

Gerhard Wagner

List of Publications by Year in descending order

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268
papers

23,816
citations

6613

79
h-index

9103

144
g-index

282
all docs

282
docs citations

282
times ranked

23312
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of RIP1 kinase as a specific cellular target of necrostatins. <i>Nature Chemical Biology</i> , 2008, 4, 313-321.	8.0	1,708
2	Protein structures in solution by nuclear magnetic resonance and distance geometry. <i>Journal of Molecular Biology</i> , 1987, 196, 611-639.	4.2	646
3	Solution Structure of the Integral Human Membrane Protein VDAC-1 in Detergent Micelles. <i>Science</i> , 2008, 321, 1206-1210.	12.6	605
4	Evidence for an Alternative Glycolytic Pathway in Rapidly Proliferating Cells. <i>Science</i> , 2010, 329, 1492-1499.	12.6	586
5	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.	2.5	578
6	Identification of small-molecule inhibitors of interaction between the BH3 domain and Bcl-xL. <i>Nature Cell Biology</i> , 2001, 3, 173-182.	10.3	536
7	Small-Molecule Inhibition of the Interaction between the Translation Initiation Factors eIF4E and eIF4G. <i>Cell</i> , 2007, 128, 257-267.	28.9	497
8	Optimized Phospholipid Bilayer Nanodiscs Facilitate High-Resolution Structure Determination of Membrane Proteins. <i>Journal of the American Chemical Society</i> , 2013, 135, 1919-1925.	13.7	445
9	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.	7.6	411
10	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.	7.1	403
11	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.	2.8	381
12	The Crystal Structure of a T Cell Receptor in Complex with Peptide and MHC Class II. <i>Science</i> , 1999, 286, 1913-1921.	12.6	376
13	An ARC/Mediator subunit required for SREBP control of cholesterol and lipid homeostasis. <i>Nature</i> , 2006, 442, 700-704.	27.8	351
14	The T Cell Receptor Is an Anisotropic Mechanosensor. <i>Journal of Biological Chemistry</i> , 2009, 284, 31028-31037.	3.4	350
15	Structure of translation factor eIF4E bound to m7GDP and interaction with 4E-binding protein. <i>Nature Structural Biology</i> , 1997, 4, 717-724.	9.7	347
16	An open-source drug discovery platform enables ultra-large virtual screens. <i>Nature</i> , 2020, 580, 663-668.	27.8	345
17	Ribosome Loading onto the mRNA Cap Is Driven by Conformational Coupling between eIF4G and eIF4E. <i>Cell</i> , 2003, 115, 739-750.	28.9	312
18	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.	13.7	308

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19	A nuclear receptor-like pathway regulating multidrug resistance in fungi. <i>Nature</i> , 2008, 452, 604-609.	27.8	294
20	Intramolecular Masking of Nuclear Import Signal on NF-AT4 by Casein Kinase I and MEKK1. <i>Cell</i> , 1998, 93, 851-861.	28.9	291
21	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.	7.1	264
22	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.	14.3	263
23	A General Framework for Development and Data Analysis of Competitive High-Throughput Screens for Small-Molecule Inhibitors of Protein-Protein Interactions by Fluorescence Polarization. <i>Biochemistry</i> , 2004, 43, 16056-16066.	2.5	243
24	NMR spectroscopy: a multifaceted approach to macromolecular structure. <i>Quarterly Reviews of Biophysics</i> , 2000, 33, 29-65.	5.7	224
25	Covalently circularized nanodiscs for studying membrane proteins and viral entry. <i>Nature Methods</i> , 2017, 14, 49-52.	19.0	221
26	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.	2.1	217
27	Structure of a Heterophilic Adhesion Complex between the Human CD2 and CD58 (LFA-3) Counterreceptors. <i>Cell</i> , 1999, 97, 791-803.	28.9	216
28	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.	7.1	209
29	Topology and Regulation of the Human eIF4A/4G/4H Helicase Complex in Translation Initiation. <i>Cell</i> , 2009, 136, 447-460.	28.9	205
30	Translation initiation: structures, mechanisms and evolution. <i>Quarterly Reviews of Biophysics</i> , 2004, 37, 197-284.	5.7	198
31	The Kinetochore-Bound Ska1 Complex Tracks Depolymerizing Microtubules and Binds to Curved Protofilaments. <i>Developmental Cell</i> , 2012, 23, 968-980.	7.0	194
32	Nuclear magnetic resonance of labile protons in the basic pancreatic trypsin inhibitor. <i>Journal of Molecular Biology</i> , 1979, 130, 1-18.	4.2	191
33	[20] Investigation of protein motions via relaxation measurements. <i>Methods in Enzymology</i> , 1994, 239, 563-596.	1.0	191
34	Electron-Transfer Reactivity and Enzymatic Activity of Hemoglobin in a SP Sephadex Membrane. <i>Analytical Chemistry</i> , 2001, 73, 2850-2854.	6.5	179
35	An Optimized 3D NOESY-HSQC. <i>Journal of Magnetic Resonance Series B</i> , 1996, 112, 200-205.	1.6	165
36	Assembly of phospholipid nanodiscs of controlled size for structural studies of membrane proteins by NMR. <i>Nature Protocols</i> , 2018, 13, 79-98.	12.0	159

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37	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.	13.7	158
38	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.	28.9	156
39	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.	7.1	154
40	In situ observation of protein phosphorylation by high-resolution NMR spectroscopy. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 321-329.	8.2	153
41	Dynamic thiolation of thioesterase structure of a non-ribosomal peptide synthetase. <i>Nature</i> , 2008, 454, 903-906.	27.8	151
42	NMR Structural Investigation of the Mitochondrial Outer Membrane Protein VDAC and Its Interaction with Antiapoptotic Bcl-xL. <i>Biochemistry</i> , 2007, 46, 514-525.	2.5	148
43	A solubility-enhancement tag (SET) for NMR studies of poorly behaving proteins. <i>Journal of Biomolecular NMR</i> , 2001, 20, 11-14.	2.8	138
44	Structural basis for the enhancement of eIF4A helicase activity by eIF4G. <i>Genes and Development</i> , 2005, 19, 2212-2223.	5.9	137
45	Solution structure of the DNA-binding domain of Cd2-GAL4 from <i>S. cerevisiae</i> . <i>Nature</i> , 1992, 356, 450-453.	27.8	134
46	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.	13.7	131
47	NMR relaxation and protein mobility. <i>Current Opinion in Structural Biology</i> , 1993, 3, 748-754.	5.7	127
48	Solution structure of the potassium channel inhibitor agitoxin 2: Caliper for probing channel geometry. <i>Protein Science</i> , 1995, 4, 1478-1489.	7.6	125
49	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.	13.7	123
50	Perspectives in magnetic resonance: NMR in the post-FFT era. <i>Journal of Magnetic Resonance</i> , 2014, 241, 60-73.	2.1	122
51	Molecular Signatures of Hemagglutinin Stem-Directed Heterosubtypic Human Neutralizing Antibodies against Influenza A Viruses. <i>PLoS Pathogens</i> , 2014, 10, e1004103.	4.7	121
52	Inhibiting fungal multidrug resistance by disrupting an activator-Mediator interaction. <i>Nature</i> , 2016, 530, 485-489.	27.8	120
53	Applications of Non-Uniform Sampling and Processing. <i>Topics in Current Chemistry</i> , 2011, 316, 125-148.	4.0	119
54	Kinetics of the exchange of individual amide protons in the basic pancreatic trypsin inhibitor. <i>Journal of Molecular Biology</i> , 1979, 130, 19-30.	4.2	117

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55	4E Binding Proteins Inhibit the Translation Factor eIF4E without Folded Structure. <i>Biochemistry</i> , 1998, 37, 9-15.	2.5	116
56	The 3D structures of VDAC represent a native conformation. <i>Trends in Biochemical Sciences</i> , 2010, 35, 514-521.	7.5	115
57	Nonmicellar systems for solution NMR spectroscopy of membrane proteins. <i>Current Opinion in Structural Biology</i> , 2010, 20, 471-479.	5.7	114
58	Structural basis for the selectivity of the external thioesterase of the surfactin synthetase. <i>Nature</i> , 2008, 454, 907-911.	27.8	112
59	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.	7.1	109
60	NMR studies of protein interactions. <i>Current Opinion in Structural Biology</i> , 2006, 16, 109-117.	5.7	106
61	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.	7.1	104
62	Unusual Rel-like architecture in the DNA-binding domain of the transcription factor NFATc. <i>Nature</i> , 1997, 385, 172-176.	27.8	103
63	Cell-free Expressed Bacteriorhodopsin in Different Soluble Membrane Mimetics: Biophysical Properties and NMR Accessibility. <i>Structure</i> , 2013, 21, 394-401.	3.3	103
64	Solution Structure of the Core NFATC1/DNA Complex. <i>Cell</i> , 1998, 92, 687-696.	28.9	101
65	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.	7.1	101
66	Application of nonlinear sampling schemes to COSY-type spectra. <i>Journal of Biomolecular NMR</i> , 1993, 3, 569-76.	2.8	97
67	Improved resolution in triple-resonance spectra by nonlinear sampling in the constant-time domain. <i>Journal of Biomolecular NMR</i> , 1994, 4, 483-490.	2.8	96
68	Solution structure of the catalytic domain of GCN5 histone acetyltransferase bound to coenzyme A. <i>Nature</i> , 1999, 400, 86-89.	27.8	96
69	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.	2.8	96
70	A constant-time three-dimensional triple-resonance pulse scheme to correlate intraresidue ^1H N, ^{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
71	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.	7.1	95
72	Tumor suppression by small molecule inhibitors of translation initiation. <i>Oncotarget</i> , 2012, 3, 869-881.	1.8	91

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73	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.	7.1	90
74	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.	13.7	89
75	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
76	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.	8.2	86
77	A new 3D HN(CA)HA experiment for obtaining fingerprint HN-H β cross peaks in ^{15}N - and ^{13}C -labeled proteins. <i>Journal of Biomolecular NMR</i> , 1992, 2, 203-210.	2.8	83
78	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
79	Aromatic ^{19}F - ^{13}C TROSY: a background-free approach to probe biomolecular structure, function, and dynamics. <i>Nature Methods</i> , 2019, 16, 333-340.	19.0	82
80	Mammalian SCAN Domain Dimer Is a Domain-Swapped Homolog of the HIV Capsid C-Terminal Domain. <i>Molecular Cell</i> , 2005, 17, 137-143.	9.7	81
81	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.	5.7	81
82	The interaction of eIF4E with 4E-BP1 is an induced fit to a completely disordered protein. <i>Protein Science</i> , 1998, 7, 1639-1642.	7.6	80
83	Dynamic interaction of CD2 with the GYF and the SH3 domain of compartmentalized effector molecules. <i>EMBO Journal</i> , 2002, 21, 5985-5995.	7.8	80
84	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.	7.1	77
85	Structure of the VP16 transactivator target in the Mediator. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 410-415.	8.2	75
86	TCR Mechanobiology: Torques and Tunable Structures Linked to Early T Cell Signaling. <i>Frontiers in Immunology</i> , 2012, 3, 76.	4.8	75
87	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
88	Overcoming the solubility limit with solubility-enhancement tags: successful applications in biomolecular NMR studies. <i>Journal of Biomolecular NMR</i> , 2010, 46, 23-31.	2.8	72
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.	7.1	72
90	Cryo-EM structure of an activated GPCR-G protein complex in lipid nanodiscs. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 258-267.	8.2	71

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91	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.	2.8	69
92	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.	14.5	69
93	Structure of the glycosylated adhesion domain of human T lymphocyte glycoprotein CD2. <i>Structure</i> , 1993, 1, 69-81.	3.3	66
94	The C-Terminal Domain of Eukaryotic Initiation Factor 5 Promotes Start Codon Recognition by Its Dynamic Interplay with eIF1 and eIF2 [†] . <i>Cell Reports</i> , 2012, 1, 689-702.	6.4	66
95	A multi-pronged approach targeting SARS-CoV-2 proteins using ultra-large virtual screening. <i>IScience</i> , 2021, 24, 102021.	4.1	66
96	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.	14.5	65
97	Lipid Dynamics and Protein-Lipid Interactions in 2D Crystals Formed with the β^2 -Barrel Integral Membrane Protein VDAC1. <i>Journal of the American Chemical Society</i> , 2012, 134, 6375-6387.	13.7	65
98	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.	13.7	63
99	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.	13.7	63
100	Quantification of Maximum-Entropy Spectrum Reconstructions. <i>Journal of Magnetic Resonance</i> , 1997, 125, 332-339.	2.1	62
101	Pre-TCR ligand binding impacts thymocyte development before β^2 TCR expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8373-8378.	7.1	62
102	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.	2.8	61
103	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.	13.7	61
104	Pre-T Cell Receptors (Pre-TCRs) Leverage β^2 Complementarity Determining Regions (CDRs) and Hydrophobic Patch in Mechanosensing Thymic Self-ligands. <i>Journal of Biological Chemistry</i> , 2016, 291, 25292-25305.	3.4	60
105	Increased Sensitivity in HNCA and HN(CO)CA Experiments by Selective C^{13} Decoupling. <i>Journal of Magnetic Resonance Series B</i> , 1996, 113, 91-96.	1.6	59
106	Fast Assignment of ^{15}N -HSQC Peaks using High-Resolution 3D HNCOCA Experiments with Non-Uniform Sampling. <i>Journal of Biomolecular NMR</i> , 2005, 33, 43-50.	2.8	59
107	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.	2.5	58
108	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.	13.7	58

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109	The T Cell Antigen Receptor $\hat{\pm}$ Transmembrane Domain Coordinates Triggering through Regulation of Bilayer Immersion and CD3 Subunit Associations. <i>Immunity</i> , 2018, 49, 829-841.e6.	14.3	58
110	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.	13.7	57
111	Modulating TRADD to restore cellular homeostasis and inhibit apoptosis. <i>Nature</i> , 2020, 587, 133-138.	27.8	57
112	Use of Selective C $\hat{\pm}$ Pulses for Improvement of HN(CA)CO $\hat{\pm}$ D and HN(COCA)NH $\hat{\pm}$ D Experiments. <i>Journal of Magnetic Resonance Series B</i> , 1996, 111, 194-198.	1.6	56
113	Molecular Framework for the Activation of RNA-dependent Protein Kinase. <i>Journal of Biological Chemistry</i> , 2007, 282, 11474-11486.	3.4	56
114	Hypoxia-inducible Factor-1 $\hat{\pm}$ (HIF-1 $\hat{\pm}$) 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.	3.4	55
115	Structural Features of the $\hat{\pm}$ $\hat{\pm}$ TCR Mechanotransduction Apparatus That Promote pMHC Discrimination. <i>Frontiers in Immunology</i> , 2015, 6, 441.	4.8	55
116	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.	6.4	54
117	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.	2.6	53
118	Solution structure of villin 14T, a domain conserved among actin $\hat{\pm}$ severing proteins. <i>Protein Science</i> , 1994, 3, 70-81.	7.6	52
119	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.	7.1	52
120	Structure and mobility of the PUT3 dimer. <i>Nature Structural Biology</i> , 1997, 4, 744-750.	9.7	51
121	Coupled Decomposition of Four-Dimensional NOESY Spectra. <i>Journal of the American Chemical Society</i> , 2009, 131, 12970-12978.	13.7	51
122	Discovery and Characterization of a Disulfide-Locked $\langle i \rangle C \langle /i \rangle \langle sub \rangle 2 \langle /sub \rangle$ -Symmetric Defensin Peptide. <i>Journal of the American Chemical Society</i> , 2014, 136, 13494-13497.	13.7	50
123	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.	3.3	49
124	1-13C amino acid selective labeling in a 2H15N background for NMR studies of large proteins. <i>Journal of Biomolecular NMR</i> , 2007, 38, 89-98.	2.8	49
125	IBIS—a tool for automated sequential assignment of protein spectra from triple resonance experiments. <i>Journal of Biomolecular NMR</i> , 2003, 26, 335-344.	2.8	48
126	NMR Methods for Studying Protein $\hat{\pm}$ Protein Interactions Involved in Translation Initiation. <i>Methods in Enzymology</i> , 2007, 430, 283-331.	1.0	48

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127	Structure refinement and membrane positioning of selectively labeled OmpX in phospholipid nanodiscs. <i>Journal of Biomolecular NMR</i> , 2015, 61, 249-260.	2.8	48
128	NMR Solution Structure and Condition-Dependent Oligomerization of the Antimicrobial Peptide Human Defensin 5. <i>Biochemistry</i> , 2012, 51, 9624-9637.	2.5	45
129	Proton resonance assignments and secondary structure of the 13.6 kDa glycosylated adhesion domain of human CD2. <i>Biochemistry</i> , 1993, 32, 10995-11006.	2.5	44
130	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.	7.6	44
131	Î²-Hairpin Loop of Eukaryotic Initiation Factor 1 (eIF1) Mediates 40 S Ribosome Binding to Regulate Initiator tRNAMet Recruitment and Accuracy of AUG Selection in Vivo. <i>Journal of Biological Chemistry</i> , 2013, 288, 27546-27562.	3.4	44
132	Structural and Functional Evidence that Nck Interaction with CD3Î¼ Regulates T-Cell Receptor Activity. <i>Journal of Molecular Biology</i> , 2008, 380, 704-716.	4.2	43
133	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.	3.4	43
134	Structure of a CGI-58 Motif Provides the Molecular Basis of Lipid Droplet Anchoring. <i>Journal of Biological Chemistry</i> , 2015, 290, 26361-26372.	3.4	43
135	Discovery of Small-Molecule Inhibitors of the NFATâˆ©Calcineurin Interaction by Competitive High-Throughput Fluorescence Polarization Screeningâ€¢. <i>Biochemistry</i> , 2004, 43, 16067-16075.	2.5	42
136	Alternate ¹³ C ¹² C Labeling for Complete Mainchain Resonance Assignments using CÎ± Direct-Detection with Applicability Toward Fast Relaxing Protein Systems. <i>Journal of the American Chemical Society</i> , 2008, 130, 17210-17211.	13.7	42
137	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.	8.2	42
138	Nitrogen detected TROSY at high field yields high resolution and sensitivity for protein NMR. <i>Journal of Biomolecular NMR</i> , 2015, 63, 323-331.	2.8	40
139	Overexpression of eIF5 or its protein mimic 5MP perturbs eIF2 function and induces ATF4 translation through delayed re-initiation. <i>Nucleic Acids Research</i> , 2016, 44, 8704-8713.	14.5	40
140	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.	7.1	40
141	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.	3.4	39
142	eIF1A augments Ago2-mediated Dicer-independent miRNA biogenesis and RNA interference. <i>Nature Communications</i> , 2015, 6, 7194.	12.8	39
143	Multiple-quantum magic-angle spinning spectroscopy using nonlinear sampling. <i>Journal of Magnetic Resonance</i> , 2003, 161, 43-55.	2.1	38
144	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.	2.8	38

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145	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.	13.7	37
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