# Peter E Wright

## List of Publications by Citations



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|---|---|---|---|
| 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 | Intrinsically unstructured proteins and their functions. *Nature Reviews Molecular Cell Biology*, **2005**, 6, 197-208 | 48.7 | 2985 |
| 331 | Intrinsically unstructured proteins: re-assessing the protein structure-function paradigm. *Journal of Molecular Biology*, **1999**, 293, 321-31 | 6.5 | 2343 |
| 330 | The role of dynamic conformational ensembles in biomolecular recognition. *Nature Chemical Biology*, **2009**, 5, 789-96 | 11.7 | 1420 |
| 329 | Intrinsically disordered proteins in cellular signalling and regulation. *Nature Reviews Molecular Cell Biology*, **2015**, 16, 18-29 | 48.7 | 1249 |
| 328 | Classification of intrinsically disordered regions and proteins. *Chemical Reviews*, **2014**, 114, 6589-631 | 68.1 | 1141 |
| 327 | Coupling of folding and binding for unstructured proteins. *Current Opinion in Structural Biology*, **2002**, 12, 54-60 | 8.1 | 1121 |
| 326 | Zinc finger proteins: new insights into structural and functional diversity. *Current Opinion in Structural Biology*, **2001**, 11, 39-46 | 8.1 | 1001 |
| 325 | Mechanism of coupled folding and binding of an intrinsically disordered protein. *Nature*, **2007**, 447, 1021-5 | 50.4 | 852 |
| 324 | Linking folding and binding. *Current Opinion in Structural Biology*, **2009**, 19, 31-8 | 8.1 | 813 |
| 323 | The dynamic energy landscape of dihydrofolate reductase catalysis. *Science*, **2006**, 313, 1638-42 | 33.3 | 778 |
| 322 | 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 |
| 321 | 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 |
| 320 | Intramolecular motions of a zinc finger DNA-binding domain from Xfin characterized by proton-detected natural abundance carbon-13 heteronuclear NMR spectroscopy. *Journal of the American Chemical Society*, **1991**, 113, 4371-4380 | 16.4 | 575 |
| 319 | Unfolded proteins and protein folding studied by NMR. *Chemical Reviews*, **2004**, 104, 3607-22 | 68.1 | 541 |
| 318 | Structural basis for DNA bending by the architectural transcription factor LEF-1. *Nature*, **1995**, 376, 791-5 | 50.4 | 524 |
| 317 | Sequence-dependent correction of random coil NMR chemical shifts. *Journal of the American Chemical Society*, **2001**, 123, 2970-8 | 16.4 | 509 |
| 316 | Conformation of peptide fragments of proteins in aqueous solution: implications for initiation of protein folding. *Biochemistry*, **1988**, 27, 7167-75 | 3.2 | 464 |

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| 315 | QRandom coilQ1H 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 |
| 314 | 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 |
| 313 | Structure, dynamics, and catalytic function of dihydrofolate reductase. *Annual Review of Biophysics and Biomolecular Structure*, **2004**, 33, 119-40 | | 384 |
| 312 | Mutual synergistic folding in recruitment of CBP/p300 by p160 nuclear receptor coactivators. *Nature*, **2002**, 415, 549-53 | 50.4 | 373 |
| 311 | An NMR perspective on enzyme dynamics. *Chemical Reviews*, **2006**, 106, 3055-79 | 68.1 | 369 |
| 310 | 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 |
| 309 | A dynamic knockout reveals that conformational fluctuations influence the chemical step of enzyme catalysis. *Science*, **2011**, 332, 234-8 | 33.3 | 350 |
| 308 | 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 |
| 307 | Structural and dynamic characterization of partially folded states of apomyoglobin and implications for protein folding. *Nature Structural Biology*, **1998**, 5, 148-55 | | 318 |
| 306 | Recommendations for the presentation of NMR structures of proteins and nucleic acids. IUPAC-IUBMB-IUPAB Inter-Union Task Group on the Standardization of Data Bases of Protein and Nucleic Acid Structures Determined by NMR Spectroscopy. *Journal of Biomolecular NMR*, **1998**, 12, 1-23 | 3 | 316 |
| 305 | 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 |
| 304 | Suppression of the effects of cross-correlation between dipolar and anisotropic chemical shift relaxation mechanisms in the measurement of spin-spin relaxation rates. *Molecular Physics*, **1992**, 75, 699-711 | 1.7 | 272 |
| 303 | High-resolution solution structures of oxidized and reduced Escherichia coli thioredoxin. *Structure*, **1994**, 2, 853-68 | 5.2 | 267 |
| 302 | 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 |
| 301 | Modulation of allostery by protein intrinsic disorder. *Nature*, **2013**, 498, 390-4 | 50.4 | 255 |
| 300 | PRAK is essential for ras-induced senescence and tumor suppression. *Cell*, **2007**, 128, 295-308 | 56.2 | 252 |
| 299 | Backbone dynamics in dihydrofolate reductase complexes: role of loop flexibility in the catalytic mechanism. *Biochemistry*, **2001**, 40, 9846-59 | 3.2 | 226 |
| 298 | Electrostatic calculations of side-chain pK(a) values in myoglobin and comparison with NMR data for histidines. *Biochemistry*, **1993**, 32, 8045-56 | 3.2 | 226 |

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| 297 | Is apomyoglobin a molten globule? Structural characterization by NMR. *Journal of Molecular Biology* , **1996**, 263, 531-8 | 6.5 | 225 |
| 296 | Backbone dynamics of the Bacillus subtilis glucose permease IIA domain determined from 15N NMR relaxation measurements. *Biochemistry*, **1992**, 31, 4394-406 | 3.2 | 223 |
| 295 | 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 |
| 294 | 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 |
| 293 | 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 |
| 292 | Peptide conformation and protein folding. *Current Opinion in Structural Biology*, **1993**, 3, 60-65 | 8.1 | 202 |
| 291 | 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 |
| 290 | 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 |
| 289 | Recommendations for the presentation of NMR structures of proteins and nucleic acids. *Journal of Molecular Biology*, **1998**, 280, 933-52 | 6.5 | 192 |
| 288 | Assemblages: functional units formed by cellular phase separation. *Journal of Cell Biology*, **2014**, 206, 579-88 | 7.3 | 187 |
| 287 | Insights into the structure and dynamics of unfolded proteins from nuclear magnetic resonance. *Advances in Protein Chemistry*, **2002**, 62, 311-40 | | 183 |
| 286 | Solution structure of the first three zinc fingers of TFIIIA bound to the cognate DNA sequence: determinants of affinity and sequence specificity. *Journal of Molecular Biology*, **1997**, 273, 183-206 | 6.5 | 171 |
| 285 | Equilibrium NMR studies of unfolded and partially folded proteins. *Nature Structural Biology*, **1998**, 5 Suppl, 499-503 | | 169 |
| 284 | 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 |
| 283 | Local structural plasticity of the prion protein. Analysis of NMR relaxation dynamics. *Biochemistry*, **2001**, 40, 2743-53 | 3.2 | 164 |
| 282 | 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 |
| 281 | 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 |
| 280 | 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 |

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| 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 | 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 |
| 277 | Structural characterization of unfolded states of apomyoglobin using residual dipolar couplings. *Journal of Molecular Biology*, **2004**, 340, 1131-42 | 6.5 | 157 |
| 276 | Biochemistry. How do proteins interact?. *Science*, **2008**, 320, 1429-30 | 33.3 | 155 |
| 275 | 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 |
| 274 | Dynamics of the dihydrofolate reductase-folate complex: catalytic sites and regions known to undergo conformational change exhibit diverse dynamical features. *Biochemistry*, **1995**, 34, 11037-48 | 3.2 | 151 |
| 273 | 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 |
| 272 | Analysis of an activator:coactivator complex reveals an essential role for secondary structure in transcriptional activation. *Molecular Cell*, **1998**, 2, 353-9 | 17.6 | 145 |
| 271 | Structural basis for cooperative transcription factor binding to the CBP coactivator. *Journal of Molecular Biology*, **2006**, 355, 1005-13 | 6.5 | 144 |
| 270 | 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 |
| 269 | 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 |
| 268 | 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 |
| 267 | Dynamics of a flexible loop in dihydrofolate reductase from Escherichia coli and its implication for catalysis. *Biochemistry*, **1994**, 33, 439-42 | 3.2 | 142 |
| 266 | 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 |
| 265 | 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 |
| 264 | Nuclear magnetic resonance methods for elucidation of structure and dynamics in disordered states. *Methods in Enzymology*, **2001**, 339, 258-70 | 1.7 | 137 |
| 263 | Insights into protein folding from NMR. *Annual Review of Physical Chemistry*, **1996**, 47, 369-95 | 15.7 | 137 |
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| 261 | Mapping of the binding interfaces of the proteins of the bacterial phosphotransferase system, HPr and IIAglc. *Biochemistry*, **1993**, 32, 32-7 | 3.2 | 134 |
| 260 | Mapping long-range contacts in a highly unfolded protein. *Journal of Molecular Biology*, **2002**, 322, 655-62 | 4.5 | 130 |
| 259 | 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 |
| 258 | 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 |
| 257 | Structure of the PHD zinc finger from human Williams-Beuren syndrome transcription factor. *Journal of Molecular Biology*, **2000**, 304, 723-9 | 6.5 | 129 |
| 256 | NMR Order Parameters of Biomolecules: A New Analytical Representation and Application to the Gaussian Axial Fluctuation Model. *Journal of the American Chemical Society*, **1994**, 116, 8426-8427 | 16.4 | 126 |
| 255 | 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 |
| 254 | Functional advantages of dynamic protein disorder. *FEBS Letters*, **2015**, 589, 2433-40 | 3.8 | 124 |
| 253 | Molecular hinges in protein folding: the urea-denatured state of apomyoglobin. *Biochemistry*, **2002**, 41, 12681-6 | 3.2 | 123 |
| 252 | 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 |
| 251 | Role of secondary structure in discrimination between constitutive and inducible activators. *Molecular and Cellular Biology*, **1999**, 19, 5601-7 | 4.8 | 122 |
| 250 | Chemical shift dispersion and secondary structure prediction in unfolded and partly folded proteins. *FEBS Letters*, **1997**, 419, 285-9 | 3.8 | 121 |
| 249 | Recommendations for the presentation of NMR structures of proteins and nucleic acids--IUPAC-IUBMB-IUPAB Inter-Union Task Group on the standardization of data bases of protein and nucleic acid structures determined by NMR spectroscopy. *FEBS Journal*, **1998**, 256, 1-15 | | 119 |
| 248 | 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 |
| 247 | Native and non-native secondary structure and dynamics in the pH 4 intermediate of apomyoglobin. *Biochemistry*, **2000**, 39, 2894-901 | 3.2 | 116 |
| 246 | Absence of a stable intermediate on the folding pathway of protein A. *Protein Science*, **1997**, 6, 1449-57 | 6.3 | 113 |
| 245 | Structural basis for recruitment of CBP/p300 coactivators by STAT1 and STAT2 transactivation domains. *EMBO Journal*, **2009**, 28, 948-58 | 13 | 108 |
| 244 | 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, 754-66 | 6.5 | 108 |

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| 243 | 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 |
| 242 | 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 |
| 241 | SANE (Structure Assisted NOE Evaluation): an automated model-based approach for NOE assignment. *Journal of Biomolecular NMR*, **2001**, 19, 321-9 | 3 | 105 |
| 240 | Divergent evolution of protein conformational dynamics in dihydrofolate reductase. *Nature Structural and Molecular Biology*, **2013**, 20, 1243-9 | 17.6 | 104 |
| 239 | 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 |
| 238 | High-resolution solution structure of reduced French bean plastocyanin and comparison with the crystal structure of poplar plastocyanin. *Journal of Molecular Biology*, **1991**, 221, 533-55 | 6.5 | 104 |
| 237 | Conformational changes in the active site loops of dihydrofolate reductase during the catalytic cycle. *Biochemistry*, **2004**, 43, 16046-55 | 3.2 | 103 |
| 236 | 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 |
| 235 | Domain packing and dynamics in the DNA complex of the N-terminal zinc fingers of TFIIIA. *Nature Structural Biology*, **1997**, 4, 605-8 | | 102 |
| 234 | 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 |
| 233 | 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 |
| 232 | Solution structure of the TAZ2 (CH3) domain of the transcriptional adaptor protein CBP. *Journal of Molecular Biology*, **2000**, 303, 243-53 | 6.5 | 101 |
| 231 | Peptide models of protein folding initiation sites. 3. The G-H helical hairpin of myoglobin. *Biochemistry*, **1993**, 32, 6356-64 | 3.2 | 101 |
| 230 | Specific interaction of the first three zinc fingers of TFIIIA with the internal control region of the Xenopus 5 S RNA gene. *Journal of Molecular Biology*, **1992**, 223, 857-71 | 6.5 | 100 |
| 229 | Hypersensitive termination of the hypoxic response by a disordered protein switch. *Nature*, **2017**, 543, 447-451 | 50.4 | 99 |
| 228 | Automated identification of functional dynamic contact networks from X-ray crystallography. *Nature Methods*, **2013**, 10, 896-902 | 21.6 | 99 |
| 227 | 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 |
| 226 | 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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| 225 | Mechanisms of transthyretin inhibition of -amyloid aggregation in vitro. *Journal of Neuroscience*, **2013**, 33, 19423-33 | 6.6 | 98 |
| 224 | Chemical shift as a probe of molecular interfaces: NMR studies of DNA binding by the three amino-terminal zinc finger domains from transcription factor IIIA. *Journal of Biomolecular NMR*, **1998**, 12, 51-71 | 3 | 98 |
| 223 | Identification of native and non-native structure in kinetic folding intermediates of apomyoglobin. *Journal of Molecular Biology*, **2006**, 355, 139-56 | 6.5 | 98 |
| 222 | Solution structure of carbonmonoxy myoglobin determined from nuclear magnetic resonance distance and chemical shift constraints. *Journal of Molecular Biology*, **1994**, 244, 183-97 | 6.5 | 97 |
| 221 | Functional role of a mobile loop of Escherichia coli dihydrofolate reductase in transition-state stabilization. *Biochemistry*, **1992**, 31, 7826-33 | 3.2 | 97 |
| 220 | 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 |
| 219 | Characterization of a folding intermediate of apoplastocyanin trapped by proline isomerization. *Biochemistry*, **1993**, 32, 12299-310 | 3.2 | 95 |
| 218 | Assignment of the proton NMR spectrum of reduced and oxidized thioredoxin: sequence-specific assignments, secondary structure, and global fold. *Biochemistry*, **1989**, 28, 7074-87 | 3.2 | 95 |
| 217 | Finding Our Way in the Dark Proteome. *Journal of the American Chemical Society*, **2016**, 138, 9730-42 | 16.4 | 93 |
| 216 | Mapping the interactions of the p53 transactivation domain with the KIX domain of CBP. *Biochemistry*, **2009**, 48, 2115-24 | 3.2 | 90 |
| 215 | Antigenic peptides. *FASEB Journal*, **1995**, 9, 37-42 | 0.9 | 89 |
| 214 | Conservation of folding pathways in evolutionarily distant globin sequences. *Nature Structural Biology*, **2000**, 7, 679-86 | | 88 |
| 213 | The apomyoglobin folding pathway revisited: structural heterogeneity in the kinetic burst phase intermediate. *Journal of Molecular Biology*, **2002**, 322, 483-9 | 6.5 | 86 |
| 212 | Peptide models of protein folding initiation sites. 2. The G-H turn region of myoglobin acts as a helix stop signal. *Biochemistry*, **1993**, 32, 6348-55 | 3.2 | 86 |
| 211 | Expanding the Paradigm: Intrinsically Disordered Proteins and Allosteric Regulation. *Journal of Molecular Biology*, **2018**, 430, 2309-2320 | 6.5 | 82 |
| 210 | Structure of the Wilms tumor suppressor protein zinc finger domain bound to DNA. *Journal of Molecular Biology*, **2007**, 372, 1227-45 | 6.5 | 82 |
| 209 | Analysis of the RelA:CBP/p300 interaction reveals its involvement in NF-B-driven transcription. *PLoS Biology*, **2013**, 11, e1001647 | 9.7 | 81 |
| 208 | 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 |

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| 207 | Quench-flow experiments combined with mass spectrometry show apomyoglobin folds through and obligatory intermediate. *Protein Science*, **1999**, 8, 45-9 | 6.3 | 80 |
| 206 | Elucidation of the protein folding landscape by NMR. *Methods in Enzymology*, **2005**, 394, 299-321 | 1.7 | 80 |
| 205 | Assignment of resonances in the 1H nuclear magnetic resonance spectrum of the carbon monoxide complex of sperm whale myoglobin by phase-sensitive two-dimensional techniques. *Journal of Molecular Biology*, **1987**, 194, 313-27 | 6.5 | 80 |
| 204 | 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 |
| 203 | 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 |
| 202 | Complete assignment of the 1H nuclear magnetic resonance spectrum of French bean plastocyanin. Application of an integrated approach to spin system identification in proteins. *Journal of Molecular Biology*, **1988**, 202, 603-22 | 6.5 | 78 |
| 201 | Improved low pH bicelle system for orienting macromolecules over a wide temperature range. *Journal of Biomolecular NMR*, **1999**, 13, 387-91 | 3 | 77 |
| 200 | Folding propensities of peptide fragments of myoglobin. *Protein Science*, **1997**, 6, 706-16 | 6.3 | 76 |
| 199 | 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 |
| 198 | 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 |
| 197 | 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 |
| 196 | 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 |
| 195 | Effect of H helix destabilizing mutations on the kinetic and equilibrium folding of apomyoglobin. *Journal of Molecular Biology*, **1999**, 285, 269-82 | 6.5 | 72 |
| 194 | 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 |
| 193 | Effect of cofactor binding and loop conformation on side chain methyl dynamics in dihydrofolate reductase. *Biochemistry*, **2004**, 43, 374-83 | 3.2 | 71 |
| 192 | A distal mutation perturbs dynamic amino acid networks in dihydrofolate reductase. *Biochemistry*, **2013**, 52, 4605-19 | 3.2 | 68 |
| 191 | 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 |
| 190 | NMR study of the interaction of plastocyanin with chromium(II) analogues of inorganic electron transfer reagents. *Biochimica Et Biophysica Acta - Bioenergetics*, **1980**, 591, 162-76 | 4.6 | 67 |

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| 189 | 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, 859-65 | 6.5 | 66 |
| 188 | NMR solution structure of the inserted domain of human leukocyte function associated antigen-1. *Journal of Molecular Biology*, **2000**, 295, 1251-64 | 6.5 | 65 |
| 187 | Changes in the apomyoglobin folding pathway caused by mutation of the distal histidine residue. *Biochemistry*, **2000**, 39, 11227-37 | 3.2 | 62 |
| 186 | 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, 533-9 | 6.5 | 62 |
| 185 | Computational methods for determining protein structures from NMR data. *Biochemical Pharmacology*, **1990**, 40, 15-22 | 6 | 62 |
| 184 | Fast and accurate fitting of relaxation dispersion data using the flexible software package GLOVE. *Journal of Biomolecular NMR*, **2013**, 56, 275-83 | 3 | 61 |
| 183 | CBP/p300 TAZ1 domain forms a structured scaffold for ligand binding. *Biochemistry*, **2005**, 44, 490-7 | 3.2 | 61 |
| 182 | Relative contributions of the zinc fingers of transcription factor IIIA to the energetics of DNA binding. *Journal of Molecular Biology*, **1994**, 244, 23-35 | 6.5 | 61 |
| 181 | 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 |
| 180 | Complete assignment of the 1H nuclear magnetic resonance spectrum of French bean plastocyanin. Sequential resonance assignments, secondary structure and global fold. *Journal of Molecular Biology*, **1988**, 202, 623-36 | 6.5 | 60 |
| 179 | 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 |
| 178 | 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 |
| 177 | Measurement of relaxation time constants for methyl groups by proton-detected heteronuclear NMR spectroscopy. *Chemical Physics Letters*, **1991**, 185, 41-46 | 2.5 | 58 |
| 176 | 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 |
| 175 | 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 |
| 174 | Localized structural fluctuations promote amyloidogenic conformations in transthyretin. *Journal of Molecular Biology*, **2013**, 425, 977-88 | 6.5 | 56 |
| 173 | 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 |
| 172 | Probing Protein/Protein Interactions with Mass Spectrometry and Isotopic Labeling: Analysis of the p21/Cdk2 Complex. *Journal of the American Chemical Society*, **1996**, 118, 5320-5321 | 16.4 | 55 |

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| 171 | Assignment of heme and distal amino acid resonances in the 1H-NMR spectra of the carbon monoxide and oxygen complexes of sperm whale myoglobin. *BBA - Proteins and Proteomics*, **1985**, 832, 175-85 | | 55 |
| 170 | High-resolution solution structure of the retinoid X receptor DNA-binding domain. *Journal of Molecular Biology*, **1998**, 281, 271-84 | 6.5 | 54 |
| 169 | NMR evidence for multiple conformations in a highly helical model peptide. *Biochemistry*, **1993**, 32, 13089-97 | 3.2 | 54 |
| 168 | Localization of sites of interaction between p23 and Hsp90 in solution. *Journal of Biological Chemistry*, **2006**, 281, 14457-64 | 5.4 | 53 |
| 167 | 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 |
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