John Lute Markley

List of Publications by Year
in descending order

316 papers	25,359 citations	15503 65 h-index	8629 146 g-index
340 all docs	340 docs citations	340 times ranked	24416 citing authors

#	Article	IF	Citations
1	CHESPA/CHESCA-SPARKY: automated NMR data analysis plugins for SPARKY to map protein allostery. Bioinformatics, 2021, 37, 1176-1177.	4.1	12
2	The Protein Data Bank Archive. Methods in Molecular Biology, 2021, 2305, 3-21.	0.9	49
3	iPick: Multiprocessing software for integrated NMR signal detection and validation. Journal of Magnetic Resonance, 2021, 328, 106995.	2.1	9
4	Coordination of Di-Acetylated Histone Ligands by the ATAD2 Bromodomain. International Journal of Molecular Sciences, 2021, 22, 9128.	4.1	9
5	Templated Collagen â€œDouble Helicesâ€•Maintain Their Structure. Journal of the American Chemical Society, 2020, 142, 1137-1141.	13.7	17
6	Structural Insights into the Recognition of Mono- and Diacetylated Histones by the ATAD2B Bromodomain. Journal of Medicinal Chemistry, 2020, 63, 12799-12813.	6.4	15
7	Probabilistic identification of saccharide moieties in biomolecules and their protein complexes. Scientific Data, 2020, 7, 210.	5.3	4
8	Uncovering a membrane-distal conformation of KRAS available to recruit RAF to the plasma membrane. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 24258-24268.	7.1	34
9	Fragment screening targeting Ebola virus nucleoprotein C-terminal domain identifies lead candidates. Antiviral Research, 2020, 180, 104822.	4.1	3
10	ISCU interacts with NFU1, and ISCU[4Fe-4S] transfers its Fe-S cluster to NFU1 leading to the production of holo-NFU1. Journal of Structural Biology, 2020, 210, 107491.	2.8	13
11	The BRPF1 bromodomain is a molecular reader of di-acetyllysine. Current Research in Structural Biology, 2020, 2, 104-115.	2.2	16
12	Metabolic Changes in Synaptosomes in an Animal Model of Schizophrenia Revealed by 1H and 1H,13C NMR Spectroscopy. Metabolites, 2020, 10, 79.	2.9	1
13	PISA-SPARKY: an interactive SPARKY plugin to analyze oriented solid-state NMR spectra of helical membrane proteins. Bioinformatics, 2020, 36, 2915-2916.	4.1	7
14	BioMagResBank (BMRB) as a Resource for Structural Biology. Methods in Molecular Biology, 2020, 2112, 187-218.	0.9	35
15	The cytotoxicity of gallium maltolate in glioblastoma cells is enhanced by metformin through combined action on mitochondrial complex 1. Oncotarget, 2020, 11, 1531-1544.	1.8	8
16	Automated evaluation of consistency within the PubChem Compound database. Scientific Data, 2019, 6, 190023.	5.3	15
17	Structure and evolution of the 4-helix bundle domain of Zuotin, a J-domain protein co-chaperone of Hsp70. PLoS ONE, 2019, 14, e0217098.	2.5	8
18	Mitochondrial metabolism promotes adaptation to proteotoxic stress. Nature Chemical Biology, 2019, 15, 681-689.	8.0	275

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19	I-PINE web server: an integrative probabilistic NMR assignment system for proteins. Journal of Biomolecular NMR, 2019, 73, 213-222.	2.8	50
20	Backbone resonance assignments and secondary structure of Ebola nucleoprotein 600â€“739 construct. Biomolecular NMR Assignments, 2019, 13, 315-319.	0.8	3
21	Function and solution structure of the Arabidopsis thaliana RALF8 peptide. Protein Science, 2019, 28, 1115-1126.	7.6	10
22	Announcing mandatory submission of PDBx/mmCIF format files for crystallographic depositions to the Protein Data Bank (PDB). Acta Crystallographica Section D: Structural Biology, 2019, 75, 451-454.	2.3	46
23	Solution structure of human myeloid-derived growth factor suggests a conserved function in the endoplasmic reticulum. Nature Communications, 2019, 10, 5612.	12.8	15
24	NMR-STAR: comprehensive ontology for representing, archiving and exchanging data from nuclear magnetic resonance spectroscopic experiments. Journal of Biomolecular NMR, 2019, 73, 5-9.	2.8	32
25	Protein Data Bank: the single global archive for 3D macromolecular structure data. Nucleic Acids Research, 2019, 47, D520-D528.	14.5	671
26	Tools for Enhanced NMR-Based Metabolomics Analysis. Methods in Molecular Biology, 2019, 2037, 413-427.	0.9	6
27	ISCU(M108I) and ISCU(D39V) Differ from Wild-Type ISCU in Their Failure To Form Cysteine Desulfurase Complexes Containing Both Frataxin and Ferredoxin. Biochemistry, 2018, 57, 1491-1500.	2.5	16
28	Caloric Restriction Engages Hepatic RNA Processing Mechanisms in Rhesus Monkeys. Cell Metabolism, 2018, 27, 677-688.e5.	16.2	56
29	PINE-SPARKY.2 for automated NMR-based protein structure research. Bioinformatics, 2018, 34, 1586-1588.	4.1	27
30	Interactions of iron-bound frataxin with ISCU and ferredoxin on the cysteine desulfurase complex leading to Fe-S cluster assembly. Journal of Inorganic Biochemistry, 2018, 183, 107-116.	3.5	51
31	Conserved Lipid and Small-Molecule Modulation of COQ8 Reveals Regulation of the Ancient Kinase-like UbiB Family. Cell Chemical Biology, 2018, 25, 154-165.e11.	5.2	63
32	NMR as a Tool to Investigate the Processes of Mitochondrial and Cytosolic Iron-Sulfur Cluster Biosynthesis. Molecules, 2018, 23, 2213.	3.8	8
33	Probing Protein-Protein Interactions Using Asymmetric Labeling and Carbonyl-Carbon Selective Heteronuclear NMR Spectroscopy. Molecules, 2018, 23, 1937.	3.8	9
34	Worldwide Protein Data Bank biocuration supporting open access to high-quality 3D structural biology data. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	45
35	Architectural Features of Human Mitochondrial Cysteine Desulfurase Complexes from Crosslinking Mass Spectrometry and Small-Angle X-Ray Scattering. Structure, 2018, 26, 1127-1136.e4.	3.3	20
36	Applications of Parametrized NMR Spin Systems of Small Molecules. Analytical Chemistry, 2018, 90, 10646-10649.	6.5	23

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37	View from Nuclear Magnetic Resonance Spectroscopy. Advances in Experimental Medicine and Biology, 2018, 1105, 19-22.	1.6	2
38	Current Solution NMR Techniques for Structure-Function Studies of Proteins and RNA Molecules. Advances in Experimental Medicine and Biology, 2018, 1105, 43-58.	1.6	1
39	Mitochondrial Cysteine Desulfurase and ISD11 Coexpressed in Escherichia coli Yield Complex Containing Acyl Carrier Protein. ACS Chemical Biology, 2017, 12, 918-921.	3.4	32
40	OneDep: Unified wwPDB System for Deposition, Biocuration, and Validation of Macromolecular Structures in the PDB Archive. Structure, 2017, 25, 536-545.	3.3	130
41	Biomolecular NMR: Past and future. Archives of Biochemistry and Biophysics, 2017, 628, 3-16.	3.0	4
42	Progressive Stereo Locking (PSL): A Residual Dipolar Coupling Based Force Field Method for Determining the Relative Configuration of Natural Products and Other Small Molecules. ACS Chemical Biology, 2017, 12, 2157-2163.	3.4	24
43	Unique identifiers for small molecules enable rigorous labeling of their atoms. Scientific Data, 2017, 4, 170073.	5.3	30
44	Protein Data Bank (PDB): The Single Global Macromolecular Structure Archive. Methods in Molecular Biology, 2017, 1607, 627-641.	0.9	592
45	Human Mitochondrial Ferredoxin 1 (FDX1) and Ferredoxin 2 (FDX2) Both Bind Cysteine Desulfurase and Donate Electrons for Ironâ€“Sulfur Cluster Biosynthesis. Biochemistry, 2017, 56, 487-499.	2.5	89
46	Spin System Modeling of Nuclear Magnetic Resonance Spectra for Applications in Metabolomics and Small Molecule Screening. Analytical Chemistry, 2017, 89, 12201-12208.	6.5	31
47	PDB-Dev: a Prototype System for Depositing Integrative/Hybrid Structural Models. Structure, 2017, 25, 1317-1318.	3.3	84
48	Chemical Genomics, Structure Elucidation, and in Vivo Studies of the Marine-Derived Anticlostridial Ecteinamycin. ACS Chemical Biology, 2017, 12, 2287-2295.	3.4	24
49	The future of NMR-based metabolomics. Current Opinion in Biotechnology, 2017, 43, 34-40.	6.6	651
50	Increasing rigor in NMR-based metabolomics through validated and open source tools. Current Opinion in Biotechnology, 2017, 43, 56-61.	6.6	20
51	NMR-Based Identification of Metabolites in Polar and Non-Polar Extracts of Avian Liver. Metabolites, 2017, 7, 61.	2.9	17
52	Relationship between recombinant protein expression and host metabolome as determined by two-dimensional NMR spectroscopy. PLoS ONE, 2017, 12, e0177233.	2.5	14
53	Broadening the functionality of a J-protein/Hsp70 molecular chaperone system. PLoS Genetics, 2017, 13, e1007084.	3.5	30
54	Structureâ€function relationships of brazzein variants with altered interactions with the human sweet taste receptor. Protein Science, 2016, 25, 711-719.	7.6	19

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55	Integrative NMR for biomolecular research. Journal of Biomolecular NMR, 2016, 64, 307-332.	2.8	47
56	The AUDANA algorithm for automated protein 3D structure determination from NMR NOE data. Journal of Biomolecular NMR, 2016, 65, 51-57.	2.8	36
57	The archiving and dissemination of biological structure data. Current Opinion in Structural Biology, 2016, 40, 17-22.	5.7	28
58	Structure and Function of the PriC DNA Replication Restart Protein. Journal of Biological Chemistry, 2016, 291, 18384-18396.	3.4	17
59	Structural/Functional Properties of Human NFU1, an Intermediate [4Fe-4S] Carrier in Human Mitochondrial Iron-Sulfur Cluster Biogenesis. Structure, 2016, 24, 2080-2091.	3.3	45
60	Mechanism of Histone H3K4me3 Recognition by the Plant Homeodomain of Inhibitor of Growth 3. Journal of Biological Chemistry, 2016, 291, 18326-18341.	3.4	26
61	Dynamical Structures of Hsp70 and Hsp70-Hsp40 Complexes. Structure, 2016, 24, 1014-1030.	3.3	91
62	Probabilistic validation of protein NMR chemical shift assignments. Journal of Biomolecular NMR, 2016, 64, 17-25.	2.8	11
63	Publication of nuclear magnetic resonance experimental data with semantic web technology and the application thereof to biomedical research of proteins. Journal of Biomedical Semantics, 2016, 7, 16.	1.6	9
64	NMRmix: A Tool for the Optimization of Compound Mixtures in 1D ¹H NMR Ligand Affinity Screens. Journal of Proteome Research, 2016, 15, 1360-1368.	3.7	19
65	The Complex Energy Landscape of the Protein IscU. Biophysical Journal, 2015, 109, 1019-1025.	0.5	14
66	Solution Structural Studies of GTP:Adenosylcobinamide-Phosphateguanylyl Transferase (CobY) from Methanocaldococcus jannaschii. PLoS ONE, 2015, 10, e0141297.	2.5	3
67	Tangled web of interactions among proteins involved in ironâ€“sulfur cluster assembly as unraveled by NMR, SAXS, chemical crosslinking, and functional studies. Biochimica Et Biophysica Acta - Molecular Cell Research, 2015, 1853, 1416-1428.	4.1	32
68	NMR Exchange Format: a unified and open standard for representation of NMR restraint data. Nature Structural and Molecular Biology, 2015, 22, 433-434.	8.2	40
69	Human Cancer Antigen Globo H Is a Cell-Surface Ligand for Human Ribonuclease 1. ACS Central Science, 2015, 1, 181-190.	11.3	14
70	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. Structure, 2015, 23, 1156-1167.	3.3	159
71	NMRFAM-SDF: a protein structure determination framework. Journal of Biomolecular NMR, 2015, 62, 481-495.	2.8	4
72	Expression platforms for producing eukaryotic proteins: a comparison of E. coli cell-based and wheat germ cell-free synthesis, affinity and solubility tags, and cloning strategies. Journal of Structural and Functional Genomics, 2015, 16, 67-80.	1.2	12

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73	MolProbity for the massesâ€“of data. Journal of Biomolecular NMR, 2015, 63, 77-83.	2.8	44
74	ADAPT-NMR 3.0: utilization of BEST-type triple-resonance NMR experiments to accelerate the process of data collection and assignment. Journal of Biomolecular NMR, 2015, 62, 247-252.	2.8	0
75	NMRFAM-SPARKY: enhanced software for biomolecular NMR spectroscopy. Bioinformatics, 2015, 31, 1325-1327.	4.1	1,507
76	Assignments of RNase A by ADAPT-NMR and enhancer. Biomolecular NMR Assignments, 2015, 9, 81-88.	0.8	3
77	Metabolic Evidence of Diminished Lipid Oxidation in Women With Polycystic Ovary Syndrome. Current Metabolomics, 2014, 1, 269-278.	0.5	51
78	Interactions between Metal-binding Domains Modulate Intracellular Targeting of Cu(I)-ATPase ATP7B, as Revealed by Nanobody Binding. Journal of Biological Chemistry, 2014, 289, 32682-32693.	3.4	33
79	The Protein Data Bank archive as an open data resource. Journal of Computer-Aided Molecular Design, 2014, 28, 1009-1014.	2.9	114
80	PONDEROSA-C/S: clientâ€“server based software package for automated protein 3D structure determination. Journal of Biomolecular NMR, 2014, 60, 73-75.	2.8	49
81	Response toOn prompt update of literature references in the Protein Data Bank. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2780-2780.	2.5	1
82	Role of IscX in Ironâ€“Sulfur Cluster Biogenesis in Escherichia coli. Journal of the American Chemical Society, 2014, 136, 7933-7942.	13.7	53
83	Cell-Free Protein Synthesis for Functional and Structural Studies. Methods in Molecular Biology, 2014, 1091, 161-178.	0.9	19
84	The Specialized Hsp70 (HscA) Interdomain Linker Binds to Its Nucleotide-Binding Domain and Stimulates ATP Hydrolysis in Both cis and trans Configurations. Biochemistry, 2014, 53, 7148-7159.	2.5	24
85	Nucleotide-Dependent Interactions within a Specialized Hsp70/Hsp40 Complex Involved in Feâ€“S Cluster Biogenesis. Journal of the American Chemical Society, 2014, 136, 11586-11589.	13.7	25
86	pH-Induced Conformational Change of IscU at Low pH Correlates with Protonation/Deprotonation of Two Conserved Histidine Residues. Biochemistry, 2014, 53, 5290-5297.	2.5	8
87	Molecular Insights into the Recognition of N-Terminal Histone Modifications by the BRPF1 Bromodomain. Journal of Molecular Biology, 2014, 426, 1661-1676.	4.2	64
88	Automated Cell-Free Protein Production Methods for Structural Studies. Methods in Molecular Biology, 2014, 1140, 117-135.	0.9	5
89	Solution Structure of the 2A Protease from a Common Cold Agent, Human Rhinovirus C2, Strain W12. PLoS ONE, 2014, 9, e97198.	2.5	7
90	Plant cell wall profiling by fast maximum likelihood reconstruction (FMLR) and region-of-interest (ROI) segmentation of solution-state 2D 1Hâ€“13C NMR spectra. Biotechnology for Biofuels, 2013, 6, 45.	6.2	18

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91	NMRbot: Python scripts enable high-throughput data collection on current Bruker BioSpin NMR spectrometers. Metabolomics, 2013, 9, 558-563.	3.0	21
92	Metamorphic protein IscU alternates conformations in the course of its role as the scaffold protein for ironâ€“sulfur cluster biosynthesis and delivery. FEBS Letters, 2013, 587, 1172-1179.	2.8	70
93	Fast automated protein NMR data collection and assignment by ADAPT-NMR on Bruker spectrometers. Journal of Magnetic Resonance, 2013, 236, 83-88.	2.1	14
94	Human Mitochondrial Chaperone (mtHSP70) and Cysteine Desulfurase (NFS1) Bind Preferentially to the Disordered Conformation, Whereas Co-chaperone (HSC20) Binds to the Structured Conformation of the Iron-Sulfur Cluster Scaffold Protein (ISCU). Journal of Biological Chemistry, 2013, 288, 28755-28770.	3.4	50
95	Recommendations of the wwPDB NMR Validation Task Force. Structure, 2013, 21, 1563-1570.	3.3	151
96	[2Fe-2S]-Ferredoxin Binds Directly to Cysteine Desulfurase and Supplies an Electron for Ironâ€“Sulfur Cluster Assembly but Is Displaced by the Scaffold Protein or Bacterial Frataxin. Journal of the American Chemical Society, 2013, 135, 8117-8120.	13.7	88
97	Temperatureâ€dependent conformational change affecting Tyr11 and sweetness loops of brazzein. Proteins: Structure, Function and Bioinformatics, 2013, 81, 919-925.	2.6	15
98	ADAPT-NMR Enhancer: complete package for reduced dimensionality in protein NMR spectroscopy. Bioinformatics, 2013, 29, 515-517.	4.1	9
99	Biophysical characterization of Î±-synuclein and its controversial structure. Intrinsically Disordered Proteins, 2013, 1, e26255.	1.9	59
100	Dosage Effects of Salt and pH Stresses on Saccharomyces cerevisiae as Monitored via Metabolites by Using Two Dimensional NMR Spectroscopy. Bulletin of the Korean Chemical Society, 2013, 34, 3602-3608.	1.9	15
101	Specialized Hsp70 Chaperone (HscA) Binds Preferentially to the Disordered Form, whereas J-protein (HscB) Binds Preferentially to the Structured Form of the Iron-Sulfur Cluster Scaffold Protein (IscU). Journal of Biological Chemistry, 2012, 287, 31406-31413.	3.4	41
102	Disordered form of the scaffold protein IscU is the substrate for iron-sulfur cluster assembly on cysteine desulfurase. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 454-459.	7.1	70
103	Regulation of Estrogen Receptor Î± N-Terminus Conformation and Function by Peptidyl Prolyl Isomerase Pin1. Molecular and Cellular Biology, 2012, 32, 445-457.	2.3	64
104	An automated system designed for large scale NMR data deposition and annotation: application to over 600 assigned chemical shift data entries to the BioMagResBank from the Riken Structural Genomics/Proteomics Initiative internal database. Journal of Biomolecular NMR, 2012, 53, 311-320.	2.8	26
105	PACSY, a relational database management system for protein structure and chemical shift analysis. Journal of Biomolecular NMR, 2012, 54, 169-179.	2.8	33
106	Metamorphic Protein IscU Changes Conformation by cisâ€“trans Isomerizations of Two Peptidylâ€“Prolyl Peptide Bonds. Biochemistry, 2012, 51, 9595-9602.	2.5	31
107	Characterization of the [2Fe-2S] Cluster of Escherichia coli Transcription Factor IscR. Biochemistry, 2012, 51, 4453-4462.	2.5	85
108	Semiautomated Device for Batch Extraction of Metabolites from Tissue Samples. Analytical Chemistry, 2012, 84, 1809-1812.	6.5	6

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109	Novel NMR and MS Approaches to Metabolomics. Methods in Pharmacology and Toxicology, 2012, , 199-230.	0.2	4
110	Three-Dimensional Structure and Determinants of Stability of the Ironâ€“Sulfur Cluster Scaffold Protein IscU from Escherichia coli. Biochemistry, 2012, 51, 5557-5563.	2.5	40
111	Use of NMR Saturation Transfer Difference Spectroscopy to Study Ligand Binding to Membrane Proteins. Methods in Molecular Biology, 2012, 914, 47-63.	0.9	38
112	PACSY database, a relational database management system for Protein structure and nuclear Magnetic Resonance chemical shift analysis. , 2012, , .		1
113	In support of the BMRB. Nature Structural and Molecular Biology, 2012, 19, 854-860.	8.2	6
114	Robust, Integrated Computational Control of NMR Experiments to Achieve Optimal Assignment by ADAPT-NMR. PLoS ONE, 2012, 7, e33173.	2.5	17
115	Databases and Software for NMR-Based Metabolomics. Current Metabolomics, 2012, 1, 28-40.	0.5	45
116	RNA-PAIRS: RNA probabilistic assignment of imino resonance shifts. Journal of Biomolecular NMR, 2012, 52, 289-302.	2.8	15
117	Tracing Metabolite Footsteps of Escherichia coli Along the Time Course of Recombinant Protein Expression by Two-Dimensional NMR Spectroscopy. Bulletin of the Korean Chemical Society, 2012, 33, 4041-4046.	1.9	8
118	Molecular Interactions in PriCâ€mediated DNA Replication Restart. FASEB Journal, 2012, 26, lb88.	0.5	0
119	Hyperfine-Shifted ¹³C Resonance Assignments in an Ironâ^'Sulfur Protein with Quantum Chemical Verification: Aliphatic Cβ'HÂ·Â·Â·S 3-Centerâ^'4-Electron Interactions. Journal of the American Chemical Society, 2011, 133, 1310-1316.	13.7	31
120	Measurement of Absolute Concentrations of Individual Compounds in Metabolite Mixtures by Gradient-Selective Time-Zero ¹Hâ€“¹³C HSQC with Two Concentration References and Fast Maximum Likelihood Reconstruction Analysis. Analytical Chemistry, 2011, 83, 9352-9360.	6.5	39
121	Deconvolution of Two-Dimensional NMR Spectra by Fast Maximum Likelihood Reconstruction: Application to Quantitative Metabolomics. Analytical Chemistry, 2011, 83, 4871-4880.	6.5	80
122	Role of aminotransferases in glutamate metabolism of human erythrocytes. Journal of Biomolecular NMR, 2011, 49, 221-229.	2.8	46
123	Two-dimensional concurrent HMQC-COSY as an approach for small molecule chemical shift assignment and compound identification. Journal of Biomolecular NMR, 2011, 49, 291-296.	2.8	13
124	Hydrogen exchange during cell-free incorporation of deuterated amino acids and an approach to its inhibition. Journal of Biomolecular NMR, 2011, 51, 467-476.	2.8	26
125	Three hydrophobic amino acids in Escherichia coli HscB make the greatest contribution to the stability of the HscB-IscU complex. BMC Biochemistry, 2011, 12, 3.	4.4	31
126	PONDEROSA, an automated 3D-NOESY peak picking program, enables automated protein structure determination. Bioinformatics, 2011, 27, 1727-1728.	4.1	29

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127	Structural Characterization of Hsp12, the Heat Shock Protein from Saccharomyces cerevisiae, in Aqueous Solution Where It Is Intrinsically Disordered and in Detergent Micelles Where It Is Locally Î±-Helical. Journal of Biological Chemistry, 2011, 286, 43447-43453.	3.4	26
128	An NMR structural study of nickel-substituted rubredoxin. Journal of Biological Inorganic Chemistry, 2010, 15, 409-420.	2.6	17
129	Differences in the Structure and Dynamics of the Apo- and Palmitate-ligated Forms of Aedes aegypti Sterol Carrier Protein 2 (AeSCP-2). Journal of Biological Chemistry, 2010, 285, 17046-17053.	3.4	9
130	NMR Method for Measuring Carbon-13 Isotopic Enrichment of Metabolites in Complex Solutions. Analytical Chemistry, 2010, 82, 4558-4563.	6.5	38
131	Key Amino Acid Residues Involved in Multi-Point Binding Interactions between Brazzein, a Sweet Protein, and the T1R2â€“T1R3 Human Sweet Receptor. Journal of Molecular Biology, 2010, 398, 584-599.	4.2	104
132	Interactions between the human sweet-sensing T1R2â€“T1R3 receptor and sweeteners detected by saturation transfer difference NMR spectroscopy. Biochimica Et Biophysica Acta - Biomembranes, 2010, 1798, 82-86.	2.6	53
133	Cell-Free Protein Synthesis Technology in NMR High-Throughput Structure Determination. Methods in Molecular Biology, 2010, 607, 127-147.	0.9	30
134	Why not highâ€throughput eukaryotic protein structures?. FASEB Journal, 2010, 24, lb229.	0.5	0
135	Role of band 3 in regulating metabolic flux of red blood cells. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18515-18520.	7.1	109
136	Probabilistic Interaction Network of Evidence Algorithm and its Application to Complete Labeling of Peak Lists from Protein NMR Spectroscopy. PLoS Computational Biology, 2009, 5, e1000307.	3.2	177
137	PINE-SPARKY: graphical interface for evaluating automated probabilistic peak assignments in protein NMR spectroscopy. Bioinformatics, 2009, 25, 2085-2087.	4.1	107
138	rNMR: open source software for identifying and quantifying metabolites in NMR spectra. Magnetic Resonance in Chemistry, 2009, 47, S123-6.	1.9	169
139	The Center for Eukaryotic Structural Genomics. Journal of Structural and Functional Genomics, 2009, 10, 165-179.	1.2	33
140	Empirical correlation between protein backbone 15N and 13C secondary chemical shifts and its application to nitrogen chemical shift re-referencing. Journal of Biomolecular NMR, 2009, 44, 95-99.	2.8	28
141	The NMR restraints grid at BMRB for 5,266 protein and nucleic acid PDB entries. Journal of Biomolecular NMR, 2009, 45, 389-396.	2.8	26
142	One-Sample Approach to Determine the Relative Orientations of Proteins in Ternary and Binary Complexes from Residual Dipolar Coupling Measurements. Journal of the American Chemical Society, 2009, 131, 14138-14139.	13.7	9
143	Structure and Dynamics of the Ironâ^'Sulfur Cluster Assembly Scaffold Protein IscU and Its Interaction with the Cochaperone HscB. Biochemistry, 2009, 48, 6062-6071.	2.5	82
144	Hyperfine-Shifted 13C and 15N NMR Signals from Clostridium pasteurianum Rubredoxin: Extensive Assignments and Quantum Chemical Verification. Journal of the American Chemical Society, 2009, 131, 15555-15563.	13.7	20

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145	Zinc-substituted Desulfovibrio gigas desulforedoxins: Resolving subunit degeneracy with nonsymmetric pseudocontact shifts. Protein Science, 2009, 11, 2464-2470.	7.6	10
146	BioMagResBank (BMRB) as a partner in the Worldwide Protein Data Bank (wwPDB): new policies affecting biomolecular NMR depositions. Journal of Biomolecular NMR, 2008, 40, 153-155.	2.8	117
147	Structure of the putative 32â€ƒkDa myrosinaseâ€bbinding protein from Arabidopsis (At3g16450.1) determined by SAILâ€NMR. FEBS Journal, 2008, 275, 5873-5884.	4.7	28
148	Metabolite identification via the Madison Metabolomics Consortium Database. Nature Biotechnology, 2008, 26, 162-164.	17.5	591
149	Data Management in Structural Genomics: An Overview. Methods in Molecular Biology, 2008, 426, 49-79.	0.9	26
150	Structure of Human J-type Co-chaperone HscB Reveals a Tetracysteine Metal-binding Domain. Journal of Biological Chemistry, 2008, 283, 30184-30192.	3.4	38
151	Efficient and rapid protein expression and purification of small high disulfide containing sweet protein brazzein in E. coli. Protein Expression and Purification, 2008, 58, 263-268.	1.3	45
152	Direct NMR Detection of the Binding of Functional Ligands to the Human Sweet Receptor, a Heterodimeric Family 3 GPCR. Journal of the American Chemical Society, 2008, 130, 7212-7213.	13.7	70
153	Solution Structure of the Ironâ^'Sulfur Cluster Cochaperone HscB and Its Binding Surface for the Ironâ^'Sulfur Assembly Scaffold Protein IscU. Biochemistry, 2008, 47, 9394-9404.	2.5	42
154	Simultaneous Detection and Deconvolution of Congested NMR Spectra Containing Three Isotopically Labeled Species. Journal of the American Chemical Society, 2008, 130, 7818-7819.	13.7	12
155	Structural basis for RNA recognition by a type II poly(A)-binding protein. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 15317-15322.	7.1	19
156	How Sweet It Is: Detailed Molecular and Functional Studies of Brazzein, a Sweet Protein and Its Analogs. ACS Symposium Series, 2008, , 560-572.	0.5	5
157	The worldwide Protein Data Bank (wwPDB): ensuring a single, uniform archive of PDB data. Nucleic Acids Research, 2007, 35, D301-D303.	14.5	992
158	Remediation of the protein data bank archive. Nucleic Acids Research, 2007, 36, D426-D433.	14.5	136
159	BioMagResBank. Nucleic Acids Research, 2007, 36, D402-D408.	14.5	1,450
160	One-step purification of bacterially expressed recombinant transducin Î±-subunit and isotopically labeled PDE6 Î³-subunit for NMR analysis. Protein Expression and Purification, 2007, 51, 187-197.	1.3	17
161	Three-dimensional Structure Determined for a Subunit of Human tRNA Splicing Endonuclease (Sen15) Reveals a Novel Dimeric Fold. Journal of Molecular Biology, 2007, 366, 155-164.	4.2	19
162	Method for Determining Molar Concentrations of Metabolites in Complex Solutions from Two-Dimensional ¹Hâ^'¹³C NMR Spectra. Analytical Chemistry, 2007, 79, 9385-9390.	6.5	262

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163	NMR analysis goes nano. Nature Biotechnology, 2007, 25, 750-751.	17.5	7
164	Reply to: Building meaningful models of glycoproteins. Nature Structural and Molecular Biology, 2007, 14, 354-355.	8.2	24
165	Solution structure of human sorting nexin 22. Protein Science, 2007, 16, 807-814.	7.6	13
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