

# Assist Beat VÃ¶geli

## List of Publications by Year in descending order

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Version: 2024-02-01

81  
papers

2,298  
citations

257450

24  
h-index

243625

44  
g-index

88  
all docs

88  
docs citations

88  
times ranked

1886  
citing authors

#	ARTICLE	IF	CITATIONS
1	On the use of residual dipolar couplings in multi-state structure calculation of two-domain proteins. Magnetic Resonance Letters, 2022, 2, 61-68.	1.3	0
2	Solution NMR backbone assignments of disordered Olduvai protein domain CON1 employing H <sub>1</sub> -detected experiments. Biomolecular NMR Assignments, 2022, , 1.	0.8	0
3	Structural Investigation of a Putative Intrinsically Disordered Region Within Deleted in Colorectal Carcinoma That Regulates Protein Synthesis. FASEB Journal, 2022, 36, .	0.5	0
4	Butyrate Analogues Mimicking Hypoxia by the Chemical Stabilization of Hypoxia Inducible Factor (HIF). FASEB Journal, 2022, 36, .	0.5	0
5	Microbiota-derived butyrate is an endogenous HIF prolyl hydroxylase inhibitor. Gut Microbes, 2021, 13, 1938380.	9.8	30
6	Recognition of non-CpG repeats in Alu and ribosomal RNAs by the Z-RNA binding domain of ADAR1 induces A-Z junctions. Nature Communications, 2021, 12, 793.	12.8	39
7	The Disordered Spindly C-terminus Interacts with RZZ Subunits ROD-1 and ZWL-1 in the Kinetochore through the Same Sites in C. Elegans. Journal of Molecular Biology, 2021, 433, 166812.	4.2	11
8	Targeting tumor-derived NLRP3 reduces melanoma progression by limiting MDSCs expansion. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	95
9	Solution NMR backbone assignments of the N-terminal Z <sup>1</sup> -linker-Z <sup>2</sup> segment from Homo sapiens ADAR1p150. Biomolecular NMR Assignments, 2021, 15, 273-279.	0.8	2
10	Microbial-derived indoles inhibit neutrophil myeloperoxidase to diminish bystander tissue damage. FASEB Journal, 2021, 35, e21552.	0.5	17
11	Microbiota-derived butyrate is an endogenous inhibitor of HIF prolyl-hydroxylases. FASEB Journal, 2021, 35, .	0.5	0
12	The Inherent Dynamics and Interaction Sites of the SARS-CoV-2 Nucleocapsid N-Terminal Region. Journal of Molecular Biology, 2021, 433, 167108.	4.2	30
13	Reconstruction of Coupled Intra- and Interdomain Protein Motion from Nuclear and Electron Magnetic Resonance. Journal of the American Chemical Society, 2021, 143, 16055-16067.	13.7	13
14	Protein Motional Details Revealed by Complementary Structural Biology Techniques. Structure, 2020, 28, 1024-1034.e3.	3.3	11
15	Protein Allostery at Atomic Resolution. Angewandte Chemie - International Edition, 2020, 59, 22132-22139.	13.8	21
16	Protein Allostery at Atomic Resolution. Angewandte Chemie, 2020, 132, 22316-22323.	2.0	1
17	Reducing the measurement time of exact NOEs by non-uniform sampling. Journal of Biomolecular NMR, 2020, 74, 717-739.	2.8	7
18	Integrating NMR and simulations reveals motions in the UUCG tetraloop. Nucleic Acids Research, 2020, 48, 5839-5848.	14.5	31

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19	Activity and Affinity of Pin1 Variants. <i>Molecules</i> , 2020, 25, 36.	3.8	7
20	Deuteration of nonexchangeable protons on proteins affects their thermal stability, side-chain dynamics, and hydrophobicity. <i>Protein Science</i> , 2020, 29, 1641-1654.	7.6	21
21	Distance-independent Cross-correlated Relaxation and Isotropic Chemical Shift Modulation in Protein Dynamics Studies. <i>ChemPhysChem</i> , 2019, 20, 178-196.	2.1	8
22	Solution NMR backbone assignment reveals interaction-free tumbling of human lineage-specific Olduvai protein domains. <i>Biomolecular NMR Assignments</i> , 2019, 13, 339-343.	0.8	4
23	Exact distance measurements for structure and dynamics in solid proteins by fast-magic-angle-spinning NMR. <i>Chemical Communications</i> , 2019, 55, 7899-7902.	4.1	20
24	A transient helix in the disordered region of dynein light intermediate chain links the motor to structurally diverse adaptors for cargo transport. <i>PLoS Biology</i> , 2019, 17, e3000100.	5.6	39
25	Backbone and side-chain chemical shift assignments of full-length, apo, human Pin1, a phosphoprotein regulator with interdomain allostery. <i>Biomolecular NMR Assignments</i> , 2019, 13, 85-89.	0.8	6
26	NOE-derived Methyl Distances from a 360-kDa Proteasome Complex. <i>Chemistry - A European Journal</i> , 2018, 24, 2270-2276.	3.3	9
27	The Sign of Nuclear Magnetic Resonance Chemical Shift Difference as a Determinant of the Origin of Binding Selectivity: Elucidation of the Position Dependence of Phosphorylation in Ligands Binding to Scribble PDZ1. <i>Biochemistry</i> , 2018, 57, 66-71.	2.5	6
28	Structure and dynamics conspire in the evolution of affinity between intrinsically disordered proteins. <i>Science Advances</i> , 2018, 4, eaau4130.	10.3	38
29	Efficient Stereospecific H <sup>1</sup> 2/3 NMR Assignment Strategy for Mid-Size Proteins. <i>Magnetochemistry</i> , 2018, 4, 25.	2.4	7
30	Extending the Applicability of Exact Nuclear Overhauser Enhancements to Large Proteins and RNA. <i>ChemBioChem</i> , 2018, 19, 1695-1701.	2.6	15
31	High-resolution small RNA structures from exact nuclear Overhauser enhancement measurements without additional restraints. <i>Communications Biology</i> , 2018, 1, 61.	4.4	23
32	Correlated motions of C <sup>15</sup> N and C <sup>13</sup> pairs in protonated and per-deuterated GB3. <i>Journal of Biomolecular NMR</i> , 2018, 72, 39-54.	2.8	5
33	Cross-correlated relaxation rates between protein backbone H-X dipolar interactions. <i>Journal of Biomolecular NMR</i> , 2017, 67, 211-232.	2.8	9
34	eNORA2 Exact NOE Analysis Program. <i>Journal of Chemical Theory and Computation</i> , 2017, 13, 4336-4346.	5.3	32
35	Detection of Correlated Protein Backbone and Side-Chain Angle Fluctuations. <i>ChemBioChem</i> , 2017, 18, 2016-2021.	2.6	5
36	The Exact Nuclear Overhauser Enhancement: Recent Advances. <i>Molecules</i> , 2017, 22, 1176.	3.8	26

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37	Enzyme Selectivity Fine-Tuned through Dynamic Control of a Loop. <i>Angewandte Chemie</i> , 2016, 128, 3148-3152.	2.0	1
38	Enzyme Selectivity Fine-Tuned through Dynamic Control of a Loop. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 3096-3100.	13.8	13
39	The Dynamic Basis for Signal Propagation in Human Pin1-WW. <i>Structure</i> , 2016, 24, 1464-1475.	3.3	20
40	Direct Investigation of Slow Correlated Dynamics in Proteins via Dipolar Interactions. <i>Journal of the American Chemical Society</i> , 2016, 138, 8412-8421.	13.7	19
41	The Exact NOE as an Alternative in Ensemble Structure Determination. <i>Biophysical Journal</i> , 2016, 110, 113-126.	0.5	39
42	Compiled data set of exact NOE distance limits, residual dipolar couplings and scalar couplings for the protein GB3. <i>Data in Brief</i> , 2015, 5, 99-106.	1.0	11
43	A Structural Ensemble for the Enzyme Cyclophilin Reveals an Orchestrated Mode of Action at Atomic Resolution. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 11657-11661.	13.8	30
44	Solution NMR Studies of Recombinant $\Delta^2(1\text{--}42)$ : From the Presence of a Micellar Entity to Residual $\beta$ -Sheet Structure in the Soluble Species. <i>ChemBioChem</i> , 2015, 16, 659-669.	2.6	42
45	Extending the eNOE data set of large proteins by evaluation of NOEs with unresolved diagonals. <i>Journal of Biomolecular NMR</i> , 2015, 62, 63-69.	2.8	23
46	The experimental accuracy of the uni-directional exact NOE. <i>Journal of Magnetic Resonance</i> , 2015, 259, 32-46.	2.1	17
47	Complementarity and congruence between exact NOEs and traditional NMR probes for spatial decoding of protein dynamics. <i>Journal of Structural Biology</i> , 2015, 191, 306-317.	2.8	19
48	Intermolecular Detergent-Membrane Protein NOEs for the Characterization of the Dynamics of Membrane Protein-Detergent Complexes. <i>Journal of Physical Chemistry B</i> , 2014, 118, 14288-14301.	2.6	5
49	The nuclear Overhauser effect from a quantitative perspective. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2014, 78, 1-46.	7.5	115
50	Towards a true protein movie: A perspective on the potential impact of the ensemble-based structure determination using exact NOEs. <i>Journal of Magnetic Resonance</i> , 2014, 241, 53-59.	2.1	31
51	The Structure of Mouse Cytomegalovirus m04 Protein Obtained from Sparse NMR Data Reveals a Conserved Fold of the m02-m06 Viral Immune Modulator Family. <i>Structure</i> , 2014, 22, 1263-1273.	3.3	23
52	Multiple-state ensemble structure determination from eNOE spectroscopy. <i>Molecular Physics</i> , 2013, 111, 437-454.	1.7	28
53	Stereospecific assignments in proteins using exact NOEs. <i>Journal of Biomolecular NMR</i> , 2013, 57, 211-218.	2.8	16
54	Full relaxation matrix analysis of apparent cross-correlated relaxation rates in four-spin systems. <i>Journal of Magnetic Resonance</i> , 2013, 226, 52-63.	2.1	3

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55	Relaxation Matrix Analysis of Spin Diffusion for the NMR Structure Calculation with eNOEs. Journal of Chemical Theory and Computation, 2012, 8, 3483-3492.	5.3	47
56	Discrete Three-dimensional Representation of Macromolecular Motion from eNOE-based Ensemble Calculation. Chimia, 2012, 66, 787.	0.6	10
57	Spatial elucidation of motion in proteins by ensemble-based structure calculation using exact NOEs. Nature Structural and Molecular Biology, 2012, 19, 1053-1057.	8.2	92
58	Temperature Dependence of $^1\text{H}$ - $^1\text{H}$ Distances in Ubiquitin As Studied by Exact Measurements of NOEs. Journal of Physical Chemistry B, 2011, 115, 7648-7660.	2.6	16
59	How uniform is the peptide plane geometry? A high-accuracy NMR study of dipolar $^1\text{C}$ - $^1\text{H}$ cross-correlated relaxation. Journal of Biomolecular NMR, 2011, 50, 315-329.	2.8	8
60	Side chain: backbone projections in aromatic and ASX residues from NMR cross-correlated relaxation. Journal of Biomolecular NMR, 2010, 46, 135-147.	2.8	9
61	Quantitative determination of NOE rates in perdeuterated and protonated proteins: Practical and theoretical aspects. Journal of Magnetic Resonance, 2010, 204, 290-302.	2.1	32
62	Comprehensive description of NMR cross-correlated relaxation under anisotropic molecular tumbling and correlated local dynamics on all time scales. Journal of Chemical Physics, 2010, 133, 014501.	3.0	20
63	Correlated Dynamics between Protein HN and HC Bonds Observed by NMR Cross Relaxation. Journal of the American Chemical Society, 2009, 131, 3668-3678.	13.7	39
64	Exact Distances and Internal Dynamics of Perdeuterated Ubiquitin from NOE Buildups. Journal of the American Chemical Society, 2009, 131, 17215-17225.	13.7	91
65	Protein backbone motions viewed by intraresidue and sequential $^1\text{H}$ - $^1\text{H}$ residual dipolar couplings. Journal of Biomolecular NMR, 2008, 41, 17-28.	2.8	27
66	NMR Determination of Amide $^1\text{N}$ - $^1\text{H}$ Equilibrium Bond Length from Concerted Dipolar Coupling Measurements. Journal of the American Chemical Society, 2008, 130, 16518-16520.	13.7	98
67	Simultaneous NMR Study of Protein Structure and Dynamics Using Conservative Mutagenesis. Journal of Physical Chemistry B, 2008, 112, 6045-6056.	2.6	87
68	Limits on Variations in Protein Backbone Dynamics from Precise Measurements of Scalar Couplings. Journal of the American Chemical Society, 2007, 129, 9377-9385.	13.7	127
69	Spin-State Selective Carbon-Detected HNCO with TROSY Optimization in All Dimensions and Double Echo Antiecho Sensitivity Enhancement in Both Indirect Dimensions. Journal of the American Chemical Society, 2007, 129, 5484-5491.	13.7	21
70	Structure and dynamics of a molten globular enzyme. Nature Structural and Molecular Biology, 2007, 14, 1202-1206.	8.2	102
71	Interference between transverse cross-correlated relaxation and longitudinal relaxation affects apparent J-coupling and transverse cross-correlated relaxation. Chemical Physics Letters, 2006, 423, 123-125.	2.6	4
72	$^{13}\text{C}$ -detected HN(CA)C and HMCNC experiments using a single methyl-reprotonated sample for unambiguous methyl resonance assignment. Journal of Biomolecular NMR, 2006, 36, 259-266.	2.8	4

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73	Measuring $^1\text{H}$ - $^1\text{H}$ and $^1\text{H}$ - $^{13}\text{C}$ RDCs in methyl groups: example of pulse sequences with numerically optimized coherence transfer schemes. <i>Journal of Magnetic Resonance</i> , 2005, 172, 36-47.	2.1	3
74	Side-chain H and C resonance assignment in protonated/partially deuterated proteins using an improved 3D $^{13}\text{C}$ -detected HCC-TOCSY. <i>Journal of Magnetic Resonance</i> , 2005, 174, 200-208.	2.1	9
75	Simultaneous $^1\text{H}$ - or $^2\text{H}$ -, $^{15}\text{N}$ - and multiple-band-selective $^{13}\text{C}$ -decoupling during acquisition in $^{13}\text{C}$ -detected experiments with proteins and oligonucleotides. <i>Journal of Biomolecular NMR</i> , 2005, 31, 1-9.	2.8	24
76	Detection of $^2\text{D}$ , $^1\text{H}$ correlations in proteins using a new time- and sensitivity-optimal experiment. <i>Journal of Biomolecular NMR</i> , 2005, 31, 273-278.	2.8	33
77	An enzymatic molten globule: Efficient coupling of folding and catalysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 12860-12864.	7.1	128
78	Measurements of Side-Chain $^{13}\text{C}$ - $^{13}\text{C}$ Residual Dipolar Couplings in Uniformly Deuterated Proteins. <i>Journal of the American Chemical Society</i> , 2004, 126, 2414-2420.	13.7	23
79	Observation of Individual Transitions in Magnetically Equivalent Spin Systems. <i>Journal of the American Chemical Society</i> , 2003, 125, 9566-9567.	13.7	10
80	Longitudinal $^1\text{H}$ Relaxation Optimization in TROSY NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2002, 124, 12898-12902.	13.7	166
81	TROSY experiment for refinement of backbone psi and phi by simultaneous measurements of cross-correlated relaxation rates and $^3\text{J}(\text{H}\alpha\text{HN})$ coupling constants. <i>Journal of Biomolecular NMR</i> , 2002, 24, 291-300.	2.8	13