G Marius Clore

List of Publications by Citations

561 papers	60,146 citations	116 h-index	232 g-index
592 ext. papers	62,995 ext. citations	8.8 avg, IF	7.49 L-index

#	Paper	IF	Citations
561	Crystallography & NMR system: A new software suite for macromolecular structure determination. *Acta Crystallographica Section D: Biological Crystallography*, **1998**, 54, 905-21		14106
560	The Xplor-NIH NMR molecular structure determination package. *Journal of Magnetic Resonance*, **2003**, 160, 65-73	3	1919
559	Solution structure of a calmodulin-target peptide complex by multidimensional NMR. *Science*, **1992**, 256, 632-8	33.3	1256
558	Deviations from the simple two-parameter model-free approach to the interpretation of nitrogen-15 nuclear magnetic relaxation of proteins. *Journal of the American Chemical Society*, **1990**, 112, 4989-4991	16.4	937
557	Overcoming the overlap problem in the assignment of 1H NMR spectra of larger proteins by use of three-dimensional heteronuclear 1H-15N Hartmann-Hahn-multiple quantum coherence and nuclear Overhauser-multiple quantum coherence spectroscopy: application to interleukin 1 beta. *Biochemistry*, **1990**, 29, 6150-6	3.2	914
556	A novel, highly stable fold of the immunoglobulin binding domain of streptococcal protein G. *Science*, **1991**, 253, 657-61	33.3	720
555	Determination of three-dimensional structures of proteins from interproton distance data by hybrid distance geometry-dynamical simulated annealing calculations. *FEBS Letters*, **1988**, 229, 317-24	3.8	665
554	Using XplorNIH for NMR molecular structure determination. *Progress in Nuclear Magnetic Resonance Spectroscopy*, **2006**, 48, 47-62	10.4	601
553	Theory, practice, and applications of paramagnetic relaxation enhancement for the characterization of transient low-population states of biological macromolecules and their complexes. *Chemical Reviews*, **2009**, 109, 4108-39	68.1	575
552	Determination of the three-dimensional solution structure of the C-terminal domain of cellobiohydrolase I from Trichoderma reesei. A study using nuclear magnetic resonance and hybrid distance geometry-dynamical simulated annealing. *Biochemistry*, **1989**, 28, 7241-57	3.2	496
551	Analysis of the backbone dynamics of interleukin-1 beta using two-dimensional inverse detected heteronuclear 15N-1H NMR spectroscopy. *Biochemistry*, **1990**, 29, 7387-401	3.2	488
550	Determination of three-dimensional structures of proteins by simulated annealing with interproton distance restraints. Application to crambin, potato carboxypeptidase inhibitor and barley serine proteinase inhibitor 2. *Protein Engineering, Design and Selection*, **1988**, 2, 27-38	1.9	467
549	Determination of three-dimensional structures of proteins from interproton distance data by dynamical simulated annealing from a random array of atoms. Circumventing problems associated with folding. *FEBS Letters*, **1988**, 239, 129-36	3.8	466
548	Molecular basis of human 46X,Y sex reversal revealed from the three-dimensional solution structure of the human SRY-DNA complex. *Cell*, **1995**, 81, 705-14	56.2	445
547	Three-dimensional structure of interleukin 8 in solution. *Biochemistry*, **1990**, 29, 1689-96	3.2	442
546	Structures of larger proteins in solution: three- and four-dimensional heteronuclear NMR spectroscopy. *Science*, **1991**, 252, 1390-9	33.3	427
545	NMR structure of a specific DNA complex of Zn-containing DNA binding domain of GATA-1. *Science*, **1993**, 261, 438-46	33.3	420

544	Use of dipolar 1H-15N and 1H-13C couplings in the structure determination of magnetically oriented macromolecules in solution. *Nature Structural Biology*, **1997**, 4, 732-8		408
543	Visualization of transient encounter complexes in protein-protein association. *Nature*, **2006**, 444, 383-6	50.4	352
542	A robust method for determining the magnitude of the fully asymmetric alignment tensor of oriented macromolecules in the absence of structural information. *Journal of Magnetic Resonance*, **1998**, 133, 216-21	3	350
541	Three-dimensional solution structure of the 44 kDa ectodomain of SIV gp41. *EMBO Journal*, **1998**, 17, 4572-84	13	348
540	Open-to-closed transition in apo maltose-binding protein observed by paramagnetic NMR. *Nature*, **2007**, 449, 1078-82	50.4	336
539	Crystal structure of interleukin 8: symbiosis of NMR and crystallography. *Proceedings of the National Academy of Sciences of the United States of America*, **1991**, 88, 502-6	11.5	324
538	Detecting transient intermediates in macromolecular binding by paramagnetic NMR. *Nature*, **2006**, 440, 1227-30	50.4	323
537	Atomic-resolution dynamics on the surface of amyloid-β protofibrils probed by solution NMR. *Nature*, **2011**, 480, 268-72	50.4	320
536	Three-dimensional structure of proteins determined by molecular dynamics with interproton distance restraints: application to crambin. *Proceedings of the National Academy of Sciences of the United States of America*, **1986**, 83, 3801-5	11.5	309
535	The solution structure of HIV-1 Nef reveals an unexpected fold and permits delineation of the binding surface for the SH3 domain of Hck tyrosine protein kinase. *Nature Structural and Molecular Biology*, **1996**, 3, 340-5	17.6	302
534	Measurement of Residual Dipolar Couplings of Macromolecules Aligned in the Nematic Phase of a Colloidal Suspension of Rod-Shaped Viruses. *Journal of the American Chemical Society*, **1998**, 120, 10571-10572	16.4	296
533	Direct structure refinement against residual dipolar couplings in the presence of rhombicity of unknown magnitude. *Journal of Magnetic Resonance*, **1998**, 131, 159-62	3	292
532	Ensemble approach for NMR structure refinement against (1)H paramagnetic relaxation enhancement data arising from a flexible paramagnetic group attached to a macromolecule. *Journal of the American Chemical Society*, **2004**, 126, 5879-96	16.4	285
531	Determination of three-dimensional structures of proteins and nucleic acids in solution by nuclear magnetic resonance spectroscopy. *Critical Reviews in Biochemistry and Molecular Biology*, **1989**, 24, 479-564	8.7	282
530	The solution structure of an HMG-I(Y)-DNA complex defines a new architectural minor groove binding motif. *Nature Structural Biology*, **1997**, 4, 657-65		281
529	High-resolution structure of the oligomerization domain of p53 by multidimensional NMR. *Science*, **1994**, 265, 386-91	33.3	278
528	Solution structure of the N-terminal zinc binding domain of HIV-1 integrase. *Nature Structural Biology*, **1997**, 4, 567-77		273
527	The solution conformation of the antibacterial peptide cecropin A: a nuclear magnetic resonance and dynamical simulated annealing study. *Biochemistry*, **1988**, 27, 7620-9	3.2	272

526	Solution structure of the DNA binding domain of HIV-1 integrase. *Biochemistry*, **1995**, 34, 9826-33	3.2	270
525	Intercalation, DNA kinking, and the control of transcription. *Science*, **1996**, 271, 778-84	33.3	270
524	Four-dimensional heteronuclear triple-resonance NMR spectroscopy of interleukin-1 beta in solution. *Science*, **1990**, 249, 411-4	33.3	270
523	Three-dimensional structure of potato carboxypeptidase inhibitor in solution. A study using nuclear magnetic resonance, distance geometry, and restrained molecular dynamics. *Biochemistry*, **1987**, 26, 8012-23	3.2	270
522	Application of molecular dynamics with interproton distance restraints to three-dimensional protein structure determination. A model study of crambin. *Journal of Molecular Biology*, **1986**, 191, 523-51	6.5	265
521	Multidimensional heteronuclear nuclear magnetic resonance of proteins. *Methods in Enzymology*, **1994**, 239, 349-63	1.7	231
520	R-factor, Free R, and Complete Cross-Validation for Dipolar Coupling Refinement of NMR Structures. *Journal of the American Chemical Society*, **1999**, 121, 9008-9012	16.4	225
519	Improving the Packing and Accuracy of NMR Structures with a Pseudopotential for the Radius of Gyration. *Journal of the American Chemical Society*, **1999**, 121, 2337-2338	16.4	225
518	Demonstration of positionally disordered water within a protein hydrophobic cavity by NMR. *Science*, **1995**, 267, 1813-7	33.3	225
517	Solution conformation of a heptadecapeptide comprising the DNA binding helix F of the cyclic AMP receptor protein of Escherichia coli. Combined use of 1H nuclear magnetic resonance and restrained molecular dynamics. *Journal of Molecular Biology*, **1985**, 186, 435-55	6.5	224
516	Solution structure of cyanovirin-N, a potent HIV-inactivating protein. *Nature Structural Biology*, **1998**, 5, 571-8		220
515	Sequence-specific determination of protein and peptide concentrations by absorbance at 205 nm. *Protein Science*, **2013**, 22, 851-8	6.3	219
514	Determining the structures of large proteins and protein complexes by NMR. *Trends in Biotechnology*, **1998**, 16, 22-34	15.1	219
513	Solution structure of human thioredoxin in a mixed disulfide intermediate complex with its target peptide from the transcription factor NF kappa B. *Structure*, **1995**, 3, 289-97	5.2	216
512	New methods of structure refinement for macromolecular structure determination by NMR. *Proceedings of the National Academy of Sciences of the United States of America*, **1998**, 95, 5891-8	11.5	215
511	High-resolution solution structure of the beta chemokine hMIP-1 beta by multidimensional NMR. *Science*, **1994**, 263, 1762-7	33.3	215
510	The three-dimensional structure of α-purothionin in solution: combined use of nuclear magnetic resonance, distance geometry and restrained molecular dynamics. *EMBO Journal*, **1986**, 5, 2729-2735	13	208
509	Minor groove-binding architectural proteins: structure, function, and DNA recognition. *Annual Review of Biophysics and Biomolecular Structure*, **1998**, 27, 105-31		207

508	Three-dimensional NMR spectroscopy of a protein in solution. *Nature*, **1988**, 332, 374-6	50.4	205
507	Identification by NMR of the binding surface for the histidine-containing phosphocarrier protein HPr on the N-terminal domain of enzyme I of the Escherichia coli phosphotransferase system. *Biochemistry*, **1997**, 36, 4393-8	3.2	202
506	Practical aspects of (1)H transverse paramagnetic relaxation enhancement measurements on macromolecules. *Journal of Magnetic Resonance*, **2007**, 184, 185-95	3	202
505	The impact of direct refinement against 13C alpha and 13C beta chemical shifts on protein structure determination by NMR. *Journal of Magnetic Resonance Series B*, **1995**, 106, 92-6		196
504	A palindromic regulatory site within vertebrate GATA-1 promoters requires both zinc fingers of the GATA-1 DNA-binding domain for high-affinity interaction. *Molecular and Cellular Biology*, **1996**, 16, 2238-47	4.8	193
503	Refined solution structure of the oligomerization domain of the tumour suppressor p53. *Nature Structural and Molecular Biology*, **1995**, 2, 321-33	17.6	190
502	Applications of three- and four-dimensional heteronuclear NMR spectroscopy to protein structure determination. *Progress in Nuclear Magnetic Resonance Spectroscopy*, **1991**, 23, 43-92	10.4	187
501	Assignment of the side-chain 1H and 13C resonances of interleukin-1 beta using double- and triple-resonance heteronuclear three-dimensional NMR spectroscopy. *Biochemistry*, **1990**, 29, 8172-84	3.2	181
500	Improving the quality of NMR and crystallographic protein structures by means of a conformational database potential derived from structure databases. *Protein Science*, **1996**, 5, 1067-80	6.3	180
499	How much backbone motion in ubiquitin is required to account for dipolar coupling data measured in multiple alignment media as assessed by independent cross-validation?. *Journal of the American Chemical Society*, **2004**, 126, 2923-38	16.4	179
498	Accurate and rapid docking of protein-protein complexes on the basis of intermolecular nuclear overhauser enhancement data and dipolar couplings by rigid body minimization. *Proceedings of the National Academy of Sciences of the United States of America*, **2000**, 97, 9021-5	11.5	178
497	Elucidating transient macromolecular interactions using paramagnetic relaxation enhancement. *Current Opinion in Structural Biology*, **2007**, 17, 603-16	8.1	177
496	Complete resonance assignment for the polypeptide backbone of interleukin 1 beta using three-dimensional heteronuclear NMR spectroscopy. *Biochemistry*, **1990**, 29, 3542-56	3.2	172
495	The solution structure of a specific GAGA factor-DNA complex reveals a modular binding mode. *Nature Structural Biology*, **1997**, 4, 122-32		171
494	Solution structure of the 40,000 Mr phosphoryl transfer complex between the N-terminal domain of enzyme I and HPr. *Nature Structural Biology*, **1999**, 6, 166-73		171
493	Improvements and extensions in the conformational database potential for the refinement of NMR and X-ray structures of proteins and nucleic acids. *Journal of Magnetic Resonance*, **1997**, 125, 171-7	3	170
492	Four-dimensional 13C/13C-edited nuclear Overhauser enhancement spectroscopy of a protein in solution: application to interleukin 1 beta. *Biochemistry*, **1991**, 30, 12-8	3.2	167
491	High-resolution three-dimensional structure of interleukin 1 beta in solution by three- and four-dimensional nuclear magnetic resonance spectroscopy. *Biochemistry*, **1991**, 30, 2315-23	3.2	167

490	A 500 ps molecular dynamics simulation study of interleukin-1 beta in water. Correlation with nuclear magnetic resonance spectroscopy and crystallography. *Journal of Molecular Biology*, **1992**, 226, 239-50	6.5	166
489	An efficient and cost-effective isotope labeling protocol for proteins expressed in Escherichia coli. *Journal of Biomolecular NMR*, **1998**, 11, 97-102	3	162
488	Kinetics of folding of the all-beta sheet protein interleukin-1 beta. *Science*, **1993**, 260, 1110-3	33.3	161
487	Solution structure of the constant region of nuclear envelope protein LAP2 reveals two LEM-domain structures: one binds BAF and the other binds DNA. *EMBO Journal*, **2001**, 20, 4399-407	13	160
486	Solution structure of the 30 kDa N-terminal domain of enzyme I of the Escherichia coli phosphoenolpyruvate:sugar phosphotransferase system by multidimensional NMR. *Biochemistry*, **1997**, 36, 2517-30	3.2	159
485	Correlation between 3hJNC and Hydrogen Bond Length in Proteins. *Journal of the American Chemical Society*, **1999**, 121, 6275-6279	16.4	157
484	Increased Resolution and Improved Spectral Quality in Four-Dimensional 13C/13C-Separated HMQC-NOESY-HMQC Spectra Using Pulsed Field Gradients. *Journal of Magnetic Resonance Series B*, **1993**, 101, 210-213		157
483	Internal coordinates for molecular dynamics and minimization in structure determination and refinement. *Journal of Magnetic Resonance*, **2001**, 152, 288-302	3	156
482	Defining long range order in NMR structure determination from the dependence of heteronuclear relaxation times on rotational diffusion anisotropy. *Nature Structural Biology*, **1997**, 4, 443-9		155
481	Solvent isotope effect and protein stability. *Nature Structural Biology*, **1995**, 2, 852-5		155
480	Three-dimensional solution structure of human interleukin-4 by multidimensional heteronuclear magnetic resonance spectroscopy. *Science*, **1992**, 256, 1673-7	33.3	155
479	NMR structural and kinetic characterization of a homeodomain diffusing and hopping on nonspecific DNA. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 15062-7	11.5	154
478	Visualizing transient dark states by NMR spectroscopy. *Quarterly Reviews of Biophysics*, **2015**, 48, 35-1167		152
477	Kinetics of amyloid beta monomer-to-oligomer exchange by NMR relaxation. *Journal of the American Chemical Society*, **2010**, 132, 9948-51	16.4	152
476	Crystal structure of cyanovirin-N, a potent HIV-inactivating protein, shows unexpected domain swapping. *Journal of Molecular Biology*, **1999**, 288, 403-12	6.5	152
475	Structural comparisons among the short-chain helical cytokines. *Structure*, **1994**, 2, 159-73	5.2	151
474	Autoprocessing of HIV-1 protease is tightly coupled to protein folding. *Nature Structural Biology*, **1999**, 6, 868-75		150
473	Solution structure of recombinant hirudin and the Lys-47----Glu mutant: a nuclear magnetic resonance and hybrid distance geometry-dynamical simulated annealing study. *Biochemistry*, **1989**, 28, 2601-17	3.2	150

472	The solution structure of human thioredoxin complexed with its target from Ref-1 reveals peptide chain reversal. *Structure*, **1996**, 4, 613-20	5.2	149
471	Detection of nuclear Overhauser effects between degenerate amide proton resonances by heteronuclear three-dimensional NMR spectroscopy. *Journal of the American Chemical Society*, **1990**, 112, 9020-9022	16.4	149
470	Assessing the quality of solution nuclear magnetic resonance structures by complete cross-validation. *Science*, **1993**, 261, 328-31	33.3	146
469	Structure and dynamics of KH domains from FBP bound to single-stranded DNA. *Nature*, **2002**, 415, 1051-	56.4	141
468	Exploring the limits of precision and accuracy of protein structures determined by nuclear magnetic resonance spectroscopy. *Journal of Molecular Biology*, **1993**, 231, 82-102	6.5	141
467	A powerful method of sequential proton resonance assignment in proteins using relayed 15N-1H multiple quantum coherence spectroscopy. *FEBS Letters*, **1989**, 243, 93-8	3.8	141
466	Identification and localization of bound internal water in the solution structure of interleukin 1 beta by heteronuclear three-dimensional 1H rotating-frame Overhauser 15N-1H multiple quantum coherence NMR spectroscopy. *Biochemistry*, **1990**, 29, 5671-6	3.2	138
465	The high-resolution three-dimensional solution structures of the oxidized and reduced states of human thioredoxin. *Structure*, **1994**, 2, 503-22	5.2	137
464	High-resolution three-dimensional structure of reduced recombinant human thioredoxin in solution. *Biochemistry*, **1991**, 30, 2685-98	3.2	137
463	Identification of a binding site for the human immunodeficiency virus type 1 nucleocapsid protein. *Proceedings of the National Academy of Sciences of the United States of America*, **1993**, 90, 5219-23	11.5	134
462	Determination of the three-dimensional solution structure of the antihypertensive and antiviral protein BDS-I from the sea anemone Anemonia sulcata: a study using nuclear magnetic resonance and hybrid distance geometry-dynamical simulated annealing. *Biochemistry*, **1989**, 28, 2188-98	3.2	132
461	Design of an expression system for detecting folded protein domains and mapping macromolecular interactions by NMR. *Protein Science*, **1997**, 6, 2359-64	6.3	131
460	Structure refinement of oligonucleotides by molecular dynamics with nuclear Overhauser effect interproton distance restraints: application to 5' d(C-G-T-A-C-G)2. *Journal of Molecular Biology*, **1986** , 188, 455-75	6.5	131
459	The impact of direct refinement against three-bond HN-C alpha H coupling constants on protein structure determination by NMR. *Journal of Magnetic Resonance Series B*, **1994**, 104, 99-103		130
458	Evaluation of cross-correlation effects and measurement of one-bond couplings in proteins with short transverse relaxation times. *Journal of Magnetic Resonance*, **2000**, 143, 184-96	3	129
457	Structural and dynamic characterization of the urea denatured state of the immunoglobulin binding domain of streptococcal protein G by multidimensional heteronuclear NMR spectroscopy. *Protein Science*, **1995**, 4, 2605-15	6.3	129
456	High-resolution three-dimensional structure of a single zinc finger from a human enhancer binding protein in solution. *Biochemistry*, **1990**, 29, 9324-34	3.2	129
455	The high-resolution, three-dimensional solution structure of human interleukin-4 determined by multidimensional heteronuclear magnetic resonance spectroscopy. *Biochemistry*, **1993**, 32, 6744-62	3.2	128

454	A common sense approach to peak picking in two-, three-, and four-dimensional spectra using automatic computer analysis of contour diagrams. 1991. *Journal of Magnetic Resonance*, **2011**, 213, 357-63	2	126
453	Molecular basis for synergistic transcriptional activation by Oct1 and Sox2 revealed from the solution structure of the 42-kDa Oct1.Sox2.Hoxb1-DNA ternary transcription factor complex. *Journal of Biological Chemistry*, **2004**, 279, 1449-57	5.4	125
452	Amplitudes of protein backbone dynamics and correlated motions in a small alpha/beta protein: correspondence of dipolar coupling and heteronuclear relaxation measurements. *Biochemistry*, **2004**, 43, 10678-91	3.2	124
451	Fast folding of a prototypic polypeptide: the immunoglobulin binding domain of streptococcal protein G. *Protein Science*, **1994**, 3, 1945-52	6.3	124
450	Four p53 DNA-binding domain peptides bind natural p53-response elements and bend the DNA. *Proceedings of the National Academy of Sciences of the United States of America*, **1995**, 92, 8591-5	11.5	123
449	Determination of three-dimensional structures of proteins in solution by nuclear magnetic resonance spectroscopy. *Protein Engineering, Design and Selection*, **1987**, 1, 275-88	1.9	122
448	Two-, three-, and four-dimensional NMR methods for obtaining larger and more precise three-dimensional structures of proteins in solution. *Annual Review of Biophysics and Biophysical Chemistry*, **1991**, 20, 29-63		120
447	A small single-"finger" peptide from the erythroid transcription factor GATA-1 binds specifically to DNA as a zinc or iron complex. *Proceedings of the National Academy of Sciences of the United States of America*, **1993**, 90, 1676-80	11.5	119
446	Docking of protein-protein complexes on the basis of highly ambiguous intermolecular distance restraints derived from 1H/15N chemical shift mapping and backbone 15N-1H residual dipolar couplings using conjoined rigid body/torsion angle dynamics. *Journal of the American Chemical Society*, **2003**, 125, 2902-12	16.4	117
445	Disordered water within a hydrophobic protein cavity visualized by x-ray crystallography. *Proceedings of the National Academy of Sciences of the United States of America*, **1999**, 96, 103-8	11.5	116
444	Relationship between electrostatics and redox function in human thioredoxin: characterization of pH titration shifts using two-dimensional homo- and heteronuclear NMR. *Biochemistry*, **1992**, 31, 3442-52	3.2	116
443	Three-dimensional structures of alpha and beta chemokines. *FASEB Journal*, **1995**, 9, 57-62	0.9	115
442	Structural basis for SRY-dependent 46-X,Y sex reversal: modulation of DNA bending by a naturally occurring point mutation. *Journal of Molecular Biology*, **2001**, 312, 481-99	6.5	114
441	The single Cys2-His2 zinc finger domain of the GAGA protein flanked by basic residues is sufficient for high-affinity specific DNA binding. *Proceedings of the National Academy of Sciences of the United States of America*, **1996**, 93, 2822-6	11.5	114
440	The solution structure of the human ETS1-DNA complex reveals a novel mode of binding and true side chain intercalation. *Cell*, **1995**, 83, 761-71	56.2	113
439	The impact of direct refinement against proton chemical shifts on protein structure determination by NMR. *Journal of Magnetic Resonance Series B*, **1995**, 107, 293-7		113
438	Visualizing transient events in amino-terminal autoprocessing of HIV-1 protease. *Nature*, **2008**, 455, 693-6	50.4	111
437	Design of a novel peptide inhibitor of HIV fusion that disrupts the internal trimeric coiled-coil of gp41. *Journal of Biological Chemistry*, **2002**, 277, 14238-45	5.4	111

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435	Molecular basis of sequence-specific single-stranded DNA recognition by KH domains: solution structure of a complex between hnRNP K KH3 and single-stranded DNA. *EMBO Journal*, **2002**, 21, 3476-85	13	107
434	The VMD-XPLOR visualization package for NMR structure refinement. *Journal of Magnetic Resonance*, **2001**, 149, 239-44	3	107
433	Concordance of residual dipolar couplings, backbone order parameters and crystallographic B-factors for a small alpha/beta protein: a unified picture of high probability, fast atomic motions in proteins. *Journal of Molecular Biology*, **2006**, 355, 879-86	6.5	105
432	A proton nuclear magnetic resonance study of the antihypertensive and antiviral protein BDS-I from the sea anemone Anemonia sulcata: sequential and stereospecific resonance assignment and secondary structure. *Biochemistry*, **1989**, 28, 2178-87	3.2	103
431	Young Investigator Award Lecture. Structures of larger proteins, protein-ligand and protein-DNA complexes by multidimensional heteronuclear NMR. *Protein Science*, **1994**, 3, 372-90	6.3	102
430	Solution structure of the 128 kDa enzyme I dimer from Escherichia coli and its 146 kDa complex with HPr using residual dipolar couplings and small- and wide-angle X-ray scattering. *Journal of the American Chemical Society*, **2010**, 132, 13026-45	16.4	100
429	Three-dimensional solution structure of the E3-binding domain of the dihydrolipoamide succinyltransferase core from the 2-oxoglutarate dehydrogenase multienzyme complex of Escherichia coli. *Biochemistry*, **1992**, 31, 3463-71	3.2	100
428	Transient, sparsely populated compact states of apo and calcium-loaded calmodulin probed by paramagnetic relaxation enhancement: interplay of conformational selection and induced fit. *Journal of the American Chemical Society*, **2011**, 133, 18966-74	16.4	99
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425	Identification of the contact surface of a streptococcal protein G domain complexed with a human Fc fragment. *Journal of Molecular Biology*, **1993**, 233, 331-5	6.5	98
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420	1.67-A X-ray structure of the B2 immunoglobulin-binding domain of streptococcal protein G and comparison to the NMR structure of the B1 domain. *Biochemistry*, **1992**, 31, 10449-57	3.2	96
419	Xplor-NIH for molecular structure determination from NMR and other data sources. *Protein Science*, **2018**, 27, 26-40	6.3	96

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417	1H?1H correlation via isotropic mixing of 13C magnetization, a new three-dimensional approach for assigning 1H and 13C spectra of 13C-enriched proteins. *Journal of Magnetic Resonance*, **1990**, 88, 425-431		95
416	Replica exchange simulations of transient encounter complexes in protein-protein association. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 12855-60	11.5	94
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414	Characterization of the low-temperature intermediates of the reaction of fully reduced soluble cytochrome oxidase with oxygen by electron-paramagnetic-resonance and optical spectroscopy. *Biochemical Journal*, **1980**, 185, 139-54	3.8	93
413	Long Distance Measurements up to 160 Å in the GroEL Tetradecamer Using Q-Band DEER EPR Spectroscopy. *Angewandte Chemie - International Edition*, **2016**, 55, 15905-15909	16.4	92
412	Ionization equilibria for side-chain carboxyl groups in oxidized and reduced human thioredoxin and in the complex with its target peptide from the transcription factor NF kappa B. *Biochemistry*, **1996**, 35, 7-13	3.2	90
411	A common sense approach to peak picking in two-, three-, and four-dimensional spectra using automatic computer analysis of contour diagrams. *Journal of Magnetic Resonance*, **1991**, 95, 214-220		90
410	A physical picture of atomic motions within the Dickerson DNA dodecamer in solution derived from joint ensemble refinement against NMR and large-angle X-ray scattering data. *Biochemistry*, **2007**, 46, 1152-66	3.2	88
409	Sources of and solutions to problems in the refinement of protein NMR structures against torsion angle potentials of mean force. *Journal of Magnetic Resonance*, **2000**, 146, 249-54	3	87
408	Refolding proteins by gel filtration chromatography. *FEBS Letters*, **1994**, 345, 125-30	3.8	86
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405	Solution structure of the phosphoryl transfer complex between the signal transducing proteins HPr and IIA(glucose) of the Escherichia coli phosphoenolpyruvate:sugar phosphotransferase system. *EMBO Journal*, **2000**, 19, 5635-49	13	84
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