

Isabella C Felli

List of Publications by Year in descending order

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citations

61857

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141
all docs

141
docs citations

141
times ranked

4375
citing authors

#	ARTICLE	IF	CITATIONS
1	13C-detected protonless NMR spectroscopy of proteins in solution. Progress in Nuclear Magnetic Resonance Spectroscopy, 2006, 48, 25-45.	3.9	210
2	The Atx1-Ccc2 complex is a metal-mediated protein-protein interaction. Nature Chemical Biology, 2006, 2, 367-368.	3.9	204
3	pE-DB: a database of structural ensembles of intrinsically disordered and of unfolded proteins. Nucleic Acids Research, 2014, 42, D326-D335.	6.5	195
4	Protonless NMR Experiments for Sequence-Specific Assignment of Backbone Nuclei in Unfolded Proteins. Journal of the American Chemical Society, 2006, 128, 3918-3919.	6.6	176
5	Structure and backbone dynamics of a microcrystalline metalloprotein by solid-state NMR. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11095-11100.	3.3	173
6	Complete Assignment of Heteronuclear Protein Resonances by Protonless NMR Spectroscopy. Angewandte Chemie - International Edition, 2005, 44, 3089-3092.	7.2	162
7	Fast Resonance Assignment and Fold Determination of Human Superoxide Dismutase by High-Resolution Proton-Detected Solid-State MAS NMR Spectroscopy. Angewandte Chemie - International Edition, 2011, 50, 11697-11701.	7.2	157
8	NMR reveals pathway for ferric mineral precursors to the central cavity of ferritin. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 545-550.	3.3	143
9	Novel 13C direct detection experiments, including extension to the third dimension, to perform the complete assignment of proteins. Journal of Magnetic Resonance, 2006, 178, 56-64.	1.2	116
10	Molecular chaperone function of Mia40 triggers consecutive induced folding steps of the substrate in mitochondrial protein import. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20190-20195.	3.3	116
11	Probing the Interaction of Cisplatin with the Human Copper Chaperone Atox1 by Solution and In-Cell NMR Spectroscopy. Journal of the American Chemical Society, 2011, 133, 18361-18369.	6.6	114
12	13C Direct Detection Experiments on the Paramagnetic Oxidized Monomeric Copper, Zinc Superoxide Dismutase. Journal of the American Chemical Society, 2003, 125, 16423-16429.	6.6	107
13	The three-dimensional structure in solution of the paramagnetic high-potential iron-sulfur protein I from Ectothiorhodospira halophila through nuclear magnetic resonance. FEBS Journal, 1994, 225, 715-725.	0.2	99
14	A Strategy for the NMR Characterization of Type II Copper(II) Proteins: The Case of the Copper Trafficking Protein CopC from Pseudomonas Syringae. Journal of the American Chemical Society, 2003, 125, 7200-7208.	6.6	98
15	Small-molecule sequestration of amyloid-β as a drug discovery strategy for Alzheimer's disease. Science Advances, 2020, 6, .	4.7	95
16	Cyanobacterial metallochaperone inhibits deleterious side reactions of copper. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 95-100.	3.3	91
17	Recent Advances in Solution NMR: Fast Methods and Heteronuclear Direct Detection. ChemPhysChem, 2009, 10, 1356-1368.	1.0	90
18	H-start for exclusively heteronuclear NMR spectroscopy: The case of intrinsically disordered proteins. Journal of Magnetic Resonance, 2009, 198, 275-281.	1.2	90

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19	Speeding Up ¹³ C Direct Detection Biomolecular NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2009, 131, 15339-15345.	6.6	88
20	The Solution Structure of Oxidized Rat Microsomal Cytochrome b ₅ . <i>Biochemistry</i> , 1998, 37, 173-184.	1.2	86
21	Copper(I)-mediated protein-protein interactions result from suboptimal interaction surfaces. <i>Biochemical Journal</i> , 2009, 422, 37-42.	1.7	85
22	Determination of RNA Sugar Pucker Mode from Cross-Correlated Relaxation in Solution NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 1999, 121, 1956-1957.	6.6	80
23	Magic Angle Spinning NMR of Paramagnetic Proteins. <i>Accounts of Chemical Research</i> , 2013, 46, 2108-2116.	7.6	78
24	Side chain to main chain hydrogen bonds stabilize a polyglutamine helix in a transcription factor. <i>Nature Communications</i> , 2019, 10, 2034.	5.8	78
25	¹³ C- ¹³ C NOESY: An Attractive Alternative for Studying Large Macromolecules. <i>Journal of the American Chemical Society</i> , 2004, 126, 464-465.	6.6	74
26	The crowd you're in with: Effects of different types of crowding agents on protein aggregation. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 346-357.	1.1	74
27	Transferred Cross-Correlated Relaxation: Application to the Determination of Sugar Pucker in an Aminoacylated tRNA-Mimetic Weakly Bound to EF-Tu. <i>Journal of the American Chemical Society</i> , 1999, 121, 1945-1948.	6.6	73
28	NMR Spectroscopic Studies of Intrinsically Disordered Proteins at Near Physiological Conditions. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 11808-11812.	7.2	71
29	The Solution Structure Refinement of the Paramagnetic Reduced High-Potential Iron-Sulfur Protein I from <i>Ectothiorhodospira Halophila</i> by Using Stable Isotope Labeling and Nuclear Relaxation. <i>FEBS Journal</i> , 1996, 241, 440-452.	0.2	69
30	NMR Methods for the Study of Intrinsically Disordered Proteins Structure, Dynamics, and Interactions: General Overview and Practical Guidelines. <i>Advances in Experimental Medicine and Biology</i> , 2015, 870, 49-122.	0.8	69
31	Structural and Dynamic Characterization of Intrinsically Disordered Human Securin by NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2008, 130, 16873-16879.	6.6	67
32	Structural and Mechanistic Implications of Metal Binding in the Small Heat-shock Protein β -crystallin. <i>Journal of Biological Chemistry</i> , 2012, 287, 1128-1138.	1.6	67
33	Speeding up sequence specific assignment of IDPs. <i>Journal of Biomolecular NMR</i> , 2012, 53, 293-301.	1.6	66
34	Novel methods based on ¹³ C detection to study intrinsically disordered proteins. <i>Journal of Magnetic Resonance</i> , 2014, 241, 115-125.	1.2	65
35	The Ambivalent Role of Proline Residues in an Intrinsically Disordered Protein: From Disorder Promoters to Compaction Facilitators. <i>Journal of Molecular Biology</i> , 2020, 432, 3093-3111.	2.0	65
36	¹³ C Direct Detection biomolecular NMR. <i>Concepts in Magnetic Resonance Part A: Bridging Education and Research</i> , 2008, 32A, 183-200.	0.2	62

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37	Sequence Context Influences the Structure and Aggregation Behavior of a PolyQ Tract. <i>Biophysical Journal</i> , 2016, 110, 2361-2366.	0.2	58
38	¹³ C Direct-Detection Biomolecular NMR Spectroscopy in Living Cells. <i>Angewandte Chemie - International Edition</i> , 2011, 50, 2339-2341.	7.2	55
39	Rapid Measurement of Pseudocontact Shifts in Metalloproteins by Proton-Detected Solid-State NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2012, 134, 14730-14733.	6.6	53
40	Recent progress in NMR spectroscopy: Toward the study of intrinsically disordered proteins of increasing size and complexity. <i>IUBMB Life</i> , 2012, 64, 473-481.	1.5	53
41	A Heteronuclear Direct-Detection NMR Spectroscopy Experiment for Protein-Backbone Assignment. <i>Angewandte Chemie - International Edition</i> , 2004, 43, 2257-2259.	7.2	52
42	A method for ^{13}C direct-detection in protonless NMR. <i>Journal of Magnetic Resonance</i> , 2007, 188, 301-310.	1.2	52
43	In-cell ¹³ C NMR spectroscopy for the study of intrinsically disordered proteins. <i>Nature Protocols</i> , 2014, 9, 2005-2016.	5.5	48
44	Hsp70 and Hsp40 inhibit an inter-domain interaction necessary for transcriptional activity in the androgen receptor. <i>Nature Communications</i> , 2019, 10, 3562.	5.8	45
45	Protein residue linking in a single spectrum for magic-angle spinning NMR assignment. <i>Journal of Biomolecular NMR</i> , 2015, 62, 253-261.	1.6	44
46	Exclusively Heteronuclear ¹³ C-Detected Amino Acid-Selective NMR Experiments for the Study of Intrinsically Disordered Proteins (IDPs). <i>ChemBioChem</i> , 2012, 13, 2425-2432.	1.3	43
47	High-dimensionality ¹³ C direct-detected NMR experiments for the automatic assignment of intrinsically disordered proteins. <i>Journal of Biomolecular NMR</i> , 2013, 57, 353-361.	1.6	42
48	Sequence-Specific Assignment of Ligand Cysteine Protons of Oxidized, Recombinant HiPIP I from <i>Ectothiorhodospira halophila</i> . <i>Inorganic Chemistry</i> , 1995, 34, 2516-2523.	1.9	40
49	The role of a conserved tyrosine residue in high-potential iron sulfur proteins. <i>Protein Science</i> , 1995, 4, 2562-2572.	3.1	39
50	Probing the Backbone Dynamics of Oxidized and Reduced Rat Microsomal Cytochrome b5 via ¹⁵ N Rotating Frame NMR Relaxation Measurements: A Biological Implications. <i>Biochemistry</i> , 1998, 37, 12320-12330.	1.2	39
51	Structure Determination of a Key Intermediate of the Enantioselective Pd Complex Catalyzed Allylic Substitution Reaction. <i>Chemistry - A European Journal</i> , 2000, 6, 3281-3286.	1.7	39
52	Linking functions: an additional role for an intrinsically disordered linker domain in the transcriptional coactivator CBP. <i>Scientific Reports</i> , 2017, 7, 4676.	1.6	39
53	Direct Carbon Detection in Paramagnetic Metalloproteins To Further Exploit Pseudocontact Shift Restraints. <i>Journal of the American Chemical Society</i> , 2004, 126, 10496-10497.	6.6	38
54	High-resolution and sensitivity through-bond correlations in ultra-fast magic angle spinning (MAS) solid-state NMR. <i>Chemical Science</i> , 2011, 2, 345-348.	3.7	38

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55	Transverse-Dephasing Optimized Homonuclear J-Decoupling in Solid-State NMR Spectroscopy of Uniformly ¹³ C-Labeled Proteins. <i>Journal of the American Chemical Society</i> , 2009, 131, 10816-10817.	6.6	36
56	Exclusively Heteronuclear NMR Experiments to Obtain Structural and Dynamic Information on Proteins. <i>ChemPhysChem</i> , 2010, 11, 689-695.	1.0	36
57	High-Resolution 2D NMR of Disordered Proteins Enhanced by Hyperpolarized Water. <i>Analytical Chemistry</i> , 2018, 90, 6169-6177.	3.2	36
58	Improving the chemical shift dispersion of multidimensional NMR spectra of intrinsically disordered proteins. <i>Journal of Biomolecular NMR</i> , 2013, 55, 231-237.	1.6	35
59	¹³ C- ¹³ C NOESY: A constructive use of ¹³ C- ¹³ C spin-diffusion. <i>Journal of Biomolecular NMR</i> , 2004, 30, 245-251.	1.6	34
60	Picometer Resolution Structure of the Coordination Sphere in the Metal-Binding Site in a Metalloprotein by NMR. <i>Journal of the American Chemical Society</i> , 2020, 142, 16757-16765.	6.6	33
61	Relaxation-optimised Hartmannâ€“Hahn transfer using a specifically Tailored MOCCA-XY16 mixing sequence for carbonylâ€“carbonyl correlation spectroscopy in ¹³ C direct detection NMR experiments. <i>Journal of Biomolecular NMR</i> , 2009, 43, 187-196.	1.6	32
62	A selective experiment for the sequential protein backbone assignment from 3D heteronuclear spectra. <i>Journal of Magnetic Resonance</i> , 2005, 172, 324-328.	1.2	31
63	Mapping proteinâ€“protein interaction by ¹³ Câ€“detected heteronuclear NMR spectroscopy. <i>Journal of Biomolecular NMR</i> , 2006, 36, 111-122.	1.6	31
64	Structural Analysis of Protein Interfaces from ¹³ C Direct-Detected Paramagnetic Relaxation Enhancements. <i>Journal of the American Chemical Society</i> , 2010, 132, 7285-7287.	6.6	31
65	Dynamics of the Intrinsically Disordered Câ€“terminal Domain of the Nipah Virus Nucleoprotein and Interaction with the X Domain of the Phosphoprotein as Unveiled by NMR Spectroscopy. <i>ChemBioChem</i> , 2015, 16, 268-276.	1.3	31
66	Cyclized NDGA modifies dynamic Î±-synuclein monomers preventing aggregation and toxicity. <i>Scientific Reports</i> , 2019, 9, 2937.	1.6	31
67	The Solution Structure of Oxidized HiPIP I from <i>Ectothiorhodospira halophila</i> ; Can NMR Spectroscopy Be Used to Probe Rearrangements Associated with Electron Transfer Processes?. <i>Chemistry - A European Journal</i> , 1995, 1, 598-607.	1.7	30
68	â€“CONâ€“assignment strategy for highly flexible intrinsically disordered proteins. <i>Journal of Biomolecular NMR</i> , 2014, 60, 209-218.	1.6	30
69	Just a Flexible Linker? The Structural and Dynamic Properties of CBP-ID4 Revealed by NMR Spectroscopy. <i>Biophysical Journal</i> , 2016, 110, 372-381.	0.2	29
70	Large-Scale Recombinant Production of the SARS-CoV-2 Proteome for High-Throughput and Structural Biology Applications. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 653148.	1.6	29
71	Determination of sugar conformation in large RNA oligonucleotides from analysis of dipole-dipole cross correlated relaxation by solution NMR spectroscopy. <i>Journal of Biomolecular NMR</i> , 1999, 15, 241-250.	1.6	28
72	Solution structure of the B form of oxidized rat microsomal cytochromeâ€“b5 and backbone dynamics via ¹⁵ N rotating-frame NMR-relaxation measurements. <i>FEBS Journal</i> , 1999, 260, 347-354.	0.2	28

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73	¹ H and ¹³ C NMR Studies of an Oxidized HiPIP. <i>Inorganic Chemistry</i> , 1997, 36, 4798-4803.	1.9	27
74	Lanthanide induced residual dipolar couplings for the conformational investigation of peripheral ¹⁵ NH ₂ moieties. <i>Journal of Biomolecular NMR</i> , 2000, 18, 347-355.	1.6	27
75	Towards a Protocol for Solution Structure Determination of Copper(II) Proteins: the Case of CullZnII Superoxide Dismutase. <i>ChemBioChem</i> , 2007, 8, 1422-1429.	1.3	26
76	The highly flexible disordered regions of the SARS-CoV-2 nucleocapsid N protein within the 1â€“248 residue construct: sequence-specific resonance assignments through NMR. <i>Biomolecular NMR Assignments</i> , 2021, 15, 219-227.	0.4	26
77	Sequence-specific assignment of the ¹ H and ¹⁵ N nuclear magnetic resonance spectra of the reduced recombinant high-potential iron-sulfur protein I from <i>Ectothiorhodospira halophila</i> . <i>FEBS Journal</i> , 1994, 225, 703-714.	0.2	25
78	Highâ€Resolution Characterization of Intrinsic Disorder in Proteins: Expanding the Suite of ¹³ Câ€Detected NMR Spectroscopy Experiments to Determine Key Observables. <i>ChemBioChem</i> , 2011, 12, 2347-2352.	1.3	25
79	C-Band ESEEM of Strongly Coupled Peptide Nitrogens in Reduced Two-Iron Ferredoxin. <i>Journal of Magnetic Resonance Series B</i> , 1995, 108, 99-102.	1.6	24
80	Proline Fingerprint in Intrinsically Disordered Proteins. <i>ChemBioChem</i> , 2018, 19, 1625-1629.	1.3	24
81	Local mobility of ¹⁵ N labeled biomolecules characterized through cross-correlation rates: Applications to paramagnetic proteins. <i>Journal of Biomolecular NMR</i> , 1998, 12, 509-521.	1.6	23
82	High Magnetic Field Consequences on the NMR Hyperfine Shifts in Solution. <i>Journal of Magnetic Resonance</i> , 1998, 134, 360-364.	1.2	23
83	Protein NMR Resonance Assignment without Spectral Analysis: 5Dâ€Solidâ€State Automated Projection Spectroscopy (SOâ€APSY). <i>Angewandte Chemie - International Edition</i> , 2020, 59, 2380-2384.	7.2	23
84	A complete relaxation matrix refinement of the solution structure of a paramagnetic metalloprotein: Reduced HiPIP I from <i>Ectothiorhodospira halophila</i> . , 1996, 24, 158-164.		22
85	Combination of DQ and ZQ Coherences for Sensitive Throughâ€Bond NMR Correlation Experiments in Biosolids under Ultraâ€Fast MAS. <i>ChemPhysChem</i> , 2012, 13, 2405-2411.	1.0	21
86	NMR Characterization of Longâ€Range Contacts in Intrinsically Disordered Proteins from Paramagnetic Relaxation Enhancement in ¹³ C Directâ€Detection Experiments. <i>ChemBioChem</i> , 2019, 20, 335-339.	1.3	21
87	Taking Simultaneous Snapshots of Intrinsically Disordered Proteins in Action. <i>Biophysical Journal</i> , 2019, 117, 46-55.	0.2	20
88	Monitoring the Interaction of Î±â€Synuclein with Calcium Ions through Exclusively Heteronuclear Nuclear Magnetic Resonance Experiments. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 18537-18545.	7.2	20
89	¹³ C Direct Detected NMR for Challenging Systems. <i>Chemical Reviews</i> , 2022, 122, 9468-9496.	23.0	20
90	Direct Detection of Hydrogen Bonds in Monomeric Superoxide Dismutase:â€ Biological Implications. <i>Biochemistry</i> , 2002, 41, 2913-2920.	1.2	19

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91	¹³ C-Detected Through-Bond Correlation Experiments for Protein Resonance Assignment by Ultra-Fast MAS Solid-State NMR. <i>ChemPhysChem</i> , 2013, 14, 3131-3137.	1.0	19
92	NMR Reveals Specific Tracts within the Intrinsically Disordered Regions of the SARS-CoV-2 Nucleocapsid Protein Involved in RNA Encountering. <i>Biomolecules</i> , 2022, 12, 929.	1.8	19
93	Sensitivity-enhanced three-dimensional and carbon-detected two-dimensional NMR of proteins using hyperpolarized water. <i>Journal of Biomolecular NMR</i> , 2020, 74, 161-171.	1.6	17
94	From NOESY Cross Peaks to Structural Constraints in a Paramagnetic Metalloprotein. <i>Magnetic Resonance in Chemistry</i> , 1996, 34, 948-950.	1.1	16
95	Side chain mobility as monitored by CH-CH cross correlation: the example of cytochrome b5. <i>Journal of Biomolecular NMR</i> , 2001, 20, 1-10.	1.6	16
96	The Heterogeneous Structural Behavior of E7 from HPV16 Revealed by NMR Spectroscopy. <i>ChemBioChem</i> , 2013, 14, 1876-1882.	1.3	16
97	An Intrinsically Disordered Domain Has a Dual Function Coupled to Compartment-Dependent Redox Control. <i>Journal of Molecular Biology</i> , 2013, 425, 594-608.	2.0	16
98	Spin-state-selective methods in solution- and solid-state biomolecular ¹³ C NMR. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2015, 84-85, 1-13.	3.9	16
99	¹³ C APSY-NMR for sequential assignment of intrinsically disordered proteins. <i>Journal of Biomolecular NMR</i> , 2018, 70, 167-175.	1.6	16
100	Structural and Dynamic Characterization of the Molecular Hub Early Region 1A (E1A) from Human Adenovirus. <i>Chemistry - A European Journal</i> , 2016, 22, 13010-13013.	1.7	15
101	Multimodal Response to Copper Binding in Superoxide Dismutase Dynamics. <i>Journal of the American Chemical Society</i> , 2020, 142, 19660-19667.	6.6	15
102	A further investigation of the cytochrome b 5-cytochrome c complex. <i>Journal of Biological Inorganic Chemistry</i> , 2003, 8, 777-786.	1.1	14
103	Monitoring HPV-16 E7 phosphorylation events. <i>Virology</i> , 2017, 503, 70-75.	1.1	14
104	Ensemble description of the intrinsically disordered N-terminal domain of the Nipah virus P/V protein from combined NMR and SAXS. <i>Scientific Reports</i> , 2020, 10, 19574.	1.6	13
105	The influence of a surface charge on the electronic and steric structure of a high potential iron-sulfur protein. <i>Journal of Biological Inorganic Chemistry</i> , 1996, 1, 257-263.	1.1	12
106	Amino acid recognition for automatic resonance assignment of intrinsically disordered proteins. <i>Journal of Biomolecular NMR</i> , 2016, 64, 239-253.	1.6	12
107	An intrinsically disordered proteins community for ELIXIR. <i>F1000Research</i> , 2019, 8, 1753.	0.8	12
108	Recent Advances in Solution NMR Studies. <i>Annual Reports on NMR Spectroscopy</i> , 2013, 80, 359-418.	0.7	11

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109	Adenoviral E1A Exploits Flexibility and Disorder to Target Cellular Proteins. <i>Biomolecules</i> , 2020, 10, 1541.	1.8	10
110	X-band ESEEM spectroscopy of ¹⁵ N substituted native and inhibitor-bound superoxide dismutase. <i>FEBS Letters</i> , 1994, 345, 55-60.	1.3	9
111	Identification of slow motions in the reduced recombinant high-potential iron sulfur protein I (HiPIP) Tj ETQq1 1 0.784314 rgBT /Overf... <i>Biomolecular NMR</i> , 1998, 12, 307-318.	1.6	9
112	Backbone and Side-chains ¹ H, ¹³ C and ¹⁵ N NMR Assignment of Human β 2-parvalbumin. <i>Journal of Biomolecular NMR</i> , 2005, 33, 137-137.	1.6	9
113	Longitudinal relaxation properties of ¹ H _N and ¹ H ₁ determined by direct-detected ¹³ C NMR experiments to study intrinsically disordered proteins (IDPs). <i>Journal of Magnetic Resonance</i> , 2015, 254, 19-26.	1.2	8
114	Fragment-Based NMR Study of the Conformational Dynamics in the bHLH Transcription Factor Ascl1. <i>Biophysical Journal</i> , 2017, 112, 1366-1373.	0.2	8
115	The free energy landscape of the oncogene protein E7 of human papillomavirus type 16 reveals a complex interplay between ordered and disordered regions. <i>Scientific Reports</i> , 2019, 9, 5822.	1.6	8
116	Exclusively heteronuclear NMR experiments for the investigation of intrinsically disordered proteins: focusing on proline residues. <i>Magnetic Resonance</i> , 2021, 2, 511-522.	0.8	7
117	Hidden α -helical propensity segments within disordered regions of the transcriptional activator CHOP. <i>PLoS ONE</i> , 2017, 12, e0189171.	1.1	6
118	Monitoring the Interaction of α -Synuclein with Calcium Ions through Exclusively Heteronuclear Nuclear Magnetic Resonance Experiments. <i>Angewandte Chemie</i> , 2020, 132, 18696-18704.	1.6	6
119	Interaction between the scaffold proteins CBP by IQGAP1 provides an interface between gene expression and cytoskeletal activity. <i>Scientific Reports</i> , 2020, 10, 5753.	1.6	6
120	Backbone-only restraints for fast determination of the protein fold: The role of paramagnetism-based restraints. Cytochrome b562 as an example. <i>Journal of Magnetic Resonance</i> , 2005, 172, 191-200.	1.2	4
121	Flexibility of the PDZ-binding motif in the micelle-bound form of Jagged-1 cytoplasmic tail. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012, 1818, 1706-1716.	1.4	3
122	A complete relaxation matrix refinement of the solution structure of a paramagnetic metalloprotein: Reduced HiPIP I from <i>Ectothiorhodospira halophila</i> . , 1996, 24, 158.		2
123	Frontispiece: Monitoring the Interaction of α -Synuclein with Calcium Ions through Exclusively Heteronuclear Nuclear Magnetic Resonance Experiments. <i>Angewandte Chemie - International Edition</i> , 2020, 59, .	7.2	1
124	The solution structure of oxidized HiPIP I from <i>Ectothiorhodospira halophila</i> . Can NMR probe rearrangements associated to electron transfer processes?. <i>Journal of Inorganic Biochemistry</i> , 1995, 59, 576.	1.5	0
125	Putting the Right Spin on It. <i>ChemPhysChem</i> , 2013, 14, 2998-2999.	1.0	0
126	Protein-NMR-Resonanzzuordnung ohne Spektralanalyse: automatisierte Festkörperlaserprojektionsspektroskopie in 5D (SO-APSY). <i>Angewandte Chemie</i> , 2020, 132, 2400-2405.	1.6	0

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127	Frontispiz: Monitoring the Interaction of α -Synuclein with Calcium Ions through Exclusively Heteronuclear Nuclear Magnetic Resonance Experiments. <i>Angewandte Chemie</i> , 2020, 132, .	1.6	0
128	Glutamine Side-Chain to Main Chain Hydrogen Bonds Can be used to Design Single Alpha-Helices that are Stable at Room Temperature. <i>Biophysical Journal</i> , 2020, 118, 369a-370a.	0.2	0