

Gerhard Wagner

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3383651/publications.pdf>

Version: 2024-02-01

268
papers

23,816
citations

6606

79
h-index

9090

144
g-index

282
all docs

282
docs citations

282
times ranked

23312
citing authors

#	ARTICLE	IF	CITATIONS
1	High fidelity sampling schedules for NMR spectra of high dynamic range. <i>Journal of Magnetic Resonance</i> , 2022, 339, 107228.	1.2	4
2	Pre- α T cell receptors topologically sample self-ligands during thymocyte \hat{I}^2 -selection. <i>Science</i> , 2021, 371, 181-185.	6.0	25
3	Allosterically Coupled Multisite Binding of Testosterone to Human Serum Albumin. <i>Endocrinology</i> , 2021, 162, .	1.4	14
4	A multi-pronged approach targeting SARS-CoV-2 proteins using ultra-large virtual screening. <i>IScience</i> , 2021, 24, 102021.	1.9	66
5	Cryo-EM structure of an activated GPCR \hat{C} protein complex in lipid nanodiscs. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 258-267.	3.6	71
6	Structural basis of the dynamic human CEACAM1 monomer-dimer equilibrium. <i>Communications Biology</i> , 2021, 4, 360.	2.0	6
7	VirtualFlow Ants \hat{C} Ultra-Large Virtual Screenings with Artificial Intelligence Driven Docking Algorithm Based on Ant Colony Optimization. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5807.	1.8	16
8	A biphenyl inhibitor of eIF4E targeting an internal binding site enables the design of cell-permeable PROTAC-degraders. <i>European Journal of Medicinal Chemistry</i> , 2021, 219, 113435.	2.6	15
9	Deep computational analysis details dysregulation of eukaryotic translation initiation complex eIF4F in human cancers. <i>Cell Systems</i> , 2021, 12, 907-923.e6.	2.9	11
10	A general chemical crosslinking strategy for structural analyses of weakly interacting proteins applied to preTCR \hat{C} pMHC complexes. <i>Journal of Biological Chemistry</i> , 2021, 296, 100255.	1.6	4
11	NUScon: a community-driven platform for quantitative evaluation of nonuniform sampling in NMR. <i>Magnetic Resonance</i> , 2021, 2, 843-861.	0.8	7
12	The Structural Basis for Low Conductance in the Membrane Protein VDAC upon \hat{I}^2 -NADH Binding and Voltage Gating. <i>Structure</i> , 2020, 28, 206-214.e4.	1.6	28
13	Conformational gating, dynamics and allostery in human monoacylglycerol lipase. <i>Scientific Reports</i> , 2020, 10, 18531.	1.6	8
14	Modulating TRADD to restore cellular homeostasis and inhibit apoptosis. <i>Nature</i> , 2020, 587, 133-138.	13.7	57
15	Nearest-neighbor NMR spectroscopy: categorizing spectral peaks by their adjacent nuclei. <i>Nature Communications</i> , 2020, 11, 5547.	5.8	10
16	Large Nanodiscs: A Potential Game Changer in Structural Biology of Membrane Protein Complexes and Virus Entry. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 539.	2.0	17
17	The precious fluorine on the ring: fluorine NMR for biological systems. <i>Journal of Biomolecular NMR</i> , 2020, 74, 365-379.	1.6	31
18	An open-source drug discovery platform enables ultra-large virtual screens. <i>Nature</i> , 2020, 580, 663-668.	13.7	345

#	ARTICLE	IF	CITATIONS
19	A newly identified Leishmania IF4E-interacting protein, Leish4E-IP2, modulates the activity of cap-binding protein paralogs. <i>Nucleic Acids Research</i> , 2020, 48, 4405-4417.	6.5	10
20	Accounting of Receptor Flexibility in Ultra-Large Virtual Screens with VirtualFlow Using a Grey Wolf Optimization Method. <i>Supercomputing Frontiers and Innovations</i> , 2020, 7, 4-12.	0.5	7
21	Discovery of small-molecule inhibitors targeting the ribosomal peptidyl transferase center (PTC) of <i>M. tuberculosis</i> . <i>Chemical Science</i> , 2019, 10, 8764-8767.	3.7	10
22	Integrative methods in structural biology. <i>Journal of Biomolecular NMR</i> , 2019, 73, 261-263.	1.6	7
23	Emerging solution NMR methods to illuminate the structural and dynamic properties of proteins. <i>Current Opinion in Structural Biology</i> , 2019, 58, 294-304.	2.6	26
24	Topological analysis of the gp41 MPER on lipid bilayers relevant to the metastable HIV-1 envelope prefusion state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 22556-22566.	3.3	22
25	Structural characterization of the human membrane protein VDAC2 in lipid bilayers by MAS NMR. <i>Journal of Biomolecular NMR</i> , 2019, 73, 451-460.	1.6	13
26	A nanobody that recognizes a 14-residue peptide epitope in the E2 ubiquitin-conjugating enzyme UBC6e modulates its activity. <i>Molecular Immunology</i> , 2019, 114, 513-523.	1.0	36
27	Aromatic 19F-13C TROSY: a background-free approach to probe biomolecular structure, function, and dynamics. <i>Nature Methods</i> , 2019, 16, 333-340.	9.0	82
28	NMR: an essential structural tool for integrative studies of T cell development, pMHC ligand recognition and TCR mechanobiology. <i>Journal of Biomolecular NMR</i> , 2019, 73, 319-332.	1.6	18
29	Nonuniform Sampling for NMR Spectroscopy. <i>Methods in Enzymology</i> , 2019, 614, 263-291.	0.4	31
30	¹⁵ N detection harnesses the slow relaxation property of nitrogen: Delivering enhanced resolution for intrinsically disordered proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1710-E1719.	3.3	40
31	Mixed pyruvate labeling enables backbone resonance assignment of large proteins using a single experiment. <i>Nature Communications</i> , 2018, 9, 356.	5.8	13
32	Cytocapsular tubes conduct cell translocation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1137-E1146.	3.3	9
33	Recent developments in solution nuclear magnetic resonance (NMR)-based molecular biology. <i>Journal of Molecular Medicine</i> , 2018, 96, 1-8.	1.7	23
34	Covalently circularized nanodiscs; challenges and applications. <i>Current Opinion in Structural Biology</i> , 2018, 51, 129-134.	2.6	31
35	Structural basis for LeishIF4E-1 modulation by an interacting protein in the human parasite <i>Leishmania major</i> . <i>Nucleic Acids Research</i> , 2018, 46, 3791-3801.	6.5	19
36	Assembly of phospholipid nanodiscs of controlled size for structural studies of membrane proteins by NMR. <i>Nature Protocols</i> , 2018, 13, 79-98.	5.5	159

#	ARTICLE	IF	CITATIONS
37	NMR-directed design of pre-TCR \hat{I}^2 and pMHC molecules implies a distinct geometry for pre-TCR relative to \hat{I}^2 TCR recognition of pMHC. <i>Journal of Biological Chemistry</i> , 2018, 293, 754-766.	1.6	14
38	High resolution X-ray and NMR structural study of human T-cell immunoglobulin and mucin domain containing protein-3. <i>Scientific Reports</i> , 2018, 8, 17512.	1.6	35
39	Cytidine monophosphate &N&/em>-acetylneuraminic acid synthetase enhances invasion of human triple-negative breast cancer cells. <i>OncoTargets and Therapy</i> , 2018, Volume 11, 6827-6838.	1.0	8
40	The T Cell Antigen Receptor \hat{I}^2 Transmembrane Domain Coordinates Triggering through Regulation of Bilayer Immersion and CD3 Subunit Associations. <i>Immunity</i> , 2018, 49, 829-841.e6.	6.6	58
41	Optimal control theory enables homonuclear decoupling without Bloch \hat{I}^2 Siebert shifts in NMR spectroscopy. <i>Nature Communications</i> , 2018, 9, 3014.	5.8	26
42	DNA-Corralled Nanodiscs for the Structural and Functional Characterization of Membrane Proteins and Viral Entry. <i>Journal of the American Chemical Society</i> , 2018, 140, 10639-10643.	6.6	57
43	Rapid convergence of optimal control in NMR using numerically-constructed toggling frames. <i>Journal of Magnetic Resonance</i> , 2017, 281, 94-103.	1.2	12
44	^1H , ^{13}C , and ^{15}N backbone chemical shift assignments of 4E-BP144 \hat{I}^2 and 4E-BP144 \hat{I}^2 bound to eIF4E. <i>Biomolecular NMR Assignments</i> , 2017, 11, 187-191.	0.4	1
45	Interpolating and extrapolating with hmsIST: seeking a tmax for optimal sensitivity, resolution and frequency accuracy. <i>Journal of Biomolecular NMR</i> , 2017, 68, 139-154.	1.6	24
46	Molecular Landscape of the Ribosome Pre-initiation Complex during mRNA Scanning: Structural Role for eIF3c and Its Control by eIF5. <i>Cell Reports</i> , 2017, 18, 2651-2663.	2.9	54
47	Covalently circularized nanodiscs for studying membrane proteins and viral entry. <i>Nature Methods</i> , 2017, 14, 49-52.	9.0	221
48	Solution Structure of the Cuz1 AN1 Zinc Finger Domain: An Exposed LDFLP Motif Defines a Subfamily of AN1 Proteins. <i>PLoS ONE</i> , 2016, 11, e0163660.	1.1	3
49	The Role of Dynamics and Allostery in the Inhibition of the eIF4E/eIF4G Translation Initiation Factor Complex. <i>Angewandte Chemie</i> , 2016, 128, 7292-7295.	1.6	1
50	The Role of Dynamics and Allostery in the Inhibition of the eIF4E/eIF4G Translation Initiation Factor Complex. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 7176-7179.	7.2	14
51	Nitrogen-detected TROSY yields comparable sensitivity to proton-detected TROSY for non-deuterated, large proteins under physiological salt conditions. <i>Journal of Biomolecular NMR</i> , 2016, 64, 143-151.	1.6	34
52	Pre-T Cell Receptors (Pre-TCRs) Leverage \hat{I}^2 Complementarity Determining Regions (CDRs) and Hydrophobic Patch in Mechanosensing Thymic Self-ligands. <i>Journal of Biological Chemistry</i> , 2016, 291, 25292-25305.	1.6	60
53	Analytical optimization of active bandwidth and quality factor for TOCSY experiments in NMR spectroscopy. <i>Journal of Biomolecular NMR</i> , 2016, 66, 9-20.	1.6	5
54	An accurately preorganized IRES RNA structure enables eIF4G capture for initiation of viral translation. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 859-864.	3.6	42

#	ARTICLE	IF	CITATIONS
55	Perspective: revisiting the field dependence of TROSY sensitivity. <i>Journal of Biomolecular NMR</i> , 2016, 66, 221-225.	1.6	19
56	Identification of DNA primase inhibitors via a combined fragment-based and virtual screening. <i>Scientific Reports</i> , 2016, 6, 36322.	1.6	18
57	Overexpression of eIF5 or its protein mimic 5MP perturbs eIF2 function and induces <i>ATF4</i> translation through delayed re-initiation. <i>Nucleic Acids Research</i> , 2016, 44, 8704-8713.	6.5	40
58	Conformational dynamics of a G-protein β subunit is tightly regulated by nucleotide binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3629-38.	3.3	77
59	Inhibiting fungal multidrug resistance by disrupting an activator-Mediator interaction. <i>Nature</i> , 2016, 530, 485-489.	13.7	120
60	UTOPIA NMR: activating unexploited magnetization using interleaved low-gamma detection. <i>Journal of Biomolecular NMR</i> , 2016, 64, 9-15.	1.6	19
61	Backbone resonance assignment of N15, N30 and D10 T cell receptor β subunits. <i>Biomolecular NMR Assignments</i> , 2016, 10, 35-39.	0.4	4
62	<i>NMR</i> studies reveal a novel grab and release mechanism for efficient catalysis of the bacterial γ -Cys peroxiredoxin machinery. <i>FEBS Journal</i> , 2015, 282, 4620-4638.	2.2	9
63	Structural Features of the β TCR Mechanotransduction Apparatus That Promote pMHC Discrimination. <i>Frontiers in Immunology</i> , 2015, 6, 441.	2.2	55
64	An RNA-binding Protein, Lin28, Recognizes and Remodels G-quartets in the MicroRNAs (miRNAs) and mRNAs It Regulates. <i>Journal of Biological Chemistry</i> , 2015, 290, 17909-17922.	1.6	32
65	Pre-TCR ligand binding impacts thymocyte development before β TCR expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8373-8378.	3.3	62
66	eIF1A augments Ago2-mediated Dicer-independent miRNA biogenesis and RNA interference. <i>Nature Communications</i> , 2015, 6, 7194.	5.8	39
67	Nitrogen detected TROSY at high field yields high resolution and sensitivity for protein NMR. <i>Journal of Biomolecular NMR</i> , 2015, 63, 323-331.	1.6	40
68	Lipid bilayer-bound conformation of an integral membrane beta barrel protein by multidimensional MAS NMR. <i>Journal of Biomolecular NMR</i> , 2015, 61, 299-310.	1.6	38
69	Magic Angle Spinning Nuclear Magnetic Resonance Characterization of Voltage-Dependent Anion Channel Gating in Two-Dimensional Lipid Crystalline Bilayers. <i>Biochemistry</i> , 2015, 54, 994-1005.	1.2	34
70	Force-dependent transition in the T-cell receptor β -subunit allosterically regulates peptide discrimination and pMHC bond lifetime. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1517-1522.	3.3	209
71	Structure refinement and membrane positioning of selectively labeled OmpX in phospholipid nanodiscs. <i>Journal of Biomolecular NMR</i> , 2015, 61, 249-260.	1.6	48
72	NMR resonance assignments of the catalytic domain of human serine/threonine phosphatase calcineurin in unligated and PVIVIT-peptide-bound states. <i>Biomolecular NMR Assignments</i> , 2015, 9, 201-205.	0.4	5

#	ARTICLE	IF	CITATIONS
73	Increased resolution of aromatic cross peaks using alternate ¹³ C labeling and TROSY. <i>Journal of Biomolecular NMR</i> , 2015, 62, 291-301.	1.6	26
74	Molecular mechanism of the dual activity of 4EGI-1: Dissociating eIF4G from eIF4E but stabilizing the binding of unphosphorylated 4E-BP1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E4036-45.	3.3	90
75	Structure of a herpesvirus nuclear egress complex subunit reveals an interaction groove that is essential for viral replication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 9010-9015.	3.3	52
76	NMR studies of membrane proteins. <i>Journal of Biomolecular NMR</i> , 2015, 61, 181-184.	1.6	6
77	The membrane anchor of the transcriptional activator SREBP is characterized by intrinsic conformational flexibility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 12390-12395.	3.3	14
78	Controlled Co-reconstitution of Multiple Membrane Proteins in Lipid Bilayer Nanodiscs Using DNA as a Scaffold. <i>ACS Chemical Biology</i> , 2015, 10, 2448-2454.	1.6	21
79	Structure of a CGI-58 Motif Provides the Molecular Basis of Lipid Droplet Anchoring. <i>Journal of Biological Chemistry</i> , 2015, 290, 26361-26372.	1.6	43
80	¹ H, ¹³ C, and ¹⁵ N backbone and sidechain chemical shift assignments for the HEAT2 domain of human eIF4GI. <i>Biomolecular NMR Assignments</i> , 2015, 9, 157-160.	0.4	0
81	Essential role of eIF5-mimic protein in animal development is linked to control of ATF4 expression. <i>Nucleic Acids Research</i> , 2014, 42, 10321-10330.	6.5	24
82	Molecular Signatures of Hemagglutinin Stem-Directed Heterosubtypic Human Neutralizing Antibodies against Influenza A Viruses. <i>PLoS Pathogens</i> , 2014, 10, e1004103.	2.1	121
83	A new broadband homonuclear mixing pulse for NMR with low applied power. <i>Journal of Chemical Physics</i> , 2014, 141, 024201.	1.2	6
84	Human Translation Initiation Factor eIF4G1 Possesses a Low-Affinity ATP Binding Site Facing the ATP-Binding Cleft of eIF4A in the eIF4G/eIF4A Complex. <i>Biochemistry</i> , 2014, 53, 6422-6425.	1.2	2
85	Backbone resonance assignment of the HEAT1-domain of the human eukaryotic translation initiation factor 4GI. <i>Biomolecular NMR Assignments</i> , 2014, 8, 89-91.	0.4	6
86	Disruption of Helix-Capping Residues 671 and 674 Reveals a Role in HIV-1 Entry for a Specialized Hinge Segment of the Membrane Proximal External Region of gp41. <i>Journal of Molecular Biology</i> , 2014, 426, 1095-1108.	2.0	34
87	G-quadruplex structures contribute to the neuroprotective effects of angiogenin-induced tRNA fragments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18201-18206.	3.3	264
88	Examining weak protein-protein interactions in start codon recognition via NMR spectroscopy. <i>FEBS Journal</i> , 2014, 281, 1965-1973.	2.2	12
89	Structure of the eukaryotic translation initiation factor eIF4E in complex with 4EGI-1 reveals an allosteric mechanism for dissociating eIF4G. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3187-95.	3.3	72
90	Quantitative phosphoproteomic analysis reveals system-wide signaling pathways downstream of SDF-1/CXCR4 in breast cancer stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2182-90.	3.3	109

#	ARTICLE	IF	CITATIONS
91	Constitutively Oxidized CXXC Motifs within the CD3 Heterodimeric Ectodomains of the T Cell Receptor Complex Enforce the Conformation of Juxtaposed Segments. <i>Journal of Biological Chemistry</i> , 2014, 289, 18880-18892.	1.6	24
92	The LxVP and PxlIT NFAT Motifs Bind Jointly to Overlapping Epitopes on Calcineurin's Catalytic Domain Distant to the Regulatory Domain. <i>Structure</i> , 2014, 22, 1016-1027.	1.6	15
93	Selective Methyl Labeling of Eukaryotic Membrane Proteins Using Cell-Free Expression. <i>Journal of the American Chemical Society</i> , 2014, 136, 11308-11310.	6.6	36
94	Solid-State NMR Structure Determination from Diagonal-Compensated, Sparsely Nonuniform-Sampled 4D Proton-Proton Restraints. <i>Journal of the American Chemical Society</i> , 2014, 136, 11002-11010.	6.6	61
95	Discovery and Characterization of a Disulfide-Locked α -Symmetric Defensin Peptide. <i>Journal of the American Chemical Society</i> , 2014, 136, 13494-13497.	6.6	50
96	Perspectives in magnetic resonance: NMR in the post-FFT era. <i>Journal of Magnetic Resonance</i> , 2014, 241, 60-73.	1.2	122
97	Structure-activity relationship study of 4EGI-1, small molecule eIF4E/eIF4G protein-protein interaction inhibitors. <i>European Journal of Medicinal Chemistry</i> , 2014, 77, 361-377.	2.6	18
98	The Use of Amphipols for NMR Structural Characterization of 7-TM Proteins. <i>Journal of Membrane Biology</i> , 2014, 247, 957-964.	1.0	26
99	Resonance assignments of the microtubule-binding domain of the <i>C. elegans</i> spindle and kinetochore-associated protein 1. <i>Biomolecular NMR Assignments</i> , 2014, 8, 275-278.	0.4	5
100	4EGI-1 targets breast cancer stem cells by selective inhibition of translation that persists in CSC maintenance, proliferation and metastasis. <i>Oncotarget</i> , 2014, 5, 6028-6037.	0.8	29
101	Cell-free Expressed Bacteriorhodopsin in Different Soluble Membrane Mimetics: Biophysical Properties and NMR Accessibility. <i>Structure</i> , 2013, 21, 394-401.	1.6	103
102	Immunogenicity of Membrane-bound HIV-1 gp41 Membrane-proximal External Region (MPER) Segments Is Dominated by Residue Accessibility and Modulated by Stereochemistry. <i>Journal of Biological Chemistry</i> , 2013, 288, 31888-31901.	1.6	43
103	Exploring new limits in complex biological structures. <i>Current Opinion in Structural Biology</i> , 2013, 23, 704-706.	2.6	2
104	Exploring signal-to-noise ratio and sensitivity in non-uniformly sampled multi-dimensional NMR spectra. <i>Journal of Biomolecular NMR</i> , 2013, 55, 167-178.	1.6	96
105	Pulse design for broadband correlation NMR spectroscopy by multi-rotating frames. <i>Journal of Biomolecular NMR</i> , 2013, 55, 291-302.	1.6	11
106	Optimized Phospholipid Bilayer Nanodiscs Facilitate High-Resolution Structure Determination of Membrane Proteins. <i>Journal of the American Chemical Society</i> , 2013, 135, 1919-1925.	6.6	445
107	Molecular Crowding Enhanced ATPase Activity of the RNA Helicase eIF4A Correlates with Compaction of Its Quaternary Structure and Association with eIF4G. <i>Journal of the American Chemical Society</i> , 2013, 135, 10040-10047.	6.6	35
108	The Interaction between Eukaryotic Initiation Factor 1A and eIF5 Retains eIF1 within Scanning Preinitiation Complexes. <i>Biochemistry</i> , 2013, 52, 9510-9518.	1.2	37

#	ARTICLE	IF	CITATIONS
109	\hat{I}^2 -Hairpin Loop of Eukaryotic Initiation Factor 1 (eIF1) Mediates 40 S Ribosome Binding to Regulate Initiator tRNA ^{Met} Recruitment and Accuracy of AUG Selection in Vivo. <i>Journal of Biological Chemistry</i> , 2013, 288, 27546-27562.	1.6	44
110	Hypoxia-inducible Factor-1 \hat{I}^{\pm} (HIF-1 \hat{I}^{\pm}) Promotes Cap-dependent Translation of Selective mRNAs through Up-regulating Initiation Factor eIF4E1 in Breast Cancer Cells under Hypoxia Conditions. <i>Journal of Biological Chemistry</i> , 2013, 288, 18732-18742.	1.6	55
111	Abstract 109: Preliminary Structural Into the Sterol Regulatory Element-Binding Protein (SREBP) Interaction With SREBP Cleavage-Activating Protein (SCAP). <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2013, 33, .	1.1	0
112	Lipid Dynamics and Proteinâ€™Lipid Interactions in 2D Crystals Formed with the \hat{I}^2 -Barrel Integral Membrane Protein VDAC1. <i>Journal of the American Chemical Society</i> , 2012, 134, 6375-6387.	6.6	65
113	Solution NMR spectroscopic characterization of human VDAC-2 in detergent micelles and lipid bilayer nanodiscs. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012, 1818, 1562-1569.	1.4	53
114	The C-Terminal Domain of Eukaryotic Initiation Factor 5 Promotes Start Codon Recognition by Its Dynamic Interplay with eIF1 and eIF2 \hat{I}^2 . <i>Cell Reports</i> , 2012, 1, 689-702.	2.9	66
115	The Kinetochore-Bound Ska1 Complex Tracks Depolymerizing Microtubules and Binds to Curved Protofilaments. <i>Developmental Cell</i> , 2012, 23, 968-980.	3.1	194
116	NMR Solution Structure and Condition-Dependent Oligomerization of the Antimicrobial Peptide Human Defensin 5. <i>Biochemistry</i> , 2012, 51, 9624-9637.	1.2	45
117	TCR Mechanobiology: Torques and Tunable Structures Linked to Early T Cell Signaling. <i>Frontiers in Immunology</i> , 2012, 3, 76.	2.2	75
118	Application of iterative soft thresholding for fast reconstruction of NMR data non-uniformly sampled with multidimensional Poisson Gap scheduling. <i>Journal of Biomolecular NMR</i> , 2012, 52, 315-327.	1.6	381
119	Editorial management of the <i>Journal of Biomolecular NMR</i> . <i>Journal of Biomolecular NMR</i> , 2012, 52, 3-4.	1.6	1
120	Tumor suppression by small molecule inhibitors of translation initiation. <i>Oncotarget</i> , 2012, 3, 869-881.	0.8	91
121	Applications of Non-Uniform Sampling and Processing. <i>Topics in Current Chemistry</i> , 2011, 316, 125-148.	4.0	119
122	Antibody mechanics on a membrane-bound HIV segment essential for GP41-targeted viral neutralization. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1235-1243.	3.6	86
123	Structure of the VP16 transactivator target in the Mediator. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 410-415.	3.6	75
124	HNCA-TOCSY-CANH experiments with alternate ¹³ C- ¹² C labeling: a set of 3D experiment with unique supra-sequential information for mainchain resonance assignment. <i>Journal of Biomolecular NMR</i> , 2011, 49, 17-26.	1.6	10
125	Speeding up direct ¹⁵ N detection: hCaN 2D NMR experiment. <i>Journal of Biomolecular NMR</i> , 2011, 51, 497-504.	1.6	23
126	Inhibition of the interactions between eukaryotic initiation factors 4E and 4G impairs long-term associative memory consolidation but not reconsolidation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 3383-3388.	3.3	95

#	ARTICLE	IF	CITATIONS
127	Molecular Characterization of Disrupted in Schizophrenia-1 Risk Variant S704C Reveals the Formation of Altered Oligomeric Assembly. <i>Journal of Biological Chemistry</i> , 2011, 286, 44266-44276.	1.6	26
128	A novel 4E-interacting protein in <i>Leishmania</i> is involved in stage-specific translation pathways. <i>Nucleic Acids Research</i> , 2011, 39, 8404-8415.	6.5	69
129	Transient Domain Interactions in Non-Ribosomal Peptide Synthetases. <i>FASEB Journal</i> , 2011, 25, .	0.2	0
130	Backbone and ILV side chain methyl group assignments of the integral human membrane protein VDAC-1. <i>Biomolecular NMR Assignments</i> , 2010, 4, 29-32.	0.4	10
131	Overcoming the solubility limit with solubility-enhancement tags: successful applications in biomolecular NMR studies. <i>Journal of Biomolecular NMR</i> , 2010, 46, 23-31.	1.6	72
132	CACA-TOCSY with alternate ^{13}C labeling: a ^{13}C direct detection experiment for mainchain resonance assignment, dihedral angle information, and amino acid type identification. <i>Journal of Biomolecular NMR</i> , 2010, 47, 55-63.	1.6	23
133	Nitrogen-detected CAN and CON experiments as alternative experiments for main chain NMR resonance assignments. <i>Journal of Biomolecular NMR</i> , 2010, 47, 271-282.	1.6	34
134	The 3D structures of VDAC represent a native conformation. <i>Trends in Biochemical Sciences</i> , 2010, 35, 514-521.	3.7	115
135	Distinctive CD3 Heterodimeric Ectodomain Topologies Maximize Antigen-Triggered Activation of $\hat{1}\hat{2}$ T Cell Receptors. <i>Journal of Immunology</i> , 2010, 185, 2951-2959.	0.4	34
136	Autoinhibitory Interaction in the Multidomain Adaptor Protein Nck: Possible Roles in Improving Specificity and Functional Diversity. <i>Biochemistry</i> , 2010, 49, 5634-5641.	1.2	11
137	Poisson-Gap Sampling and Forward Maximum Entropy Reconstruction for Enhancing the Resolution and Sensitivity of Protein NMR Data. <i>Journal of the American Chemical Society</i> , 2010, 132, 2145-2147.	6.6	308
138	High-Resolution 3D CANCA NMR Experiments for Complete Mainchain Assignments Using $\hat{1}\hat{2}$ Direct Detection. <i>Journal of the American Chemical Society</i> , 2010, 132, 2945-2951.	6.6	25
139	Nonmicellar systems for solution NMR spectroscopy of membrane proteins. <i>Current Opinion in Structural Biology</i> , 2010, 20, 471-479.	2.6	114
140	Evidence for an Alternative Glycolytic Pathway in Rapidly Proliferating Cells. <i>Science</i> , 2010, 329, 1492-1499.	6.0	586
141	The $\hat{1}\hat{2}$ T Cell Receptor Is an Anisotropic Mechanosensor. <i>Journal of Biological Chemistry</i> , 2009, 284, 31028-31037.	1.6	350
142	Evolutionary changes in the <i>Leishmania</i> eIF4F complex involve variations in the eIF4E-eIF4G interactions. <i>Nucleic Acids Research</i> , 2009, 37, 3243-3253.	6.5	65
143	Coupled Decomposition of Four-Dimensional NOESY Spectra. <i>Journal of the American Chemical Society</i> , 2009, 131, 12970-12978.	6.6	51
144	Broadly neutralizing anti-HIV-1 antibodies disrupt a hinge-related function of gp41 at the membrane interface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 9057-9062.	3.3	104

#	ARTICLE	IF	CITATIONS
145	The role of solution NMR in the structure determinations of VDAC-1 and other membrane proteins. <i>Current Opinion in Structural Biology</i> , 2009, 19, 396-401.	2.6	81
146	The T-lock: automated compensation of radio-frequency induced sample heating. <i>Journal of Biomolecular NMR</i> , 2009, 44, 69-76.	1.6	6
147	FM reconstruction of non-uniformly sampled protein NMR data at higher dimensions and optimization by distillation. <i>Journal of Biomolecular NMR</i> , 2009, 45, 283-294.	1.6	69
148	Time-shared HSQC-NOESY for accurate distance constraints measured at high-field in ¹⁵ N- ¹³ C-ILV methyl labeled proteins. <i>Journal of Biomolecular NMR</i> , 2009, 45, 311-318.	1.6	14
149	Topology and Regulation of the Human eIF4A/4G/4H Helicase Complex in Translation Initiation. <i>Cell</i> , 2009, 136, 447-460.	13.5	205
150	A Double TROSY hNCANH Experiment for Efficient Assignment of Large and Challenging Proteins. <i>Journal of the American Chemical Society</i> , 2009, 131, 12880-12881.	6.6	23
151	Structural and Functional Characterization of the Integral Membrane Protein VDAC-1 in Lipid Bilayer Nanodiscs. <i>Journal of the American Chemical Society</i> , 2009, 131, 17777-17779.	6.6	158
152	A nuclear receptor-like pathway regulating multidrug resistance in fungi. <i>Nature</i> , 2008, 452, 604-609.	13.7	294
153	Structural basis for the selectivity of the external thioesterase of the surfactin synthetase. <i>Nature</i> , 2008, 454, 907-911.	13.7	112
154	Dynamic thiolation of thioesterase structure of a non-ribosomal peptide synthetase. <i>Nature</i> , 2008, 454, 903-906.	13.7	151
155	In situ observation of protein phosphorylation by high-resolution NMR spectroscopy. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 321-329.	3.6	153
156	Identification of RIP1 kinase as a specific cellular target of necrostatins. <i>Nature Chemical Biology</i> , 2008, 4, 313-321.	3.9	1,708
157	Structural and Functional Evidence that Nck Interaction with CD3 ζ Regulates T-Cell Receptor Activity. <i>Journal of Molecular Biology</i> , 2008, 380, 704-716.	2.0	43
158	HIV-1 Broadly Neutralizing Antibody Extracts Its Epitope from a Kinked gp41 Ectodomain Region on the Viral Membrane. <i>Immunity</i> , 2008, 28, 52-63.	6.6	263
159	Solution Structure of the Integral Human Membrane Protein VDAC-1 in Detergent Micelles. <i>Science</i> , 2008, 321, 1206-1210.	6.0	605
160	Alternate ¹³ C α ¹² C Labeling for Complete Mainchain Resonance Assignments using C β Direct-Detection with Applicability Toward Fast Relaxing Protein Systems. <i>Journal of the American Chemical Society</i> , 2008, 130, 17210-17211.	6.6	42
161	Effects of Redox Potential and Ca ²⁺ on the Inositol 1,4,5-Trisphosphate Receptor L3-1 Loop Region. <i>Journal of Biological Chemistry</i> , 2008, 283, 25567-25575.	1.6	39
162	Modern NMR in Undergraduate Education: Introduction. <i>ACS Symposium Series</i> , 2007, , 1-6.	0.5	0

#	ARTICLE	IF	CITATIONS
163	Molecular Framework for the Activation of RNA-dependent Protein Kinase. <i>Journal of Biological Chemistry</i> , 2007, 282, 11474-11486.	1.6	56
164	Importance of the CD3 β Ectodomain Terminal β 2-Strand and Membrane Proximal Stalk in Thymic Development and Receptor Assembly. <i>Journal of Immunology</i> , 2007, 178, 3668-3679.	0.4	22
165	Small-Molecule Inhibition of the Interaction between the Translation Initiation Factors eIF4E and eIF4G. <i>Cell</i> , 2007, 128, 257-267.	13.5	497
166	NMR Methods for Studying Protein-Protein Interactions Involved in Translation Initiation. <i>Methods in Enzymology</i> , 2007, 430, 283-331.	0.4	48
167	Ultrahigh-Resolution ^1H - ^{13}C HSQC Spectra of Metabolite Mixtures Using Nonlinear Sampling and Forward Maximum Entropy Reconstruction. <i>Journal of the American Chemical Society</i> , 2007, 129, 5108-5116.	6.6	131
168	NMR Structural Investigation of the Mitochondrial Outer Membrane Protein VDAC and Its Interaction with Antiapoptotic Bcl-xL. <i>Biochemistry</i> , 2007, 46, 514-525.	1.2	148
169	Sequence and structure evolved separately in a ribosomal ubiquitin variant. <i>EMBO Journal</i> , 2007, 26, 3474-3483.	3.5	21
170	Structure of the Calcineurin-NFAT Complex: Defining a T Cell Activation Switch Using Solution NMR and Crystal Coordinates. <i>Structure</i> , 2007, 15, 587-597.	1.6	49
171	^1H - ^{13}C amino acid selective labeling in a ^2H - ^{15}N background for NMR studies of large proteins. <i>Journal of Biomolecular NMR</i> , 2007, 38, 89-98.	1.6	49
172	The role of cross-interface salt bridges in SCAN domain dimerization specificity. <i>FASEB Journal</i> , 2007, 21, A271.	0.2	0
173	Non-uniformly Sampled Double-TROSY hNcaNH Experiments for NMR Sequential Assignments of Large Proteins. <i>Journal of the American Chemical Society</i> , 2006, 128, 5757-5763.	6.6	63
174	NMR Distinction of Single- and Multiple-Mode Binding of Small-Molecule Protein Ligands. <i>Journal of the American Chemical Society</i> , 2006, 128, 2160-2161.	6.6	37
175	Mapping of the Auto-inhibitory Interactions of Protein Kinase R by Nuclear Magnetic Resonance. <i>Journal of Molecular Biology</i> , 2006, 364, 352-363.	2.0	35
176	An ARC/Mediator subunit required for SREBP control of cholesterol and lipid homeostasis. <i>Nature</i> , 2006, 442, 700-704.	13.7	351
177	Determination of all NOEs in ^1H - ^{13}C -Me-ILV-U- ^2H - ^{15}N Proteins with Two Time-Shared Experiments. <i>Journal of Biomolecular NMR</i> , 2006, 34, 31-40.	1.6	36
178	Solution Structure of the First Src Homology 3 Domain of Human Nck2. <i>Journal of Biomolecular NMR</i> , 2006, 34, 203-208.	1.6	14
179	Identification of individual protein-ligand NOEs in the limit of intermediate exchange. <i>Journal of Biomolecular NMR</i> , 2006, 36, 1-11.	1.6	23
180	NMR studies of protein interactions. <i>Current Opinion in Structural Biology</i> , 2006, 16, 109-117.	2.6	106

#	ARTICLE	IF	CITATIONS
181	Amplitudes and directions of internal protein motions from a JAM analysis of ^{15}N relaxation data. <i>Magnetic Resonance in Chemistry</i> , 2006, 44, S130-S142.	1.1	6
182	Structure of eukaryotic initiation factors at interfaces within ribosomal preinitiation complexes: Yeast perspectives. <i>FASEB Journal</i> , 2006, 20, A502.	0.2	0
183	Correspondence between spin-dynamic phases and pulse program phases of NMR spectrometers. <i>Journal of Magnetic Resonance</i> , 2005, 174, 325-330.	1.2	14
184	Fast Assignment of ^{15}N -HSQC Peaks using High-Resolution 3D HNCOCANH Experiments with Non-Uniform Sampling. <i>Journal of Biomolecular NMR</i> , 2005, 33, 43-50.	1.6	59
185	Unambiguous Assignment of NMR Protein Backbone Signals with a Time-shared Triple-resonance Experiment. <i>Journal of Biomolecular NMR</i> , 2005, 33, 187-196.	1.6	31
186	High-resolution aliphatic side-chain assignments in 3D HCOCNH experiments with joint ^1H - ^{13}C evolution and non-uniform sampling. <i>Journal of Biomolecular NMR</i> , 2005, 32, 55-60.	1.6	29
187	Structural basis for the enhancement of eIF4A helicase activity by eIF4G. <i>Genes and Development</i> , 2005, 19, 2212-2223.	2.7	137
188	Mammalian SCAN Domain Dimer Is a Domain-Swapped Homolog of the HIV Capsid C-Terminal Domain. <i>Molecular Cell</i> , 2005, 17, 137-143.	4.5	81
189	Solution structure of the CD3 ϵ ectodomain and comparison with CD3 δ as a basis for modeling T cell receptor topology and signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 16867-16872.	3.3	101
190	Selective inhibition of calcineurin-NFAT signaling by blocking protein-protein interaction with small organic molecules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7554-7559.	3.3	154
191	Accelerated acquisition of high resolution triple-resonance spectra using non-uniform sampling and maximum entropy reconstruction. <i>Journal of Magnetic Resonance</i> , 2004, 170, 15-21.	1.2	217
192	Discovery of Small-Molecule Inhibitors of the NFAT \sim Calcineurin Interaction by Competitive High-Throughput Fluorescence Polarization Screening. <i>Biochemistry</i> , 2004, 43, 16067-16075.	1.2	42
193	A General Framework for Development and Data Analysis of Competitive High-Throughput Screens for Small-Molecule Inhibitors of Protein \sim Protein Interactions by Fluorescence Polarization. <i>Biochemistry</i> , 2004, 43, 16056-16066.	1.2	243
194	Translation initiation: structures, mechanisms and evolution. <i>Quarterly Reviews of Biophysics</i> , 2004, 37, 197-284.	2.4	198
195	Letter to the Editor: Rapid backbone (^1H), (^{13}C), and (^{15}N) assignment of the V1 domain of human PKC iota using the new program IBIS. <i>Journal of Biomolecular NMR</i> , 2003, 26, 373-374.	1.6	2
196	IBIS—a tool for automated sequential assignment of protein spectra from triple resonance experiments. <i>Journal of Biomolecular NMR</i> , 2003, 26, 335-344.	1.6	48
197	Structural investigations of a GYF domain covalently linked to a proline-rich peptide. <i>Journal of Biomolecular NMR</i> , 2003, 27, 143-149.	1.6	24
198	A sensitive and robust method for obtaining intermolecular NOEs between side chains in large protein complexes. <i>Journal of Biomolecular NMR</i> , 2003, 25, 235-242.	1.6	61

#	ARTICLE	IF	CITATIONS
199	Multiple-quantum magic-angle spinning spectroscopy using nonlinear sampling. <i>Journal of Magnetic Resonance</i> , 2003, 161, 43-55.	1.2	38
200	Broadband ^{13}C – ^{13}C adiabatic mixing in solution optimized for high fields. <i>Journal of Magnetic Resonance</i> , 2003, 165, 59-79.	1.2	12
201	Ribosome Loading onto the mRNA Cap Is Driven by Conformational Coupling between eIF4G and eIF4E. <i>Cell</i> , 2003, 115, 739-750.	13.5	312
202	Structural basis for recruitment of CBP/p300 by hypoxia-inducible factor-1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 5367-5372.	3.3	403
203	TreeDock: A Tool for Protein Docking Based on Minimizing van der Waals Energies. <i>Journal of the American Chemical Society</i> , 2002, 124, 1241-1250.	6.6	63
204	A Novel Approach for Characterizing Protein Ligand Complexes: A Molecular Basis for Specificity of Small-Molecule Bcl-2 Inhibitors. <i>Journal of the American Chemical Society</i> , 2002, 124, 1234-1240.	6.6	123
205	Dynamic interaction of CD2 with the GYF and the SH3 domain of compartmentalized effector molecules. <i>EMBO Journal</i> , 2002, 21, 5985-5995.	3.5	80
206	Mechanisms Contributing to T Cell Receptor Signaling and Assembly Revealed by the Solution Structure of an Ectodomain Fragment of the CD3 μ η Heterodimer. <i>Cell</i> , 2001, 105, 913-923.	13.5	156
207	An unmediated hydrogen peroxide biosensor based on hemoglobin incorporated in a montmorillonite membrane. <i>Analyst</i> , 2001, 126, 1086-1089.	1.7	29
208	Electron-Transfer Reactivity and Enzymatic Activity of Hemoglobin in a SP Sephadex Membrane. <i>Analytical Chemistry</i> , 2001, 73, 2850-2854.	3.2	179
209	Incorporation of Horseradish Peroxidase in a Kieselguhr Membrane and the Application to a Mediator-free Hydrogen Peroxide Sensor. <i>Analytical Sciences</i> , 2001, 17, 273-276.	0.8	25
210	A solubility-enhancement tag (SET) for NMR studies of poorly behaving proteins. <i>Journal of Biomolecular NMR</i> , 2001, 20, 11-14.	1.6	138
211	Solution structure and backbone dynamics of an omega-conotoxin precursor. <i>Protein Science</i> , 2001, 10, 538-550.	3.1	21
212	Identification of small-molecule inhibitors of interaction between the BH3 domain and Bcl-xL. <i>Nature Cell Biology</i> , 2001, 3, 173-182.	4.6	536
213	Structure and dynamics of scTCR investigated by a new NMR structural refinement methodology. <i>Seibutsu Butsuri</i> , 2000, 40, S26.	0.0	0
214	NMR spectroscopy: a multifaceted approach to macromolecular structure. <i>Quarterly Reviews of Biophysics</i> , 2000, 33, 29-65.	2.4	224
215	Recombinant decorsin: Dynamics of the RGD recognition site. <i>Protein Science</i> , 2000, 9, 1428-1438.	3.1	18
216	Utilization of Site-Directed Spin Labeling and High-Resolution Heteronuclear Nuclear Magnetic Resonance for Global Fold Determination of Large Proteins with Limited Nuclear Overhauser Effect Data. <i>Biochemistry</i> , 2000, 39, 5355-5365.	1.2	578

#	ARTICLE	IF	CITATIONS
217	Efficient Synthesis of ¹³ C, ¹⁵ N-Labeled RNA Containing the Cap Structure m ⁷ GpppA. <i>Journal of the American Chemical Society</i> , 2000, 122, 2417-2421.	6.6	20
218	The GYF domain is a novel structural fold that is involved in lymphoid signaling through proline-rich sequences. <i>Nature Structural Biology</i> , 1999, 6, 656-660.	9.7	86
219	Solution structure of the catalytic domain of GCN5 histone acetyltransferase bound to coenzyme A. <i>Nature</i> , 1999, 400, 86-89.	13.7	96
220	Solution structure of the hRPABC14.4 subunit of human RNA polymerases. <i>Nature Structural Biology</i> , 1999, 6, 1039-1042.	9.7	14
221	Structure, specificity and CDR mobility of a class II restricted single-chain T-cell receptor. <i>Nature Structural Biology</i> , 1999, 6, 574-581.	9.7	83
222	Efficient side-chain and backbone assignment in large proteins: application to tGCN5. <i>Journal of Biomolecular NMR</i> , 1999, 15, 227-239.	1.6	36
223	Application of automated NOE assignment to three-dimensional structure refinement of a 28 kDa single-chain T cell receptor. , 1999, 15, 103-113.		13
224	The Crystal Structure of a T Cell Receptor in Complex with Peptide and MHC Class II. <i>Science</i> , 1999, 286, 1913-1921.	6.0	376
225	Structure of a Heterophilic Adhesion Complex between the Human CD2 and CD58 (LFA-3) Counterreceptors. <i>Cell</i> , 1999, 97, 791-803.	13.5	216
226	Identification by NMR Spectroscopy of Residues at Contact Surfaces in Large, Slowly Exchanging Macromolecular Complexes. <i>Journal of the American Chemical Society</i> , 1999, 121, 9903-9904.	6.6	89
227	Internal and overall motions of the translation factor eIF4E: cap binding and insertion in a CHAPS detergent micelle. <i>Journal of Biomolecular NMR</i> , 1998, 12, 73-88.	1.6	21
228	The interaction of eIF4E with 4Eâ€œBP1 is an induced fit to a completely disordered protein. <i>Protein Science</i> , 1998, 7, 1639-1642.	3.1	80
229	Solution Structure of the Core NFATC1/DNA Complex. <i>Cell</i> , 1998, 92, 687-696.	13.5	101
230	Intramolecular Masking of Nuclear Import Signal on NF-AT4 by Casein Kinase I and MEKK1. <i>Cell</i> , 1998, 93, 851-861.	13.5	291
231	4E Binding Proteins Inhibit the Translation Factor eIF4E without Folded Structureâ€œ. <i>Biochemistry</i> , 1998, 37, 9-15.	1.2	116
232	A Simple Method to Distinguish Intermonomer Nuclear Overhauser Effects in Homodimeric Proteins with C ₂ Symmetry. <i>Journal of the American Chemical Society</i> , 1997, 119, 5958-5959.	6.6	58
233	Unusual Rel-like architecture in the DNA-binding domain of the transcription factor NFATc. <i>Nature</i> , 1997, 385, 172-176.	13.7	103
234	Structure of translation factor eIF4E bound to m ⁷ GDP and interaction with 4E-binding protein. <i>Nature Structural Biology</i> , 1997, 4, 717-724.	9.7	347

#	ARTICLE	IF	CITATIONS
235	Structure and mobility of the PUT3 dimer. <i>Nature Structural Biology</i> , 1997, 4, 744-750.	9.7	51
236	Dimerization of the UmuD' protein in solution and its implications for regulation of SOS mutagenesis. <i>Nature Structural Biology</i> , 1997, 4, 979-982.	9.7	73
237	Refined solution structure of the DNA-binding domain of GAL4 and use of 3J(113Cd,1H) in structure determination. <i>Journal of Biomolecular NMR</i> , 1997, 10, 397-401.	1.6	17
238	The counterreceptor binding site of human CD2 exhibits an extended surface patch with multiple conformations fluctuating with millisecond to microsecond motions. <i>Protein Science</i> , 1997, 6, 534-542.	3.1	44
239	Refined structure of villin 14T and a detailed comparison with other actin- \bar{c} severing domains. <i>Protein Science</i> , 1997, 6, 1197-1209.	3.1	28
240	Quantification of Maximum-Entropy Spectrum Reconstructions. <i>Journal of Magnetic Resonance</i> , 1997, 125, 332-339.	1.2	62
241	Local Mobility within Villin 14T Probed via Heteronuclear Relaxation Measurements and a Reduced Spectral Density Mapping. <i>Biochemistry</i> , 1996, 35, 1722-1732.	1.2	36
242	Use of Selective \bar{c} -Pulses for Improvement of HN(CA)CO- \bar{c} D and HN(COCA)NH- \bar{c} D Experiments. <i>Journal of Magnetic Resonance Series B</i> , 1996, 111, 194-198.	1.6	56
243	An Optimized 3D NOESY- \bar{c} HSQC. <i>Journal of Magnetic Resonance Series B</i> , 1996, 112, 200-205.	1.6	165
244	Increased Sensitivity in HNCA and HN(CO)CA Experiments by Selective \bar{c} ² Decoupling. <i>Journal of Magnetic Resonance Series B</i> , 1996, 113, 91-96.	1.6	59
245	Solution structure of the potassium channel inhibitor agitoxin 2: Caliper for probing channel geometry. <i>Protein Science</i> , 1995, 4, 1478-1489.	3.1	125
246	The importance of being floppy. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 255-257.	3.6	27
247	Composition and Sequence Specific Resonance Assignments of the Heterogeneous N-Linked Glycan in the 13.6 kDa Adhesion Domain of Human Cluster of Differentiation 2 (CD2) as Determined by NMR on the Intact Glycoprotein. <i>Biochemistry</i> , 1995, 34, 1622-1634.	1.2	58
248	[20] Investigation of protein motions via relaxation measurements. <i>Methods in Enzymology</i> , 1994, 239, 563-596.	0.4	191
249	Improved resolution in triple-resonance spectra by nonlinear sampling in the constant-time domain. <i>Journal of Biomolecular NMR</i> , 1994, 4, 483-490.	1.6	96
250	Solution structure of villin 14T, a domain conserved among actin- \bar{c} severing proteins. <i>Protein Science</i> , 1994, 3, 70-81.	3.1	52
251	Thin end of the wedge. <i>Nature Structural Biology</i> , 1994, 1, 497-498.	9.7	5
252	Application of nonlinear sampling schemes to COSY-type spectra. <i>Journal of Biomolecular NMR</i> , 1993, 3, 569-76.	1.6	97

#	ARTICLE	IF	CITATIONS
253	Structure of the glycosylated adhesion domain of human T lymphocyte glycoprotein CD2. <i>Structure</i> , 1993, 1, 69-81.	1.6	66
254	Proton resonance assignments and secondary structure of the 13.6 kDa glycosylated adhesion domain of human CD2. <i>Biochemistry</i> , 1993, 32, 10995-11006.	1.2	44
255	NMR relaxation and protein mobility. <i>Current Opinion in Structural Biology</i> , 1993, 3, 748-754.	2.6	127
256	Design, synthesis and solution structure of a renin inhibitor Structural constraints from NOE, and homonuclear and heteronuclear coupling constants combined with distance geometry calculations. <i>FEBS Letters</i> , 1992, 302, 97-103.	1.3	9
257	The solution structure of eglin c based on measurements of many NOEs and coupling constants and its comparison with X-ray structures. <i>Protein Science</i> , 1992, 1, 736-751.	3.1	411
258	Effects of DNA binding and metal substitution on the dynamics of the GAL4 DNA-binding domain as studied by amide proton exchange. <i>Protein Science</i> , 1992, 1, 1403-1412.	3.1	21
259	Solution structure of the DNA-binding domain of C ₂ -GAL4 from <i>S. cerevisiae</i> . <i>Nature</i> , 1992, 356, 450-453.	13.7	134
260	A constant-time three-dimensional triple-resonance pulse scheme to correlate intraresidue ¹ HN, ¹⁵ N, and ¹³ C chemical shifts in ¹⁵ N-, ¹³ C-labelled proteins. <i>Journal of Magnetic Resonance</i> , 1992, 97, 213-217.	0.5	95
261	A triple-resonance pulse scheme for selectively correlating amide ¹ HN and ¹⁵ N nuclei with the ¹ H α proton of the preceding residue. <i>Journal of Biomolecular NMR</i> , 1992, 2, 389-394.	1.6	26
262	A new 3D HN(CA)HA experiment for obtaining fingerprint HN-H α cross peaks in ¹⁵ N- and ¹³ C-labeled proteins. <i>Journal of Biomolecular NMR</i> , 1992, 2, 203-210.	1.6	83
263	NMR studies of structure and dynamics of isotope enriched proteins. <i>Biopolymers</i> , 1992, 32, 381-390.	1.2	12
264	Methotrexate binds in a non-productive orientation to human dihydrofolate reductase in solution, based on NMR spectroscopy. <i>FEBS Letters</i> , 1991, 283, 267-269.	1.3	14
265	Protein structures in solution by nuclear magnetic resonance and distance geometry. <i>Journal of Molecular Biology</i> , 1987, 196, 611-639.	2.0	646
266	Nuclear magnetic resonance of labile protons in the basic pancreatic trypsin inhibitor. <i>Journal of Molecular Biology</i> , 1979, 130, 1-18.	2.0	191
267	Kinetics of the exchange of individual amide protons in the basic pancreatic trypsin inhibitor. <i>Journal of Molecular Biology</i> , 1979, 130, 19-30.	2.0	117
268	Chapter 2. Low- γ ; Nuclei Detection Experiments for Biomolecular NMR. <i>RSC Biomolecular Sciences</i> , 0, , 25-52.	0.4	9