H Jane Dyson

List of Publications by Citations

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	Intrinsically unstructured proteins and their functions. *Nature Reviews Molecular Cell Biology*, **2005**, 6, 197-208	48.7	2985
277	Intrinsically unstructured proteins: re-assessing the protein structure-function paradigm. *Journal of Molecular Biology*, **1999**, 293, 321-31	6.5	2343
276	1H, 13C and 15N chemical shift referencing in biomolecular NMR. *Journal of Biomolecular NMR*, **1995**, 6, 135-40	3	2054
275	Intrinsically disordered proteins in cellular signalling and regulation. *Nature Reviews Molecular Cell Biology*, **2015**, 16, 18-29	48.7	1249
274	Coupling of folding and binding for unstructured proteins. *Current Opinion in Structural Biology*, **2002**, 12, 54-60	8.1	1121
273	Mechanism of coupled folding and binding of an intrinsically disordered protein. *Nature*, **2007**, 447, 1021-5	56.4	852
272	Linking folding and binding. *Current Opinion in Structural Biology*, **2009**, 19, 31-8	8.1	813
271	The dynamic energy landscape of dihydrofolate reductase catalysis. *Science*, **2006**, 313, 1638-42	33.3	778
270	Solution structure of the KIX domain of CBP bound to the transactivation domain of CREB: a model for activator:coactivator interactions. *Cell*, **1997**, 91, 741-52	56.2	648
269	Folding of immunogenic peptide fragments of proteins in water solution. I. Sequence requirements for the formation of a reverse turn. *Journal of Molecular Biology*, **1988**, 201, 161-200	6.5	634
268	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, 13452-7	11.5	626
267	Unfolded proteins and protein folding studied by NMR. *Chemical Reviews*, **2004**, 104, 3607-22	68.1	541
266	Sequence-dependent correction of random coil NMR chemical shifts. *Journal of the American Chemical Society*, **2001**, 123, 2970-8	16.4	509
265	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, 2042-7	11.5	485
264	Conformation of peptide fragments of proteins in aqueous solution: implications for initiation of protein folding. *Biochemistry*, **1988**, 27, 7167-75	3.2	464
263	Random coil 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	3	453
262	Folding of immunogenic peptide fragments of proteins in water solution. II. The nascent helix. *Journal of Molecular Biology*, **1988**, 201, 201-17	6.5	449

261	Structure, dynamics, and catalytic function of dihydrofolate reductase. *Annual Review of Biophysics and Biomolecular Structure*, **2004**, 33, 119-40		384
260	Mutual synergistic folding in recruitment of CBP/p300 by p160 nuclear receptor coactivators. *Nature*, **2002**, 415, 549-53	50.4	373
259	An NMR perspective on enzyme dynamics. *Chemical Reviews*, **2006**, 106, 3055-79	68.1	369
258	Folding of peptide fragments comprising the complete sequence of proteins. Models for initiation of protein folding. I. Myohemerythrin. *Journal of Molecular Biology*, **1992**, 226, 795-817	6.5	351
257	A dynamic knockout reveals that conformational fluctuations influence the chemical step of enzyme catalysis. *Science*, **2011**, 332, 234-8	33.3	350
256	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
255	Structural and dynamic characterization of partially folded states of apomyoglobin and implications for protein folding. *Nature Structural Biology*, **1998**, 5, 148-55		318
254	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
253	High-resolution solution structures of oxidized and reduced Escherichia coli thioredoxin. *Structure*, **1994**, 2, 853-68	5.2	267
252	Random coil chemical shifts in acidic 8 M urea: implementation of random coil shift data in NMRView. *Journal of Biomolecular NMR*, **2000**, 18, 43-8	3	258
251	Backbone dynamics in dihydrofolate reductase complexes: role of loop flexibility in the catalytic mechanism. *Biochemistry*, **2001**, 40, 9846-59	3.2	226
250	The immunodominant site of a synthetic immunogen has a conformational preference in water for a type-II reverse turn. *Nature*, **1985**, 318, 480-3	50.4	221
249	Folding of peptide fragments comprising the complete sequence of proteins. Models for initiation of protein folding. II. Plastocyanin. *Journal of Molecular Biology*, **1992**, 226, 819-35	6.5	215
248	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
247	Peptide conformation and protein folding. *Current Opinion in Structural Biology*, **1993**, 3, 60-65	8.1	202
246	Peptide models of protein folding initiation sites. 1. Secondary structure formation by peptides corresponding to the G- and H-helices of myoglobin. *Biochemistry*, **1993**, 32, 6337-47	3.2	198
245	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
244	Insights into the structure and dynamics of unfolded proteins from nuclear magnetic resonance. *Advances in Protein Chemistry*, **2002**, 62, 311-40		183

243	Effects of buried charged groups on cysteine thiol ionization and reactivity in Escherichia coli thioredoxin: structural and functional characterization of mutants of Asp 26 and Lys 57. *Biochemistry*, **1997**, 36, 2622-36	3.2	176
242	What's in a name? Why these proteins are intrinsically disordered: Why these proteins are intrinsically disordered. *Intrinsically Disordered Proteins*, **2013**, 1, e24157		171
241	Equilibrium NMR studies of unfolded and partially folded proteins. *Nature Structural Biology*, **1998**, 5 Suppl, 499-503		169
240	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
239	Local structural plasticity of the prion protein. Analysis of NMR relaxation dynamics. *Biochemistry*, **2001**, 40, 2743-53	3.2	164
238	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
237	Three-dimensional solution structure of the reduced form of Escherichia coli thioredoxin determined by nuclear magnetic resonance spectroscopy. *Biochemistry*, **1990**, 29, 4129-36	3.2	161
236	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
235	Structural characterization of unfolded states of apomyoglobin using residual dipolar couplings. *Journal of Molecular Biology*, **2004**, 340, 1131-42	6.5	157
234	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
233	Solution conformational preferences of immunogenic peptides derived from the principal neutralizing determinant of the HIV-1 envelope glycoprotein gp120. *Biochemistry*, **1991**, 30, 9187-94	3.2	147
232	1H NMR studies of the solution conformations of an analogue of the C-peptide of ribonuclease A. *Biochemistry*, **1989**, 28, 7059-64	3.2	146
231	Structural basis for cooperative transcription factor binding to the CBP coactivator. *Journal of Molecular Biology*, **2006**, 355, 1005-13	6.5	144
230	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
229	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
228	Stabilization of a type VI turn in a family of linear peptides in water solution. *Journal of Molecular Biology*, **1994**, 243, 736-53	6.5	143
227	Comparison of backbone and tryptophan side-chain dynamics of reduced and oxidized Escherichia coli thioredoxin using 15N NMR relaxation measurements. *Biochemistry*, **1993**, 32, 426-35	3.2	140
226	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

225	Nuclear magnetic resonance methods for elucidation of structure and dynamics in disordered states. *Methods in Enzymology*, **2001**, 339, 258-70	1.7	137
224	Insights into protein folding from NMR. *Annual Review of Physical Chemistry*, **1996**, 47, 369-95	15.7	137
223	Solution structure and acetyl-lysine binding activity of the GCN5 bromodomain. *Journal of Molecular Biology*, **2000**, 304, 355-70	6.5	135
222	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
221	Expanding the proteome: disordered and alternatively folded proteins. *Quarterly Reviews of Biophysics*, **2011**, 44, 467-518	7	132
220	Mapping long-range contacts in a highly unfolded protein. *Journal of Molecular Biology*, **2002**, 322, 655-62	4.5	130
219	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
218	DNA-induced alpha-helix capping in conserved linker sequences is a determinant of binding affinity in Cys(2)-His(2) zinc fingers. *Journal of Molecular Biology*, **2000**, 295, 719-27	6.5	129
217	Conformational preferences in the Ser133-phosphorylated and non-phosphorylated forms of the kinase inducible transactivation domain of CREB. *FEBS Letters*, **1998**, 430, 317-22	3.8	125
216	Functional advantages of dynamic protein disorder. *FEBS Letters*, **2015**, 589, 2433-40	3.8	124
215	Molecular hinges in protein folding: the urea-denatured state of apomyoglobin. *Biochemistry*, **2002**, 41, 12681-6	3.2	123
214	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
213	Chemical shift dispersion and secondary structure prediction in unfolded and partly folded proteins. *FEBS Letters*, **1997**, 419, 285-9	3.8	121
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211	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
210	Native and non-native secondary structure and dynamics in the pH 4 intermediate of apomyoglobin. *Biochemistry*, **2000**, 39, 2894-901	3.2	116
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208	Structural basis for recruitment of CBP/p300 coactivators by STAT1 and STAT2 transactivation domains. *EMBO Journal*, **2009**, 28, 948-58	13	108

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206	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
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203	Divergent evolution of protein conformational dynamics in dihydrofolate reductase. *Nature Structural and Molecular Biology*, **2013**, 20, 1243-9	17.6	104
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201	Molecular basis for modulation of biological function by alternate splicing of the WilmsPtumor suppressor protein. *Proceedings of the National Academy of Sciences of the United States of America*, **2000**, 97, 11932-5	11.5	103
200	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
199	Solution structure of the cysteine-rich domain of the Escherichia coli chaperone protein DnaJ. *Journal of Molecular Biology*, **2000**, 300, 805-18	6.5	102
198	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
197	Solution structure of the TAZ2 (CH3) domain of the transcriptional adaptor protein CBP. *Journal of Molecular Biology*, **2000**, 303, 243-53	6.5	101
196	Peptide models of protein folding initiation sites. 3. The G-H helical hairpin of myoglobin. *Biochemistry*, **1993**, 32, 6356-64	3.2	101
195	Hypersensitive termination of the hypoxic response by a disordered protein switch. *Nature*, **2017**, 543, 447-451	50.4	99
194	NMR characterization of the metallo-beta-lactamase from Bacteroides fragilis and its interaction with a tight-binding inhibitor: role of an active-site loop. *Biochemistry*, **1999**, 38, 14507-14	3.2	99
193	Use of chemical shifts and coupling constants in nuclear magnetic resonance structural studies on peptides and proteins. *Methods in Enzymology*, **1994**, 239, 392-416	1.7	99
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187	Finding Our Way in the Dark Proteome. *Journal of the American Chemical Society*, **2016**, 138, 9730-42	16.4	93
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179	Expanding the Paradigm: Intrinsically Disordered Proteins and Allosteric Regulation. *Journal of Molecular Biology*, **2018**, 430, 2309-2320	6.5	82
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169	Folding propensities of peptide fragments of myoglobin. *Protein Science*, **1997**, 6, 706-16	6.3	76
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