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	Intrinsically unstructured proteins and their functions. Nature Reviews Molecular Cell Biology, 2005, 6, 197-208.	16.1	3,403
2	Intrinsically unstructured proteins: re-assessing the protein structure-function paradigm. Journal of Molecular Biology, 1999, 293, 321-331.	2.0	2,668
3	1H, 13C and 15N chemical shift referencing in biomolecular NMR. Journal of Biomolecular NMR, 1995, 6, 135-140.	1.6	2,216
4	Intrinsically disordered proteins in cellular signalling and regulation. Nature Reviews Molecular Cell Biology, 2015, 16, 18-29.	16.1	1,849
5	Coupling of folding and binding for unstructured proteins. Current Opinion in Structural Biology, 2002, 12, 54-60.	2.6	1,223
6	Mechanism of coupled folding and binding of an intrinsically disordered protein. Nature, 2007, 447, 1021-1025.	13.7	984
7	Linking folding and binding. Current Opinion in Structural Biology, 2009, 19, 31-38.	2.6	932
8	The Dynamic Energy Landscape of Dihydrofolate Reductase Catalysis. Science, 2006, 313, 1638-1642.	6.0	877
9	Solution Structure of the KIX Domain of CBP Bound to the Transactivation Domain of CREB: A Model for Activator:Coactivator Interactions. Cell, 1997, 91, 741-752.	13.5	705
10	Folding of immunogenic peptide fragments of proteins in water solution. Journal of Molecular Biology, 1988, 201, 161-200.	2.0	685
11	Structure of the recombinant full-length hamster prion protein PrP(29-231): The N terminus is highly flexible. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 13452-13457.	3.3	665
12	Unfolded Proteins and Protein Folding Studied by NMR. Chemical Reviews, 2004, 104, 3607-3622.	23.0	596
13	Sequence-Dependent Correction of Random Coil NMR Chemical Shifts. Journal of the American Chemical Society, 2001, 123, 2970-2978.	6.6	562
14	Copper binding to the prion protein: Structural implications of four identical cooperative binding sites. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 2042-2047.	3.3	520
15	Conformation of peptide fragments of proteins in aqueous solution: implications for initiation of protein folding. Biochemistry, 1988, 27, 7167-7175.	1.2	505
16	Folding of immunogenic peptide fragments of proteins in water solution. Journal of Molecular Biology, 1988, 201, 201-217.	2.0	477
17	â€˜Random coilâ€™ 1H chemical shifts obtained as a function of temperature and trifluoroethanol concentration for the peptide series GGXGG. Journal of Biomolecular NMR, 1995, 5, 14-24.	1.6	476
18	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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19	An NMR Perspective on Enzyme Dynamics. Chemical Reviews, 2006, 106, 3055-3079.	23.0	424
20	Mutual synergistic folding in recruitment of CBP/p300 by p160 nuclear receptor coactivators. Nature, 2002, 415, 549-553.	13.7	423
21	A Dynamic Knockout Reveals That Conformational Fluctuations Influence the Chemical Step of Enzyme Catalysis. Science, 2011, 332, 234-238.	6.0	414
22	Folding of peptide fragments comprising the complete sequence of proteins. Journal of Molecular Biology, 1992, 226, 795-817.	2.0	385
23	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
24	Structural and dynamic characterization of partially folded states of apomyoglobin and implications for protein folding. Nature Structural Biology, 1998, 18, 148-155.	9.7	344
25	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
26	High-resolution solution structures of oxidized and reduced Escherichia coli thioredoxin. Structure, 1994, 2, 853-868.	1.6	281
27	Random coil chemical shifts in acidic 8 M urea: implementation of random coil shift data in NMRView. Journal of Biomolecular NMR, 2000, 18, 43-48.	1.6	272
28	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
29	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
30	The immunodominant site of a synthetic immunogen has a conformational preference in water for a type-II reverse turn. Nature, 1985, 318, 480-483.	13.7	246
31	Backbone Dynamics in Dihydrofolate Reductase Complexes:Â Role of Loop Flexibility in the Catalytic Mechanismâ€. Biochemistry, 2001, 40, 9846-9859.	1.2	246
32	Peptide conformation and protein folding. Current Opinion in Structural Biology, 1993, 3, 60-65.	2.6	232
33	Folding of peptide fragments comprising the complete sequence of proteins. Journal of Molecular Biology, 1992, 226, 819-835.	2.0	226
34	Whatâ€™s in a name? Why these proteins are intrinsically disordered. Intrinsically Disordered Proteins, 2013, 1, e24157.	1.9	226
35	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
36	NMR Structural and Dynamic Characterization of the Acid-Unfolded State of Apomyoglobin Provides Insights into the Early Events in Protein Foldingâ€,â€¡. Biochemistry, 2001, 40, 3561-3571.	1.2	212

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37	Peptide models of protein folding initiation sites. 1. Secondary structure formation by peptides corresponding to the G- and H-helixes of myoglobin. Biochemistry, 1993, 32, 6337-6347.	1.2	209
38	Insights into the structure and dynamics of unfolded proteins from nuclear magnetic resonance. Advances in Protein Chemistry, 2002, 62, 311-340.	4.4	208
39	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
40	Effects of Buried Charged Groups on Cysteine Thiol Ionization and Reactivity inEscherichia coliThioredoxin:Â Structural and Functional Characterization of Mutants of Asp 26 and Lys 57â€. Biochemistry, 1997, 36, 2622-2636.	1.2	192
41	Equilibrium NMR studies of unfolded and partially folded proteins. Nature Structural Biology, 1998, 5, 499-503.	9.7	187
42	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
43	Three-dimensional solution structure of the reduced form of Escherichia coli thioredoxin determined by nuclear magnetic resonance spectroscopy. Biochemistry, 1990, 29, 4129-4136.	1.2	177
44	Local Structural Plasticity of the Prion Protein. Analysis of NMR Relaxation Dynamicsâ€. Biochemistry, 2001, 40, 2743-2753.	1.2	171
45	Cooperativity in Transcription Factor Binding to the Coactivator CREB-binding Protein (CBP). Journal of Biological Chemistry, 2002, 277, 43168-43174.	1.6	166
46	Structural Basis for Cooperative Transcription Factor Binding to the CBP Coactivator. Journal of Molecular Biology, 2006, 355, 1005-1013.	2.0	166
47	Structural Characterization of Unfolded States of Apomyoglobin using Residual Dipolar Couplings. Journal of Molecular Biology, 2004, 340, 1131-1142.	2.0	165
48	Proton NMR studies of the solution conformations of an analog of the C-peptide of ribonuclease A. Biochemistry, 1989, 28, 7059-7064.	1.2	162
49	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
50	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
51	Functional advantages of dynamic protein disorder. FEBS Letters, 2015, 589, 2433-2440.	1.3	162
52	Solution conformational preferences of immunogenic peptides derived from the principal neutralizing determinant of the HIV-1 envelope glycoprotein gp120. Biochemistry, 1991, 30, 9187-9194.	1.2	155
53	Divergent evolution of protein conformational dynamics in dihydrofolate reductase. Nature Structural and Molecular Biology, 2013, 20, 1243-1249.	3.6	153
54	Stabilization of a type VI turn in a family of linear peptides in water solution. Journal of Molecular Biology, 1994, 243, 736-753.	2.0	152

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55	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
56	Expanding the proteome: disordered and alternatively folded proteins. Quarterly Reviews of Biophysics, 2011, 44, 467-518.	2.4	150
57	Comparison of backbone and tryptophan side-chain dynamics of reduced and oxidized Escherichia coli thioredoxin using nitrogen-15 NMR relaxation measurements. Biochemistry, 1993, 32, 426-435.	1.2	148
58	Nuclear Magnetic Resonance Methods for Elucidation of Structure and Dynamics in Disordered States. Methods in Enzymology, 2001, 339, 258-270.	0.4	148
59	Two different neurodegenerative diseases caused by proteins with similar structures. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 2352-2357.	3.3	147
60	Structural basis for recruitment of CBP/p300 coactivators by STAT1 and STAT2 transactivation domains. EMBO Journal, 2009, 28, 948-958.	3.5	147
61	INSIGHTS INTO PROTEIN FOLDING FROM NMR. Annual Review of Physical Chemistry, 1996, 47, 369-395.	4.8	144
62	Solution structure and acetyl-lysine binding activity of the GCN5 bromodomain. Journal of Molecular Biology, 2000, 304, 355-370.	2.0	141
63	Mapping Long-range Contacts in a Highly Unfolded Protein. Journal of Molecular Biology, 2002, 322, 655-662.	2.0	140
64	Hypersensitive termination of the hypoxic response by a disordered protein switch. Nature, 2017, 543, 447-451.	13.7	140
65	Conformational preferences in the Ser133 -phosphorylated and non-phosphorylated forms of the kinase inducible transactivation domain of CREB. FEBS Letters, 1998, 430, 317-322.	1.3	137
66	DNA-induced Î±-helix capping in conserved linker sequences is a determinant of binding affinity in Cys2-His2 zinc fingers. Journal of Molecular Biology, 2000, 295, 719-727.	2.0	137
67	Chemical shift dispersion and secondary structure prediction in unfolded and partly folded proteins. FEBS Letters, 1997, 419, 285-289.	1.3	135
68	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
69	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
70	Amylin Proprotein Processing Generates Progressively More Amyloidogenic Peptides that Initially Sample the Helical State. Biochemistry, 2008, 47, 9900-9910.	1.2	132
71	Molecular Hinges in Protein Folding:Â the Urea-Denatured State of Apomyoglobinâ€. Biochemistry, 2002, 41, 12681-12686.	1.2	130
72	Solution Structure of the Cysteine-rich Domain of the Escherichia coli Chaperone Protein DnaJ. Journal of Molecular Biology, 2000, 300, 805-818.	2.0	121

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73	Solution structure of the TAZ2 (CH3) domain of the transcriptional adaptor protein CBP. Journal of Molecular Biology, 2000, 303, 243-253.	2.0	121
74	Native and Non-native Secondary Structure and Dynamics in the pH 4 Intermediate of Apomyoglobinâ€. Biochemistry, 2000, 39, 2894-2901.	1.2	121
75	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
76	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
77	Conformational Changes in the Active Site Loops of Dihydrofolate Reductase during the Catalytic Cycleâ€. Biochemistry, 2004, 43, 16046-16055.	1.2	119
78	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
79	Three-dimensional structure of a type VI turn in a linear peptide in water solution Evidence for stacking of aromatic rings as a major stabilizing factor. Journal of Molecular Biology, 1994, 243, 754-766.	2.0	118
80	Absence of a stable intermediate on the folding pathway of protein A. Protein Science, 1997, 6, 1449-1457.	3.1	117
81	Molecular basis for modulation of biological function by alternate splicing of the Wilms' tumor suppressor protein. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 11932-11935.	3.3	115
82	SANE (Structure Assisted NOE Evaluation): an automated model-based approach for NOE assignment. Journal of Biomolecular NMR, 2001, 19, 321-329.	1.6	113
83	Comparison of protein solution structures refined by molecular dynamics simulation in vacuum, with a generalized Born model, and with explicit water. Journal of Biomolecular NMR, 2002, 22, 317-331.	1.6	112
84	Identification of Native and Non-native Structure in Kinetic Folding Intermediates of Apomyoglobin. Journal of Molecular Biology, 2006, 355, 139-156.	2.0	112
85	[13] Use of chemical shifts and coupling constants in nuclear magnetic resonance structural studies on peptides and proteins. Methods in Enzymology, 1994, 239, 392-416.	0.4	111
86	Finding Our Way in the Dark Proteome. Journal of the American Chemical Society, 2016, 138, 9730-9742.	6.6	111
87	Peptide models of protein folding initiation sites. 3. The G-H helical hairpin of myoglobin. Biochemistry, 1993, 32, 6356-6364.	1.2	109
88	Mapping the Interactions of the p53 Transactivation Domain with the KIX Domain of CBP. Biochemistry, 2009, 48, 2115-2124.	1.2	109
89	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
90	Expanding the Paradigm: Intrinsically Disordered Proteins and Allosteric Regulation. Journal of Molecular Biology, 2018, 430, 2309-2320.	2.0	105

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91	NMR Solution Structure of Cu(I) Rusticyanin fromThiobacillus ferrooxidans: Structural Basis for the Extreme Acid Stability and Redox Potential. Journal of Molecular Biology, 1996, 263, 752-767.	2.0	104
92	NMR Characterization of the Metallo-Î²-lactamase from Bacteroides fragilis and Its Interaction with a Tight-Binding Inhibitor:â€‰ Role of an Active-Site Loop. Biochemistry, 1999, 38, 14507-14514.	1.2	104
93	Characterization of a folding intermediate of apoplastocyanin trapped by proline isomerization. Biochemistry, 1993, 32, 12299-12310.	1.2	103
94	Assignment of the proton NMR spectrum of reduced and oxidized thioredoxin: sequence-specific assignments, secondary structure, and global fold. Biochemistry, 1989, 28, 7074-7087.	1.2	102
95	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
96	Activation of the Redox-regulated Chaperone Hsp33 by Domain Unfolding. Journal of Biological Chemistry, 2004, 279, 20529-20538.	1.6	100
97	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
98	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
99	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
100	Antigenic peptides. FASEB Journal, 1995, 9, 37-42.	0.2	96
101	Proton Sharing between Cysteine Thiols in Escherichia coli Thioredoxin: Implications for the Mechanism of Protein Disulfide Reduction. Biochemistry, 1995, 34, 10101-10105.	1.2	96
102	Conservation of folding pathways in evolutionarily distant globin sequences. Nature Structural Biology, 2000, 7, 679-686.	9.7	95
103	Conformational preferences of synthetic peptides derived from the immunodominant site of the circumsporozoite protein of Plasmodium falciparum by proton NMR. Biochemistry, 1990, 29, 7828-7837.	1.2	94
104	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
105	Quenchâ€flow experiments combined with mass spectrometry show apomyoglobin folds through an obligatory intermediate. Protein Science, 1999, 8, 45-49.	3.1	93
106	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
107	Peptide models of protein folding initiation sites. 2. The G-H turn region of myoglobin acts as a helix stop signal. Biochemistry, 1993, 32, 6348-6355.	1.2	92
108	Structure of the Wilms Tumor Suppressor Protein Zinc Finger Domain Bound to DNA. Journal of Molecular Biology, 2007, 372, 1227-1245.	2.0	91

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109	Elucidation of the Protein Folding Landscape by NMR. Methods in Enzymology, 2005, 394, 299-321.	0.4	90
110	The Apomyoglobin Folding Pathway Revisited: Structural Heterogeneity in the Kinetic Burst Phase Intermediate. Journal of Molecular Biology, 2002, 322, 483-489.	2.0	89
111	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
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	Structural and Energetic Basis of Carbohydrateâ€“Aromatic Packing Interactions in Proteins. Journal of the American Chemical Society, 2013, 135, 9877-9884.	6.6	85
114	Improved low pH bicelle system for orienting macromolecules over a wide temperature range. Journal of Biomolecular NMR, 1999, 13, 387-391.	1.6	84
115	Folding propensities of peptide fragments of myoglobin. Protein Science, 1997, 6, 706-716.	3.1	82
116	Calculations of Electrostatic Interactions and pKas in the Active Site of Escherichia coli Thioredoxin,. Biochemistry, 1998, 37, 10298-10306.	1.2	82
117	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
118	Making Sense of Intrinsically Disordered Proteins. Biophysical Journal, 2016, 110, 1013-1016.	0.2	81
119	Effect of H helix destabilizing mutations on the kinetic and equilibrium folding of apomyoglobin 1 1Edited by F. Cohen. Journal of Molecular Biology, 1999, 285, 269-282.	2.0	79
120	Structural and dynamic characterization of an unfolded state of poplar apo-plastocyanin formed under nondenaturing conditions. Protein Science, 2001, 10, 1056-1066.	3.1	79
121	Structure-based design of a constrained peptide mimic of the HIV-1 V3 loop neutralization site 1 1 Edited by F.E. Cohen. Journal of Molecular Biology, 1997, 266, 31-39.	2.0	77
122	A Distal Mutation Perturbs Dynamic Amino Acid Networks in Dihydrofolate Reductase. Biochemistry, 2013, 52, 4605-4619.	1.2	77
123	Proton-transfer effects in the active-site region of Escherichia coli thioredoxin using two-dimensional proton NMR. Biochemistry, 1991, 30, 4262-4268.	1.2	76
124	CBP/p300 TAZ1 Domain Forms a Structured Scaffold for Ligand Binding,. Biochemistry, 2005, 44, 490-497.	1.2	76
125	Roles of intrinsic disorder in proteinâ€“nucleic acid interactions. Molecular BioSystems, 2012, 8, 97-104.	2.9	76
126	NMR solution structure of the inserted domain of human leukocyte function associated antigen-1. Journal of Molecular Biology, 2000, 295, 1251-1264.	2.0	74

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127	Glycosylation of Threonine of the Repeating Unit of RNA Polymerase II with Î²-LinkedN-Acetylglucosame Leads to a Turnlike Structure. Journal of the American Chemical Society, 1998, 120, 11567-11575.	6.6	73
128	Effect of Cofactor Binding and Loop Conformation on Side Chain Methyl Dynamics in Dihydrofolate Reductase. Biochemistry, 2004, 43, 374-383.	1.2	73
129	Direct Measurement of the Aspartic Acid 26 pKafor ReducedEscherichia coliThioredoxin by13C NMRâ€. Biochemistry, 1996, 35, 1-6.	1.2	72
130	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
131	Dynamic Interaction of Hsp90 with Its Client Protein p53. Journal of Molecular Biology, 2011, 411, 158-173.	2.0	72
132	Solution structure of Escherichia coli glutaredoxin-2 shows similarity to mammalian glutathione-S-transferases. Journal of Molecular Biology, 2001, 310, 907-918.	2.0	71
133	Structural analyses of CREB-CBP transcriptional activator-coactivator complexes by NMR spectroscopy: implications for mapping the boundaries of structural domains. Journal of Molecular Biology, 1999, 287, 859-865.	2.0	68
134	Changes in the Apomyoglobin Folding Pathway Caused by Mutation of the Distal Histidine Residue. Biochemistry, 2000, 39, 11227-11237.	1.2	68
135	Genomic-scale comparison of sequence- and structure-based methods of function prediction: Does structure provide additional insight?. Protein Science, 2001, 10, 1005-1014.	3.1	68
136	Gene Synthesis, High-Level Expression, and Mutagenesis of Thiobacillus ferrooxidans Rusticyanin: His 85 Is a Ligand to the Blue Copper Center. Biochemistry, 1995, 34, 6640-6648.	1.2	66
137	DNA-induced conformational changes are the basis for cooperative dimerization by the DNA binding domain of the retinoid X receptor. Journal of Molecular Biology, 1998, 284, 533-539.	2.0	66
138	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
139	Localized Structural Fluctuations Promote Amyloidogenic Conformations in Transthyretin. Journal of Molecular Biology, 2013, 425, 977-988.	2.0	65
140	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
141	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
142	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
143	Comparison of the Hydrogen-Exchange Behavior of Reduced and Oxidized Escherichia Coli Thioredoxin. Biochemistry, 1995, 34, 611-619.	1.2	61
144	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

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145	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
146	NMR illuminates intrinsic disorder. Current Opinion in Structural Biology, 2021, 70, 44-52.	2.6	60
147	Dynamics of the Metallo-Î²-Lactamase from Bacteroides fragilis in the Presence and Absence of a Tight-Binding Inhibitor. Biochemistry, 2000, 39, 13356-13364.	1.2	59
148	High-resolution solution structure of the retinoid X receptor DNA-binding domain. Journal of Molecular Biology, 1998, 281, 271-284.	2.0	58
149	Alternative Splicing of Wilms' Tumor Suppressor Protein Modulates DNA Binding Activity through Isoform-Specific DNA-Induced Conformational Changesâ€. Biochemistry, 2000, 39, 5341-5348.	1.2	58
150	Localization of Sites of Interaction between p23 and Hsp90 in Solution. Journal of Biological Chemistry, 2006, 281, 14457-14464.	1.6	58
151	Polypeptide backbone resonance assignments and secondary structure of Bacillus subtilis enzyme IIIglc determined by two-dimensional and three-dimensional heteronuclear NMR spectroscopy. Biochemistry, 1991, 30, 6896-6907.	1.2	56
152	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
153	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
154	Efficient Inhibition of Escherichia Coli RNA Polymerase by the Bacteriophage T4 AsiA Protein Requires that AsiA Binds First to Free Ïƒ70. Journal of Molecular Biology, 2000, 304, 731-739.	2.0	55
155	Sequence Determinants of a Protein Folding Pathway. Journal of Molecular Biology, 2005, 351, 383-392.	2.0	54
156	Populating the equilibrium molten globule state of apomyoglobin under conditions suitable for structural characterization by NMR. FEBS Letters, 1997, 417, 92-96.	1.3	53
157	The Intrinsically Disordered RNR Inhibitor Sml1 Is a Dynamic Dimer. Biochemistry, 2008, 47, 13428-13437.	1.2	53
158	Conformational Relaxation following Hydride Transfer Plays a Limiting Role in Dihydrofolate Reductase Catalysisâ€. Biochemistry, 2008, 47, 9227-9233.	1.2	53
159	Prion Proteins with Pathogenic and Protective Mutations Show Similar Structure and Dynamics. Biochemistry, 2009, 48, 8120-8128.	1.2	53
160	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
161	Tailoring Relaxation Dispersion Experiments for Fast-Associating Protein Complexes. Journal of the American Chemical Society, 2007, 129, 13406-13407.	6.6	52
162	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

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163	Prediction of the Rotational Tumbling Time for Proteins with Disordered Segments. Journal of the American Chemical Society, 2009, 131, 6814-6821.	6.6	48
164	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
165	Conformational and Dynamic Characterization of the Molten Globule State of an Apomyoglobin Mutant with an Altered Folding Pathwayâ€. Biochemistry, 2001, 40, 14459-14467.	1.2	45
166	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
167	Contribution of Increased Length and Intact Capping Sequences to the Conformational Preference for Helix in a 31-Residue Peptide from the C Terminus of Myohemerythrin. Biochemistry, 1997, 36, 5234-5244.	1.2	44
168	Potential bias in NMR relaxation data introduced by peak intensity analysis and curve fitting methods. Journal of Biomolecular NMR, 2001, 21, 1-9.	1.6	44
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