Geerten W Vuister

List of Publications by Year
in descending order

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92 papers	6,257 citations	66343 42 h-index	69250 77 g-index
96 all docs	96 docs citations	96 times ranked	6213 citing authors

#	Article	IF	Citations
1	Quantitative J correlation: a new approach for measuring homonuclear three-bond J(HNH.alpha.) coupling constants in 15N-enriched proteins. Journal of the American Chemical Society, 1993, 115, 7772-7777.	13.7	1,074
2	[2] Measurement of homo- and heteronuclear J couplings from quantitative J correlation. Methods in Enzymology, 1994, 239, 79-105.	1.0	373
3	CcpNmr AnalysisAssign: a flexible platform for integrated NMR analysis. Journal of Biomolecular NMR, 2016, 66, 111-124.	2.8	231
4	Ca2+ Regulation in the Na+/Ca2+ Exchanger Involves Two Markedly Different Ca2+ Sensors. Molecular Cell, 2006, 22, 15-25.	9.7	184
5	WeNMR: Structural Biology on the Grid. Journal of Grid Computing, 2012, 10, 743-767.	3.9	170
6	Measurement of three-bond nitrogen-carbon J couplings in proteins uniformly enriched in nitrogen-15 and carbon-13. Journal of the American Chemical Society, 1993, 115, 5334-5335.	13.7	167
7	Structural and dynamic changes of photoactive yellow protein during its photocycle in solution. Nature Structural Biology, 1998, 5, 568-570.	9.7	155
8	Recommendations of the wwPDB NMR Validation Task Force. Structure, 2013, 21, 1563-1570.	3.3	151
9	Solution Structure and Backbone Dynamics of the Photoactive Yellow Proteinâ€‚â€¡. Biochemistry, 1998, 37, 12689-12699.	2.5	129
10	Gradient-enhanced HMQC and HSQC spectroscopy. Applications to 15N-labeled Mnt repressor. Journal of the American Chemical Society, 1991, 113, 9688-9690.	13.7	128
11	2D and 3D NMR Study of Phenylalanine Residues in Proteins by Reverse Isotopic Labeling. Journal of the American Chemical Society, 1994, 116, 9206-9210.	13.7	126
12	The solution structure and DNA-binding properties of the cold-shock domain of the human Y-box protein YB-1. Journal of Molecular Biology, 2002, 316, 317-326.	4.2	121
13	Resolution enhancement and spectral editing of uniformly 13C-enriched proteins by homonuclear broadband 13C decoupling. Journal of Magnetic Resonance, 1992, 98, 428-435.	0.5	117
14	Solution structure of the DNA-binding domain of Drosophila heat shock transcription factor. Nature Structural and Molecular Biology, 1994, 1, 605-614.	8.2	115
15	CING: an integrated residue-based structure validation program suite. Journal of Biomolecular NMR, 2012, 54, 267-283.	2.8	106
16	A Cell-penetrating Peptide Derived from Human Lactoferrin with Conformation-dependent Uptake Efficiency. Journal of Biological Chemistry, 2009, 284, 36099-36108.	3.4	105
17	Demonstration of Long-Range Interactions in a PDZ Domain by NMR, Kinetics, and Protein Engineering. Structure, 2006, 14, 1801-1809.	3.3	103
18	ATP-induced conformational changes of the nucleotide-binding domain of Na,K-ATPase. Nature Structural and Molecular Biology, 2003, 10, 468-474.	8.2	97

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19	Quantitative Measurement of Relaxation Interference Effects between1HNCSA and1Hâ^'15N Dipolar Interaction:Â Correlation with Secondary Structure. Journal of the American Chemical Society, 1997, 119, 8985-8990.	13.7	94
20	DRESS: a database of REfined solution NMR structures. Proteins: Structure, Function and Bioinformatics, 2004, 55, 483-486.	2.6	91
21	Improving the quality of protein structures derived by NMR spectroscopy. Journal of Biomolecular NMR, 2002, 22, 281-289.	2.8	88
22	Binding of the AVR4 Elicitor of Cladosporium fulvum to Chitotriose Units Is Facilitated by Positive Allosteric Protein-Protein Interactions. Journal of Biological Chemistry, 2004, 279, 16786-16796.	3.4	83
23	Quantitative Evaluation of Experimental NMR Restraints. Journal of the American Chemical Society, 2003, 125, 12026-12034.	13.7	81
24	CASD-NMR: critical assessment of automated structure determination by NMR. Nature Methods, 2009, 6, 625-626.	19.0	80
25	Molecular Mechanisms of Calmodulin Action on TRPV5 and Modulation by Parathyroid Hormone. Molecular and Cellular Biology, 2011, 31, 2845-2853.	2.3	78
26	Traditional Biomolecular Structure Determination by NMR Spectroscopy Allows for Major Errors. PLoS Computational Biology, 2006, 2, e9.	3.2	76
27	Blind Testing of Routine, Fully Automated Determination of Protein Structures from NMR Data. Structure, 2012, 20, 227-236.	3.3	75
28	The precision of NMR structure ensembles revisited. Journal of Biomolecular NMR, 2003, 25, 225-234.	2.8	74
29	Ca ²⁺ regulation in the Na ⁺ /Ca ²⁺ exchanger features a dual electrostatic switch mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 14333-14338.	7.1	73
30	Structure, dynamics and binding characteristics of the second PDZ domain of PTP-BL. Journal of Molecular Biology, 2002, 316, 1101-1110.	4.2	72
31	Structural diversity in twin-arginine signal peptide-binding proteins. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 15641-15646.	7.1	71
32	Validation of protein structures derived by NMR spectroscopy. Progress in Nuclear Magnetic Resonance Spectroscopy, 2004, 45, 315-337.	7.5	70
33	A PDZ domain recapitulates a unifying mechanism for protein folding. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 128-133.	7.1	69
34	An empirical correlation between 1JC.alpha.H.alpha. and protein backbone conformation. Journal of the American Chemical Society, 1992, 114, 9674-9675.	13.7	68
35	Structure calculation, refinement and validation usingCcpNmr Analysis. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 154-161.	2.5	67
36	The use of 1JC?H? coupling constants as a probe for protein backbone conformation. Journal of Biomolecular NMR, 1993, 3, 67-80.	2.8	65

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37	An Allosteric Intramolecular PDZâ^'PDZ Interaction Modulates PTP-BL PDZ2 Binding Specificity. Biochemistry, 2007, 46, 13629-13637.	2.5	56
38	The Mad1-Sin3B interaction involves a novel helical fold. Nature Structural Biology, 2000, 7, 1100-1104.	9.7	52
39	Measurement of two-bond JCOHÎ± coupling constants in proteins uniformly enriched with13C. Journal of Biomolecular NMR, 1992, 2, 401-405.	2.8	50
40	Kinetic folding mechanism of PDZ2 from PTP-BL. Protein Engineering, Design and Selection, 2005, 18, 389-395.	2.1	50
41	Resonance assignment of methionine methyl groups and ?3angular information from long-range proton?carbon and carbon?carbon J correlation in a calmodulin?peptide complex. Journal of Biomolecular NMR, 1994, 4, 787-797.	2.8	49
42	Structural analysis of calmodulin binding to ion channels demonstrates the role of its plasticity in regulation. Pflugers Archiv European Journal of Physiology, 2013, 465, 1507-1519.	2.8	42
43	NMR Exchange Format: a unified and open standard for representation of NMR restraint data. Nature Structural and Molecular Biology, 2015, 22, 433-434.	8.2	40
44	Measurement of (15)N- (1)H coupling constants in uniformly (15)N-labeled proteins: Application to the photoactive yellow protein. Journal of Biomolecular NMR, 1997, 10, 301-306.	2.8	38
45	Homonuclear three-dimensional proton NMR spectroscopy of pike parvalbumin. Comparison of short- and medium-range NOEs from 2D and 3D NMR. Journal of the American Chemical Society, 1990, 112, 5024-5030.	13.7	36
46	NRG-CING: integrated validation reports of remediated experimental biomolecular NMR data and coordinates in wwPDB. Nucleic Acids Research, 2012, 40, D519-D524.	14.5	34
47	An overview of tools for the validation of protein NMR structures. Journal of Biomolecular NMR, 2014, 58, 259-285.	2.8	34
48	Extension of the Binding Motif of the Sin3 Interacting Domain of the Mad Family Proteinsâ€,â€¡. Biochemistry, 2004, 43, 46-54.	2.5	32
49	A novel experiment for the quantitative measurement of CSA(1H(N))/CSA(15N) cross-correlated relaxation in 15N-labeled proteins. Journal of Biomolecular NMR, 2000, 16, 171-174.	2.8	30
50	Structure and Dynamics of Ca2+-Binding Domain 1 of the Na+/Ca2+ Exchanger in the Presence and in the Absence of Ca2+. Journal of Molecular Biology, 2008, 377, 945-955.	4.2	30
51	The TRPV5/6 calcium channels contain multiple calmodulin binding sites with differential binding properties. Journal of Structural and Functional Genomics, 2012, 13, 91-100.	1.2	30
52	A Closed Binding Pocket and Global Destabilization Modify the Binding Properties of an Alternatively Spliced Form of the Second PDZ Domain of PTP-BL. Structure, 2004, 12, 11-20.	3.3	29
53	Gradient-enhanced 3D NOESY-HMQC spectroscopy. Journal of Biomolecular NMR, 1992, 2, 301-305.	2.8	27
54	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.	2.8	27

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55	A Novel Mechanism for Calmodulin-Dependent Inactivation of Transient Receptor Potential Vanilloid 6. Biochemistry, 2018, 57, 2611-2622.	2.5	27
56	Sin3A recruits Tet1 to the PAH1 domain via a highly conserved Sin3-Interaction Domain. Scientific Reports, 2018, 8, 14689.	3.3	27
57	The NMR restraints grid at BMRB for 5,266 protein and nucleic acid PDB entries. Journal of Biomolecular NMR, 2009, 45, 389-396.	2.8	26
58	Accurate Prediction of the Dynamical Changes within the Second PDZ Domain of PTP1e. PLoS Computational Biology, 2012, 8, e1002794.	3.2	25
59	Structural Basis for Ca2+ Regulation in the Na+/Ca2+ Exchanger. Annals of the New York Academy of Sciences, 2007, 1099, 7-15.	3.8	19
60	Simple highâ€resolution <scp>NMR</scp> spectroscopy as a tool in molecular biology. FEBS Journal, 2019, 286, 2035-2042.	4.7	19
61	NMR Experiments for the Study of Photointermediates: Application to the Photoactive Yellow Protein. Journal of Magnetic Resonance, 1999, 137, 443-447.	2.1	18
62	Cold Shock Domain of the Human Y-Box Protein YB-1. Backbone Dynamics and Equilibrium between the Native State and a Partially Unfolded Stateâ€. Biochemistry, 2004, 43, 10237-10246.	2.5	18
63	The Structural Basis of Calcium-Dependent Inactivation of the Transient Receptor Potential Vanilloid 5 Channel. Biochemistry, 2018, 57, 2623-2635.	2.5	18
64	Role of Structural and Dynamical Plasticity in Sin3: The Free PAH2 Domain is a Folded Module in mSin3B. Journal of Molecular Biology, 2006, 358, 485-497.	4.2	17
65	Binding of calcium is sensed structurally and dynamically throughout the second calciumâ€binding domain of the sodium/calcium exchanger. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1813-1824.	2.6	17
66	The Second Ca²⁺-Binding Domain of NCX1 Binds Mg²⁺ with High Affinity. Biochemistry, 2011, 50, 8804-8812.	2.5	17
67	Overlapping transport and chaperoneâ€binding functions within a bacterial twinâ€arginine signal peptide. Molecular Microbiology, 2012, 83, 1254-1267.	2.5	16
68	Structural Analysis of an Epidermal Growth Factor/Transforming Growth Factor-Î± Chimera with Unique ErbB Binding Specificity. Journal of Biological Chemistry, 2003, 278, 39114-39123.	3.4	15
69	Concepts and tools for NMR restraint analysis and validation. Concepts in Magnetic Resonance, 2004, 22A, 90-105.	1.3	14
70	Solution Structure of the Second PDZ Domain of the Neuronal Adaptor X11Î± and its Interaction with the C-terminal Peptide of the Human Copper Chaperone for Superoxide Dismutase. Journal of Biomolecular NMR, 2005, 32, 209-218.	2.8	14
71	Fragment-Based Drug Discovery by NMR. Where Are the Successes and Where can It Be Improved?. Frontiers in Molecular Biosciences, 2022, 9, 834453.	3.5	14
72	The interaction of PTP-BL PDZ domains with RIL: An enigmatic role for the RIL LIM domain. Molecular Biology Reports, 2005, 31, 203-215.	2.3	13

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73	Sulfonylurea receptors regulate the channel pore in ATP-sensitive potassium channels via an intersubunit salt bridge. Biochemical Journal, 2014, 464, 343-354.	3.7	13
74	A 15n-filtered 2D 1H TOCSY experiment for assignment of aromatic ring resonances and selective identification of tyrosine ring resonances in proteins: Description and application to Photoactive Yellow Protein. Journal of Biomolecular NMR, 1997, 9, 313-316.	2.8	12
75	Definition of a New Information-Based Per-Residue Quality Parameter. Journal of Biomolecular NMR, 2005, 33, 123-134.	2.8	12
76	CEESY:Â Characterizing the Conformation of Unobservable Protein States. Journal of the American Chemical Society, 2006, 128, 3856-3857.	13.7	9
77	Overview on the Use of NMR to Examine Protein Structure. Current Protocols in Protein Science, 2011, 64, Unit17.5.	2.8	9
78	Statistical analysis of double NOE transfer pathways in proteins as measured in 3D NOE-NOE spectroscopy. Journal of Biomolecular NMR, 1991, 1, 421-438.	2.8	8
79	CcpNmr AnalysisScreen, a new software programme with dedicated automated analysis tools for fragment-based drug discovery by NMR. Journal of Biomolecular NMR, 2020, 74, 565-577.	2.8	8
80	Expression and purification of the C-terminal fragments of TRPV5/6 channels. Protein Expression and Purification, 2011, 80, 28-33.	1.3	7
81	Structural and dynamic aspects of Ca2+ and Mg2+ binding of the regulatory domains of the Na+/Ca2+ exchanger. Biochemical Society Transactions, 2012, 40, 409-414.	3.4	7
82	NMR structure note: solution structure of Ca2+ binding domain 2B of the third isoform of the Na+/Ca2+ exchanger. Journal of Biomolecular NMR, 2012, 54, 115-121.	2.8	6
83	Pulse Sequences for Measuring Coupling Constants. , 2002, , 195-257.		5
84	NMR-Based Modeling and Refinement of Protein 3D Structures. Methods in Molecular Biology, 2015, 1215, 351-380.	0.9	5
85	Sequence-specific assignment of the PAH2 domain of Sin3B free and bound to Mad1. Journal of Biomolecular NMR, 2001, 19, 377-378.	2.8	4
86	Analysis of the structural quality of the CASD-NMR 2013 entries. Journal of Biomolecular NMR, 2015, 62, 527-540.	2.8	4
87	Resonance assignment and secondary structure of the cold shock domain of the human YB-1 protein. Journal of Biomolecular NMR, 1998, 12, 463-464.	2.8	3
88	Sequence-specific 1H, 13C and 15N assignment of the EH1 domain of mouse Eps15. Journal of Biomolecular NMR, 1998, 12, 465-466.	2.8	2
89	A 3D doubly sensitivity enhanced X-filtered TOCSY-TOCSY experiment. Journal of Biomolecular NMR, 2002, 24, 155-160.	2.8	2
90	Sequence-specific 1H, 13C and 15N assignment and secondary structure of the apo EH2 domain of mouse Eps15. Journal of Biomolecular NMR, 1999, 14, 97-98.	2.8	1

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91	Sequence-specific 1H, 13C and 15N assignment of the single-stranded DNA binding protein of the bacteriophage phi 29. Journal of Biomolecular NMR, 1999, 13, 303-304.	2.8	0
92	Recent Developments in Protein NMR Spectroscopy. , 1996, , 117-120.		0