Peter E Wright

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

332 papers	41,206 citations	101 h-index	197 g-index
364 ext. papers	44,773 ext. citations	8.8 avg, IF	7.64 L-index

#	Paper	IF	Citations
332	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
331	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
330	Thermodynamic Stability and Aggregation Kinetics of EF Helix and EF Loop Variants of Transthyretin. *Biochemistry*, **2021**, 60, 756-764	3.2	4
329	Modeling of Hidden Structures Using Sparse Chemical Shift Data from NMR Relaxation Dispersion. *Biophysical Journal*, **2021**, 120, 296-305	2.9	2
328	Role of Active Site Loop Dynamics in Mediating Ligand Release from Dihydrofolate Reductase. *Biochemistry*, **2021**, 60, 2663-2671	3.2	1
327	The molecular basis of allostery in a facilitated dissociation process. *Structure*, **2021**, 29, 1327-1338.e5	5.2	1
326	NMR illuminates intrinsic disorder. *Current Opinion in Structural Biology*, **2021**, 70, 44-52	8.1	21
325	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
324	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
323	Determining Binding Kinetics of Intrinsically Disordered Proteins by NMR Spectroscopy. *Methods in Molecular Biology*, **2020**, 2141, 663-681	1.4	1
322	A Disorder-to-Order Transition Activates an ATP-Independent Membrane Protein Chaperone. *Journal of Molecular Biology*, **2020**, 432, 166708	6.5	5
321	An allosteric peptide inhibitor of HIF-1 regulates hypoxia-induced retinal neovascularization. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 28297-28306	11.5	8
320	RNA Binding by the KTS Splice Variants of Wilms Tumor Suppressor Protein WT1. *Biochemistry*, **2020**, 59, 3889-3901	3.2	1
319	Comparison of backbone dynamics of the p50 dimerization domain of NF in the homodimeric transcription factor NF 1 and in its heterodimeric complex with RelA (p65). *Protein Science*, **2019**, 28, 2064-2072	6.3	4
318	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
317	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
316	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

315	Expanding the Paradigm: Intrinsically Disordered Proteins and Allosteric Regulation. *Journal of Molecular Biology*, **2018**, 430, 2309-2320	6.5	82
314	Slow Dynamics of Tryptophan-Water Networks in Proteins. *Journal of the American Chemical Society*, **2018**, 140, 675-682	16.4	20
313	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
312	How Do Intrinsically Disordered Viral Proteins Hijack the Cell?. *Biochemistry*, **2018**, 57, 4045-4046	3.2	12
311	Tight complexes from disordered proteins. *Nature*, **2018**, 555, 37-38	50.4	2
310	NMR Measurements Reveal the Structural Basis of Transthyretin Destabilization by Pathogenic Mutations. *Biochemistry*, **2018**, 57, 4421-4430	3.2	16
309	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
308	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
307	Mispacking of the Phe87 Side Chain Reduces the Kinetic Stability of Human Transthyretin. *Biochemistry*, **2018**, 57, 6919-6922	3.2	3
306	Structural Basis for Graded Inhibition of CREB:DNA Interactions by Multisite Phosphorylation. *Biochemistry*, **2018**, 57, 6964-6972	3.2	2
305	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
304	Hypersensitive termination of the hypoxic response by a disordered protein switch. *Nature*, **2017**, 543, 447-451	50.4	99
303	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
302	How Does Your Protein Fold? Elucidating the Apomyoglobin Folding Pathway. *Accounts of Chemical Research*, **2017**, 50, 105-111	24.3	28
301	Fluorotryptophan Incorporation Modulates the Structure and Stability of Transthyretin in a Site-Specific Manner. *Biochemistry*, **2017**, 56, 5570-5581	3.2	13
300	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
299	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
298	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

297	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
296	Conformational dynamics of a membrane protein chaperone enables spatially regulated substrate capture and release. *Proceedings of the National Academy of Sciences of the United States of America* , **2016**, 113, E1615-24	11.5	23
295	Multi-probe relaxation dispersion measurements increase sensitivity to protein dynamics. *Physical Chemistry Chemical Physics*, **2016**, 18, 5789-98	3.6	7
294	Finding Our Way in the Dark Proteome. *Journal of the American Chemical Society*, **2016**, 138, 9730-42	16.4	93
293	NMR Characterization of Information Flow and Allosteric Communities in the MAP Kinase p38 *Scientific Reports*, **2016**, 6, 28655	4.9	16
292	Solid-State NMR Studies Reveal Native-like Sheet Structures in Transthyretin Amyloid. *Biochemistry*, **2016**, 55, 5272-8	3.2	21
291	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
290	Functional advantages of dynamic protein disorder. *FEBS Letters*, **2015**, 589, 2433-40	3.8	124
289	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
288	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
287	Intrinsically disordered proteins in cellular signalling and regulation. *Nature Reviews Molecular Cell Biology*, **2015**, 16, 18-29	48.7	1249
286	Integrated description of protein dynamics from room-temperature X-ray crystallography and NMR. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, E445-54	11.5	106
285	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
284	Side chain conformational averaging in human dihydrofolate reductase. *Biochemistry*, **2014**, 53, 1134-45	3.2	4
283	Probing the non-native H helix translocation in apomyoglobin folding intermediates. *Biochemistry*, **2014**, 53, 3767-80	3.2	10
282	Accurate scoring of non-uniform sampling schemes for quantitative NMR. *Journal of Magnetic Resonance*, **2014**, 246, 31-5	3	37
281	Classification of intrinsically disordered regions and proteins. *Chemical Reviews*, **2014**, 114, 6589-631	68.1	1141
280	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

279	pE-DB: a database of structural ensembles of intrinsically disordered and of unfolded proteins. *Nucleic Acids Research*, **2014**, 42, D326-35	20.1	159
278	Combinatorial regulation of a signal-dependent activator by phosphorylation and acetylation. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 17116-21	11.5	18
277	Assemblages: functional units formed by cellular phase separation. *Journal of Cell Biology*, **2014**, 206, 579-88	7.3	187
276	Automated identification of functional dynamic contact networks from X-ray crystallography. *Nature Methods*, **2013**, 10, 896-902	21.6	99
275	Fast and accurate fitting of relaxation dispersion data using the flexible software package GLOVE. *Journal of Biomolecular NMR*, **2013**, 56, 275-83	3	61
274	The CH2 domain of CBP/p300 is a novel zinc finger. *FEBS Letters*, **2013**, 587, 2506-11	3.8	9
273	Divergent evolution of protein conformational dynamics in dihydrofolate reductase. *Nature Structural and Molecular Biology*, **2013**, 20, 1243-9	17.6	104
272	Localized structural fluctuations promote amyloidogenic conformations in transthyretin. *Journal of Molecular Biology*, **2013**, 425, 977-88	6.5	56
271	A distal mutation perturbs dynamic amino acid networks in dihydrofolate reductase. *Biochemistry*, **2013**, 52, 4605-19	3.2	68
270	Modulation of allostery by protein intrinsic disorder. *Nature*, **2013**, 498, 390-4	50.4	255
269	Side-chain conformational heterogeneity of intermediates in the Escherichia coli dihydrofolate reductase catalytic cycle. *Biochemistry*, **2013**, 52, 3464-77	3.2	15
268	Analysis of the RelA:CBP/p300 interaction reveals its involvement in NF-B-driven transcription. *PLoS Biology*, **2013**, 11, e1001647	9.7	81
267	Mechanisms of transthyretin inhibition of amyloid aggregation in vitro. *Journal of Neuroscience*, **2013**, 33, 19423-33	6.6	98
266	Functional Interactions of Intrinsically Disordered Proteins in Signaling Networks. *FASEB Journal*, **2013**, 27, 459.3	0.9	
265	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
264	Quantitative analysis of multisite protein-ligand interactions by NMR: binding of intrinsically disordered p53 transactivation subdomains with the TAZ2 domain of CBP. *Journal of the American Chemical Society*, **2012**, 134, 3792-803	16.4	104
263	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
262	Structural Basis for Cooperative Transcription Factor Binding to the CBP Coactivator. *FASEB Journal* , **2012**, 26, lb266	0.9	

261	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
260	Identification of endogenous ligands bound to bacterially expressed human and E. coli dihydrofolate reductase by 2D NMR. *FEBS Letters*, **2011**, 585, 3528-32	3.8	13
259	A dynamic knockout reveals that conformational fluctuations influence the chemical step of enzyme catalysis. *Science*, **2011**, 332, 234-8	33.3	350
258	Measurement of protein unfolding/refolding kinetics and structural characterization of hidden intermediates by NMR relaxation dispersion. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 9078-83	11.5	58
257	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	
256	Graded enhancement of p53 binding to CREB-binding protein (CBP) by multisite phosphorylation. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 19290-5	11.5	163
255	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
254	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
253	Energetic frustration of apomyoglobin folding: role of the B helix. *Journal of Molecular Biology*, **2010**, 396, 1319-28	6.5	16
252	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
251	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
250	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
249	Linking folding and binding. *Current Opinion in Structural Biology*, **2009**, 19, 31-8	8.1	813
248	The role of dynamic conformational ensembles in biomolecular recognition. *Nature Chemical Biology*, **2009**, 5, 789-96	11.7	1420
247	Mapping the interactions of the p53 transactivation domain with the KIX domain of CBP. *Biochemistry*, **2009**, 48, 2115-24	3.2	90
246	Prion proteins with pathogenic and protective mutations show similar structure and dynamics. *Biochemistry*, **2009**, 48, 8120-8	3.2	49
245	Structural basis for recruitment of CBP/p300 coactivators by STAT1 and STAT2 transactivation domains. *EMBO Journal*, **2009**, 28, 948-58	13	108
244	Prediction of the rotational tumbling time for proteins with disordered segments. *Journal of the American Chemical Society*, **2009**, 131, 6814-21	16.4	39

243	Biochemistry. How do proteins interact?. *Science*, **2008**, 320, 1429-30	33.3	155
242	The kinetic and equilibrium molten globule intermediates of apoleghemoglobin differ in structure. *Journal of Molecular Biology*, **2008**, 378, 715-25	6.5	23
241	Overexpression of post-translationally modified peptides in Escherichia coli by co-expression with modifying enzymes. *Protein Expression and Purification*, **2008**, 57, 108-15	2	28
240	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
239	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
238	The intrinsically disordered RNR inhibitor Sml1 is a dynamic dimer. *Biochemistry*, **2008**, 47, 13428-37	3.2	45
237	Conformational relaxation following hydride transfer plays a limiting role in dihydrofolate reductase catalysis. *Biochemistry*, **2008**, 47, 9227-33	3.2	50
236	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
235	Structural characterization of partially folded intermediates of apomyoglobin H64F. *Protein Science* , **2008**, 17, 313-21	6.3	15
234	Mechanism of coupled folding and binding of an intrinsically disordered protein. *Nature*, **2007**, 447, 1021-5	56.4	852
233	S03A3 Metastable structure detected by relaxation dispersion NMR spectroscopy(Visualising Dynamical Aspects of A Protein Molecule). *Seibutsu Butsuri*, **2007**, 47, S4	0	
232	PRAK is essential for ras-induced senescence and tumor suppression. *Cell*, **2007**, 128, 295-308	56.2	252
231	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
230	Structure of the Wilms tumor suppressor protein zinc finger domain bound to DNA. *Journal of Molecular Biology*, **2007**, 372, 1227-45	6.5	82
229	Tailoring relaxation dispersion experiments for fast-associating protein complexes. *Journal of the American Chemical Society*, **2007**, 129, 13406-7	16.4	49
228	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
227	Localization of sites of interaction between p23 and Hsp90 in solution. *Journal of Biological Chemistry*, **2006**, 281, 14457-64	5.4	53
226	The dynamic energy landscape of dihydrofolate reductase catalysis. *Science*, **2006**, 313, 1638-42	33.3	778

225	An NMR perspective on enzyme dynamics. *Chemical Reviews*, **2006**, 106, 3055-79	68.1	369
224	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
223	Structural basis for cooperative transcription factor binding to the CBP coactivator. *Journal of Molecular Biology*, **2006**, 355, 1005-13	6.5	144
222	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
221	Identification of native and non-native structure in kinetic folding intermediates of apomyoglobin. *Journal of Molecular Biology*, **2006**, 355, 139-56	6.5	98
220	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
219	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
218	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
217	Inhibition of DNA binding by human estrogen-related receptor 2 and estrogen receptor alpha with minor groove binding polyamides. *Biochemistry*, **2005**, 44, 4196-203	3.2	39
216	CBP/p300 TAZ1 domain forms a structured scaffold for ligand binding. *Biochemistry*, **2005**, 44, 490-7	3.2	61
215	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
214	Sequence determinants of a protein folding pathway. *Journal of Molecular Biology*, **2005**, 351, 383-92	6.5	46
213	Elucidation of the protein folding landscape by NMR. *Methods in Enzymology*, **2005**, 394, 299-321	1.7	80
212	Structure and Function of the CBP/p300 TAZ Domains **2005**, 114-120		2
211	Intrinsically unstructured proteins and their functions. *Nature Reviews Molecular Cell Biology*, **2005**, 6, 197-208	48.7	2985
210	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
209	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
208	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

207	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
206	Model-free analysis of protein dynamics: assessment of accuracy and model selection protocols based on molecular dynamics simulation. *Journal of Biomolecular NMR*, **2004**, 29, 243-57	3	56
205	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
204	Effect of cofactor binding and loop conformation on side chain methyl dynamics in dihydrofolate reductase. *Biochemistry*, **2004**, 43, 374-83	3.2	71
203	Conformational changes in the active site loops of dihydrofolate reductase during the catalytic cycle. *Biochemistry*, **2004**, 43, 16046-55	3.2	103
202	Unfolded proteins and protein folding studied by NMR. *Chemical Reviews*, **2004**, 104, 3607-22	68.1	541
201	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
200	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
199	Structural characterization of unfolded states of apomyoglobin using residual dipolar couplings. *Journal of Molecular Biology*, **2004**, 340, 1131-42	6.5	157
198	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
197	Structure, dynamics, and catalytic function of dihydrofolate reductase. *Annual Review of Biophysics and Biomolecular Structure*, **2004**, 33, 119-40		384
196	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
195	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
194	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
193	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
192	Structure of the nuclear factor ALY: insights into post-transcriptional regulatory and mRNA nuclear export processes. *Biochemistry*, **2003**, 42, 7348-57	3.2	19
191	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
190	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

189	Folding of a beta-sheet protein monitored by real-time NMR spectroscopy. *Journal of Molecular Biology*, **2003**, 328, 1161-71	6.5	28
188	Coupling of folding and binding for unstructured proteins. *Current Opinion in Structural Biology*, **2002**, 12, 54-60	8.1	1121
187	Mutual synergistic folding in recruitment of CBP/p300 by p160 nuclear receptor coactivators. *Nature*, **2002**, 415, 549-53	50.4	373
186	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
185	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
184	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
183	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
182	Molecular hinges in protein folding: the urea-denatured state of apomyoglobin. *Biochemistry*, **2002**, 41, 12681-6	3.2	123
181	Insights into the structure and dynamics of unfolded proteins from nuclear magnetic resonance. *Advances in Protein Chemistry*, **2002**, 62, 311-40		183
180	The apomyoglobin folding pathway revisited: structural heterogeneity in the kinetic burst phase intermediate. *Journal of Molecular Biology*, **2002**, 322, 483-9	6.5	86
179	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
178	High pressure NMR reveals that apomyoglobin is an equilibrium mixture from the native to the unfolded. *Journal of Molecular Biology*, **2002**, 320, 311-9	6.5	72
177	Mapping long-range contacts in a highly unfolded protein. *Journal of Molecular Biology*, **2002**, 322, 655-62	6.5	130
176	SANE (Structure Assisted NOE Evaluation): an automated model-based approach for NOE assignment. *Journal of Biomolecular NMR*, **2001**, 19, 321-9	3	105
175	Anisotropic rotational diffusion in model-free analysis for a ternary DHFR complex. *Journal of Biomolecular NMR*, **2001**, 19, 209-30	3	42
174	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
173	Zinc finger proteins: new insights into structural and functional diversity. *Current Opinion in Structural Biology*, **2001**, 11, 39-46	8.1	1001
172	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

171	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
170	Backbone dynamics in dihydrofolate reductase complexes: role of loop flexibility in the catalytic mechanism. *Biochemistry*, **2001**, 40, 9846-59	3.2	226
169	Nuclear magnetic resonance methods for elucidation of structure and dynamics in disordered states. *Methods in Enzymology*, **2001**, 339, 258-70	1.7	137
168	Sequence-dependent correction of random coil NMR chemical shifts. *Journal of the American Chemical Society*, **2001**, 123, 2970-8	16.4	509
167	Solution structure of Escherichia coli glutaredoxin-2 shows similarity to mammalian glutathione-S-transferases. *Journal of Molecular Biology*, **2001**, 310, 907-18	6.5	67
166	Solution structure of the third immunoglobulin domain of the neural cell adhesion molecule N-CAM: can solution studies define the mechanism of homophilic binding?. *Journal of Molecular Biology*, **2001**, 311, 161-72	6.5	23
165	Conformational and dynamic characterization of the molten globule state of an apomyoglobin mutant with an altered folding pathway. *Biochemistry*, **2001**, 40, 14459-67	3.2	43
164	Local structural plasticity of the prion protein. Analysis of NMR relaxation dynamics. *Biochemistry*, **2001**, 40, 2743-53	3.2	164
163	Amide proton hydrogen exchange rates for sperm whale myoglobin obtained from 15N-1H NMR spectra. *Protein Science*, **2000**, 9, 186-93	6.3	18
162	Conservation of folding pathways in evolutionarily distant globin sequences. *Nature Structural Biology*, **2000**, 7, 679-86		88
161	Assessment of zinc finger orientations by residual dipolar coupling constants. *Journal of Biomolecular NMR*, **2000**, 16, 9-21	3	40
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