Robert Powers

List of Publications by Year
in descending order

174 papers	9,697 citations	36303 51 h-index	43889 91 g-index
245 all docs	245 docs citations	245 times ranked	12941 citing authors

#	Article	IF	Citations
1	Multivariate Analysis in Metabolomics. Current Metabolomics, 2012, 1, 92-107.	0.5	804
2	The future of NMR-based metabolomics. Current Opinion in Biotechnology, 2017, 43, 34-40.	6.6	651
3	MUC1 and HIF-1alpha Signaling Crosstalk Induces Anabolic Glucose Metabolism to Impart Gemcitabine Resistance to Pancreatic Cancer. Cancer Cell, 2017, 32, 71-87.e7.	16.8	373
4	Automated analysis of protein NMR assignments using methods from artificial intelligence. Journal of Molecular Biology, 1997, 269, 592-610.	4.2	292
5	PCA as a Practical Indicator of OPLS-DA Model Reliability. Current Metabolomics, 2016, 4, 97-103.	0.5	284
6	Protein NMR Recall, Precision, andF-measure Scores (RPF Scores):Â Structure Quality Assessment Measures Based on Information Retrieval Statistics. Journal of the American Chemical Society, 2005, 127, 1665-1674.	13.7	246
7	A common sense approach to peak picking in two-, three-, and four-dimensional spectra using automatic computer analysis of contour diagrams. Journal of Magnetic Resonance, 1991, 95, 214-220.	0.5	233
8	MUC1 mucin stabilizes and activates hypoxia-inducible factor 1 alpha to regulate metabolism in pancreatic cancer. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13787-13792.	7.1	207
9	Metabolic reprogramming induced by ketone bodies diminishes pancreatic cancer cachexia. Cancer & Metabolism, 2014, 2, 18.	5.0	182
10	Three-Dimensional Solution Structure of Human Interleukin-4 by Multidimensional Heteronuclear Magnetic Resonance Spectroscopy. Science, 1992, 256, 1673-1677.	12.6	169
11	Beyond the paradigm: Combining mass spectrometry and nuclear magnetic resonance for metabolomics. Progress in Nuclear Magnetic Resonance Spectroscopy, 2017, 100, 1-16.	7.5	168
12	Utilities for quantifying separation in PCA/PLS-DA scores plots. Analytical Biochemistry, 2013, 433, 102-104.	2.4	160
13	The high-resolution, three-dimensional solution structure of human interleukin-4 determined by multidimensional heteronuclear magnetic resonance spectroscopy. Biochemistry, 1993, 32, 6744-6762.	2.5	143
14	Amino Acid Catabolism in <i>Staphylococcus aureus</i> and the Function of Carbon Catabolite Repression. MBio, 2017, 8, .	4.1	136
15	A common sense approach to peak picking in two-, three-, and four-dimensional spectra using automatic computer analysis of contour diagrams. Journal of Magnetic Resonance, 2011, 213, 357-363.	2.1	133
16	Structure-Based Design of a Novel, Potent, and Selective Inhibitor for MMP-13 Utilizing NMR Spectroscopy and Computer-Aided Molecular Design. Journal of the American Chemical Society, 2000, 122, 9648-9654.	13.7	124
17	A topology-constrained distance network algorithm for protein structure determination from NOESY data. Proteins: Structure, Function and Bioinformatics, 2005, 62, 587-603.	2.6	121
18	Application of NMR Metabolomics to Search for Human Disease Biomarkers. Combinatorial Chemistry and High Throughput Screening, 2012, 15, 595-610.	1.1	116

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19	Metabolic Dysfunction in Parkinson's Disease: Bioenergetics, Redox Homeostasis and Central Carbon Metabolism. Brain Research Bulletin, 2017, 133, 12-30.	3.0	115
20	New frontiers in metabolomics: from measurement to insight. F1000Research, 2017, 6, 1148.	1.6	115
21	Properly Oriented Heparin‑Decasaccharide-Induced Dimers Are the Biologically Active Form of Basic Fibroblast Growth Factor†,‡. Biochemistry, 1997, 36, 4782-4791.	2.5	111
22	O-GlcNAc Transferase Suppresses Inflammation and Necroptosis by Targeting Receptor-Interacting Serine/Threonine-Protein Kinase 3. Immunity, 2019, 50, 576-590.e6.	14.3	111
23	Mitochondrial dysfunction in glial cells: Implications for neuronal homeostasis and survival. Toxicology, 2017, 391, 109-115.	4.2	107
24	MVAPACK: A Complete Data Handling Package for NMR Metabolomics. ACS Chemical Biology, 2014, 9, 1138-1144.	3.4	96
25	Estimating Protein‑Ligand Binding Affinity Using High-Throughput Screening by NMR. ACS Combinatorial Science, 2008, 10, 948-958.	3.3	95
26	NMR metabolomics and drug discovery. Magnetic Resonance in Chemistry, 2009, 47, S2-11.	1.9	92
27	CcpA Regulates Arginine Biosynthesis in Staphylococcus aureus through Repression of Proline Catabolism. PLoS Pathogens, 2012, 8, e1003033.	4.7	91
28	Analysis of bacterial biofilms using NMR-based metabolomics. Future Medicinal Chemistry, 2012, 4, 1273-1306.	2.3	89
29	MS/NMR: A Structure-Based Approach for Discovering Protein Ligands and for Drug Design by Coupling Size Exclusion Chromatography, Mass Spectrometry, and Nuclear Magnetic Resonance Spectroscopy. Analytical Chemistry, 2001, 73, 571-581.	6.5	85
30	Analysis of the backbone dynamics of the ribonuclease H domain of the human immunodeficiency virus reverse transcriptase using nitrogen-15 relaxation measurements. Biochemistry, 1992, 31, 9150-9157.	2.5	83
31	Alterations in Energy/Redox Metabolism Induced by Mitochondrial and Environmental Toxins: A Specific Role for Glucose-6-Phosphate-Dehydrogenase and the Pentose Phosphate Pathway in Paraquat Toxicity. ACS Chemical Biology, 2014, 9, 2032-2048.	3.4	82
32	Urease is an essential component of the acid response network of Staphylococcus aureus and is required for a persistent murine kidney infection. PLoS Pathogens, 2019, 15, e1007538.	4.7	82
33	Quantitative NMR-Based Biomedical Metabolomics: Current Status and Applications. Molecules, 2020, 25, 5128.	3.8	81
34	Predicting the <i>in Vivo</i> Mechanism of Action for Drug Leads Using NMR Metabolomics. ACS Chemical Biology, 2012, 7, 166-171.	3.4	78
35	Solution Structure of B. subtilis Acyl Carrier Protein. Structure, 2001, 9, 277-287.	3.3	76
36	Staphylococcus aureus Metabolic Adaptations during the Transition from a Daptomycin Susceptibility Phenotype to a Daptomycin Nonsusceptibility Phenotype. Antimicrobial Agents and Chemotherapy, 2015, 59, 4226-4238.	3.2	75

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37	Comparison of protein active site structures for functional annotation of proteins and drug design. Proteins: Structure, Function and Bioinformatics, 2006, 65, 124-135.	2.6	73
38	Tricarboxylic Acid Cycle-Dependent Regulation of <i>Staphylococcus epidermidis</i> Polysaccharide Intercellular Adhesin Synthesis. Journal of Bacteriology, 2008, 190, 7621-7632.	2.2	73
39	Negative impact of noise on the principal component analysis of NMR data. Journal of Magnetic Resonance, 2006, 178, 88-95.	2.1	71
40	Use of NMR Metabolomics To Analyze the Targets of <scp>d</scp>-Cycloserine in Mycobacteria: Role of <scp>d</scp>-Alanine Racemase. Journal of Proteome Research, 2007, 6, 4608-4614.	3.7	68
41	Inactivation of the Pta-AckA Pathway Causes Cell Death in Staphylococcus aureus. Journal of Bacteriology, 2013, 195, 3035-3044.	2.2	68
42	An Integrated Platform for Automated Analysis of Protein NMR Structures. Methods in Enzymology, 2005, 394, 111-141.	1.0	67
43	High-Resolution Solution Structure of Basic Fibroblast Growth Factor Determined by Multidimensional Heteronuclear Magnetic Resonance Spectroscopy. Biochemistry, 1996, 35, 13552-13561.	2.5	63
44	Metabolomics Analysis Identifies <scp>d</scp>-Alanine-<scp>d</scp>-Alanine Ligase as the Primary Lethal Target of <scp>d</scp>-Cycloserine in Mycobacteria. Journal of Proteome Research, 2014, 13, 1065-1076.	3.7	61
45	Combining DI-ESIâ€"MS and NMR datasets for metabolic profiling. Metabolomics, 2015, 11, 391-402.	3.0	60
46	Proton, nitrogen-15, carbon-13, carbon-13 monoxide assignments of human interleukin-4 using three-dimensional double- and triple-resonance heteronuclear magnetic resonance spectroscopy. Biochemistry, 1992, 31, 4334-4346.	2.5	59
47	High-resolution solution structure of the catalytic fragment of human collagenase-3 (MMP-13) complexed with a hydroxamic acid inhibitor. Journal of Molecular Biology, 2000, 302, 671-689.	4.2	56
48	Impact of Mobility on Structure-Based Drug Design for the MMPs. Journal of the American Chemical Society, 2002, 124, 12658-12659.	13.7	56
49	Influence of Iron and Aeration on Staphylococcus aureus Growth, Metabolism, and Transcription. Journal of Bacteriology, 2014, 196, 2178-2189.	2.2	55
50	Rapid Proteinâˆ¼Ligand Costructures Using Chemical Shift Perturbations. Journal of the American Chemical Society, 2008, 130, 535-545.	13.7	54
51	Analysis of metabolomic PCA data using tree diagrams. Analytical Biochemistry, 2010, 399, 58-63.	2.4	54
52	Solution Structure of ZipA, a Crucial Component ofEscherichia coliCell Divisionâ€. Biochemistry, 2000, 39, 9146-9156.	2.5	52
53	Solution structure of human IL-13 and implication for receptor binding11Edited by P. E. Wright. Journal of Molecular Biology, 2001, 310, 219-230.	4.2	52
54	Structure and Function of Human DnaJ Homologue Subfamily A Member 1 (DNAJA1) and Its Relationship to Pancreatic Cancer. Biochemistry, 2014, 53, 1360-1372.	2.5	52

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55	The Current State of Drug Discovery and a Potential Role for NMR Metabolomics. Journal of Medicinal Chemistry, 2014, 57, 5860-5870.	6.4	52
56	Structural Relatedness of Distinct Determinants Recognized by Monoclonal Antibody TP25.99 on β2-Microglobulin-Associated and β2-Microglobulin-Free HLA Class I Heavy Chains. Journal of Immunology, 2000, 165, 3275-3283.	0.8	49
57	NMR Solution Structure of the Catalytic Fragment of Human Fibroblast Collagenase Complexed with a Sulfonamide Derivative of a Hydroxamic Acid Compound. Biochemistry, 1999, 38, 7085-7096.	2.5	48
58	FAST-NMR: Functional Annotation Screening Technology Using NMR Spectroscopy. Journal of the American Chemical Society, 2006, 128, 15292-15299.	13.7	48
59	The discovery of anthranilic acid-based MMP inhibitors. Part 1: SAR of the 3-position. Bioorganic and Medicinal Chemistry Letters, 2001, 11, 235-238.	2.2	47
60	NMR Analysis of a Stress Response Metabolic Signaling Network. Journal of Proteome Research, 2011, 10, 3743-3754.	3.7	46
61	The Application of X-ray, NMR, and Molecular Modeling in the Design of MMP Inhibitors. Current Topics in Medicinal Chemistry, 2004, 4, 1311-1327.	2.1	45
62	Using NMR Metabolomics to Investigate Tricarboxylic Acid Cycle-dependent Signal Transduction in Staphylococcus epidermidis. Journal of Biological Chemistry, 2010, 285, 36616-36624.	3.4	45
63	A Urinary Metabolic Signature for Multiple Sclerosis and Neuromyelitis Optica. Journal of Proteome Research, 2016, 15, 659-666.	3.7	45
64	Combining Mass Spectrometry and NMR Improves Metabolite Detection and Annotation. Journal of Proteome Research, 2018, 17, 4017-4022.	3.7	45
65	Solution structure of the tumor necrosis factor receptor-1 death domain. Journal of Molecular Biology, 2001, 310, 895-906.	4.2	44
66	Advances in nuclear magnetic resonance for drug discovery. Expert Opinion on Drug Discovery, 2009, 4, 1077-1098.	5.0	42
67	High-Resolution Solution Structure of the Inhibitor-Free Catalytic Fragment of Human Fibroblast Collagenase Determined by Multidimensional NMR‡. Biochemistry, 1998, 37, 1495-1504.	2.5	40
68	Glucose Metabolism and AMPK Signaling Regulate Dopaminergic Cell Death Induced by Gene (α-Synuclein)-Environment (Paraquat) Interactions. Molecular Neurobiology, 2017, 54, 3825-3842.	4.0	40
69	Three-dimensional triple-resonance NMR of 13C/15N-enriched proteins using constant-time evolution. Journal of Magnetic Resonance, 1991, 94, 209-213.	0.5	39
70	Application of NMR and Molecular Docking in Structure-Based Drug Discovery. Topics in Current Chemistry, 2011, 326, 1-34.	4.0	39
71	Revisiting Protocols for the NMR Analysis of Bacterial Metabolomes. Journal of Integrated OMICS, 2013, 3, 120-137.	0.5	39
72	Metabolic Investigations of the Molecular Mechanisms Associated with Parkinson's Disease. Metabolites, 2017, 7, 22.	2.9	39

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73	NMR Structure of Free RGS4 Reveals an Induced Conformational Change upon Binding GÎ±. Biochemistry, 2000, 39, 7063-7073.	2.5	38
74	Catabolite Control Protein E (CcpE) Is a LysR-type Transcriptional Regulator of Tricarboxylic Acid Cycle Activity in Staphylococcus aureus. Journal of Biological Chemistry, 2013, 288, 36116-36128.	3.4	38
75	The application of machine-learning and Raman spectroscopy for the rapid detection of edible oils type and adulteration. Food Chemistry, 2022, 373, 131471.	8.2	38
76	Deterministic multidimensional nonuniform gap sampling. Journal of Magnetic Resonance, 2015, 261, 19-26.	2.1	36
77	Secondary structure of the ribonuclease H domain of the human immunodeficiency virus reverse transcriptase in solution using three-dimensional double and triple resonance heteronuclear magnetic resonance spectroscopy. Journal of Molecular Biology, 1991, 221, 1081-1090.	4.2	35
78	The application of FAST-NMR for the identification of novel drug discovery targets. Drug Discovery Today, 2008, 13, 172-179.	6.4	34
79	Mutational analysis and NMR studies of the death domain of the tumor necrosis factor receptor-111Edited by P. E. Wright. Journal of Molecular Biology, 2000, 300, 1323-1333.	4.2	33
80	NMR Metabolic Profiling ofAspergillusnidulansto Monitor Drug and Protein Activity. Journal of Proteome Research, 2006, 5, 1916-1923.	3.7	33
81	Assignments, secondary structure and dynamics of the inhibitor-free catalytic fragment of human fibroblast collagenase. Journal of Biomolecular NMR, 1997, 10, 9-19.	2.8	32
82	Metabolic Mitigation of Staphylococcus aureus Vancomycin Intermediate-Level Susceptibility. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	32
83	Nitrite Derived from Endogenous Bacterial Nitric Oxide Synthase Activity Promotes Aerobic Respiration. MBio, 2017, 8, .	4.1	31
84	NMR Metabolomics Analysis of Parkinson&#39;s Disease. Current Metabolomics, 2013, 1, 191-209.	0.5	29
85	TWo-Dimensional1H and31P NMR Spectra and Restrained Molecular Dynamics Structure of an Oligodeoxyribonucleotide Duplex Refined via a Hybrid Relaxation Matrix Procedure. Journal of Biomolecular Structure and Dynamics, 1990, 8, 253-294.	3.5	27
86	1H, 15N, 13C and 13CO assignments and secondary structure determination of basic fibroblast growth factor using 3D heteronuclear NMR spectroscopy. Journal of Biomolecular NMR, 1995, 6, 245-54.	2.8	27
87	Glucose Limitation Alters Glutamine Metabolism in MUC1-Overexpressing Pancreatic Cancer Cells. Journal of Proteome Research, 2017, 16, 3536-3546.	3.7	27
88	The effect of cysteine oxidation on DJ-1 cytoprotective function in human alveolar type II cells. Cell Death and Disease, 2019, 10, 638.	6.3	27
89	Phosphorus NMR and Its Application to Metabolomics. Analytical Chemistry, 2020, 92, 9536-9545.	6.5	27
90	Two-dimensional proton and phosphorus-31 NMR spectra and restrained molecular dynamics structure of a covalent CPI-CDPI2-oligodeoxyribonucleotide decamer complex. Biochemistry, 1990, 29, 9994-10008.	2.5	26

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91	Determination of the secondary structure and folding topology of human interleukin-4 using three-dimensional heteronuclear magnetic resonance spectroscopy. Biochemistry, 1992, 31, 4347-4353.	2.5	26
92	Determining the optimal size of small molecule mixtures for high throughput NMR screening. Journal of Biomolecular NMR, 2005, 31, 243-258.	2.8	26
93	Redox Imbalance Underlies the Fitness Defect Associated with Inactivation of the Pta-AckA Pathway in <i>Staphylococcus aureus</i>. Journal of Proteome Research, 2016, 15, 1205-1212.	3.7	26
94	Solution structure ofArchaeglobus fulgidispeptidyl-tRNA hydrolase (Pth2) provides evidence for an extensive conserved family of Pth2 enzymes in archea, bacteria, and eukaryotes. Protein Science, 2005, 14, 2849-2861.	7.6	25
95	Unique opportunities for NMR methods in structural genomics. Journal of Structural and Functional Genomics, 2009, 10, 101-106.	1.2	25
96	Insights into gemcitabine resistance and the potential for therapeutic monitoring. Metabolomics, 2018, 14, 156.	3.0	25
97	A community resource of experimental data for <scp>NMR</scp> / <scp>X</scp>â€ray crystal structure pairs. Protein Science, 2016, 25, 30-45.	7.6	24
98	Design and Characterization of a Functional Library for NMR Screening Against Novel Protein Targets. Combinatorial Chemistry and High Throughput Screening, 2006, 9, 515-534.	1.1	23
99	Expanding the Coverage of the Metabolome with Nitrogen-Based NMR. Analytical Chemistry, 2018, 90, 4521-4528.	6.5	23
100	Applications of NMR to structure-based drug design in structural genomics. Journal of Structural and Functional Genomics, 2002, 2, 113-123.	1.2	22
101	Resonance assignments for Oncostatin M, a 24-kDa ?-helical protein. Journal of Biomolecular NMR, 1996, 7, 273-82.	2.8	21
102	A Multi-Step NMR Screen for the Identification and Evaluation of Chemical Leads for Drug Discovery. Combinatorial Chemistry and High Throughput Screening, 2009, 12, 285-295.	1.1	21
103	Functional evolution of PLP-dependent enzymes based on active-site structural similarities. Proteins: Structure, Function and Bioinformatics, 2014, 82, 2597-2608.	2.6	21
104	Generalized adaptive intelligent binning of multiway data. Chemometrics and Intelligent Laboratory Systems, 2015, 146, 42-46.	3.5	21
105	Nanoformulated copper/zinc superoxide dismutase exerts differential effects on glucose vs lipid homeostasis depending on the diet composition possibly via altered AMPK signaling. Translational Research, 2017, 188, 10-26.	5.0	20
106	Two-Dimensional¹H and³¹P NMR Spectra of a Decamer Oligodeoxyribonucleotide Duplex and a Quinoxaline ([MeCys³,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50.142 Td (MeCys<sup: 1989, 7, 515-556.	3.5	19
107	Evaluation of Multivariate Classification Models for Analyzing NMR Metabolomics Data. Journal of Proteome Research, 2019, 18, 3282-3294.	3.7	19
108	Simultaneous phase and scatter correction for NMR datasets. Chemometrics and Intelligent Laboratory Systems, 2014, 131, 1-6.	3.5	18

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109	Solution conformation of a synthetic fragment of human pituitary growth hormone. Two-dimensional NMR of an .alpha.-helical dimer. Biochemistry, 1989, 28, 1048-1054.	2.5	17
110	Potential of Urinary Metabolites for Diagnosing Multiple Sclerosis. ACS Chemical Biology, 2013, 8, 684-690.	3.4	17
111	Evaluation of Non-Uniform Sampling 2D 1Hâ€"13C HSQC Spectra for Semi-Quantitative Metabolomics. Metabolites, 2020, 10, 203.	2.9	17
112	Radiation exposure induces cross-species temporal metabolic changes that are mitigated in mice by amifostine. Scientific Reports, 2021, 11, 14004.	3.3	17
113	Sample Preparation of Mycobacterium tuberculosis Extracts for Nuclear Magnetic Resonance Metabolomic Studies. Journal of Visualized Experiments, 2012, , e3673.	0.3	16
114	13C NMR Reveals No Evidence of nâˆ'Ï€* Interactions in Proteins. PLoS ONE, 2012, 7, e42075.	2.5	16
115	A sequential algorithm for multiblock orthogonal projections to latent structures. Chemometrics and Intelligent Laboratory Systems, 2015, 149, 33-39.	3.5	16
116	GPR55 receptor antagonist decreases glycolytic activity in PANCâ€1 pancreatic cancer cell line and tumor xenografts. International Journal of Cancer, 2017, 141, 2131-2142.	5.1	16
117	Combination of two analytical techniques improves wine classification by Vineyard, Region, and vintage. Food Chemistry, 2021, 354, 129531.	8.2	16
118	NMR Metabolomics Protocols for Drug Discovery. Methods in Molecular Biology, 2019, 2037, 265-311.	0.9	16
119	Validity of Using the Radius of Gyration as a Restraint in NMR Protein Structure Determination. Journal of the American Chemical Society, 2001, 123, 3834-3835.	13.7	15
120	Comparing normalization methods and the impact of noise. Metabolomics, 2018, 14, 108.	3.0	15
121	HYPER: a hierarchical algorithm for automatic determination of protein dihedral-angle constraints and stereospecific C beta H2 resonance assignments from NMR data. Journal of Biomolecular NMR, 1999, 15, 251-264.	2.8	14
122	Evaluation of the Utility of NMR Structures Determined from Minimal NOE-Based Restraints for Structure-Based Drug Design, Using MMP-1 as an Example. Biochemistry, 2000, 39, 13365-13375.	2.5	14
123	Metabolomics Analyses from Tissues in Parkinsonâ€™s Disease. Methods in Molecular Biology, 2019, 1996, 217-257.	0.9	14
124	Metabolic profiling of historical and modern wheat cultivars using proton nuclear magnetic resonance spectroscopy. Scientific Reports, 2021, 11, 3080.	3.3	14
125	Structure and function of <i>Pseudomonas aeruginosa</i> protein PA1324 (21â€"170). Protein Science, 2009, 18, 606-618.	7.6	13
126	Solution structure and function of YndB, an AHSA1 protein from<i>Bacillus subtilis</i>. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3328-3340.	2.6	13

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127	Metabolic Feedback Inhibition Influences Metabolite Secretion by the Human Gut Symbiont Bacteroides thetaiotaomicron. MSystems, 2020, 5, .	3.8	13
128	Solution structure of the <i>Pseudomonas putida</i> protein PpPutA45 and its DNA complex. Proteins: Structure, Function and Bioinformatics, 2009, 75, 12-27.	2.6	12
129	Correlation between Protein Function and Ligand Binding Profiles. Journal of Proteome Research, 2011, 10, 2538-2545.	3.7	12
130	Searching the protein structure database for ligand-binding site similarities using CPASS v.2. BMC Research Notes, 2011, 4, 17.	1.4	12
131	Assessment of Metabolic Changes in <i>Mycobacterium smegmatis</i> Wild-Type and <i>alr</i> Mutant Strains: Evidence of a New Pathway of <scp>d</scp>-Alanine Biosynthesis. Journal of Proteome Research, 2017, 16, 1270-1279.	3.7	12
132	Functional Genomics and NMR Spectroscopy. Combinatorial Chemistry and High Throughput Screening, 2007, 10, 676-697.	1.1	11
133	Structural and Functional Similarity between the Bacterial Type III Secretion System Needle Protein PrgI and the Eukaryotic Apoptosis Bcl-2 Proteins. PLoS ONE, 2009, 4, e7442.	2.5	11
134	Bacterial protein structures reveal phylum dependent divergence. Computational Biology and Chemistry, 2011, 35, 24-33.	2.3	10
135	Transient sampling of aggregationâ€prone conformations causes pathogenic instability of a parkinsonian mutant of <scp>DJ</scp>â€‘1 at physiological temperature. Protein Science, 2015, 24, 1671-1685.	7.6	10
136	Homology Model for Oncostatin M Based on NMR Structural Data. Biochemistry, 1998, 37, 10581-10588.	2.5	9
137	Letter to the editor: 1H, 15N, 13C, and 13CO assignments and secondary structure determination of collagenase-3 (MMP-13) complexed with a hydroxamic acid inhibitor. Journal of Biomolecular NMR, 2000, 17, 269-270.	2.8	9
138	Growth and Preparation of Staphylococcus epidermidis for NMR Metabolomic Analysis. Methods in Molecular Biology, 2014, 1106, 71-91.	0.9	8
139	Metabolic changes associated with adaptive resistance to daptomycin in Streptococcus mitis-oralis. BMC Microbiology, 2020, 20, 162.	3.3	8
140	The Applicability of Molecular Descriptors for Designing an Electrospray Ionization Mass Spectrometry Compatible Library for Drug Discovery. Combinatorial Chemistry and High Throughput Screening, 2012, 15, 806-815.	1.1	8
141	Understanding interactions of Citropin 1.1 analogues with model membranes and their influence on biological activity. Peptides, 2019, 119, 170119.	2.4	7
142	APPLICATIONS OF NUCLEAR MAGNETIC RESONANCE AND MASS SPECTROMETRY TO ANTICANCER DRUG DISCOVERY. , 2006, , 107-190.		6
143	PROFESS: a PROtein Function, Evolution, Structure and Sequence database. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq011-baq011.	3.0	6
144	15N CEST data and traditional model-free analysis capture fast internal dynamics of DJ-1. Analytical Biochemistry, 2018, 542, 24-28.	2.4	6

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145	DNAJA1 Dysregulates Metabolism Promoting an Antiapoptotic Phenotype in Pancreatic Ductal Adenocarcinoma. Journal of Proteome Research, 2021, 20, 3925-3939.	3.7	6
146	MnTE-2-PyP protects fibroblast mitochondria from hyperglycemia and radiation exposure. Redox Biology, 2022, 52, 102301.	9.0	6
147	Letter to the editor: 1H, 15N, 13C, and 13CO assignments and secondary structure determination of ZipA. Journal of Biomolecular NMR, 2000, 17, 275-276.	2.8	5
148	Development of Cyclobuteneâ€•and Cyclobutaneâ€Functionalized Fatty Acids with Inhibitory Activity against <i>Mycobacterium tuberculosis</i>. ChemMedChem, 2014, 9, 1838-1849.	3.2	5
149	Novel Amphiphilic Cyclobutene and Cyclobutane cis-C18 Fatty Acid Derivatives Inhibit Mycobacterium avium subsp. paratuberculosis Growth. Veterinary Sciences, 2019, 6, 46.	1.7	5
150	Closing the gap between in vivo and in vitro omics: using QA/QC to strengthen ex vivo NMR metabolomics. NMR in Biomedicine, 2021, , e4594.	2.8	5
151	Properly Oriented Heparinâˆ'Decasaccharide-Induced Dimers Are the Biologically Active Form of Basic Fibroblast Growth Factor. Biochemistry, 1997, 36, 7936-7936.	2.5	5
152	1H, 13C, and 15N NMR assignments for the Bacillus subtilis yndB START domain. Biomolecular NMR Assignments, 2009, 3, 191-194.	0.8	4
153	Integrative network analyses of transcriptomics data reveal potential drug targets for acute radiation syndrome. Scientific Reports, 2021, 11, 5585.	3.3	4
154	A reversed phase ultra-high-performance liquid chromatography-data independent mass spectrometry method for the rapid identification of mycobacterial lipids. Journal of Chromatography A, 2022, 1662, 462739.	3.7	4
155	Peptidomics analysis reveals changes in small urinary peptides in patients with interstitial cystitis/bladder pain syndrome. Scientific Reports, 2022, 12, 8289.	3.3	4
156	Analysis by NMR Spectroscopy of the Structural Homology between the Linear and the Cyclic Peptide Recognized by Anti-human Leukocyte Antigen Class I Monoclonal Antibody TP25.99*. Journal of Biological Chemistry, 2000, 275, 24679-24685.	3.4	3
157	Identification of Lowâ€Molecularâ€Weight Compounds Inhibiting Growth of Corynebacteria: Potential Lead Compounds for Antibiotics. ChemMedChem, 2014, 9, 282-285.	3.2	3
158	Functional Evolution of Proteins. Proteins: Structure, Function and Bioinformatics, 2019, 87, 492-501.	2.6	3
159	Gadolinium-Based Paramagnetic Relaxation Enhancement Agent Enhances Sensitivity for NUS Multidimensional NMR-Based Metabolomics. Molecules, 2021, 26, 5115.	3.8	3
160	Deciphering the mechanism of action of antitubercular compounds with metabolomics. Computational and Structural Biotechnology Journal, 2021, 19, 4284-4299.	4.1	3
161	Shifting-corrected regularized regression for 1<i>H</i> NMR metabolomics identification and quantification. Biostatistics, 2022, 24, 140-160.	1.5	3
162	Human Serum Alters the Metabolism and Antibiotic Susceptibility of <i>Staphylococcus aureus</i>. Journal of Proteome Research, 2022, 21, 1467-1474.	3.7	3

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163	An inexpensive high-throughput nuclear magnetic resonance tube cleaning apparatus. Analytical Biochemistry, 2011, 416, 234-236.	2.4	2
164	1H, 13C, and 15N NMR assignments for the helicase interaction domain of Staphylococcus aureus DnaG primase. Biomolecular NMR Assignments, 2012, 6, 35-38.	0.8	2
165	Statistical removal of background signals from high-throughput 1H NMR line-broadening ligand-affinity screens. Journal of Biomolecular NMR, 2015, 63, 53-58.	2.8	2
166	Identification of a Ligand-Binding Site on the <i>Staphylococcus aureus</i> DnaG Primase C-Terminal Domain. Biochemistry, 2017, 56, 932-943.	2.5	2
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168	Letter to the Editor:1H,13C and15N assignments for the Archaeglobus fulgidis protein AF2095. Journal of Biomolecular NMR, 2004, 30, 107-108.	2.8	1
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