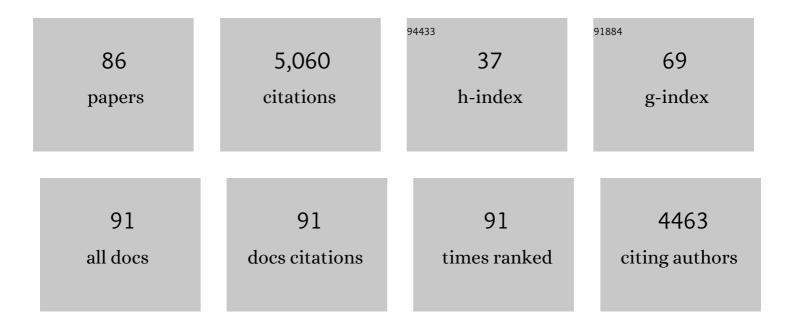
## Bernhard Brutscher

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	SOFAST-HMQC Experiments for Recording Two-dimensional Deteronuclear Correlation Spectra of Proteins within a Few Seconds. Journal of Biomolecular NMR, 2005, 33, 199-211.	2.8	603
2	Very Fast Two-Dimensional NMR Spectroscopy for Real-Time Investigation of Dynamic Events in Proteins on the Time Scale of Seconds. Journal of the American Chemical Society, 2005, 127, 8014-8015.	13.7	592
3	A set of BEST triple-resonance experiments for time-optimized protein resonance assignment. Journal of Magnetic Resonance, 2007, 187, 163-169.	2.1	311
4	Speeding Up Three-Dimensional Protein NMR Experiments to a Few Minutes. Journal of the American Chemical Society, 2006, 128, 9042-9043.	13.7	272
5	Recovering lost magnetization: polarization enhancement in biomolecular NMR. Journal of Biomolecular NMR, 2011, 49, 9-15.	2.8	200
6	BEST-TROSY experiments for time-efficient sequential resonance assignment of large disordered proteins. Journal of Biomolecular NMR, 2013, 55, 311-321.	2.8	193
7	Backbone Dynamics and Structural Characterization of the Partially Folded A State of Ubiquitin by 1H, 13C, and 15N Nuclear Magnetic Resonance Spectroscopy. Biochemistry, 1997, 36, 13043-13053.	2.5	181
8	Protein folding and unfolding studied at atomic resolution by fast two-dimensional NMR spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 11257-11262.	7.1	144
9	Improved Sensitivity and Resolution in1Hâ^13C NMR Experiments of RNA. Journal of the American Chemical Society, 1998, 120, 11845-11851.	13.7	101
10	UltraSOFAST HMQC NMR and the Repetitive Acquisition of 2D Protein Spectra at Hz Rates. Journal of the American Chemical Society, 2007, 129, 1372-1377.	13.7	99
11	Fast Two-Dimensional NMR Spectroscopy of High Molecular Weight Protein Assemblies. Journal of the American Chemical Society, 2009, 131, 3448-3449.	13.7	99
12	Recent Advances in Solution NMR: Fast Methods and Heteronuclear Direct Detection. ChemPhysChem, 2009, 10, 1356-1368.	2.1	90
13	Longitudinal-Relaxation-Enhanced NMR Experiments for the Study of Nucleic Acids in Solution. Journal of the American Chemical Society, 2009, 131, 8571-8577.	13.7	90
14	Guidelines for the use of band-selective radiofrequency pulses in hetero-nuclear NMR: Example of longitudinal-relaxation-enhanced BEST-type 1H–15N correlation experiments. Journal of Magnetic Resonance, 2010, 203, 190-198.	2.1	85
15	NMR Spectroscopic Studies of Intrinsically Disordered Proteins at Nearâ€Physiological Conditions. Angewandte Chemie - International Edition, 2013, 52, 11808-11812.	13.8	71
16	NMR Methods for the Study of Instrinsically Disordered Proteins Structure, Dynamics, and Interactions: General Overview and Practical Guidelines. Advances in Experimental Medicine and Biology, 2015, 870, 49-122.	1.6	69
17	Resolution Enhancement in Multidimensional Solid-State NMR Spectroscopy of Proteins Using Spin-State Selection. Journal of the American Chemical Society, 2003, 125, 11816-11817.	13.7	66
18	HET-SOFAST NMR for fast detection of structural compactness and heterogeneity along polypeptide chains. Magnetic Resonance in Chemistry, 2006, 44, S177-S184.	1.9	62

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19	Solution Structure of the C-Terminal Nucleoprotein–RNA Binding Domain of the Vesicular Stomatitis Virus Phosphoprotein. Journal of Molecular Biology, 2008, 382, 525-538.	4.2	59
20	Hadamard Amino-Acid-Type Edited NMR Experiment for Fast Protein Resonance Assignment. Journal of the American Chemical Society, 2008, 130, 5014-5015.	13.7	56
21	RNA binding and chaperone activity of the <i>E. coli</i> cold-shock protein CspA. Nucleic Acids Research, 2017, 45, gkx044.	14.5	56
22	Native-unlike Long-lived Intermediates along the Folding Pathway of the Amyloidogenic Protein β2-Microglobulin Revealed by Real-time Two-dimensional NMR. Journal of Biological Chemistry, 2010, 285, 5827-5835.	3.4	55
23	Assignment of NMR spectra of proteins using triple-resonance two-dimensional experiments. Journal of Biomolecular NMR, 1994, 4, 325-33.	2.8	53
24	Principles and applications of cross-correlated relaxation in biomolecules. Concepts in Magnetic Resonance, 2000, 12, 207-229.	1.3	51
25	Transient Structure and SH3 Interaction Sites in an Intrinsically Disordered Fragment of the Hepatitis C Virus Protein NS5A. Journal of Molecular Biology, 2012, 420, 310-323.	4.2	49
26	Intraresidue HNCA and COHNCA Experiments for Protein Backbone Resonance Assignment. Journal of Magnetic Resonance, 2002, 156, 155-159.	2.1	48
27	Accurate characterization of weak macromolecular interactions by titration of NMR residual dipolar couplings: application to the CD2AP SH3-C:ubiquitin complex. Nucleic Acids Research, 2009, 37, e70-e70.	14.5	46
28	Real-Time NMR Characterization of Structure and Dynamics in a Transiently Populated Protein Folding Intermediate. Journal of the American Chemical Society, 2012, 134, 8066-8069.	13.7	46
29	NMRlib: user-friendly pulse sequence tools for Bruker NMR spectrometers. Journal of Biomolecular NMR, 2019, 73, 199-211.	2.8	46
30	Title is missing!. Journal of Biomolecular NMR, 1999, 14, 241-252.	2.8	45
31	<sup>13</sup> C-Labeled Heparan Sulfate Analogue as a Tool To Study Protein/Heparan Sulfate Interactions by NMR Spectroscopy: Application to the CXCL12α Chemokine. Journal of the American Chemical Society, 2011, 133, 9642-9645.	13.7	45
32	Highly Efficient NMR Assignment of Intrinsically Disordered Proteins: Application to B- and T Cell Receptor Domains. PLoS ONE, 2013, 8, e62947.	2.5	44
33	NMR Determination of Sugar Puckers in Nucleic Acids from CSAâ^'Dipolar Cross-Correlated Relaxation. Journal of the American Chemical Society, 2000, 122, 6779-6780.	13.7	43
34	How Detergent Impacts Membrane Proteins: Atomic-Level Views of Mitochondrial Carriers in Dodecylphosphocholine. Journal of Physical Chemistry Letters, 2018, 9, 933-938.	4.6	41
35	Sensitivity-enhanced IPAP-SOFAST-HMQC for fast-pulsing 2D NMR with reduced radiofrequency load. Journal of Magnetic Resonance, 2008, 190, 333-338.	2.1	40
36	Computer assignment of the backbone resonances of labelled proteins using two-dimensional correlation experiments. Journal of Biomolecular NMR, 1995, 5, 154-60.	2.8	38

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37	High-resolution 3D HNCOCA experiment applied to a 28 kDa paramagnetic protein. Journal of Biomolecular NMR, 1995, 5, 202-6.	2.8	38
38	An improved ultrafast 2D NMR experiment: Towards atom-resolved real-time studies of protein kinetics at multi-Hz rates. Journal of Biomolecular NMR, 2009, 43, 1-10.	2.8	38
39	Optimized set of two-dimensional experiments for fast sequential assignment, secondary structure determination, and backbone fold validation of 13C/15N-labelled proteins. Journal of Biomolecular NMR, 2003, 27, 57-67.	2.8	37
40	Hyperdimensional Protein NMR Spectroscopy in Peptide-Sequence Space. Journal of the American Chemical Society, 2007, 129, 11916-11917.	13.7	37
41	Accurate Measurement of Small Spin–Spin Couplings in Partially Aligned Molecules Using a Novel J-Mismatch Compensated Spin-State-Selection Filter. Journal of Magnetic Resonance, 2001, 151, 332-338.	2.1	36
42	Determination of an Initial Set of NOE-Derived Distance Constraints for the Structure Determination of 15N/13C-Labeled Proteins. Journal of Magnetic Resonance Series B, 1995, 109, 238-242.	1.6	34
43	Hadamard frequency-encoded SOFAST-HMQC for ultrafast two-dimensional protein NMR. Journal of Magnetic Resonance, 2006, 178, 334-339.	2.1	34
44	Amino Acid-Type Edited NMR Experiments for Methylâ^'Methyl Distance Measurement in13C-Labeled Proteins. Journal of the American Chemical Society, 2004, 126, 9584-9591.	13.7	32
45	Automated Spectral Compression for Fast Multidimensional NMR and Increased Time Resolution in Real-Time NMR Spectroscopy. Journal of the American Chemical Society, 2007, 129, 2756-2757.	13.7	32
46	"CON-CON―assignment strategy for highly flexible intrinsically disordered proteins. Journal of Biomolecular NMR, 2014, 60, 209-218.	2.8	30
47	Direct Structure Determination Using Residual Dipolar Couplings: Reaction-Site Conformation of Methionine Sulfoxide Reductase in Solution. Journal of the American Chemical Society, 2002, 124, 13709-13715.	13.7	24
48	Combined frequency- and time-domain NMR spectroscopy. Application to fast protein resonance assignment. Journal of Biomolecular NMR, 2004, 29, 57-64.	2.8	24
49	Transverse relaxation optimized HCN experiment for nucleic acids: combining the advantages of TROSY and MQ spin evolution. Journal of Biomolecular NMR, 2001, 21, 367-372.	2.8	23
50	Solution Structure of the Sulfite Reductase Flavodoxin-like Domain from Escherichia coli,. Biochemistry, 2005, 44, 9086-9095.	2.5	23
51	Fast Realâ€Time NMR Methods for Characterizing Shortâ€Lived Molecular States. ChemPhysChem, 2013, 14, 3059-3070.	2.1	22
52	Extensive1H NMR resonance assignment of proteins using natural abundance gradient-enhanced13Câ^'1H correlation spectroscopy. FEBS Letters, 1993, 333, 251-256.	2.8	21
53	Base-type-selective high-resolution 13C edited NOESY for sequential assignment of large RNAs. Journal of Biomolecular NMR, 2001, 19, 141-151.	2.8	21
54	Biophysical characterization of the MerP-like amino-terminal extension of the mercuric reductase from Ralstonia metallidurans CH34. Journal of Biological Inorganic Chemistry, 2004, 9, 49-58.	2.6	21

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55	Interaction of Nonstructural Protein 5A of the Hepatitis C Virus with Src Homology 3 Domains Using Noncanonical Binding Sites. Biochemistry, 2013, 52, 6160-6168.	2.5	21
56	Probing Conformational Exchange Dynamics in a Short-Lived Protein Folding Intermediate by Real-Time Relaxation–Dispersion NMR. Journal of the American Chemical Society, 2017, 139, 1065-1068.	13.7	21
57	Highly automated protein backbone resonance assignment within a few hours: the «BATCH» strategy and software package. Journal of Biomolecular NMR, 2009, 44, 43-57.	2.8	20
58	Reactivity, Secondary Structure, and Molecular Topology of theEscherichia coliSulfite Reductase Flavodoxin-like Domainâ€. Biochemistry, 2002, 41, 3770-3780.	2.5	19
59	HNCA+, HNCO+, and HNCACB+ experiments: improved performance by simultaneous detection of orthogonal coherence transfer pathways. Journal of Biomolecular NMR, 2014, 60, 1-9.	2.8	19
60	The Disordered Region of the HCV Protein NS5A: Conformational Dynamics, SH3 Binding, and Phosphorylation. Biophysical Journal, 2015, 109, 1483-1496.	0.5	19
61	Side Chain Orientation from Methyl1Hâ^'1H Residual Dipolar Couplings Measured in Highly Deuterated Proteins. Journal of the American Chemical Society, 2002, 124, 14616-14625.	13.7	18
62	Rapid measurement of residual dipolar couplings for fast fold elucidation of proteins. Journal of Biomolecular NMR, 2011, 51, 369-378.	2.8	18
63	iHADAMAC: A complementary tool for sequential resonance assignment of globular and highly disordered proteins. Journal of Magnetic Resonance, 2012, 214, 329-334.	2.1	18
64	ssNMRlib: a comprehensive library and tool box for acquisition of solid-state nuclear magnetic resonance experiments on Bruker spectrometers. Magnetic Resonance, 2020, 1, 331-345.	1.9	13
65	NMR Study of the Interaction between Zn(II) Ligated Bleomycin andStreptoalloteichus hindustanusBleomycin Resistance Proteinâ€. Biochemistry, 2003, 42, 651-663.	2.5	11
66	Optimized fast mixing device for real-time NMR applications. Journal of Magnetic Resonance, 2017, 281, 125-129.	2.1	11
67	DEPT spectral editing in HCCONH-type experiments. Application to fast protein backbone and side chain assignment. Journal of Magnetic Resonance, 2004, 167, 178-184.	2.1	10
68	NMR Reveals Light-Induced Changes in the Dynamics of a Photoswitchable Fluorescent Protein. Biophysical Journal, 2019, 117, 2087-2100.	0.5	10
69	Detection and assignment of phosphoserine and phosphothreonine residues by 13C–31P spin-echo difference NMR spectroscopy. Journal of Biomolecular NMR, 2009, 43, 31-37.	2.8	9
70	1H, 13C, and 15N resonance assignment of a 179 residue fragment of hepatitis C virus non-structural protein 5A. Biomolecular NMR Assignments, 2011, 5, 241-243.	0.8	9
71	Measuring hydrogen exchange in proteins by selective water saturation in 1H–15N SOFAST/BEST-type experiments: advantages and limitations. Journal of Biomolecular NMR, 2014, 60, 99-107.	2.8	9
72	Longitudinal relaxation properties of 1HN and 1Hα determined by direct-detected 13C NMR experiments to study intrinsically disordered proteins (IDPs). Journal of Magnetic Resonance, 2015, 254, 19-26.	2.1	8

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73	Fragment-Based NMR Study of the Conformational Dynamics in the bHLH Transcription Factor Ascl1. Biophysical Journal, 2017, 112, 1366-1373.	0.5	8
74	BEST and SOFAST experiments for resonance assignment of histidine and tyrosine side chains in 13C/15N labeled proteins. Journal of Biomolecular NMR, 2018, 72, 115-124.	2.8	8
75	Parallel screening and optimization of protein constructs for structural studies. Protein Science, 2009, 18, 434-439.	7.6	7
76	Spectral editing of intra- and inter-chain methyl–methyl NOEs in protein complexes. Journal of Biomolecular NMR, 2020, 74, 83-94.	2.8	7
77	Disentangling Chromophore States in a Reversibly Switchable Green Fluorescent Protein: Mechanistic Insights from NMR Spectroscopy. Journal of the American Chemical Society, 2021, 143, 7521-7530.	13.7	7
78	Sensitivity-optimized experiment for the measurement of residual dipolar couplings between amide protons. Journal of Biomolecular NMR, 2007, 38, 47-55.	2.8	6
79	1H, 13C and 15N assignment of the flavodoxin-like domain of the Escherichia coli sulfite reductase. Journal of Biomolecular NMR, 2001, 21, 71-72.	2.8	5
80	Suppression of artifacts induced by homonuclear decoupling in amino-acid-type edited methyl 1H–13C correlation experiments. Journal of Magnetic Resonance, 2004, 170, 199-205.	2.1	5
81	Resolution-Enhanced Base-Type-Edited HCN Experiment for RNA. Journal of Biomolecular NMR, 2005, 32, 263-271.	2.8	4
82	NMR assignments of human linker histone H1x N-terminal domain and globular domain in the presence and absence of perchlorate. Biomolecular NMR Assignments, 2019, 13, 249-254.	0.8	3
83	Fast Protein Backbone NMR Resonance Assignment Using the BATCH Strategy. Methods in Molecular Biology, 2012, 831, 407-428.	0.9	3
84	Aromatic SOFAST-HMBC for proteins at natural 13C abundance. Journal of Magnetic Resonance, 2019, 300, 95-102.	2.1	2
85	The non-structural protein 5A (NS5A) of hepatitis C virus interacts with the SH3 domain of human Bin1 using non-canonical binding sites. European Journal of Medical Research, 2014, 19, .	2.2	0
86	Raw nuclear magnetic resonance data of human linker histone H1x, lacking the C-terminal domain (NGH1x), and trajectory data of nanosecond molecular dynamics simulations of GH1x- and NGH1x-chromatosomes. Data in Brief, 2020, 31, 105865.	1.0	0