Martin Billeter

List of Publications by Year
in descending order

83 papers	14,648 citations	87723 38 h-index	60497 81 g-index
85 all docs	85 docs citations	85 times ranked	10523 citing authors

#	Article	IF	Citations
1	MOLMOL: A program for display and analysis of macromolecular structures. Journal of Molecular Graphics, 1996, 14, 51-55.	1.7	6,760
2	The program XEASY for computer-supported NMR spectral analysis of biological macromolecules. Journal of Biomolecular NMR, 1995, 6, 1-10.	1.6	1,570
3	Polypeptide secondary structure determination by nuclear magnetic resonance observation of short proton-proton distances. Journal of Molecular Biology, 1984, 180, 715-740.	2.0	771
4	Homeodomain-DNA recognition. Cell, 1994, 78, 211-223.	13.5	770
5	Sequential resonance assignments in protein 1H nuclear magnetic resonance spectra. Journal of Molecular Biology, 1982, 155, 321-346.	2.0	608
6	Determination of the Nuclear Magnetic Resonance Solution Structure of an Antennapedia Homeodomain-DNA Complex. Journal of Molecular Biology, 1993, 234, 1084-1097.	2.0	278
7	Efficient analysis of protein 2D NMR spectra using the software packageEASY. Journal of Biomolecular NMR, 1991, 1, 111-130.	1.6	265
8	Optimizing resolution in multidimensional NMR by three-way decomposition. Journal of Biomolecular NMR, 2003, 27, 165-173.	1.6	166
9	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.	2.0	157
10	MUNIN: a new approach to multi-dimensional NMR spectra interpretation. Journal of Biomolecular NMR, 2001, 20, 49-60.	1.6	152
11	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.	2.0	134
12	GARANT-a general algorithm for resonance assignment of multidimensional nuclear magnetic resonance spectra. , 1997, 18, 139-149.		129
13	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.	2.0	122
14	Automated Peak Picking and Peak Integration in Macromolecular NMR Spectra Using AUTOPSY. Journal of Magnetic Resonance, 1998, 135, 288-297.	1.2	121
15	Automated sequence-specific NMR assignment of homologous proteins using the program GARANT. Journal of Biomolecular NMR, 1996, 7, 207-13.	1.6	117
16	Precise vicinal coupling constants3JHNÎ± in proteins from nonlinear fits of J-modulated [15N,1H]-COSY experiments. Journal of Biomolecular NMR, 1992, 2, 257-274.	1.6	112
17	Hydration and DNA Recognition by Homeodomains. Cell, 1996, 85, 1057-1065.	13.5	112
18	NMR structure of oxidized Escherichia coli glutaredoxin: Comparison with reduced E. coli glutaredoxin and functionally related proteins. Protein Science, 1992, 1, 310-321.	3.1	111

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19	Solution NMR structure determination of proteins revisited. Journal of Biomolecular NMR, 2008, 42, 155-158.	1.6	100
20	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.	2.0	92
21	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.	2.4	91
22	MUNIN: application of three-way decomposition to the analysis of heteronuclear NMR relaxation data. Journal of Biomolecular NMR, 2001, 21, 263-268.	1.6	82
23	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.	2.0	80
24	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.	6.5	80
25	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.	1.5	78
26	Many-body potential for molecular interactions. Journal of the American Chemical Society, 1988, 110, 6984-6991.	6.6	75
27	Multiway Decomposition of NMR Spectra with Coupled Evolution Periods. Journal of the American Chemical Society, 2005, 127, 13486-13487.	6.6	74
28	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.	6.6	73
29	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.	2.0	70
30	8-hydroxyflavonoid glucuronides from Malva sylvestris. Phytochemistry, 1991, 30, 987-990.	1.4	59
31	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.	1.6	57
32	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.	1.0	55
33	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.	1.3	54
34	Conformational analysis of protein and nucleic acid fragments with the new grid search algorithm FOUND. Journal of Biomolecular NMR, 1998, 12, 543-548.	1.6	53
35	NMR studies of the hydration of biological macromolecules. Faraday Discussions, 1996, 103, 245-253.	1.6	52
36	Propagation of Dynamic Changes in Barnase Upon Binding of Barstar: An NMR and Computational Study. Journal of Molecular Biology, 2007, 367, 1079-1092.	2.0	52

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37	Fully automated sequence-specific resonance assignments of hetero- nuclear protein spectra. Journal of Biomolecular NMR, 2003, 27, 69-79.	1.6	50
38	Minor-Groove Binding Drugs: Where Is the Second Hoechst 33258 Molecule?. Journal of Physical Chemistry B, 2013, 117, 5820-5830.	1.2	46
39	Structural Role of a Buried Salt Bridge in the 434 Repressor DNA-binding Domain. Journal of Molecular Biology, 1996, 264, 1002-1012.	2.0	45
40	Three-way decomposition of a complete 3D 15N-NOESY-HSQC. Journal of Biomolecular NMR, 2002, 24, 191-201.	1.6	40
41	Hydration water molecules seen by NMR and by X-ray crystallography. Progress in Nuclear Magnetic Resonance Spectroscopy, 1995, 27, 635-645.	3.9	38
42	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.	1.6	38
43	Homeodomain-type DNA recognition. Progress in Biophysics and Molecular Biology, 1996, 66, 211-225.	1.4	37
44	Dynamics-modulated Biological Activity of Transforming Growth Factor Î²3. Journal of Biological Chemistry, 2002, 277, 46273-46279.	1.6	35
45	High-throughput analysis of protein NMR spectra. Progress in Nuclear Magnetic Resonance Spectroscopy, 2005, 46, 109-129.	3.9	33
46	NMR detection of multiple transitions to low-populated states in azurin. Protein Science, 2003, 12, 56-65.	3.1	32
47	The Sequence and Conformation of Human Pancreatic Procarboxypeptidase A2. Journal of Biological Chemistry, 1995, 270, 6651-6657.	1.6	31
48	NMR studies of DNA duplexes singly cross-linked by different synthetic linkers. Nucleic Acids Research, 1995, 23, 4827-4835.	6.5	31
49	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.	2.0	30
50	Lysozyme's lectin-like characteristics facilitates its immune defense function. Quarterly Reviews of Biophysics, 2017, 50, e9.	2.4	29
51	Signal identification in NMR spectra with coupled evolution periods. Journal of Magnetic Resonance, 2005, 176, 47-53.	1.2	28
52	Essential domain motions in barnase revealed by MD simulations. Proteins: Structure, Function and Bioinformatics, 2002, 46, 250-258.	1.5	26
53	Automated Analysis of Large Sets of Heteronuclear Correlation Spectra in NMR-Based Drug Discovery. Journal of Medicinal Chemistry, 2002, 45, 5649-5654.	2.9	24
54	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.	1.7	24

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55	Non-uniform sampling in biomolecular NMR. Journal of Biomolecular NMR, 2017, 68, 65-66.	1.6	24
56	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.	1.6	23
57	Prion protein structural features indicate possible relations to signal peptidases. FEBS Letters, 1998, 426, 291-296.	1.3	22
58	Robust and versatile interpretation of spectra with coupled evolution periods using multi-way decomposition. Magnetic Resonance in Chemistry, 2006, 44, S185-S195.	1.1	21
59	Assignment of protein NMR spectra based on projections, multi-way decomposition and a fast correlation approach. Journal of Biomolecular NMR, 2008, 42, 87-97.	1.6	21
60	Specific DNA recognition by theAntp homeodomain: MD simulations of specific and nonspecific complexes. Proteins: Structure, Function and Bioinformatics, 2004, 57, 772-782.	1.5	20
61	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.	2.0	19
62	Stepwise Evolution of the Herpes Simplex Virus Origin Binding Protein and Origin of Replication. Journal of Biological Chemistry, 2009, 284, 16246-16255.	1.6	16
63	Backbone dynamics of the channel-forming antibiotic zervamicin IIB studied by 15 N NMR relaxation. FEBS Letters, 2001, 495, 52-55.	1.3	15
64	Accuracy and robustness of three-way decomposition applied to NMR data. Journal of Magnetic Resonance, 2005, 174, 188-199.	1.2	15
65	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.	2.0	14
66	Accurate relaxation parameters for large proteins. Journal of Magnetic Resonance, 2004, 167, 107-113.	1.2	13
67	Molecular Basis of the Receptor Interactions of Polysialic Acid (polySia), polySia Mimetics, and Sulfated Polysaccharides. ChemMedChem, 2016, 11, 990-1002.	1.6	11
68	Nanomedical Relevance of the Intermolecular Interaction Dynamicsâ€"Examples from Lysozymes and Insulins. ACS Omega, 2019, 4, 4206-4220.	1.6	11
69	Appendix: Model Studies Relating Nuclear Magnetic Resonance Data with the Three-dimensional Structure of Protein-DNA Complexes. Journal of Molecular Biology, 1993, 234, 1094.	2.0	9
70	PRODECOMPv3: decompositions of NMR projections for protein backbone and side-chain assignments and structural studies. Bioinformatics, 2008, 24, 2258-2259.	1.8	8
71	NUScon: a community-driven platform for quantitative evaluation of nonuniform sampling in NMR. Magnetic Resonance, 2021, 2, 843-861.	0.8	7
72	NMR for structural studies in drug discovery. Journal of Computer - Aided Molecular Design, 1995, 3, 151-167.	1.0	6

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73	Automated protein backbone assignment using the projection-decomposition approach. Journal of Biomolecular NMR, 2012, 54, 43-51.	1.6	5
74	Automated protein structure determination by NMR. Journal of Biomolecular NMR, 2015, 62, 411-412.	1.6	4
75	Structural characterisation of a histone domain by projectionâ€“decomposition. Journal of Magnetic Resonance, 2012, 217, 48-52.	1.2	3
76	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.	0.4	2
77	A Consensus on Protein Structure Accuracy in NMR?. Structure, 2015, 23, 255-256.	1.6	2
78	Interactive model building of proteins from NMR data. Magnetic Resonance in Chemistry, 2003, 41, S33-S36.	1.1	1
79	Multi-way decomposition of projected spectra obtained in protein NMR. Proceedings in Applied Mathematics and Mechanics, 2007, 7, 1110103-1110104.	0.2	1
80	DIADECOMP: A new approach to analyze decompositions from projection spectroscopy. Journal of Magnetic Resonance, 2016, 273, 1-8.	1.2	1
81	Complete protein assignment from sets of spectra recorded overnight. Journal of Biomolecular NMR, 2019, 73, 59-70.	1.6	1
82	[8] Computer-assisted resonance assignments. Methods in Enzymology, 1989, 177, 150-158.	0.4	0
83	The indelible mark of computation on bio-NMR. Journal of Biomolecular NMR, 2014, 58, 231-232.	1.6	0