Ronald J Moore

List of Publications by Year
in descending order

43 papers	4,833 citations	159585 30 h-index	243625 44 g-index
49 all docs	49 docs citations	49 times ranked	6236 citing authors

#	Article	IF	Citations
1	Three-dimensional feature matching improves coverage for single-cell proteomics based on ion mobility filtering. Cell Systems, 2022, 13, 426-434.e4.	6.2	49
2	Hanging drop sample preparation improves sensitivity of spatial proteomics. Lab on A Chip, 2022, 22, 2869-2877.	6.0	12
3	Surfactant-assisted one-pot sample preparation for label-free single-cell proteomics. Communications Biology, 2021, 4, 265.	4.4	46
4	Enhancing Top-Down Proteomics of Brain Tissue with FAIMS. Journal of Proteome Research, 2021, 20, 2780-2795.	3.7	36
5	MetFish: a Metabolomics Pipeline for Studying Microbial Communities in Chemically Extreme Environments. MSystems, 2021, 6, e0105820.	3.8	5
6	Mass spectrometry-based direct detection of multiple types of protein thiol modifications in pancreatic beta cells under endoplasmic reticulum stress. Redox Biology, 2021, 46, 102111.	9.0	27
7	High-throughput and high-efficiency sample preparation for single-cell proteomics using a nested nanowell chip. Nature Communications, 2021, 12, 6246.	12.8	76
8	Automated mass spectrometry imaging of over 2000 proteins from tissue sections at 100-μm spatial resolution. Nature Communications, 2020, 11, 8.	12.8	178
9	A proteome-wide assessment of the oxidative stress paradigm for metal and metal-oxide nanomaterials in human macrophages. NanoImpact, 2020, 17, 100194.	4.5	29
10	Stochiometric quantification of the thiol redox proteome of macrophages reveals subcellular compartmentalization and susceptibility to oxidative perturbations. Redox Biology, 2020, 36, 101649.	9.0	34
11	High-Throughput Large-Scale Targeted Proteomics Assays for Quantifying Pathway Proteins in Pseudomonas putida KT2440. Frontiers in Bioengineering and Biotechnology, 2020, 8, 603488.	4.1	10
12	Sensitive Top-Down Proteomics Analysis of a Low Number of Mammalian Cells Using a Nanodroplet Sample Processing Platform. Analytical Chemistry, 2020, 92, 7087-7095.	6.5	38
13	Block Design with Common Reference Samples Enables Robust Large-Scale Label-Free Quantitative Proteome Profiling. Journal of Proteome Research, 2020, 19, 2863-2872.	3.7	10
14	Picoflow Liquid Chromatography–Mass Spectrometry for Ultrasensitive Bottom-Up Proteomics Using 2-μm-i.d. Open Tubular Columns. Analytical Chemistry, 2020, 92, 4711-4715.	6.5	55
15	Automated Coupling of Nanodroplet Sample Preparation with Liquid Chromatography–Mass Spectrometry for High-Throughput Single-Cell Proteomics. Analytical Chemistry, 2020, 92, 10588-10596.	6.5	105
16	An Improved Boosting to Amplify Signal with Isobaric Labeling (iBASIL) Strategy for Precise Quantitative Single-cell Proteomics. Molecular and Cellular Proteomics, 2020, 19, 828-838.	3.8	121
17	Tandem Mass Tag Labeling Facilitates Reversed-Phase Liquid Chromatography-Mass Spectrometry Analysis of Hydrophilic Phosphopeptides. Analytical Chemistry, 2019, 91, 11606-11613.	6.5	22
18	High-Throughput Single Cell Proteomics Enabled by Multiplex Isobaric Labeling in a Nanodroplet Sample Preparation Platform. Analytical Chemistry, 2019, 91, 13119-13127.	6.5	156

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19	Automated Nanoflow Two-Dimensional Reversed-Phase Liquid Chromatography System Enables In-Depth Proteome and Phosphoproteome Profiling of Nanoscale Samples. Analytical Chemistry, 2019, 91, 9707-9715.	6.5	36
20	Rapidly Assessing the Quality of Targeted Proteomics Experiments through Monitoring Stable-Isotope Labeled Standards. Journal of Proteome Research, 2019, 18, 694-699.	3.7	11
21	Nanodroplet processing platform for deep and quantitative proteome profiling of 10â€"100 mammalian cells. Nature Communications, 2018, 9, 882.	12.8	384
22	Quality Control Analysis in Real-time (QC-ART): A Tool for Real-time Quality Control Assessment of Mass Spectrometry-based Proteomics Data. Molecular and Cellular Proteomics, 2018, 17, 1824-1836.	3.8	25
23	Subnanogram proteomics: Impact of LC column selection, MS instrumentation and data analysis strategy on proteome coverage for trace samples. International Journal of Mass Spectrometry, 2018, 427, 4-10.	1.5	67
24	Proteome Profiling of 1 to 5 Spiked Circulating Tumor Cells Isolated from Whole Blood Using Immunodensity Enrichment, Laser Capture Microdissection, Nanodroplet Sample Processing, and Ultrasensitive nanoLCâ€"MS. Analytical Chemistry, 2018, 90, 11756-11759.	6.5	60
25	Proteomic Analysis of Single Mammalian Cells Enabled by Microfluidic Nanodroplet Sample Preparation and Ultrasensitive NanoLCâ€"MS. Angewandte Chemie - International Edition, 2018, 57, 12370-12374.	13.8	186
26	Spatially Resolved Proteome Mapping of Laser Capture Microdissected Tissue with Automated Sample Transfer to Nanodroplets. Molecular and Cellular Proteomics, 2018, 17, 1864-1874.	3.8	105
27	Reproducible workflow for multiplexed deep-scale proteome and phosphoproteome analysis of tumor tissues by liquid chromatographyâ€"mass spectrometry. Nature Protocols, 2018, 13, 1632-1661.	12.0	377
28	Nanowell-mediated two-dimensional liquid chromatography enables deep proteome profiling of <1000 mammalian cells. Chemical Science, 2018, 9, 6944-6951.	7.4	33
29	Time-resolved proteome profiling of normal lung development. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2018, 315, L11-L24.	2.9	25
30	Proteomic Analysis of Single Mammalian Cells Enabled by Microfluidic Nanodroplet Sample Preparation and Ultrasensitive NanoLCâ€"MS. Angewandte Chemie, 2018, 130, 12550-12554.	2.0	31
31	Informed-Proteomics: open-source software package for top-down proteomics. Nature Methods, 2017, 14, 909-914.	19.0	126
32	Spatially-Resolved Proteomics: Rapid Quantitative Analysis of Laser Capture Microdissected Alveolar Tissue Samples. Scientific Reports, 2016, 6, 39223.	3.3	69
33	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. Cell, 2016, 166, 755-765.	28.9	804
34	SNaPP: Simplified Nanoproteomics Platform for Reproducible Global Proteomic Analysis of Nanogram Protein Quantities. Endocrinology, 2016, 157, 1307-1314.	2.8	48
35	Sources of Technical Variability in Quantitative LCâ€"MS Proteomics: Human Brain Tissue Sample Analysis. Journal of Proteome Research, 2013, 12, 2128-2137.	3.7	162
36	Antibody-free, targeted mass-spectrometric approach for quantification of proteins at low picogram per milliliter levels in human plasma/serum. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 15395-15400.	7.1	211

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37	Large-Scale Multiplexed Quantitative Discovery Proteomics Enabled by the Use of an 18O-Labeled â€œUniversalâ€•Reference Sample. Journal of Proteome Research, 2009, 8, 290-299.	3.7	59
38	Fully Automated Four-Column Capillary LCâ€'MS System for Maximizing Throughput in Proteomic Analyses. Analytical Chemistry, 2008, 80, 294-302.	6.5	130
39	Chemically Etched Open Tubular and Monolithic Emitters for Nanoelectrospray Ionization Mass Spectrometry. Analytical Chemistry, 2006, 78, 7796-7801.	6.5	233
40	Comparative proteome analyses of human plasma followingin vivo lipopolysaccharide administration using multidimensional separations coupled with tandem mass spectrometry. Proteomics, 2005, 5, 572-584.	2.2	125
41	Quantitative Proteome Analysis of Human Plasma following in Vivo Lipopolysaccharide Administration Using 16O/18O Labeling and the Accurate Mass and Time Tag Approach. Molecular and Cellular Proteomics, 2005, 4, 700-709.	3.8	156
42	Automated 20 kpsi RPLC-MS and MS/MS with Chromatographic Peak Capacities of 1000â€'1500 and Capabilities in Proteomics and Metabolomics. Analytical Chemistry, 2005, 77, 3090-3100.	6.5	227
43	High-Efficiency On-Line Solid-Phase Extraction Coupling to 15â€'150-Î¼m-i.d. Column Liquid Chromatography for Proteomic Analysis. Analytical Chemistry, 2003, 75, 3596-3605.	6.5	104