

# John Lute Markley

## List of Publications by Citations

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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
3 <sup>17</sup>	The CCPN data model for NMR spectroscopy: development of a software pipeline. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2005</b> , 59, 687-96	4.2	2232
3 <sup>16</sup>	<sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N chemical shift referencing in biomolecular NMR. <i>Journal of Biomolecular NMR</i> , <b>1995</b> , 6, 135-40	3	2054
3 <sup>15</sup>	BioMagResBank. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D402-8	20.1	1217
3 <sup>14</sup>	NMRFAM-SPARKY: enhanced software for biomolecular NMR spectroscopy. <i>Bioinformatics</i> , <b>2015</b> , 31, 1325-7	7.2	879
3 <sup>13</sup>	The worldwide Protein Data Bank (wwPDB): ensuring a single, uniform archive of PDB data. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D301-3	20.1	807
3 <sup>12</sup>	Metabolite identification via the Madison Metabolomics Consortium Database. <i>Nature Biotechnology</i> , <b>2008</b> , 26, 162-4	44.5	546
3 <sup>11</sup>	The future of NMR-based metabolomics. <i>Current Opinion in Biotechnology</i> , <b>2017</b> , 43, 34-40	11.4	500
3 <sup>10</sup>	Observation of histidine residues in proteins by nuclear magnetic resonance spectroscopy. <i>Accounts of Chemical Research</i> , <b>1975</b> , 8, 70-80	24.3	379
3 <sup>09</sup>	A relational database for sequence-specific protein NMR data. <i>Journal of Biomolecular NMR</i> , <b>1991</b> , 1, 217-36	3	332
3 <sup>08</sup>	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. <i>Journal of Biomolecular NMR</i> , <b>1998</b> , 12, 1-23	3	316
3 <sup>07</sup>	Protein Data Bank: the single global archive for 3D macromolecular structure data. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D520-D528	20.1	308
3 <sup>06</sup>	RECOORD: a recalculated coordinate database of 500+ proteins from the PDB using restraints from the BioMagResBank. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2005</b> , 59, 662-72	4.2	285
3 <sup>05</sup>	Protein Data Bank (PDB): The Single Global Macromolecular Structure Archive. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1607, 627-641	1.4	271
3 <sup>04</sup>	Recommendations for the presentation of NMR structures of proteins and nucleic acids (IUPAC Recommendations 1998). <i>Pure and Applied Chemistry</i> , <b>1998</b> , 70, 117-142	2.1	263
3 <sup>03</sup>	Method for determining molar concentrations of metabolites in complex solutions from two-dimensional <sup>1</sup> H- <sup>13</sup> C NMR spectra. <i>Analytical Chemistry</i> , <b>2007</b> , 79, 9385-90	7.8	233
3 <sup>02</sup>	Spin-Lattice Relaxation Measurements in Slowly Relaxing Complex Spectra. <i>Journal of Chemical Physics</i> , <b>1971</b> , 55, 3604-3605	3.9	229
3 <sup>01</sup>	Probabilistic interaction network of evidence algorithm and its application to complete labeling of peak lists from protein NMR spectroscopy. <i>PLoS Computational Biology</i> , <b>2009</b> , 5, e1000307	5	162

300	rNMR: open source software for identifying and quantifying metabolites in NMR spectra. <i>Magnetic Resonance in Chemistry</i> , <b>2009</b> , 47 Suppl 1, S123-6	2.1	149
299	Correlation proton magnetic resonance studies at 250 MHz of bovine pancreatic ribonuclease. I. Reinvestigation of the histidine peak assignments. <i>Biochemistry</i> , <b>1975</b> , 14, 3546-54	3.2	143
298	Effects of amino acid substitutions on the pressure denaturation of staphylococcal nuclease as monitored by fluorescence and nuclear magnetic resonance spectroscopy. <i>Biochemistry</i> , <b>1993</b> , 32, 5222-32	3.2	136
297	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , <b>2015</b> , 23, 1156-67	5.2	131
296	Remediation of the protein data bank archive. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D426-33	20.1	124
295	Cell-free protein production and labeling protocol for NMR-based structural proteomics. <i>Nature Methods</i> , <b>2004</b> , 1, 149-53	21.6	123
294	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. <i>FEBS Journal</i> , <b>1998</b> , 256, 1-15		119
293	Recommendations of the wwPDB NMR Validation Task Force. <i>Structure</i> , <b>2013</b> , 21, 1563-70	5.2	117
292	Nuclear magnetic resonance studies of helix-coil transitions in polyamino acids. <i>Journal of Molecular Biology</i> , <b>1967</b> , 27, 25-40	6.5	108
291	BioMagResBank (BMRB) as a partner in the Worldwide Protein Data Bank (wwPDB): new policies affecting biomolecular NMR depositions. <i>Journal of Biomolecular NMR</i> , <b>2008</b> , 40, 153-5	3	99
290	Structure of the oxidized long-chain flavodoxin from Anabaena 7120 at 2 Å resolution. <i>Protein Science</i> , <b>1992</b> , 1, 1413-27	6.3	98
289	Protein energetic conformational analysis from NMR chemical shifts (PECAN) and its use in determining secondary structural elements. <i>Journal of Biomolecular NMR</i> , <b>2005</b> , 32, 71-81	3	97
288	High-resolution iterative frequency identification for NMR as a general strategy for multidimensional data collection. <i>Journal of the American Chemical Society</i> , <b>2005</b> , 127, 12528-36	16.4	96
287	Solution structure of the thermostable sweet-tasting protein brazzein. <i>Nature Structural Biology</i> , <b>1998</b> , 5, 427-31		94
286	Protonation-state dependence of hydrogen bond strengths and exchange rates in a serine protease catalytic triad: bovine chymotrypsinogen A. <i>Biochemistry</i> , <b>1996</b> , 35, 11092-7	3.2	92
285	Correlation of carbon-13 and nitrogen-15 chemical shifts in selectively and uniformly labeled proteins by heteronuclear two-dimensional NMR spectroscopy. <i>Journal of the American Chemical Society</i> , <b>1988</b> , 110, 6256-8	16.4	92
284	Role of band 3 in regulating metabolic flux of red blood cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 18515-20	11.5	88
283	Hydrogen bonding in proteins as studied by amide hydrogen D/H fractionation factors: application to staphylococcal nuclease. <i>Biochemistry</i> , <b>1994</b> , 33, 1029-36	3.2	88

282	Key amino acid residues involved in multi-point binding interactions between brazzein, a sweet protein, and the T1R2-T1R3 human sweet receptor. <i>Journal of Molecular Biology</i> , <b>2010</b> , 398, 584-99	6.5	87
281	Hydrogen exchange in unligated and ligated staphylococcal nuclease. <i>Biochemistry</i> , <b>1993</b> , 32, 11022-8	3.2	87
280	OneDep: Unified wwPDB System for Deposition, Biocuration, and Validation of Macromolecular Structures in the PDB Archive. <i>Structure</i> , <b>2017</b> , 25, 536-545	5.2	86
279	NMR Investigations of Clostridium pasteurianum Rubredoxin. Origin of Hyperfine <sup>1</sup> H, <sup>2</sup> H, <sup>13</sup> C, and <sup>15</sup> N NMR Chemical Shifts in Iron-Sulfur Proteins As Determined by Comparison of Experimental Data with Hybrid Density Functional Calculations <i>Journal of the American Chemical Society</i> , <b>1998</b> , 120, 4806-4814	16.4	86
278	The Protein Data Bank archive as an open data resource. <i>Journal of Computer-Aided Molecular Design</i> , <b>2014</b> , 28, 1009-14	4.2	85
277	PINE-SPARKY: graphical interface for evaluating automated probabilistic peak assignments in protein NMR spectroscopy. <i>Bioinformatics</i> , <b>2009</b> , 25, 2085-7	7.2	85
276	Solution structure of a late embryogenesis abundant protein (LEA14) from Arabidopsis thaliana, a cellular stress-related protein. <i>Protein Science</i> , <b>2005</b> , 14, 2601-9	6.3	84
275	Zymogen activation in serine proteinases. Proton magnetic resonance pH titration studies of the two histidines of bovine chymotrypsinogen A and chymotrypsin Aalpha. <i>Biochemistry</i> , <b>1978</b> , 17, 4627-40	3.2	83
274	Auto-induction medium for the production of [U- <sup>15</sup> N]- and [U- <sup>13</sup> C, U- <sup>15</sup> N]-labeled proteins for NMR screening and structure determination. <i>Protein Expression and Purification</i> , <b>2005</b> , 40, 268-78	2	81
273	Project management system for structural and functional proteomics: Sesame. <i>Journal of Structural and Functional Genomics</i> , <b>2003</b> , 4, 11-23		80
272	Sweetness determinant sites of brazzein, a small, heat-stable, sweet-tasting protein. <i>Archives of Biochemistry and Biophysics</i> , <b>2000</b> , 376, 259-65	4.1	77
271	[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. <i>Journal of the American Chemical Society</i> , <b>2013</b> , 135, 8117-20	16.4	76
270	Changes in hydrogen-bond strengths explain reduction potentials in 10 rubredoxin variants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 14581-6	11.5	75
269	Nuclear magnetic resonance studies of the copper binding sites of blue copper proteins: oxidized, reduced, and apoplastocyanin. <i>Biochemistry</i> , <b>1975</b> , 14, 4428-33	3.2	75
268	Structure and dynamics of the iron-sulfur cluster assembly scaffold protein IscU and its interaction with the cochaperone HscB. <i>Biochemistry</i> , <b>2009</b> , 48, 6062-71	3.2	73
267	Dynamical Structures of Hsp70 and Hsp70-Hsp40 Complexes. <i>Structure</i> , <b>2016</b> , 24, 1014-30	5.2	71
266	Characterization of the [2Fe-2S] cluster of Escherichia coli transcription factor IscR. <i>Biochemistry</i> , <b>2012</b> , 51, 4453-62	3.2	71
265	Deconvolution of two-dimensional NMR spectra by fast maximum likelihood reconstruction: application to quantitative metabolomics. <i>Analytical Chemistry</i> , <b>2011</b> , 83, 4871-80	7.8	71

264	Practical introduction to theory and implementation of multinuclear, multidimensional nuclear magnetic resonance experiments. <i>Methods in Enzymology</i> , <b>1994</b> , 239, 3-79	1.7	71
263	(13)C[(13)C] 2D NMR: a novel strategy for the study of paramagnetic proteins with slow electronic relaxation rates. <i>Journal of the American Chemical Society</i> , <b>2002</b> , 124, 3204-5	16.4	70
262	Addressing the intrinsic disorder bottleneck in structural proteomics. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2005</b> , 59, 444-53	4.2	69
261	Nuclear magnetic resonance studies of trypsin inhibitors. Histidines of virgin and modified soybean trypsin inhibitor (Kunitz). <i>Biochemistry</i> , <b>1973</b> , 12, 2245-50	3.2	63
260	Mitochondrial metabolism promotes adaptation to proteotoxic stress. <i>Nature Chemical Biology</i> , <b>2019</b> , 15, 681-689	11.7	62
259	Disordered form of the scaffold protein IscU is the substrate for iron-sulfur cluster assembly on cysteine desulfurase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 454-9	11.5	62
258	Linear analysis of carbon-13 chemical shift differences and its application to the detection and correction of errors in referencing and spin system identifications. <i>Journal of Biomolecular NMR</i> , <b>2005</b> , 32, 13-22	3	62
257	Direct NMR detection of the binding of functional ligands to the human sweet receptor, a heterodimeric family 3 GPCR. <i>Journal of the American Chemical Society</i> , <b>2008</b> , 130, 7212-3	16.4	61
256	PDB-Dev: a Prototype System for Depositing Integrative/Hybrid Structural Models. <i>Structure</i> , <b>2017</b> , 25, 1317-1318	5.2	58
255	Regulation of estrogen receptor [N-terminus conformation and function by peptidyl prolyl isomerase Pin1. <i>Molecular and Cellular Biology</i> , <b>2012</b> , 32, 445-57	4.8	58
254	Metamorphic protein IscU alternates conformations in the course of its role as the scaffold protein for iron-sulfur cluster biosynthesis and delivery. <i>FEBS Letters</i> , <b>2013</b> , 587, 1172-9	3.8	57
253	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. <i>Journal of the American Chemical Society</i> , <b>1995</b> , 117, 5347-5350	16.4	57
252	Wheat germ cell-free platform for eukaryotic protein production. <i>FEBS Journal</i> , <b>2006</b> , 273, 4160-9	5.7	56
251	Theory and application of the maximum likelihood principle to NMR parameter estimation of multidimensional NMR data. <i>Journal of Biomolecular NMR</i> , <b>1995</b> , 5, 245-58	3	56
250	Concerted two-dimensional NMR approaches to hydrogen-1, carbon-13, and nitrogen-15 resonance assignments in proteins. <i>Biochemistry</i> , <b>1989</b> , 28, 230-6	3.2	56
249	Hydrogen bonds in serine proteinases and their complexes with protein proteinase inhibitors. Proton nuclear magnetic resonance studies. <i>Biochemistry</i> , <b>1978</b> , 17, 4648-56	3.2	56
248	Coupling between local structure and global stability of a protein: mutants of staphylococcal nuclease. <i>Biochemistry</i> , <b>1990</b> , 29, 4516-25	3.2	53
247	The charge-relay system of serine proteinases: proton magnetic resonance titration studies of the four histidines of porcine trypsin. <i>Journal of Molecular Biology</i> , <b>1976</b> , 102, 487-509	6.5	53

246	Biophysical characterization of Eynuclein and its controversial structure. <i>Intrinsically Disordered Proteins</i> , <b>2013</b> , 1, 18-39		52
245	Probabilistic Identification of Spin Systems and their Assignments including Coil-Helix Inference as Output (PISTACHIO). <i>Journal of Biomolecular NMR</i> , <b>2005</b> , 32, 219-33	3	52
244	Comparison of cell-based and cell-free protocols for producing target proteins from the Arabidopsis thaliana genome for structural studies. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2005</b> , 59, 633-43	4.2	52
243	Hydrogen-1 NMR evidence for three interconverting forms of staphylococcal nuclease: effects of mutations and solution conditions on their distribution. <i>Biochemistry</i> , <b>1989</b> , 28, 204-11	3.2	51
242	Soybean trypsin inhibitor (Kunitz) and its complex with trypsin. Carbon-13 nuclear magnetic resonance studies of the reactive site arginine. <i>Biochemistry</i> , <b>1980</b> , 19, 5703	3.2	51
241	High-pressure denaturation of staphylococcal nuclease proline-to-glycine substitution mutants. <i>Biochemistry</i> , <b>1996</b> , 35, 3857-64	3.2	48
240	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 <sup>+</sup> cluster. <i>Biochemistry</i> , <b>1991</b> , 30, 7363-8	3.2	48
239	Role of IscX in iron-sulfur cluster biogenesis in Escherichia coli. <i>Journal of the American Chemical Society</i> , <b>2014</b> , 136, 7933-42	16.4	47
238	Molecular insights into the recognition of N-terminal histone modifications by the BRPF1 bromodomain. <i>Journal of Molecular Biology</i> , <b>2014</b> , 426, 1661-76	6.5	47
237	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. <i>Biochemistry</i> , <b>1988</b> , 27, 136-42	3.2	47
236	<sup>1</sup> H NMR of intact muscle at 11 T. <i>FEBS Letters</i> , <b>1984</b> , 165, 231-7	3.8	47
235	Human Mitochondrial Ferredoxin 1 (FDX1) and Ferredoxin 2 (FDX2) Both Bind Cysteine Desulfurase and Donate Electrons for Iron-Sulfur Cluster Biosynthesis. <i>Biochemistry</i> , <b>2017</b> , 56, 487-499	3.2	46
234	Two-dimensional NMR strategies for carbon-carbon correlations and sequence-specific assignments in carbon-13 labeled proteins. <i>Journal of the American Chemical Society</i> , <b>1988</b> , 110, 4093-4095	16.4	46
233	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). <i>Journal of Biological Chemistry</i> , <b>2013</b> , 288, 28755-70	5.4	44
232	(Diisopropylphosphoryl)serine proteinases. Proton and phosphorus-31 nuclear magnetic resonance-pH titration studies. <i>Biochemistry</i> , <b>1979</b> , 18, 4108-16	3.2	44
231	Interactions between the human sweet-sensing T1R2-T1R3 receptor and sweeteners detected by saturation transfer difference NMR spectroscopy. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , <b>2010</b> , 1798, 82-6	3.8	43
230	BioMagResBank databases DOCR and FRED containing converted and filtered sets of experimental NMR restraints and coordinates from over 500 protein PDB structures. <i>Journal of Biomolecular NMR</i> , <b>2005</b> , 32, 1-12	3	43
229	Calculations of one-, two- and three-bond nuclear spin-spin couplings in a model peptide and correlations with experimental data. <i>Journal of Biomolecular NMR</i> , <b>1994</b> , 4, 519-42	3	42



228	Hydrogen-1 nuclear magnetic resonance investigation of high-potential iron-sulfur proteins from <i>Ectothiorhodospira halophila</i> and <i>Ectothiorhodospira vacuolata</i> : a comparative study of hyperfine-shifted resonances. <i>Biochemistry</i> , <b>1986</b> , 25, 60-7	3.2	42
227	High-resolution proton nuclear magnetic resonance studies of the nickel(II) derivative of azurin. <i>Biochemistry</i> , <b>1982</b> , 21, 6253-8	3.2	42
226	New bioinformatics resources for metabolomics. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , <b>2007</b> , 157-68	1.3	42
225	Trans-hydrogen-bond (h2)J(NN) and (h1)J(NH) couplings in the DNA A-T base pair: natural bond orbital analysis. <i>Journal of the American Chemical Society</i> , <b>2002</b> , 124, 1190-1	16.4	41
224	Engineered disulfide bonds in staphylococcal nuclease: effects on the stability and conformation of the folded protein. <i>Biochemistry</i> , <b>1996</b> , 35, 10328-38	3.2	41
223	NMR assignments of the four histidines of staphylococcal nuclease in native and denatured states. <i>Biochemistry</i> , <b>1988</b> , 27, 2158-65	3.2	41
222	Databases and Software for NMR-Based Metabolomics. <i>Current Metabolomics</i> , <b>2013</b> , 1,	1	40
221	Theoretical Studies of Protium/Deuterium Fractionation Factors and Cooperative Hydrogen Bonding in Peptides. <i>Journal of the American Chemical Society</i> , <b>1995</b> , 117, 9619-9624	16.4	40
220	Elimination of cross-relaxation effects from two-dimensional chemical-exchange spectra of macromolecules. <i>Journal of the American Chemical Society</i> , <b>1990</b> , 112, 2574-2577	16.4	40
219	Conserved Lipid and Small-Molecule Modulation of COQ8 Reveals Regulation of the Ancient Kinase-like UbiB Family. <i>Cell Chemical Biology</i> , <b>2018</b> , 25, 154-165.e11	8.2	40
218	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. <i>Biochemistry</i> , <b>2003</b> , 42, 2847-56	3.2	39
217	Solution structure of the iron-sulfur cluster cochaperone HscB and its binding surface for the iron-sulfur assembly scaffold protein IscU. <i>Biochemistry</i> , <b>2008</b> , 47, 9394-404	3.2	38
216	Coupling between trans/cis proline isomerization and protein stability in staphylococcal nuclease. <i>Protein Science</i> , <b>1996</b> , 5, 1907-16	6.3	38
215	Correlation proton magnetic resonance studies at 250 MHz of bovine pancreatic ribonuclease. III. Mutual electrostatic interaction between histidine residues 12 and 119. <i>Biochemistry</i> , <b>1975</b> , 14, 3562-6	3.2	38
214	Caloric Restriction Engages Hepatic RNA Processing Mechanisms in Rhesus Monkeys. <i>Cell Metabolism</i> , <b>2018</b> , 27, 677-688.e5	24.6	37
213	Structural/Functional Properties of Human NFU1, an Intermediate [4Fe-4S] Carrier in Human Mitochondrial Iron-Sulfur Cluster Biogenesis. <i>Structure</i> , <b>2016</b> , 24, 2080-2091	5.2	37
212	Metabolic Evidence of Diminished Lipid Oxidation in Women With Polycystic Ovary Syndrome. <i>Current Metabolomics</i> , <b>2014</b> , 2, 269-278	1	37
211	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). <i>Journal of Biological Chemistry</i> , <b>2012</b> , 287, 31406-13	5.4	37

210	Efficient and rapid protein expression and purification of small high disulfide containing sweet protein brazzein in <i>E. coli</i> . <i>Protein Expression and Purification</i> , <b>2008</b> , 58, 263-8	2	37
209	Lack of evidence for a tetrahedral intermediate in the hydrolysis of nitroanilide substrates by serine proteinases. Subzero-temperature stopped-flow experiments. <i>FEBS Journal</i> , <b>1981</b> , 120, 477-85		37
208	Integrative NMR for biomolecular research. <i>Journal of Biomolecular NMR</i> , <b>2016</b> , 64, 307-32	3	36
207	Interactions of iron-bound frataxin with ISCU and ferredoxin on the cysteine desulfurase complex leading to Fe-S cluster assembly. <i>Journal of Inorganic Biochemistry</i> , <b>2018</b> , 183, 107-116	4.2	35
206	Comparison of the accuracy of protein solution structures derived from conventional and network-edited NOESY data. <i>Protein Science</i> , <b>1995</b> , 4, 2289-99	6.3	35
205	Three-dimensional structure and determinants of stability of the iron-sulfur cluster scaffold protein IscU from <i>Escherichia coli</i> . <i>Biochemistry</i> , <b>2012</b> , 51, 5557-63	3.2	34
204	Use of NMR saturation transfer difference spectroscopy to study ligand binding to membrane proteins. <i>Methods in Molecular Biology</i> , <b>2012</b> , 914, 47-63	1.4	34
203	Role of aminotransferases in glutamate metabolism of human erythrocytes. <i>Journal of Biomolecular NMR</i> , <b>2011</b> , 49, 221-9	3	34
202	NMR method for measuring carbon-13 isotopic enrichment of metabolites in complex solutions. <i>Analytical Chemistry</i> , <b>2010</b> , 82, 4558-63	7.8	34
201	Two-dimensional NMR studies of Kazal proteinase inhibitors. 1. Sequence-specific assignments and secondary structure of turkey ovomucoid third domain. <i>Biochemistry</i> , <b>1988</b> , 27, 2519-29	3.2	34
200	Connectivity of proton and carbon spectra of the blue copper protein, plastocyanin, established by two-dimensional nuclear magnetic resonance. <i>FEBS Letters</i> , <b>1983</b> , 162, 52-56	3.8	34
199	Measurement of absolute concentrations of individual compounds in metabolite mixtures by gradient-selective time-zero <sup>1</sup> H- <sup>13</sup> C HSQC with two concentration references and fast maximum likelihood reconstruction analysis. <i>Analytical Chemistry</i> , <b>2011</b> , 83, 9352-60	7.8	33
198	Structure of human J-type co-chaperone HscB reveals a tetracysteine metal-binding domain. <i>Journal of Biological Chemistry</i> , <b>2008</b> , 283, 30184-92	5.4	33
197	Redox-Dependent Magnetic Alignment of <i>Clostridium pasteurianum</i> Rubredoxin: Measurement of Magnetic Susceptibility Anisotropy and Prediction of Pseudocontact Shift Contributions. <i>Journal of the American Chemical Society</i> , <b>1999</b> , 121, 4677-4683	16.4	33
196	Announcing mandatory submission of PDBx/mmCIF format files for crystallographic depositions to the Protein Data Bank (PDB). <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2019</b> , 75, 451-454	5.5	32
195	PONDEROSA-C/S: client-server based software package for automated protein 3D structure determination. <i>Journal of Biomolecular NMR</i> , <b>2014</b> , 60, 73-5	3	31
194	Worldwide Protein Data Bank biocuration supporting open access to high-quality 3D structural biology data. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2018</b> , 2018,	5	31
193	MolProbity for the masses-of data. <i>Journal of Biomolecular NMR</i> , <b>2015</b> , 63, 77-83	3	30



192	Tangled web of interactions among proteins involved in iron-sulfur cluster assembly as unraveled by NMR, SAXS, chemical crosslinking, and functional studies. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , <b>2015</b> , 1853, 1416-28	4.9	30
191	Three hydrophobic amino acids in Escherichia coli HscB make the greatest contribution to the stability of the HscB-IscU complex. <i>BMC Biochemistry</i> , <b>2011</b> , 12, 3	4.8	30
190	Correlation between hydrogen bond lengths and reduction potentials in Clostridium pasteurianum rubredoxin. <i>Journal of the American Chemical Society</i> , <b>2003</b> , 125, 1464-5	16.4	30
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