H Jane Dyson

List of Publications by Year
in descending order

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291 papers	40,446 citations	2669 95 h-index	2617 194 g-index
402 all docs	402 docs citations	402 times ranked	27477 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, .	3.3	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.	1.2	4
3	A transthyretin monomer intermediate undergoes local unfolding and transient interaction with oligomers in a kinetically concerted aggregation pathway. Journal of Biological Chemistry, 2022, 298, 102162.	1.6	5
4	Modeling of Hidden Structures Using Sparse Chemical Shift Data from NMR Relaxation Dispersion. Biophysical Journal, 2021, 120, 296-305.	0.2	4
5	Backbone and side-chain chemical shift assignments of p50 subunit of NF-Î°B transcription factor. Biomolecular NMR Assignments, 2021, 15, 29-33.	0.4	2
6	Using NMR to identify binding regions for N and C-terminal Hsp90 inhibitors using Hsp90 domains. RSC Medicinal Chemistry, 2021, 12, 410-415.	1.7	4
7	Thermodynamic Stability and Aggregation Kinetics of EF Helix and EF Loop Variants of Transthyretin. Biochemistry, 2021, 60, 756-764.	1.2	14
8	Early Strides in NMR Dynamics Measurements. Biochemistry, 2021, 60, 3452-3454.	1.2	0
9	Diversity at BJ: The editors, the reviewers, theÂauthors. Biophysical Journal, 2021, 120, E1-E2.	0.2	0
10	Role of Active Site Loop Dynamics in Mediating Ligand Release from E. coli Dihydrofolate Reductase. Biochemistry, 2021, 60, 2663-2671.	1.2	4
11	The molecular basis of allostery in a facilitated dissociation process. Structure, 2021, 29, 1327-1338.e5.	1.6	6
12	NMR illuminates intrinsic disorder. Current Opinion in Structural Biology, 2021, 70, 44-52.	2.6	60
13	More pandemic reflections. Biophysical Journal, 2021, 120, E1-E2.	0.2	0
14	A phosphorylation-dependent switch in the disordered p53 transactivation domain regulates DNA binding. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	33
15	Characterization of the High-Affinity Fuzzy Complex between the Disordered Domain of the E7 Oncoprotein from High-Risk HPV and the TAZ2 Domain of CBP. Biochemistry, 2021, 60, 3887-3898.	1.2	9
16	Reflections on the Pandemic. Biophysical Journal, 2020, 119, E1.	0.2	0
17	RNA Binding by the KTS Splice Variants of Wilmsâ€™ Tumor Suppressor Protein WT1. Biochemistry, 2020, 59, 3889-3901.	1.2	4
18	A Conformational Switch in the Zinc Finger Protein Kaiso Mediates Differential Readout of Specific and Methylated DNA Sequences. Biochemistry, 2020, 59, 1909-1926.	1.2	7

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19	Management of Hsp90-Dependent Protein Folding by Small Molecules Targeting the Aha1 Co-Chaperone. Cell Chemical Biology, 2020, 27, 292-305.e6.	2.5	13
20	Editorsâ€™ Note. Biophysical Journal, 2020, 119, E1.	0.2	0
21	Comparison of backbone dynamics of the p50 dimerization domain of NFÎºB in the homodimeric transcription factor NFÎºB1 and in its heterodimeric complex with RelA (p65). Protein Science, 2019, 28, 2064-2072.	3.1	7
22	Perspective: the essential role of NMR in the discovery and characterization of intrinsically disordered proteins. Journal of Biomolecular NMR, 2019, 73, 651-659.	1.6	48
23	Aggregation of zincâ€free p53 is inhibited by Hsp90 but not other chaperones. Protein Science, 2019, 28, 2020-2023.	3.1	7
24	Economics and Politics of Publishing in Our Mission-Driven Society. Biophysical Journal, 2019, 116, E1-E2.	0.2	0
25	A Journal for All Biophysics. Biophysical Journal, 2019, 116, E1.	0.2	0
26	Role of Backbone Dynamics in Modulating the Interactions of Disordered Ligands with the TAZ1 Domain of the CREB-Binding Protein. Biochemistry, 2019, 58, 1354-1362.	1.2	33
27	A Dynamic Switch in Inactive p38Î³ Leads to an Excited State on the Pathway to an Active Kinase. Biochemistry, 2019, 58, 5160-5172.	1.2	7
28	Expanding the Paradigm: Intrinsically Disordered Proteins and Allosteric Regulation. Journal of Molecular Biology, 2018, 430, 2309-2320.	2.0	105
29	Slow Dynamics of Tryptophanâ€“Water Networks in Proteins. Journal of the American Chemical Society, 2018, 140, 675-682.	6.6	26
30	Characterization of an Hsp90-Independent Interaction between Co-Chaperone p23 and Transcription Factor p53. Biochemistry, 2018, 57, 935-944.	1.2	13
31	Is the BJ Review Process Gender-Biased?. Biophysical Journal, 2018, 114, E1.	0.2	0
32	CHÂ·Â·Â·O Hydrogen Bonds Mediate Highly Specific Recognition of Methylated CpG Sites by the Zinc Finger Protein Kaiso. Biochemistry, 2018, 57, 2109-2120.	1.2	19
33	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
34	Mispacking of the Phe87 Side Chain Reduces the Kinetic Stability of Human Transthyretin. Biochemistry, 2018, 57, 6919-6922.	1.2	8
35	Structural Basis for Graded Inhibition of CREB:DNA Interactions by Multisite Phosphorylation. Biochemistry, 2018, 57, 6964-6972.	1.2	7
36	Structural basis for cooperative regulation of KIX-mediated transcription pathways by the HTLV-1 HBZ activation domain. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 10040-10045.	3.3	18

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37	How Do Intrinsically Disordered Viral Proteins Hijack the Cell?. Biochemistry, 2018, 57, 4045-4046.	1.2	22
38	NMR Measurements Reveal the Structural Basis of Transthyretin Destabilization by Pathogenic Mutations. Biochemistry, 2018, 57, 4421-4430.	1.2	30
39	Kinetic analysis of the multistep aggregation pathway of human transthyretin. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E6201-E6208.	3.3	29
40	Hypersensitive termination of the hypoxic response by a disordered protein switch. Nature, 2017, 543, 447-451.	13.7	140
41	Functional importance of stripping in NFÎºB signaling revealed by a stripping-impaired IÎºBÎ± mutant. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1916-1921.	3.3	32
42	Role of the CBP catalytic core in intramolecular SUMOylation and control of histone H3 acetylation. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E5335-E5342.	3.3	56
43	How Does Your Protein Fold? Elucidating the Apomyoglobin Folding Pathway. Accounts of Chemical Research, 2017, 50, 105-111.	7.6	44
44	Fluorotryptophan Incorporation Modulates the Structure and Stability of Transthyretin in a Site-Specific Manner. Biochemistry, 2017, 56, 5570-5581.	1.2	20
45	Defining the Structural Basis for Allosteric Product Release from E. coli Dihydrofolate Reductase Using NMR Relaxation Dispersion. Journal of the American Chemical Society, 2017, 139, 11233-11240.	6.6	27
46	Structural Basis for Interaction of the Tandem Zinc Finger Domains of Human Muscleblind with Cognate RNA from Human Cardiac Troponin T. Biochemistry, 2017, 56, 4154-4168.	1.2	27
47	Greetings from Your New Editor-in-Chief. Biophysical Journal, 2017, 113, E1.	0.2	0
48	Finding Our Way in the Dark Proteome. Journal of the American Chemical Society, 2016, 138, 9730-9742.	6.6	111
49	Structural characterization of the ternary complex that mediates termination of NF-Î°B signaling by IÎ°BÎ±. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 6212-6217.	3.3	8
50	Mapping the interactions of adenoviral E1A proteins with the p160 nuclear receptor coactivator binding domain of CBP. Protein Science, 2016, 25, 2256-2267.	3.1	18
51	<scp>NMR</scp> characterization of a 72 k<scp>D</scp>a transcription factor using differential isotopic labeling. Protein Science, 2016, 25, 597-604.	3.1	8
52	The Dependence of Carbohydrateâ€“Aromatic Interaction Strengths on the Structure of the Carbohydrate. Journal of the American Chemical Society, 2016, 138, 7636-7648.	6.6	44
53	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
54	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

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55	Making Sense of Intrinsically Disordered Proteins. Biophysical Journal, 2016, 110, 1013-1016.	0.2	81
56	Classic Analysis of Biopolymer Dynamics Is Model Free. Biophysical Journal, 2016, 110, 3-6.	0.2	4
57	Functional advantages of dynamic protein disorder. FEBS Letters, 2015, 589, 2433-2440.	1.3	162
58	Cofactor-Mediated Conformational Dynamics Promote Product Release From Escherichia coli Dihydrofolate Reductase via an Allosteric Pathway. Journal of the American Chemical Society, 2015, 137, 9459-9468.	6.6	45
59	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
60	Biomolecular Systems Interactions, Dynamics, and Allostery: Reflections and New Directions. Biophysical Journal, 2015, 109, E01-E02.	0.2	0
61	Intrinsically disordered proteins in cellular signalling and regulation. Nature Reviews Molecular Cell Biology, 2015, 16, 18-29.	16.1	1,849
62	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
63	Side Chain Conformational Averaging in Human Dihydrofolate Reductase. Biochemistry, 2014, 53, 1134-1145.	1.2	8
64	Probing the Non-Native H Helix Translocation in Apomyoglobin Folding Intermediates. Biochemistry, 2014, 53, 3767-3780.	1.2	16
65	Structural Characterization of Interactions between the Double-Stranded RNA-Binding Zinc Finger Protein JAZ and Nucleic Acids. Biochemistry, 2014, 53, 1495-1510.	1.2	20
66	The CH2 domain of CBP/p300 is a novel zinc finger. FEBS Letters, 2013, 587, 2506-2511.	1.3	12
67	Divergent evolution of protein conformational dynamics in dihydrofolate reductase. Nature Structural and Molecular Biology, 2013, 20, 1243-1249.	3.6	153
68	Localized Structural Fluctuations Promote Amyloidogenic Conformations in Transthyretin. Journal of Molecular Biology, 2013, 425, 977-988.	2.0	65
69	Long-Range Effects and Functional Consequences of Stabilizing Mutations in the Ankyrin Repeat Domain of Î²Bî±. Journal of Molecular Biology, 2013, 425, 902-913.	2.0	10
70	A Distal Mutation Perturbs Dynamic Amino Acid Networks in Dihydrofolate Reductase. Biochemistry, 2013, 52, 4605-4619.	1.2	77
71	Structural and Energetic Basis of Carbohydrateâ€“Aromatic Packing Interactions in Proteins. Journal of the American Chemical Society, 2013, 135, 9877-9884.	6.6	85
72	Side-Chain Conformational Heterogeneity of Intermediates in the Escherichia coli Dihydrofolate Reductase Catalytic Cycle. Biochemistry, 2013, 52, 3464-3477.	1.2	16

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73	Whatâ€™s in a name? Why these proteins are intrinsically disordered. Intrinsically Disordered Proteins, 2013, 1, e24157.	1.9	226
74	Identification of Cys255 in HIFâ€1Î± as a novel site for development of covalent inhibitors of HIFâ€1Î±/ARNT PasB domain proteinâ€“protein interaction. Protein Science, 2012, 21, 1885-1896.	3.1	64
75	CheShift-2 resolves a local inconsistency between two X-ray crystal structures. Journal of Biomolecular NMR, 2012, 54, 193-198.	1.6	4
76	Homodimerization of the PAS-B Domains of Hypoxia-Inducible Factors. Journal of Physical Chemistry B, 2012, 116, 6960-6965.	1.2	5
77	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
78	Roles of intrinsic disorder in proteinâ€“nucleic acid interactions. Molecular BioSystems, 2012, 8, 97-104.	2.9	76
79	Role of disorder in IÎºBâ€“NFÎºB interaction. IUBMB Life, 2012, 64, 499-505.	1.5	41
80	Kaiso uses all three zinc fingers and adjacent sequence motifs for high affinity binding to sequenceâ€specific and methylâ€CpG DNA targets. FEBS Letters, 2012, 586, 734-739.	1.3	17
81	Structural Basis for Cooperative Transcription Factor Binding to the CBP Coactivator. FASEB Journal, 2012, 26, lb266.	0.2	0
82	A Dynamic Knockout Reveals That Conformational Fluctuations Influence the Chemical Step of Enzyme Catalysis. Science, 2011, 332, 234-238.	6.0	414
83	Expanding the proteome: disordered and alternatively folded proteins. Quarterly Reviews of Biophysics, 2011, 44, 467-518.	2.4	150
84	The RelA Nuclear Localization Signal Folds upon Binding to IκBα. Journal of Molecular Biology, 2011, 405, 754-764.	2.0	29
85	Consequences of Stabilizing the Natively Disordered F Helix for the Folding Pathway of Apomyoglobin. Journal of Molecular Biology, 2011, 411, 248-263.	2.0	16
86	Dynamic Interaction of Hsp90 with Its Client Protein p53. Journal of Molecular Biology, 2011, 411, 158-173.	2.0	72
87	The client protein p53 adopts a molten globuleâ€like state in the presence of Hsp90. Nature Structural and Molecular Biology, 2011, 18, 537-541.	3.6	121
88	Detection of a ternary complex of NF-κB and IκBα with DNA provides insights into how IκBα removes NF-κB from transcription sites. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1367-1372.	3.3	26
89	Leu628 of the KIX domain of CBP is a key residue for the interaction with the MLL transactivation domain. FEBS Letters, 2010, 584, 4500-4504.	1.3	32
90	3P040 Mapping the Interactions of the Intrinsically Disordered p53 Transactivation Subdomains with the TAZ2 Domain of CBP by NMR(Protein: Structure & Function,The 48th Annual Meeting of the) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5	0.0	0

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91	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
92	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
93	Energetic Frustration of Apomyoglobin Folding: Role of the B Helix. Journal of Molecular Biology, 2010, 396, 1319-1328.	2.0	17
94	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
95	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
96	Evaluating Î²-turn mimics as Î²-sheet folding nucleators. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11067-11072.	3.3	97
97	Linking folding and binding. Current Opinion in Structural Biology, 2009, 19, 31-38.	2.6	932
98	Diagnostic chemical shift markers for loop conformation and substrate and cofactor binding in dihydrofolate reductase complexes. Protein Science, 2009, 12, 2230-2238.	3.1	38
99	Mapping the Interactions of the p53 Transactivation Domain with the KIX Domain of CBP. Biochemistry, 2009, 48, 2115-2124.	1.2	109
100	Prion Proteins with Pathogenic and Protective Mutations Show Similar Structure and Dynamics. Biochemistry, 2009, 48, 8120-8128.	1.2	53
101	Interaction of the IÎºBÎ± C-terminal PEST Sequence with NF-ÎºB: Insights into the Inhibition of NF-ÎºB DNA Binding by IÎºBÎ±. Journal of Molecular Biology, 2009, 388, 824-838.	2.0	28
102	Functional Dynamics of the Folded Ankyrin Repeats of IÎºBÎ± Revealed by Nuclear Magnetic Resonance. Biochemistry, 2009, 48, 8023-8031.	1.2	22
103	Structural basis for recruitment of CBP/p300 coactivators by STAT1 and STAT2 transactivation domains. EMBO Journal, 2009, 28, 948-958.	3.5	147
104	Prediction of the Rotational Tumbling Time for Proteins with Disordered Segments. Journal of the American Chemical Society, 2009, 131, 6814-6821.	6.6	48
105	Structure discrimination for the C-terminal domain of Escherichia coli trigger factor in solution. Journal of Biomolecular NMR, 2008, 40, 23-30.	1.6	17
106	Structural characterization of partially folded intermediates of apomyoglobin H64F. Protein Science, 2008, 17, 313-321.	3.1	16
107	Hydrogenâ€“deuterium exchange strategy for delineation of contact sites in protein complexes. FEBS Letters, 2008, 582, 1495-1500.	1.3	16
108	The Kinetic and Equilibrium Molten Globule Intermediates of Apoleghemoglobin Differ in Structure. Journal of Molecular Biology, 2008, 378, 715-725.	2.0	26

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109	Transfer of Flexibility between Ankyrin Repeats in IÎºBÎ± upon Formation of the NF-Îº B Complex. Journal of Molecular Biology, 2008, 380, 917-931.	2.0	61
110	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
111	Amylin Proprotein Processing Generates Progressively More Amyloidogenic Peptides that Initially Sample the Helical State. Biochemistry, 2008, 47, 9900-9910.	1.2	132
112	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
113	The Intrinsically Disordered RNR Inhibitor Sml1 Is a Dynamic Dimer. Biochemistry, 2008, 47, 13428-13437.	1.2	53
114	Conformational Relaxation following Hydride Transfer Plays a Limiting Role in Dihydrofolate Reductase Catalysisâ€. Biochemistry, 2008, 47, 9227-9233.	1.2	53
115	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
116	Embryonic Neural Inducing Factor Churchill Is not a DNA-binding Zinc Finger Protein: Solution Structure Reveals a Solvent-exposed Î²-Sheet and Zinc Binuclear Cluster. Journal of Molecular Biology, 2007, 371, 1274-1289.	2.0	21
117	Structure of the Wilms Tumor Suppressor Protein Zinc Finger Domain Bound to DNA. Journal of Molecular Biology, 2007, 372, 1227-1245.	2.0	91
118	Tailoring Relaxation Dispersion Experiments for Fast-Associating Protein Complexes. Journal of the American Chemical Society, 2007, 129, 13406-13407.	6.6	52
119	NMR detection of adventitious xylose binding to the quorum-sensing protein SdiA of Escherichia coli. Bioorganic and Medicinal Chemistry Letters, 2007, 17, 6202-6205.	1.0	7
120	Mechanism of coupled folding and binding of an intrinsically disordered protein. Nature, 2007, 447, 1021-1025.	13.7	984
121	Dynamics of IκBa Probed by NMR. FASEB Journal, 2007, 21, A655.	0.2	0
122	The Dynamic Energy Landscape of Dihydrofolate Reductase Catalysis. Science, 2006, 313, 1638-1642.	6.0	877
123	An NMR Perspective on Enzyme Dynamics. Chemical Reviews, 2006, 106, 3055-3079.	23.0	424
124	NMR Solution Structure of the Peptide Fragment 1â^'30, Derived from Unprocessed Mouse Doppel Protein, in DHPC Micellesâ€. Biochemistry, 2006, 45, 159-166.	1.2	19
125	The Reduced, Denatured Somatomedin B Domain of Vitronectin Refolds into a Stable, Biologically Active Molecule. Biochemistry, 2006, 45, 3297-3306.	1.2	11
126	Structural Basis for Cooperative Transcription Factor Binding to the CBP Coactivator. Journal of Molecular Biology, 2006, 355, 1005-1013.	2.0	166

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127	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
128	Identification of Native and Non-native Structure in Kinetic Folding Intermediates of Apomyoglobin. Journal of Molecular Biology, 2006, 355, 139-156.	2.0	112
129	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
130	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
131	According to current textbooks, a well-defined three-dimensional structure is a prerequisite for the function of a protein. Is this correct?. IUBMB Life, 2006, 58, 107-109.	1.5	20
132	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
133	Localization of Sites of Interaction between p23 and Hsp90 in Solution. Journal of Biological Chemistry, 2006, 281, 14457-14464.	1.6	58
134	Structure and Function of the CBP/p300 TAZ Domains. , 2005, , 114-120.		4
135	Intrinsically unstructured proteins and their functions. Nature Reviews Molecular Cell Biology, 2005, 6, 197-208.	16.1	3,403
136	Generation of native-like protein structures from limited NMR data, modern force fields and advanced conformational sampling. Journal of Biomolecular NMR, 2005, 31, 59-64.	1.6	36
137	Letter to the Editor: Backbone and side chain 1H, 13C and 15N assignments for Escherichia coli SdiA1-171, the autoinducer-binding domain of a quorum sensing protein. Journal of Biomolecular NMR, 2005, 31, 373-374.	1.6	7
138	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
139	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
140	CBP/p300 TAZ1 Domain Forms a Structured Scaffold for Ligand Binding,. Biochemistry, 2005, 44, 490-497.	1.2	76
141	Solution Structure of the N-terminal Zinc Fingers of the Xenopus laevis double-stranded RNA-binding Protein ZFa. Journal of Molecular Biology, 2005, 351, 718-730.	2.0	18
142	Sequence Determinants of a Protein Folding Pathway. Journal of Molecular Biology, 2005, 351, 383-392.	2.0	54
143	Elucidation of the Protein Folding Landscape by NMR. Methods in Enzymology, 2005, 394, 299-321.	0.4	90
144	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

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145	Activation of the Redox-regulated Chaperone Hsp33 by Domain Unfolding. Journal of Biological Chemistry, 2004, 279, 20529-20538.	1.6	100
146	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
147	Unfolded Proteins and Protein Folding Studied by NMR. ChemInform, 2004, 35, no.	0.1	1
148	Disulfide Bonding Arrangements in Active Forms of the Somatomedin B Domain of Human Vitronectinâ€. Biochemistry, 2004, 43, 6519-6534.	1.2	37
149	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
150	Effect of Cofactor Binding and Loop Conformation on Side Chain Methyl Dynamics in Dihydrofolate Reductase. Biochemistry, 2004, 43, 374-383.	1.2	73
151	Conformational Changes in the Active Site Loops of Dihydrofolate Reductase during the Catalytic Cycleâ€. Biochemistry, 2004, 43, 16046-16055.	1.2	119
152	Unfolded Proteins and Protein Folding Studied by NMR. Chemical Reviews, 2004, 104, 3607-3622.	23.0	596
153	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
154	Introduction:â€‰ Biological Nuclear Magnetic Resonance. Chemical Reviews, 2004, 104, 3517-3518.	23.0	2
155	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
156	Structural Characterization of Unfolded States of Apomyoglobin using Residual Dipolar Couplings. Journal of Molecular Biology, 2004, 340, 1131-1142.	2.0	165
157	The Zinc-dependent Redox Switch Domain of the Chaperone Hsp33 has a Novel Fold. Journal of Molecular Biology, 2004, 341, 893-899.	2.0	52
158	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
159	Structure, Dynamics, and Catalytic Function of Dihydrofolate Reductase. Annual Review of Biophysics and Biomolecular Structure, 2004, 33, 119-140.	18.3	444
160	The CBP/p300 TAZ1 domain in its native state is not a binding partner of MDM2. Biochemical Journal, 2004, 381, 685-691.	1.7	41
161	Changes in structure and dynamics of the Fv fragment of a catalytic antibody upon binding of inhibitor. Protein Science, 2003, 12, 1386-1394.	3.1	14
162	Role of a solvent-exposed tryptophan in the recognition and binding of antibiotic substrates for a metallo-Î²-lactamase. Protein Science, 2003, 12, 1368-1375.	3.1	56

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163	Structure of the Nuclear Factor ALY:â€‰ Insights into Post-Transcriptional Regulatory and mRNA Nuclear Export Processes. Biochemistry, 2003, 42, 7348-7357.	1.2	20
164	Role of the B Helix in Early Folding Events in Apomyoglobin: Evidence from Site-directed Mutagenesis for Native-like Long Range Interactions. Journal of Molecular Biology, 2003, 334, 293-307.	2.0	51
165	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
166	Folding of a Î²-sheet Protein Monitored by Real-time NMR Spectroscopy. Journal of Molecular Biology, 2003, 328, 1161-1171.	2.0	29
167	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
168	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
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