# Lewis E Kay

## List of Publications by Year in Descending Order



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|---|---|---|---|
| 178 papers | 26,523 citations | 81 h-index | 162 g-index |
| 178 ext. papers | 28,278 ext. citations | 10.3 avg, IF | 6.96 L-index |

| # | Paper | IF | Citations |
|---|---|---|---|
| 178 | Interaction hot spots for phase separation revealed by NMR studies of a CAPRIN1 condensed phase. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118, | 11.5 | 11 |
| 177 | Allovalency observed by transferred NOE: interactions of sulfated tyrosine residues in the N-terminal segment of CCR5 with the CCL5 chemokine. *FEBS Journal*, **2021**, 288, 1648-1663 | 5.7 | 2 |
| 176 | A methyl-TROSY approach for NMR studies of high-molecular-weight DNA with application to the nucleosome core particle. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 12836-12846 | 11.5 | 18 |
| 175 | The methyl C-edited/C-filtered transferred NOE for studying protein interactions with short linear motifs. *Journal of Biomolecular NMR*, **2020**, 74, 681-693 | 3 | 3 |
| 174 | An NMR View of Protein Dynamics in Health and Disease. *Annual Review of Biophysics*, **2019**, 48, 297-319 | 21.1 | 60 |
| 173 | A Methyl-TROSY-Based H Relaxation Dispersion Experiment for Studies of Conformational Exchange in High Molecular Weight Proteins. *Angewandte Chemie - International Edition*, **2019**, 58, 6250-6254 | 16.4 | 18 |
| 172 | The evolution of solution state NMR pulse sequences through the @yesQof triple-resonance spectroscopy. *Journal of Magnetic Resonance*, **2019**, 306, 48-54 | 3 | 1 |
| 171 | A Methyl-TROSY-Based 1H Relaxation Dispersion Experiment for Studies of Conformational Exchange in High Molecular Weight Proteins. *Angewandte Chemie*, **2019**, 131, 6316-6320 | 3.6 | 1 |
| 170 | Revisiting H CPMG relaxation dispersion experiments: a simple modification can eliminate large artifacts. *Journal of Biomolecular NMR*, **2019**, 73, 641-650 | 3 | 4 |
| 169 | Probing Conformational Exchange in Weakly Interacting, Slowly Exchanging Protein Systems via Off-Resonance R Experiments: Application to Studies of Protein Phase Separation. *Journal of the American Chemical Society*, **2018**, 140, 2115-2126 | 16.4 | 22 |
| 168 | A methyl H double quantum CPMG experiment to study protein conformational exchange. *Journal of Biomolecular NMR*, **2018**, 72, 79-91 | 3 | 11 |
| 167 | Measuring Solvent Hydrogen Exchange Rates by Multifrequency Excitation N CEST: Application to Protein Phase Separation. *Journal of Physical Chemistry B*, **2018**, 122, 11206-11217 | 3.4 | 10 |
| 166 | Longitudinal relaxation optimized amide H-CEST experiments for studying slow chemical exchange processes in fully protonated proteins. *Journal of Biomolecular NMR*, **2017**, 67, 295-307 | 3 | 13 |
| 165 | Probing conformational dynamics in biomolecules via chemical exchange saturation transfer: a primer. *Journal of Biomolecular NMR*, **2017**, 67, 243-271 | 3 | 78 |
| 164 | Structural and hydrodynamic properties of an intrinsically disordered region of a germ cell-specific protein on phase separation. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, E8194-E8203 | 11.5 | 227 |
| 163 | Evolution of magnetization due to asymmetric dimerization: theoretical considerations and application to aberrant oligomers formed by apoSOD1(2SH). *Physical Chemistry Chemical Physics*, **2016**, 18, 5720-8 | 3.6 | 6 |
| 162 | Probing the free energy landscapes of ALS disease mutants of SOD1 by NMR spectroscopy. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, E6939-E6945 | 11.5 | 35 |

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| 161 | A magnet moment silenced: A tribute to my friend and mentor Alex D. Bain. *Concepts in Magnetic Resonance Part A: Bridging Education and Research*, **2016**, 45A, e21420 | 0.6 | |
| 160 | Quantitative measurement of exchange dynamics in proteins via (13)C relaxation dispersion of (13)CHD2-labeled samples. *Journal of Biomolecular NMR*, **2016**, 65, 59-64 | 3 | 8 |
| 159 | Solution NMR Spectroscopy Provides an Avenue for the Study of Functionally Dynamic Molecular Machines: The Example of Protein Disaggregation. *Journal of the American Chemical Society*, **2016**, 138, 1466-77 | 16.4 | 24 |
| 158 | Evaluating the influence of initial magnetization conditions on extracted exchange parameters in NMR relaxation experiments: applications to CPMG and CEST. *Journal of Biomolecular NMR*, **2016**, 65, 143-156 | 3 | 2 |
| 157 | Probing Invisible, Excited Protein States by Non-Uniformly Sampled Pseudo-4D CEST Spectroscopy. *Angewandte Chemie*, **2015**, 127, 10653-10657 | 3.6 | 5 |
| 156 | Probing Invisible, Excited Protein States by Non-Uniformly Sampled Pseudo-4D CEST Spectroscopy. *Angewandte Chemie - International Edition*, **2015**, 54, 10507-11 | 16.4 | 22 |
| 155 | (13)CHD2-CEST NMR spectroscopy provides an avenue for studies of conformational exchange in high molecular weight proteins. *Journal of Biomolecular NMR*, **2015**, 63, 187-99 | 3 | 26 |
| 154 | Thermal fluctuations of immature SOD1 lead to separate folding and misfolding pathways. *ELife*, **2015**, 4, e07296 | 8.9 | 67 |
| 153 | Visualizing side chains of invisible protein conformers by solution NMR. *Journal of Molecular Biology* , **2014**, 426, 763-74 | 6.5 | 48 |
| 152 | A similar in vitro and in cell lysate folding intermediate for the FF domain. *Journal of Molecular Biology*, **2014**, 426, 3214-3220 | 6.5 | 12 |
| 151 | Probing the free energy landscape of the fast-folding gpW protein by relaxation dispersion NMR. *Journal of the American Chemical Society*, **2014**, 136, 7444-51 | 16.4 | 28 |
| 150 | Bringing dynamic molecular machines into focus by methyl-TROSY NMR. *Annual Review of Biochemistry*, **2014**, 83, 291-315 | 29.1 | 162 |
| 149 | Measuring hydrogen exchange rates in invisible protein excited states. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 8820-5 | 11.5 | 37 |
| 148 | Probing non-specific interactions of Ca□+-calmodulin in E. coli lysate. *Journal of Biomolecular NMR*, **2013**, 55, 239-47 | 3 | 21 |
| 147 | An R(1□)expression for a spin in chemical exchange between two sites with unequal transverse relaxation rates. *Journal of Biomolecular NMR*, **2013**, 55, 211-8 | 3 | 27 |
| 146 | A comparative CEST NMR study of slow conformational dynamics of small GTPases complexed with GTP and GTP analogues. *Angewandte Chemie - International Edition*, **2013**, 52, 10771-4 | 16.4 | 28 |
| 145 | A Comparative CEST NMR Study of Slow Conformational Dynamics of Small GTPases Complexed with GTP and GTP Analogues. *Angewandte Chemie*, **2013**, 125, 10971-10974 | 3.6 | 5 |
| 144 | Probing slow chemical exchange at carbonyl sites in proteins by chemical exchange saturation transfer NMR spectroscopy. *Angewandte Chemie - International Edition*, **2013**, 52, 4156-9 | 16.4 | 33 |

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| 143 | Probing Slow Chemical Exchange at Carbonyl Sites in Proteins by Chemical Exchange Saturation Transfer NMR Spectroscopy. *Angewandte Chemie*, **2013**, 125, 4250-4253 | 3.6 | 4 |
| 142 | Folding of the four-helix bundle FF domain from a compact on-pathway intermediate state is governed predominantly by water motion. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 19268-73 | 11.5 | 15 |
| 141 | Structure of an intermediate state in protein folding and aggregation. *Science*, **2012**, 336, 362-6 | 33.3 | 292 |
| 140 | Studying "invisible" excited protein states in slow exchange with a major state conformation. *Journal of the American Chemical Society*, **2012**, 134, 8148-61 | 16.4 | 321 |
| 139 | NMR studies of protein structure and dynamics. 2005. *Journal of Magnetic Resonance*, **2011**, 213, 477-91 | 3 | 10 |
| 138 | Divided-evolution-based pulse scheme for quantifying exchange processes in proteins: powerful complement to relaxation dispersion experiments. *Journal of the American Chemical Society*, **2011**, 133, 1935-45 | 16.4 | 11 |
| 137 | Determining valine side-chain rotamer conformations in proteins from methyl 13C chemical shifts: application to the 360 kDa half-proteasome. *Journal of the American Chemical Society*, **2011**, 133, 8272-81 | 16.4 | 47 |
| 136 | Kay, Lewis E.: Structure and Dynamics of Proteins Big and Small **2010**, | | 1 |
| 135 | Determination of Leu side-chain conformations in excited protein states by NMR relaxation dispersion. *Journal of the American Chemical Society*, **2010**, 132, 42-3 | 16.4 | 59 |
| 134 | Protein dynamics and conformational disorder in molecular recognition. *Journal of Molecular Recognition*, **2010**, 23, 105-16 | 2.6 | 277 |
| 133 | Methyl groups as probes of supra-molecular structure, dynamics and function. *Journal of Biomolecular NMR*, **2010**, 46, 75-87 | 3 | 133 |
| 132 | Measurement of signs of chemical shift differences between ground and excited protein states: a comparison between H(S/M)QC and R1rho methods. *Journal of Biomolecular NMR*, **2010**, 46, 205-16 | 3 | 20 |
| 131 | Observing biological dynamics at atomic resolution using NMR. *Trends in Biochemical Sciences*, **2009** , 34, 601-11 | 10.3 | 256 |
| 130 | CPMG relaxation dispersion NMR experiments measuring glycine 1H alpha and 13C alpha chemical shifts in the invisible excited states of proteins. *Journal of Biomolecular NMR*, **2009**, 45, 45-55 | 3 | 34 |
| 129 | Measuring 13Cbeta chemical shifts of invisible excited states in proteins by relaxation dispersion NMR spectroscopy. *Journal of Biomolecular NMR*, **2009**, 44, 139-55 | 3 | 38 |
| 128 | NMR spectroscopy brings invisible protein states into focus. *Nature Chemical Biology*, **2009**, 5, 808-14 | 11.7 | 342 |
| 127 | Isotope labeling methods for studies of excited protein states by relaxation dispersion NMR spectroscopy. *Nature Protocols*, **2009**, 4, 1641-8 | 18.8 | 44 |
| 126 | Accurate measurement of alpha proton chemical shifts of excited protein states by relaxation dispersion NMR spectroscopy. *Journal of the American Chemical Society*, **2009**, 131, 1915-26 | 16.4 | 65 |

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| 125 | Measurement of methyl group motional parameters of invisible, excited protein states by NMR spectroscopy. *Journal of the American Chemical Society*, **2009**, 131, 12745-54 | 16.4 | 26 |
| 124 | An analysis of the effects of 1HN-(1)HN dipolar couplings on the measurement of amide bond vector orientations in invisible protein states by relaxation dispersion NMR. *Journal of Physical Chemistry B*, **2009**, 113, 9968-77 | 3.4 | 6 |
| 123 | An improved 15N relaxation dispersion experiment for the measurement of millisecond time-scale dynamics in proteins. *Journal of Physical Chemistry B*, **2008**, 112, 5898-904 | 3.4 | 144 |
| 122 | Probing invisible, low-populated States of protein molecules by relaxation dispersion NMR spectroscopy: an application to protein folding. *Accounts of Chemical Research*, **2008**, 41, 442-51 | 24.3 | 212 |
| 121 | Probing chemical shifts of invisible states of proteins with relaxation dispersion NMR spectroscopy: how well can we do?. *Journal of the American Chemical Society*, **2008**, 130, 2667-75 | 16.4 | 142 |
| 120 | Probing structure in invisible protein states with anisotropic NMR chemical shifts. *Journal of the American Chemical Society*, **2008**, 130, 2734-5 | 16.4 | 56 |
| 119 | Using relaxation dispersion NMR spectroscopy to determine structures of excited, invisible protein states. *Journal of Biomolecular NMR*, **2008**, 41, 113-20 | 3 | 95 |
| 118 | Measurement of carbonyl chemical shifts of excited protein states by relaxation dispersion NMR spectroscopy: comparison between uniformly and selectively (13)C labeled samples. *Journal of Biomolecular NMR*, **2008**, 42, 35-47 | 3 | 62 |
| 117 | Probing side-chain dynamics in the proteasome by relaxation violated coherence transfer NMR spectroscopy. *Journal of the American Chemical Society*, **2007**, 129, 1743-50 | 16.4 | 97 |
| 116 | Three-Dimensional HMQC-NOESY, NOESY-HMQC, and NOESY-HSQC **2007**, | | 1 |
| 115 | Solution NMR of supramolecular complexes: providing new insights into function. *Nature Methods*, **2007**, 4, 697-703 | 21.6 | 138 |
| 114 | Quantitative dynamics and binding studies of the 20S proteasome by NMR. *Nature*, **2007**, 445, 618-22 | 50.4 | 415 |
| 113 | Strong coupling effects during X-pulse CPMG experiments recorded on heteronuclear ABX spin systems: artifacts and a simple solution. *Journal of Biomolecular NMR*, **2007**, 38, 41-6 | 3 | 18 |
| 112 | A single-quantum methyl 13C-relaxation dispersion experiment with improved sensitivity. *Journal of Biomolecular NMR*, **2007**, 38, 79-88 | 3 | 96 |
| 111 | Fractional 13C enrichment of isolated carbons using [1-13C]- or [2- 13C]-glucose facilitates the accurate measurement of dynamics at backbone Calpha and side-chain methyl positions in proteins. *Journal of Biomolecular NMR*, **2007**, 38, 199-212 | 3 | 145 |
| 110 | Phi-value analysis of a three-state protein folding pathway by NMR relaxation dispersion spectroscopy. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 15717-22 | 11.5 | 46 |
| 109 | Conformational instability of the MARK3 UBA domain compromises ubiquitin recognition and promotes interaction with the adjacent kinase domain. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 14336-41 | 11.5 | 39 |
| 108 | Measurement of bond vector orientations in invisible excited states of proteins. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 18473-7 | 11.5 | 154 |

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| 107 | The folding pathway of an FF domain: characterization of an on-pathway intermediate state under folding conditions by (15)N, (13)C(alpha) and (13)C-methyl relaxation dispersion and (1)H/(2)H-exchange NMR spectroscopy. *Journal of Molecular Biology*, **2007**, 372, 497-512 | 6.5 | 51 |
| 106 | New tools provide new insights in NMR studies of protein dynamics. *Science*, **2006**, 312, 224-8 | 33.3 | 638 |
| 105 | Abp1p and Fyn SH3 domains fold through similar low-populated intermediate states. *Biochemistry*, **2006**, 45, 10175-83 | 3.2 | 37 |
| 104 | Functional dynamics of human FKBP12 revealed by methyl 13C rotating frame relaxation dispersion NMR spectroscopy. *Journal of the American Chemical Society*, **2006**, 128, 5718-27 | 16.4 | 55 |
| 103 | Identification of a collapsed intermediate with non-native long-range interactions on the folding pathway of a pair of Fyn SH3 domain mutants by NMR relaxation dispersion spectroscopy. *Journal of Molecular Biology*, **2006**, 363, 958-76 | 6.5 | 73 |
| 102 | Multiple-site exchange in proteins studied with a suite of six NMR relaxation dispersion experiments: an application to the folding of a Fyn SH3 domain mutant. *Journal of the American Chemical Society*, **2005**, 127, 15602-11 | 16.4 | 84 |
| 101 | Side-chain interactions in the folding pathway of a Fyn SH3 domain mutant studied by relaxation dispersion NMR spectroscopy. *Biochemistry*, **2005**, 44, 15430-6 | 3.2 | 28 |
| 100 | Solution structure and dynamics of integral membrane proteins by NMR: a case study involving the enzyme PagP. *Methods in Enzymology*, **2005**, 394, 335-50 | 1.7 | 27 |
| 99 | NMR studies of protein structure and dynamics. *Journal of Magnetic Resonance*, **2005**, 173, 193-207 | 3 | 229 |
| 98 | Intrinsic dynamics of an enzyme underlies catalysis. *Nature*, **2005**, 438, 117-21 | 50.4 | 925 |
| 97 | Quantitative NMR spectroscopy of supramolecular complexes: dynamic side pores in ClpP are important for product release. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 16678-83 | 11.5 | 175 |
| 96 | Low-populated folding intermediates of Fyn SH3 characterized by relaxation dispersion NMR. *Nature*, **2004**, 430, 586-90 | 50.4 | 410 |
| 95 | An isotope labeling strategy for methyl TROSY spectroscopy. *Journal of Biomolecular NMR*, **2004**, 28, 165-72 | 3 | 192 |
| 94 | Nuclear magnetic resonance spectroscopy of high-molecular-weight proteins. *Annual Review of Biochemistry*, **2004**, 73, 107-46 | 29.1 | 218 |
| 93 | Model selection for the interpretation of protein side chain methyl dynamics. *Journal of Biomolecular NMR*, **2003**, 25, 325-33 | 3 | 13 |
| 92 | Methyl TROSY: explanation and experimental verification. *Magnetic Resonance in Chemistry*, **2003**, 41, 843-852 | 2.1 | 153 |
| 91 | Side chain assignments of Ile delta 1 methyl groups in high molecular weight proteins: an application to a 46 ns tumbling molecule. *Journal of the American Chemical Society*, **2003**, 125, 5701-6 | 16.4 | 45 |
| 90 | Probing residual interactions in unfolded protein states using NMR spin relaxation techniques: an application to delta131delta. *Journal of the American Chemical Society*, **2003**, 125, 11988-92 | 16.4 | 19 |

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| 89 | Ile, Leu, and Val methyl assignments of the 723-residue malate synthase G using a new labeling strategy and novel NMR methods. *Journal of the American Chemical Society*, **2003**, 125, 13868-78 | 16.4 | 279 |
| 88 | Side chain dynamics in unfolded protein states: an NMR based 2H spin relaxation study of delta131delta. *Journal of the American Chemical Society*, **2003**, 125, 1748-58 | 16.4 | 43 |
| 87 | The effects of mutations on motions of side-chains in protein L studied by 2H NMR dynamics and scalar couplings. *Journal of Molecular Biology*, **2003**, 329, 551-63 | 6.5 | 54 |
| 86 | A "three-pronged" binding mechanism for the SAP/SH2D1A SH2 domain: structural basis and relevance to the XLP syndrome. *EMBO Journal*, **2002**, 21, 314-23 | 13 | 73 |
| 85 | Solution structure and dynamics of the outer membrane enzyme PagP by NMR. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 13560-5 | 11.5 | 282 |
| 84 | Multidimensional 2H-Based NMR Methods for Resonance Assignment, Structure Determination, and The Study of Protein Dynamics **2002**, 27-74 | | 2 |
| 83 | Four-dimensional NMR spectroscopy of a 723-residue protein: chemical shift assignments and secondary structure of malate synthase g. *Journal of the American Chemical Society*, **2002**, 124, 10025-35 | 16.4 | 205 |
| 82 | Reconstructing NMR spectra of "invisible" excited protein states using HSQC and HMQC experiments. *Journal of the American Chemical Society*, **2002**, 124, 12352-60 | 16.4 | 155 |
| 81 | Distribution of molecular size within an unfolded state ensemble using small-angle X-ray scattering and pulse field gradient NMR techniques. *Journal of Molecular Biology*, **2002**, 316, 101-12 | 6.5 | 158 |
| 80 | Deuterium spin probes of side-chain dynamics in proteins. 2. Spectral density mapping and identification of nanosecond time-scale side-chain motions. *Journal of the American Chemical Society*, **2002**, 124, 6449-60 | 16.4 | 115 |
| 79 | Direct structure refinement of high molecular weight proteins against residual dipolar couplings and carbonyl chemical shift changes upon alignment: an application to maltose binding protein. *Journal of Biomolecular NMR*, **2001**, 21, 31-40 | 3 | 46 |
| 78 | Multidimensional NMR methods for protein structure determination. *IUBMB Life*, **2001**, 52, 291-302 | 4.7 | 95 |
| 77 | Latent and active p53 are identical in conformation. *Nature Structural Biology*, **2001**, 8, 756-60 | | 227 |
| 76 | Studying excited states of proteins by NMR spectroscopy. *Nature Structural Biology*, **2001**, 8, 932-5 | | 332 |
| 75 | Slow dynamics in folded and unfolded states of an SH3 domain. *Journal of the American Chemical Society*, **2001**, 123, 11341-52 | 16.4 | 408 |
| 74 | Nuclear magnetic resonance methods for high molecular weight proteins: a study involving a complex of maltose binding protein and beta-cyclodextrin. *Methods in Enzymology*, **2001**, 339, 174-203 | 1.7 | 47 |
| 73 | Ligand-induced structural changes to maltodextrin-binding protein as studied by solution NMR spectroscopy. *Journal of Molecular Biology*, **2001**, 309, 961-74 | 6.5 | 114 |
| 72 | Measurement of (13)C(alpha)-(13)C(beta) dipolar couplings in (15)N,(13)C,(2)H-labeled proteins: application to domain orientation in maltose binding protein. *Journal of the American Chemical Society*, **2001**, 123, 2858-64 | 16.4 | 25 |

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|---|---|---|---|
| 71 | The NMR structure of the 38 kDa U1A protein - PIE RNA complex reveals the basis of cooperativity in regulation of polyadenylation by human U1A protein. *Nature Structural Biology*, **2000**, 7, 329-35 | | 110 |
| 70 | New developments in isotope labeling strategies for protein solution NMR spectroscopy. *Current Opinion in Structural Biology*, **2000**, 10, 585-92 | 8.1 | 190 |
| 69 | Assignment of 1H(N), 15N, 13C(alpha), 13CO and 13C(beta) resonances in a 67 kDa p53 dimer using 4D-TROSY NMR spectroscopy. *Journal of Biomolecular NMR*, **2000**, 18, 173-6 | 3 | 27 |
| 68 | A method for incorporating dipolar couplings into structure calculations in cases of (near) axial symmetry of alignment. *Journal of Biomolecular NMR*, **2000**, 18, 183-8 | 3 | 13 |
| 67 | Orienting domains in proteins using dipolar couplings measured by liquid-state NMR: differences in solution and crystal forms of maltodextrin binding protein loaded with beta-cyclodextrin. *Journal of Molecular Biology*, **2000**, 295, 1265-73 | 6.5 | 181 |
| 66 | Global folds of proteins with low densities of NOEs using residual dipolar couplings: application to the 370-residue maltodextrin-binding protein. *Journal of Molecular Biology*, **2000**, 300, 197-212 | 6.5 | 147 |
| 65 | A 4D TROSY-based pulse scheme for correlating 1HNi,15Ni,13Calphai,13CO□1 chemical shifts in high molecular weight, 15N,13C, 2H labeled proteins. *Journal of Biomolecular NMR*, **1999**, 15, 309-13 | 3 | 44 |
| 64 | TROSY-based HNCO pulse sequences for the measurement of 1HN-15N, 15N-13CO, 1HN-13CO, 13CO-13C□and 1HN-13C□dipolar couplings in 15N, 13C, 2H-labeled proteins. *Journal of Biomolecular NMR*, **1999**, 14, 333-343 | 3 | 100 |
| 63 | A robust and cost-effective method for the production of Val, Leu, Ile (delta 1) methyl-protonated 15N-, 13C-, 2H-labeled proteins. *Journal of Biomolecular NMR*, **1999**, 13, 369-74 | 3 | 420 |
| 62 | TROSY Triple-Resonance Four-Dimensional NMR Spectroscopy of a 46 ns Tumbling Protein. *Journal of the American Chemical Society*, **1999**, 121, 2571-2575 | 16.4 | 139 |
| 61 | NOE data demonstrating a compact unfolded state for an SH3 domain under non-denaturing conditions. *Journal of Molecular Biology*, **1999**, 289, 619-38 | 6.5 | 149 |
| 60 | An HNCO-based Pulse Scheme for the Measurement of 13C□1H□One-bond Dipolar couplings in 15N, 13C Labeled Proteins. *Journal of Biomolecular NMR*, **1998**, 12, 325-32 | 3 | 50 |
| 59 | Subunit-specific backbone NMR assignments of a 64 kDa trp repressor/DNA complex: a role for N-terminal residues in tandem binding. *Journal of Biomolecular NMR*, **1998**, 11, 307-18 | 3 | 19 |
| 58 | Analytical description of the effect of adiabatic pulses on IS, I2S, and I3S spin systems. *Journal of Magnetic Resonance*, **1998**, 130, 169-75 | 3 | 13 |
| 57 | Independent ligand-induced folding of the RNA-binding domain and two functionally distinct antitermination regions in the phage lambda N protein. *Molecular Cell*, **1998**, 1, 265-75 | 17.6 | 84 |
| 56 | NMR structure of the bacteriophage lambda N peptide/boxB RNA complex: recognition of a GNRA fold by an arginine-rich motif. *Cell*, **1998**, 93, 289-99 | 56.2 | 229 |
| 55 | Solution structure of a TBP-TAF(II)230 complex: protein mimicry of the minor groove surface of the TATA box unwound by TBP. *Cell*, **1998**, 94, 573-83 | 56.2 | 191 |
| 54 | NMR studies of tandem WW domains of Nedd4 in complex with a PY motif-containing region of the epithelial sodium channel. *Biochemistry and Cell Biology*, **1998**, 76, 341-350 | 3.6 | 34 |

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| 53 | Significantly Improved Resolution for NOE Correlations from Valine and Isoleucine (C□) Methyl Groups in 15N,13C- and 15N,13C,2H-Labeled Proteins. *Journal of the American Chemical Society*, **1998**, 120, 4825-4831 | 16.4 | 28 |
| 52 | A study of protein side-chain dynamics from new 2H auto-correlation and 13C cross-correlation NMR experiments: application to the N-terminal SH3 domain from drk. *Journal of Molecular Biology*, **1998**, 276, 939-54 | 6.5 | 108 |
| 51 | Backbone and methyl dynamics of the regulatory domain of troponin C: anisotropic rotational diffusion and contribution of conformational entropy to calcium affinity. *Journal of Molecular Biology*, **1998**, 278, 667-86 | 6.5 | 118 |
| 50 | The use of 2H, 13C, 15N multidimensional NMR to study the structure and dynamics of proteins. *Annual Review of Biophysics and Biomolecular Structure*, **1998**, 27, 357-406 | | 511 |
| 49 | The Development of NMR Methods to Study Protein Structure and Dynamics **1998**, 285-293 | | |
| 48 | Global folds of highly deuterated, methyl-protonated proteins by multidimensional NMR. *Biochemistry*, **1997**, 36, 1389-401 | 3.2 | 231 |
| 47 | Production and Incorporation of 15N, 13C, 2H (1H-□ Methyl) Isoleucine into Proteins for Multidimensional NMR Studies. *Journal of the American Chemical Society*, **1997**, 119, 7599-7600 | 16.4 | 221 |
| 46 | Characterization of the backbone dynamics of folded and denatured states of an SH3 domain. *Biochemistry*, **1997**, 36, 2390-402 | 3.2 | 148 |
| 45 | Methods for Measurement of Intermolecular NOEs by Multinuclear NMR Spectroscopy: □ Application to a Bacteriophage □N-Peptide/boxBRNA Complex. *Journal of the American Chemical Society*, **1997**, 119, 6711-6721 | 16.4 | 529 |
| 44 | Comprehensive NOE characterization of a partially folded large fragment of staphylococcal nuclease Delta131Delta, using NMR methods with improved resolution. *Journal of Molecular Biology*, **1997**, 272, 9-20 | 6.5 | 56 |
| 43 | Contributions to protein entropy and heat capacity from bond vector motions measured by NMR spin relaxation. *Journal of Molecular Biology*, **1997**, 272, 790-804 | 6.5 | 134 |
| 42 | Solution NMR spectroscopy beyond 25 kDa. *Current Opinion in Structural Biology*, **1997**, 7, 722-31 | 8.1 | 153 |
| 41 | Specific (15)N, NH correlations for residues in(15) N, (13)C and fractionally deuterated proteins that immediately follow methyl-containing amino acids. *Journal of Biomolecular NMR*, **1997**, 10, 283-8 | 3 | 11 |
| 40 | Stereospecific assignment of the NH2 resonances from the primary amides of asparagine and glutamine side chains in isotopically labeled proteins. *Journal of Biomolecular NMR*, **1997**, 9, 306-12 | 3 | 29 |
| 39 | Triple-resonance NOESY-based experiments with improved spectral resolution: applications to structural characterization of unfolded, partially folded and folded proteins. *Journal of Biomolecular NMR*, **1997**, 9, 181-200 | 3 | 69 |
| 38 | Structure and dynamics of bacteriophage IKe major coat protein in MPG micelles by solution NMR. *Biochemistry*, **1996**, 35, 5145-57 | 3.2 | 75 |
| 37 | Assignment of 15N, 13C□13C□ and HN Resonances in an 15N,13C,2H Labeled 64 kDa Trp Repressor□Operator Complex Using Triple-Resonance NMR Spectroscopy and 2H-Decoupling. *Journal of the American Chemical Society*, **1996**, 118, 6570-6579 | 16.4 | 127 |
| 36 | Selective methyl group protonation of perdeuterated proteins. *Journal of Molecular Biology*, **1996**, 263, 627-36 | 6.5 | 272 |

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| 35 | An (H)C(CO)NH-TOCSY pulse scheme for sequential assignment of protonated methyl groups in otherwise deuterated (15)N, (13)C-labeled proteins. *Journal of Biomolecular NMR*, **1996**, 8, 351-6 | 3 | 85 |
| 34 | Protein Dynamics as Studied by Solution NMR Techniques **1996**, 241-279 | | 12 |
| 33 | Structural, Dynamic, and Folding Studies of SH2 and SH3 Domains **1996**, 35-47 | | |
| 32 | Spectral density function mapping using 15N relaxation data exclusively. *Journal of Biomolecular NMR*, **1995**, 6, 153-62 | 3 | 454 |
| 31 | Direct demonstration of an intramolecular SH2-phosphotyrosine interaction in the Crk protein. *Nature*, **1995**, 374, 477-9 | 50.4 | 128 |
| 30 | Pulsed field gradient multi-dimensional NMR methods for the study of protein structure and dynamics in solution. *Progress in Biophysics and Molecular Biology*, **1995**, 63, 277-99 | 4.7 | 126 |
| 29 | Solution Structure of a Cellulose-Binding Domain from Cellulomonas fimi by Nuclear Magnetic Resonance Spectroscopy. *Biochemistry*, **1995**, 34, 6993-7009 | 3.2 | 217 |
| 28 | Measurement of 2H T1 and T1.rho. Relaxation Times in Uniformly 13C-Labeled and Fractionally 2H-Labeled Proteins in Solution. *Journal of the American Chemical Society*, **1995**, 117, 11536-11544 | 16.4 | 263 |
| 27 | Field gradient techniques in NMR spectroscopy. *Current Opinion in Structural Biology*, **1995**, 5, 674-81 | 8.1 | 60 |
| 26 | Backbone 1H and 15N resonance assignments of the N-terminal SH3 domain of drk in folded and unfolded states using enhanced-sensitivity pulsed field gradient NMR techniques. *Journal of Biomolecular NMR*, **1994**, 4, 845-58 | 3 | 617 |
| 25 | Backbone dynamics of a free and phosphopeptide-complexed Src homology 2 domain studied by 15N NMR relaxation. *Biochemistry*, **1994**, 33, 5984-6003 | 3.2 | 1979 |
| 24 | NMR Experiments for the Measurement of Carbon Relaxation Properties in Highly Enriched, Uniformly 13C,15N-Labeled Proteins: Application to 13C.alpha. Carbons. *Journal of the American Chemical Society*, **1994**, 116, 8266-8278 | 16.4 | 167 |
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