John Lute Markley

List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/8042635/john-lute-markley-publications-by-year.pdf
Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.
The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

317 papers	20,402 citations	61 h-index	134 g-index
340 ext. papers	23,161 ext. citations	6.1 avg, IF	6.62 L-index

#	Paper	IF	Citations
317	CHESPA/CHESCA-SPARKY: automated NMR data analysis plugins for SPARKY to map protein allostery. *Bioinformatics*, **2021**, 37, 1176-1177	7.2	5
316	The Protein Data Bank Archive. *Methods in Molecular Biology*, **2021**, 2305, 3-21	1.4	12
315	iPick: Multiprocessing software for integrated NMR signal detection and validation. *Journal of Magnetic Resonance*, **2021**, 328, 106995	3	2
314	Coordination of Di-Acetylated Histone Ligands by the ATAD2 Bromodomain. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	3
313	Fragment screening targeting Ebola virus nucleoprotein C-terminal domain identifies lead candidates. *Antiviral Research*, **2020**, 180, 104822	10.8	1
312	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	3.4	10
311	The BRPF1 bromodomain is a molecular reader of di-acetyllysine. *Current Research in Structural Biology*, **2020**, 2, 104-115	2.8	5
310	PISA-SPARKY: an interactive SPARKY plugin to analyze oriented solid-state NMR spectra of helical membrane proteins. *Bioinformatics*, **2020**, 36, 2915-2916	7.2	4
309	The cytotoxicity of gallium maltolate in glioblastoma cells is enhanced by metformin through combined action on mitochondrial complex 1. *Oncotarget*, **2020**, 11, 1531-1544	3.3	4
308	Templated Collagen "Double Helices" Maintain Their Structure. *Journal of the American Chemical Society*, **2020**, 142, 1137-1141	16.4	10
307	Structural Insights into the Recognition of Mono- and Diacetylated Histones by the ATAD2B Bromodomain. *Journal of Medicinal Chemistry*, **2020**, 63, 12799-12813	8.3	5
306	Probabilistic identification of saccharide moieties in biomolecules and their protein complexes. *Scientific Data*, **2020**, 7, 210	8.2	4
305	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	11.5	12
304	BioMagResBank (BMRB) as a Resource for Structural Biology. *Methods in Molecular Biology*, **2020**, 2112, 187-218	1.4	18
303	Structure and evolution of the 4-helix bundle domain of Zuotin, a J-domain protein co-chaperone of Hsp70. *PLoS ONE*, **2019**, 14, e0217098	3.7	2
302	Mitochondrial metabolism promotes adaptation to proteotoxic stress. *Nature Chemical Biology*, **2019**, 15, 681-689	11.7	62
301	I-PINE web server: an integrative probabilistic NMR assignment system for proteins. *Journal of Biomolecular NMR*, **2019**, 73, 213-222	3	26

300	Backbone resonance assignments and secondary structure of Ebola nucleoprotein 600-739 construct. *Biomolecular NMR Assignments*, **2019**, 13, 315-319	0.7	1
299	Function and solution structure of the Arabidopsis thaliana RALF8 peptide. *Protein Science*, **2019**, 28, 1115-1126	6.3	5
298	Automated evaluation of consistency within the PubChem Compound database. *Scientific Data*, **2019**, 6, 190023	8.2	7
297	Approach to Improving the Quality of Open Data in the Universe of Small Molecules. *Lecture Notes in Business Information Processing*, **2019**, 519-530	0.6	
296	Tools for Enhanced NMR-Based Metabolomics Analysis. *Methods in Molecular Biology*, **2019**, 2037, 413-427	1.4	3
295	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	5.5	32
294	Solution structure of human myeloid-derived growth factor suggests a conserved function in the endoplasmic reticulum. *Nature Communications*, **2019**, 10, 5612	17.4	7
293	NMR-STAR: comprehensive ontology for representing, archiving and exchanging data from nuclear magnetic resonance spectroscopic experiments. *Journal of Biomolecular NMR*, **2019**, 73, 5-9	3	17
292	Protein Data Bank: the single global archive for 3D macromolecular structure data. *Nucleic Acids Research*, **2019**, 47, D520-D528	20.1	308
291	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	3.2	12
290	Caloric Restriction Engages Hepatic RNA Processing Mechanisms in Rhesus Monkeys. *Cell Metabolism*, **2018**, 27, 677-688.e5	24.6	37
289	PINE-SPARKY.2 for automated NMR-based protein structure research. *Bioinformatics*, **2018**, 34, 1586-1588	7.2	17
288	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	4.2	35
287	Architectural Features of Human Mitochondrial Cysteine Desulfurase Complexes from Crosslinking Mass Spectrometry and Small-Angle X-Ray Scattering. *Structure*, **2018**, 26, 1127-1136.e4	5.2	15
286	Applications of Parametrized NMR Spin Systems of Small Molecules. *Analytical Chemistry*, **2018**, 90, 10646-10649	7.8	15
285	Current Solution NMR Techniques for Structure-Function Studies of Proteins and RNA Molecules. *Advances in Experimental Medicine and Biology*, **2018**, 1105, 43-58	3.6	
284	View from Nuclear Magnetic Resonance Spectroscopy. *Advances in Experimental Medicine and Biology*, **2018**, 1105, 19-22	3.6	2
283	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	8.2	40

282	Structural Proteomics **2018**, 99-128		
281	NMR as a Tool to Investigate the Processes of Mitochondrial and Cytosolic Iron-Sulfur Cluster Biosynthesis. *Molecules*, **2018**, 23,	4.8	5
280	Probing Protein-Protein Interactions Using Asymmetric Labeling and Carbonyl-Carbon Selective Heteronuclear NMR Spectroscopy. *Molecules*, **2018**, 23,	4.8	9
279	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,	5	31
278	Mitochondrial Cysteine Desulfurase and ISD11 Coexpressed in Escherichia coli Yield Complex Containing Acyl Carrier Protein. *ACS Chemical Biology*, **2017**, 12, 918-921	4.9	23
277	OneDep: Unified wwPDB System for Deposition, Biocuration, and Validation of Macromolecular Structures in the PDB Archive. *Structure*, **2017**, 25, 536-545	5.2	86
276	Biomolecular NMR: Past and future. *Archives of Biochemistry and Biophysics*, **2017**, 628, 3-16	4.1	3
275	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	4.9	16
274	Unique identifiers for small molecules enable rigorous labeling of their atoms. *Scientific Data*, **2017**, 4, 170073	8.2	19
273	Protein Data Bank (PDB): The Single Global Macromolecular Structure Archive. *Methods in Molecular Biology*, **2017**, 1607, 627-641	1.4	271
272	Human Mitochondrial Ferredoxin 1 (FDX1) and Ferredoxin 2 (FDX2) Both Bind Cysteine Desulfurase and Donate Electrons for Iron-Sulfur Cluster Biosynthesis. *Biochemistry*, **2017**, 56, 487-499	3.2	46
271	Spin System Modeling of Nuclear Magnetic Resonance Spectra for Applications in Metabolomics and Small Molecule Screening. *Analytical Chemistry*, **2017**, 89, 12201-12208	7.8	19
270	Relationship between recombinant protein expression and host metabolome as determined by two-dimensional NMR spectroscopy. *PLoS ONE*, **2017**, 12, e0177233	3.7	10
269	PDB-Dev: a Prototype System for Depositing Integrative/Hybrid Structural Models. *Structure*, **2017**, 25, 1317-1318	5.2	58
268	Chemical Genomics, Structure Elucidation, and in Vivo Studies of the Marine-Derived Anticlostridial Ecteinamycin. *ACS Chemical Biology*, **2017**, 12, 2287-2295	4.9	19
267	The future of NMR-based metabolomics. *Current Opinion in Biotechnology*, **2017**, 43, 34-40	11.4	500
266	Increasing rigor in NMR-based metabolomics through validated and open source tools. *Current Opinion in Biotechnology*, **2017**, 43, 56-61	11.4	17
265	NMR-Based Identification of Metabolites in Polar and Non-Polar Extracts of Avian Liver. *Metabolites* , **2017**, 7,	5.6	9

264	Broadening the functionality of a J-protein/Hsp70 molecular chaperone system. *PLoS Genetics*, **2017**, 13, e1007084	6	19
263	Structure and Function of the PriC DNA Replication Restart Protein. *Journal of Biological Chemistry*, **2016**, 291, 18384-96	5.4	11
262	Structural/Functional Properties of Human NFU1, an Intermediate [4Fe-4S] Carrier in Human Mitochondrial Iron-Sulfur Cluster Biogenesis. *Structure*, **2016**, 24, 2080-2091	5.2	37
261	Mechanism of Histone H3K4me3 Recognition by the Plant Homeodomain of Inhibitor of Growth 3. *Journal of Biological Chemistry*, **2016**, 291, 18326-41	5.4	18
260	Dynamical Structures of Hsp70 and Hsp70-Hsp40 Complexes. *Structure*, **2016**, 24, 1014-30	5.2	71
259	Probabilistic validation of protein NMR chemical shift assignments. *Journal of Biomolecular NMR*, **2016**, 64, 17-25	3	8
258	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	2.2	7
257	NMRmix: A Tool for the Optimization of Compound Mixtures in 1D (1)H NMR Ligand Affinity Screens. *Journal of Proteome Research*, **2016**, 15, 1360-8	5.6	17
256	Structure-function relationships of brazzein variants with altered interactions with the human sweet taste receptor. *Protein Science*, **2016**, 25, 711-9	6.3	13
255	Integrative NMR for biomolecular research. *Journal of Biomolecular NMR*, **2016**, 64, 307-32	3	36
254	The AUDANA algorithm for automated protein 3D structure determination from NMR NOE data. *Journal of Biomolecular NMR*, **2016**, 65, 51-7	3	24
253	The archiving and dissemination of biological structure data. *Current Opinion in Structural Biology*, **2016**, 40, 17-22	8.1	23
252	Human Cancer Antigen Globo H Is a Cell-Surface Ligand for Human Ribonuclease 1. *ACS Central Science*, **2015**, 1, 181-190	16.8	13
251	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. *Structure*, **2015**, 23, 1156-67	5.2	131
250	NMRFAM-SDF: a protein structure determination framework. *Journal of Biomolecular NMR*, **2015**, 62, 481-95	3	4
249	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		10
248	MolProbity for the masses-of data. *Journal of Biomolecular NMR*, **2015**, 63, 77-83	3	30
247	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, 247-52	3	

246	NMRFAM-SPARKY: enhanced software for biomolecular NMR spectroscopy. *Bioinformatics*, **2015**, 31, 1325-7	7.2	879
245	Assignments of RNase A by ADAPT-NMR and enhancer. *Biomolecular NMR Assignments*, **2015**, 9, 81-8	0.7	2
244	The Complex Energy Landscape of the Protein IscU. *Biophysical Journal*, **2015**, 109, 1019-25	2.9	10
243	Solution Structural Studies of GTP:Adenosylcobinamide-Phosphateguanylyl Transferase (CobY) from Methanocaldococcus jannaschii. *PLoS ONE*, **2015**, 10, e0141297	3.7	2
242	Tangled web of interactions among proteins involved in iron-sulfur cluster assembly as unraveled by NMR, SAXS, chemical crosslinking, and functional studies. *Biochimica Et Biophysica Acta - Molecular Cell Research*, **2015**, 1853, 1416-28	4.9	30
241	NMR Exchange Format: a unified and open standard for representation of NMR restraint data. *Nature Structural and Molecular Biology*, **2015**, 22, 433-4	17.6	26
240	Role of IscX in iron-sulfur cluster biogenesis in Escherichia coli. *Journal of the American Chemical Society*, **2014**, 136, 7933-42	16.4	47
239	Cell-free protein synthesis for functional and structural studies. *Methods in Molecular Biology*, **2014**, 1091, 161-78	1.4	16
238	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, 7148-59	3.2	20
237	Nucleotide-dependent interactions within a specialized Hsp70/Hsp40 complex involved in Fe-S cluster biogenesis. *Journal of the American Chemical Society*, **2014**, 136, 11586-9	16.4	20
236	pH-induced conformational change of IscU at low pH correlates with protonation/deprotonation of two conserved histidine residues. *Biochemistry*, **2014**, 53, 5290-7	3.2	6
235	Molecular insights into the recognition of N-terminal histone modifications by the BRPF1 bromodomain. *Journal of Molecular Biology*, **2014**, 426, 1661-76	6.5	47
234	Metabolic Evidence of Diminished Lipid Oxidation in Women With Polycystic Ovary Syndrome. *Current Metabolomics*, **2014**, 2, 269-278	1	37
233	Interactions between metal-binding domains modulate intracellular targeting of Cu(I)-ATPase ATP7B, as revealed by nanobody binding. *Journal of Biological Chemistry*, **2014**, 289, 32682-93	5.4	28
232	The Protein Data Bank archive as an open data resource. *Journal of Computer-Aided Molecular Design*, **2014**, 28, 1009-14	4.2	85
231	PONDEROSA-C/S: client-server based software package for automated protein 3D structure determination. *Journal of Biomolecular NMR*, **2014**, 60, 73-5	3	31
230	Response to On prompt update of literature references in the Protein Data Bank. *Acta Crystallographica Section D: Biological Crystallography*, **2014**, 70, 2780		1
229	Solution structure of the 2A protease from a common cold agent, human rhinovirus C2, strain W12. *PLoS ONE*, **2014**, 9, e97198	3.7	7

228	Automated cell-free protein production methods for structural studies. *Methods in Molecular Biology*, **2014**, 1140, 117-35	1.4	5
227	Plant cell wall profiling by fast maximum likelihood reconstruction (FMLR) and region-of-interest (ROI) segmentation of solution-state 2D 1H-13C NMR spectra. *Biotechnology for Biofuels*, **2013**, 6, 45	7.8	18
226	NMRbot: Python scripts enable high-throughput data collection on current Bruker BioSpin NMR spectrometers. *Metabolomics*, **2013**, 9, 558-563	4.7	16
225	Metamorphic protein IscU alternates conformations in the course of its role as the scaffold protein for iron-sulfur cluster biosynthesis and delivery. *FEBS Letters*, **2013**, 587, 1172-9	3.8	57
224	Fast automated protein NMR data collection and assignment by ADAPT-NMR on Bruker spectrometers. *Journal of Magnetic Resonance*, **2013**, 236, 83-8	3	12
223	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, 28755-70	5.4	44
222	Recommendations of the wwPDB NMR Validation Task Force. *Structure*, **2013**, 21, 1563-70	5.2	117
221	Databases and Software for NMR-Based Metabolomics. *Current Metabolomics*, **2013**, 1,	1	40
220	[2Fe-2S]-ferredoxin binds directly to cysteine desulfurase and supplies an electron for iron-sulfur cluster assembly but is displaced by the scaffold protein or bacterial frataxin. *Journal of the American Chemical Society*, **2013**, 135, 8117-20	16.4	76
219	Temperature-dependent conformational change affecting Tyr11 and sweetness loops of brazzein. *Proteins: Structure, Function and Bioinformatics*, **2013**, 81, 919-25	4.2	10
218	ADAPT-NMR Enhancer: complete package for reduced dimensionality in protein NMR spectroscopy. *Bioinformatics*, **2013**, 29, 515-7	7.2	7
217	Biophysical characterization of synuclein and its controversial structure. *Intrinsically Disordered Proteins*, **2013**, 1, 18-39		52
216	Dosage Effects of Salt and pH Stresses on as Monitored Metabolites by Using Two Dimensional NMR Spectroscopy. *Bulletin of the Korean Chemical Society*, **2013**, 34, 3602-3608	1.2	10
215	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, 311-20	3	20
214	PACSY, a relational database management system for protein structure and chemical shift analysis. *Journal of Biomolecular NMR*, **2012**, 54, 169-79	3	22
213	Metamorphic protein IscU changes conformation by cis-trans isomerizations of two peptidyl-prolyl peptide bonds. *Biochemistry*, **2012**, 51, 9595-602	3.2	24
212	Characterization of the [2Fe-2S] cluster of Escherichia coli transcription factor IscR. *Biochemistry*, **2012**, 51, 4453-62	3.2	71
211	Semiautomated device for batch extraction of metabolites from tissue samples. *Analytical Chemistry*, **2012**, 84, 1809-12	7.8	3

210	Novel NMR and MS Approaches to Metabolomics. *Methods in Pharmacology and Toxicology*, **2012**, 199-230	1.1	1
209	Three-dimensional structure and determinants of stability of the iron-sulfur cluster scaffold protein IscU from Escherichia coli. *Biochemistry*, **2012**, 51, 5557-63	3.2	34
208	Use of NMR saturation transfer difference spectroscopy to study ligand binding to membrane proteins. *Methods in Molecular Biology*, **2012**, 914, 47-63	1.4	34
207	In support of the BMRB. *Nature Structural and Molecular Biology*, **2012**, 19, 854-60	17.6	5
206	Robust, integrated computational control of NMR experiments to achieve optimal assignment by ADAPT-NMR. *PLoS ONE*, **2012**, 7, e33173	3.7	15
205	RNA-PAIRS: RNA probabilistic assignment of imino resonance shifts. *Journal of Biomolecular NMR*, **2012**, 52, 289-302	3	13
204	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, 31406-13	5.4	37
203	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, 454-9	11.5	62
202	Regulation of estrogen receptor N-terminus conformation and function by peptidyl prolyl isomerase Pin1. *Molecular and Cellular Biology*, **2012**, 32, 445-57	4.8	58
201	Tracing Metabolite Footsteps of Along the Time Course of Recombinant Protein Expression by Two-Dimensional NMR Spectroscopy. *Bulletin of the Korean Chemical Society*, **2012**, 33, 4041-4046	1.2	8
200	Molecular Interactions in PriC-mediated DNA Replication Restart. *FASEB Journal*, **2012**, 26, lb88	0.9	
199	Deconvolution of two-dimensional NMR spectra by fast maximum likelihood reconstruction: application to quantitative metabolomics. *Analytical Chemistry*, **2011**, 83, 4871-80	7.8	71
198	Role of aminotransferases in glutamate metabolism of human erythrocytes. *Journal of Biomolecular NMR*, **2011**, 49, 221-9	3	34
197	Two-dimensional concurrent HMQC-COSY as an approach for small molecule chemical shift assignment and compound identification. *Journal of Biomolecular NMR*, **2011**, 49, 291-6	3	11
196	Hydrogen exchange during cell-free incorporation of deuterated amino acids and an approach to its inhibition. *Journal of Biomolecular NMR*, **2011**, 51, 467-76	3	24
195	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	4.8	30
194	Hyperfine-shifted 13C resonance assignments in an iron-sulfur protein with quantum chemical verification: aliphatic C-H S 3-center-4-electron interactions. *Journal of the American Chemical Society*, **2011**, 133, 1310-6	16.4	28
193	Measurement of absolute concentrations of individual compounds in metabolite mixtures by gradient-selective time-zero 1H-13C HSQC with two concentration references and fast maximum likelihood reconstruction analysis. *Analytical Chemistry*, **2011**, 83, 9352-60	7.8	33

192	PONDEROSA, an automated 3D-NOESY peak picking program, enables automated protein structure determination. *Bioinformatics*, **2011**, 27, 1727-8	7.2	24
191	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 helical. *Journal of Biological Chemistry*, **2011**, 286, 43447-53	5.4	22
190	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, 17046-53	5.4	9
189	NMR method for measuring carbon-13 isotopic enrichment of metabolites in complex solutions. *Analytical Chemistry*, **2010**, 82, 4558-63	7.8	34
188	Key amino acid residues involved in multi-point binding interactions between brazzein, a sweet protein, and the T1R2-T1R3 human sweet receptor. *Journal of Molecular Biology*, **2010**, 398, 584-99	6.5	87
187	Interactions between the human sweet-sensing T1R2-T1R3 receptor and sweeteners detected by saturation transfer difference NMR spectroscopy. *Biochimica Et Biophysica Acta - Biomembranes*, **2010**, 1798, 82-6	3.8	43
186	An NMR structural study of nickel-substituted rubredoxin. *Journal of Biological Inorganic Chemistry*, **2010**, 15, 409-20	3.7	13
185	Cell-free protein synthesis technology in NMR high-throughput structure determination. *Methods in Molecular Biology*, **2010**, 607, 127-47	1.4	29
184	Why not high-throughput eukaryotic protein structures?. *FASEB Journal*, **2010**, 24, lb229	0.9	
183	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, 18515-20	11.5	88
182	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	5	162
181	PINE-SPARKY: graphical interface for evaluating automated probabilistic peak assignments in protein NMR spectroscopy. *Bioinformatics*, **2009**, 25, 2085-7	7.2	85
180	rNMR: open source software for identifying and quantifying metabolites in NMR spectra. *Magnetic Resonance in Chemistry*, **2009**, 47 Suppl 1, S123-6	2.1	149
179	The Center for Eukaryotic Structural Genomics. *Journal of Structural and Functional Genomics*, **2009**, 10, 165-79		25
178	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, 95-9	3	23
177	The NMR restraints grid at BMRB for 5,266 protein and nucleic acid PDB entries. *Journal of Biomolecular NMR*, **2009**, 45, 389-96	3	25
176	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, 14138-9	16.4	9
175	Structure and dynamics of the iron-sulfur cluster assembly scaffold protein IscU and its interaction with the cochaperone HscB. *Biochemistry*, **2009**, 48, 6062-71	3.2	73

174	Hyperfine-shifted (13)C and (15)N NMR signals from Clostridium pasteurianum rubredoxin: extensive assignments and quantum chemical verification. *Journal of the American Chemical Society*, **2009**, 131, 15555-63	16.4	14
173	Metabolite identification via the Madison Metabolomics Consortium Database. *Nature Biotechnology*, **2008**, 26, 162-4	44.5	546
172	Data management in structural genomics: an overview. *Methods in Molecular Biology*, **2008**, 426, 49-79	1.4	22
171	Structure of human J-type co-chaperone HscB reveals a tetracysteine metal-binding domain. *Journal of Biological Chemistry*, **2008**, 283, 30184-92	5.4	33
170	Efficient and rapid protein expression and purification of small high disulfide containing sweet protein brazzein in E. coli. *Protein Expression and Purification*, **2008**, 58, 263-8	2	37
169	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, 7212-3	16.4	61
168	Solution structure of the iron-sulfur cluster cochaperone HscB and its binding surface for the iron-sulfur assembly scaffold protein IscU. *Biochemistry*, **2008**, 47, 9394-404	3.2	38
167	Simultaneous detection and deconvolution of congested NMR spectra containing three isotopically labeled species. *Journal of the American Chemical Society*, **2008**, 130, 7818-9	16.4	12
166	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, 15317-22	11.5	17
165	How Sweet It Is: Detailed Molecular and Functional Studies of Brazzein, a Sweet Protein and Its Analogs. *ACS Symposium Series*, **2008**, 560-572	0.4	4
164	BioMagResBank (BMRB) as a partner in the Worldwide Protein Data Bank (wwPDB): new policies affecting biomolecular NMR depositions. *Journal of Biomolecular NMR*, **2008**, 40, 153-5	3	99
163	Structure of the putative 32 kDa myrosinase-binding protein from Arabidopsis (At3g16450.1) determined by SAIL-NMR. *FEBS Journal*, **2008**, 275, 5873-84	5.7	25
162	Remediation of the protein data bank archive. *Nucleic Acids Research*, **2008**, 36, D426-33	20.1	124
161	BioMagResBank. *Nucleic Acids Research*, **2008**, 36, D402-8	20.1	1217
160	Method for determining molar concentrations of metabolites in complex solutions from two-dimensional 1H-13C NMR spectra. *Analytical Chemistry*, **2007**, 79, 9385-90	7.8	233
159	NMR analysis goes nano. *Nature Biotechnology*, **2007**, 25, 750-1	44.5	7
158	Reply to: Building meaningful models of glycoproteins. *Nature Structural and Molecular Biology*, **2007**, 14, 354-355	17.6	22
157	Solution structure of human sorting nexin 22. *Protein Science*, **2007**, 16, 807-14	6.3	13

156	Structures of proteins of biomedical interest from the Center for Eukaryotic Structural Genomics. *Journal of Structural and Functional Genomics*, **2007**, 8, 73-84		9
155	Small-scale, semi-automated purification of eukaryotic proteins for structure determination. *Journal of Structural and Functional Genomics*, **2007**, 8, 153-66		27
154	A graphical approach to tracking and reporting target status in structural genomics. *Journal of Structural and Functional Genomics*, **2007**, 8, 209-16		4
153	HIFI-C: a robust and fast method for determining NMR couplings from adaptive 3D to 2D projections. *Journal of Biomolecular NMR*, **2007**, 38, 341-51	3	12
152	Carbonyl carbon label selective (CCLS) 1H-15N HSQC experiment for improved detection of backbone 13C-15N cross peaks in larger proteins. *Journal of Biomolecular NMR*, **2007**, 39, 177-85	3	14
151	Nearest-neighbor effects on backbone alpha and beta carbon chemical shifts in proteins. *Journal of Biomolecular NMR*, **2007**, 39, 247-57	3	16
150	The worldwide Protein Data Bank (wwPDB): ensuring a single, uniform archive of PDB data. *Nucleic Acids Research*, **2007**, 35, D301-3	20.1	807
149	One-step purification of bacterially expressed recombinant transducin alpha-subunit and isotopically labeled PDE6 gamma-subunit for NMR analysis. *Protein Expression and Purification*, **2007**, 51, 187-97	2	16
148	Three-dimensional structure determined for a subunit of human tRNA splicing endonuclease (Sen15) reveals a novel dimeric fold. *Journal of Molecular Biology*, **2007**, 366, 155-64	6.5	13
147	New bioinformatics resources for metabolomics. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2007**, 157-68	1.3	42
146	Wheat germ cell-free expression system for protein production. *Current Protocols in Protein Science* , **2006**, Chapter 5, Unit 5.18	3.1	20
145	Preparation of isotopically labeled spinach acyl-acyl carrier protein for NMR structural studies. *Protein Expression and Purification*, **2006**, 46, 446-55	2	9
144	Wheat germ cell-free platform for eukaryotic protein production. *FEBS Journal*, **2006**, 273, 4160-9	5.7	56
143	Probabilistic approach to determining unbiased random-coil carbon-13 chemical shift values from the protein chemical shift database. *Journal of Biomolecular NMR*, **2006**, 35, 155-65	3	13
142	High-resolution iterative frequency identification for NMR as a general strategy for multidimensional data collection. *Journal of the American Chemical Society*, **2005**, 127, 12528-36	16.4	96
141	Solution structure of isoform 1 of Roadblock/LC7, a light chain in the dynein complex. *Journal of Molecular Biology*, **2005**, 354, 1043-51	6.5	24
140	Probing the sweet determinants of brazzein: wild-type brazzein and a tasteless variant, brazzein-ins(R18a-I18b), exhibit different pH-dependent NMR chemical shifts. *Biochemical and Biophysical Research Communications*, **2005**, 335, 256-63	3.4	5
139	Auto-induction medium for the production of [U-15N]- and [U-13C, U-15N]-labeled proteins for NMR screening and structure determination. *Protein Expression and Purification*, **2005**, 40, 268-78	2	81

138	Solution structure of At3g04780.1-des15, an Arabidopsis thaliana ortholog of the C-terminal domain of human thioredoxin-like protein. *Protein Science*, **2005**, 14, 1059-63	6.3	10
137	Macromolecular Structure Determination by NMR Spectroscopy. *Methods of Biochemical Analysis*, **2005**, 89-113		3
136	Three-dimensional structure of the AAH26994.1 protein from Mus musculus, a putative eukaryotic Urm1. *Protein Science*, **2005**, 14, 2095-102	6.3	21
135	Solution structure of a late embryogenesis abundant protein (LEA14) from Arabidopsis thaliana, a cellular stress-related protein. *Protein Science*, **2005**, 14, 2601-9	6.3	84
134	1H, 15N and 13C resonance assignments of a protein involved in the autophagy process, At4g21980.1 from Arabidopsis thaliana. *Journal of Biomolecular NMR*, **2005**, 32, 337	3	3
133	Linear analysis of carbon-13 chemical shift differences and its application to the detection and correction of errors in referencing and spin system identifications. *Journal of Biomolecular NMR*, **2005**, 32, 13-22	3	62
132	BioMagResBank databases DOCR and FRED containing converted and filtered sets of experimental NMR restraints and coordinates from over 500 protein PDB structures. *Journal of Biomolecular NMR*, **2005**, 32, 1-12	3	43
131	Protein energetic conformational analysis from NMR chemical shifts (PECAN) and its use in determining secondary structural elements. *Journal of Biomolecular NMR*, **2005**, 32, 71-81	3	97
130	Probabilistic Identification of Spin Systems and their Assignments including Coil-Helix Inference as Output (PISTACHIO). *Journal of Biomolecular NMR*, **2005**, 32, 219-33	3	52
129	1H, 15N and 13C resonance assignments of the putative Bet v 1 family protein At1g24000.1 from Arabidopsis thaliana. *Journal of Biomolecular NMR*, **2005**, 32, 335	3	1
128	RECOORD: a recalculated coordinate database of 500+ proteins from the PDB using restraints from the BioMagResBank. *Proteins: Structure, Function and Bioinformatics*, **2005**, 59, 662-72	4.2	285
127	Comparison of cell-based and cell-free protocols for producing target proteins from the Arabidopsis thaliana genome for structural studies. *Proteins: Structure, Function and Bioinformatics*, **2005**, 59, 633-43	4.2	52
126	Addressing the intrinsic disorder bottleneck in structural proteomics. *Proteins: Structure, Function and Bioinformatics*, **2005**, 59, 444-53	4.2	69
125	The CCPN data model for NMR spectroscopy: development of a software pipeline. *Proteins: Structure, Function and Bioinformatics*, **2005**, 59, 687-96	4.2	2232
124	Changes in hydrogen-bond strengths explain reduction potentials in 10 rubredoxin variants. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 14581-6	11.5	75
123	High-throughput automated platform for nuclear magnetic resonance-based structural proteomics. *Expert Review of Proteomics*, **2005**, 2, 49-55	4.2	26
122	Cell-free protein production and labeling protocol for NMR-based structural proteomics. *Nature Methods*, **2004**, 1, 149-53	21.6	123
121	Hypothetical protein At2g24940.1 from Arabidopsis thaliana has a cytochrome b5 like fold. *Journal of Biomolecular NMR*, **2004**, 30, 215-8	3	12

120	Production in two-liter beverage bottles of proteins for NMR structure determination labeled with either 15N- or 13C-15N. *Journal of Structural and Functional Genomics*, **2004**, 5, 87-93		22
119	Solution structure of a calmodulin-like calcium-binding domain from Arabidopsis thaliana. *Journal of Biomolecular NMR*, **2004**, 30, 451-6	3	8
118	Crystal structure of At2g03760, a putative steroid sulfotransferase from Arabidopsis thaliana. *Proteins: Structure, Function and Bioinformatics*, **2004**, 57, 854-7	4.2	14
117	Prevention of aggregation after refolding by balanced stabilization-destabilization: production of the Arabidopsis thaliana protein APG8a (At4g21980) for NMR structure determination. *Protein Expression and Purification*, **2004**, 34, 280-3	2	9
116	Project management system for structural and functional proteomics: Sesame. *Journal of Structural and Functional Genomics*, **2003**, 4, 11-23		80
115	Mixing apparatus for preparing NMR samples under pressure. *Journal of Magnetic Resonance*, **2003**, 164, 84-91	3	8
114	NMR determination of pKa values for Asp, Glu, His, and Lys mutants at each variable contiguous enzyme-inhibitor contact position of the turkey ovomucoid third domain. *Biochemistry*, **2003**, 42, 2847-56	3.2	39
113	Protein inhibitors of serine proteinases: role of backbone structure and dynamics in controlling the hydrolysis constant. *Biochemistry*, **2003**, 42, 5186-94	3.2	11
112	Correlation between hydrogen bond lengths and reduction potentials in Clostridium pasteurianum rubredoxin. *Journal of the American Chemical Society*, **2003**, 125, 1464-5	16.4	30
111	Two conformational states of Turkey ovomucoid third domain at low pH: three-dimensional structures, internal dynamics, and interconversion kinetics and thermodynamics. *Biochemistry*, **2003** , 42, 6380-91	3.2	15
110	Monkey electrophysiological and human psychophysical responses to mutants of the sweet protein brazzein: delineating brazzein sweetness. *Chemical Senses*, **2003**, 28, 491-8	4.8	24
109	Correlation of the sweetness of variants of the protein brazzein with patterns of hydrogen bonds detected by NMR spectroscopy. *Journal of Biological Chemistry*, **2003**, 278, 31331-9	5.4	27
108	Macromolecular structure determination by NMR spectroscopy. *Methods of Biochemical Analysis*, **2003**, 44, 89-113		20
107	Zinc-substituted Desulfovibrio gigas desulforedoxins: resolving subunit degeneracy with nonsymmetric pseudocontact shifts. *Protein Science*, **2002**, 11, 2464-70	6.3	9
106	Early formation of a beta hairpin during folding of staphylococcal nuclease H124L as detected by pulsed hydrogen exchange. *Protein Science*, **2002**, 11, 82-91	6.3	18
105	Evidence for a strong hydrogen bond in the catalytic dyad of transition-state analogue inhibitor complexes of chymotrypsin from proton-triton NMR isotope shifts. *Journal of the American Chemical Society*, **2002**, 124, 4196-7	16.4	27
104	Quantum chemical calculations on structural models of the catalytic site of chymotrypsin: comparison of calculated results with experimental data from NMR spectroscopy. *Journal of the American Chemical Society*, **2002**, 124, 14373-81	16.4	23
103	Trans-hydrogen-bond (h2)J(NN) and (h1)J(NH) couplings in the DNA A-T base pair: natural bond orbital analysis. *Journal of the American Chemical Society*, **2002**, 124, 1190-1	16.4	41

102	(13)C[(13)C] 2D NMR: a novel strategy for the study of paramagnetic proteins with slow electronic relaxation rates. *Journal of the American Chemical Society*, **2002**, 124, 3204-5	16.4	70
101	NMR chemical shift mapping of the binding site of a protein proteinase inhibitor: changes in the (1)H, (13)C and (15)N NMR chemical shifts of turkey ovomucoid third domain upon binding to bovine chymotrypsin A(alpha). *Journal of Molecular Recognition*, **2001**, 14, 166-71	2.6	14
100	Solution structure of the toluene 4-monooxygenase effector protein (T4moD). *Biochemistry*, **2001**, 40, 3512-24	3.2	26
99	Electron-nuclear interactions in two prototypical [2Fe-2S] proteins: selective (chiral) deuteration and analysis of (1)H and (2)H NMR signals from the alpha and beta hydrogens of cysteinyl residues that ligate the iron in the active sites of human ferredoxin and Anabaena 7120 vegetative ferredoxin. *Archives of Biochemistry and Biophysics*, **2000**, 373, 328-34	4.1	13
98	Sweetness determinant sites of brazzein, a small, heat-stable, sweet-tasting protein. *Archives of Biochemistry and Biophysics*, **2000**, 376, 259-65	4.1	77
97	NMR studies of retinoid-protein interactions: the conformation of [13C]-beta-ionones bound to beta-lactoglobulin B. *Pharmaceutical Research*, **1999**, 16, 651-9	4.5	8
96	Redox-Dependent Magnetic Alignment of Clostridium pasteurianum Rubredoxin: Measurement of Magnetic Susceptibility Anisotropy and Prediction of Pseudocontact Shift Contributions. *Journal of the American Chemical Society*, **1999**, 121, 4677-4683	16.4	33
95	Detection and classification of hyperfine-shifted 1H, 2H, and 15N resonances of the Rieske ferredoxin component of toluene 4-monooxygenase. *Biochemistry*, **1999**, 38, 727-39	3.2	29
94	Properties of the His57-Asp102 dyad of rat trypsin D189S in the zymogen, activated enzyme, and alpha1-proteinase inhibitor complexed forms. *Archives of Biochemistry and Biophysics*, **1999**, 362, 254-64	4.1	16
93	Practical model fitting approaches to the direct extraction of NMR parameters simultaneously from all dimensions of multidimensional NMR spectra. *Journal of Biomolecular NMR*, **1998**, 12, 277-97	3	18
92	Complete 1H and partial 13C resonance assignments at 37 and 22 degrees C for brazzein, an intensely sweet protein. *Journal of Biomolecular NMR*, **1998**, 11, 231-2	3	8
91	Recommendations for the presentation of NMR structures of proteins and nucleic acids. IUPAC-IUBMB-IUPAB Inter-Union Task Group on the Standardization of Data Bases of Protein and Nucleic Acid Structures Determined by NMR Spectroscopy. *Journal of Biomolecular NMR*, **1998**, 12, 1-23	3	316
90	Solution structure of the thermostable sweet-tasting protein brazzein. *Nature Structural Biology*, **1998**, 5, 427-31		94
89	Recommendations for the presentation of NMR structures of proteins and nucleic acids--IUPAC-IUBMB-IUPAB Inter-Union Task Group on the standardization of data bases of protein and nucleic acid structures determined by NMR spectroscopy. *FEBS Journal*, **1998**, 256, 1-15		119
88	Amplification of One-Bond1H/2H Isotope Effects on15N Chemical Shifts inClostridium pasteurianumRubredoxin by Fermi-Contact Effects through Hydrogen Bonds. *Journal of the American Chemical Society*, **1998**, 120, 4893-4894	16.4	23
87	Inadequacies of the Point-Dipole Approximation for Describing Electron–Nuclear Interactions in Paramagnetic Proteins: Hybrid Density Functional Calculations and the Analysis of NMR Relaxation of High-Spin Iron(III) Rubredoxin. *Journal of Physical Chemistry B*, **1998**, 102, 8300-8305	3.4	26
86	NMR Investigations of Clostridium pasteurianum Rubredoxin. Origin of Hyperfine 1H, 2H, 13C, and 15N NMR Chemical Shifts in Iron–Sulfur Proteins As Determined by Comparison of Experimental Data with Hybrid Density Functional Calculations. *Journal of the American Chemical Society*, **1998**, 120, 4806-4814	16.4	86
85	Recommendations for the presentation of NMR structures of proteins and nucleic acids (IUPAC Recommendations 1998). *Pure and Applied Chemistry*, **1998**, 70, 117-142	2.1	263

84	Probing the influence of mutations on the stability of a ferredoxin by mass spectrometry. *The Protein Journal*, **1997**, 16, 527-32		11
83	Assignment of 1H, 13C, and 15N signals of oxidized Clostridium pasteurianum rubredoxin. *Journal of Biomolecular NMR*, **1997**, 10, 409-10	3	13
82	Assignment of 1H, 13C, and 15N signals of reduced Clostridium pasteurianum rubredoxin: oxidation state-dependent changes in chemical shifts and relaxation rates. *Journal of Biomolecular NMR*, **1997** , 10, 411-2	3	14
81	Solution structures of staphylococcal nuclease from multidimensional, multinuclear NMR: nuclease-H124L and its ternary complex with Ca2+ and thymidine-3P,5Pbisphosphate. *Journal of Biomolecular NMR*, **1997**, 10, 143-64	3	26
80	Protonation-state dependence of hydrogen bond strengths and exchange rates in a serine protease catalytic triad: bovine chymotrypsinogen A. *Biochemistry*, **1996**, 35, 11092-7	3.2	92
79	High-pressure denaturation of staphylococcal nuclease proline-to-glycine substitution mutants. *Biochemistry*, **1996**, 35, 3857-64	3.2	48
78	Effects of experimentally achievable improvements in the quality of NMR distance constraints on the accuracy of calculated protein structures. *Journal of Molecular Biology*, **1996**, 258, 334-48	6.5	13
77	Engineered disulfide bonds in staphylococcal nuclease: effects on the stability and conformation of the folded protein. *Biochemistry*, **1996**, 35, 10328-38	3.2	41
76	Coupling between trans/cis proline isomerization and protein stability in staphylococcal nuclease. *Protein Science*, **1996**, 5, 1907-16	6.3	38
75	Approaches to the Determination of More Accurate Cross-Relaxation Rates and the Effects of Improved Distance Constraints on Protein Solution Structures **1996**, 73-111		
74	Theory and application of the maximum likelihood principle to NMR parameter estimation of multidimensional NMR data. *Journal of Biomolecular NMR*, **1995**, 5, 245-58	3	56
73	1H, 13C and 15N chemical shift referencing in biomolecular NMR. *Journal of Biomolecular NMR*, **1995**, 6, 135-40	3	2054
72	Mutations of surface residues in Anabaena vegetative and heterocyst ferredoxin that affect thermodynamic stability as determined by guanidine hydrochloride denaturation. *Protein Science*, **1995**, 4, 58-64	6.3	12
71	Comparison of the accuracy of protein solution structures derived from conventional and network-edited NOESY data. *Protein Science*, **1995**, 4, 2289-99	6.3	35
70	Ab Initio Calculations of Protium/Deuterium Fractionation Factors in O2H5+ Clusters. *The Journal of Physical Chemistry*, **1995**, 99, 8013-8016		15
69	Detection and Classification of Hyperfine-Shifted 1H, 2H, and 15N Resonances from the Four Cysteines That Ligate Iron in Oxidized and Reduced Clostridium pasteurianum Rubredoxin. *Journal of the American Chemical Society*, **1995**, 117, 5347-5350	16.4	57
68	Theoretical Studies of Protium/Deuterium Fractionation Factors and Cooperative Hydrogen Bonding in Peptides. *Journal of the American Chemical Society*, **1995**, 117, 9619-9624	16.4	40
67	NOE Measurements in the Absence of Spin Diffusion: Application to Methylene Groups in Proteins and Effects on Local Structural Parameters. *Journal of the American Chemical Society*, **1995**, 117, 5610-5611	16.4	13

66	Protein engineering for the elucidation of the mechanism of electron transfer in redox proteins. *Biochemical Society Transactions*, **1994**, 22, 796-800	5.1	8
65	Calculations of one-, two- and three-bond nuclear spin-spin couplings in a model peptide and correlations with experimental data. *Journal of Biomolecular NMR*, **1994**, 4, 519-42	3	42
64	Two-dimensional exchange spectroscopy of proteins. *Methods in Enzymology*, **1994**, 239, 106-44	1.7	29
63	Practical introduction to theory and implementation of multinuclear, multidimensional nuclear magnetic resonance experiments. *Methods in Enzymology*, **1994**, 239, 3-79	1.7	71
62	Solution structure of turkey ovomucoid third domain as determined from nuclear magnetic resonance data. *Journal of Molecular Biology*, **1994**, 242, 203-14	6.5	30
61	Solution structure of reactive-site hydrolyzed turkey ovomucoid third domain by nuclear magnetic resonance and distance geometry methods. *Journal of Molecular Biology*, **1994**, 242, 215-30	6.5	10
60	Hydrogen bonding in proteins as studied by amide hydrogen D/H fractionation factors: application to staphylococcal nuclease. *Biochemistry*, **1994**, 33, 1029-36	3.2	88
59	Hydrogen exchange in unligated and ligated staphylococcal nuclease. *Biochemistry*, **1993**, 32, 11022-8	3.2	87
58	Effects of amino acid substitutions on the pressure denaturation of staphylococcal nuclease as monitored by fluorescence and nuclear magnetic resonance spectroscopy. *Biochemistry*, **1993**, 32, 5222-32	3.2	136
57	Calculation of nuclear spin-spin coupling constants with ab initio molecular orbital wave functions. *The Journal of Physical Chemistry*, **1993**, 97, 11657-11665		23
56	Overexpression and purification of avian ovomucoid third domains in Escherichia coli. *Protein Engineering, Design and Selection*, **1993**, 6, 221-7	1.9	13
55	A perifusion loop-gap resonator NMR probe for aerobic cell suspensions. *Magnetic Resonance in Medicine*, **1993**, 29, 563-6	4.4	2
54	Topological Editing of Cross-Relaxation Networks. *Israel Journal of Chemistry*, **1992**, 32, 245-256	3.4	13
53	Structure of the oxidized long-chain flavodoxin from Anabaena 7120 at 2 A resolution. *Protein Science*, **1992**, 1, 1413-27	6.3	98
52	Elucidation of amino acid spin systems in proteins and determination of heteronuclear coupling constants by carbon-proton-proton three-dimensional NMR. *Journal of Magnetic Resonance*, **1991**, 92, 434-438		12
51	A relational database for sequence-specific protein NMR data. *Journal of Biomolecular NMR*, **1991**, 1, 217-36	3	332
50	Two-dimensional magnetization exchange spectroscopy of Anabaena 7120 ferredoxin. Nuclear Overhauser effect and electron self-exchange cross peaks from amino acid residues surrounding the 2Fe-2S* cluster. *Biochemistry*, **1991**, 30, 7363-8	3.2	48
49	1H NMR spectra of vertebrate [2Fe-2S] ferredoxins. Hyperfine resonances suggest different electron delocalization patterns from plant ferredoxins. *Biochemistry*, **1991**, 30, 9078-83	3.2	30

48	Refinement of the NMR solution structure of a protein to remove distortions arising from neglect of internal motion. *Biochemistry*, **1991**, 30, 3807-11	3.2	27
47	Two-dimensional spectra of intact tissue: homonuclear Hartmann-Hahn spectroscopy provides increased sensitivity and information content as compared to COSY. *Magnetic Resonance in Medicine*, **1990**, 15, 142-51	4.4	11
46	Coupling between local structure and global stability of a protein: mutants of staphylococcal nuclease. *Biochemistry*, **1990**, 29, 4516-25	3.2	53
45	Elimination of cross-relaxation effects from two-dimensional chemical-exchange spectra of macromolecules. *Journal of the American Chemical Society*, **1990**, 112, 2574-2577	16.4	40
44	1H, 13C, and 15N resonance assignments for a ferrocytochrome c553 heme by multinuclear NMR spectroscopy. *Archives of Biochemistry and Biophysics*, **1990**, 276, 369-73	4.1	11
43	Two-dimensional correlated spectroscopy (COSY) of intact frog muscle: spectral pattern characterization and lactate quantitation. *Magnetic Resonance in Medicine*, **1989**, 11, 316-30	4.4	28
42	Concerted two-dimensional NMR approaches to hydrogen-1, carbon-13, and nitrogen-15 resonance assignments in proteins. *Biochemistry*, **1989**, 28, 230-6	3.2	56
41	Hydrogen-1 NMR evidence for three interconverting forms of staphylococcal nuclease: effects of mutations and solution conditions on their distribution. *Biochemistry*, **1989**, 28, 204-11	3.2	51
40	Staphylococcal nuclease active-site amino acids: pH dependence of tyrosines and arginines by 13C NMR and correlation with kinetic studies. *Biochemistry*, **1989**, 28, 2116-24	3.2	20
39	Two-dimensional NMR studies of Kazal proteinase inhibitors. 1. Sequence-specific assignments and secondary structure of turkey ovomucoid third domain. *Biochemistry*, **1988**, 27, 2519-29	3.2	34
38	Correlation of carbon-13 and nitrogen-15 chemical shifts in selectively and uniformly labeled proteins by heteronuclear two-dimensional NMR spectroscopy. *Journal of the American Chemical Society*, **1988**, 110, 6256-8	16.4	92
37	NMR assignments of the four histidines of staphylococcal nuclease in native and denatured states. *Biochemistry*, **1988**, 27, 2158-65	3.2	41
36	Two-dimensional NMR studies of Kazal proteinase inhibitors. 2. Sequence-specific assignments and secondary structure of reactive site modified turkey ovomucoid third domain. *Biochemistry*, **1988**, 27, 2529-39	3.2	16
35	Detailed analysis of carbon-13 NMR spin systems in a uniformly carbon-13 enriched protein: flavodoxin from Anabaena 7120. *Journal of the American Chemical Society*, **1988**, 110, 4095-4096	16.4	25
34	Flavodoxin from Anabaena 7120: uniform nitrogen-15 enrichment and hydrogen-1, nitrogen-15, and phosphorus-31 NMR investigations of the flavin mononucleotide binding site in the reduced and oxidized states. *Biochemistry*, **1988**, 27, 136-42	3.2	47
33	Two-dimensional NMR strategies for carbon-carbon correlations and sequence-specific assignments in carbon-13 labeled proteins. *Journal of the American Chemical Society*, **1988**, 110, 4093-4095	16.4	46
32	NMR in Biology and Medicine edited by Shu Chien and Chien Ho. *Medical Physics*, **1987**, 14, 891-892	4.4	
31	One- and two-dimensional NMR spectral analysis of the consequences of single amino acid replacements in proteins. *Journal of Cellular Biochemistry*, **1986**, 30, 291-309	4.7	8

30	Hydrogen-1 nuclear magnetic resonance investigation of high-potential iron-sulfur proteins from Ectothiorhodospira halophila and Ectothiorhodospira vacuolata: a comparative study of hyperfine-shifted resonances. *Biochemistry*, **1986**, 25, 60-7	3.2	42
29	Turnip yellow mosaic virus and its capsid have thermal stabilities with opposite pH dependence: studies by differential scanning calorimetry and 31P nuclear magnetic resonance spectroscopy. *Virology*, **1985**, 146, 213-20	3.6	11
28	Water permeability of chloroplast envelope membranes. In vivo measurement by saturation-transfer NMR. *FEBS Letters*, **1985**, 183, 353-8	3.8	26
27	Natural abundance 13C NMR spectra of human muscle, normal and diseased. *Magnetic Resonance in Medicine*, **1984**, 1, 30-43	4.4	29
26	1H NMR of intact muscle at 11 T. *FEBS Letters*, **1984**, 165, 231-7	3.8	47
25	Nuclear magnetic resonance studies of two-iron-two-sulfur ferredoxins. 5. Hyperfine-shifted peaks in proton and carbon-13 spectra. *Biochemistry*, **1983**, 22, 6008-6010	3.2	17
24	Connectivity of proton and carbon spectra of the blue copper protein, plastocyanin, established by two-dimensional nuclear magnetic resonance. *FEBS Letters*, **1983**, 162, 52-56	3.8	34
23	High-resolution proton nuclear magnetic resonance studies of the nickel(II) derivative of azurin. *Biochemistry*, **1982**, 21, 6253-8	3.2	42
22	Proton NMR spectroscopy of the active site histidine of alpha-lytic proteinase. Effects of adjacent 13C and 15N labels. *FEBS Letters*, **1982**, 138, 233-5	3.8	8
21	Heteronuclear (proton, carbon-13) two-dimensional chemical shift correlation NMR spectroscopy of a protein. Ferredoxin from Anabaena variabilis. *Journal of the American Chemical Society*, **1982**, 104, 4010-4011	16.4	28
20	Lack of evidence for a tetrahedral intermediate in the hydrolysis of nitroanilide substrates by serine proteinases. Subzero-temperature stopped-flow experiments. *FEBS Journal*, **1981**, 120, 477-85		37
19	Soybean trypsin inhibitor (Kunitz) and its complex with trypsin. Carbon-13 nuclear magnetic resonance studies of the reactive site arginine. *Biochemistry*, **1980**, 19, 5703	3.2	51
18	(Diisopropylphosphoryl)serine proteinases. Proton and phosphorus-31 nuclear magnetic resonance-pH titration studies. *Biochemistry*, **1979**, 18, 4108-16	3.2	44
17	Hydrogen bonds in serine proteinases and their complexes with protein proteinase inhibitors. Proton nuclear magnetic resonance studies. *Biochemistry*, **1978**, 17, 4648-56	3.2	56
16	Zymogen activation in serine proteinases. Proton magnetic resonance pH titration studies of the two histidines of bovine chymotrypsinogen A and chymotrypsin Aalpha. *Biochemistry*, **1978**, 17, 4627-40	3.2	83
15	Active site in zymogens. Proton magnetic resonance pH titration curves of histidine-57 in porcine and bovine trypsinogens and in their complexes with bovine pancreatic trypsin inhibitor (Kunitz). *Biochemistry*, **1978**, 17, 4640-7	3.2	28
14	Spinach plastocyanin: comparison of reduced and oxidized forms by natural abundance carbon-13 nuclear magnetic resonance spectroscopy. *Biochemical and Biophysical Research Communications*, **1977**, 78, 106-14	3.4	15
13	The charge-relay system of serine proteinases: proton magnetic resonance titration studies of the four histidines of porcine trypsin. *Journal of Molecular Biology*, **1976**, 102, 487-509	6.5	53

12	Correlation proton magnetic resonance studies at 250 MHz of bovine pancreatic ribonuclease. I. Reinvestigation of the histidine peak assignments. *Biochemistry*, **1975**, 14, 3546-54	3.2	143
11	Assignment of the histidine proton magnetic resonance peaks of soybean trypsin inhibitor (Kunitz) by a differertial deuterium exchange technique. *Biochemistry*, **1975**, 14, 3234-7	3.2	18
10	Correlation proton magnetic resonance studies at 250 MHz of bovine pancreatic ribonuclease. III. Mutual electrostatic interaction between histidine residues 12 and 119. *Biochemistry*, **1975**, 14, 3562-6	3.2	38
9	Nuclear magnetic resonance studies of the copper binding sites of blue copper proteins: oxidized, reduced, and apoplastocyanin. *Biochemistry*, **1975**, 14, 4428-33	3.2	75
8	Observation of histidine residues in proteins by nuclear magnetic resonance spectroscopy. *Accounts of Chemical Research*, **1975**, 8, 70-80	24.3	379
7	High-resolution proton magnetic resonance studies of two trypsin inhibitors: soybean trypsin inhibitor (Kunitz) and ovomucoid (hen egg white). *Annals of the New York Academy of Sciences*, **1973** , 222, 347-73	6.5	14
6	Nuclear magnetic resonance studies of trypsin inhibitors. Histidines of virgin and modified soybean trypsin inhibitor (Kunitz). *Biochemistry*, **1973**, 12, 2245-50	3.2	63
5	Spin-Lattice Relaxation Measurements in Slowly Relaxing Complex Spectra. *Journal of Chemical Physics*, **1971**, 55, 3604-3605	3.9	229
4	Nuclear magnetic resonance studies of helix-coil transitions in polyamino acids. *Journal of Molecular Biology*, **1967**, 27, 25-40	6.5	108
3	Structural Proteomics99-128		
2	Robust nomenclature and software for enhanced reproducibility in molecular modeling of small molecules		2
1	Chapter 5:Acquisition and Post-processing of Reduced Dimensionality NMR Experiments. *New Developments in NMR*,96-118	0.9	2