Peter E Wright

List of Publications by Year
in descending order

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341 papers	47,694 citations	1463 107 h-index	1900 208 g-index
364 all docs	364 docs citations	364 times ranked	31397 citing authors

#	Article	IF	Citations
1	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, .	7.1	22
2	Interactions of a Long Noncoding RNA with Domains of NF-Î°B and IÎ°BÎ±: Implications for the Inhibition of Non-Signal-Related Phosphorylation. Biochemistry, 2022, 61, 367-376.	2.5	4
3	Structural Biology â€“ Painting the Mechanistic Landscape of Biomolecules. Journal of Molecular Biology, 2022, 434, 167566.	4.2	1
4	Client Specificity of an ATPâ€independent Chaperone is Regulated by a Temperature Sensitive Switch. FASEB Journal, 2022, 36, .	0.5	0
5	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.	3.4	5
6	Modeling of Hidden Structures Using Sparse Chemical Shift Data from NMR Relaxation Dispersion. Biophysical Journal, 2021, 120, 296-305.	0.5	4
7	Thermodynamic Stability and Aggregation Kinetics of EF Helix and EF Loop Variants of Transthyretin. Biochemistry, 2021, 60, 756-764.	2.5	14
8	Role of Active Site Loop Dynamics in Mediating Ligand Release from E. coli Dihydrofolate Reductase. Biochemistry, 2021, 60, 2663-2671.	2.5	4
9	The molecular basis of allostery in a facilitated dissociation process. Structure, 2021, 29, 1327-1338.e5.	3.3	6
10	NMR illuminates intrinsic disorder. Current Opinion in Structural Biology, 2021, 70, 44-52.	5.7	60
11	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, .	7.1	33
12	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.	2.5	9
13	A Disorder-to-Order Transition Activates an ATP-Independent Membrane Protein Chaperone. Journal of Molecular Biology, 2020, 432, 166708.	4.2	8
14	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.	7.1	31
15	RNA Binding by the KTS Splice Variants of Wilmsâ€™ Tumor Suppressor Protein WT1. Biochemistry, 2020, 59, 3889-3901.	2.5	4
16	A Conformational Switch in the Zinc Finger Protein Kaiso Mediates Differential Readout of Specific and Methylated DNA Sequences. Biochemistry, 2020, 59, 1909-1926.	2.5	7
17	Determining Binding Kinetics of Intrinsically Disordered Proteins by NMR Spectroscopy. Methods in Molecular Biology, 2020, 2141, 663-681.	0.9	3
18	Comparison of backbone dynamics of the p50 dimerization domain of NFÎ°B in the homodimeric transcription factor NFÎ°B1 and in its heterodimeric complex with RelA (p65). Protein Science, 2019, 28, 2064-2072.	7.6	7

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19	Perspective: the essential role of NMR in the discovery and characterization of intrinsically disordered proteins. Journal of Biomolecular NMR, 2019, 73, 651-659.	2.8	48
20	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.	2.5	33
21	A Dynamic Switch in Inactive p38Î³ Leads to an Excited State on the Pathway to an Active Kinase. Biochemistry, 2019, 58, 5160-5172.	2.5	7
22	Expanding the Paradigm: Intrinsically Disordered Proteins and Allosteric Regulation. Journal of Molecular Biology, 2018, 430, 2309-2320.	4.2	105
23	Slow Dynamics of Tryptophanâ€“Water Networks in Proteins. Journal of the American Chemical Society, 2018, 140, 675-682.	13.7	26
24	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.	2.5	19
25	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.	7.1	93
26	Mispacking of the Phe87 Side Chain Reduces the Kinetic Stability of Human Transthyretin. Biochemistry, 2018, 57, 6919-6922.	2.5	8
27	Structural Basis for Graded Inhibition of CREB:DNA Interactions by Multisite Phosphorylation. Biochemistry, 2018, 57, 6964-6972.	2.5	7
28	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.	7.1	18
29	How Do Intrinsically Disordered Viral Proteins Hijack the Cell?. Biochemistry, 2018, 57, 4045-4046.	2.5	22
30	Tight complexes from disordered proteins. Nature, 2018, 555, 37-38.	27.8	3
31	NMR Measurements Reveal the Structural Basis of Transthyretin Destabilization by Pathogenic Mutations. Biochemistry, 2018, 57, 4421-4430.	2.5	30
32	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.	7.1	29
33	Hypersensitive termination of the hypoxic response by a disordered protein switch. Nature, 2017, 543, 447-451.	27.8	140
34	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.	7.1	56
35	How Does Your Protein Fold? Elucidating the Apomyoglobin Folding Pathway. Accounts of Chemical Research, 2017, 50, 105-111.	15.6	44
36	Fluorotryptophan Incorporation Modulates the Structure and Stability of Transthyretin in a Site-Specific Manner. Biochemistry, 2017, 56, 5570-5581.	2.5	20

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37	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.	13.7	27
38	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.	2.5	27
39	Finding Our Way in the Dark Proteome. Journal of the American Chemical Society, 2016, 138, 9730-9742.	13.7	111
40	NMR Characterization of Information Flow and Allosteric Communities in the MAP Kinase p38Î³. Scientific Reports, 2016, 6, 28655.	3.3	19
41	Solid-State NMR Studies Reveal Native-like Î²-Sheet Structures in Transthyretin Amyloid. Biochemistry, 2016, 55, 5272-5278.	2.5	25
42	Mapping the interactions of adenoviral E1A proteins with the p160 nuclear receptor coactivator binding domain of CBP. Protein Science, 2016, 25, 2256-2267.	7.6	18
43	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.	7.1	94
44	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.	3.4	251
45	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.	7.1	33
46	Multi-probe relaxation dispersion measurements increase sensitivity to protein dynamics. Physical Chemistry Chemical Physics, 2016, 18, 5789-5798.	2.8	9
47	Functional advantages of dynamic protein disorder. FEBS Letters, 2015, 589, 2433-2440.	2.8	162
48	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.	13.7	45
49	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.	7.1	222
50	Intrinsically disordered proteins in cellular signalling and regulation. Nature Reviews Molecular Cell Biology, 2015, 16, 18-29.	37.0	1,849
51	pE-DB: a database of structural ensembles of intrinsically disordered and of unfolded proteins. Nucleic Acids Research, 2014, 42, D326-D335.	14.5	195
52	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.	7.1	20
53	Assemblages: Functional units formed by cellular phase separation. Journal of Cell Biology, 2014, 206, 579-588.	5.2	227
54	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.	7.1	142

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55	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.	4.2	61
56	Side Chain Conformational Averaging in Human Dihydrofolate Reductase. Biochemistry, 2014, 53, 1134-1145.	2.5	8
57	Probing the Non-Native H Helix Translocation in Apomyoglobin Folding Intermediates. Biochemistry, 2014, 53, 3767-3780.	2.5	16
58	Accurate scoring of non-uniform sampling schemes for quantitative NMR. Journal of Magnetic Resonance, 2014, 246, 31-35.	2.1	57
59	Classification of Intrinsically Disordered Regions and Proteins. Chemical Reviews, 2014, 114, 6589-6631.	47.7	1,618
60	Structural Characterization of Interactions between the Double-Stranded RNA-Binding Zinc Finger Protein JAZ and Nucleic Acids. Biochemistry, 2014, 53, 1495-1510.	2.5	20
61	Automated identification of functional dynamic contact networks from X-ray crystallography. Nature Methods, 2013, 10, 896-902.	19.0	130
62	Fast and accurate fitting of relaxation dispersion data using the flexible software package GLOVE. Journal of Biomolecular NMR, 2013, 56, 275-283.	2.8	71
63	The CH2 domain of CBP/p300 is a novel zinc finger. FEBS Letters, 2013, 587, 2506-2511.	2.8	12
64	Divergent evolution of protein conformational dynamics in dihydrofolate reductase. Nature Structural and Molecular Biology, 2013, 20, 1243-1249.	8.2	153
65	Localized Structural Fluctuations Promote Amyloidogenic Conformations in Transthyretin. Journal of Molecular Biology, 2013, 425, 977-988.	4.2	65
66	A Distal Mutation Perturbs Dynamic Amino Acid Networks in Dihydrofolate Reductase. Biochemistry, 2013, 52, 4605-4619.	2.5	77
67	Modulation of allostery by protein intrinsic disorder. Nature, 2013, 498, 390-394.	27.8	295
68	Side-Chain Conformational Heterogeneity of Intermediates in the Escherichia coli Dihydrofolate Reductase Catalytic Cycle. Biochemistry, 2013, 52, 3464-3477.	2.5	16
69	Analysis of the RelA:CBP/p300 Interaction Reveals Its Involvement in NF-Î¹B-Driven Transcription. PLoS Biology, 2013, 11, e1001647.	5.6	118
70	Mechanisms of Transthyretin Inhibition of Î²-Amyloid AggregationIn Vitro. Journal of Neuroscience, 2013, 33, 19423-19433.	3.6	118
71	Functional Interactions of Intrinsically Disordered Proteins in Signaling Networks. FASEB Journal, 2013, 27, 459.3.	0.5	0
72	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.	7.1	101

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73	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.	13.7	123
74	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.	2.8	17
75	Structural Basis for Cooperative Transcription Factor Binding to the CBP Coactivator. FASEB Journal, 2012, 26, lb266.	0.5	0
76	A Dynamic Knockout Reveals That Conformational Fluctuations Influence the Chemical Step of Enzyme Catalysis. Science, 2011, 332, 234-238.	12.6	414
77	Consequences of Stabilizing the Natively Disordered F Helix for the Folding Pathway of Apomyoglobin. Journal of Molecular Biology, 2011, 411, 248-263.	4.2	16
78	Identification of endogenous ligands bound to bacterially expressed human andE. colidihydrofolate reductase by 2D NMR. FEBS Letters, 2011, 585, 3528-3532.	2.8	14
79	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.	7.1	70
80	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.	2.8	32
81	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 ETQq1 1 0.784314 rgBT /Overlock	3.14	
82	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.	7.1	188
83	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.	7.1	133
84	Structure of the p53 Transactivation Domain in Complex with the Nuclear Receptor Coactivator Binding Domain of CREB Binding Protein. Biochemistry, 2010, 49, 9964-9971.	2.5	162
85	Energetic Frustration of Apomyoglobin Folding: Role of the B Helix. Journal of Molecular Biology, 2010, 396, 1319-1328.	4.2	17
86	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.	7.1	197
87	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.	7.1	119
88	Linking folding and binding. Current Opinion in Structural Biology, 2009, 19, 31-38.	5.7	932
89	The role of dynamic conformational ensembles in biomolecular recognition. Nature Chemical Biology, 2009, 5, 789-796.	8.0	1,649
90	Diagnostic chemical shift markers for loop conformation and substrate and cofactor binding in dihydrofolate reductase complexes. Protein Science, 2009, 12, 2230-2238.	7.6	38

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91	Mapping the Interactions of the p53 Transactivation Domain with the KIX Domain of CBP. Biochemistry, 2009, 48, 2115-2124.	2.5	109
92	Prion Proteins with Pathogenic and Protective Mutations Show Similar Structure and Dynamics. Biochemistry, 2009, 48, 8120-8128.	2.5	53
93	Editorial from the Editor-in-Chief. Journal of Molecular Biology, 2009, 385, 1-2.	4.2	1
94	Structural basis for recruitment of CBP/p300 coactivators by STAT1 and STAT2 transactivation domains. EMBO Journal, 2009, 28, 948-958.	7.8	147
95	Prediction of the Rotational Tumbling Time for Proteins with Disordered Segments. Journal of the American Chemical Society, 2009, 131, 6814-6821.	13.7	48
96	Structural characterization of partially folded intermediates of apomyoglobin H64F. Protein Science, 2008, 17, 313-321.	7.6	16
97	How Do Proteins Interact?. Science, 2008, 320, 1429-1430.	12.6	174
98	The Kinetic and Equilibrium Molten Globule Intermediates of Apoleghemoglobin Differ in Structure. Journal of Molecular Biology, 2008, 378, 715-725.	4.2	26
99	Overexpression of post-translationally modified peptides in Escherichia coli by co-expression with modifying enzymes. Protein Expression and Purification, 2008, 57, 108-115.	1.3	30
100	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.	7.1	89
101	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.	2.5	86
102	The Intrinsically Disordered RNR Inhibitor Sml1 Is a Dynamic Dimer. Biochemistry, 2008, 47, 13428-13437.	2.5	53
103	Conformational Relaxation following Hydride Transfer Plays a Limiting Role in Dihydrofolate Reductase Catalysisâ€. Biochemistry, 2008, 47, 9227-9233.	2.5	53
104	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.	7.1	105
105	S03A3 Metastable structure detected by relaxation dispersion NMR spectroscopy(Visualising) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.P	0
106	PRAK Is Essential for ras-Induced Senescence and Tumor Suppression. Cell, 2007, 128, 295-308.	28.9	286
107	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.	4.2	21
108	Structure of the Wilms Tumor Suppressor Protein Zinc Finger Domain Bound to DNA. Journal of Molecular Biology, 2007, 372, 1227-1245.	4.2	91

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109	Tailoring Relaxation Dispersion Experiments for Fast-Associating Protein Complexes. Journal of the American Chemical Society, 2007, 129, 13406-13407.	13.7	52
110	Mechanism of coupled folding and binding of an intrinsically disordered protein. Nature, 2007, 447, 1021-1025.	27.8	984
111	The Dynamic Energy Landscape of Dihydrofolate Reductase Catalysis. Science, 2006, 313, 1638-1642.	12.6	877
112	An NMR Perspective on Enzyme Dynamics. Chemical Reviews, 2006, 106, 3055-3079.	47.7	424
113	NMR Solution Structure of the Peptide Fragment 1â˜30, Derived from Unprocessed Mouse Doppel Protein, in DHPC Micellesâ€. Biochemistry, 2006, 45, 159-166.	2.5	19
114	Structural Basis for Cooperative Transcription Factor Binding to the CBP Coactivator. Journal of Molecular Biology, 2006, 355, 1005-1013.	4.2	166
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.	4.2	162
116	Identification of Native and Non-native Structure in Kinetic Folding Intermediates of Apomyoglobin. Journal of Molecular Biology, 2006, 355, 139-156.	4.2	112
117	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.	4.2	72
118	Solution Structure of the Hdm2 C2H2C4 RING, a Domain Critical for Ubiquitination of p53. Journal of Molecular Biology, 2006, 363, 433-450.	4.2	120
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.	3.4	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.	7.1	266
121	Localization of Sites of Interaction between p23 and Hsp90 in Solution. Journal of Biological Chemistry, 2006, 281, 14457-14464.	3.4	58
122	Structure and Function of the CBP/p300 TAZ Domains. , 2005, , 114-120.		4
123	Intrinsically unstructured proteins and their functions. Nature Reviews Molecular Cell Biology, 2005, 6, 197-208.	37.0	3,403
124	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.	7.1	152
125	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.	7.1	62
126	Inhibition of DNA Binding by Human Estrogen-Related Receptor 2 and Estrogen Receptor Î± with Minor Groove Binding Polyamidesâ€. Biochemistry, 2005, 44, 4196-4203.	2.5	42

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127	CBP/p300 TAZ1 Domain Forms a Structured Scaffold for Ligand Binding,. Biochemistry, 2005, 44, 490-497.	2.5	76
128	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.	4.2	18
129	Sequence Determinants of a Protein Folding Pathway. Journal of Molecular Biology, 2005, 351, 383-392.	4.2	54
130	Elucidation of the Protein Folding Landscape by NMR. Methods in Enzymology, 2005, 394, 299-321.	1.0	90
131	Interaction of the TAZ1 Domain of the CREB-Binding Protein with the Activation Domain of CITED2. Journal of Biological Chemistry, 2004, 279, 3042-3049.	3.4	97
132	Recognition of the mRNA AU-rich element by the zinc finger domain of TIS11d. Nature Structural and Molecular Biology, 2004, 11, 257-264.	8.2	320
133	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.	2.8	60
134	Unfolded Proteins and Protein Folding Studied by NMR. ChemInform, 2004, 35, no.	0.0	1
135	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.	2.5	62
136	Effect of Cofactor Binding and Loop Conformation on Side Chain Methyl Dynamics in Dihydrofolate Reductase. Biochemistry, 2004, 43, 374-383.	2.5	73
137	Conformational Changes in the Active Site Loops of Dihydrofolate Reductase during the Catalytic Cycleâ€. Biochemistry, 2004, 43, 16046-16055.	2.5	119
138	Unfolded Proteins and Protein Folding Studied by NMR. Chemical Reviews, 2004, 104, 3607-3622.	47.7	596
139	Packing, specificity, and mutability at the binding interface between the p160 coactivator and CREB-binding protein. Protein Science, 2004, 13, 203-210.	7.6	66
140	Introduction:â€‰ Biological Nuclear Magnetic Resonance. Chemical Reviews, 2004, 104, 3517-3518.	47.7	2
141	Solution Structure of the KIX Domain of CBP Bound to the Transactivation Domain of c-Myb. Journal of Molecular Biology, 2004, 337, 521-534.	4.2	181
142	Structural Characterization of Unfolded States of Apomyoglobin using Residual Dipolar Couplings. Journal of Molecular Biology, 2004, 340, 1131-1142.	4.2	165
143	ZZ Domain of CBP: an Unusual Zinc Finger Fold in a Protein Interaction Module. Journal of Molecular Biology, 2004, 343, 1081-1093.	4.2	81
144	Structure, Dynamics, and Catalytic Function of Dihydrofolate Reductase. Annual Review of Biophysics and Biomolecular Structure, 2004, 33, 119-140.	18.3	444

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145	The CBP/p300 TAZ1 domain in its native state is not a binding partner of MDM2. Biochemical Journal, 2004, 381, 685-691.	3.7	41
146	Changes in structure and dynamics of the Fv fragment of a catalytic antibody upon binding of inhibitor. Protein Science, 2003, 12, 1386-1394.	7.6	14
147	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.	7.6	56
148	Structure of the Nuclear Factor ALY:â€‰ Insights into Post-Transcriptional Regulatory and mRNA Nuclear Export Processes. Biochemistry, 2003, 42, 7348-7357.	2.5	20
149	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.	4.2	51
150	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.	4.2	97
151	Folding of a Î²-sheet Protein Monitored by Real-time NMR Spectroscopy. Journal of Molecular Biology, 2003, 328, 1161-1171.	4.2	29
152	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.	3.4	134
153	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.	7.1	376
154	Molecular Hinges in Protein Folding:Â the Urea-Denatured State of Apomyoglobinâ€. Biochemistry, 2002, 41, 12681-12686.	2.5	130
155	Insights into the structure and dynamics of unfolded proteins from nuclear magnetic resonance. Advances in Protein Chemistry, 2002, 62, 311-340.	4.4	208
156	The Apomyoglobin Folding Pathway Revisited: Structural Heterogeneity in the Kinetic Burst Phase Intermediate. Journal of Molecular Biology, 2002, 322, 483-489.	4.2	89
157	Cooperativity in Transcription Factor Binding to the Coactivator CREB-binding Protein (CBP). Journal of Biological Chemistry, 2002, 277, 43168-43174.	3.4	166
158	High Pressure NMR Reveals that Apomyoglobin is an Equilibrium Mixture from the Native to the Unfolded. Journal of Molecular Biology, 2002, 320, 311-319.	4.2	81
159	Mapping Long-range Contacts in a Highly Unfolded Protein. Journal of Molecular Biology, 2002, 322, 655-662.	4.2	140
160	Coupling of folding and binding for unstructured proteins. Current Opinion in Structural Biology, 2002, 12, 54-60.	5.7	1,223
161	Mutual synergistic folding in recruitment of CBP/p300 by p160 nuclear receptor coactivators. Nature, 2002, 415, 549-553.	27.8	423
162	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.	2.8	112

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163	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.	2.8	6
164	Structural and dynamic characterization of an unfolded state of poplar apo-plastocyanin formed under nondenaturing conditions. Protein Science, 2001, 10, 1056-1066.	7.6	79
165	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.	2.5	212
166	Backbone Dynamics in Dihydrofolate Reductase Complexes:Â Role of Loop Flexibility in the Catalytic Mechanismâ€. Biochemistry, 2001, 40, 9846-9859.	2.5	246
167	Nuclear Magnetic Resonance Methods for Elucidation of Structure and Dynamics in Disordered States. Methods in Enzymology, 2001, 339, 258-270.	1.0	148
168	Sequence-Dependent Correction of Random Coil NMR Chemical Shifts. Journal of the American Chemical Society, 2001, 123, 2970-2978.	13.7	562
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