

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

257101

24
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243296

44
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88
all docs

88
docs citations

88
times ranked

1886
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Longitudinal ^1H Relaxation Optimization in TROSY NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2002, 124, 12898-12902. | 6.6 | 166 |
| 2 | 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. | 3.3 | 128 |
| 3 | Limits on Variations in Protein Backbone Dynamics from Precise Measurements of Scalar Couplings. <i>Journal of the American Chemical Society</i> , 2007, 129, 9377-9385. | 6.6 | 127 |
| 4 | The nuclear Overhauser effect from a quantitative perspective. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2014, 78, 1-46. | 3.9 | 115 |
| 5 | Structure and dynamics of a molten globular enzyme. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 1202-1206. | 3.6 | 102 |
| 6 | NMR Determination of Amide N-H Equilibrium Bond Length from Concerted Dipolar Coupling Measurements. <i>Journal of the American Chemical Society</i> , 2008, 130, 16518-16520. | 6.6 | 98 |
| 7 | Targeting tumor-derived NLRP3 reduces melanoma progression by limiting MDSCs expansion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, . | 3.3 | 95 |
| 8 | Spatial elucidation of motion in proteins by ensemble-based structure calculation using exact NOEs. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1053-1057. | 3.6 | 92 |
| 9 | Exact Distances and Internal Dynamics of Perdeuterated Ubiquitin from NOE Buildups. <i>Journal of the American Chemical Society</i> , 2009, 131, 17215-17225. | 6.6 | 91 |
| 10 | Simultaneous NMR Study of Protein Structure and Dynamics Using Conservative Mutagenesis. <i>Journal of Physical Chemistry B</i> , 2008, 112, 6045-6056. | 1.2 | 87 |
| 11 | Relaxation Matrix Analysis of Spin Diffusion for the NMR Structure Calculation with eNOEs. <i>Journal of Chemical Theory and Computation</i> , 2012, 8, 3483-3492. | 2.3 | 47 |
| 12 | Solution NMR Studies of Recombinant β_2 (1 α -42): From the Presence of a Micellar Entity to Residual β -Sheet Structure in the Soluble Species. <i>ChemBioChem</i> , 2015, 16, 659-669. | 1.3 | 42 |
| 13 | Correlated Dynamics between Protein HN and HC Bonds Observed by NMR Cross Relaxation. <i>Journal of the American Chemical Society</i> , 2009, 131, 3668-3678. | 6.6 | 39 |
| 14 | The Exact NOE as an Alternative in Ensemble Structure Determination. <i>Biophysical Journal</i> , 2016, 110, 113-126. | 0.2 | 39 |
| 15 | 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. | 2.6 | 39 |
| 16 | Recognition of non-CpG repeats in Alu and ribosomal RNAs by the Z-RNA binding domain of ADAR1 induces A-Z junctions. <i>Nature Communications</i> , 2021, 12, 793. | 5.8 | 39 |
| 17 | Structure and dynamics conspire in the evolution of affinity between intrinsically disordered proteins. <i>Science Advances</i> , 2018, 4, eaau4130. | 4.7 | 38 |
| 18 | Detection of $\text{C}^{\alpha^2}, \text{C}^{\beta}$ correlations in proteins using a new time- and sensitivity-optimal experiment. <i>Journal of Biomolecular NMR</i> , 2005, 31, 273-278. | 1.6 | 33 |

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|----|--|-----|-----------|
| 19 | Quantitative determination of NOE rates in perdeuterated and protonated proteins: Practical and theoretical aspects. <i>Journal of Magnetic Resonance</i> , 2010, 204, 290-302. | 1.2 | 32 |
| 20 | eNORA2 Exact NOE Analysis Program. <i>Journal of Chemical Theory and Computation</i> , 2017, 13, 4336-4346. | 2.3 | 32 |
| 21 | 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. | 1.2 | 31 |
| 22 | Integrating NMR and simulations reveals motions in the UUCG tetraloop. <i>Nucleic Acids Research</i> , 2020, 48, 5839-5848. | 6.5 | 31 |
| 23 | 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. | 7.2 | 30 |
| 24 | Microbiota-derived butyrate is an endogenous HIF prolyl hydroxylase inhibitor. <i>Gut Microbes</i> , 2021, 13, 1938380. | 4.3 | 30 |
| 25 | The Inherent Dynamics and Interaction Sites of the SARS-CoV-2 Nucleocapsid N-Terminal Region. <i>Journal of Molecular Biology</i> , 2021, 433, 167108. | 2.0 | 30 |
| 26 | Multiple-state ensemble structure determination from eNOE spectroscopy. <i>Molecular Physics</i> , 2013, 111, 437-454. | 0.8 | 28 |
| 27 | Protein backbone motions viewed by intraresidue and sequential ^1H - ^1H residual dipolar couplings. <i>Journal of Biomolecular NMR</i> , 2008, 41, 17-28. | 1.6 | 27 |
| 28 | The Exact Nuclear Overhauser Enhancement: Recent Advances. <i>Molecules</i> , 2017, 22, 1176. | 1.7 | 26 |
| 29 | Simultaneous ^1H - or ^2H -, ^{15}N - and multiple-band-selective ^{13}C -decoupling during acquisition in ^{13}C -detected experiments with proteins and oligonucleotides. <i>Journal of Biomolecular NMR</i> , 2005, 31, 1-9. | 1.6 | 24 |
| 30 | Measurements of Side-Chain ^{13}C - ^{13}C Residual Dipolar Couplings in Uniformly Deuterated Proteins. <i>Journal of the American Chemical Society</i> , 2004, 126, 2414-2420. | 6.6 | 23 |
| 31 | 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. | 1.6 | 23 |
| 32 | 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. | 1.6 | 23 |
| 33 | High-resolution small RNA structures from exact nuclear Overhauser enhancement measurements without additional restraints. <i>Communications Biology</i> , 2018, 1, 61. | 2.0 | 23 |
| 34 | Spin-State Selective Carbon-Detected HNC0 with TROSY Optimization in All Dimensions and Double Echo Antiecho Sensitivity Enhancement in Both Indirect Dimensions. <i>Journal of the American Chemical Society</i> , 2007, 129, 5484-5491. | 6.6 | 21 |
| 35 | Protein Allostery at Atomic Resolution. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 22132-22139. | 7.2 | 21 |
| 36 | Deuteration of nonexchangeable protons on proteins affects their thermal stability, side chain dynamics, and hydrophobicity. <i>Protein Science</i> , 2020, 29, 1641-1654. | 3.1 | 21 |

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|----|---|-----|-----------|
| 37 | Comprehensive description of NMR cross-correlated relaxation under anisotropic molecular tumbling and correlated local dynamics on all time scales. <i>Journal of Chemical Physics</i> , 2010, 133, 014501. | 1.2 | 20 |
| 38 | The Dynamic Basis for Signal Propagation in Human Pin1-WW. <i>Structure</i> , 2016, 24, 1464-1475. | 1.6 | 20 |
| 39 | Exact distance measurements for structure and dynamics in solid proteins by fast-magic-angle-spinning NMR. <i>Chemical Communications</i> , 2019, 55, 7899-7902. | 2.2 | 20 |
| 40 | 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. | 1.3 | 19 |
| 41 | Direct Investigation of Slow Correlated Dynamics in Proteins via Dipolar Interactions. <i>Journal of the American Chemical Society</i> , 2016, 138, 8412-8421. | 6.6 | 19 |
| 42 | The experimental accuracy of the uni-directional exact NOE. <i>Journal of Magnetic Resonance</i> , 2015, 259, 32-46. | 1.2 | 17 |
| 43 | Microbial-derived indoles inhibit neutrophil myeloperoxidase to diminish bystander tissue damage. <i>FASEB Journal</i> , 2021, 35, e21552. | 0.2 | 17 |
| 44 | Temperature Dependence of ^1H - ^1H Distances in Ubiquitin As Studied by Exact Measurements of NOEs. <i>Journal of Physical Chemistry B</i> , 2011, 115, 7648-7660. | 1.2 | 16 |
| 45 | Stereospecific assignments in proteins using exact NOEs. <i>Journal of Biomolecular NMR</i> , 2013, 57, 211-218. | 1.6 | 16 |
| 46 | Extending the Applicability of Exact Nuclear Overhauser Enhancements to Large Proteins and RNA. <i>ChemBioChem</i> , 2018, 19, 1695-1701. | 1.3 | 15 |
| 47 | TROSY experiment for refinement of backbone psi and phi by simultaneous measurements of cross-correlated relaxation rates and $^3,4\text{J}(\text{H}\alpha\text{HN})$ coupling constants. <i>Journal of Biomolecular NMR</i> , 2002, 24, 291-300. | 1.6 | 13 |
| 48 | Enzyme Selectivity Fine-Tuned through Dynamic Control of a Loop. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 3096-3100. | 7.2 | 13 |
| 49 | Reconstruction of Coupled Intra- and Interdomain Protein Motion from Nuclear and Electron Magnetic Resonance. <i>Journal of the American Chemical Society</i> , 2021, 143, 16055-16067. | 6.6 | 13 |
| 50 | 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. | 0.5 | 11 |
| 51 | Protein Motional Details Revealed by Complementary Structural Biology Techniques. <i>Structure</i> , 2020, 28, 1024-1034.e3. | 1.6 | 11 |
| 52 | The Disordered Spindly C-terminus Interacts with RZZ Subunits ROD-1 and ZWL-1 in the Kinetochores through the Same Sites in <i>C. Elegans</i> . <i>Journal of Molecular Biology</i> , 2021, 433, 166812. | 2.0 | 11 |
| 53 | Observation of Individual Transitions in Magnetically Equivalent Spin Systems. <i>Journal of the American Chemical Society</i> , 2003, 125, 9566-9567. | 6.6 | 10 |
| 54 | Discrete Three-dimensional Representation of Macromolecular Motion from eNOE-based Ensemble Calculation. <i>Chimia</i> , 2012, 66, 787. | 0.3 | 10 |

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|----|---|-----|-----------|
| 55 | Side-chain H and C resonance assignment in protonated/partially deuterated proteins using an improved 3D ¹³ C-detected HCC ¹³ C-TOCSY. <i>Journal of Magnetic Resonance</i> , 2005, 174, 200-208. | 1.2 | 9 |
| 56 | Side chain: backbone projections in aromatic and ASX residues from NMR cross-correlated relaxation. <i>Journal of Biomolecular NMR</i> , 2010, 46, 135-147. | 1.6 | 9 |
| 57 | Cross-correlated relaxation rates between protein backbone H ¹⁵ N dipolar interactions. <i>Journal of Biomolecular NMR</i> , 2017, 67, 211-232. | 1.6 | 9 |
| 58 | NOE ¹³ C-Derived Methyl Distances from a 360 ¹³ C...kDa Proteasome Complex. <i>Chemistry - A European Journal</i> , 2018, 24, 2270-2276. | 1.7 | 9 |
| 59 | How uniform is the peptide plane geometry? A high-accuracy NMR study of dipolar C ¹³ -C ¹³ /HN ¹⁵ N cross-correlated relaxation. <i>Journal of Biomolecular NMR</i> , 2011, 50, 315-329. | 1.6 | 8 |
| 60 | Distance ¹³ C-independent Cross ¹³ C-correlated Relaxation and Isotropic Chemical Shift Modulation in Protein Dynamics Studies. <i>ChemPhysChem</i> , 2019, 20, 178-196. | 1.0 | 8 |
| 61 | Efficient Stereospecific H ¹³ C ² /3 NMR Assignment Strategy for Mid-Size Proteins. <i>Magnetochemistry</i> , 2018, 4, 25. | 1.0 | 7 |
| 62 | Reducing the measurement time of exact NOEs by non-uniform sampling. <i>Journal of Biomolecular NMR</i> , 2020, 74, 717-739. | 1.6 | 7 |
| 63 | Activity and Affinity of Pin1 Variants. <i>Molecules</i> , 2020, 25, 36. | 1.7 | 7 |
| 64 | 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. | 1.2 | 6 |
| 65 | 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. | 0.4 | 6 |
| 66 | Intermolecular Detergent ¹³ C-Membrane Protein NOEs for the Characterization of the Dynamics of Membrane Protein ¹³ C-Detergent Complexes. <i>Journal of Physical Chemistry B</i> , 2014, 118, 14288-14301. | 1.2 | 5 |
| 67 | Detection of Correlated Protein Backbone and Side ¹³ C-Chain Angle Fluctuations. <i>ChemBioChem</i> , 2017, 18, 2016-2021. | 1.3 | 5 |
| 68 | Correlated motions of C ¹³ - ¹⁵ N and C ¹³ - ¹³ C ² pairs in protonated and per-deuterated GB3. <i>Journal of Biomolecular NMR</i> , 2018, 72, 39-54. | 1.6 | 5 |
| 69 | Interference between transverse cross-correlated relaxation and longitudinal relaxation affects apparent J-coupling and transverse cross-correlated relaxation. <i>Chemical Physics Letters</i> , 2006, 423, 123-125. | 1.2 | 4 |
| 70 | ¹³ C-detected HN(CA)C and HMCMC experiments using a single methyl-reprotonated sample for unambiguous methyl resonance assignment. <i>Journal of Biomolecular NMR</i> , 2006, 36, 259-266. | 1.6 | 4 |
| 71 | Solution NMR backbone assignment reveals interaction-free tumbling of human lineage-specific Olduvai protein domains. <i>Biomolecular NMR Assignments</i> , 2019, 13, 339-343. | 0.4 | 4 |
| 72 | Measuring ¹ H ¹ H and ¹ H ¹³ 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. | 1.2 | 3 |

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|----|---|-----|-----------|
| 73 | Full relaxation matrix analysis of apparent cross-correlated relaxation rates in four-spin systems. Journal of Magnetic Resonance, 2013, 226, 52-63. | 1.2 | 3 |
| 74 | Solution NMR backbone assignments of the N-terminal Z ¹ -linker-Z ² segment from Homo sapiens ADAR1p150. Biomolecular NMR Assignments, 2021, 15, 273-279. | 0.4 | 2 |
| 75 | Enzyme Selectivity Fine-Tuned through Dynamic Control of a Loop. Angewandte Chemie, 2016, 128, 3148-3152. | 1.6 | 1 |
| 76 | Protein Allostery at Atomic Resolution. Angewandte Chemie, 2020, 132, 22316-22323. | 1.6 | 1 |
| 77 | Microbiota-derived butyrate is an endogenous inhibitor of HIF prolyl-hydroxylases. FASEB Journal, 2021, 35, . | 0.2 | 0 |
| 78 | On the use of residual dipolar couplings in multi-state structure calculation of two-domain proteins. Magnetic Resonance Letters, 2022, 2, 61-68. | 0.7 | 0 |
| 79 | Solution NMR backbone assignments of disordered Olduvai protein domain CON1 employing H ¹ -detected experiments. Biomolecular NMR Assignments, 2022, , 1. | 0.4 | 0 |
| 80 | Structural Investigation of a Putative Intrinsically Disordered Region Within Deleted in Colorectal Carcinoma That Regulates Protein Synthesis. FASEB Journal, 2022, 36, . | 0.2 | 0 |
| 81 | Butyrate Analogues Mimicking Hypoxia by the Chemical Stabilization of Hypoxia Inducible Factor (HIF). FASEB Journal, 2022, 36, . | 0.2 | 0 |