Timothy A Cross

List of Publications by Year
in descending order

146	9,065	31976	48315
papers	citations	53 h-index	88 g-index

146	146	146	4802
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Emulating Membrane Protein Environmentsâ”€How Much Lipid Is Required for a Native Structure: Influenza S31N M2. Journal of the American Chemical Society, 2022, 144, 2137-2148.	13.7	5
2	Surprising Rigidity of Functionally Important Water Molecules Buried in the Lipid Headgroup Region. Journal of the American Chemical Society, 2022, 144, 7881-7888.	13.7	12
3	Fuzzy Association of an Intrinsically Disordered Protein with Acidic Membranes. Jacs Au, 2021, 1, 66-78.	7.9	21
4	Functional stability of water wireâ€“carbonyl interactions in an ion channel. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 11908-11915.	7.1	32
5	Observation of the Imidazole-Imidazolium Hydrogen Bonds Responsible for Selective Proton Conductance in the Influenza A M2 Channel. Journal of the American Chemical Society, 2020, 142, 2115-2119.	13.7	29
6	Influenza A M2 Channel Clustering at High Protein/Lipid Ratios: Viral Budding Implications. Biophysical Journal, 2019, 116, 1075-1084.	0.5	33
7	Perturbations of Native Membrane Protein Structure in Alkyl Phosphocholine Detergents: A Critical Assessment of NMR and Biophysical Studies. Chemical Reviews, 2018, 118, 3559-3607.	47.7	132
8	False positives in using the zymogram assay for identification of peptidoglycan hydrolases. Analytical Biochemistry, 2018, 543, 162-166.	2.4	9
9	YidC: Evaluating the Importance of the Native Environment. Structure, 2018, 26, 2-4.	3.3	1
10	Binding and Proton Blockage by Amantadine Variants of the Influenza M2_{WT} and M2_{S31N} Explained. Journal of Medicinal Chemistry, 2017, 60, 1716-1733.	6.4	17
11	Beyond Structural Biology to Functional Biology: Solid-State NMR Experiments and Strategies for Understanding the M2 Proton Channel Conductance. Journal of Physical Chemistry B, 2017, 121, 4799-4809.	2.6	7
12	NMR spectroscopy up to 35.2 T using a series-connected hybrid magnet. Journal of Magnetic Resonance, 2017, 284, 125-136.	2.1	122
13	¹⁷O MAS NMR Correlation Spectroscopy at High Magnetic Fields. Journal of the American Chemical Society, 2017, 139, 17953-17963.	13.7	44
14	Structural Influences: Cholesterol, Drug, and Proton Binding to Full-Length Influenza A M2 Protein. Biophysical Journal, 2016, 110, 1391-1399.	0.5	37
15	Probing Hydronium Ion Histidine NH Exchange Rate Constants in the M2 Channel via Indirect Observation of Dipolar-Dephased ¹⁵N Signals in Magic-Angle-Spinning NMR. Journal of the American Chemical Society, 2016, 138, 15801-15804.	13.7	14
16	Differential Binding of Rimantadine Enantiomers to Influenza A M2 Proton Channel. Journal of the American Chemical Society, 2016, 138, 1506-1509.	13.7	28
17	Structure of CrgA, a cell division structural and regulatory protein from Mycobacterium tuberculosis , in lipid bilayers. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E119-26.	7.1	45
18	Dynamic Short Hydrogen Bonds in Histidine Tetrad of Full-Length M2 Proton Channel Reveal Tetrameric Structural Heterogeneity and Functional Mechanism. Structure, 2015, 23, 2300-2308.	3.3	53

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19	Solid state NMR: The essential technology for helical membrane protein structural characterization. Journal of Magnetic Resonance, 2014, 239, 100-109.	2.1	31
20	Binding of MgtR, a Salmonella Transmembrane Regulatory Peptide, to MgtC, a Mycobacterium tuberculosis Virulence Factor: A Structural Study. Journal of Molecular Biology, 2014, 426, 436-446.	4.2	21
21	Assignment of oriented sample NMR resonances from a three transmembrane helix protein. Journal of Magnetic Resonance, 2014, 240, 34-44.	2.1	10
22	Membrane Protein Structural Validation by Oriented Sample Solid-State NMR: Diacylglycerol Kinase. Biophysical Journal, 2014, 106, 1559-1569.	0.5	22
23	Aminoadamantanes with Persistent in Vitro Efficacy against H1N1 (2009) Influenza A. Journal of Medicinal Chemistry, 2014, 57, 4629-4639.	6.4	62
24	Identifying inter-residue resonances in crowded 2D 13Câ€“13C chemical shift correlation spectra of membrane proteins by solid-state MAS NMR difference spectroscopy. Journal of Biomolecular NMR, 2013, 56, 265-273.	2.8	18
25	Lipid bilayer preparations of membrane proteins for oriented and magic-angle spinning solid-state NMR samples. Nature Protocols, 2013, 8, 2256-2270.	12.0	61
26	Helical membrane protein conformations and their environment. European Biophysics Journal, 2013, 42, 731-755.	2.2	55
27	Solid state NMR and proteinâ€“protein interactions in membranes. Current Opinion in Structural Biology, 2013, 23, 919-928.	5.7	32
28	Solid State NMR Strategy for Characterizing Native Membrane Protein Structures. Accounts of Chemical Research, 2013, 46, 2172-2181.	15.6	81
29	Influences of Membrane Mimetic Environments on Membrane Protein Structures. Annual Review of Biophysics, 2013, 42, 361-392.	10.0	237
30	Modeling the membrane environment has implications for membrane protein structure and function: Influenza A M2 protein. Protein Science, 2013, 22, 381-394.	7.6	46
31	Ab initio calculations and validation of the pH-dependent structures of the His37-Trp41 quartet, the heart of acid activation and proton conductance in the M2 protein of Influenza A virus. Chemical Science, 2013, 4, 2776.	7.4	21
32	Mycobacterium tuberculosis CwsA Interacts with CrgA and Wag31, and the CrgA-CwsA Complex Is Involved in Peptidoglycan Synthesis and Cell Shape Determination. Journal of Bacteriology, 2012, 194, 6398-6409.	2.2	65
33	M2 protein from Influenza A: from multiple structures to biophysical and functional insights. Current Opinion in Virology, 2012, 2, 128-133.	5.4	58
34	Recent progress in structure-based anti-influenza drug design. Drug Discovery Today, 2012, 17, 1111-1120.	6.4	64
35	Magic Angle Spinning and Oriented Sample Solid-State NMR Structural Restraints Combine for Influenza A M2 Protein Functional Insights. Journal of the American Chemical Society, 2012, 134, 9022-9025.	13.7	48
36	In support of the BMRB. Nature Structural and Molecular Biology, 2012, 19, 854-860.	8.2	6

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37	M2 Proton Channel Structural Validation from Fullâ€Length Protein Samples in Synthetic Bilayers and E.â€...coli Membranes. Angewandte Chemie - International Edition, 2012, 51, 8383-8386.	13.8	84
38	Modeling the Membrane Environment for Membrane Proteins. Biophysical Journal, 2011, 100, 2073-2074.	0.5	16
39	Drug sensitivity, drug-resistant mutations, and structures of three conductance domains of viral porins. Biochimica Et Biophysica Acta - Biomembranes, 2011, 1808, 538-546.	2.6	16
40	A systematic assessment of mature MBP in membrane protein production: Overexpression, membrane targeting and purification. Protein Expression and Purification, 2011, 80, 34-40.	1.3	28
41	Influence of solubilizing environments on membrane protein structures. Trends in Biochemical Sciences, 2011, 36, 117-125.	7.5	186
42	Geometry of kinked protein helices from NMR data. Journal of Magnetic Resonance, 2011, 210, 82-89.	2.1	6
43	Characterization of CrgA, a New Partner of the Mycobacterium tuberculosis Peptidoglycan Polymerization Complexes. Journal of Bacteriology, 2011, 193, 3246-3256.	2.2	61
44	Insight into the Mechanism of the Influenza A Proton Channel from a Structure in a Lipid Bilayer. Science, 2010, 330, 509-512.	12.6	422
45	Gramicidin Channels Are Internally Gated. Biophysical Journal, 2010, 98, 1486-1493.	0.5	13
46	Backbone structure of a small helical integral membrane protein: A unique structural characterization. Protein Science, 2009, 18, 134-146.	7.6	34
47	Ligand Binding in the Conserved Interhelical Loop of CorA, a Magnesium Transporter from Mycobacterium tuberculosis. Journal of Biological Chemistry, 2009, 284, 15619-15628.	3.4	18
48	Solid phase peptide synthesis of 15N-gramicidins A, B, and C and high performance liquid chromatographic purification. International Journal of Peptide and Protein Research, 2009, 33, 298-303.	0.1	89
49	Flu BM2 structure and function. Nature Structural and Molecular Biology, 2009, 16, 1207-1209.	8.2	7
50	Initial structural and dynamic characterization of the M2 protein transmembrane and amphipathic helices in lipid bilayers. Protein Science, 2009, 12, 2597-2605.	7.6	119
51	Conformational heterogeneity of the M2 proton channel and a structural model for channel activation. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 13311-13316.	7.1	102
52	1H, 15N and 13C backbone resonance assignment of Rv1567c, an integral membrane protein from Mycobacterium tuberculosis. Biomolecular NMR Assignments, 2008, 2, 47-49.	0.8	1
53	Structure of the transmembrane region of the M2 protein H+ channel. Protein Science, 2008, 10, 2241-2250.	7.6	221
54	Transmembrane Helix Uniformity Examined by Spectral Mapping of Torsion Angles. Structure, 2008, 16, 787-797.	3.3	77

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55	Proton Transport through Influenza A Virus M2 Protein Reconstituted in Vesicles. Biophysical Journal, 2008, 94, 434-445.	0.5	55
56	Solid-State NMR and MD Simulations of the Antiviral Drug Amantadine Solubilized in DMPC Bilayers. Biophysical Journal, 2008, 94, 1295-1302.	0.5	45
57	A Secondary Gate As a Mechanism for Inhibition of the M2 Proton Channel by Amantadine. Journal of Physical Chemistry B, 2008, 112, 7977-7979.	2.6	106
58	Solid-State ¹⁹F NMR Spectroscopy Reveals That Trp₄₁ Participates in the Gating Mechanism of the M2 Proton Channel of Influenza A Virus. Journal of the American Chemical Society, 2008, 130, 918-924.	13.7	47
59	Expression of membrane proteins from Mycobacterium tuberculosis in Escherichia coli as fusions with maltose binding protein. Protein Expression and Purification, 2007, 53, 24-30.	1.3	46
60	Uniformly Aligned Full-Length Membrane Proteins in Liquid Crystalline Bilayers for Structural Characterization. Journal of the American Chemical Society, 2007, 129, 5304-5305.	13.7	32
61	Backbone Structure of the Amantadine-Blocked Trans-Membrane Domain M2 Proton Channel from Influenza A Virus. Biophysical Journal, 2007, 92, 4335-4343.	0.5	175
62	The Chemical and Dynamical Influence of the Anti-Viral Drug Amantadine on the M2 Proton Channel Transmembrane Domain. Biophysical Journal, 2007, 93, 276-283.	0.5	72
63	Lipid bilayers: an essential environment for the understanding of membrane proteins. Magnetic Resonance in Chemistry, 2007, 45, S2-S11.	1.9	49
64	Structural biology of transmembrane domains: Efficient production and characterization of transmembrane peptides by NMR. Protein Science, 2007, 16, 2153-2165.	7.6	38
65	Flow-Through Lipid Nanotube Arrays for Structure-Function Studies of Membrane Proteins by Solid-State NMR Spectroscopy. Biophysical Journal, 2006, 91, 3076-3084.	0.5	36
66	Ion-Binding Study by17O Solid-State NMR Spectroscopy in the Model Peptide Gly-Gly-Gly at 19.6 T. Journal of the American Chemical Society, 2006, 128, 9849-9855.	13.7	53
67	Comprehensive evaluation of solution nuclear magnetic resonance spectroscopy sample preparation for helical integral membrane proteins. Journal of Structural and Functional Genomics, 2006, 7, 51-64.	1.2	77
68	Histidines, heart of the hydrogen ion channel from influenza A virus: Toward an understanding of conductance and proton selectivity. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6865-6870.	7.1	236
69	Ultra-wide bore 900MHz high-resolution NMR at the National High Magnetic Field Laboratory. Journal of Magnetic Resonance, 2005, 177, 1-8.	2.1	121
70	Ion Solvation by Channel Carbonyls Characterized by 17O Solid-State NMR at 21 T. Journal of the American Chemical Society, 2005, 127, 11922-11923.	13.7	56
71	Identification ofMycobacteriumtuberculosisH37Rv Integral Membrane Proteins by One-Dimensional Gel Electrophoresis and Liquid Chromatography Electrospray Ionization Tandem Mass Spectrometry. Journal of Proteome Research, 2005, 4, 855-861.	3.7	104
72	Cloning and expression of multiple integral membrane proteins from Mycobacterium tuberculosis in Escherichia coli. Protein Science, 2005, 14, 148-158.	7.6	86

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73	Mathematical aspects of protein structure determination with NMR orientational restraints. Bulletin of Mathematical Biology, 2004, 66, 1705-1730.	1.9	19
74	Proton Conductance of Influenza Virus M2 Protein in Planar Lipid Bilayers. Biophysical Journal, 2004, 87, 1697-1704.	0.5	53
75	Structural Restraints and Heterogeneous Orientation of the Gramicidin A Channel Closed State in Lipid Bilayers. Biophysical Journal, 2004, 86, 2837-2845.	0.5	11
76	Seeking Higher Resolution and Sensitivity for NMR of Quadrupolar Nuclei at Ultrahigh Magnetic Fields. Journal of the American Chemical Society, 2002, 124, 5634-5635.	13.7	108
77	Noncontact Dipole Effects on Channel Permeation. VI. 5F- and 6F-Trp Gramicidin Channel Currents. Biophysical Journal, 2002, 83, 1974-1986.	0.5	25
78	Uniformity, Ideality, and Hydrogen Bonds in Transmembrane Î±-Helices. Biophysical Journal, 2002, 83, 2084-2095.	0.5	75
79	The Role of Trp Side Chains in Tuning Single Proton Conduction through Gramicidin Channels. Biophysical Journal, 2002, 83, 880-898.	0.5	27
80	Solid-State 19F-NMR Analysis of 19F-Labeled Tryptophan in Gramicidin A in Oriented Membranes. Biophysical Journal, 2002, 83, 3336-3350.	0.5	56
81	Noncontact Dipole Effects on Channel Permeation. IV. Kinetic Model of 5F-Trp13 Gramicidin A Currents. Biophysical Journal, 2001, 81, 1245-1254.	0.5	26
82	Noncontact Dipole Effects on Channel Permeation. V. Computed Potentials for Fluorinated Gramicidin. Biophysical Journal, 2001, 81, 1255-1264.	0.5	20
83	Complete Cross-Validation andR-Factor Calculation of a Solid-State NMR Derived Structure. Journal of the American Chemical Society, 2001, 123, 7292-7298.	13.7	25
84	Protein structure in anisotropic environments: Development of orientational constraints. Concepts in Magnetic Resonance, 2000, 12, 55-70.	1.3	42
85	Protein structure in anisotropic environments: Unique structural fold from orientational constraints. Concepts in Magnetic Resonance, 2000, 12, 71-82.	1.3	24
86	Inter- and intramolecular distance measurements by solid-state MAS NMR: determination of gramicidin A channel dimer structure in hydrated phospholipid bilayers. Journal of Biomolecular NMR, 2000, 16, 261-268.	2.8	34
87	Identification and minimization of sources of temporal instabilities in high field (>23 T) resistive magnets. Review of Scientific Instruments, 2000, 71, 2882-2889.	1.3	21
88	Helix tilt of the M2 transmembrane peptide from influenza A virus: an intrinsic property. Journal of Molecular Biology, 2000, 295, 117-125.	4.2	143
89	Transmembrane Domain of M2 Protein from Influenza A Virus Studied by Solid-State 15N Polarization Inversion Spin Exchange at Magic Angle NMR. Biophysical Journal, 2000, 79, 767-775.	0.5	93
90	Water: Foldase activity in catalyzing polypeptide conformational rearrangements. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 9057-9061.	7.1	50

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91	SOLID-STATE NUCLEAR MAGNETIC RESONANCE INVESTIGATION OF PROTEIN AND POLYPEPTIDE STRUCTURE. Annual Review of Biophysics and Biomolecular Structure, 1999, 28, 235-268.	18.3	105
92	Validation of the single-stranded channel conformation of gramicidin A by solid-state NMR. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 7910-7915.	7.1	73
93	Gramicidin channel controversy--revisited. Nature Structural Biology, 1999, 6, 610-611.	9.7	58
94	Noncontact Dipole Effects on Channel Permeation. III. Anomalous Proton Conductance Effects in Gramicidin. Biophysical Journal, 1999, 77, 2492-2501.	0.5	42
95	Solid-State NMR and Hydrogen-Deuterium Exchange in a Bilayer-Solubilized Peptide: Structural and Mechanistic Implications. Biophysical Journal, 1999, 76, 1179-1189.	0.5	46
96	Cation transport: an example of structural based selectivity 1 1Edited by I. B. Holland. Journal of Molecular Biology, 1999, 285, 1993-2003.	4.2	65
97	Noncontact Dipole Effects on Channel Permeation. I. Experiments with (5F-Indole)Trp13 Gramicidin A Channels. Biophysical Journal, 1998, 75, 2830-2844.	0.5	115
98	15N NMR. Studies in Physical and Theoretical Chemistry, 1998, 84, 218-235.	0.0	0
99	[31] Solid-state nuclear magnetic resonance characterization of gramicidin channel structure. Methods in Enzymology, 1997, 289, 672-IN4.	1.0	83
100	Protein stability and conformational rearrangements in lipid bilayers: linear gramicidin, a model system. Biophysical Journal, 1997, 73, 614-623.	0.5	35
101	Transmembrane four-helix bundle of influenza A M2 protein channel: structural implications from helix tilt and orientation. Biophysical Journal, 1997, 73, 2511-2517.	0.5	184
102	Protein structural analysis from solid-state NMR-derived orientational constraints. Biophysical Journal, 1997, 72, 2342-2348.	0.5	24
103	High-resolution polypeptide structure in a lamellar phase lipid environment from solid state NMR derived orientational constraints. Structure, 1997, 5, 1655-1669.	3.3	269
104	High resolution and high fields in biological solid state NMR. Solid State Nuclear Magnetic Resonance, 1997, 9, 77-80.	2.3	14
105	A Catalytic Role for Protic Solvents in Conformational Interconversion. Journal of the American Chemical Society, 1996, 118, 9176-9177.	13.7	18
106	Conformational trapping in a membrane environment: a regulatory mechanism for protein activity?. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 5872-5876.	7.1	49
107	Hydrogen exchange in the lipid bilayer-bound gramicidin channel. Solid State Nuclear Magnetic Resonance, 1996, 7, 177-183.	2.3	9
108	Macromolecular structural elucidation with solid-state NMR-derived orientational constraints. Journal of Biomolecular NMR, 1996, 8, 1-14.	2.8	137

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109	Low-Temperature Solid-State 15N NMR Characterization of Polypeptide Backbone Librations. Journal of Magnetic Resonance Series B, 1995, 107, 43-50.	1.6	38
110	Structural analysis of highly oriented poly(p-phenylene-terephthalamide) by 15N solid-state nuclear magnetic resonance. Solid State Nuclear Magnetic Resonance, 1994, 3, 209-218.	2.3	18
111	Structure and dynamics from solid-state NMR spectroscopy. Structure, 1994, 2, 699-701.	3.3	18
112	Side-chain structure and dynamics at the lipid-protein interface: Val1 of the gramicidin A channel. Biophysical Journal, 1994, 66, 1380-1387.	0.5	39
113	Polypeptide Conformational Space. Journal of Molecular Biology, 1994, 241, 431-439.	4.2	12
114	Analysis of Polypeptide Backbone T1 Relaxation Data Using an Experimentally Derived Model. Journal of Magnetic Resonance Series B, 1993, 101, 35-43.	1.6	16
115	High-resolution structure and dynamic implications for a double-helical gramicidin A conformer. Journal of Biomolecular NMR, 1993, 3, 495-513.	2.8	37
116	Orientational constraints as threeâ€dimensional structural constraints from chemical shift anisotropy: The polypeptide backbone of gramicidin A in a lipid bilayer. Protein Science, 1993, 2, 532-542.	7.6	78
117	Rapidly Frozen Polypeptide Samples for Characterization of High-Definition Dynamics by Solid-State NMR Spectroscopy. Biochemical and Biophysical Research Communications, 1993, 197, 904-909.	2.1	26
118	High-resolution conformation of gramicidin A in a lipid bilayer by solid-state NMR. Science, 1993, 261, 1457-1460.	12.6	685
119	Structural analysis of uniaxially aligned polymers using solid-state nitrogen-15 NMR. Macromolecules, 1993, 26, 6660-6663.	4.8	29
120	2H NMR determination of the global correlation time of the gramicidin channel in a lipid bilayer. Biophysical Journal, 1993, 65, 1162-1167.	0.5	49
121	Anisotropy and NMR of macromolecules. Biophysical Journal, 1993, 64, 301-302.	0.5	6
122	Solid-state 13C NMR spectroscopy of a 13C carbonyl-labeled polypeptide. Biophysical Journal, 1992, 61, 1550-1556.	0.5	17
123	Determination of the carbon-13 chemical shift and nitrogen-14 electric field gradient tensor orientations with respect to the molecular frame in a polypeptide. Journal of the American Chemical Society, 1992, 114, 5312-5321.	13.7	107
124	Structure of an isolated gramicidin A double helical species by high-resolution nuclear magnetic resonance. Journal of Molecular Biology, 1992, 226, 1101-1109.	4.2	40
125	Molecular dynamics computations and solid state nuclear magnetic resonance of the gramicidin cation channel. Biophysical Journal, 1991, 60, 974-978.	0.5	30
126	Experimental determination of torsion angles in the polypeptide backbone of the gramicidin a channel by solid state nuclear magnetic resonance. Journal of Molecular Biology, 1991, 218, 607-619.	4.2	63

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127	Solid-state nuclear magnetic resonance derived model for dynamics in the polypeptide backbone of the gramicidin a channel. Journal of Molecular Biology, 1991, 218, 621-637.	4.2	43
128	A method for the analytic determination of polypeptide structure using solid state nuclear magnetic resonance: The â€˜â€˜metric methodâ€™â€™. Journal of Chemical Physics, 1990, 92, 1483-1494.	3.0	26
129	Optimizing and characterizing alignment of oriented lipid bilayers containing gramicidin D. Biophysical Journal, 1990, 57, 351-362.	0.5	98
130	Nitrogen-hydrogen bond length determinations and implications for the gramicidin channel conformation and dynamics from nitrogen-15-proton dipolar interactions. Journal of the American Chemical Society, 1989, 111, 1910-1912.	13.7	32
131	Experimental observation of orientational dispersion in the peptide backbone of the gramicidin cation channel. Journal of the American Chemical Society, 1989, 111, 400-401.	13.7	15
132	Solvent history dependence of gramicidin A conformations in hydrated lipid bilayers. Biophysical Journal, 1988, 54, 259-267.	0.5	103
133	Solid-phase peptide synthesis and solid-state NMR spectroscopy of [Ala3-15N][Val1]gramicidin A.. Proceedings of the National Academy of Sciences of the United States of America, 1988, 85, 1384-1388.	7.1	66
134	A Solid State Nuclear Magnetic Resonance Approach for Determining the Structure of Gramicidin a without Model Fitting. Biophysical Journal, 1986, 49, 124-126.	0.5	24
135	Cerebral Metabolic Studies in Situ by 31P-: Nuclear Magnetic Resonance after Hypothermic Circulatory Arrest. Pediatric Research, 1986, 20, 867-871.	2.3	30
136	Protein structure by solid state nuclear magnetic resonance. Journal of Molecular Biology, 1985, 182, 367-381.	4.2	118
137	Nitrogen-15 spin exchange in a protein. Journal of the American Chemical Society, 1983, 105, 7471-7473.	13.7	57
138	31P nuclear magnetic resonance of the RNA in tobacco mosaic virus. Journal of Molecular Biology, 1983, 170, 1037-1043.	4.2	19
139	Protein structure by solid-state NMR. Journal of the American Chemical Society, 1983, 105, 306-308.	13.7	105
140	Protein dynamics by solid-state NMR: aromatic rings of the coat protein in fd bacteriophage.. Proceedings of the National Academy of Sciences of the United States of America, 1982, 79, 101-105.	7.1	96
141	Strategy for nitrogen NMR analysis of biopolymers. Journal of the American Chemical Society, 1982, 104, 1759-1761.	13.7	72
142	Protein dynamics by solid-state nuclear magnetic resonance spectroscopy. Journal of Molecular Biology, 1982, 159, 543-549.	4.2	43
143	Structure and architecture of the bacterial virus fd. an infrared linear dichroism study. Biophysical Chemistry, 1981, 14, 283-291.	2.8	13
144	Nuclear magnetic resonance of the filamentous bacteriophage fd. Biophysical Journal, 1980, 32, 531-548.	0.5	35

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145	Structural properties of fd coat protein in sodium dodecyl sulfate micelles. Biochemical and Biophysical Research Communications, 1980, 92, 478-484.	2.1	51
146	NMR of fd coat protein. Journal of Supramolecular Structure, 1979, 11, 139-145.	2.3	20