

Carine van Heijenoort

List of Publications by Year in descending order

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57
papers

1,415
citations

430874

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330143

37
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60
all docs

60
docs citations

60
times ranked

1656
citing authors

#	ARTICLE	IF	CITATIONS
1	Optimisation of spatially encoded diffusion ordered NMR spectroscopy for the analysis of mixtures. <i>Magnetic Resonance in Chemistry</i> , 2022, 60, 121-138.	1.9	8
2	Fluorinated Triazole Foldamers: Folded or Extended Conformational Preferences. <i>ChemPlusChem</i> , 2021, 86, 241-251.	2.8	3
3	Structural and dynamic characterization of the C-terminal tail of ErbB2: Disordered but not random. <i>Biophysical Journal</i> , 2021, 120, 1869-1882.	0.5	5
4	$\hat{\text{I}}^2$ -Hairpin Peptide Mimics Decrease Human Islet Amyloid Polypeptide (hIAPP) Aggregation. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 729001.	3.7	6
5	Expanding the Disorder-Function Paradigm in the C-Terminal Tails of Erbbs. <i>Biomolecules</i> , 2021, 11, 1690.	4.0	2
6	^{13}C , ^{15}N and ^{15}N assignments of human Grb2 free of ligands. <i>Biomolecular NMR Assignments</i> , 2020, 14, 323-327.	0.8	0
7	NMR Characterization of the Influence of Zinc(II) Ions on the Structural and Dynamic Behavior of the New Delhi Metallo- $\hat{\text{I}}^2$ -Lactamase-1 and on the Binding with Flavonols as Inhibitors. <i>ACS Omega</i> , 2020, 5, 10466-10480.	3.5	19
8	Structural Characterization of N-WASP Domain V Using MD Simulations with NMR and SAXS Data. <i>Biophysical Journal</i> , 2019, 116, 1216-1227.	0.5	18
9	Single Scan Diffusion Ordered NMR Spectroscopy of SABRE Hyperpolarized Mixtures. <i>ChemPhysChem</i> , 2019, 20, 392-398.	2.1	14
10	^1H , ^{13}C and ^{15}N assignments of the C-terminal intrinsically disordered cytosolic fragment of the receptor tyrosine kinase ErbB2. <i>Biomolecular NMR Assignments</i> , 2018, 12, 23-26.	0.8	5
11	Structure-activity relationships of $\hat{\text{I}}^2$ -hairpin mimics as modulators of amyloid $\hat{\text{I}}^2$ -peptide aggregation. <i>European Journal of Medicinal Chemistry</i> , 2018, 154, 280-293.	5.5	15
12	Modulation of the HIV nucleocapsid dynamics finely tunes its RNA-binding properties during virion genesis. <i>Nucleic Acids Research</i> , 2018, 46, 9699-9710.	14.5	6
13	Spatially encoded diffusion-ordered NMR spectroscopy of reaction mixtures in organic solvents. <i>Analyst</i> , 2018, 143, 3458-3464.	3.5	17
14	Spatially encoded 2D and 3D diffusion-ordered NMR spectroscopy. <i>Chemical Communications</i> , 2017, 53, 701-704.	4.1	48
15	Efficient simulation of ultrafast magnetic resonance experiments. <i>Physical Chemistry Chemical Physics</i> , 2017, 19, 17577-17586.	2.8	16
16	Single Scan ^{13}C Diffusion Ordered NMR Spectroscopy of DNP Hyperpolarised Substrates. <i>Chemistry - A European Journal</i> , 2017, 23, 16722-16727.	3.3	34
17	Frontispiece: Single Scan ^{13}C Diffusion Ordered NMR Spectroscopy of DNP Hyperpolarised Substrates. <i>Chemistry - A European Journal</i> , 2017, 23, .	3.3	0
18	Mutations in actin used for structural studies partially disrupt $\hat{\text{I}}^2$ -thymosin/WH2 domains interaction. <i>FEBS Letters</i> , 2016, 590, 3690-3699.	2.8	3

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19	Robust and low cost uniform ¹⁵ N-labeling of proteins expressed in Drosophila S2 cells and Spodoptera frugiperda Sf9 cells for NMR applications. <i>Journal of Structural Biology</i> , 2014, 188, 71-78.	2.8	19
20	Structural features and interfacial properties of WH2, $\hat{\gamma}$ -thymosin domains and other intrinsically disordered domains in the regulation of actin cytoskeleton dynamics. <i>Cytoskeleton</i> , 2013, 70, 686-705.	2.0	23
21	How a single residue in individual $\hat{\gamma}$ -thymosin/WH2 domains controls their functions in actin assembly. <i>EMBO Journal</i> , 2012, 31, 1000-1013.	7.8	53
22	Amphipols From A to Z. <i>Annual Review of Biophysics</i> , 2011, 40, 379-408.	10.0	226
23	An unfolding model for the GDP/GTP conformational switch of the GTPase Arf6. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2011, 67, C347-C347.	0.3	0
24	What makes homologous small GTPases specific? A combined X-ray, SAXS and NMR study. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2011, 67, C120-C121.	0.3	0
25	Solution NMR mapping of water-accessible residues in the transmembrane $\hat{\gamma}$ -barrel of OmpX. <i>European Biophysics Journal</i> , 2010, 39, 623-630.	2.2	56
26	Robust structure-based resonance assignment for functional protein studies by NMR. <i>Journal of Biomolecular NMR</i> , 2010, 46, 157-173.	2.8	17
27	NMR structure note: oxidized microsomal human cytochrome b5. <i>Journal of Biomolecular NMR</i> , 2010, 47, 289-295.	2.8	12
28	Structural study of the membrane protein Mscl using cell-free expression and solid-state NMR. <i>Journal of Magnetic Resonance</i> , 2010, 204, 155-159.	2.1	32
29	Multifunctionality of the $\hat{\gamma}$ -thymosin/WH2 module: $\hat{\gamma}$ -actin sequestration, actin filament growth, nucleation, and severing. <i>Annals of the New York Academy of Sciences</i> , 2010, 1194, 44-52.	3.8	29
30	Insight into the Role of Dynamics in the Conformational Switch of the Small GTP-binding Protein Arf1*. <i>Journal of Biological Chemistry</i> , 2010, 285, 37987-37994.	3.4	9
31	Cell-penetrating Peptides with Intracellular Actin-remodeling Activity in Malignant Fibroblasts. <i>Journal of Biological Chemistry</i> , 2010, 285, 7712-7721.	3.4	31
32	Structure of a GPCR Ligand in Its Receptor-Bound State: Leukotriene B4 Adopts a Highly Constrained Conformation When Associated to Human BLT2. <i>Journal of the American Chemical Society</i> , 2010, 132, 9049-9057.	13.7	66
33	SAXS and X-ray Crystallography Suggest an Unfolding Model for the GDP/GTP Conformational Switch of the Small GTPase Arf6. <i>Journal of Molecular Biology</i> , 2010, 402, 696-707.	4.2	13
34	NOE networks for NMR resonance assignment of proteins with known 3D structure. <i>Bioinformatics</i> , 2009, 25, 474-481.	4.1	16
35	Inter- and intramolecular contacts in a membrane protein/surfactant complex observed by heteronuclear dipole-to-dipole cross-relaxation. <i>Journal of Magnetic Resonance</i> , 2009, 197, 91-95.	2.1	40
36	Structure and inhibition of Arf GTPases. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2008, 64, C333-C333.	0.3	0

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37	Structure of the Histone Chaperone Asf1 Bound to the Histone H3 C-Terminal Helix and Functional Insights. <i>Structure</i> , 2007, 15, 191-199.	3.3	43
38	Structure, Function, and Evolution of the beta-Thymosin/WH2 (WASP-Homology2) Actin-Binding Module. <i>Annals of the New York Academy of Sciences</i> , 2007, 1112, 67-75.	3.8	26
39	¹ H, ¹³ C and ¹⁵ N resonance assignment of the first N-terminal RNA recognition motif (RRM) of the human heterogeneous nuclear ribonucleoprotein H (hnRNP H). <i>Biomolecular NMR Assignments</i> , 2007, 1, 221-223.	0.8	0
40	Coupling of Folding and Binding of Thymosin β 24 upon Interaction with Monomeric Actin Monitored by Nuclear Magnetic Resonance. <i>Journal of Biological Chemistry</i> , 2004, 279, 23637-23645.	3.4	97
41	Analysis of slow motions in the microsecond range on domain 1 of annexin I. <i>Comptes Rendus Chimie</i> , 2004, 7, 253-258.	0.5	0
42	The β 2-Thymosin/WH2 Domain. <i>Cell</i> , 2004, 117, 611-623.	28.9	201
43	Dynamical characterization of residual and non-native structures in a partially folded protein by ¹⁵ N NMR relaxation using a model based on a distribution of correlation times. <i>Protein Science</i> , 2002, 11, 957-964.	7.6	26
44	¹ H, ¹³ C and ¹⁵ N chemical shift assignment of the honeybee odorant-binding protein ASP2. <i>Journal of Biomolecular NMR</i> , 2001, 21, 181-182.	2.8	11
45	¹⁵ N NMR relaxation as a probe for helical intrinsic propensity: the case of the unfolded D2 domain of annexin I. <i>Journal of Biomolecular NMR</i> , 2001, 19, 3-18.	2.8	25
46	New ¹⁵ N NMR Exchange Experiments for the Unambiguous Assignment of ¹ H/ ¹⁵ N Resonances of Proteins in Complexes in Slow Chemical Exchange with Free Form. <i>Journal of Magnetic Resonance</i> , 2000, 142, 276-279.	2.1	9
47	NMR characterization of a kissing complex formed between the TAR RNA element of HIV-1 and a DNA aptamer. <i>Nucleic Acids Research</i> , 2000, 28, 3386-3391.	14.5	38
48	Dynamics of the DNA Binding Domain of the Fructose Repressor from the Analysis of Linear Correlations between the ¹⁵ N- ¹ H Bond Spectral Densities Obtained by Nuclear Magnetic Resonance Spectroscopy. <i>Biochemistry</i> , 1998, 37, 5060-5073.	2.5	17
49	Three-dimensional structure determination of capsicein: A toxin of fungus origin. <i>Toxicon</i> , 1996, 34, 1077-1078.	1.6	0
50	Resonance assignment, cysteine-pairing elucidation and secondary-structure determination of capsicein, an alpha-elicitin, by three-dimensional ¹ H NMR. <i>FEBS Journal</i> , 1994, 220, 427-438.	0.2	17
51	¹ H and ¹⁵ N Resonance Assignment and Secondary Structure of Capsicein, an .alpha.-Elicitin, Determined by Three-Dimensional Heteronuclear NMR. <i>Biochemistry</i> , 1994, 33, 8188-8197.	2.5	17
52	Analysis of the backbone dynamics of capsicein using ¹⁵ N NMR relaxation rate measurements. <i>Journal De Chimie Physique Et De Physico-Chimie Biologique</i> , 1994, 91, 776-784.	0.2	1
53	Application of homonuclear three-dimensional NMR spectroscopy to the study of a protein in solution. <i>Journal De Chimie Physique Et De Physico-Chimie Biologique</i> , 1992, 89, 147-156.	0.2	4
54	Application de la RMN tridimensionnelle à l'étude des protéines : quelques développements récents. <i>Journal De Chimie Physique Et De Physico-Chimie Biologique</i> , 1992, 89, 125-133.	0.2	0

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55	Application of Maximum Entropy Methods to NMR Spectra of Proteins. , 1991, , 163-174.		1
56	Insight into protein nuclear magnetic resonance research. Biochimie, 1990, 72, 531-535.	2.6	3
57	Reassessment of Structural Characteristics of the d(CGCG) ₂ :Actinomycin D Complex from Complete ¹ H and ³¹ P NMR. Journal of Biomolecular Structure and Dynamics, 1989, 7, 557-589.	3.5	18