

Michael R Hoopmann

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

4,374
citations

147801

31
h-index

149698

56
g-index

66
all docs

66
docs citations

66
times ranked

6830
citing authors

#	ARTICLE	IF	CITATIONS
1	Discovery and Visualization of Uncharacterized Drug-Protein Adducts Using Mass Spectrometry. <i>Analytical Chemistry</i> , 2022, 94, 3501-3509.	6.5	7
2	Roles of bacteriophages, plasmids and CRISPR immunity in microbial community dynamics revealed using time-series integrated meta-omics. <i>Nature Microbiology</i> , 2021, 6, 123-135.	13.3	47
3	SPACEPro: A Software Tool for Analysis of Protein Sample Cleavage for Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2021, 20, 1911-1917.	3.7	3
4	A redox-active crosslinker reveals an essential and inhibitable oxidative folding network in the endoplasmic reticulum of malaria parasites. <i>PLoS Pathogens</i> , 2021, 17, e1009293.	4.7	9
5	2021 Special Issue on Software Tools and Resources: Finding the Right Tools for the Job. <i>Journal of Proteome Research</i> , 2021, 20, 1819-1820.	3.7	0
6	Lung proteomic biomarkers associated with chronic obstructive pulmonary disease. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2021, 321, L1119-L1130.	2.9	14
7	Hallstatt miners consumed blue cheese and beer during the Iron Age and retained a non-Westernized gut microbiome until the Baroque period. <i>Current Biology</i> , 2021, 31, 5149-5162.e6.	3.9	22
8	<i>Plasmodium falciparum</i> Calcium-Dependent Protein Kinase 4 is Critical for Male Gametogenesis and Transmission to the Mosquito Vector. <i>MBio</i> , 2021, 12, e0257521.	4.1	26
9	Absence of full-length dystrophin impairs normal maturation and contraction of cardiomyocytes derived from human-induced pluripotent stem cells. <i>Cardiovascular Research</i> , 2020, 116, 368-382.	3.8	47
10	Integration of time-series meta-omics data reveals how microbial ecosystems respond to disturbance. <i>Nature Communications</i> , 2020, 11, 5281.	12.8	57
11	DIALib-QC an assessment tool for spectral libraries in data-independent acquisition proteomics. <i>Nature Communications</i> , 2020, 11, 5251.	12.8	32
12	Insights from the First Phosphopeptide Challenge of the MS Resource Pillar of the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2020, 19, 4754-4765.	3.7	7
13	PTMProphet: Fast and Accurate Mass Modification Localization for the Trans-Proteomic Pipeline. <i>Journal of Proteome Research</i> , 2019, 18, 4262-4272.	3.7	80
14	Special Issue on Software Tools and Resources: Acknowledging the Toolmakers of Science. <i>Journal of Proteome Research</i> , 2019, 18, 575-575.	3.7	1
15	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019, 91, 6953-6961.	6.5	100
16	A Protein Standard That Emulates Homology for the Characterization of Protein Inference Algorithms. <i>Journal of Proteome Research</i> , 2018, 17, 1879-1886.	3.7	22
17	StPeter: Seamless Label-Free Quantification with the Trans-Proteomic Pipeline. <i>Journal of Proteome Research</i> , 2018, 17, 1314-1320.	3.7	19
18	Robust determination of differential abundance in shotgun proteomics using nonparametric statistics. <i>Molecular Omics</i> , 2018, 14, 424-436.	2.8	0

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19	ABRF Proteome Informatics Research Group (iPRG) 2016 Study: Inferring Proteoforms from Bottom-up Proteomics Data. <i>Journal of Biomolecular Techniques</i> , 2018, 29, 39-45.	1.5	6
20	The Iceman's Last Meal Consisted of Fat, Wild Meat, and Cereals. <i>Current Biology</i> , 2018, 28, 2348-2355.e9.	3.9	39
21	ABRF Proteome Informatics Research Group (iPRG) 2015 Study: Detection of Differentially Abundant Proteins in Label-Free Quantitative LC-MS/MS Experiments. <i>Journal of Proteome Research</i> , 2017, 16, 945-957.	3.7	42
22	An Open Data Format for Visualization and Analysis of Cross-Linked Mass Spectrometry Results. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 1728-1734.	2.8	9
23	Human SRMAtlas: A Resource of Targeted Assays to Quantify the Complete Human Proteome. <i>Cell</i> , 2016, 166, 766-778.	28.9	295
24	Testing and Validation of Computational Methods for Mass Spectrometry. <i>Journal of Proteome Research</i> , 2016, 15, 809-814.	3.7	34
25	The 5300-year-old <i>Helicobacter pylori</i> genome of the Iceman. <i>Science</i> , 2016, 351, 162-165.	12.6	200
26	The molecular architecture of the Dam1 kinetochore complex is defined by cross-linking based structural modelling. <i>Nature Communications</i> , 2015, 6, 8673.	12.8	51
27	Comparative integrated omics: identification of key functionalities in microbial community-wide metabolic networks. <i>Npj Biofilms and Microbiomes</i> , 2015, 1, 15007.	6.4	82
28	Quantitative proteogenomic profiling of epidermal barrier formation in vitro. <i>Journal of Dermatological Science</i> , 2015, 78, 173-180.	1.9	0
29	A Deeper Look into Comet's Implementation and Features. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 1865-1874.	2.8	175
30	Kojak: Efficient Analysis of Chemically Cross-Linked Protein Complexes. <i>Journal of Proteome Research</i> , 2015, 14, 2190-2198.	3.7	155
31	reSpect: Software for Identification of High and Low Abundance Ion Species in Chimeric Tandem Mass Spectra. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 1837-1847.	2.8	17
32	Decreased Gap Width in a Cylindrical High-Field Asymmetric Waveform Ion Mobility Spectrometry Device Improves Protein Discovery. <i>Analytical Chemistry</i> , 2015, 87, 12230-12237.	6.5	10
33	Kinetochore Biorientation in <i>Saccharomyces cerevisiae</i> Requires a Tightly Folded Conformation of the Ndc80 Complex. <i>Genetics</i> , 2014, 198, 1483-1493.	2.9	17
34	Community-integrated omics links dominance of a microbial generalist to fine-tuned resource usage. <i>Nature Communications</i> , 2014, 5, 5603.	12.8	75
35	Crux: Rapid Open Source Protein Tandem Mass Spectrometry Analysis. <i>Journal of Proteome Research</i> , 2014, 13, 4488-4491.	3.7	130
36	Performance evaluation of a dual linear ion trap-Fourier transform ion cyclotron resonance mass spectrometer for proteomics research. <i>Journal of Proteomics</i> , 2013, 88, 109-119.	2.4	25

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37	The State of the Human Proteome in 2012 as Viewed through PeptideAtlas. <i>Journal of Proteome Research</i> , 2013, 12, 162-171.	3.7	115
38	Comet: An open-source MS/MS sequence database search tool. <i>Proteomics</i> , 2013, 13, 22-24.	2.2	1,175
39	Current algorithmic solutions for peptide-based proteomics data generation and identification. <i>Current Opinion in Biotechnology</i> , 2013, 24, 31-38.	6.6	49
40	Mass Fingerprinting of Complex Mixtures: Protein Inference from High-Resolution Peptide Masses and Predicted Retention Times. <i>Journal of Proteome Research</i> , 2013, 12, 5730-5741.	3.7	15
41	Nanospray FAIMS Fractionation Provides Significant Increases in Proteome Coverage of Unfractionated Complex Protein Digests. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014985.	3.8	51
42	In Vivo Application of Photocleavable Protein Interaction Reporter Technology. <i>Journal of Proteome Research</i> , 2012, 11, 1027-1041.	3.7	29
43	Accurate Peptide Fragment Mass Analysis: Multiplexed Peptide Identification and Quantification. <i>Journal of Proteome Research</i> , 2012, 11, 1621-1632.	3.7	86
44	Recognizing Uncertainty Increases Robustness and Reproducibility of Mass Spectrometry-based Protein Inferences. <i>Journal of Proteome Research</i> , 2012, 11, 5586-5591.	3.7	36
45	Identification of Peptide Features in Precursor Spectra Using HardkÅr and KrÅnik. <i>Current Protocols in Bioinformatics</i> , 2012, 37, Unit13.18.	25.8	15
46	The Fasted/Fed Mouse Metabolic Acetylome: N6-Acetylation Differences Suggest Acetylation Coordinates Organ-Specific Fuel Switching. <i>Journal of Proteome Research</i> , 2011, 10, 4134-4149.	3.7	68
47	SILACTor: Software To Enable Dynamic SILAC Studies. <i>Analytical Chemistry</i> , 2011, 83, 8403-8410.	6.5	13
48	Quantitative Proteomic and Interaction Network Analysis of Cisplatin Resistance in HeLa Cells. <i>PLoS ONE</i> , 2011, 6, e19892.	2.5	37
49	Identification of ejaculated proteins in the house mouse (<i>Mus domesticus</i>) via isotopic labeling. <i>BMC Genomics</i> , 2011, 12, 306.	2.8	58
50	Cross-linking Measurements of In Vivo Protein Complex Topologies. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.006841.	3.8	81
51	Comparison of Database Search Strategies for High Precursor Mass Accuracy MS/MS Data. <i>Journal of Proteome Research</i> , 2010, 9, 1138-1143.	3.7	109
52	Deconvolution of Mixture Spectra from Ion-Trap Data-Independent-Acquisition Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2010, 82, 833-841.	6.5	124
53	Improved Strategies for Rapid Identification of Chemically Cross-Linked Peptides Using Protein Interaction Reporter Technology. <i>Journal of Proteome Research</i> , 2010, 9, 6323-6333.	3.7	32
54	Isotope Signatures Allow Identification of Chemically Cross-Linked Peptides by Mass Spectrometry: A Novel Method to Determine Interresidue Distances in Protein Structures through Cross-Linking. <i>Journal of Proteome Research</i> , 2010, 9, 3583-3589.	3.7	32

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55	Post Analysis Data Acquisition for the Iterative MS/MS Sampling of Proteomics Mixtures. <i>Journal of Proteome Research</i> , 2009, 8, 1870-1875.	3.7	56
56	Label-Free Comparative Analysis of Proteomics Mixtures Using Chromatographic Alignment of High-Resolution LC-MS Data. <i>Analytical Chemistry</i> , 2008, 80, 961-971.	6.5	60
57	Assessing the Dynamic Range and Peak Capacity of Nanoflow LC-FAIMS-MS on an Ion Trap Mass Spectrometer for Proteomics. <i>Analytical Chemistry</i> , 2008, 80, 6888-6897.	6.5	78
58	High-Speed Data Reduction, Feature Detection, and MS/MS Spectrum Quality Assessment of Shotgun Proteomics Data Sets Using High-Resolution Mass Spectrometry. <i>Analytical Chemistry</i> , 2007, 79, 5620-5632.	6.5	154