Isabella C Felli

List of Publications by Year
in descending order

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128 papers	6,033 citations	61857 43 h-index	85405 71 g-index
141 all docs	141 docs citations	141 times ranked	4375 citing authors

#	Article	IF	Citations
1	¹³C Direct Detected NMR for Challenging Systems. Chemical Reviews, 2022, 122, 9468-9496.	23.0	20
2	NMR Reveals Specific Tracts within the Intrinsically Disordered Regions of the SARS-CoV-2 Nucleocapsid Protein Involved in RNA Encountering. Biomolecules, 2022, 12, 929.	1.8	19
3	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. Biomolecular NMR Assignments, 2021, 15, 219-227.	0.4	26
4	Large-Scale Recombinant Production of the SARS-CoV-2 Proteome for High-Throughput and Structural Biology Applications. Frontiers in Molecular Biosciences, 2021, 8, 653148.	1.6	29
5	Exclusively heteronuclear NMR experiments for the investigation of intrinsically disordered proteins: focusing on proline residues. Magnetic Resonance, 2021, 2, 511-522.	0.8	7
6	Proteinâ€NMRâ€Resonanzzuordnung ohne Spektralanalyse: automatisierte FestkÃ¶rperâ€Projektionsspektroskopie in 5D (SOâ€APSY). Angewandte Chemie, 2020, 132, 2400-2405.	1.6	0
7	Protein NMR Resonance Assignment without Spectral Analysis: 5Dâ€‰SOlidâ€State Automated Projection SpectroscopY (SOâ€APSY). Angewandte Chemie - International Edition, 2020, 59, 2380-2384.	7.2	23
8	The Ambivalent Role of Proline Residues in an Intrinsically Disordered Protein: From Disorder Promoters to Compaction Facilitators. Journal of Molecular Biology, 2020, 432, 3093-3111.	2.0	65
9	Adenoviral E1A Exploits Flexibility and Disorder to Target Cellular Proteins. Biomolecules, 2020, 10, 1541.	1.8	10
10	Monitoring the Interaction of Î±â€Synuclein with Calcium Ions through Exclusively Heteronuclear Nuclear Magnetic Resonance Experiments. Angewandte Chemie, 2020, 132, 18696-18704.	1.6	6
11	Monitoring the Interaction of Î±â€Synuclein with Calcium Ions through Exclusively Heteronuclear Nuclear Magnetic Resonance Experiments. Angewandte Chemie - International Edition, 2020, 59, 18537-18545.	7.2	20
12	Picometer Resolution Structure of the Coordination Sphere in the Metal-Binding Site in a Metalloprotein by NMR. Journal of the American Chemical Society, 2020, 142, 16757-16765.	6.6	33
13	Ensemble description of the intrinsically disordered N-terminal domain of the Nipah virus P/V protein from combined NMR and SAXS. Scientific Reports, 2020, 10, 19574.	1.6	13
14	Multimodal Response to Copper Binding in Superoxide Dismutase Dynamics. Journal of the American Chemical Society, 2020, 142, 19660-19667.	6.6	15
15	Frontispiz: Monitoring the Interaction of Î±â€Synuclein with Calcium Ions through Exclusively Heteronuclear Nuclear Magnetic Resonance Experiments. Angewandte Chemie, 2020, 132, .	1.6	0
16	Frontispiece: Monitoring the Interaction of Î±â€Synuclein with Calcium Ions through Exclusively Heteronuclear Nuclear Magnetic Resonance Experiments. Angewandte Chemie - International Edition, 2020, 59, .	7.2	1
17	Small-molecule sequestration of amyloid-Î² as a drug discovery strategy for Alzheimerâ€™s disease. Science Advances, 2020, 6, .	4.7	95
18	Glutamine Side-Chain to Main Chain Hydrogen Bonds Can be used to Design Single Alpha-Helices that are Stable at Room Temperature. Biophysical Journal, 2020, 118, 369a-370a.	0.2	0

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19	Sensitivity-enhanced three-dimensional and carbon-detected two-dimensional NMR of proteins using hyperpolarized water. Journal of Biomolecular NMR, 2020, 74, 161-171.	1.6	17
20	Interaction between the scaffold proteins CBP by IQGAP1 provides an interface between gene expression and cytoskeletal activity. Scientific Reports, 2020, 10, 5753.	1.6	6
21	Hsp70 and Hsp40 inhibit an inter-domain interaction necessary for transcriptional activity in the androgen receptor. Nature Communications, 2019, 10, 3562.	5.8	45
22	Taking Simultaneous Snapshots of Intrinsically Disordered Proteins in Action. Biophysical Journal, 2019, 117, 46-55.	0.2	20
23	Side chain to main chain hydrogen bonds stabilize a polyglutamine helix in a transcription factor. Nature Communications, 2019, 10, 2034.	5.8	78
24	Cyclized NDGA modifies dynamic Î±-synuclein monomers preventing aggregation and toxicity. Scientific Reports, 2019, 9, 2937.	1.6	31
25	The free energy landscape of the oncogene protein E7 of human papillomavirus type 16 reveals a complex interplay between ordered and disordered regions. Scientific Reports, 2019, 9, 5822.	1.6	8
26	NMR Characterization of Longâ€Range Contacts in Intrinsically Disordered Proteins from Paramagnetic Relaxation Enhancement in ¹³C Directâ€Detection Experiments. ChemBioChem, 2019, 20, 335-339.	1.3	21
27	An intrinsically disordered proteins community for ELIXIR. F1000Research, 2019, 8, 1753.	0.8	12
28	13C APSY-NMR for sequential assignment of intrinsically disordered proteins. Journal of Biomolecular NMR, 2018, 70, 167-175.	1.6	16
29	High-Resolution 2D NMR of Disordered Proteins Enhanced by Hyperpolarized Water. Analytical Chemistry, 2018, 90, 6169-6177.	3.2	36
30	Proline Fingerprint in Intrinsically Disordered Proteins. ChemBioChem, 2018, 19, 1625-1629.	1.3	24
31	Monitoring HPV-16 E7 phosphorylation events. Virology, 2017, 503, 70-75.	1.1	14
32	Fragment-Based NMR Study of the Conformational Dynamics in the bHLH Transcription Factor Ascl1. Biophysical Journal, 2017, 112, 1366-1373.	0.2	8
33	Linking functions: an additional role for an intrinsically disordered linker domain in the transcriptional coactivator CBP. Scientific Reports, 2017, 7, 4676.	1.6	39
34	Hidden Î±-helical propensity segments within disordered regions of the transcriptional activator CHOP. PLoS ONE, 2017, 12, e0189171.	1.1	6
35	Amino acid recognition for automatic resonance assignment of intrinsically disordered proteins. Journal of Biomolecular NMR, 2016, 64, 239-253.	1.6	12
36	Structural and Dynamic Characterization of the Molecular Hub Early Region 1A (E1A) from Human Adenovirus. Chemistry - A European Journal, 2016, 22, 13010-13013.	1.7	15

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37	Sequence Context Influences the Structure and Aggregation Behavior of a PolyQ Tract. Biophysical Journal, 2016, 110, 2361-2366.	0.2	58
38	Just a Flexible Linker? The Structural and Dynamic Properties of CBP-ID4 Revealed by NMR Spectroscopy. Biophysical Journal, 2016, 110, 372-381.	0.2	29
39	Longitudinal relaxation properties of 1HN and 1HÎ± determined by direct-detected 13C NMR experiments to study intrinsically disordered proteins (IDPs). Journal of Magnetic Resonance, 2015, 254, 19-26.	1.2	8
40	Protein residue linking in a single spectrum for magic-angle spinning NMR assignment. Journal of Biomolecular NMR, 2015, 62, 253-261.	1.6	44
41	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.	0.8	69
42	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. ChemBioChem, 2015, 16, 268-276.	1.3	31
43	Spin-state-selective methods in solution- and solid-state biomolecular 13C NMR. Progress in Nuclear Magnetic Resonance Spectroscopy, 2015, 84-85, 1-13.	3.9	16
44	pE-DB: a database of structural ensembles of intrinsically disordered and of unfolded proteins. Nucleic Acids Research, 2014, 42, D326-D335.	6.5	195
45	â€œCON-CONâ€•assignment strategy for highly flexible intrinsically disordered proteins. Journal of Biomolecular NMR, 2014, 60, 209-218.	1.6	30
46	The crowd you're in with: Effects of different types of crowding agents on protein aggregation. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 346-357.	1.1	74
47	In-cell 13C NMR spectroscopy for the study of intrinsically disordered proteins. Nature Protocols, 2014, 9, 2005-2016.	5.5	48
48	Novel methods based on 13C detection to study intrinsically disordered proteins. Journal of Magnetic Resonance, 2014, 241, 115-125.	1.2	65
49	The Heterogeneous Structural Behavior of E7 from HPV16 Revealed by NMR Spectroscopy. ChemBioChem, 2013, 14, 1876-1882.	1.3	16
50	An Intrinsically Disordered Domain Has a Dual Function Coupled to Compartment-Dependent Redox Control. Journal of Molecular Biology, 2013, 425, 594-608.	2.0	16
51	Recent Advances in Solution NMR Studies. Annual Reports on NMR Spectroscopy, 2013, 80, 359-418.	0.7	11
52	High-dimensionality 13C direct-detected NMR experiments for the automatic assignment of intrinsically disordered proteins. Journal of Biomolecular NMR, 2013, 57, 353-361.	1.6	42
53	NMR Spectroscopic Studies of Intrinsically Disordered Proteins at Nearâ€Physiological Conditions. Angewandte Chemie - International Edition, 2013, 52, 11808-11812.	7.2	71
54	Magic Angle Spinning NMR of Paramagnetic Proteins. Accounts of Chemical Research, 2013, 46, 2108-2116.	7.6	78

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55	¹³Câ€Detected Throughâ€Bond Correlation Experiments for Protein Resonance Assignment by Ultraâ€Fast MAS Solidâ€State NMR. ChemPhysChem, 2013, 14, 3131-3137.	1.0	19
56	Improving the chemical shift dispersion of multidimensional NMR spectra of intrinsically disordered proteins. Journal of Biomolecular NMR, 2013, 55, 231-237.	1.6	35
57	Putting the Right Spin on It. ChemPhysChem, 2013, 14, 2998-2999.	1.0	0
58	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
59	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
60	Structural and Mechanistic Implications of Metal Binding in the Small Heat-shock Protein Î±B-crystallin. Journal of Biological Chemistry, 2012, 287, 1128-1138.	1.6	67
61	Exclusively Heteronuclear ¹³Câ€Detected Aminoâ€Acidâ€Selective NMR Experiments for the Study of Intrinsically Disordered Proteins (IDPs). ChemBioChem, 2012, 13, 2425-2432.	1.3	43
62	Speeding up sequence specific assignment of IDPs. Journal of Biomolecular NMR, 2012, 53, 293-301.	1.6	66
63	Rapid Measurement of Pseudocontact Shifts in Metalloproteins by Proton-Detected Solid-State NMR Spectroscopy. Journal of the American Chemical Society, 2012, 134, 14730-14733.	6.6	53
64	Flexibility of the PDZ-binding motif in the micelle-bound form of Jagged-1 cytoplasmic tail. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 1706-1716.	1.4	3
65	Recent progress in NMR spectroscopy: Toward the study of intrinsically disordered proteins of increasing size and complexity. IUBMB Life, 2012, 64, 473-481.	1.5	53
66	Combination of DQ and ZQ Coherences for Sensitive Throughâ€Bond NMR Correlation Experiments in Biosolids under Ultraâ€Fast MAS. ChemPhysChem, 2012, 13, 2405-2411.	1.0	21
67	High-resolution and sensitivity through-bond correlations in ultra-fast magic angle spinning (MAS) solid-state NMR. Chemical Science, 2011, 2, 345-348.	3.7	38
68	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
69	¹³C Directâ€Detection Biomolecular NMR Spectroscopy in Living Cells. Angewandte Chemie - International Edition, 2011, 50, 2339-2341.	7.2	55
70	Fast Resonance Assignment and Fold Determination of Human Superoxide Dismutase by Highâ€Resolution Protonâ€Detected Solidâ€State MAS NMR Spectroscopy. Angewandte Chemie - International Edition, 2011, 50, 11697-11701.	7.2	157
71	Highâ€Resolution Characterization of Intrinsic Disorder in Proteins: Expanding the Suite of ¹³Câ€Detected NMR Spectroscopy Experiments to Determine Key Observables. ChemBioChem, 2011, 12, 2347-2352.	1.3	25
72	Exclusively Heteronuclear NMR Experiments to Obtain Structural and Dynamic Information on Proteins. ChemPhysChem, 2010, 11, 689-695.	1.0	36

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73	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
74	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
75	Structural Analysis of Protein Interfaces from 13C Direct-Detected Paramagnetic Relaxation Enhancements. Journal of the American Chemical Society, 2010, 132, 7285-7287.	6.6	31
76	Recent Advances in Solution NMR: Fast Methods and Heteronuclear Direct Detection. ChemPhysChem, 2009, 10, 1356-1368.	1.0	90
77	H-start for exclusively heteronuclear NMR spectroscopy: The case of intrinsically disordered proteins. Journal of Magnetic Resonance, 2009, 198, 275-281.	1.2	90
78	Relaxation-optimised Hartmannâ€“Hahn transfer using a specifically Tailored MOCCA-XY16 mixing sequence for carbonylâ€“carbonyl correlation spectroscopy in 13C direct detection NMR experiments. Journal of Biomolecular NMR, 2009, 43, 187-196.	1.6	32
79	Speeding Up ¹³C Direct Detection Biomolecular NMR Spectroscopy. Journal of the American Chemical Society, 2009, 131, 15339-15345.	6.6	88
80	Transverse-Dephasing Optimized Homonuclear J-Decoupling in Solid-State NMR Spectroscopy of Uniformly 13C-Labeled Proteins. Journal of the American Chemical Society, 2009, 131, 10816-10817.	6.6	36
81	Copper(I)-mediated proteinâ€“protein interactions result from suboptimal interaction surfaces. Biochemical Journal, 2009, 422, 37-42.	1.7	85
82	¹³C Directâ€detection biomolecular NMR. Concepts in Magnetic Resonance Part A: Bridging Education and Research, 2008, 32A, 183-200.	0.2	62
83	Structural and Dynamic Characterization of Intrinsically Disordered Human Securin by NMR Spectroscopy. Journal of the American Chemical Society, 2008, 130, 16873-16879.	6.6	67
84	Towards a Protocol for Solution Structure Determination of Copper(II) Proteins: the Case of CuIIZnII Superoxide Dismutase. ChemBioChem, 2007, 8, 1422-1429.	1.3	26
85	A method for CÎ± direct-detection in protonless NMR. Journal of Magnetic Resonance, 2007, 188, 301-310.	1.2	52
86	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
87	The Atx1-Ccc2 complex is a metal-mediated protein-protein interaction. Nature Chemical Biology, 2006, 2, 367-368.	3.9	204
88	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
89	Mapping proteinâ€“protein interaction by 13Câ€²-detected heteronuclear NMR spectroscopy. Journal of Biomolecular NMR, 2006, 36, 111-122.	1.6	31
90	13C-detected protonless NMR spectroscopy of proteins in solution. Progress in Nuclear Magnetic Resonance Spectroscopy, 2006, 48, 25-45.	3.9	210

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91	Complete Assignment of Heteronuclear Protein Resonances by Protonless NMR Spectroscopy. Angewandte Chemie - International Edition, 2005, 44, 3089-3092.	7.2	162
92	Backbone-only restraints for fast determination of the protein fold: The role of paramagnetism-based restraints. Cytochrome b562 as an example. Journal of Magnetic Resonance, 2005, 172, 191-200.	1.2	4
93	A selective experiment for the sequential protein backbone assignment from 3D heteronuclear spectra. Journal of Magnetic Resonance, 2005, 172, 324-328.	1.2	31
94	Backbone and Side-chains 1H, 13C and 15N NMR Assignment of Human Î²-parvalbumin. Journal of Biomolecular NMR, 2005, 33, 137-137.	1.6	9
95	13C-13C NOESY: A constructive use of 13C-13C spin-diffusion. Journal of Biomolecular NMR, 2004, 30, 245-251.	1.6	34
96	A Heteronuclear Direct-Detection NMR Spectroscopy Experiment for Protein-Backbone Assignment. Angewandte Chemie - International Edition, 2004, 43, 2257-2259.	7.2	52
97	13Câ''13C NOESY:Â An Attractive Alternative for Studying Large Macromolecules. Journal of the American Chemical Society, 2004, 126, 464-465.	6.6	74
98	Direct Carbon Detection in Paramagnetic Metalloproteins To Further Exploit Pseudocontact Shift Restraints. Journal of the American Chemical Society, 2004, 126, 10496-10497.	6.6	38
99	A further investigation of the cytochrome b 5â€"cytochrome c complex. Journal of Biological Inorganic Chemistry, 2003, 8, 777-786.	1.1	14
100	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
101	A Strategy for the NMR Characterization of Type II Copper(II) Proteins:Â the Case of the Copper Trafficking Protein CopC fromPseudomonasSyringae. Journal of the American Chemical Society, 2003, 125, 7200-7208.	6.6	98
102	Direct Detection of Hydrogen Bonds in Monomeric Superoxide Dismutase:â€‰ Biological Implications. Biochemistry, 2002, 41, 2913-2920.	1.2	19
103	Side chain mobility as monitored by CH-CH cross correlation: the example of cytochrome b5. Journal of Biomolecular NMR, 2001, 20, 1-10.	1.6	16
104	Structure Determination of a Key Intermediate of the Enantioselective Pd Complex Catalyzed Allylic Substitution Reaction. Chemistry - A European Journal, 2000, 6, 3281-3286.	1.7	39
105	Lanthanide induced residual dipolar couplings for the conformational investigation of peripheral 15NH2 moieties. Journal of Biomolecular NMR, 2000, 18, 347-355.	1.6	27
106	Determination of sugar conformation in large RNA oligonucleotides from analysis of dipole-dipole cross correlated relaxation by solution NMR spectroscopy. Journal of Biomolecular NMR, 1999, 15, 241-250.	1.6	28
107	Solution structure of the B form of oxidized rat microsomal cytochromeâ€ƒb5and backbone dynamics via15N rotating-frame NMR-relaxation measurements. FEBS Journal, 1999, 260, 347-354.	0.2	28
108	TransferredÂCross-CorrelatedÂRelaxation:ÂApplication to the Determination of Sugar Pucker in an Aminoacylated tRNA-Mimetic Weakly Bound to EF-Tu. Journal of the American Chemical Society, 1999, 121, 1945-1948.	6.6	73

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109	Determination of RNA Sugar Pucker Mode from Cross-Correlated Relaxation in Solution NMR Spectroscopy. Journal of the American Chemical Society, 1999, 121, 1956-1957.	6.6	80
110	Identification of slow motions in the reduced recombinant high-potential iron sulfur protein I (HiPIP) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Biomolecular NMR, 1998, 12, 307-318.	1.6	9
111	Local mobility of 15N labeled biomolecules characterized through cross-correlation rates: Applications to paramagnetic proteins. Journal of Biomolecular NMR, 1998, 12, 509-521.	1.6	23
112	High Magnetic Field Consequences on the NMR Hyperfine Shifts in Solution. Journal of Magnetic Resonance, 1998, 134, 360-364.	1.2	23
113	The Solution Structure of Oxidized Rat Microsomal Cytochromeb5â€‚â€¡. Biochemistry, 1998, 37, 173-184.	1.2	86
114	Probing the Backbone Dynamics of Oxidized and Reduced Rat Microsomal Cytochromeb5via15N Rotating Frame NMR Relaxation Measurements:Â Biological Implicationsâ€. Biochemistry, 1998, 37, 12320-12330.	1.2	39
115	1H and 13C NMR Studies of an Oxidized HiPIP. Inorganic Chemistry, 1997, 36, 4798-4803.	1.9	27
116	The influence of a surface charge on the electronic and steric structure of a high potential iron-sulfur protein. Journal of Biological Inorganic Chemistry, 1996, 1, 257-263.	1.1	12
117	The Solution Structure Refinement of the Paramagnetic Reduced High-Potential Iron-Sulfur Protein I from Ectothiorhodospira Halophila by Using Stable Isotope Labeling and Nuclear Relaxation. FEBS Journal, 1996, 241, 440-452.	0.2	69
118	A complete relaxation matrix refinement of the solution structure of a paramagnetic metalloprotein: Reduced HiPIP I fromEctothiorhodospira halophila. , 1996, 24, 158-164.		22
119	From NOESY Cross Peaks to Structural Constraints in a Paramagnetic Metalloprotein. Magnetic Resonance in Chemistry, 1996, 34, 948-950.	1.1	16
120	A complete relaxation matrix refinement of the solution structure of a paramagnetic metalloprotein: Reduced HiPIP I from Ectothiorhodospira halophila. , 1996, 24, 158.		2
121	The Solution Structure of Oxidized HiPIP I from Ectothiorhodospira halophila; Can NMR Spectroscopy Be Used to Probe Rearrangements Associated with Electron Transfer Processes?. Chemistry - A European Journal, 1995, 1, 598-607.	1.7	30
122	C-Band ESEEM of Strongly Coupled Peptide Nitrogens in Reduced Two-Iron Ferredoxin. Journal of Magnetic Resonance Series B, 1995, 108, 99-102.	1.6	24
123	The role of a conserved tyrosine residue in highâ€potential iron sulfur proteins. Protein Science, 1995, 4, 2562-2572.	3.1	39
124	The solution structure of oxidized HiPIP I from Echtothiorhodospira halophila. Can NMR probe rearrangements associated to electron transfer processes?. Journal of Inorganic Biochemistry, 1995, 59, 576.	1.5	0
125	Sequence-Specific Assignment of Ligand Cysteine Protons of Oxidized, Recombinant HiPIP I from Ectothiorhodospira halophila. Inorganic Chemistry, 1995, 34, 2516-2523.	1.9	40
126	Sequence-specific assignment of the 1H and 15N nuclear magnetic resonance spectra of the reduced recombinant high-potential iron-sulfur protein I from Ectothiorhodospira halophila. FEBS Journal, 1994, 225, 703-714.	0.2	25

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127	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
128	X-band ESEEM spectroscopy of15N substituted native and inhibitor-bound superoxide dismutase. FEBS Letters, 1994, 345, 55-60.	1.3	9