

Torsten Herrmann

List of Publications by Year in descending order

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58
papers

5,784
citations

117625

34
h-index

128289

60
g-index

62
all docs

62
docs citations

62
times ranked

6256
citing authors

#	ARTICLE	IF	CITATIONS
1	Protein NMR Structure Determination with Automated NOE Assignment Using the New Software CANDID and the Torsion Angle Dynamics Algorithm DYANA. <i>Journal of Molecular Biology</i> , 2002, 319, 209-227.	4.2	1,408
2	Protein NMR structure determination with automated NOE-identification in the NOESY spectra using the new software ATNOS. <i>Journal of Biomolecular NMR</i> , 2002, 24, 171-189.	2.8	448
3	A new type V toxin-antitoxin system where mRNA for toxin GhoT is cleaved by antitoxin GhoS. <i>Nature Chemical Biology</i> , 2012, 8, 855-861.	8.0	268
4	Rapid Proton-Detected NMR Assignment for Proteins with Fast Magic Angle Spinning. <i>Journal of the American Chemical Society</i> , 2014, 136, 12489-12497.	13.7	254
5	Structure of fully protonated proteins by proton-detected magic-angle spinning NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9187-9192.	7.1	224
6	Prion protein NMR structures of cats, dogs, pigs, and sheep. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 640-645.	7.1	203
7	NMR structure of the calreticulin P-domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 3133-3138.	7.1	178
8	Structure and backbone dynamics of a microcrystalline metalloprotein by solid-state NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 11095-11100.	7.1	173
9	WeNMR: Structural Biology on the Grid. <i>Journal of Grid Computing</i> , 2012, 10, 743-767.	3.9	170
10	Fast Resonance Assignment and Fold Determination of Human Superoxide Dismutase by High-Resolution Proton-Detected Solid-State MAS NMR Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2011, 50, 11697-11701.	13.8	157
11	Protein Structure Determination from ¹³ C Spin-Diffusion Solid-State NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2008, 130, 3959-3966.	13.7	155
12	Recommendations of the wwPDB NMR Validation Task Force. <i>Structure</i> , 2013, 21, 1563-1570.	3.3	151
13	Novel Î ² -Barrel Fold in the Nuclear Magnetic Resonance Structure of the Replicase Nonstructural Protein 1 from the Severe Acute Respiratory Syndrome Coronavirus. <i>Journal of Virology</i> , 2007, 81, 3151-3161.	3.4	127
14	NMR Structure of the Apoptosis- and Inflammation-Related NALP1 Pyrin Domain. <i>Structure</i> , 2003, 11, 1199-1205.	3.3	124
15	NMR Structure and Metal Interactions of the CopZ Copper Chaperone. <i>Journal of Biological Chemistry</i> , 1999, 274, 22597-22603.	3.4	116
16	Automated sequence-specific protein NMR assignment using the memetic algorithm MATCH. <i>Journal of Biomolecular NMR</i> , 2008, 41, 127-138.	2.8	111
17	Structural basis of chaperone-subunit complex recognition by the type 1 pilus assembly platform FimD. <i>EMBO Journal</i> , 2005, 24, 2075-2086.	7.8	100
18	Automated NMR structure determination and disulfide bond identification of the myotoxin crotamine from <i>Crotalus durissus terrificus</i> . <i>Toxicon</i> , 2005, 46, 759-767.	1.6	84

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19	Advances in automated NMR protein structure determination. Quarterly Reviews of Biophysics, 2011, 44, 257-309.	5.7	84
20	CASD-NMR: critical assessment of automated structure determination by NMR. Nature Methods, 2009, 6, 625-626.	19.0	80
21	Nuclear Magnetic Resonance Structure of the N-Terminal Domain of Nonstructural Protein 3 from the Severe Acute Respiratory Syndrome Coronavirus. Journal of Virology, 2007, 81, 12049-12060.	3.4	75
22	Blind Testing of Routine, Fully Automated Determination of Protein Structures from NMR Data. Structure, 2012, 20, 227-236.	3.3	75
23	Automated amino acid side-chain NMR assignment of proteins using ¹³ C- and ¹⁵ N-resolved 3D [1H,1H]-NOESY. Journal of Biomolecular NMR, 2008, 42, 23-33.	2.8	66
24	Structural Genomics of the Severe Acute Respiratory Syndrome Coronavirus: Nuclear Magnetic Resonance Structure of the Protein nsP7. Journal of Virology, 2005, 79, 12905-12913.	3.4	58
25	The J-UNIO protocol for automated protein structure determination by NMR in solution. Journal of Biomolecular NMR, 2012, 53, 341-354.	2.8	57
26	NMR Structures of 36 and 73-residue Fragments of the Calreticulin P-domain. Journal of Molecular Biology, 2002, 322, 773-784.	4.2	55
27	Rapid Measurement of Pseudocontact Shifts in Metalloproteins by Proton-Detected Solid-State NMR Spectroscopy. Journal of the American Chemical Society, 2012, 134, 14730-14733.	13.7	53
28	Comprehensive Automation for NMR Structure Determination of Proteins. Methods in Molecular Biology, 2012, 831, 429-451.	0.9	50
29	NMR structure of a KlbA intein precursor from Methanococcus jannaschii. Protein Science, 2007, 16, 1316-1328.	7.6	44
30	Protein residue linking in a single spectrum for magic-angle spinning NMR assignment. Journal of Biomolecular NMR, 2015, 62, 253-261.	2.8	44
31	Three-dimensional structure topology of the calreticulin P-domain based on NMR assignment. FEBS Letters, 2001, 488, 69-73.	2.8	41
32	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
33	Temporal Ordering in Endocytic Clathrin-Coated Vesicle Formation via AP2 Phosphorylation. Developmental Cell, 2019, 50, 494-508.e11.	7.0	40
34	The Solution Structure and Dynamics of Full-length Human Cerebral Dopamine Neurotrophic Factor and Its Neuroprotective Role against α -Synuclein Oligomers. Journal of Biological Chemistry, 2015, 290, 20527-20540.	3.4	39
35	Solution Structure and Intermolecular Interactions of the Third Metal-binding Domain of ATP7A, the Menkes Disease Protein. Journal of Biological Chemistry, 2006, 281, 29141-29147.	3.4	38
36	Structural Analysis of the Conserved Ubiquitin-binding Motifs (UBMs) of the Translesion Polymerase ϵ in Complex with Ubiquitin. Journal of Biological Chemistry, 2011, 286, 1364-1373.	3.4	36

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37	NMR for structural proteomics of <i>Thermotoga maritima</i> : Screening and structure determination. <i>Journal of Structural and Functional Genomics</i> , 2004, 5, 205-215.	1.2	31
38	NMR Structure of the <i>Escherichia coli</i> Type 1 Pilus Subunit FimF and Its Interactions with Other Pilus Subunits. <i>Journal of Molecular Biology</i> , 2008, 375, 752-763.	4.2	26
39	Structural studies suggest aggregation as one of the modes of action for teixobactin. <i>Chemical Science</i> , 2018, 9, 8850-8859.	7.4	24
40	APSY-NMR for protein backbone assignment in high-throughput structural biology. <i>Journal of Biomolecular NMR</i> , 2015, 61, 47-53.	2.8	22
41	A Residue Specific Insight into the Arkadia E3 Ubiquitin Ligase Activity and Conformational Plasticity. <i>Journal of Molecular Biology</i> , 2017, 429, 2373-2386.	4.2	22
42	A consistent calculation of dispersion corrections in elastic electron-deuteron scattering. <i>European Physical Journal A</i> , 1998, 2, 29-40.	2.5	19
43	Letter to the Editor: NMR Structure Determination of the Hypothetical Protein TM1290 from <i>Thermotoga Maritima</i> using Automated NOESY Analysis. <i>Journal of Biomolecular NMR</i> , 2004, 29, 403-406.	2.8	19
44	Solution structure of Asl1650, an acyl carrier protein from <i>Anabaena</i> sp. PCC 7120 with a variant phosphopantetheinylation-site sequence. <i>Protein Science</i> , 2006, 15, 1030-1041.	7.6	19
45	Comparison of NMR and crystal structures highlights conformational isomerism in protein active sites. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1393-1405.	0.7	18
46	Cold-adapted signal proteins: NMR structures of pheromones from the antarctic ciliate <i>Euplotes nobilii</i> . <i>IUBMB Life</i> , 2007, 59, 578-585.	3.4	17
47	Targeted projection NMR spectroscopy for unambiguous metabolic profiling of complex mixtures. <i>Magnetic Resonance in Chemistry</i> , 2010, 48, 727-733.	1.9	17
48	CASD-NMR 2: robust and accurate unsupervised analysis of raw NOESY spectra and protein structure determination with UNIO. <i>Journal of Biomolecular NMR</i> , 2015, 62, 473-480.	2.8	16
49	NMR structure of the conserved hypothetical protein TM0487 from <i>Thermotoga maritima</i> : Implications for 216 homologous DUF59 proteins. <i>Protein Science</i> , 2005, 14, 2880-2886.	7.6	14
50	Comparison of NMR and crystal structures for the proteins TM1112 and TM1367. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1381-1392.	0.7	14
51	Automated Protein NMR Structure Determination in Crude Cell-Extract. <i>Journal of Biomolecular NMR</i> , 2006, 34, 3-11.	2.8	11
52	Solution structures of the putative anti- λ -factor antagonist TM1442 from <i>Thermotoga maritima</i> in the free and phosphorylated states. <i>Magnetic Resonance in Chemistry</i> , 2006, 44, S61-S70.	1.9	11
53	NMR structure determination of the conserved hypothetical protein TM1816 from <i>Thermotoga maritima</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 552-557.	2.6	7
54	Revealing the mechanism of repressor inactivation during switching of a temperate bacteriophage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 20576-20585.	7.1	6

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55	NMR structure of the conserved hypothetical protein TM0979 from <i>Thermotoga maritima</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 59, 387-390.	2.6	4
56	Structural and DNA binding properties of mycobacterial integration host factor mIHF. <i>Journal of Structural Biology</i> , 2020, 209, 107434.	2.8	3
57	Applications of Projection NMR Techniques. <i>Annual Reports on NMR Spectroscopy</i> , 2013, 78, 55-102.	1.5	1
58	Nuclear overhauser spectroscopy of chiral CHD methylene groups. <i>Journal of Biomolecular NMR</i> , 2016, 64, 27-37.	2.8	1