

Peter E Wright

List of Publications by Year in descending order

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341
papers

47,694
citations

1713

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364
all docs

364
docs citations

364
times ranked

35267
citing authors

#	ARTICLE	IF	CITATIONS
1	Multivalency enables unidirectional switch-like competition between intrinsically disordered proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	22
2	Interactions of a Long Noncoding RNA with Domains of NF- κ B and I κ B β : Implications for the Inhibition of Non-Signal-Related Phosphorylation. <i>Biochemistry</i> , 2022, 61, 367-376.	1.2	4
3	Structural Biology â€“ Painting the Mechanistic Landscape of Biomolecules. <i>Journal of Molecular Biology</i> , 2022, 434, 167566.	2.0	1
4	Client Specificity of an ATPâ€independent Chaperone is Regulated by a Temperature Sensitive Switch. <i>FASEB Journal</i> , 2022, 36, .	0.2	0
5	A transthyretin monomer intermediate undergoes local unfolding and transient interaction with oligomers in a kinetically concerted aggregation pathway. <i>Journal of Biological Chemistry</i> , 2022, 298, 102162.	1.6	5
6	Modeling of Hidden Structures Using Sparse Chemical Shift Data from NMR Relaxation Dispersion. <i>Biophysical Journal</i> , 2021, 120, 296-305.	0.2	4
7	Thermodynamic Stability and Aggregation Kinetics of EF Helix and EF Loop Variants of Transthyretin. <i>Biochemistry</i> , 2021, 60, 756-764.	1.2	14
8	Role of Active Site Loop Dynamics in Mediating Ligand Release from <i>E. coli</i> Dihydrofolate Reductase. <i>Biochemistry</i> , 2021, 60, 2663-2671.	1.2	4
9	The molecular basis of allostery in a facilitated dissociation process. <i>Structure</i> , 2021, 29, 1327-1338.e5.	1.6	6
10	NMR illuminates intrinsic disorder. <i>Current Opinion in Structural Biology</i> , 2021, 70, 44-52.	2.6	60
11	A phosphorylation-dependent switch in the disordered p53 transactivation domain regulates DNA binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	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. <i>Biochemistry</i> , 2021, 60, 3887-3898.	1.2	9
13	A Disorder-to-Order Transition Activates an ATP-Independent Membrane Protein Chaperone. <i>Journal of Molecular Biology</i> , 2020, 432, 166708.	2.0	8
14	An allosteric peptide inhibitor of HIF-1 α regulates hypoxia-induced retinal neovascularization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 28297-28306.	3.3	31
15	RNA Binding by the KTS Splice Variants of Wilmsâ€™ Tumor Suppressor Protein WT1. <i>Biochemistry</i> , 2020, 59, 3889-3901.	1.2	4
16	A Conformational Switch in the Zinc Finger Protein Kaiso Mediates Differential Readout of Specific and Methylated DNA Sequences. <i>Biochemistry</i> , 2020, 59, 1909-1926.	1.2	7
17	Determining Binding Kinetics of Intrinsically Disordered Proteins by NMR Spectroscopy. <i>Methods in Molecular Biology</i> , 2020, 2141, 663-681.	0.4	3
18	Comparison of backbone dynamics of the p50 dimerization domain of NF κ B in the homodimeric transcription factor NF κ B1 and in its heterodimeric complex with RelA (p65). <i>Protein Science</i> , 2019, 28, 2064-2072.	3.1	7

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19	Perspective: the essential role of NMR in the discovery and characterization of intrinsically disordered proteins. <i>Journal of Biomolecular NMR</i> , 2019, 73, 651-659.	1.6	48
20	Role of Backbone Dynamics in Modulating the Interactions of Disordered Ligands with the TAZ1 Domain of the CREB-Binding Protein. <i>Biochemistry</i> , 2019, 58, 1354-1362.	1.2	33
21	A Dynamic Switch in Inactive p38 ^β Leads to an Excited State on the Pathway to an Active Kinase. <i>Biochemistry</i> , 2019, 58, 5160-5172.	1.2	7
22	Expanding the Paradigm: Intrinsically Disordered Proteins and Allosteric Regulation. <i>Journal of Molecular Biology</i> , 2018, 430, 2309-2320.	2.0	105
23	Slow Dynamics of Tryptophan-Water Networks in Proteins. <i>Journal of the American Chemical Society</i> , 2018, 140, 675-682.	6.6	26
24	CH ₂ -O Hydrogen Bonds Mediate Highly Specific Recognition of Methylated CpG Sites by the Zinc Finger Protein Kaiso. <i>Biochemistry</i> , 2018, 57, 2109-2120.	1.2	19
25	Long-range regulation of p53 DNA binding by its intrinsically disordered N-terminal transactivation domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11302-E11310.	3.3	93
26	Mispacking of the Phe87 Side Chain Reduces the Kinetic Stability of Human Transthyretin. <i>Biochemistry</i> , 2018, 57, 6919-6922.	1.2	8
27	Structural Basis for Graded Inhibition of CREB:DNA Interactions by Multisite Phosphorylation. <i>Biochemistry</i> , 2018, 57, 6964-6972.	1.2	7
28	Structural basis for cooperative regulation of KIX-mediated transcription pathways by the HTLV-1 HBZ activation domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 10040-10045.	3.3	18
29	How Do Intrinsically Disordered Viral Proteins Hijack the Cell?. <i>Biochemistry</i> , 2018, 57, 4045-4046.	1.2	22
30	Tight complexes from disordered proteins. <i>Nature</i> , 2018, 555, 37-38.	13.7	3
31	NMR Measurements Reveal the Structural Basis of Transthyretin Destabilization by Pathogenic Mutations. <i>Biochemistry</i> , 2018, 57, 4421-4430.	1.2	30
32	Kinetic analysis of the multistep aggregation pathway of human transthyretin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E6201-E6208.	3.3	29
33	Hypersensitive termination of the hypoxic response by a disordered protein switch. <i>Nature</i> , 2017, 543, 447-451.	13.7	140
34	Role of the CBP catalytic core in intramolecular SUMOylation and control of histone H3 acetylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5335-E5342.	3.3	56
35	How Does Your Protein Fold? Elucidating the Apomyoglobin Folding Pathway. <i>Accounts of Chemical Research</i> , 2017, 50, 105-111.	7.6	44
36	Fluorotryptophan Incorporation Modulates the Structure and Stability of Transthyretin in a Site-Specific Manner. <i>Biochemistry</i> , 2017, 56, 5570-5581.	1.2	20

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37	Defining the Structural Basis for Allosteric Product Release from <i>E. coli</i> Dihydrofolate Reductase Using NMR Relaxation Dispersion. <i>Journal of the American Chemical Society</i> , 2017, 139, 11233-11240.	6.6	27
38	Structural Basis for Interaction of the Tandem Zinc Finger Domains of Human Muscleblind with Cognate RNA from Human Cardiac Troponin T. <i>Biochemistry</i> , 2017, 56, 4154-4168.	1.2	27
39	Finding Our Way in the Dark Proteome. <i>Journal of the American Chemical Society</i> , 2016, 138, 9730-9742.	6.6	111
40	NMR Characterization of Information Flow and Allosteric Communities in the MAP Kinase p38 β . <i>Scientific Reports</i> , 2016, 6, 28655.	1.6	19
41	Solid-State NMR Studies Reveal Native-like β -Sheet Structures in Transthyretin Amyloid. <i>Biochemistry</i> , 2016, 55, 5272-5278.	1.2	25
42	Mapping the interactions of adenoviral E1A proteins with the p160 nuclear receptor coactivator binding domain of CBP. <i>Protein Science</i> , 2016, 25, 2256-2267.	3.1	18
43	Recognition of the disordered p53 transactivation domain by the transcriptional adapter zinc finger domains of CREB-binding protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1853-62.	3.3	94
44	Role of Intrinsic Protein Disorder in the Function and Interactions of the Transcriptional Coactivators CREB-binding Protein (CBP) and p300. <i>Journal of Biological Chemistry</i> , 2016, 291, 6714-6722.	1.6	251
45	Conformational dynamics of a membrane protein chaperone enables spatially regulated substrate capture and release. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1615-24.	3.3	33
46	Multi-probe relaxation dispersion measurements increase sensitivity to protein dynamics. <i>Physical Chemistry Chemical Physics</i> , 2016, 18, 5789-5798.	1.3	9
47	Functional advantages of dynamic protein disorder. <i>FEBS Letters</i> , 2015, 589, 2433-2440.	1.3	162
48	Cofactor-Mediated Conformational Dynamics Promote Product Release From <i>Escherichia coli</i> Dihydrofolate Reductase via an Allosteric Pathway. <i>Journal of the American Chemical Society</i> , 2015, 137, 9459-9468.	6.6	45
49	Conformational propensities of intrinsically disordered proteins influence the mechanism of binding and folding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 9614-9619.	3.3	222
50	Intrinsically disordered proteins in cellular signalling and regulation. <i>Nature Reviews Molecular Cell Biology</i> , 2015, 16, 18-29.	16.1	1,849
51	pE-DB: a database of structural ensembles of intrinsically disordered and of unfolded proteins. <i>Nucleic Acids Research</i> , 2014, 42, D326-D335.	6.5	195
52	Combinatorial regulation of a signal-dependent activator by phosphorylation and acetylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17116-17121.	3.3	20
53	Assemblages: Functional units formed by cellular phase separation. <i>Journal of Cell Biology</i> , 2014, 206, 579-588.	2.3	227
54	Integrated description of protein dynamics from room-temperature X-ray crystallography and NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E445-54.	3.3	142

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55	The High-Risk HPV16 E7 Oncoprotein Mediates Interaction between the Transcriptional Coactivator CBP and the Retinoblastoma Protein pRb. <i>Journal of Molecular Biology</i> , 2014, 426, 4030-4048.	2.0	61
56	Side Chain Conformational Averaging in Human Dihydrofolate Reductase. <i>Biochemistry</i> , 2014, 53, 1134-1145.	1.2	8
57	Probing the Non-Native H Helix Translocation in Apomyoglobin Folding Intermediates. <i>Biochemistry</i> , 2014, 53, 3767-3780.	1.2	16
58	Accurate scoring of non-uniform sampling schemes for quantitative NMR. <i>Journal of Magnetic Resonance</i> , 2014, 246, 31-35.	1.2	57
59	Classification of Intrinsically Disordered Regions and Proteins. <i>Chemical Reviews</i> , 2014, 114, 6589-6631.	23.0	1,618
60	Structural Characterization of Interactions between the Double-Stranded RNA-Binding Zinc Finger Protein JAZ and Nucleic Acids. <i>Biochemistry</i> , 2014, 53, 1495-1510.	1.2	20
61	Automated identification of functional dynamic contact networks from X-ray crystallography. <i>Nature Methods</i> , 2013, 10, 896-902.	9.0	130
62	Fast and accurate fitting of relaxation dispersion data using the flexible software package GLOVE. <i>Journal of Biomolecular NMR</i> , 2013, 56, 275-283.	1.6	71
63	The CH2 domain of CBP/p300 is a novel zinc finger. <i>FEBS Letters</i> , 2013, 587, 2506-2511.	1.3	12
64	Divergent evolution of protein conformational dynamics in dihydrofolate reductase. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1243-1249.	3.6	153
65	Localized Structural Fluctuations Promote Amyloidogenic Conformations in Transthyretin. <i>Journal of Molecular Biology</i> , 2013, 425, 977-988.	2.0	65
66	A Distal Mutation Perturbs Dynamic Amino Acid Networks in Dihydrofolate Reductase. <i>Biochemistry</i> , 2013, 52, 4605-4619.	1.2	77
67	Modulation of allostery by protein intrinsic disorder. <i>Nature</i> , 2013, 498, 390-394.	13.7	295
68	Side-Chain Conformational Heterogeneity of Intermediates in the <i>Escherichia coli</i> Dihydrofolate Reductase Catalytic Cycle. <i>Biochemistry</i> , 2013, 52, 3464-3477.	1.2	16
69	Analysis of the RelA:CBP/p300 Interaction Reveals Its Involvement in NF- κ B-Driven Transcription. <i>PLoS Biology</i> , 2013, 11, e1001647.	2.6	118
70	Mechanisms of Transthyretin Inhibition of β 2-Microglobulin Amyloid Aggregation <i>In Vitro</i> . <i>Journal of Neuroscience</i> , 2013, 33, 19423-19433.	1.7	118
71	Functional Interactions of Intrinsically Disordered Proteins in Signaling Networks. <i>FASEB Journal</i> , 2013, 27, 459.3.	0.2	0
72	Molecular basis for recognition of methylated and specific DNA sequences by the zinc finger protein Kaiso. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15229-15234.	3.3	101

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73	Quantitative Analysis of Multisite Protein-Ligand Interactions by NMR: Binding of Intrinsically Disordered p53 Transactivation Subdomains with the TAZ2 Domain of CBP. <i>Journal of the American Chemical Society</i> , 2012, 134, 3792-3803.	6.6	123
74	Kaiso uses all three zinc fingers and adjacent sequence motifs for high affinity binding to sequence-specific and methyl-CpG DNA targets. <i>FEBS Letters</i> , 2012, 586, 734-739.	1.3	17
75	Structural Basis for Cooperative Transcription Factor Binding to the CBP Coactivator. <i>FASEB Journal</i> , 2012, 26, lb266.	0.2	0
76	A Dynamic Knockout Reveals That Conformational Fluctuations Influence the Chemical Step of Enzyme Catalysis. <i>Science</i> , 2011, 332, 234-238.	6.0	414
77	Consequences of Stabilizing the Natively Disordered F Helix for the Folding Pathway of Apomyoglobin. <i>Journal of Molecular Biology</i> , 2011, 411, 248-263.	2.0	16
78	Identification of endogenous ligands bound to bacterially expressed human and <i>E. coli</i> dihydrofolate reductase by 2D NMR. <i>FEBS Letters</i> , 2011, 585, 3528-3532.	1.3	14
79	Measurement of protein unfolding/refolding kinetics and structural characterization of hidden intermediates by NMR relaxation dispersion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9078-9083.	3.3	70
80	Leu628 of the KIX domain of CBP is a key residue for the interaction with the MLL transactivation domain. <i>FEBS Letters</i> , 2010, 584, 4500-4504.	1.3	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 IUPAC) 10.784614 rgBT (Overl	1.0	0
82	Graded enhancement of p53 binding to CREB-binding protein (CBP) by multisite phosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19290-19295.	3.3	188
83	Millisecond timescale fluctuations in dihydrofolate reductase are exquisitely sensitive to the bound ligands. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 1373-1378.	3.3	133
84	Structure of the p53 Transactivation Domain in Complex with the Nuclear Receptor Coactivator Binding Domain of CREB Binding Protein. <i>Biochemistry</i> , 2010, 49, 9964-9971.	1.2	162
85	Energetic Frustration of Apomyoglobin Folding: Role of the B Helix. <i>Journal of Molecular Biology</i> , 2010, 396, 1319-1328.	2.0	17
86	Cooperative regulation of p53 by modulation of ternary complex formation with CBP/p300 and HDM2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6591-6596.	3.3	197
87	Structural basis for subversion of cellular control mechanisms by the adenoviral E1A oncoprotein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 13260-13265.	3.3	119
88	Linking folding and binding. <i>Current Opinion in Structural Biology</i> , 2009, 19, 31-38.	2.6	932
89	The role of dynamic conformational ensembles in biomolecular recognition. <i>Nature Chemical Biology</i> , 2009, 5, 789-796.	3.9	1,649
90	Diagnostic chemical shift markers for loop conformation and substrate and cofactor binding in dihydrofolate reductase complexes. <i>Protein Science</i> , 2009, 12, 2230-2238.	3.1	38

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91	Mapping the Interactions of the p53 Transactivation Domain with the KIX Domain of CBP. <i>Biochemistry</i> , 2009, 48, 2115-2124.	1.2	109
92	Prion Proteins with Pathogenic and Protective Mutations Show Similar Structure and Dynamics. <i>Biochemistry</i> , 2009, 48, 8120-8128.	1.2	53
93	Editorial from the Editor-in-Chief. <i>Journal of Molecular Biology</i> , 2009, 385, 1-2.	2.0	1
94	Structural basis for recruitment of CBP/p300 coactivators by STAT1 and STAT2 transactivation domains. <i>EMBO Journal</i> , 2009, 28, 948-958.	3.5	147
95	Prediction of the Rotational Tumbling Time for Proteins with Disordered Segments. <i>Journal of the American Chemical Society</i> , 2009, 131, 6814-6821.	6.6	48
96	Structural characterization of partially folded intermediates of apomyoglobin H64F. <i>Protein Science</i> , 2008, 17, 313-321.	3.1	16
97	How Do Proteins Interact?. <i>Science</i> , 2008, 320, 1429-1430.	6.0	174
98	The Kinetic and Equilibrium Molten Globule Intermediates of Apoleghemoglobin Differ in Structure. <i>Journal of Molecular Biology</i> , 2008, 378, 715-725.	2.0	26
99	Overexpression of post-translationally modified peptides in <i>Escherichia coli</i> by co-expression with modifying enzymes. <i>Protein Expression and Purification</i> , 2008, 57, 108-115.	0.6	30
100	Hierarchical folding mechanism of apomyoglobin revealed by ultra-fast H/D exchange coupled with 2D NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 13859-13864.	3.3	89
101	NMR Relaxation Study of the Complex Formed Between CBP and the Activation Domain of the Nuclear Hormone Receptor Coactivator ACTR. <i>Biochemistry</i> , 2008, 47, 1299-1308.	1.2	86
102	The Intrinsically Disordered RNR Inhibitor Sml1 Is a Dynamic Dimer. <i>Biochemistry</i> , 2008, 47, 13428-13437.	1.2	53
103	Conformational Relaxation following Hydride Transfer Plays a Limiting Role in Dihydrofolate Reductase Catalysis. <i>Biochemistry</i> , 2008, 47, 9227-9233.	1.2	53
104	Modeling transient collapsed states of an unfolded protein to provide insights into early folding events. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 6278-6283.	3.3	105
105	S03A3 Metastable structure detected by relaxation dispersion NMR spectroscopy(Visualising) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.9	0
106	PRAK Is Essential for ras-Induced Senescence and Tumor Suppression. <i>Cell</i> , 2007, 128, 295-308.	13.5	286
107	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. <i>Journal of Molecular Biology</i> , 2007, 371, 1274-1289.	2.0	21
108	Structure of the Wilms Tumor Suppressor Protein Zinc Finger Domain Bound to DNA. <i>Journal of Molecular Biology</i> , 2007, 372, 1227-1245.	2.0	91

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109	Tailoring Relaxation Dispersion Experiments for Fast-Associating Protein Complexes. <i>Journal of the American Chemical Society</i> , 2007, 129, 13406-13407.	6.6	52
110	Mechanism of coupled folding and binding of an intrinsically disordered protein. <i>Nature</i> , 2007, 447, 1021-1025.	13.7	984
111	The Dynamic Energy Landscape of Dihydrofolate Reductase Catalysis. <i>Science</i> , 2006, 313, 1638-1642.	6.0	877
112	An NMR Perspective on Enzyme Dynamics. <i>Chemical Reviews</i> , 2006, 106, 3055-3079.	23.0	424
113	NMR Solution Structure of the Peptide Fragment 1 [~] 30, Derived from Unprocessed Mouse Doppel Protein, in DHPC Micelles. <i>Biochemistry</i> , 2006, 45, 159-166.	1.2	19
114	Structural Basis for Cooperative Transcription Factor Binding to the CBP Coactivator. <i>Journal of Molecular Biology</i> , 2006, 355, 1005-1013.	2.0	166
115	Structure of the <i>Escherichia coli</i> Quorum Sensing Protein SdiA: Activation of the Folding Switch by Acyl Homoserine Lactones. <i>Journal of Molecular Biology</i> , 2006, 355, 262-273.	2.0	162
116	Identification of Native and Non-native Structure in Kinetic Folding Intermediates of Apomyoglobin. <i>Journal of Molecular Biology</i> , 2006, 355, 139-156.	2.0	112
117	Induced Fit and "Lock and Key" Recognition of 5S RNA by Zinc Fingers of Transcription Factor IIIA. <i>Journal of Molecular Biology</i> , 2006, 357, 275-291.	2.0	72
118	Solution Structure of the Hdm2 C2H2C4 RING, a Domain Critical for Ubiquitination of p53. <i>Journal of Molecular Biology</i> , 2006, 363, 433-450.	2.0	120
119	According to current textbooks, a well-defined three-dimensional structure is a prerequisite for the function of a protein. Is this correct?. <i>IUBMB Life</i> , 2006, 58, 107-109.	1.5	20
120	The role of hydrophobic interactions in initiation and propagation of protein folding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 13057-13061.	3.3	266
121	Localization of Sites of Interaction between p23 and Hsp90 in Solution. <i>Journal of Biological Chemistry</i> , 2006, 281, 14457-14464.	1.6	58
122	Structure and Function of the CBP/p300 TAZ Domains. , 2005, , 114-120.		4
123	Intrinsically unstructured proteins and their functions. <i>Nature Reviews Molecular Cell Biology</i> , 2005, 6, 197-208.	16.1	3,403
124	Defining the role of active-site loop fluctuations in dihydrofolate reductase catalysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5032-5037.	3.3	152
125	Enhanced picture of protein-folding intermediates using organic solvents in H/D exchange and quench-flow experiments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 4765-4770.	3.3	62
126	Inhibition of DNA Binding by Human Estrogen-Related Receptor 2 and Estrogen Receptor β with Minor Groove Binding Polyamides. <i>Biochemistry</i> , 2005, 44, 4196-4203.	1.2	42

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127	CBP/p300 TAZ1 Domain Forms a Structured Scaffold for Ligand Binding. <i>Biochemistry</i> , 2005, 44, 490-497.	1.2	76
128	Solution Structure of the N-terminal Zinc Fingers of the <i>Xenopus laevis</i> double-stranded RNA-binding Protein ZFa. <i>Journal of Molecular Biology</i> , 2005, 351, 718-730.	2.0	18
129	Sequence Determinants of a Protein Folding Pathway. <i>Journal of Molecular Biology</i> , 2005, 351, 383-392.	2.0	54
130	Elucidation of the Protein Folding Landscape by NMR. <i>Methods in Enzymology</i> , 2005, 394, 299-321.	0.4	90
131	Interaction of the TAZ1 Domain of the CREB-Binding Protein with the Activation Domain of CITED2. <i>Journal of Biological Chemistry</i> , 2004, 279, 3042-3049.	1.6	97
132	Recognition of the mRNA AU-rich element by the zinc finger domain of TIS11d. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 257-264.	3.6	320
133	Model-free Analysis of Protein Dynamics: Assessment of Accuracy and Model Selection Protocols Based on Molecular Dynamics Simulation. <i>Journal of Biomolecular NMR</i> , 2004, 29, 243-257.	1.6	60
134	Unfolded Proteins and Protein Folding Studied by NMR. <i>ChemInform</i> , 2004, 35, no.	0.1	1
135	The LEF-1 High-Mobility Group Domain Undergoes a Disorder-to-Order Transition upon Formation of a Complex with Cognate DNA. <i>Biochemistry</i> , 2004, 43, 8725-8734.	1.2	62
136	Effect of Cofactor Binding and Loop Conformation on Side Chain Methyl Dynamics in Dihydrofolate Reductase. <i>Biochemistry</i> , 2004, 43, 374-383.	1.2	73
137	Conformational Changes in the Active Site Loops of Dihydrofolate Reductase during the Catalytic Cycle. <i>Biochemistry</i> , 2004, 43, 16046-16055.	1.2	119
138	Unfolded Proteins and Protein Folding Studied by NMR. <i>Chemical Reviews</i> , 2004, 104, 3607-3622.	23.0	596
139	Packing, specificity, and mutability at the binding interface between the p160 coactivator and CREB-binding protein. <i>Protein Science</i> , 2004, 13, 203-210.	3.1	66
140	Introduction: Biological Nuclear Magnetic Resonance. <i>Chemical Reviews</i> , 2004, 104, 3517-3518.	23.0	2
141	Solution Structure of the KIX Domain of CBP Bound to the Transactivation Domain of c-Myb. <i>Journal of Molecular Biology</i> , 2004, 337, 521-534.	2.0	181
142	Structural Characterization of Unfolded States of Apomyoglobin using Residual Dipolar Couplings. <i>Journal of Molecular Biology</i> , 2004, 340, 1131-1142.	2.0	165
143	ZZ Domain of CBP: an Unusual Zinc Finger Fold in a Protein Interaction Module. <i>Journal of Molecular Biology</i> , 2004, 343, 1081-1093.	2.0	81
144	Structure, Dynamics, and Catalytic Function of Dihydrofolate Reductase. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 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. <i>Biochemical Journal</i> , 2004, 381, 685-691.	1.7	41
146	Changes in structure and dynamics of the Fv fragment of a catalytic antibody upon binding of inhibitor. <i>Protein Science</i> , 2003, 12, 1386-1394.	3.1	14
147	Role of a solvent-exposed tryptophan in the recognition and binding of antibiotic substrates for a metallo- β -lactamase. <i>Protein Science</i> , 2003, 12, 1368-1375.	3.1	56
148	Structure of the Nuclear Factor κ B: Insights into Post-Transcriptional Regulatory and mRNA Nuclear Export Processes. <i>Biochemistry</i> , 2003, 42, 7348-7357.	1.2	20
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