Hunter N B Moseley

List of Publications by Year
in descending order

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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	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
2	Scan-Centric, Frequency-Based Method for Characterizing Peaks from Direct Injection Fourier Transform Mass Spectrometry Experiments. Metabolites, 2022, 12, 515.	2.9	0
3	MEScan: a powerful statistical framework for genome-scale mutual exclusivity analysis of cancer mutations. Bioinformatics, 2021, 37, 1189-1197.	4.1	7
4	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
5	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
6	Hierarchical Harmonization of Atom-Resolved Metabolic Reactions across Metabolic Databases. Metabolites, 2021, 11, 431.	2.9	4
7	Cellular Origins of EGFRâ€Driven Lung Cancer Cells Determine Sensitivity to Therapy. Advanced Science, 2021, 8, e2101999.	11.2	13
8	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
9	A chemical interpretation of protein electron density maps in the worldwide protein data bank. PLoS ONE, 2020, 15, e0236894.	2.5	5
10	Atom Identifiers Generated by a Neighborhood-Specific Graph Coloring Method Enable Compound Harmonization across Metabolic Databases. Metabolites, 2020, 10, 368.	2.9	6
11	SSIF: Subsumption-based Sub-term Inference Framework to audit Gene Ontology. Bioinformatics, 2020, 36, 3207-3214.	4.1	7
12	GOcats: A tool for categorizing Gene Ontology into subgraphs of user-defined concepts. PLoS ONE, 2020, 15, e0233311.	2.5	7
13	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
14	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
15	Robust Moiety Model Selection Using Mass Spectrometry Measured Isotopologues. Metabolites, 2020, 10, 118.	2.9	8
16	Deriving Lipid Classification Based on Molecular Formulas. Metabolites, 2020, 10, 122.	2.9	9
17	GOcats: A tool for categorizing Gene Ontology into subgraphs of user-defined concepts. , 2020, 15, e0233311.		0
18	GOcats: A tool for categorizing Gene Ontology into subgraphs of user-defined concepts. , 2020, 15, e0233311.		0

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19	GOcats: A tool for categorizing Gene Ontology into subgraphs of user-defined concepts. , 2020, 15, e0233311.		0
20	GOcats: A tool for categorizing Gene Ontology into subgraphs of user-defined concepts. , 2020, 15, e0233311.		0
21	A chemical interpretation of protein electron density maps in the worldwide protein data bank. , 2020, 15, e0236894.		0
22	A chemical interpretation of protein electron density maps in the worldwide protein data bank. , 2020, 15, e0236894.		0
23	A chemical interpretation of protein electron density maps in the worldwide protein data bank. , 2020, 15, e0236894.		0
24	A chemical interpretation of protein electron density maps in the worldwide protein data bank. , 2020, 15, e0236894.		0
25	A chemical interpretation of protein electron density maps in the worldwide protein data bank. , 2020, 15, e0236894.		0
26	A chemical interpretation of protein electron density maps in the worldwide protein data bank. , 2020, 15, e0236894.		0
27	Advances in gene ontology utilization improve statistical power of annotation enrichment. PLoS ONE, 2019, 14, e0220728.	2.5	10
28	Moiety modeling framework for deriving moiety abundances from mass spectrometry measured isotopologues. BMC Bioinformatics, 2019, 20, 524.	2.6	10
29	Finding High-Quality Metal Ion-Centric Regions Across the Worldwide Protein Data Bank. Molecules, 2019, 24, 3179.	3.8	4
30	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
31	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
32	BaMORC: A Software Package for Accurate and Robust 13C Reference Correction of Protein NMR Spectra. Natural Product Communications, 2019, 14, 1934578X1984914.	0.5	0
33	Characterization of Squamous Cell Lung Cancers from Appalachian Kentucky. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 348-356.	2.5	5
34	A Python library for FAIRer access and deposition to the Metabolomics Workbench Data Repository. Metabolomics, 2018, 14, 64.	3.0	9
35	A Lexical Approach to Identifying Subtype Inconsistencies in Biomedical Terminologies. , 2018, , .		5
36	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

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37	Automatic 13C chemical shift reference correction for unassigned protein NMR spectra. Journal of Biomolecular NMR, 2018, 72, 11-28.	2.8	4
38	Aberrant coordination geometries discovered in the most abundant metalloproteins. Proteins: Structure, Function and Bioinformatics, 2017, 85, 885-907.	2.6	8
39	Perspectives and expectations in structural bioinformatics of metalloproteins. Proteins: Structure, Function and Bioinformatics, 2017, 85, 938-944.	2.6	7
40	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
41	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
42	Cover Image, Volume 85, Issue 5. Proteins: Structure, Function and Bioinformatics, 2017, 85, C1-C1.	2.6	0
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	Auditing subtype inconsistencies among gene ontology concepts. , 2017, , .		7
45	A lessâ€biased analysis of metalloproteins reveals novel zinc coordination geometries. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1470-1487.	2.6	23
46	A less biased analysis of metalloproteins' coordination geometries. , 2015, , .		1
47	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
48	Genome-Wide Profiling of PARP1 Reveals an Interplay with Gene Regulatory Regions and DNA Methylation. PLoS ONE, 2015, 10, e0135410.	2.5	55
49	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
50	Development of large-scale metabolite identification methods for metabolomics. BMC Bioinformatics, 2014, 15, P36.	2.6	0
51	Coordination characterization of zinc metalloproteins. BMC Bioinformatics, 2014, 15, .	2.6	1
52	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
53	ERROR ANALYSIS AND PROPAGATION IN METABOLOMICS DATA ANALYSIS. Computational and Structural Biotechnology Journal, 2013, 4, e201301006.	4.1	43
54	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

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55	Stable isotope-resolved metabolomics and applications for drug development. , 2012, 133, 366-391.		186
56	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
57	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
58	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
59	Isotopomer analysis of lipid biosynthesis by high resolution mass spectrometry and NMR. Analytica Chimica Acta, 2009, 651, 201-208.	5.4	79
60	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
61	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
62	An Integrated Platform for Automated Analysis of Protein NMR Structures. Methods in Enzymology, 2005, 394, 111-141.	1.0	67
63	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
64	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
65	Automated Analysis of Protein NMR Assignments and Structures. ChemInform, 2004, 35, no.	0.0	0
66	Automated Analysis of Protein NMR Assignments and Structures. Chemical Reviews, 2004, 104, 3541-3556.	47.7	90
67	Automated protein fold determination using a minimal NMR constraint strategy. Protein Science, 2003, 12, 1232-1246.	7.6	53
68	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
69	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
70	Structural Proteomics of Eukaryotic Gene Families. Scientific World Journal, The, 2002, 2, 32-32.	2.1	0
71	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
72	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

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73	Automatic Determination of Protein Backbone Resonance Assignments from Triple Resonance Nuclear Magnetic Resonance Data. Methods in Enzymology, 2001, 339, 91-108.	1.0	154
74	Automated analysis of NMR assignments and structures for proteins. Current Opinion in Structural Biology, 1999, 9, 635-642.	5.7	176
75	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
76	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
77	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
78	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
79	Identification of Interactive Determinants on Idiotypic-Anti-idiotypic Antibodies through Comparison of Their Hydropathic Profiles. ImmunoMethods, 1994, 5, 107-113.	0.8	17