H Jane Dyson

List of Publications by Year in Descending Order

278 papers	35,255 citations	92 h-index	185 g-index
402 ext. papers	38,132 ext. citations	7.7 avg, IF	7.52 L-index

#	Paper	IF	Citations
278	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,	11.5	4
277	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,	11.5	7
276	Thermodynamic Stability and Aggregation Kinetics of EF Helix and EF Loop Variants of Transthyretin. *Biochemistry*, **2021**, 60, 756-764	3.2	4
275	Early Strides in NMR Dynamics Measurements. *Biochemistry*, **2021**, 60, 3452-3454	3.2	
274	Modeling of Hidden Structures Using Sparse Chemical Shift Data from NMR Relaxation Dispersion. *Biophysical Journal*, **2021**, 120, 296-305	2.9	2
273	Backbone and side-chain chemical shift assignments of p50 subunit of NF-B transcription factor. *Biomolecular NMR Assignments*, **2021**, 15, 29-33	0.7	0
272	Using NMR to identify binding regions for N and C-terminal Hsp90 inhibitors using Hsp90 domains. *RSC Medicinal Chemistry*, **2021**, 12, 410-415	3.5	1
271	Role of Active Site Loop Dynamics in Mediating Ligand Release from Dihydrofolate Reductase. *Biochemistry*, **2021**, 60, 2663-2671	3.2	1
270	The molecular basis of allostery in a facilitated dissociation process. *Structure*, **2021**, 29, 1327-1338.e5	5.2	1
269	NMR illuminates intrinsic disorder. *Current Opinion in Structural Biology*, **2021**, 70, 44-52	8.1	21
268	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	3.2	0
267	A Conformational Switch in the Zinc Finger Protein Kaiso Mediates Differential Readout of Specific and Methylated DNA Sequences. *Biochemistry*, **2020**, 59, 1909-1926	3.2	3
266	Management of Hsp90-Dependent Protein Folding by Small Molecules Targeting the Aha1 Co-Chaperone. *Cell Chemical Biology*, **2020**, 27, 292-305.e6	8.2	8
265	RNA Binding by the KTS Splice Variants of WilmsPTumor Suppressor Protein WT1. *Biochemistry*, **2020**, 59, 3889-3901	3.2	1
264	Comparison of backbone dynamics of the p50 dimerization domain of NFB in the homodimeric transcription factor NFB1 and in its heterodimeric complex with RelA (p65). *Protein Science*, **2019**, 28, 2064-2072	6.3	4
263	Perspective: the essential role of NMR in the discovery and characterization of intrinsically disordered proteins. *Journal of Biomolecular NMR*, **2019**, 73, 651-659	3	20
262	Aggregation of zinc-free p53 is inhibited by Hsp90 but not other chaperones. *Protein Science*, **2019**, 28, 2020-2023	6.3	3

261	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	3.2	20
260	A Dynamic Switch in Inactive p38 Leads to an Excited State on the Pathway to an Active Kinase. *Biochemistry*, **2019**, 58, 5160-5172	3.2	3
259	Expanding the Paradigm: Intrinsically Disordered Proteins and Allosteric Regulation. *Journal of Molecular Biology*, **2018**, 430, 2309-2320	6.5	82
258	Slow Dynamics of Tryptophan-Water Networks in Proteins. *Journal of the American Chemical Society* , **2018**, 140, 675-682	16.4	20
257	Characterization of an Hsp90-Independent Interaction between Co-Chaperone p23 and Transcription Factor p53. *Biochemistry*, **2018**, 57, 935-944	3.2	8
256	CH O Hydrogen Bonds Mediate Highly Specific Recognition of Methylated CpG Sites by the Zinc Finger Protein Kaiso. *Biochemistry*, **2018**, 57, 2109-2120	3.2	10
255	How Do Intrinsically Disordered Viral Proteins Hijack the Cell?. *Biochemistry*, **2018**, 57, 4045-4046	3.2	12
254	NMR Measurements Reveal the Structural Basis of Transthyretin Destabilization by Pathogenic Mutations. *Biochemistry*, **2018**, 57, 4421-4430	3.2	16
253	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	11.5	16
252	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	11.5	42
251	Mispacking of the Phe87 Side Chain Reduces the Kinetic Stability of Human Transthyretin. *Biochemistry*, **2018**, 57, 6919-6922	3.2	3
250	Structural Basis for Graded Inhibition of CREB:DNA Interactions by Multisite Phosphorylation. *Biochemistry*, **2018**, 57, 6964-6972	3.2	2
249	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	11.5	10
248	Hypersensitive termination of the hypoxic response by a disordered protein switch. *Nature*, **2017**, 543, 447-451	50.4	99
247	Functional importance of stripping in NFB signaling revealed by a stripping-impaired IB mutant. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 1916-1921	11.5	21
246	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	11.5	33
245	How Does Your Protein Fold? Elucidating the Apomyoglobin Folding Pathway. *Accounts of Chemical Research*, **2017**, 50, 105-111	24.3	28
244	Fluorotryptophan Incorporation Modulates the Structure and Stability of Transthyretin in a Site-Specific Manner. *Biochemistry*, **2017**, 56, 5570-5581	3.2	13

243	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	16.4	19
242	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	3.2	15
241	NMR characterization of a 72 kDa transcription factor using differential isotopic labeling. *Protein Science*, **2016**, 25, 597-604	6.3	6
240	The Dependence of Carbohydrate-Aromatic Interaction Strengths on the Structure of the Carbohydrate. *Journal of the American Chemical Society*, **2016**, 138, 7636-48	16.4	38
239	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	11.5	56
238	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, 6714-22	5.4	168
237	Making Sense of Intrinsically Disordered Proteins. *Biophysical Journal*, **2016**, 110, 1013-6	2.9	55
236	Classic Analysis of Biopolymer Dynamics Is Model Free. *Biophysical Journal*, **2016**, 110, 3-6	2.9	0
235	Finding Our Way in the Dark Proteome. *Journal of the American Chemical Society*, **2016**, 138, 9730-42	16.4	93
234	Structural characterization of the ternary complex that mediates termination of NF-B signaling by IB *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 6212-7	11.5	6
233	Mapping the interactions of adenoviral E1A proteins with the p160 nuclear receptor coactivator binding domain of CBP. *Protein Science*, **2016**, 25, 2256-2267	6.3	12
232	Functional advantages of dynamic protein disorder. *FEBS Letters*, **2015**, 589, 2433-40	3.8	124
231	Cofactor-Mediated Conformational Dynamics Promote Product Release From Escherichia coli Dihydrofolate Reductase via an Allosteric Pathway. *Journal of the American Chemical Society*, **2015**, 137, 9459-68	16.4	37
230	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, 9614-9	11.5	161
229	Intrinsically disordered proteins in cellular signalling and regulation. *Nature Reviews Molecular Cell Biology*, **2015**, 16, 18-29	48.7	1249
228	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	6.5	42
227	Side chain conformational averaging in human dihydrofolate reductase. *Biochemistry*, **2014**, 53, 1134-45	3.2	4
226	Probing the non-native H helix translocation in apomyoglobin folding intermediates. *Biochemistry*, **2014**, 53, 3767-80	3.2	10

225	Structural characterization of interactions between the double-stranded RNA-binding zinc finger protein JAZ and nucleic acids. *Biochemistry*, **2014**, 53, 1495-510	3.2	14
224	The CH2 domain of CBP/p300 is a novel zinc finger. *FEBS Letters*, **2013**, 587, 2506-11	3.8	9
223	Divergent evolution of protein conformational dynamics in dihydrofolate reductase. *Nature Structural and Molecular Biology*, **2013**, 20, 1243-9	17.6	104
222	Localized structural fluctuations promote amyloidogenic conformations in transthyretin. *Journal of Molecular Biology*, **2013**, 425, 977-88	6.5	56
221	Long-range effects and functional consequences of stabilizing mutations in the ankyrin repeat domain of IB. *Journal of Molecular Biology*, **2013**, 425, 902-13	6.5	10
220	A distal mutation perturbs dynamic amino acid networks in dihydrofolate reductase. *Biochemistry*, **2013**, 52, 4605-19	3.2	68
219	Structural and energetic basis of carbohydrate-aromatic packing interactions in proteins. *Journal of the American Chemical Society*, **2013**, 135, 9877-84	16.4	77
218	Side-chain conformational heterogeneity of intermediates in the Escherichia coli dihydrofolate reductase catalytic cycle. *Biochemistry*, **2013**, 52, 3464-77	3.2	15
217	What's in a name? Why these proteins are intrinsically disordered: Why these proteins are intrinsically disordered. *Intrinsically Disordered Proteins*, **2013**, 1, e24157		171
216	Identification of Cys255 in HIF-1 as a novel site for development of covalent inhibitors of HIF-1/ARNT PasB domain protein-protein interaction. *Protein Science*, **2012**, 21, 1885-96	6.3	47
215	CheShift-2 resolves a local inconsistency between two X-ray crystal structures. *Journal of Biomolecular NMR*, **2012**, 54, 193-8	3	3
214	Homodimerization of the PAS-B domains of hypoxia-inducible factors. *Journal of Physical Chemistry B*, **2012**, 116, 6960-5	3.4	5
213	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, 15229-34	11.5	80
212	Roles of intrinsic disorder in protein-nucleic acid interactions. *Molecular BioSystems*, **2012**, 8, 97-104		60
211	Role of disorder in IB-NFB interaction. *IUBMB Life*, **2012**, 64, 499-505	4.7	35
210	Kaiso uses all three zinc fingers and adjacent sequence motifs for high affinity binding to sequence-specific and methyl-CpG DNA targets. *FEBS Letters*, **2012**, 586, 734-9	3.8	16
209	Structural Basis for Cooperative Transcription Factor Binding to the CBP Coactivator. *FASEB Journal* , **2012**, 26, lb266	0.9	
208	Expanding the proteome: disordered and alternatively folded proteins. *Quarterly Reviews of Biophysics*, **2011**, 44, 467-518	7	132

207	The RelA nuclear localization signal folds upon binding to IB. *Journal of Molecular Biology*, **2011**, 405, 754-64	6.5	28
206	Consequences of stabilizing the natively disordered f helix for the folding pathway of apomyoglobin. *Journal of Molecular Biology*, **2011**, 411, 248-63	6.5	14
205	Dynamic Interaction of Hsp90 with Its Client Protein p53. *Journal of Molecular Biology*, **2011**, 411, 158-73	6.5	58
204	The client protein p53 adopts a molten globule-like state in the presence of Hsp90. *Nature Structural and Molecular Biology*, **2011**, 18, 537-41	17.6	105
203	A dynamic knockout reveals that conformational fluctuations influence the chemical step of enzyme catalysis. *Science*, **2011**, 332, 234-8	33.3	350
202	Detection of a ternary complex of NF-kappaB and IkappaBalpha with DNA provides insights into how IkappaBalpha removes NF-kappaB from transcription sites. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 1367-72	11.5	20
201	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 Biophysical Society of Japan). *Seibutsu Butsuri*, **2010**, 50, S152	0	
200	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, 1373-8	11.5	118
199	Structure of the p53 transactivation domain in complex with the nuclear receptor coactivator binding domain of CREB binding protein. *Biochemistry*, **2010**, 49, 9964-71	3.2	129
198	Energetic frustration of apomyoglobin folding: role of the B helix. *Journal of Molecular Biology*, **2010**, 396, 1319-28	6.5	16
197	Leu628 of the KIX domain of CBP is a key residue for the interaction with the MLL transactivation domain. *FEBS Letters*, **2010**, 584, 4500-4	3.8	26
196	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, 6591-6	11.5	159
195	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, 13260-5	11.5	102
194	Evaluating beta-turn mimics as beta-sheet folding nucleators. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 11067-72	11.5	84
193	Linking folding and binding. *Current Opinion in Structural Biology*, **2009**, 19, 31-8	8.1	813
192	Mapping the interactions of the p53 transactivation domain with the KIX domain of CBP. *Biochemistry*, **2009**, 48, 2115-24	3.2	90
191	Prion proteins with pathogenic and protective mutations show similar structure and dynamics. *Biochemistry*, **2009**, 48, 8120-8	3.2	49
190	Interaction of the IkappaBalpha C-terminal PEST sequence with NF-kappaB: insights into the inhibition of NF-kappaB DNA binding by IkappaBalpha. *Journal of Molecular Biology*, **2009**, 388, 824-38	6.5	25

189	Functional dynamics of the folded ankyrin repeats of I kappa B alpha revealed by nuclear magnetic resonance. *Biochemistry*, **2009**, 48, 8023-31	3.2	21
188	Structural basis for recruitment of CBP/p300 coactivators by STAT1 and STAT2 transactivation domains. *EMBO Journal*, **2009**, 28, 948-58	13	108
187	Prediction of the rotational tumbling time for proteins with disordered segments. *Journal of the American Chemical Society*, **2009**, 131, 6814-21	16.4	39
186	Hydrogen-deuterium exchange strategy for delineation of contact sites in protein complexes. *FEBS Letters*, **2008**, 582, 1495-500	3.8	12
185	The kinetic and equilibrium molten globule intermediates of apoleghemoglobin differ in structure. *Journal of Molecular Biology*, **2008**, 378, 715-25	6.5	23
184	Transfer of flexibility between ankyrin repeats in IkappaB* upon formation of the NF-kappaB complex. *Journal of Molecular Biology*, **2008**, 380, 917-31	6.5	56
183	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, 13859-64	11.5	79
182	Amylin proprotein processing generates progressively more amyloidogenic peptides that initially sample the helical state. *Biochemistry*, **2008**, 47, 9900-10	3.2	121
181	NMR relaxation study of the complex formed between CBP and the activation domain of the nuclear hormone receptor coactivator ACTR. *Biochemistry*, **2008**, 47, 1299-308	3.2	71
180	The intrinsically disordered RNR inhibitor Sml1 is a dynamic dimer. *Biochemistry*, **2008**, 47, 13428-37	3.2	45
179	Conformational relaxation following hydride transfer plays a limiting role in dihydrofolate reductase catalysis. *Biochemistry*, **2008**, 47, 9227-33	3.2	50
178	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, 6278-83	11.5	95
177	Structure discrimination for the C-terminal domain of Escherichia coli trigger factor in solution. *Journal of Biomolecular NMR*, **2008**, 40, 23-30	3	14
176	Structural characterization of partially folded intermediates of apomyoglobin H64F. *Protein Science* , **2008**, 17, 313-21	6.3	15
175	Thioredoxin and Glutaredoxin **2007**,		1
174	NMR detection of adventitious xylose binding to the quorum-sensing protein SdiA of Escherichia coli. *Bioorganic and Medicinal Chemistry Letters*, **2007**, 17, 6202-5	2.9	7
173	Mechanism of coupled folding and binding of an intrinsically disordered protein. *Nature*, **2007**, 447, 1021-5	55.4	852
172	Embryonic neural inducing factor churchill is not a DNA-binding zinc finger protein: solution structure reveals a solvent-exposed beta-sheet and zinc binuclear cluster. *Journal of Molecular Biology*, **2007**, 371, 1274-89	6.5	20

171	Structure of the Wilms tumor suppressor protein zinc finger domain bound to DNA. *Journal of Molecular Biology*, **2007**, 372, 1227-45	6.5	82
170	Tailoring relaxation dispersion experiments for fast-associating protein complexes. *Journal of the American Chemical Society*, **2007**, 129, 13406-7	16.4	49
169	Dynamics of IkBa Probed by NMR. *FASEB Journal*, **2007**, 21, A655	0.9	
168	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, 13057-61	11.5	195
167	Localization of sites of interaction between p23 and Hsp90 in solution. *Journal of Biological Chemistry*, **2006**, 281, 14457-64	5.4	53
166	The dynamic energy landscape of dihydrofolate reductase catalysis. *Science*, **2006**, 313, 1638-42	33.3	778
165	An NMR perspective on enzyme dynamics. *Chemical Reviews*, **2006**, 106, 3055-79	68.1	369
164	NMR solution structure of the peptide fragment 1-30, derived from unprocessed mouse Doppel protein, in DHPC micelles. *Biochemistry*, **2006**, 45, 159-66	3.2	18
163	The reduced, denatured somatomedin B domain of vitronectin refolds into a stable, biologically active molecule. *Biochemistry*, **2006**, 45, 3297-306	3.2	11
162	Structural basis for cooperative transcription factor binding to the CBP coactivator. *Journal of Molecular Biology*, **2006**, 355, 1005-13	6.5	144
161	Structure of the Escherichia coli quorum sensing protein SdiA: activation of the folding switch by acyl homoserine lactones. *Journal of Molecular Biology*, **2006**, 355, 262-73	6.5	143
160	Identification of native and non-native structure in kinetic folding intermediates of apomyoglobin. *Journal of Molecular Biology*, **2006**, 355, 139-56	6.5	98
159	Induced fit and "lock and key" recognition of 5S RNA by zinc fingers of transcription factor IIIA. *Journal of Molecular Biology*, **2006**, 357, 275-91	6.5	60
158	Solution structure of the Hdm2 C2H2C4 RING, a domain critical for ubiquitination of p53. *Journal of Molecular Biology*, **2006**, 363, 433-50	6.5	101
157	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, 107-9	4.7	18
156	CBP/p300 TAZ1 domain forms a structured scaffold for ligand binding. *Biochemistry*, **2005**, 44, 490-7	3.2	61
155	Solution structure of the N-terminal zinc fingers of the Xenopus laevis double-stranded RNA-binding protein ZFa. *Journal of Molecular Biology*, **2005**, 351, 718-30	6.5	16
154	Sequence determinants of a protein folding pathway. *Journal of Molecular Biology*, **2005**, 351, 383-92	6.5	46

153	Elucidation of the protein folding landscape by NMR. *Methods in Enzymology*, **2005**, 394, 299-321	1.7	80
152	Structure and Function of the CBP/p300 TAZ Domains **2005**, 114-120		2
151	Intrinsically unstructured proteins and their functions. *Nature Reviews Molecular Cell Biology*, **2005**, 6, 197-208	48.7	2985
150	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	3	35
149	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, 373-4	3	6
148	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, 5032-7	11.5	143
147	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, 4765-70	11.5	52
146	Interaction of the TAZ1 domain of the CREB-binding protein with the activation domain of CITED2: regulation by competition between intrinsically unstructured ligands for non-identical binding sites. *Journal of Biological Chemistry*, **2004**, 279, 3042-9	5.4	76
145	Activation of the redox-regulated chaperone Hsp33 by domain unfolding. *Journal of Biological Chemistry*, **2004**, 279, 20529-38	5.4	75
144	Recognition of the mRNA AU-rich element by the zinc finger domain of TIS11d. *Nature Structural and Molecular Biology*, **2004**, 11, 257-64	17.6	280
143	Disulfide bonding arrangements in active forms of the somatomedin B domain of human vitronectin. *Biochemistry*, **2004**, 43, 6519-34	3.2	35
142	The LEF-1 high-mobility group domain undergoes a disorder-to-order transition upon formation of a complex with cognate DNA. *Biochemistry*, **2004**, 43, 8725-34	3.2	57
141	Effect of cofactor binding and loop conformation on side chain methyl dynamics in dihydrofolate reductase. *Biochemistry*, **2004**, 43, 374-83	3.2	71
140	Conformational changes in the active site loops of dihydrofolate reductase during the catalytic cycle. *Biochemistry*, **2004**, 43, 16046-55	3.2	103
139	Unfolded proteins and protein folding studied by NMR. *Chemical Reviews*, **2004**, 104, 3607-22	68.1	541
138	Packing, specificity, and mutability at the binding interface between the p160 coactivator and CREB-binding protein. *Protein Science*, **2004**, 13, 203-10	6.3	59
137	Solution structure of the KIX domain of CBP bound to the transactivation domain of c-Myb. *Journal of Molecular Biology*, **2004**, 337, 521-34	6.5	154
136	Structural characterization of unfolded states of apomyoglobin using residual dipolar couplings. *Journal of Molecular Biology*, **2004**, 340, 1131-42	6.5	157

135	The zinc-dependent redox switch domain of the chaperone Hsp33 has a novel fold. *Journal of Molecular Biology*, **2004**, 341, 893-9	6.5	35
134	ZZ domain of CBP: an unusual zinc finger fold in a protein interaction module. *Journal of Molecular Biology*, **2004**, 343, 1081-93	6.5	72
133	Structure, dynamics, and catalytic function of dihydrofolate reductase. *Annual Review of Biophysics and Biomolecular Structure*, **2004**, 33, 119-40		384
132	The CBP/p300 TAZ1 domain in its native state is not a binding partner of MDM2. *Biochemical Journal*, **2004**, 381, 685-91	3.8	37
131	Diagnostic chemical shift markers for loop conformation and substrate and cofactor binding in dihydrofolate reductase complexes. *Protein Science*, **2003**, 12, 2230-8	6.3	38
130	Changes in structure and dynamics of the Fv fragment of a catalytic antibody upon binding of inhibitor. *Protein Science*, **2003**, 12, 1386-94	6.3	13
129	Role of a solvent-exposed tryptophan in the recognition and binding of antibiotic substrates for a metallo-beta-lactamase. *Protein Science*, **2003**, 12, 1368-75	6.3	53
128	Structure of the nuclear factor ALY: insights into post-transcriptional regulatory and mRNA nuclear export processes. *Biochemistry*, **2003**, 42, 7348-57	3.2	19
127	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	6.5	48
126	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, 819-32	6.5	79
125	Folding of a beta-sheet protein monitored by real-time NMR spectroscopy. *Journal of Molecular Biology*, **2003**, 328, 1161-71	6.5	28
124	Coupling of folding and binding for unstructured proteins. *Current Opinion in Structural Biology*, **2002**, 12, 54-60	8.1	1121
123	Mutual synergistic folding in recruitment of CBP/p300 by p160 nuclear receptor coactivators. *Nature*, **2002**, 415, 549-53	50.4	373
122	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, 317-31	3	105
121	Assignment of a 15 kDa protein complex formed between the p160 coactivator ACTR and CREB binding protein. *Journal of Biomolecular NMR*, **2002**, 22, 377-8	3	6
120	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, 42241-8	5.4	122
119	Structural basis for Hif-1 alpha /CBP recognition in the cellular hypoxic response. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 5271-6	11.5	333
118	Molecular hinges in protein folding: the urea-denatured state of apomyoglobin. *Biochemistry*, **2002**, 41, 12681-6	3.2	123

117	Insights into the structure and dynamics of unfolded proteins from nuclear magnetic resonance. *Advances in Protein Chemistry*, **2002**, 62, 311-40		183
116	The apomyoglobin folding pathway revisited: structural heterogeneity in the kinetic burst phase intermediate. *Journal of Molecular Biology*, **2002**, 322, 483-9	6.5	86
115	Cooperativity in transcription factor binding to the coactivator CREB-binding protein (CBP). The mixed lineage leukemia protein (MLL) activation domain binds to an allosteric site on the KIX domain. *Journal of Biological Chemistry*, **2002**, 277, 43168-74	5.4	139
114	Mapping long-range contacts in a highly unfolded protein. *Journal of Molecular Biology*, **2002**, 322, 655-62	6.5	130
113	SANE (Structure Assisted NOE Evaluation): an automated model-based approach for NOE assignment. *Journal of Biomolecular NMR*, **2001**, 19, 321-9	3	105
112	Potential bias in NMR relaxation data introduced by peak intensity analysis and curve fitting methods. *Journal of Biomolecular NMR*, **2001**, 21, 1-9	3	42
111	Genomic-scale comparison of sequence- and structure-based methods of function prediction: does structure provide additional insight?. *Protein Science*, **2001**, 10, 1005-14	6.3	64
110	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, 2352-7	11.5	134
109	Structural and dynamic characterization of an unfolded state of poplar apo-plastocyanin formed under nondenaturing conditions. *Protein Science*, **2001**, 10, 1056-66	6.3	75
108	NMR structural and dynamic characterization of the acid-unfolded state of apomyoglobin provides insights into the early events in protein folding. *Biochemistry*, **2001**, 40, 3561-71	3.2	203
107	Backbone dynamics in dihydrofolate reductase complexes: role of loop flexibility in the catalytic mechanism. *Biochemistry*, **2001**, 40, 9846-59	3.2	226
106	Nuclear magnetic resonance methods for elucidation of structure and dynamics in disordered states. *Methods in Enzymology*, **2001**, 339, 258-70	1.7	137
105	Sequence-dependent correction of random coil NMR chemical shifts. *Journal of the American Chemical Society*, **2001**, 123, 2970-8	16.4	509
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