Gaetano T Montelione

List of Publications by Year
in descending order

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153 papers	10,497 citations	31902 53 h-index	39575 94 g-index
164 all docs	164 docs citations	164 times ranked	10912 citing authors

#	Article	IF	Citations
1	Structural evolution of the ancient enzyme, dissimilatory sulfite reductase. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1331-1345.	1.5	5
2	SETD4-mediated KU70 methylation suppresses apoptosis. Cell Reports, 2022, 39, 110794.	2.9	4
3	Oligomeric interactions maintain activeâ€site structure in a noncooperative enzyme family. EMBO Journal, 2022, 41, .	3.5	10
4	REDCRAFT: A computational platform using residual dipolar coupling NMR data for determining structures of perdeuterated proteins in solution. PLoS Computational Biology, 2021, 17, e1008060.	1.5	8
5	Hepatitis C virus drugs that inhibit SARS-CoV-2 papain-like protease synergize with remdesivir to suppress viral replication in cell culture. Cell Reports, 2021, 35, 109133.	2.9	53
6	Role of backbone strain in de novo design of complex Î±/Î² protein structures. Nature Communications, 2021, 12, 3921.	5.8	16
7	A common binding motif in the ET domain of BRD3 forms polymorphic structural interfaces with host and viral proteins. Structure, 2021, 29, 886-898.e6.	1.6	16
8	Assessment of prediction methods for protein structures determined by <scp>NMR</scp> in <scp>CASP14</scp>: Impact of <scp>AlphaFold2</scp>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1959-1976.	1.5	30
9	ZapG (YhcB/DUF1043), a novel cell division protein in gamma-proteobacteria linking the Z-ring to septal peptidoglycan synthesis. Journal of Biological Chemistry, 2021, 296, 100700.	1.6	9
10	De novo protein design by deep network hallucination. Nature, 2021, 600, 547-552.	13.7	280
11	Evolutionary coupling saturation mutagenesis: Coevolutionâ€guided identification of distant sites influencing Bacillus naganoensis pullulanase activity. FEBS Letters, 2020, 594, 799-812.	1.3	22
12	High-Throughput PIXE as an Essential Quantitative Assay for Accurate Metalloprotein Structural Analysis: Development and Application. Journal of the American Chemical Society, 2020, 142, 185-197.	6.6	24
13	A double-stranded RNA platform is required for the interaction between a host restriction factor and the NS1 protein of influenza A virus. Nucleic Acids Research, 2020, 48, 304-315.	6.5	14
14	Tribute to Harold A. Scheraga. Journal of Physical Chemistry B, 2020, 124, 10301-10302.	1.2	0
15	Protein structure prediction assisted with sparse NMR data in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1315-1332.	1.5	21
16	Structural Basis by Which the N-Terminal Polypeptide Segment of Rhizopus chinensis Lipase Regulates Its Substrate Binding Affinity. Biochemistry, 2019, 58, 3943-3954.	1.2	14
17	De novo protein design by citizen scientists. Nature, 2019, 570, 390-394.	13.7	105
18	A Proteomic Screen of Neuronal Cell-Surface Molecules Reveals IgLONs as Structurally Conserved Interaction Modules at the Synapse. Structure, 2019, 27, 893-906.e9.	1.6	44

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19	Combining Evolutionary Covariance and NMR Data for Protein Structure Determination. Methods in Enzymology, 2019, 614, 363-392.	0.4	8
20	The copBL operon protects Staphylococcus aureus from copper toxicity: CopL is an extracellular membraneâ€“associated copper-binding protein. Journal of Biological Chemistry, 2019, 294, 4027-4044.	1.6	34
21	An ELISA-Based Screening Platform for Ligandâ€“Receptor Discovery. Methods in Enzymology, 2019, 615, 453-475.	0.4	18
22	Effect of mitochondrial uncouplers niclosamide ethanolamine (NEN) and oxyclozanide on hepatic metastasis of colon cancer. Cell Death and Disease, 2018, 9, 215.	2.7	62
23	A toolbox of immunoprecipitation-grade monoclonal antibodies to human transcription factors. Nature Methods, 2018, 15, 330-338.	9.0	58
24	Backbone and Ile-Î´1, Leu, Val methyl 1H, 15N, and 13C, chemical shift assignments for Rhizopus chinensis lipase. Biomolecular NMR Assignments, 2018, 12, 63-68.	0.4	3
25	A Hybrid Approach for Protein Structure Determination Combining Sparse NMR with Evolutionary Coupling Sequence Data. Advances in Experimental Medicine and Biology, 2018, 1105, 153-169.	0.8	7
26	Antiparallel Coiled-Coil Interactions Mediate the Homodimerization of the DNA Damage-Repair Protein PALB2. Biochemistry, 2018, 57, 6581-6591.	1.2	17
27	Minimal Heterochiral de Novo Designed 4Feâ€“4S Binding Peptide Capable of Robust Electron Transfer. Journal of the American Chemical Society, 2018, 140, 11210-11213.	6.6	42
28	Xâ€ray crystal structure of the Nâ€terminal region of <scp>M</scp>oloney murine leukemia virus integrase and its implications for viral DNA recognition. Proteins: Structure, Function and Bioinformatics, 2017, 85, 647-656.	1.5	9
29	Principles for designing proteins with cavities formed by curved Î² sheets. Science, 2017, 355, 201-206.	6.0	117
30	Multiple helical conformations of the helixâ€turnâ€helix region revealed by NOEâ€restrained MD simulations of tryptophan aporepressor, TrpR. Proteins: Structure, Function and Bioinformatics, 2017, 85, 731-740.	1.5	6
31	Cover Image, Volume 85, Issue 4. Proteins: Structure, Function and Bioinformatics, 2017, 85, C1.	1.5	0
32	¹³C metabolic flux profiling of Pichia pastoris grown in aerobic batch cultures on glucose revealed high relative anabolic use of <scp>TCA</scp> cycle and limited incorporation of provided precursors of branchedâ€chain amino acids. FEBS Journal, 2017, 284, 3100-3113.	2.2	10
33	NMR characterization of HtpG, the E. coli Hsp90, using sparse labeling with 13C-methyl alanine. Journal of Biomolecular NMR, 2017, 68, 225-236.	1.6	15
34	Aromatic claw: A new fold with high aromatic content that evades structural prediction. Protein Science, 2017, 26, 208-217.	3.1	0
35	Introduction of a polar core into the de novo designed protein <scp>T</scp>op7. Protein Science, 2016, 25, 1299-1307.	3.1	7
36	Efficient production of 2H, 13C, 15N-enriched industrial enzyme Rhizopus chinensis lipase with native disulfide bonds. Microbial Cell Factories, 2016, 15, 123.	1.9	8

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37	A community resource of experimental data for <scp>NMR</scp> / <scp>X</scp>â€ray crystal structure pairs. Protein Science, 2016, 25, 30-45.	3.1	24
38	A Second RNA-Binding Site in the NS1 Protein of Influenza B Virus. Structure, 2016, 24, 1562-1572.	1.6	12
39	Structural/Functional Properties of Human NFU1, an Intermediate [4Fe-4S] Carrier in Human Mitochondrial Iron-Sulfur Cluster Biogenesis. Structure, 2016, 24, 2080-2091.	1.6	45
40	Precise assembly of complex beta sheet topologies from de novo designed building blocks. ELife, 2015, 4, .	2.8	15
41	Aspirinâ€™s Active Metabolite Salicylic Acid Targets High Mobility Group Box 1 to Modulate Inflammatory Responses. Molecular Medicine, 2015, 21, 526-535.	1.9	97
42	NMR Exchange Format: a unified and open standard for representation of NMR restraint data. Nature Structural and Molecular Biology, 2015, 22, 433-434.	3.6	40
43	Structural and sequencing analysis of local target DNA recognition by MLV integrase. Nucleic Acids Research, 2015, 43, 5647-5663.	6.5	26
44	A hybrid NMR/SAXSâ€based approach for discriminating oligomeric protein interfaces using <scp>R</scp>osetta. Proteins: Structure, Function and Bioinformatics, 2015, 83, 309-317.	1.5	33
45	The RAS-Binding Domain of Human BRAF Protein Serine/Threonine Kinase Exhibits Allosteric Conformational Changes upon Binding HRAS. Structure, 2015, 23, 1382-1393.	1.6	31
46	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. Structure, 2015, 23, 1156-1167.	1.6	159
47	Protein structure determination by combining sparse NMR data with evolutionary couplings. Nature Methods, 2015, 12, 751-754.	9.0	75
48	The second round of Critical Assessment of Automated Structure Determination of Proteins by NMR: CASD-NMR-2013. Journal of Biomolecular NMR, 2015, 62, 413-424.	1.6	27
49	Control over overall shape and size in de novo designed proteins. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5478-85.	3.3	113
50	Analysis of the structural quality of the CASD-NMR 2013 entries. Journal of Biomolecular NMR, 2015, 62, 527-540.	1.6	4
51	Guiding automated NMR structure determination using a global optimization metric, the NMR DP score. Journal of Biomolecular NMR, 2015, 62, 439-451.	1.6	16
52	A General Computational Approach for Repeat Protein Design. Journal of Molecular Biology, 2015, 427, 563-575.	2.0	72
53	Polypeptide backbone, CÎ² and methyl group resonance assignments of the 24ÂkDa plectin repeat domain 6 from human protein plectin. Biomolecular NMR Assignments, 2015, 9, 135-138.	0.4	0
54	Structural and Functional Characterization of DUF1471 Domains of Salmonella Proteins SrfN, YdgH/SssB, and YahO. PLoS ONE, 2014, 9, e101787.	1.1	13

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55	The expanded FindCore method for identification of a core atom set for assessment of protein structure prediction. Proteins: Structure, Function and Bioinformatics, 2014, 82, 219-230.	1.5	20
56	Assessment of templateâ€based protein structure predictions in CASP10. Proteins: Structure, Function and Bioinformatics, 2014, 82, 43-56.	1.5	93
57	Allosteric regulation and substrate activation in cytosolic nucleotidase <scp>II</scp> from <scp>L</scp>egionellaÂpneumophila. FEBS Journal, 2014, 281, 1613-1628.	2.2	29
58	Altering murine leukemia virus integration through disruption of the integrase and BET protein family interaction. Nucleic Acids Research, 2014, 42, 5917-5928.	6.5	63
59	Structure of the DNA-Binding and RNA-Polymerase-Binding Region of Transcription Antitermination Factor Î»Q. Structure, 2014, 22, 488-495.	1.6	14
60	Protein NMR Structures Refined with Rosetta Have Higher Accuracy Relative to Corresponding X-ray Crystal Structures. Journal of the American Chemical Society, 2014, 136, 1893-1906.	6.6	65
61	Structure-Guided Functional Characterization of Enediyne Self-Sacrifice Resistance Proteins, CalU16 and CalU19. ACS Chemical Biology, 2014, 9, 2347-2358.	1.6	24
62	19F NMR Reveals Multiple Conformations at the Dimer Interface of the Nonstructural Protein 1 Effector Domain from Influenza A Virus. Structure, 2014, 22, 515-525.	1.6	41
63	DisMeta: A Meta Server for Construct Design and Optimization. Methods in Molecular Biology, 2014, 1091, 3-16.	0.4	64
64	Comparing Chemistry to Outcome: The Development of a Chemical Distance Metric, Coupled with Clustering and Hierarchal Visualization Applied to Macromolecular Crystallography. PLoS ONE, 2014, 9, e100782.	1.1	14
65	PDBStat: a universal restraint converter and restraint analysis software package for protein NMR. Journal of Biomolecular NMR, 2013, 56, 337-351.	1.6	59
66	Quality assessment of protein NMR structures. Current Opinion in Structural Biology, 2013, 23, 715-724.	2.6	31
67	Recommendations of the wwPDB NMR Validation Task Force. Structure, 2013, 21, 1563-1570.	1.6	151
68	RPF: a quality assessment tool for protein NMR structures. Nucleic Acids Research, 2012, 40, W542-W546.	6.5	55
69	Determination of solution structures of proteins up to 40ÂkDa using CS-Rosetta with sparse NMR data from deuterated samples. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 10873-10878.	3.3	188
70	Principles for designing ideal protein structures. Nature, 2012, 491, 222-227.	13.7	522
71	Accurate protein structure modeling using sparse NMR data and homologous structure information. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9875-9880.	3.3	37
72	Solution NMR Structure of Yeast Succinate Dehydrogenase Flavinylation Factor Sdh5 Reveals a Putative Sdh1 Binding Site. Biochemistry, 2012, 51, 8475-8477.	1.2	29

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73	Structure of a Specialized Acyl Carrier Protein Essential for Lipid A Biosynthesis with Very Long-Chain Fatty Acids in Open and Closed Conformations. Biochemistry, 2012, 51, 7239-7249.	1.2	14
74	Blind Testing of Routine, Fully Automated Determination of Protein Structures from NMR Data. Structure, 2012, 20, 227-236.	1.6	75
75	The Protein Structure Initiative: achievements and visions for the future. F1000 Biology Reports, 2012, 4, 7.	4.0	49
76	Determination of the Structures of Symmetric Protein Oligomers from NMR Chemical Shifts and Residual Dipolar Couplings. Journal of the American Chemical Society, 2011, 133, 6288-6298.	6.6	65
77	Preparation of Protein Samples for NMR Structure, Function, and Small-Molecule Screening Studies. Methods in Enzymology, 2011, 493, 21-60.	0.4	89
78	Improved Technologies Now Routinely Provide Protein NMR Structures Useful for Molecular Replacement. Structure, 2011, 19, 757-766.	1.6	34
79	The Use of the Condensed Single Protein Production System for Isotope-Labeled Outer Membrane Proteins, OmpA and OmpX in E. coli. Molecular Biotechnology, 2011, 47, 205-210.	1.3	16
80	Small angle Xâ€ray scattering as a complementary tool for highâ€throughput structural studies. Biopolymers, 2011, 95, 517-530.	1.2	69
81	Dimer Interface of the Effector Domain of Non-structural Protein 1 from Influenza A Virus. Journal of Biological Chemistry, 2011, 286, 26050-26060.	1.6	58
82	Structural basis for the sequence-specific recognition of human ISG15 by the NS1 protein of influenza B virus. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 13468-13473.	3.3	56
83	A microscale protein NMR sample screening pipeline. Journal of Biomolecular NMR, 2010, 46, 11-22.	1.6	106
84	Efficient condensed-phase production of perdeuterated soluble and membrane proteins. Journal of Structural and Functional Genomics, 2010, 11, 143-154.	1.2	18
85	Engineering of a wheat germ expression system to provide compatibility with a high throughput pET-based cloning platform. Journal of Structural and Functional Genomics, 2010, 11, 201-209.	1.2	10
86	Threeâ€dimensional structure of the weakly associated protein homodimer SeR13 using RDCs and paramagnetic surface mapping. Protein Science, 2010, 19, 1673-1685.	3.1	19
87	NMR Structure Determination for Larger Proteins Using Backbone-Only Data. Science, 2010, 327, 1014-1018.	6.0	245
88	Accurate Automated Protein NMR Structure Determination Using Unassigned NOESY Data. Journal of the American Chemical Society, 2010, 132, 202-207.	6.6	47
89	The high-throughput protein sample production platform of the Northeast Structural Genomics Consortium. Journal of Structural Biology, 2010, 172, 21-33.	1.3	125
90	Advances in protein NMR provided by the NIGMS Protein Structure Initiative: impact on drug discovery. Current Opinion in Drug Discovery & Development, 2010, 13, 335-49.	1.9	7

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91	Unique opportunities for NMR methods in structural genomics. Journal of Structural and Functional Genomics, 2009, 10, 101-106.	1.2	25
92	Independently inducible system of gene expression for condensed single protein production (cSPP) suitable for high efficiency isotope enrichment. Journal of Structural and Functional Genomics, 2009, 10, 219-225.	1.2	18
93	Improving NMR protein structure quality by Rosetta refinement: A molecular replacement study. Proteins: Structure, Function and Bioinformatics, 2009, 75, 147-167.	1.5	57
94	Construct optimization for protein NMR structure analysis using amide hydrogen/deuterium exchange mass spectrometry. Proteins: Structure, Function and Bioinformatics, 2009, 76, 882-894.	1.5	33
95	CASD-NMR: critical assessment of automated structure determination by NMR. Nature Methods, 2009, 6, 625-626.	9.0	80
96	Assessing model accuracy using the homology modeling automatically software. Proteins: Structure, Function and Bioinformatics, 2008, 70, 105-118.	1.5	42
97	Protein production and purification. Nature Methods, 2008, 5, 135-146.	9.0	763
98	Contributions to the NIH-NIGMS Protein Structure Initiative from the PSI Production Centers. Structure, 2008, 16, 5-11.	1.6	58
99	Targeting the Human Cancer Pathway Protein Interaction Network by Structural Genomics. Molecular and Cellular Proteomics, 2008, 7, 2048-2060.	2.5	70
100	Structural basis for suppression of a host antiviral response by influenza A virus. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 13093-13098.	3.3	193
101	Conserved Surface Features Form the Double-stranded RNA Binding Site of Non-structural Protein 1 (NS1) from Influenza A and B Viruses. Journal of Biological Chemistry, 2007, 282, 20584-20592.	1.6	80
102	A large data set comparison of protein structures determined by crystallography and NMR: Statistical test for structural differences and the effect of crystal packing. Proteins: Structure, Function and Bioinformatics, 2007, 69, 449-465.	1.5	113
103	Novel leverage of structural genomics. Nature Biotechnology, 2007, 25, 849-851.	9.4	59
104	SPINS: A laboratory information management system for organizing and archiving intermediate and final results from NMR protein structure determinations. Proteins: Structure, Function and Bioinformatics, 2006, 62, 843-851.	1.5	11
105	Evaluating protein structures determined by structural genomics consortia. Proteins: Structure, Function and Bioinformatics, 2006, 66, 778-795.	1.5	663
106	Proteins flex to function. Nature, 2005, 438, 36-37.	13.7	84
107	Clustering algorithms for identifying core atom sets and for assessing the precision of protein structure ensembles. Proteins: Structure, Function and Bioinformatics, 2005, 59, 673-686.	1.5	46
108	Assessing precision and accuracy of protein structures derived from NMR data. Proteins: Structure, Function and Bioinformatics, 2005, 59, 655-661.	1.5	51

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109	A topology-constrained distance network algorithm for protein structure determination from NOESY data. Proteins: Structure, Function and Bioinformatics, 2005, 62, 587-603.	1.5	121
110	An Integrated Platform for Automated Analysis of Protein NMR Structures. Methods in Enzymology, 2005, 394, 111-141.	0.4	67
111	Robotic Cloning and Protein Production Platform of the Northeast Structural Genomics Consortium. Methods in Enzymology, 2005, 394, 210-243.	0.4	118
112	NMR data collection and analysis protocol for high-throughput protein structure determination. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10487-10492.	3.3	108
113	Protein NMR Recall, Precision, andF-measure Scores (RPF Scores):Â Structure Quality Assessment Measures Based on Information Retrieval Statistics. Journal of the American Chemical Society, 2005, 127, 1665-1674.	6.6	246
114	Assignment validation software suite for the evaluation and presentation of protein resonance assignment data. Journal of Biomolecular NMR, 2004, 28, 341-355.	1.6	94
115	Biophysical Characterization of the Complex between Double-Stranded RNA and the N-Terminal Domain of the NS1 Protein from Influenza A Virus:â€‰ Evidence for a Novel RNA-Binding Mode. Biochemistry, 2004, 43, 1950-1962.	1.2	107
116	Automated Analysis of Protein NMR Assignments and Structures. Chemical Reviews, 2004, 104, 3541-3556.	23.0	90
117	TOUCHSTONEX: Protein structure prediction with sparse NMR data. Proteins: Structure, Function and Bioinformatics, 2003, 53, 290-306.	1.5	38
118	Automated protein fold determination using a minimal NMR constraint strategy. Protein Science, 2003, 12, 1232-1246.	3.1	53
119	SPINE 2: a system for collaborative structural proteomics within a federated database framework. Nucleic Acids Research, 2003, 31, 2833-2838.	6.5	55
120	Structural Proteomics of Eukaryotic Gene Families. Scientific World Journal, The, 2002, 2, 32-32.	0.8	0
121	Rapid analysis of protein backbone resonance assignments using cryogenic probes, a distributed Linux-based computing architecture, and an integrated set of spectral analysis tools. Journal of Structural and Functional Genomics, 2002, 2, 93-101.	1.2	38
122	SPINS: standardized protein NMR storage. A data dictionary and object-oriented relational database for archiving protein NMR spectra. Journal of Biomolecular NMR, 2002, 24, 113-121.	1.6	19
123	Automatic Determination of Protein Backbone Resonance Assignments from Triple Resonance Nuclear Magnetic Resonance Data. Methods in Enzymology, 2001, 339, 91-108.	0.4	154
124	X-ray crystal structure of MTH938 fromMethanobacterium thermoautotrophicumat 2.2 Ã... resolution reveals a novel tertiary protein fold. Proteins: Structure, Function and Bioinformatics, 2001, 45, 486-488.	1.5	5
125	Resonance assignments for the N-terminal domain from human RNA-binding protein with multiple splicing (RBP-MS). Journal of Biomolecular NMR, 2001, 19, 285-286.	1.6	0
126	Resonance assignments for cold-shock protein ribosome-binding factor A (RbfA) from Escherichia coli. Journal of Biomolecular NMR, 2001, 21, 389-390.	1.6	7

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127	Lipari-Szabo mapping: A graphical approach to Lipari-Szabo analysis of NMR relaxation data using reduced spectral density mapping. Journal of Biomolecular NMR, 2000, 18, 83-100.	1.6	18
128	Partial NMR assignments for uniformly (13C, 15N)-enriched BPTI in the solid state. Journal of Biomolecular NMR, 2000, 16, 209-219.	1.6	232
129	Solution NMR evidence for a cis Tyrâ€Ala peptide group in the structure of [Pro93Ala] bovine pancreatic ribonuclease A. Protein Science, 2000, 9, 421-426.	3.1	10
130	Structural genomics: keystone for a Human Proteome Project. , 1999, 6, 11-12.		115
131	Comparison of Local and Global Stability of an Analogue of a Disulfide-Folding Intermediate with Those of the Wild-Type Protein in Bovine Pancreatic Ribonuclease A:Â Identification of Specific Regions of Stable Structure along the Oxidative Folding Pathwayâ€. Biochemistry, 1999, 38, 16432-16442.	1.2	15
132	RNA binding by the novel helical domain of the influenza virus NS1 protein requires its dimer structure and a small number of specific basic amino acids. Rna, 1999, 5, 195-205.	1.6	225
133	Propagation of experimental uncertainties using the Lipari-Szabo model-free analysis of protein dynamics. Journal of Biomolecular NMR, 1998, 12, 471-492.	1.6	35
134	Homology modeling of an RNP domain from a human RNA-binding protein: Homology-constrained energy optimization provides a criterion for distinguishing potential sequence alignments. , 1998, 33, 558-566.		11
135	Solution NMR Structure and Backbone Dynamics of the Major Cold-Shock Protein (CspA) fromEscherichia coli:Â Evidence for Conformational Dynamics in the Single-Stranded RNA-Binding Siteâ€,â€¡. Biochemistry, 1998, 37, 10881-10896.	1.2	105
136	Automated analysis of protein NMR assignments using methods from artificial intelligence. Journal of Molecular Biology, 1997, 269, 592-610.	2.0	292
137	A novel RNA-binding motif in influenza A virus non-structural protein 1. Nature Structural and Molecular Biology, 1997, 4, 891-895.	3.6	110
138	Crystal structure of the unique RNA-binding domain of the influenza virus NS1 protein. Nature Structural and Molecular Biology, 1997, 4, 896-899.	3.6	120
139	Application of multiple-quantum line narrowing with simultaneous 1H and 13C constant-time scalar-coupling evolution in PFG-HACANH and PFG-HACA(CO)NH triple-resonance experiments. Journal of Biomolecular NMR, 1997, 9, 105-111.	1.6	16
140	Homology modeling using simulated annealing of restrained molecular dynamics and conformational search calculations with CONGEN: Application in predicting the threeâ€dimensional structure of murine homeodomain Msxâ€1. Protein Science, 1997, 6, 956-970.	3.1	42
141	The Mechanism of Binding Staphylococcal Protein A to Immunoglobin G Does Not Involve Helix Unwindingâ€. Biochemistry, 1996, 35, 22-31.	1.2	82
142	Phase labeling of C?H and C?C spin-system topologies: Application in constant-time PFG-CBCA(CO)NH experiments for discriminating amino acid spin-system types. Journal of Biomolecular NMR, 1996, 8, 345-350.	1.6	34
143	Phase labeling of C?H and C?C spin-system topologies: Application in PFG-HACANH and PFG-HACA(CO)NH triple-resonance experiments for determining backbone resonance assignments in proteins. Journal of Biomolecular NMR, 1996, 8, 98-104.	1.6	38
144	High-level production of uniformly 15N-and 13C-enriched fusion proteins in Escherichia coli. Journal of Biomolecular NMR, 1996, 7, 131-41.	1.6	164

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145	Simulated annealing with restrained molecular dynamics using CONGEN: Energy refinement of the NMR solution structures of epidermal and typeâ€Î± transforming growth factors. Protein Science, 1996, 5, 578-592.	3.1	37
146	Simulated annealing with restrained molecular dynamics using a flexible restraint potential: Theory and evaluation with simulated NMR constraints. Protein Science, 1996, 5, 593-603.	3.1	29
147	Combined use of 13C chemical shift and 1H??13C? heteronuclear NOE data in monitoring a protein NMR structure refinement. Journal of Biomolecular NMR, 1995, 5, 161-72.	1.6	36
148	Classification of amino acid spin systems using PFG HCC(CO)NH-TOCSY with constant-time aliphatic 13C frequency labeling. Journal of Biomolecular NMR, 1995, 6, 211-216.	1.6	21
149	Crankshaft motions of the polypeptide backbone in molecular dynamics simulations of human type-Î± transforming growth factor. Journal of Biomolecular NMR, 1995, 6, 221-226.	1.6	70
150	A general approach for determining scalar coupling constants in polypeptides and proteins. Biopolymers, 1992, 32, 327-334.	1.2	34
151	Human epidermal growth factor. FEBS Letters, 1990, 271, 47-50.	1.3	61
152	2D Chemical exchange NMR spectroscopy by proton-detected heteronuclear correlation. Journal of the American Chemical Society, 1989, 111, 3096-3098.	6.6	117
153	AlphaFold Models of Small Proteins Rival the Accuracy of Solution NMR Structures. Frontiers in Molecular Biosciences, 0, 9, .	1.6	21