Hunter N B Moseley

List of Publications by Year
in descending order

79	2,180	331670 21	265206 42
papers	citations	h-index	g-index

104	104	104	2292
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Reduced-dimensionality NMR spectroscopy for high-throughput protein resonance assignment. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 8009-8014.	7.1	186
2	Stable isotope-resolved metabolomics and applications for drug development. , 2012, 133, 366-391.		186
3	Automated analysis of NMR assignments and structures for proteins. Current Opinion in Structural Biology, 1999, 9, 635-642.	5.7	176
4	Automatic Determination of Protein Backbone Resonance Assignments from Triple Resonance Nuclear Magnetic Resonance Data. Methods in Enzymology, 2001, 339, 91-108.	1.0	154
5	Assignment validation software suite for the evaluation and presentation of protein resonance assignment data. Journal of Biomolecular NMR, 2004, 28, 341-355.	2.8	94
6	Correcting for the effects of natural abundance in stable isotope resolved metabolomics experiments involving ultra-high resolution mass spectrometry. BMC Bioinformatics, 2010, 11, 139.	2.6	94
7	Automated Analysis of Protein NMR Assignments and Structures. Chemical Reviews, 2004, 104, 3541-3556.	47.7	90
8	Complete Relaxation and Conformational Exchange Matrix (CORCEMA) Analysis of NOESY Spectra of Interacting Systems; Two-Dimensional Transferred NOESY. Journal of Magnetic Resonance Series B, 1995, 108, 243-261.	1.6	88
9	Identification of Zinc-ligated Cysteine Residues Based on 13CÎ± and 13CÎ² Chemical Shift Data. Journal of Biomolecular NMR, 2006, 34, 259-269.	2.8	84
10	Isotopomer analysis of lipid biosynthesis by high resolution mass spectrometry and NMR. Analytica Chimica Acta, 2009, 651, 201-208.	5.4	79
11	A novel deconvolution method for modeling UDP-N-acetyl-D-glucosamine biosynthetic pathways based on 13C mass isotopologue profiles under non-steady-state conditions. BMC Biology, 2011, 9, 37.	3.8	73
12	An Integrated Platform for Automated Analysis of Protein NMR Structures. Methods in Enzymology, 2005, 394, 111-141.	1.0	67
13	Genome-Wide Profiling of PARP1 Reveals an Interplay with Gene Regulatory Regions and DNA Methylation. PLoS ONE, 2015, 10, e0135410.	2.5	55
14	Automated protein fold determination using a minimal NMR constraint strategy. Protein Science, 2003, 12, 1232-1246.	7.6	53
15	ERROR ANALYSIS AND PROPAGATION IN METABOLOMICS DATA ANALYSIS. Computational and Structural Biotechnology Journal, 2013, 4, e201301006.	4.1	43
16	Stable Isotope-Labeled Tracers for Metabolic Pathway Elucidation by GC-MS and FT-MS. Methods in Molecular Biology, 2014, 1198, 147-167.	0.9	42
17	Rapid analysis of protein backbone resonance assignments using cryogenic probes, a distributed Linux-based computing architecture, and an integrated set of spectral analysis tools. Journal of Structural and Functional Genomics, 2002, 2, 93-101.	1.2	38
18	A generalized approach to automated NMR peak list editing: application to reduced dimensionality triple resonance spectra. Journal of Magnetic Resonance, 2004, 170, 263-277.	2.1	38

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19	A Computational Framework for High-Throughput Isotopic Natural Abundance Correction of Omics-Level Ultra-High Resolution FT-MS Datasets. Metabolites, 2013, 3, 853-866.	2.9	30
20	Automated protein resonance assignments of magic angle spinning solid-state NMR spectra of Î²1 immunoglobulin binding domain of protein G (GB1). Journal of Biomolecular NMR, 2010, 48, 123-128.	2.8	27
21	Loss of CLN3, the gene mutated in juvenile neuronal ceroid lipofuscinosis, leads to metabolic impairment and autophagy induction in retinal pigment epithelium. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2020, 1866, 165883.	3.8	24
22	Development and in silico evaluation of large-scale metabolite identification methods using functional group detection for metabolomics. Frontiers in Genetics, 2014, 5, 237.	2.3	23
23	A lessâ€biased analysis of metalloproteins reveals novel zinc coordination geometries. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1470-1487.	2.6	23
24	Chemoselective detection and discrimination of carbonyl-containing compounds in metabolite mixtures by ¹ H-detected ¹⁵ N nuclear magnetic resonance. Magnetic Resonance in Chemistry, 2015, 53, 337-343.	1.9	22
25	Hepatic kinome atlas: An inâ€depth identification of kinase pathways in liver fibrosis of humans and rodents. Hepatology, 2022, 76, 1376-1388.	7.3	22
26	Relative Effects of Protein-Mediated and Ligand-Mediated Spin-Diffusion Pathways on Transferred NOESY, and Implications on the Accuracy of the Bound Ligand Conformation. Journal of Magnetic Resonance Series B, 1995, 107, 289-292.	1.6	21
27	Quantitative Determination of Conformational, Dynamic, and Kinetic Parameters of a Ligand-Protein/DNA Complex from a Complete Relaxation and Conformational Exchange Matrix Analysis of Intermolecular Transferred NOESYâ€. Biochemistry, 1997, 36, 5293-5299.	2.5	21
28	SPINS: standardized protein NMR storage. A data dictionary and object-oriented relational database for archiving protein NMR spectra. Journal of Biomolecular NMR, 2002, 24, 113-121.	2.8	19
29	CORCEMA evaluation of the potential role of intermolecular transferred NOESY in the characterization of ligand-receptor complexes. Journal of Computer-Aided Molecular Design, 1996, 10, 361-371.	2.9	18
30	Identification of Interactive Determinants on Idiotypic-Anti-idiotypic Antibodies through Comparison of Their Hydropathic Profiles. ImmunoMethods, 1994, 5, 107-113.	0.8	17
31	Untargeted Stable Isotope Probing of the Gut Microbiota Metabolome Using ¹³C-Labeled Dietary Fibers. Journal of Proteome Research, 2021, 20, 2904-2913.	3.7	16
32	New methods to identify high peak density artifacts in Fourier transform mass spectra and to mitigate their effects on high-throughput metabolomic data analysis. Metabolomics, 2018, 14, 125.	3.0	14
33	Cellular Origins of EGFRâ€Driven Lung Cancer Cells Determine Sensitivity to Therapy. Advanced Science, 2021, 8, e2101999.	11.2	13
34	MAIMS: a software tool for sensitive metabolic tracer analysis through the deconvolution of 13C mass isotopologue profiles of large composite metabolites. Metabolomics, 2017, 13, 1.	3.0	12
35	SPINS: A laboratory information management system for organizing and archiving intermediate and final results from NMR protein structure determinations. Proteins: Structure, Function and Bioinformatics, 2006, 62, 843-851.	2.6	11
36	Small Molecule Isotope Resolved Formula Enumeration: A Methodology for Assigning Isotopologues and Metabolite Formulas in Fourier Transform Mass Spectra. Analytical Chemistry, 2019, 91, 8933-8940.	6.5	11

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37	Advances in gene ontology utilization improve statistical power of annotation enrichment. PLoS ONE, 2019, 14, e0220728.	2.5	10
38	Moiety modeling framework for deriving moiety abundances from mass spectrometry measured isotopologues. BMC Bioinformatics, 2019, 20, 524.	2.6	10
39	The mwtab Python Library for RESTful Access and Enhanced Quality Control, Deposition, and Curation of the Metabolomics Workbench Data Repository. Metabolites, 2021, 11, 163.	2.9	10
40	A Python library for FAIRer access and deposition to the Metabolomics Workbench Data Repository. Metabolomics, 2018, 14, 64.	3.0	9
41	Deriving Lipid Classification Based on Molecular Formulas. Metabolites, 2020, 10, 122.	2.9	9
42	Aberrant coordination geometries discovered in the most abundant metalloproteins. Proteins: Structure, Function and Bioinformatics, 2017, 85, 885-907.	2.6	8
43	A fast and efficient python library for interfacing with the Biological Magnetic Resonance Data Bank. BMC Bioinformatics, 2017, 18, 175.	2.6	8
44	Robust Moiety Model Selection Using Mass Spectrometry Measured Isotopologues. Metabolites, 2020, 10, 118.	2.9	8
45	Untargeted Lipidomics of Non-Small Cell Lung Carcinoma Demonstrates Differentially Abundant Lipid Classes in Cancer vs. Non-Cancer Tissue. Metabolites, 2021, 11, 740.	2.9	8
46	Complete Relaxation and Conformational Exchange Matrix (CORCEMA) Analysis of NOESY Spectra of Reversibly Forming Ligand-Receptor Complexes Application to Transferred NOESY. , 2002, , 223-307.		7
47	Perspectives and expectations in structural bioinformatics of metalloproteins. Proteins: Structure, Function and Bioinformatics, 2017, 85, 938-944.	2.6	7
48	Auditing subtype inconsistencies among gene ontology concepts. , 2017, , .		7
49	SSIF: Subsumption-based Sub-term Inference Framework to audit Gene Ontology. Bioinformatics, 2020, 36, 3207-3214.	4.1	7
50	GOcats: A tool for categorizing Gene Ontology into subgraphs of user-defined concepts. PLoS ONE, 2020, 15, e0233311.	2.5	7
51	MEScan: a powerful statistical framework for genome-scale mutual exclusivity analysis of cancer mutations. Bioinformatics, 2021, 37, 1189-1197.	4.1	7
52	Detecting and accounting for multiple sources of positional variance in peak list registration analysis and spin system grouping. Journal of Biomolecular NMR, 2017, 68, 281-296.	2.8	6
53	Deregulation of a Network of mRNA and miRNA Genes Reveals That CK2 and MEK Inhibitors May Synergize to Induce Apoptosis KRAS-Active NSCLC. Cancer Informatics, 2019, 18, 117693511984350.	1.9	6
54	Atom Identifiers Generated by a Neighborhood-Specific Graph Coloring Method Enable Compound Harmonization across Metabolic Databases. Metabolites, 2020, 10, 368.	2.9	6

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55	A Lexical Approach to Identifying Subtype Inconsistencies in Biomedical Terminologies. , 2018, , .		5
56	Characterization of Squamous Cell Lung Cancers from Appalachian Kentucky. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 348-356.	2.5	5
57	A chemical interpretation of protein electron density maps in the worldwide protein data bank. PLoS ONE, 2020, 15, e0236894.	2.5	5
58	Automatic 13C chemical shift reference correction for unassigned protein NMR spectra. Journal of Biomolecular NMR, 2018, 72, 11-28.	2.8	4
59	Finding High-Quality Metal Ion-Centric Regions Across the Worldwide Protein Data Bank. Molecules, 2019, 24, 3179.	3.8	4
60	Hierarchical Harmonization of Atom-Resolved Metabolic Reactions across Metabolic Databases. Metabolites, 2021, 11, 431.	2.9	4
61	Entropy based analysis of vertebrate sperm protamines sequences: evidence of potential dityrosine and cysteine-tyrosine cross-linking in sperm protamines. BMC Genomics, 2020, 21, 277.	2.8	2
62	Coordination characterization of zinc metalloproteins. BMC Bioinformatics, 2014, 15, .	2.6	1
63	A less biased analysis of metalloproteins' coordination geometries. , 2015, , .		1
64	Structural Proteomics of Eukaryotic Gene Families. Scientific World Journal, The, 2002, 2, 32-32.	2.1	0
65	Automated Analysis of Protein NMR Assignments and Structures. ChemInform, 2004, 35, no.	0.0	0
66	Development of large-scale metabolite identification methods for metabolomics. BMC Bioinformatics, 2014, 15, P36.	2.6	0
67	Cover Image, Volume 85, Issue 5. Proteins: Structure, Function and Bioinformatics, 2017, 85, C1-C1.	2.6	0
68	BaMORC: A Software Package for Accurate and Robust 13C Reference Correction of Protein NMR Spectra. Natural Product Communications, 2019, 14, 1934578X1984914.	0.5	0
69	GOcats: A tool for categorizing Gene Ontology into subgraphs of user-defined concepts. , 2020, 15, e0233311.		0
70	GOcats: A tool for categorizing Gene Ontology into subgraphs of user-defined concepts. , 2020, 15, e0233311.		0
71	GOcats: A tool for categorizing Gene Ontology into subgraphs of user-defined concepts. , 2020, 15, e0233311.		0
72	GOcats: A tool for categorizing Gene Ontology into subgraphs of user-defined concepts. , 2020, 15, e0233311.		0

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73	A chemical interpretation of protein electron density maps in the worldwide protein data bank. , 2020, 15, e0236894.		0
74	A chemical interpretation of protein electron density maps in the worldwide protein data bank. , 2020, 15, e0236894.		0
75	A chemical interpretation of protein electron density maps in the worldwide protein data bank. , 2020, 15, e0236894.		0
76	A chemical interpretation of protein electron density maps in the worldwide protein data bank. , 2020, 15, e0236894.		0
77	A chemical interpretation of protein electron density maps in the worldwide protein data bank. , 2020, 15, e0236894.		0
78	A chemical interpretation of protein electron density maps in the worldwide protein data bank. , 2020, 15, e0236894.		0
79	Scan-Centric, Frequency-Based Method for Characterizing Peaks from Direct Injection Fourier Transform Mass Spectrometry Experiments. Metabolites, 2022, 12, 515.	2.9	0