Geerten W Vuister

List of Publications by Year
in descending order

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92 papers	6,257 citations	66234 42 h-index	69108 77 g-index
96 all docs	96 docs citations	96 times ranked	6213 citing authors

#	Article	IF	Citations
1	Fragment-Based Drug Discovery by NMR. Where Are the Successes and Where can It Be Improved?. Frontiers in Molecular Biosciences, 2022, 9, 834453.	1.6	14
2	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.	1.6	8
3	Simple highâ€resolution <scp>NMR</scp> spectroscopy as a tool in molecular biology. FEBS Journal, 2019, 286, 2035-2042.	2.2	19
4	A Novel Mechanism for Calmodulin-Dependent Inactivation of Transient Receptor Potential Vanilloid 6. Biochemistry, 2018, 57, 2611-2622.	1.2	27
5	The Structural Basis of Calcium-Dependent Inactivation of the Transient Receptor Potential Vanilloid 5 Channel. Biochemistry, 2018, 57, 2623-2635.	1.2	18
6	Sin3A recruits Tet1 to the PAH1 domain via a highly conserved Sin3-Interaction Domain. Scientific Reports, 2018, 8, 14689.	1.6	27
7	CcpNmr AnalysisAssign: a flexible platform for integrated NMR analysis. Journal of Biomolecular NMR, 2016, 66, 111-124.	1.6	231
8	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
9	Structure calculation, refinement and validation usingCcpNmr Analysis. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 154-161.	2.5	67
10	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
11	Analysis of the structural quality of the CASD-NMR 2013 entries. Journal of Biomolecular NMR, 2015, 62, 527-540.	1.6	4
12	NMR-Based Modeling and Refinement of Protein 3D Structures. Methods in Molecular Biology, 2015, 1215, 351-380.	0.4	5
13	Sulfonylurea receptors regulate the channel pore in ATP-sensitive potassium channels via an intersubunit salt bridge. Biochemical Journal, 2014, 464, 343-354.	1.7	13
14	An overview of tools for the validation of protein NMR structures. Journal of Biomolecular NMR, 2014, 58, 259-285.	1.6	34
15	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.	1.3	42
16	Recommendations of the wwPDB NMR Validation Task Force. Structure, 2013, 21, 1563-1570.	1.6	151
17	NRG-CING: integrated validation reports of remediated experimental biomolecular NMR data and coordinates in wwPDB. Nucleic Acids Research, 2012, 40, D519-D524.	6.5	34
18	Accurate Prediction of the Dynamical Changes within the Second PDZ Domain of PTP1e. PLoS Computational Biology, 2012, 8, e1002794.	1.5	25

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19	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.	1.6	7
20	WeNMR: Structural Biology on the Grid. Journal of Grid Computing, 2012, 10, 743-767.	2.5	170
21	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.	1.6	6
22	CING: an integrated residue-based structure validation program suite. Journal of Biomolecular NMR, 2012, 54, 267-283.	1.6	106
23	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
24	Overlapping transport and chaperoneâ€binding functions within a bacterial twinâ€arginine signal peptide. Molecular Microbiology, 2012, 83, 1254-1267.	1.2	16
25	Blind Testing of Routine, Fully Automated Determination of Protein Structures from NMR Data. Structure, 2012, 20, 227-236.	1.6	75
26	The Second Ca²⁺-Binding Domain of NCX1 Binds Mg²⁺ with High Affinity. Biochemistry, 2011, 50, 8804-8812.	1.2	17
27	Expression and purification of the C-terminal fragments of TRPV5/6 channels. Protein Expression and Purification, 2011, 80, 28-33.	0.6	7
28	Overview on the Use of NMR to Examine Protein Structure. Current Protocols in Protein Science, 2011, 64, Unit17.5.	2.8	9
29	Molecular Mechanisms of Calmodulin Action on TRPV5 and Modulation by Parathyroid Hormone. Molecular and Cellular Biology, 2011, 31, 2845-2853.	1.1	78
30	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.	1.5	17
31	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.	3.3	73
32	A Cell-penetrating Peptide Derived from Human Lactoferrin with Conformation-dependent Uptake Efficiency. Journal of Biological Chemistry, 2009, 284, 36099-36108.	1.6	105
33	The NMR restraints grid at BMRB for 5,266 protein and nucleic acid PDB entries. Journal of Biomolecular NMR, 2009, 45, 389-396.	1.6	26
34	CASD-NMR: critical assessment of automated structure determination by NMR. Nature Methods, 2009, 6, 625-626.	9.0	80
35	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.	2.0	30
36	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.	3.3	71

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37	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.	3.3	69
38	An Allosteric Intramolecular PDZâˆ’PDZ Interaction Modulates PTP-BL PDZ2 Binding Specificity. Biochemistry, 2007, 46, 13629-13637.	1.2	56
39	Structural Basis for Ca2+ Regulation in the Na+/Ca2+ Exchanger. Annals of the New York Academy of Sciences, 2007, 1099, 7-15.	1.8	19
40	CEESY:Â Characterizing the Conformation of Unobservable Protein States. Journal of the American Chemical Society, 2006, 128, 3856-3857.	6.6	9
41	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.	2.0	17
42	Ca2+ Regulation in the Na+/Ca2+ Exchanger Involves Two Markedly Different Ca2+ Sensors. Molecular Cell, 2006, 22, 15-25.	4.5	184
43	Demonstration of Long-Range Interactions in a PDZ Domain by NMR, Kinetics, and Protein Engineering. Structure, 2006, 14, 1801-1809.	1.6	103
44	Traditional Biomolecular Structure Determination by NMR Spectroscopy Allows for Major Errors. PLoS Computational Biology, 2006, 2, e9.	1.5	76
45	Definition of a New Information-Based Per-Residue Quality Parameter. Journal of Biomolecular NMR, 2005, 33, 123-134.	1.6	12
46	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.	1.6	14
47	The interaction of PTP-BL PDZ domains with RIL: An enigmatic role for the RIL LIM domain. Molecular Biology Reports, 2005, 31, 203-215.	1.0	13
48	Kinetic folding mechanism of PDZ2 from PTP-BL. Protein Engineering, Design and Selection, 2005, 18, 389-395.	1.0	50
49	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.	1.6	83
50	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.	1.6	29
51	DRESS: a database of REfined solution NMR structures. Proteins: Structure, Function and Bioinformatics, 2004, 55, 483-486.	1.5	91
52	Concepts and tools for NMR restraint analysis and validation. Concepts in Magnetic Resonance, 2004, 22A, 90-105.	1.3	14
53	Validation of protein structures derived by NMR spectroscopy. Progress in Nuclear Magnetic Resonance Spectroscopy, 2004, 45, 315-337.	3.9	70
54	Extension of the Binding Motif of the Sin3 Interacting Domain of the Mad Family Proteinsâ€,â€¡. Biochemistry, 2004, 43, 46-54.	1.2	32

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55	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.	1.2	18
56	The precision of NMR structure ensembles revisited. Journal of Biomolecular NMR, 2003, 25, 225-234.	1.6	74
57	ATP-induced conformational changes of the nucleotide-binding domain of Na,K-ATPase. Nature Structural and Molecular Biology, 2003, 10, 468-474.	3.6	97
58	Quantitative Evaluation of Experimental NMR Restraints. Journal of the American Chemical Society, 2003, 125, 12026-12034.	6.6	81
59	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.	1.6	15
60	Pulse Sequences for Measuring Coupling Constants. , 2002, , 195-257.		5
61	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.	2.0	121
62	Structure, dynamics and binding characteristics of the second PDZ domain of PTP-BL. Journal of Molecular Biology, 2002, 316, 1101-1110.	2.0	72
63	Improving the quality of protein structures derived by NMR spectroscopy. Journal of Biomolecular NMR, 2002, 22, 281-289.	1.6	88
64	A 3D doubly sensitivity enhanced X-filtered TOCSY-TOCSY experiment. Journal of Biomolecular NMR, 2002, 24, 155-160.	1.6	2
65	Sequence-specific assignment of the PAH2 domain of Sin3B free and bound to Mad1. Journal of Biomolecular NMR, 2001, 19, 377-378.	1.6	4
66	The Mad1-Sin3B interaction involves a novel helical fold. Nature Structural Biology, 2000, 7, 1100-1104.	9.7	52
67	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.	1.6	30
68	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.	1.6	0
69	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.	1.6	1
70	NMR Experiments for the Study of Photointermediates: Application to the Photoactive Yellow Protein. Journal of Magnetic Resonance, 1999, 137, 443-447.	1.2	18
71	Resonance assignment and secondary structure of the cold shock domain of the human YB-1 protein. Journal of Biomolecular NMR, 1998, 12, 463-464.	1.6	3
72	Sequence-specific 1H, 13C and 15N assignment of the EH1 domain of mouse Eps15. Journal of Biomolecular NMR, 1998, 12, 465-466.	1.6	2

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73	Solution Structure and Backbone Dynamics of the Photoactive Yellow Proteinâ€,â€¡. Biochemistry, 1998, 37, 12689-12699.	1.2	129
74	Structural and dynamic changes of photoactive yellow protein during its photocycle in solution. Nature Structural Biology, 1998, 5, 568-570.	9.7	155
75	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.	6.6	94
76	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.	1.6	38
77	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.	1.6	12
78	Recent Developments in Protein NMR Spectroscopy. , 1996, , 117-120.		0
79	[2] Measurement of homo- and heteronuclear J couplings from quantitative J correlation. Methods in Enzymology, 1994, 239, 79-105.	0.4	373
80	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.	1.6	49
81	Solution structure of the DNA-binding domain of Drosophila heat shock transcription factor. Nature Structural and Molecular Biology, 1994, 1, 605-614.	3.6	115
82	2D and 3D NMR Study of Phenylalanine Residues in Proteins by Reverse Isotopic Labeling. Journal of the American Chemical Society, 1994, 116, 9206-9210.	6.6	126
83	The use of 1JC?H? coupling constants as a probe for protein backbone conformation. Journal of Biomolecular NMR, 1993, 3, 67-80.	1.6	65
84	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.	6.6	1,074
85	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.	6.6	167
86	An empirical correlation between 1JC.alpha.H.alpha. and protein backbone conformation. Journal of the American Chemical Society, 1992, 114, 9674-9675.	6.6	68
87	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
88	Measurement of two-bond JCOHÎ± coupling constants in proteins uniformly enriched with13C. Journal of Biomolecular NMR, 1992, 2, 401-405.	1.6	50
89	Gradient-enhanced 3D NOESY-HMQC spectroscopy. Journal of Biomolecular NMR, 1992, 2, 301-305.	1.6	27
90	Gradient-enhanced HMQC and HSQC spectroscopy. Applications to 15N-labeled Mnt repressor. Journal of the American Chemical Society, 1991, 113, 9688-9690.	6.6	128

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91	Statistical analysis of double NOE transfer pathways in proteins as measured in 3D NOE-NOE spectroscopy. Journal of Biomolecular NMR, 1991, 1, 421-438.	1.6	8
92	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.	6.6	36