G Marius Clore

List of Publications by Year
in descending order

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571	67,188	643 123	893 242
papers	citations	h-index	g-index

592	592	592	31996
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Crystallography & NMR System: A New Software Suite for Macromolecular Structure Determination. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 905-921.	2.5	14,711
2	The Xplor-NIH NMR molecular structure determination package. Journal of Magnetic Resonance, 2003, 160, 65-73.	2.1	2,165
3	Solution structure of a calmodulin-target peptide complex by multidimensional NMR. Science, 1992, 256, 632-638.	12.6	1,381
4	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.	13.7	1,021
5	Overcoming the overlap problem in the assignment of proton NMR spectra of larger proteins by use of three-dimensional heteronuclear proton-nitrogen-15 Hartmann-Hahn-multiple quantum coherence and nuclear Overhauser-multiple quantum coherence spectroscopy: application to interleukin 1.beta.. Biochemistry, 1989, 28, 6150-6156.	2.5	970
6	A novel, highly stable fold of the immunoglobulin binding domain of streptococcal protein G. Science, 1991, 253, 657-661.	12.6	792
7	Determination of three-dimensional structures of proteins from interproton distance data by hybrid distance geometry-dynamical simulated annealing calculations. FEBS Letters, 1988, 229, 317-324.	2.8	756
8	Using Xplorâ€“NIH for NMR molecular structure determination. Progress in Nuclear Magnetic Resonance Spectroscopy, 2006, 48, 47-62.	7.5	700
9	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, 4108-4139.	47.7	692
10	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, 7241-7257.	2.5	542
11	Analysis of the backbone dynamics of interleukin-1.beta. using two-dimensional inverse detected heteronuclear nitrogen-15-proton NMR spectroscopy. Biochemistry, 1990, 29, 7387-7401.	2.5	524
12	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, 129-136.	2.8	517
13	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.	2.1	513
14	Molecular basis of human 46X,Y sex reversal revealed from the three-dimensional solution structure of the human SRY-DNA complex. Cell, 1995, 81, 705-714.	28.9	496
15	Three-dimensional structure of interleukin 8 in solution. Biochemistry, 1990, 29, 1689-1696.	2.5	482
16	NMR structure of a specific DNA complex of Zn-containing DNA binding domain of GATA-1. Science, 1993, 261, 438-446.	12.6	477
17	Structures of larger proteins in solution: three- and four-dimensional heteronuclear NMR spectroscopy. Science, 1991, 252, 1390-1399.	12.6	470
18	Use of dipolar 1Hâ€“15N and 1Hâ€“13C couplings in the structure determination of magnetically oriented macromolecules in solution. Nature Structural Biology, 1997, 4, 732-738.	9.7	456

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19	Visualization of transient encounter complexes in proteinâ€“protein association. Nature, 2006, 444, 383-386.	27.8	397
20	Open-to-closed transition in apo maltose-binding protein observed by paramagnetic NMR. Nature, 2007, 449, 1078-1082.	27.8	390
21	Three-dimensional solution structure of the 44kDa ectodomain of SIV gp41. EMBO Journal, 1998, 17, 4572-4584.	7.8	386
22	Atomic-resolution dynamics on the surface of amyloid-Î² protofibrils probed by solution NMR. Nature, 2011, 480, 268-272.	27.8	374
23	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, 216-221.	2.1	368
24	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, 502-506.	7.1	353
25	Detecting transient intermediates in macromolecular binding by paramagnetic NMR. Nature, 2006, 440, 1227-1230.	27.8	349
26	Sequenceâ€specific determination of protein and peptide concentrations by absorbance at 205 nm. Protein Science, 2013, 22, 851-858.	7.6	342
27	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, 3801-3805.	7.1	339
28	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, 340-345.	8.2	337
29	The solution structure of an HMG-I(Y)â€“DNA complex defines a new architectural minor groove binding motif. Nature Structural Biology, 1997, 4, 657-665.	9.7	337
30	Determination of Three-Dimensional Structures of Proteins and Nucleic Acids in Solution by Nuclear Magnetic Resonance Spectroscop. Critical Reviews in Biochemistry and Molecular Biology, 1989, 24, 479-564.	5.2	330
31	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.	13.7	324
32	Four-dimensional heteronuclear triple-resonance NMR spectroscopy of interleukin-1 beta in solution. Science, 1990, 249, 411-414.	12.6	322
33	Solution Structure of the DNA Binding Domain of HIV-1 Integrase. Biochemistry, 1995, 34, 9826-9833.	2.5	321
34	Solution structure of the N-terminal zinc binding domain of HIV-1 integrase. Nature Structural Biology, 1997, 4, 567-577.	9.7	320
35	Ensemble Approach for NMR Structure Refinement against1H Paramagnetic Relaxation Enhancement Data Arising from a Flexible Paramagnetic Group Attached to a Macromolecule. Journal of the American Chemical Society, 2004, 126, 5879-5896.	13.7	317
36	High-resolution structure of the oligomerization domain of p53 by multidimensional NMR. Science, 1994, 265, 386-391.	12.6	311

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37	Direct Structure Refinement against Residual Dipolar Couplings in the Presence of Rhombicity of Unknown Magnitude. Journal of Magnetic Resonance, 1998, 131, 159-162.	2.1	303
38	Intercalation, DNA Kinking, and the Control of Transcription. Science, 1996, 271, 778-784.	12.6	297
39	The solution conformation of the antibacterial peptide cecropin A: a nuclear magnetic resonance and dynamical simulated annealing study. Biochemistry, 1988, 27, 7620-7629.	2.5	296
40	Application of molecular dynamics with interproton distance restraints to three-dimensional protein structure determination. Journal of Molecular Biology, 1986, 191, 523-551.	4.2	288
41	Three-dimensional structure of potato carboxypeptidase inhibitor in solution. A study using nuclear magnetic resonance, distance geometry, and restrained molecular dynamics. Biochemistry, 1987, 26, 8012-8023.	2.5	279
42	Three-dimensional NMR spectroscopy of a protein in solution. Nature, 1988, 332, 374-376.	27.8	258
43	Solution conformation of a heptadecapeptide comprising the DNA binding helix F of the cyclic AMP receptor protein of Escherichia coli. Journal of Molecular Biology, 1985, 186, 435-455.	4.2	256
44	[11] Multidimensional heteronuclear nuclear magnetic resonance of proteins. Methods in Enzymology, 1994, 239, 349-363.	1.0	250
45	Demonstration of positionally disordered water within a protein hydrophobic cavity by NMR. Science, 1995, 267, 1813-1817.	12.6	250
46	Solution structure of cyanovirin-N, a potent HIV-inactivating protein. Nature Structural Biology, 1998, 5, 571-578.	9.7	249
47	R-factor, FreeR, and Complete Cross-Validation for Dipolar Coupling Refinement of NMR Structures. Journal of the American Chemical Society, 1999, 121, 9008-9012.	13.7	245
48	The three-dimensional structure of Î±1-purothionin in solution: combined use of nuclear magnetic resonance, distance geometry and restrained molecular dynamics. EMBO Journal, 1986, 5, 2729-2735.	7.8	241
49	Practical aspects of 1H transverse paramagnetic relaxation enhancement measurements on macromolecules. Journal of Magnetic Resonance, 2007, 184, 185-195.	2.1	239
50	Determining the structures of large proteins and protein complexes by NMR. Trends in Biotechnology, 1998, 16, 22-34.	9.3	238
51	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.	13.7	237
52	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.	0.5	233
53	MINOR GROOVE-BINDING ARCHITECTURAL PROTEINS: Structure, Function, and DNA Recognition. Annual Review of Biophysics and Biomolecular Structure, 1998, 27, 105-131.	18.3	233
54	Applications of three- and four-dimensional heteronuclear NMR spectroscopy to protein structure determination. Progress in Nuclear Magnetic Resonance Spectroscopy, 1991, 23, 43-92.	7.5	232

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55	High-resolution solution structure of the beta chemokine hMIP-1 beta by multidimensional NMR. Science, 1994, 263, 1762-1767.	12.6	232
56	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, 5891-5898.	7.1	231
57	Solution structure of human thioredoxin in a mixed disulfide intermediate complex with its target peptide from the transcription factor NFÎºB. Structure, 1995, 3, 289-297.	3.3	228
58	Refined solution structure of the oligomerization domain of the tumour suppressor p53. Nature Structural and Molecular Biology, 1995, 2, 321-333.	8.2	218
59	Identification by NMR of the Binding Surface for the Histidine-Containing Phosphocarrier Protein HPr on the N-Terminal Domain of Enzyme I of theEscherichia coliPhosphotransferase Systemâ€. Biochemistry, 1997, 36, 4393-4398.	2.5	212
60	The Impact of Direct Refinement against 13CÎ± and 13CÎ² Chemical Shifts on Protein Structure Determination by NMR. Journal of Magnetic Resonance Series B, 1995, 106, 92-96.	1.6	203
61	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, 2238-2247.	2.3	203
62	Elucidating transient macromolecular interactions using paramagnetic relaxation enhancement. Current Opinion in Structural Biology, 2007, 17, 603-616.	5.7	201
63	Assignment of the side-chain proton and carbon-13 resonances of interleukin-1.beta. using double- and triple-resonance heteronuclear three-dimensional NMR spectroscopy. Biochemistry, 1990, 29, 8172-8184.	2.5	200
64	The solution structure of a specific GAGA factorâ€“DNA complex reveals a modular binding mode. Nature Structural Biology, 1997, 4, 122-132.	9.7	198
65	Improving the quality of NMR and crystallographic protein structures by means of a conformational database potential derived from structure databases. Protein Science, 1996, 5, 1067-1080.	7.6	197
66	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, 166-173.	9.7	194
67	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, 2923-2938.	13.7	194
68	Visualizing transient dark states by NMR spectroscopy. Quarterly Reviews of Biophysics, 2015, 48, 35-116.	5.7	194
69	1Hî—‚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.	0.5	190
70	Complete resonance assignment for the polypeptide backbone of interleukin 1.beta. using three-dimensional heteronuclear NMR spectroscopy. Biochemistry, 1990, 29, 3542-3556.	2.5	189
71	High-resolution three-dimensional structure of interleukin 1.beta. in solution by three- and four-dimensional nuclear magnetic resonance spectroscopy. Biochemistry, 1991, 30, 2315-2323.	2.5	189
72	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, 9021-9025.	7.1	186

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73	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, 4399-4407.	7.8	186
74	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, 171-177.	2.1	185
75	Four-dimensional carbon-13/carbon-13-edited nuclear Overhauser enhancement spectroscopy of a protein in solution: application to interleukin 1.beta.. Biochemistry, 1991, 30, 12-18.	2.5	182
76	Kinetics of Amyloid Î² Monomer-to-Oligomer Exchange by NMR Relaxation. Journal of the American Chemical Society, 2010, 132, 9948-9951.	13.7	179
77	Kinetics of folding of the all-beta sheet protein interleukin-1 beta. Science, 1993, 260, 1110-1113.	12.6	178
78	A 500 ps molecular dynamics simulation study of interleukin-1Î² in water. Journal of Molecular Biology, 1992, 226, 239-250.	4.2	177
79	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.	1.6	177
80	An efficient and cost-effective isotope labeling protocol for proteins expressed in Escherichia coli. Journal of Biomolecular NMR, 1998, 11, 97-102.	2.8	176
81	Defining long range order in NMR structure determination from the dependence of heteronuclear relaxation times on rotational diffusion anisotropy. Nature Structural Biology, 1997, 4, 443-449.	9.7	174
82	Solution structure of recombinant hirudin and the Lys-47 .fwdarw. Glu mutants: a nuclear magnetic resonance and hybrid distance geometry-dynamical simulated annealing study. Biochemistry, 1989, 28, 2601-2617.	2.5	173
83	A powerful method of sequential proton resonance assignment in proteins using relayed15N-1H multiple quantum coherence spectroscopy. FEBS Letters, 1989, 243, 93-98.	2.8	173
84	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, 5219-5223.	7.1	172
85	Solvent isotope effect and protein stability. Nature Structural Biology, 1995, 2, 852-855.	9.7	172
86	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, 15062-15067.	7.1	172
87	Internal Coordinates for Molecular Dynamics and Minimization in Structure Determination and Refinement. Journal of Magnetic Resonance, 2001, 152, 288-302.	2.1	170
88	Three-Dimensional Solution Structure of Human Interleukin-4 by Multidimensional Heteronuclear Magnetic Resonance Spectroscopy. Science, 1992, 256, 1673-1677.	12.6	169
89	Autoprocessing of HIV-1 protease is tightly coupled to protein folding. Nature Structural Biology, 1999, 6, 868-875.	9.7	168
90	Xplorâ€NIH for molecular structure determination from NMR and other data sources. Protein Science, 2018, 27, 26-40.	7.6	167

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91	Solution Structure of the 30 kDa N-Terminal Domain of Enzyme I of theEscherichia coliPhosphoenolpyruvate:Sugar Phosphotransferase System by Multidimensional NMRâ€. Biochemistry, 1997, 36, 2517-2530.	2.5	165
92	Correlation between3hJNCâ€˜and Hydrogen Bond Length in Proteins. Journal of the American Chemical Society, 1999, 121, 6275-6279.	13.7	165
93	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.	13.7	164
94	Theory and applications of the transferred nuclear overhauser effect to the study of the conformations of small ligands bound to proteins. Journal of Magnetic Resonance, 1982, 48, 402-417.	0.5	162
95	Structural comparisons among the short-chain helical cytokines. Structure, 1994, 2, 159-173.	3.3	162
96	Crystal structure of cyanovirin-N, a potent HIV-inactivating protein, shows unexpected domain swapping. Journal of Molecular Biology, 1999, 288, 403-412.	4.2	160
97	The solution structure of human thioredoxin complexed with its target from Ref-1 reveals peptide chain reversal. Structure, 1996, 4, 613-620.	3.3	157
98	Exploring the Limits of Precision and Accuracy of Protein Structures Determined by Nuclear Magnetic Resonance Spectroscopy. Journal of Molecular Biology, 1993, 231, 82-102.	4.2	156
99	Assessing the quality of solution nuclear magnetic resonance structures by complete cross-validation. Science, 1993, 261, 328-331.	12.6	155
100	Determination of three-dimensional structures of proteins in solution by nuclear magnetic resonance spectroscopy. Protein Engineering, Design and Selection, 1987, 1, 275-288.	2.1	153
101	Identification and localization of bound internal water in the solution structure of interleukin 1.beta. by heteronuclear three-dimensional proton rotating-fram Overhauser nitrogen-15-proton multiple quantum coherence NMR spectroscopy. Biochemistry, 1990, 29, 5671-5676.	2.5	153
102	Structure refinement of oligonucleotides by molecular dynamics with nuclear overhauser effect interproton distance restraints: Application to 5â€² d(C-G-T-A-C-G)2. Journal of Molecular Biology, 1986, 188, 455-475.	4.2	152
103	High-resolution three-dimensional structure of reduced recombinant human thioredoxin in solution. Biochemistry, 1991, 30, 2685-2698.	2.5	151
104	Structure and dynamics of KH domains from FBP bound to single-stranded DNA. Nature, 2002, 415, 1051-1056.	27.8	150
105	The high-resolution three-dimensional solution structures of the oxidized and reduced states of human thioredoxin. Structure, 1994, 2, 503-522.	3.3	149
106	Molecular Basis for Synergistic Transcriptional Activation by Oct1 and Sox2 Revealed from the Solution Structure of the 42-kDa Oct1Â·Sox2Â·Hoxb1-DNA Ternary Transcription Factor Complex. Journal of Biological Chemistry, 2004, 279, 1449-1457.	3.4	147
107	The high-resolution, three-dimensional solution structure of human interleukin-4 determined by multidimensional heteronuclear magnetic resonance spectroscopy. Biochemistry, 1993, 32, 6744-6762.	2.5	143
108	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, 2188-2198.	2.5	142

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109	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.	12.2	142
110	Evaluation of Cross-Correlation Effects and Measurement of One-Bond Couplings in Proteins with Short Transverse Relaxation Times. Journal of Magnetic Resonance, 2000, 143, 184-196.	2.1	142
111	Design of an expression system for detecting folded protein domains and mapping macromolecular interactions by NMR. Protein Science, 1997, 6, 2359-2364.	7.6	142
112	High-resolution three-dimensional structure of a single zinc finger from a human enhancer binding protein in solution. Biochemistry, 1990, 29, 9324-9334.	2.5	139
113	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, 2605-2615.	7.6	136
114	NMR structure determination of proteins and protein complexes larger than 20 kDa. Current Opinion in Chemical Biology, 1998, 2, 564-570.	6.1	134
115	Amplitudes of Protein Backbone Dynamics and Correlated Motions in a Small Î±/Î² Protein:â€‰Correspondence of Dipolar Coupling and Heteronuclear Relaxation Measurements. Biochemistry, 2004, 43, 10678-10691.	2.5	134
116	The Impact of Direct Refinement against Three-Bond HN-CÎ±H Coupling Constants on Protein Structure Determination by NMR. Journal of Magnetic Resonance Series B, 1994, 104, 99-103.	1.6	133
117	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, 2011, 213, 357-363.	2.1	133
118	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, 8591-8595.	7.1	132
119	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, 481-499.	4.2	132
120	Fast folding of a prototypic polypeptide: The immunoglobulin binding domain of streptococcal protein G. Protein Science, 1994, 3, 1945-1952.	7.6	131
121	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, 1676-1680.	7.1	130
122	Threeâ€dimensional structures of Î± and Î² chemokines. FASEB Journal, 1995, 9, 57-62.	0.5	130
123	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, 3476-3485.	7.8	128
124	Long Distance Measurements up to 160â€…Ã… in the GroEL Tetradecamer Using Qâ€Band DEER EPR Spectroscopy. Angewandte Chemie - International Edition, 2016, 55, 15905-15909.	13.8	128
125	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, 2822-2826.	7.1	127
126	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, 103-108.	7.1	126

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127	Design of a Novel Peptide Inhibitor of HIV Fusion That Disrupts the Internal Trimeric Coiled-coil of gp41. Journal of Biological Chemistry, 2002, 277, 14238-14245.	3.4	125
128	Docking of Proteinâ^'Protein Complexes on the Basis of Highly Ambiguous Intermolecular Distance Restraints Derived from1HN/15N Chemical Shift Mapping and Backbone15Nâ^'1H Residual Dipolar Couplings Using Conjoined Rigid Body/Torsion Angle Dynamics. Journal of the American Chemical Society, 2003, 125, 2902-2912.	13.7	125
129	Relationship between electrostatics and redox function in human thioredoxin: characterization of pH titration shifts using two-dimensional homo- and heteronuclear NMR. Biochemistry, 1992, 31, 3442-3452.	2.5	124
130	The solution structure of the human ETS1-DNA complex reveals a novel mode of binding and true side chain intercalation. Cell, 1995, 83, 761-771.	28.9	124
131	Visualizing transient events in amino-terminal autoprocessing of HIV-1 protease. Nature, 2008, 455, 693-696.	27.8	123
132	The Impact of Direct Refinement against Proton Chemical Shifts on Protein Structure Determination by NMR. Journal of Magnetic Resonance Series B, 1995, 107, 293-297.	1.6	119
133	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, 13026-13045.	13.7	118
134	Structure and Dynamics of Full-Length HIV-1 Capsid Protein in Solution. Journal of the American Chemical Society, 2013, 135, 16133-16147.	13.7	114
135	Solution structure of the cellular factor BAF responsible for protecting retroviral DNA from autointegration. Nature Structural Biology, 1998, 5, 903-909.	9.7	113
136	Water suppression in two-dimensional spin-locked NMR experiments using a novel phase-cycling procedure. Journal of the American Chemical Society, 1987, 109, 6511-6513.	13.7	112
137	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, 18966-18974.	13.7	112
138	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, 2178-2187.	2.5	110
139	The VMD-XPLOR Visualization Package for NMR Structure Refinement. Journal of Magnetic Resonance, 2001, 149, 239-244.	2.1	110
140	Theory of the time dependent transferred nuclear Overhauser effect: Applications to structural analysis of ligand-protein complexes in solution. Journal of Magnetic Resonance, 1983, 53, 423-442.	0.5	109
141	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, 3463-3471.	2.5	109
142	1H-Nmr stereospecific assignments by conformational data-base searches. Biopolymers, 1990, 29, 813-822.	2.4	108
143	Impact of Residual Dipolar Couplings on the Accuracy of NMR Structures Determined from a Minimal Number of NOE Restraints. Journal of the American Chemical Society, 1999, 121, 6513-6514.	13.7	108
144	Concordance of Residual Dipolar Couplings, Backbone Order Parameters and Crystallographic B-factors for a Small Î±/Î² Protein: A Unified Picture of High Probability, Fast Atomic Motions in Proteins. Journal of Molecular Biology, 2006, 355, 879-886.	4.2	108

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145	Structures of larger proteins, proteinâ€ligand and proteinâ€DNA complexes by multidimensional heteronuclear NMR. Protein Science, 1994, 3, 372-390.	7.6	107
146	Replica exchange simulations of transient encounter complexes in proteinâ€“protein association. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 12855-12860.	7.1	107
147	Stereospecific assignment of Î²-methylene protons in larger proteins using 3D15N-separated Hartmann-Hahn and13C-separated rotating frame Overhauser spectroscopy. Journal of Biomolecular NMR, 1991, 1, 13-22.	2.8	106
148	The pKa values of two histidine residues in human haemoglobin, the Bohr effect, and the dipole moments of Î±-helices. Journal of Molecular Biology, 1985, 183, 491-498.	4.2	103
149	Mapping the Topology and Determination of a Low-Resolution Three-Dimensional Structure of the Calmodulinâ^'Melittin Complex by Chemical Cross-Linking and High-Resolution FTICRMS:Â Direct Demonstration of Multiple Binding Modesâ€. Biochemistry, 2004, 43, 4703-4715.	2.5	103
150	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, 139-154.	3.7	102
151	Identification of the Contact Surface of a Streptococcal Protein G Domain Complexed with a Human Fc Fragment. Journal of Molecular Biology, 1993, 233, 331-335.	4.2	102
152	1.67-.ANG. 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, 10449-10457.	2.5	101
153	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 Dataâ€. Biochemistry, 2007, 46, 1152-1166.	2.5	99
154	Probing exchange kinetics and atomic resolution dynamics in high-molecular-weight complexes using dark-state exchange saturation transfer NMR spectroscopy. Nature Protocols, 2012, 7, 1523-1533.	12.0	98
155	The conformations of hirudin in solution: a study using nuclear magnetic resonance, distance geometry and restrained molecular dynamics. EMBO Journal, 1987, 6, 529-537.	7.8	97
156	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 NFÎºBâ€. Biochemistry, 1996, 35, 7-13.	2.5	97
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