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	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
2	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
3	MnTE-2-PyP protects fibroblast mitochondria from hyperglycemia and radiation exposure. Redox Biology, 2022, 52, 102301.	9.0	6
4	Shifting-corrected regularized regression for 1H NMR metabolomics identification and quantification. Biostatistics, 2022, 24, 140-160.	1.5	3
5	Human Serum Alters the Metabolism and Antibiotic Susceptibility of Staphylococcus aureus. Journal of Proteome Research, 2022, 21, 1467-1474.	3.7	3
6	Peptidomics analysis reveals changes in small urinary peptides in patients with interstitial cystitis/bladder pain syndrome. Scientific Reports, 2022, 12, 8289.	3.3	4
7	Metabolic profiling of historical and modern wheat cultivars using proton nuclear magnetic resonance spectroscopy. Scientific Reports, 2021, 11, 3080.	3.3	14
8	Integrative network analyses of transcriptomics data reveal potential drug targets for acute radiation syndrome. Scientific Reports, 2021, 11, 5585.	3.3	4
9	Radiation exposure induces cross-species temporal metabolic changes that are mitigated in mice by amifostine. Scientific Reports, 2021, 11, 14004.	3.3	17
10	DNAJA1 Dysregulates Metabolism Promoting an Antiapoptotic Phenotype in Pancreatic Ductal Adenocarcinoma. Journal of Proteome Research, 2021, 20, 3925-3939.	3.7	6
11	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
12	Gadolinium-Based Paramagnetic Relaxation Enhancement Agent Enhances Sensitivity for NUS Multidimensional NMR-Based Metabolomics. Molecules, 2021, 26, 5115.	3.8	3
13	Combination of two analytical techniques improves wine classification by Vineyard, Region, and vintage. Food Chemistry, 2021, 354, 129531.	8.2	16
14	Deciphering the mechanism of action of antitubercular compounds with metabolomics. Computational and Structural Biotechnology Journal, 2021, 19, 4284-4299.	4.1	3
15	Quantitative NMR-Based Biomedical Metabolomics: Current Status and Applications. Molecules, 2020, 25, 5128.	3.8	81
16	Metabolic Feedback Inhibition Influences Metabolite Secretion by the Human Gut Symbiont Bacteroides thetaiotaomicron. MSystems, 2020, 5, .	3.8	13
17	Evaluation of Non-Uniform Sampling 2D 1Hâ€“13C HSQC Spectra for Semi-Quantitative Metabolomics. Metabolites, 2020, 10, 203.	2.9	17
18	Phosphorus NMR and Its Application to Metabolomics. Analytical Chemistry, 2020, 92, 9536-9545.	6.5	27

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19	Metabolic changes associated with adaptive resistance to daptomycin in Streptococcus mitis-oralis. BMC Microbiology, 2020, 20, 162.	3.3	8
20	Evaluation of Multivariate Classification Models for Analyzing NMR Metabolomics Data. Journal of Proteome Research, 2019, 18, 3282-3294.	3.7	19
21	Understanding interactions of Citropin 1.1 analogues with model membranes and their influence on biological activity. Peptides, 2019, 119, 170119.	2.4	7
22	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
23	Metabolomics Analyses from Tissues in Parkinsonâ€™s Disease. Methods in Molecular Biology, 2019, 1996, 217-257.	0.9	14
24	Novel Amphiphilic Cyclobutene and Cyclobutane cis-C18 Fatty Acid Derivatives Inhibit Mycobacterium avium subsp. paratuberculosis Growth. Veterinary Sciences, 2019, 6, 46.	1.7	5
25	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
26	Functional Evolution of Proteins. Proteins: Structure, Function and Bioinformatics, 2019, 87, 492-501.	2.6	3
27	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
28	NMR Metabolomics Protocols for Drug Discovery. Methods in Molecular Biology, 2019, 2037, 265-311.	0.9	16
29	Expanding the Coverage of the Metabolome with Nitrogen-Based NMR. Analytical Chemistry, 2018, 90, 4521-4528.	6.5	23
30	15N CEST data and traditional model-free analysis capture fast internal dynamics of DJ-1. Analytical Biochemistry, 2018, 542, 24-28.	2.4	6
31	Metabolic Mitigation of Staphylococcus aureus Vancomycin Intermediate-Level Susceptibility. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	32
32	Insights into gemcitabine resistance and the potential for therapeutic monitoring. Metabolomics, 2018, 14, 156.	3.0	25
33	Combining Mass Spectrometry and NMR Improves Metabolite Detection and Annotation. Journal of Proteome Research, 2018, 17, 4017-4022.	3.7	45
34	Comparing normalization methods and the impact of noise. Metabolomics, 2018, 14, 108.	3.0	15
35	Glucose Metabolism and AMPK Signaling Regulate Dopaminergic Cell Death Induced by Gene (Î±-Synuclein)-Environment (Paraquat) Interactions. Molecular Neurobiology, 2017, 54, 3825-3842.	4.0	40
36	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

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37	The NMR solution structure and function of RPA3313: a putative ribosomal transport protein from Rhodopseudomonas palustris. Proteins: Structure, Function and Bioinformatics, 2017, 85, 93-102.	2.6	1
38	Identification of a Ligand-Binding Site on the Staphylococcus aureus DnaG Primase C-Terminal Domain. Biochemistry, 2017, 56, 932-943.	2.5	2
39	Assessment of Metabolic Changes in Mycobacterium smegmatis Wild-Type and alr Mutant Strains: Evidence of a New Pathway of <scp>d</scp>-Alanine Biosynthesis. Journal of Proteome Research, 2017, 16, 1270-1279.	3.7	12
40	Amino Acid Catabolism in Staphylococcus aureus and the Function of Carbon Catabolite Repression. MBio, 2017, 8, .	4.1	136
41	Metabolic Dysfunction in Parkinsonâ€™s Disease: Bioenergetics, Redox Homeostasis and Central Carbon Metabolism. Brain Research Bulletin, 2017, 133, 12-30.	3.0	115
42	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
43	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
44	Glucose Limitation Alters Glutamine Metabolism in MUC1-Overexpressing Pancreatic Cancer Cells. Journal of Proteome Research, 2017, 16, 3536-3546.	3.7	27
45	Nitrite Derived from Endogenous Bacterial Nitric Oxide Synthase Activity Promotes Aerobic Respiration. MBio, 2017, 8, .	4.1	31
46	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
47	Mitochondrial dysfunction in glial cells: Implications for neuronal homeostasis and survival. Toxicology, 2017, 391, 109-115.	4.2	107
48	The future of NMR-based metabolomics. Current Opinion in Biotechnology, 2017, 43, 34-40.	6.6	651
49	Metabolic Investigations of the Molecular Mechanisms Associated with Parkinsonâ€™s Disease. Metabolites, 2017, 7, 22.	2.9	39
50	New frontiers in metabolomics: from measurement to insight. F1000Research, 2017, 6, 1148.	1.6	115
51	PCA as a Practical Indicator of OPLS-DA Model Reliability. Current Metabolomics, 2016, 4, 97-103.	0.5	284
52	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
53	A Urinary Metabolic Signature for Multiple Sclerosis and Neuromyelitis Optica. Journal of Proteome Research, 2016, 15, 659-666.	3.7	45
54	Redox Imbalance Underlies the Fitness Defect Associated with Inactivation of the Pta-AckA Pathway in Staphylococcus aureus. Journal of Proteome Research, 2016, 15, 1205-1212.	3.7	26

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55	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
56	Preface: â€œThe Whole is Greater Than the Sum of its Parts.â€• Aristotle. Current Metabolomics, 2015, 3, 2-3.	0.5	0
57	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
58	A sequential algorithm for multiblock orthogonal projections to latent structures. Chemometrics and Intelligent Laboratory Systems, 2015, 149, 33-39.	3.5	16
59	Generalized adaptive intelligent binning of multiway data. Chemometrics and Intelligent Laboratory Systems, 2015, 146, 42-46.	3.5	21
60	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
61	Deterministic multidimensional nonuniform gap sampling. Journal of Magnetic Resonance, 2015, 261, 19-26.	2.1	36
62	Combining DI-ESIâ€“MS and NMR datasets for metabolic profiling. Metabolomics, 2015, 11, 391-402.	3.0	60
63	Abstract 1172: (R,Râ€™)-4â€²-Methoxy-1-naphthylfenoterol decreases glycolytic activity in the PANC-1 pancreatic cancer cell line. , 2015, , .		0
64	Metabolic reprogramming induced by ketone bodies diminishes pancreatic cancer cachexia. Cancer & Metabolism, 2014, 2, 18.	5.0	182
65	Development of Cyclobuteneâ€and Cyclobutaneâ€Functionalized Fatty Acids with Inhibitory Activity against Mycobacterium tuberculosis. ChemMedChem, 2014, 9, 1838-1849.	3.2	5
66	Identification of Lowâ€Molecularâ€Weight Compounds Inhibiting Growth of Corynebacteria: Potential Lead Compounds for Antibiotics. ChemMedChem, 2014, 9, 282-285.	3.2	3
67	Simultaneous phase and scatter correction for NMR datasets. Chemometrics and Intelligent Laboratory Systems, 2014, 131, 1-6.	3.5	18
68	MVAPACK: A Complete Data Handling Package for NMR Metabolomics. ACS Chemical Biology, 2014, 9, 1138-1144.	3.4	96
69	Influence of Iron and Aeration on Staphylococcus aureus Growth, Metabolism, and Transcription. Journal of Bacteriology, 2014, 196, 2178-2189.	2.2	55
70	Growth and Preparation of Staphylococcus epidermidis for NMR Metabolomic Analysis. Methods in Molecular Biology, 2014, 1106, 71-91.	0.9	8
71	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
72	The Current State of Drug Discovery and a Potential Role for NMR Metabolomics. Journal of Medicinal Chemistry, 2014, 57, 5860-5870.	6.4	52

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73	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
74	Functional evolution of PLP-dependent enzymes based on active-site structural similarities. Proteins: Structure, Function and Bioinformatics, 2014, 82, 2597-2608.	2.6	21
75	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
76	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
77	Potential of Urinary Metabolites for Diagnosing Multiple Sclerosis. ACS Chemical Biology, 2013, 8, 684-690.	3.4	17
78	Utilities for quantifying separation in PCA/PLS-DA scores plots. Analytical Biochemistry, 2013, 433, 102-104.	2.4	160
79	Inactivation of the Pta-AckA Pathway Causes Cell Death in Staphylococcus aureus. Journal of Bacteriology, 2013, 195, 3035-3044.	2.2	68
80	NMR Metabolomics Analysis of Parkinson's Disease. Current Metabolomics, 2013, 1, 191-209.	0.5	29
81	Revisiting Protocols for the NMR Analysis of Bacterial Metabolomes. Journal of Integrated OMICS, 2013, 3, 120-137.	0.5	39
82	CcpA Regulates Arginine Biosynthesis in Staphylococcus aureus through Repression of Proline Catabolism. PLoS Pathogens, 2012, 8, e1003033.	4.7	91
83	Sample Preparation of Mycobacterium tuberculosis Extracts for Nuclear Magnetic Resonance Metabolomic Studies. Journal of Visualized Experiments, 2012, , e3673.	0.3	16
84	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
85	Application of NMR Metabolomics to Search for Human Disease Biomarkers. Combinatorial Chemistry and High Throughput Screening, 2012, 15, 595-610.	1.1	116
86	Analysis of bacterial biofilms using NMR-based metabolomics. Future Medicinal Chemistry, 2012, 4, 1273-1306.	2.3	89
87	Predicting the in Vivo Mechanism of Action for Drug Leads Using NMR Metabolomics. ACS Chemical Biology, 2012, 7, 166-171.	3.4	78
88	13C NMR Reveals No Evidence of nâ^Ï€* Interactions in Proteins. PLoS ONE, 2012, 7, e42075.	2.5	16
89	Multivariate Analysis in Metabolomics. Current Metabolomics, 2012, 1, 92-107.	0.5	804
90	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

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91	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
92	Abstract 5152: Targeting HIF1Î±-mediated metabolic alterations in pancreatic cancer. , 2012, , .		0
93	NMR Analysis of a Stress Response Metabolic Signaling Network. Journal of Proteome Research, 2011, 10, 3743-3754.	3.7	46
94	Correlation between Protein Function and Ligand Binding Profiles. Journal of Proteome Research, 2011, 10, 2538-2545.	3.7	12
95	Application of NMR and Molecular Docking in Structure-Based Drug Discovery. Topics in Current Chemistry, 2011, 326, 1-34.	4.0	39
96	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
97	Searching the protein structure database for ligand-binding site similarities using CPASS v.2. BMC Research Notes, 2011, 4, 17.	1.4	12
98	Bacterial protein structures reveal phylum dependent divergence. Computational Biology and Chemistry, 2011, 35, 24-33.	2.3	10
99	An inexpensive high-throughput nuclear magnetic resonance tube cleaning apparatus. Analytical Biochemistry, 2011, 416, 234-236.	2.4	2
100	Research Spotlight: Research in bioanalysis and separations at the University of Nebraska â€“ Lincoln. Bioanalysis, 2011, 3, 1065-1076.	1.5	0
101	Analysis of metabolomic PCA data using tree diagrams. Analytical Biochemistry, 2010, 399, 58-63.	2.4	54
102	Solution structure and function of YndB, an AHSA1 protein fromBacillus subtilis. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3328-3340.	2.6	13
103	PROFESS: a PROtein Function, Evolution, Structure and Sequence database. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq011-baq011.	3.0	6
104	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
105	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
106	NMR metabolomics and drug discovery. Magnetic Resonance in Chemistry, 2009, 47, S2-11.	1.9	92
107	Unique opportunities for NMR methods in structural genomics. Journal of Structural and Functional Genomics, 2009, 10, 101-106.	1.2	25
108	1H, 13C, and 15N NMR assignments for the Bacillus subtilis yndB START domain. Biomolecular NMR Assignments, 2009, 3, 191-194.	0.8	4

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109	Solution structure of the Pseudomonas putida protein PpPutA45 and its DNA complex. Proteins: Structure, Function and Bioinformatics, 2009, 75, 12-27.	2.6	12
110	Structure and function of Pseudomonas aeruginosa protein PA1324 (21â€“170). Protein Science, 2009, 18, 606-618.	7.6	13
111	Advances in nuclear magnetic resonance for drug discovery. Expert Opinion on Drug Discovery, 2009, 4, 1077-1098.	5.0	42
112	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
113	The application of FAST-NMR for the identification of novel drug discovery targets. Drug Discovery Today, 2008, 13, 172-179.	6.4	34
114	Estimating Proteinâ^'Ligand Binding Affinity Using High-Throughput Screening by NMR. ACS Combinatorial Science, 2008, 10, 948-958.	3.3	95
115	Rapid Proteinâ^'Ligand Costructures Using Chemical Shift Perturbations. Journal of the American Chemical Society, 2008, 130, 535-545.	13.7	54
116	Tricarboxylic Acid Cycle-Dependent Regulation of Staphylococcus epidermidis Polysaccharide Intercellular Adhesin Synthesis. Journal of Bacteriology, 2008, 190, 7621-7632.	2.2	73
117	Functional Genomics and NMR Spectroscopy. Combinatorial Chemistry and High Throughput Screening, 2007, 10, 676-697.	1.1	11
118	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
119	APPLICATIONS OF NUCLEAR MAGNETIC RESONANCE AND MASS SPECTROMETRY TO ANTICANCER DRUG DISCOVERY. , 2006, , 107-190.		6
120	NMR Metabolic Profiling ofAspergillusnidulansto Monitor Drug and Protein Activity. Journal of Proteome Research, 2006, 5, 1916-1923.	3.7	33
121	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
122	Negative impact of noise on the principal component analysis of NMR data. Journal of Magnetic Resonance, 2006, 178, 88-95.	2.1	71
123	FAST-NMR:Â Functional Annotation Screening Technology Using NMR Spectroscopy. Journal of the American Chemical Society, 2006, 128, 15292-15299.	13.7	48
124	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
125	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
126	Determining the optimal size of small molecule mixtures for high throughput NMR screening. Journal of Biomolecular NMR, 2005, 31, 243-258.	2.8	26

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127	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
128	An Integrated Platform for Automated Analysis of Protein NMR Structures. Methods in Enzymology, 2005, 394, 111-141.	1.0	67
129	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
130	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
131	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
132	Impact of Mobility on Structure-Based Drug Design for the MMPs. Journal of the American Chemical Society, 2002, 124, 12658-12659.	13.7	56
133	Applications of NMR to structure-based drug design in structural genomics. Journal of Structural and Functional Genomics, 2002, 2, 113-123.	1.2	22
134	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
135	Solution structure of the tumor necrosis factor receptor-1 death domain. Journal of Molecular Biology, 2001, 310, 895-906.	4.2	44
136	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
137	MS/NMR:Â 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
138	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
139	Solution Structure of B. subtilis Acyl Carrier Protein. Structure, 2001, 9, 277-287.	3.3	76
140	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
141	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
142	Structural Relatedness of Distinct Determinants Recognized by Monoclonal Antibody TP25.99 on Î²2-Microglobulin-Associated and Î²2-Microglobulin-Free HLA Class I Heavy Chains. Journal of Immunology, 2000, 165, 3275-3283.	0.8	49
143	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
144	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

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145	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
146	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
147	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
148	Solution Structure of ZipA, a Crucial Component ofEscherichia coliCell Divisionâ€. Biochemistry, 2000, 39, 9146-9156.	2.5	52
149	NMR Structure of Free RGS4 Reveals an Induced Conformational Change upon Binding GÎ±. Biochemistry, 2000, 39, 7063-7073.	2.5	38
150	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
151	1H, 15N, 13C, and 13CO assignments and secondary structure determination of RGS4. Journal of Biomolecular NMR, 1999, 15, 339-340.	2.8	1
152	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
153	Homology Model for Oncostatin M Based on NMR Structural Data. Biochemistry, 1998, 37, 10581-10588.	2.5	9
154	High-Resolution Solution Structure of the Inhibitor-Free Catalytic Fragment of Human Fibroblast Collagenase Determined by Multidimensional NMRâ€¡. Biochemistry, 1998, 37, 1495-1504.	2.5	40
155	Properly Oriented Heparinâ^'Decasaccharide-Induced Dimers Are the Biologically Active Form of Basic Fibroblast Growth Factorâ€,â€¡. Biochemistry, 1997, 36, 4782-4791.	2.5	111
156	Automated analysis of protein NMR assignments using methods from artificial intelligence. Journal of Molecular Biology, 1997, 269, 592-610.	4.2	292
157	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
158	Properly Oriented Heparinâ^'Decasaccharide-Induced Dimers Are the Biologically Active Form of Basic Fibroblast Growth Factor. Biochemistry, 1997, 36, 7936-7936.	2.5	5
159	High-Resolution Solution Structure of Basic Fibroblast Growth Factor Determined by Multidimensional Heteronuclear Magnetic Resonance Spectroscopy. Biochemistry, 1996, 35, 13552-13561.	2.5	63
160	Resonance assignments for Oncostatin M, a 24-kDa ?-helical protein. Journal of Biomolecular NMR, 1996, 7, 273-82.	2.8	21
161	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
162	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

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163	Three-Dimensional Solution Structure of Human Interleukin-4 by Multidimensional Heteronuclear Magnetic Resonance Spectroscopy. Science, 1992, 256, 1673-1677.	12.6	169
164	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
165	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
166	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
167	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
168	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
169	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
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