

Torsten Herrmann

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8193754/publications.pdf>

Version: 2024-02-01

58
papers

5,784
citations

117571

34
h-index

128225

60
g-index

62
all docs

62
docs citations

62
times ranked

6256
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural and DNA binding properties of mycobacterial integration host factor mIHF. <i>Journal of Structural Biology</i> , 2020, 209, 107434.	1.3	3
2	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.	3.3	6
3	Temporal Ordering in Endocytic Clathrin-Coated Vesicle Formation via AP2 Phosphorylation. <i>Developmental Cell</i> , 2019, 50, 494-508.e11.	3.1	40
4	Structural studies suggest aggregation as one of the modes of action for teixobactin. <i>Chemical Science</i> , 2018, 9, 8850-8859.	3.7	24
5	A Residue Specific Insight into the Arkadia E3 Ubiquitin Ligase Activity and Conformational Plasticity. <i>Journal of Molecular Biology</i> , 2017, 429, 2373-2386.	2.0	22
6	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.	3.3	224
7	Nuclear overhauser spectroscopy of chiral CHD methylene groups. <i>Journal of Biomolecular NMR</i> , 2016, 64, 27-37.	1.6	1
8	APSY-NMR for protein backbone assignment in high-throughput structural biology. <i>Journal of Biomolecular NMR</i> , 2015, 61, 47-53.	1.6	22
9	NMR Exchange Format: a unified and open standard for representation of NMR restraint data. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 433-434.	3.6	40
10	Protein residue linking in a single spectrum for magic-angle spinning NMR assignment. <i>Journal of Biomolecular NMR</i> , 2015, 62, 253-261.	1.6	44
11	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.	1.6	16
12	The Solution Structure and Dynamics of Full-length Human Cerebral Dopamine Neurotrophic Factor and Its Neuroprotective Role against α -Synuclein Oligomers. <i>Journal of Biological Chemistry</i> , 2015, 290, 20527-20540.	1.6	39
13	Rapid Proton-Detected NMR Assignment for Proteins with Fast Magic Angle Spinning. <i>Journal of the American Chemical Society</i> , 2014, 136, 12489-12497.	6.6	254
14	Recommendations of the wwPDB NMR Validation Task Force. <i>Structure</i> , 2013, 21, 1563-1570.	1.6	151
15	Applications of Projection NMR Techniques. <i>Annual Reports on NMR Spectroscopy</i> , 2013, 78, 55-102.	0.7	1
16	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.	3.3	173
17	WeNMR: Structural Biology on the Grid. <i>Journal of Grid Computing</i> , 2012, 10, 743-767.	2.5	170
18	The J-UNIO protocol for automated protein structure determination by NMR in solution. <i>Journal of Biomolecular NMR</i> , 2012, 53, 341-354.	1.6	57

#	ARTICLE	IF	CITATIONS
19	Rapid Measurement of Pseudocontact Shifts in Metalloproteins by Proton-Detected Solid-State NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2012, 134, 14730-14733.	6.6	53
20	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.	3.9	268
21	Blind Testing of Routine, Fully Automated Determination of Protein Structures from NMR Data. <i>Structure</i> , 2012, 20, 227-236.	1.6	75
22	Comprehensive Automation for NMR Structure Determination of Proteins. <i>Methods in Molecular Biology</i> , 2012, 831, 429-451.	0.4	50
23	Advances in automated NMR protein structure determination. <i>Quarterly Reviews of Biophysics</i> , 2011, 44, 257-309.	2.4	84
24	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.	7.2	157
25	Structural Analysis of the Conserved Ubiquitin-binding Motifs (UBMs) of the Translesion Polymerase <i>iota</i> in Complex with Ubiquitin. <i>Journal of Biological Chemistry</i> , 2011, 286, 1364-1373.	1.6	36
26	Targeted projection NMR spectroscopy for unambiguous metabolic profiling of complex mixtures. <i>Magnetic Resonance in Chemistry</i> , 2010, 48, 727-733.	1.1	17
27	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
28	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
29	CASD-NMR: critical assessment of automated structure determination by NMR. <i>Nature Methods</i> , 2009, 6, 625-626.	9.0	80
30	Automated sequence-specific protein NMR assignment using the memetic algorithm MATCH. <i>Journal of Biomolecular NMR</i> , 2008, 41, 127-138.	1.6	111
31	Automated amino acid side-chain NMR assignment of proteins using ¹³ C- and ¹⁵ N-resolved 3D [1H,1H]-NOESY. <i>Journal of Biomolecular NMR</i> , 2008, 42, 23-33.	1.6	66
32	NMR Structure of the Escherichia coli Type 1 Pilus Subunit FimF and Its Interactions with Other Pilus Subunits. <i>Journal of Molecular Biology</i> , 2008, 375, 752-763.	2.0	26
33	Protein Structure Determination from ¹³ C Spin-Diffusion Solid-State NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2008, 130, 3959-3966.	6.6	155
34	Novel Î2-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.	1.5	127
35	Nuclear Magnetic Resonance Structure of the N-Terminal Domain of Nonstructural Protein 3 from the Severe Acute Respiratory Syndrome Coronavirus. <i>Journal of Virology</i> , 2007, 81, 12049-12060.	1.5	75
36	NMR structure of a KlbA intein precursor from <i>Methanococcus jannaschii</i> . <i>Protein Science</i> , 2007, 16, 1316-1328.	3.1	44

#	ARTICLE	IF	CITATIONS
37	Cold-adapted signal proteins: NMR structures of pheromones from the antarctic ciliate <i>Euplotes nobilii</i> . <i>IUBMB Life</i> , 2007, 59, 578-585.	1.5	17
38	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.	3.1	19
39	Automated Protein NMR Structure Determination in Crude Cell-Extract. <i>Journal of Biomolecular NMR</i> , 2006, 34, 3-11.	1.6	11
40	Solution structures of the putative anti- γ -factor antagonist TM1442 from <i>Thermotoga maritima</i> in the free and phosphorylated states. <i>Magnetic Resonance in Chemistry</i> , 2006, 44, S61-S70.	1.1	11
41	Solution Structure and Intermolecular Interactions of the Third Metal-binding Domain of ATP7A, the Menkes Disease Protein. <i>Journal of Biological Chemistry</i> , 2006, 281, 29141-29147.	1.6	38
42	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.	3.1	14
43	Structural basis of chaperone-subunit complex recognition by the type 1 pilus assembly platform FimD. <i>EMBO Journal</i> , 2005, 24, 2075-2086.	3.5	100
44	NMR structure of the conserved hypothetical protein TM0979 from <i>Thermotoga maritima</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 59, 387-390.	1.5	4
45	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.	1.5	7
46	Structural Genomics of the Severe Acute Respiratory Syndrome Coronavirus: Nuclear Magnetic Resonance Structure of the Protein nsP7. <i>Journal of Virology</i> , 2005, 79, 12905-12913.	1.5	58
47	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.	3.3	203
48	Automated NMR structure determination and disulfide bond identification of the myotoxin crostamine from <i>Crotalus durissus terrificus</i> . <i>Toxicon</i> , 2005, 46, 759-767.	0.8	84
49	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.	1.6	19
50	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
51	NMR Structure of the Apoptosis- and Inflammation-Related NALP1 Pyrin Domain. <i>Structure</i> , 2003, 11, 1199-1205.	1.6	124
52	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.	2.0	1,408
53	NMR Structures of 36 and 73-residue Fragments of the Calreticulin P-domain. <i>Journal of Molecular Biology</i> , 2002, 322, 773-784.	2.0	55
54	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.	1.6	448

#	ARTICLE	IF	CITATIONS
55	Three-dimensional structure topology of the calreticulin P-domain based on NMR assignment. FEBS Letters, 2001, 488, 69-73.	1.3	41
56	NMR structure of the calreticulin P-domain. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 3133-3138.	3.3	178
57	NMR Structure and Metal Interactions of the CopZ Copper Chaperone. Journal of Biological Chemistry, 1999, 274, 22597-22603.	1.6	116
58	A consistent calculation of dispersion corrections in elastic electron-deuteron scattering. European Physical Journal A, 1998, 2, 29-40.	1.0	19