journal of Biomolecular NMR, 2002, 22, 377-378.	1.6	6
161	Structural and dynamic characterization of an unfolded state of poplar apo-plastocyanin formed under nondenaturing conditions. Protein Science, 2001, 10, 1056-1066.	3.5	80
162	NMR Structural and Dynamic Characterization of the Acid-Unfolded State of Apomyoglobin Provides Insights into the Early Events in Protein Folding†,‡. Biochemistry, 2001, 40, 3561-3571.	1.5	215

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163	Backbone Dynamics in Dihydrofolate Reductase Complexes: Role of Loop Flexibility in the Catalytic Mechanism†. Biochemistry, 2001, 40, 9846-9859.	1.5	253
164	Sequence-Dependent Correction of Random Coil NMR Chemical Shifts. Journal of the American Chemical Society, 2001, 123, 2970-2978.	11.7	597
165	Solution structure of Escherichia coli glutaredoxin-2 shows similarity to mammalian glutathione-S-transferases. Journal of Molecular Biology, 2001, 310, 907-918.	2.9	72
166	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.	2.9	25
167	Conformational and Dynamic Characterization of the Molten Globule State of an Apomyoglobin Mutant with an Altered Folding Pathway†. Biochemistry, 2001, 40, 14459-14467.	1.5	47
168	Local Structural Plasticity of the Prion Protein. Analysis of NMR Relaxation Dynamics†. Biochemistry, 2001, 40, 2743-2753.	1.5	175
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