Michael J MacCoss

List of Publications by Year
in descending order

37 papers	2,354 citations	430874 18 h-index	345221 36 g-index
39 all docs	39 docs citations	39 times ranked	3203 citing authors

#	Article	IF	Citations
1	Does Data-Independent Acquisition Data Contain Hidden Gems? A Case Study Related to Alzheimer's Disease. Journal of Proteome Research, 2022, 21, 118-131.	3.7	15
2	Putting Humpty Dumpty Back Together Again: What Does Protein Quantification Mean in Bottom-Up Proteomics?. Journal of Proteome Research, 2022, 21, 891-898.	3.7	35
3	Discovery and Visualization of Uncharacterized Drug–Protein Adducts Using Mass Spectrometry. Analytical Chemistry, 2022, 94, 3501-3509.	6.5	7
4	Skyline Batch: An Intuitive User Interface for Batch Processing with Skyline. Journal of Proteome Research, 2022, 21, 289-294.	3.7	4
5	Development and Application of Multidimensional Lipid Libraries to Investigate Lipidomic Dysregulation Related to Smoke Inhalation Injury Severity. Journal of Proteome Research, 2022, 21, 232-242.	3.7	18
6	Prebiotic Membranes and Micelles Do Not Inhibit Peptide Formation During Dehydration. ChemBioChem, 2022, 23, .	2.6	3
7	Quantitative Isotope-Labeled Cross-Linker Proteomics Reveals Developmental Variation in Protein Interactions and Post-Translational Modifications in <i>Diaphorina citri</i>, the Citrus Greening Insect Vector. ACS Agricultural Science and Technology, 2022, 2, 486-500.	2.3	3
8	Building Spectral Libraries from Narrow-Window Data-Independent Acquisition Mass Spectrometry Data. Journal of Proteome Research, 2022, 21, 1382-1391.	3.7	6
9	CM1-driven assembly and activation of yeast γ-tubulin small complex underlies microtubule nucleation. ELife, 2021, 10, .	6.0	23
10	Affinity Purification–Mass Spectrometry Identifies a Novel Interaction between a Polerovirus and a Conserved Innate Immunity Aphid Protein that Regulates Transmission Efficiency. Journal of Proteome Research, 2021, 20, 3365-3387.	3.7	8
11	University of Washington Nathan Shock Center: innovation to advance aging research. GeroScience, 2021, 43, 2161-2165.	4.6	1
12	Comparison of Unit Resolution Versus High-Resolution Accurate Mass for Parallel Reaction Monitoring. Journal of Proteome Research, 2021, 20, 4435-4442.	3.7	18
13	Proteomic profiling dataset of chemical perturbations in multiple biological backgrounds. Scientific Data, 2021, 8, 226.	5.3	9
14	De novo design of tyrosine and serine kinase-driven protein switches. Nature Structural and Molecular Biology, 2021, 28, 762-770.	8.2	14
15	The Skyline ecosystem: Informatics for quantitative mass spectrometry proteomics. Mass Spectrometry Reviews, 2020, 39, 229-244.	5.4	469
16	Avant-garde: an automated data-driven DIA data curation tool. Nature Methods, 2020, 17, 1237-1244.	19.0	22
17	Highly Multiplex Targeted Proteomics Enabled by Real-Time Chromatographic Alignment. Analytical Chemistry, 2020, 92, 11809-11817.	6.5	17
18	Matrix-Matched Calibration Curves for Assessing Analytical Figures of Merit in Quantitative Proteomics. Journal of Proteome Research, 2020, 19, 1147-1153.	3.7	41

#	Article	IF	Citations
19	Peptidomics Approaches for the Identification of Bioactive Molecules from *Diaphorina citri*. Journal of Proteome Research, 2020, 19, 1392-1408.	3.7	11
20	Acquiring and Analyzing Data Independent Acquisition Proteomics Experiments without Spectrum Libraries. Molecular and Cellular Proteomics, 2020, 19, 1088-1103.	3.8	164
21	Thesaurus: quantifying phosphopeptide positional isomers. Nature Methods, 2019, 16, 703-706.	19.0	44
22	Improving Precursor Selectivity in Data-Independent Acquisition Using Overlapping Windows. Journal of the American Society for Mass Spectrometry, 2019, 30, 669-684.	2.8	101
23	Improving mitochondrial function with SS-31 reverses age-related redox stress and improves exercise tolerance in aged mice. Free Radical Biology and Medicine, 2019, 134, 268-281.	2.9	101
24	Specter: linear deconvolution for targeted analysis of data-independent acquisition mass spectrometry proteomics. Nature Methods, 2018, 15, 371-378.	19.0	58
25	Chromatogram libraries improve peptide detection and quantification by data independent acquisition mass spectrometry. Nature Communications, 2018, 9, 5128.	12.8	337
26	Calibration Using a Single-Point External Reference Material Harmonizes Quantitative Mass Spectrometry Proteomics Data between Platforms and Laboratories. Analytical Chemistry, 2018, 90, 13112-13117.	6.5	30
27	Proteomics Analysis Identifies Orthologs of Human Chitinase-Like Proteins as Inducers of Tube Morphogenesis Defects in *Drosophila melanogaster*. Genetics, 2017, 206, 973-984.	2.9	16
28	Statistical control of peptide and protein error rates in large-scale targeted data-independent acquisition analyses. Nature Methods, 2017, 14, 921-927.	19.0	189
29	PECAN: library-free peptide detection for data-independent acquisition tandem mass spectrometry data. Nature Methods, 2017, 14, 903-908.	19.0	158
30	A targeted proteomic strategy for the measurement of oral cancer candidate biomarkers in human saliva. Proteomics, 2016, 16, 159-173.	2.2	66
31	Visualization and Dissemination of Multidimensional Proteomics Data Comparing Protein Abundance During *Caenorhabditis elegans* Development. Journal of the American Society for Mass Spectrometry, 2015, 26, 1827-1836.	2.8	5
32	Peptide-Centric Proteome Analysis: An Alternative Strategy for the Analysis of Tandem Mass Spectrometry Data. Molecular and Cellular Proteomics, 2015, 14, 2301-2307.	3.8	146
33	Using Data Independent Acquisition (DIA) to Model High-responding Peptides for Targeted Proteomics Experiments. Molecular and Cellular Proteomics, 2015, 14, 2331-2340.	3.8	47
34	Proteomic analysis of adducted butyrylcholinesterase for biomonitoring organophosphorus exposures. Chemico-Biological Interactions, 2013, 203, 85-90.	4.0	12
35	The development of selected reaction monitoring methods for targeted proteomics via empirical refinement. Proteomics, 2012, 12, 1134-1141.	2.2	101
36	A method to determine the kinetics of multiple proteins in human infants with respiratory distress syndrome. Analytical and Bioanalytical Chemistry, 2012, 403, 2397-2402.	3.7	4

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37	Comparison between procedures using SDS for shotgun proteomic analyses of complex samples. Proteomics, 2011, 11, 2931-2935.	2.2	49