Martin Billeter

List of Publications by Year
in descending order

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83	14,648	81900 39	58581 82
papers	citations	h-index	g-index

85	85	85	10523
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	NUScon: a community-driven platform for quantitative evaluation of nonuniform sampling in NMR. Magnetic Resonance, 2021, 2, 843-861.	1.9	7
2	Complete protein assignment from sets of spectra recorded overnight. Journal of Biomolecular NMR, 2019, 73, 59-70.	2.8	1
3	Nanomedical Relevance of the Intermolecular Interaction Dynamicsâ€"Examples from Lysozymes and Insulins. ACS Omega, 2019, 4, 4206-4220.	3.5	11
4	Non-uniform sampling in biomolecular NMR. Journal of Biomolecular NMR, 2017, 68, 65-66.	2.8	24
5	Lysozyme's lectin-like characteristics facilitates its immune defense function. Quarterly Reviews of Biophysics, 2017, 50, e9.	5.7	29
6	DIADECOMP: A new approach to analyze decompositions from projection spectroscopy. Journal of Magnetic Resonance, 2016, 273, 1-8.	2.1	1
7	Molecular Basis of the Receptor Interactions of Polysialic Acid (polySia), polySia Mimetics, and Sulfated Polysaccharides. ChemMedChem, 2016, 11, 990-1002.	3.2	11
8	A Consensus on Protein Structure Accuracy in NMR?. Structure, 2015, 23, 255-256.	3.3	2
9	Automated protein structure determination by NMR. Journal of Biomolecular NMR, 2015, 62, 411-412.	2.8	4
10	The indelible mark of computation on bio-NMR. Journal of Biomolecular NMR, 2014, 58, 231-232.	2.8	0
11	Minor-Groove Binding Drugs: Where Is the Second Hoechst 33258 Molecule?. Journal of Physical Chemistry B, 2013, 117, 5820-5830.	2.6	46
12	Initial DNA Interactions of the Binuclear Threading Intercalator Î›,Î›â€[Î¼â€bidppz(bipy)₄Ru₂]⁴⁺: An NMR Study with [d(CGCGAATTCGCG)]₂. Chemistry - A European Journal, 2013, 19, 5401-5410.	3.3	24
13	Automated protein backbone assignment using the projection-decomposition approach. Journal of Biomolecular NMR, 2012, 54, 43-51.	2.8	5
14	TSAR: a program for automatic resonance assignment using 2D cross-sections of high dimensionality, high-resolution spectra. Journal of Biomolecular NMR, 2012, 54, 81-95.	2.8	23
15	Structural characterisation of a histone domain by projectionâ€"decomposition. Journal of Magnetic Resonance, 2012, 217, 48-52.	2.1	3
16	Stepwise Evolution of the Herpes Simplex Virus Origin Binding Protein and Origin of Replication. Journal of Biological Chemistry, 2009, 284, 16246-16255.	3.4	16
17	Assignment of protein NMR spectra based on projections, multi-way decomposition and a fast correlation approach. Journal of Biomolecular NMR, 2008, 42, 87-97.	2.8	21
18	Solution NMR structure determination of proteins revisited. Journal of Biomolecular NMR, 2008, 42, 155-158.	2.8	100

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19	PRODECOMPv3: decompositions of NMR projections for protein backbone and side-chain assignments and structural studies. Bioinformatics, 2008, 24, 2258-2259.	4.1	8
20	Propagation of Dynamic Changes in Barnase Upon Binding of Barstar: An NMR and Computational Study. Journal of Molecular Biology, 2007, 367, 1079-1092.	4.2	52
21	Multi-way decomposition of projected spectra obtained in protein NMR. Proceedings in Applied Mathematics and Mechanics, 2007, 7, 1110103-1110104.	0.2	1
22	Assignment of 1H, 13C, and 15N resonances of YgiT, a putative DNA interacting protein from E.Âcoli, containing one HTH and two CxxC motifs. Biomolecular NMR Assignments, 2007, 1, 217-219.	0.8	2
23	Robust and versatile interpretation of spectra with coupled evolution periods using multi-way decomposition. Magnetic Resonance in Chemistry, 2006, 44, S185-S195.	1.9	21
24	Accuracy and robustness of three-way decomposition applied to NMR data. Journal of Magnetic Resonance, 2005, 174, 188-199.	2.1	15
25	Signal identification in NMR spectra with coupled evolution periods. Journal of Magnetic Resonance, 2005, 176, 47-53.	2.1	28
26	High-throughput analysis of protein NMR spectra. Progress in Nuclear Magnetic Resonance Spectroscopy, 2005, 46, 109-129.	7.5	33
27	Multiway Decomposition of NMR Spectra with Coupled Evolution Periods. Journal of the American Chemical Society, 2005, 127, 13486-13487.	13.7	74
28	DNA adopts normal B-form upon incorporation of highly fluorescent DNA base analogue tC: NMR structure and UV-Vis spectroscopy characterization. Nucleic Acids Research, 2004, 32, 5087-5095.	14.5	80
29	Accurate relaxation parameters for large proteins. Journal of Magnetic Resonance, 2004, 167, 107-113.	2.1	13
30	Specific DNA recognition by theAntp homeodomain: MD simulations of specific and nonspecific complexes. Proteins: Structure, Function and Bioinformatics, 2004, 57, 772-782.	2.6	20
31	Gated Electron Transfers and Electron Pathways in Azurin: A NMR Dynamic Study at Multiple Fields and Temperatures. Journal of Molecular Biology, 2004, 342, 1599-1611.	4.2	30
32	Fully automated sequence-specific resonance assignments of hetero- nuclear protein spectra. Journal of Biomolecular NMR, 2003, 27, 69-79.	2.8	50
33	Optimizing resolution in multidimensional NMR by three-way decomposition. Journal of Biomolecular NMR, 2003, 27, 165-173.	2.8	166
34	Interactive model building of proteins from NMR data. Magnetic Resonance in Chemistry, 2003, 41, S33-S36.	1.9	1
35	NMR detection of multiple transitions to low-populated states in azurin. Protein Science, 2003, 12, 56-65.	7.6	32
36	Dynamics-modulated Biological Activity of Transforming Growth Factor Î²3. Journal of Biological Chemistry, 2002, 277, 46273-46279.	3.4	35

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37	Automated Analysis of Large Sets of Heteronuclear Correlation Spectra in NMR-Based Drug Discovery. Journal of Medicinal Chemistry, 2002, 45, 5649-5654.	6.4	24
38	Essential domain motions in barnase revealed by MD simulations. Proteins: Structure, Function and Bioinformatics, 2002, 46, 250-258.	2.6	26
39	Three-way decomposition of a complete 3D 15N-NOESY-HSQC. Journal of Biomolecular NMR, 2002, 24, 191-201.	2.8	40
40	Backbone dynamics of the channel-forming antibiotic zervamicin IIB studied by 15 N NMR relaxation. FEBS Letters, 2001, 495, 52-55.	2.8	15
41	MUNIN: a new approach to multi-dimensional NMR spectra interpretation. Journal of Biomolecular NMR, 2001, 20, 49-60.	2.8	152
42	MUNIN: application of three-way decomposition to the analysis of heteronuclear NMR relaxation data. Journal of Biomolecular NMR, 2001, 21, 263-268.	2.8	82
43	NMR structure of the chimeric hybrid duplex r(gcaguggc).r(gcca)d(CTGC) comprising the tRNA-DNA junction formed during initiation of HIV-1 reverse transcription. Journal of Biomolecular NMR, 1999, 13, 343-355.	2.8	38
44	Conformational Changes of the BS2 Operator DNA upon Complex Formation with the Antennapedia Homeodomain Studied by NMR with13C/15N-labeled DNA. Journal of Molecular Biology, 1999, 292, 609-617.	4.2	14
45	Conformational analysis of protein and nucleic acid fragments with the new grid search algorithm FOUND. Journal of Biomolecular NMR, 1998, 12, 543-548.	2.8	53
46	Automated Peak Picking and Peak Integration in Macromolecular NMR Spectra Using AUTOPSY. Journal of Magnetic Resonance, 1998, 135, 288-297.	2.1	121
47	Prion protein structural features indicate possible relations to signal peptidases. FEBS Letters, 1998, 426, 291-296.	2.8	22
48	The NMR solution structure of the non-classical homeodomain from the rat liver LFB1/HNF1 transcription factor 1 1Edited by P. E. Wright. Journal of Molecular Biology, 1997, 267, 673-683.	4.2	19
49	GARANT-a general algorithm for resonance assignment of multidimensional nuclear magnetic resonance spectra. Journal of Computational Chemistry, 1997, 18, 139-149.	3.3	129
50	Structural Role of a Buried Salt Bridge in the 434 Repressor DNA-binding Domain. Journal of Molecular Biology, 1996, 264, 1002-1012.	4.2	45
51	Hydration and DNA Recognition by Homeodomains. Cell, 1996, 85, 1057-1065.	28.9	112
52	NMR studies of the hydration of biological macromolecules. Faraday Discussions, 1996, 103, 245-253.	3.2	52
53	Homeodomain-type DNA recognition. Progress in Biophysics and Molecular Biology, 1996, 66, 211-225.	2.9	37
54	MOLMOL: A program for display and analysis of macromolecular structures. Journal of Molecular Graphics, 1996, 14, 51-55.	1.1	6,760

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55	Automated sequence-specific NMR assignment of homologous proteins using the program GARANT. Journal of Biomolecular NMR, 1996, 7, 207-13.	2.8	117
56	NMR for structural studies in drug discovery. Journal of Computer - Aided Molecular Design, 1995, 3, 151-167.	1.0	6
57	The program XEASY for computer-supported NMR spectral analysis of biological macromolecules. Journal of Biomolecular NMR, 1995, 6, 1-10.	2.8	1,570
58	Hydration water molecules seen by NMR and by X-ray crystallography. Progress in Nuclear Magnetic Resonance Spectroscopy, 1995, 27, 635-645.	7.5	38
59	The Sequence and Conformation of Human Pancreatic Procarboxypeptidase A2. Journal of Biological Chemistry, 1995, 270, 6651-6657.	3.4	31
60	NMR studies of DNA duplexes singly cross-linked by different synthetic linkers. Nucleic Acids Research, 1995, 23, 4827-4835.	14.5	31
61	Homeodomain-DNA recognition. Cell, 1994, 78, 211-223.	28.9	770
62	The Nuclear Magnetic Resonance Solution Structure of the Mixed Disulfide between Escherichia coli Glutaredoxin(C14S) and Glutathione. Journal of Molecular Biology, 1994, 235, 1585-1597.	4.2	134
63	Warum Pentose- und nicht Hexose-NucleinsÃuren??. Teil VI. â€˜Homo-DNSâ€™:1H-,13C-,31P-und15N-NMR-spektroskopische Untersuchung von ddGlc(A-A-A-A-A-T-T-T-T-T) in wÃssriger LÃ¶sung. Helvetica Chimica Acta, 1993, 76, 2701-2756.	1.6	55
64	Determination of the NMR solution structure of the Hoechst 33258-d(GTGGAATTCCAC)2 complex and comparison with the X-ray crystal structure. Structure, 1993, 1, 177-186.	3.3	57
65	Nuclear Magnetic Resonance Spectroscopy of a DNA Complex with the Uniformly 13C-Labeled Antennapedia Homeodomain and Structure Determination of the DNA-bound Homeodomain. Journal of Molecular Biology, 1993, 234, 1070-1083.	4.2	80
66	Determination of the Nuclear Magnetic Resonance Solution Structure of an Antennapedia Homeodomain-DNA Complex. Journal of Molecular Biology, 1993, 234, 1084-1097.	4.2	278
67	Appendix: Model Studies Relating Nuclear Magnetic Resonance Data with the Three-dimensional Structure of Protein-DNA Complexes. Journal of Molecular Biology, 1993, 234, 1094.	4.2	9
68	Comparison of protein structures determined by NMR in solution and by X-ray diffraction in single crystals. Quarterly Reviews of Biophysics, 1992, 25, 325-377.	5.7	91
69	Determination of the nuclear magnetic resonance solution structure of the DNA-binding domain (residues 1 to 69) of the 434 repressor and comparison with the X-ray crystal structure. Journal of Molecular Biology, 1992, 223, 743-767.	4.2	70
70	NMR structure of oxidized Escherichia coli glutaredoxin: Comparison with reduced E. coli glutaredoxin and functionally related proteins. Protein Science, 1992, 1, 310-321.	7.6	111
71	Precise vicinal coupling constants3JHNÎ± in proteins from nonlinear fits of J-modulated [15N,1H]-COSY experiments. Journal of Biomolecular NMR, 1992, 2, 257-274.	2.8	112
72	Sequence-specific1H n.m.r. assignments and determination of the three-dimensional structure of reduced escherichia coli glutaredoxin. Journal of Molecular Biology, 1991, 221, 1311-1324.	4.2	92

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73	8-hydroxyflavonoid glucuronides from Malva sylvestris. Phytochemistry, 1991, 30, 987-990.	2.9	59
74	Efficient analysis of protein 2D NMR spectra using the software packageEASY. Journal of Biomolecular NMR, 1991, 1, 111-130.	2.8	265
75	Determination of the three-dimensional structure of theAntennapedia homeodomain fromDrosophila in solution by1H nuclear magnetic resonance spectroscopy. Journal of Molecular Biology, 1990, 214, 183-197.	4.2	122
76	Three-dimensional structure of the neurotoxin ATX Ia fromAnemonia sulcata in aqueous solution determined by nuclear magnetic resonance spectroscopy. Proteins: Structure, Function and Bioinformatics, 1989, 6, 357-371.	2.6	78
77	Comparison of the high-resolution structures of the Î±-amylase inhibitor tendamistat determined by nuclear magnetic resonance in solution and by X-ray diffraction in single crystals. Journal of Molecular Biology, 1989, 206, 677-687.	4.2	157
78	[8] Computer-assisted resonance assignments. Methods in Enzymology, 1989, 177, 150-158.	1.0	0
79	Many-body potential for molecular interactions. Journal of the American Chemical Society, 1988, 110, 6984-6991.	13.7	75
80	A new technique to calculate low-energy conformations of cyclic molecules utilizing the ellipsoid algorithm and molecular dynamics: application to 18-crown-6. Journal of the American Chemical Society, 1988, 110, 8385-8391.	13.7	73
81	Spatial arrangement of the three Î± helices in the solution conformation of E. coli lac represser DNA-binding domain. FEBS Letters, 1984, 174, 243-247.	2.8	54
82	Polypeptide secondary structure determination by nuclear magnetic resonance observation of short proton-proton distances. Journal of Molecular Biology, 1984, 180, 715-740.	4.2	771
83	Sequential resonance assignments in protein 1H nuclear magnetic resonance spectra. Journal of Molecular Biology, 1982, 155, 321-346.	4.2	608