

Ronald J Moore

List of Publications by Year in descending order

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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	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016, 166, 755-765.	28.9	804
2	Nanodroplet processing platform for deep and quantitative proteome profiling of 10 ⁴ -100 mammalian cells. <i>Nature Communications</i> , 2018, 9, 882.	12.8	384
3	Reproducible workflow for multiplexed deep-scale proteome and phosphoproteome analysis of tumor tissues by liquid chromatography-mass spectrometry. <i>Nature Protocols</i> , 2018, 13, 1632-1661.	12.0	377
4	Chemically Etched Open Tubular and Monolithic Emitters for Nanoelectrospray Ionization Mass Spectrometry. <i>Analytical Chemistry</i> , 2006, 78, 7796-7801.	6.5	233
5	Automated 20 kpsi RPLC-MS and MS/MS with Chromatographic Peak Capacities of 1000 ⁺ 1500 and Capabilities in Proteomics and Metabolomics. <i>Analytical Chemistry</i> , 2005, 77, 3090-3100.	6.5	227
6	Antibody-free, targeted mass-spectrometric approach for quantification of proteins at low picogram per milliliter levels in human plasma/serum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15395-15400.	7.1	211
7	Proteomic Analysis of Single Mammalian Cells Enabled by Microfluidic Nanodroplet Sample Preparation and Ultrasensitive NanoLC-MS. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 12370-12374.	13.8	186
8	Automated mass spectrometry imaging of over 2000 proteins from tissue sections at 100- $\frac{1}{4}$ m spatial resolution. <i>Nature Communications</i> , 2020, 11, 8.	12.8	178
9	Sources of Technical Variability in Quantitative LC-MS Proteomics: Human Brain Tissue Sample Analysis. <i>Journal of Proteome Research</i> , 2013, 12, 2128-2137.	3.7	162
10	Quantitative Proteome Analysis of Human Plasma following in Vivo Lipopolysaccharide Administration Using ¹⁶ O/ ¹⁸ O Labeling and the Accurate Mass and Time Tag Approach. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 700-709.	3.8	156
11	High-Throughput Single Cell Proteomics Enabled by Multiplex Isobaric Labeling in a Nanodroplet Sample Preparation Platform. <i>Analytical Chemistry</i> , 2019, 91, 13119-13127.	6.5	156
12	Fully Automated Four-Column Capillary LC-MS System for Maximizing Throughput in Proteomic Analyses. <i>Analytical Chemistry</i> , 2008, 80, 294-302.	6.5	130
13	Informed-Proteomics: open-source software package for top-down proteomics. <i>Nature Methods</i> , 2017, 14, 909-914.	19.0	126
14	Comparative proteome analyses of human plasma following in vivo lipopolysaccharide administration using multidimensional separations coupled with tandem mass spectrometry. <i>Proteomics</i> , 2005, 5, 572-584.	2.2	125
15	An Improved Boosting to Amplify Signal with Isobaric Labeling (iBASIL) Strategy for Precise Quantitative Single-cell Proteomics. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 828-838.	3.8	121
16	Spatially Resolved Proteome Mapping of Laser Capture Microdissected Tissue with Automated Sample Transfer to Nanodroplets. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1864-1874.	3.8	105
17	Automated Coupling of Nanodroplet Sample Preparation with Liquid Chromatography-Mass Spectrometry for High-Throughput Single-Cell Proteomics. <i>Analytical Chemistry</i> , 2020, 92, 10588-10596.	6.5	105
18	High-Efficiency On-Line Solid-Phase Extraction Coupling to 15 ⁺ 150- $\frac{1}{4}$ m-i.d. Column Liquid Chromatography for Proteomic Analysis. <i>Analytical Chemistry</i> , 2003, 75, 3596-3605.	6.5	104

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19	High-throughput and high-efficiency sample preparation for single-cell proteomics using a nested nanowell chip. <i>Nature Communications</i> , 2021, 12, 6246.	12.8	76
20	Spatially-Resolved Proteomics: Rapid Quantitative Analysis of Laser Capture Microdissected Alveolar Tissue Samples. <i>Scientific Reports</i> , 2016, 6, 39223.	3.3	69
21	Subnanogram proteomics: Impact of LC column selection, MS instrumentation and data analysis strategy on proteome coverage for trace samples. <i>International Journal of Mass Spectrometry</i> , 2018, 427, 4-10.	1.5	67
22	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 nanoLC-MS. <i>Analytical Chemistry</i> , 2018, 90, 11756-11759.	6.5	60
23	Large-Scale Multiplexed Quantitative Discovery Proteomics Enabled by the Use of an ¹⁸ O-Labeled α -Universal-Reference Sample. <i>Journal of Proteome Research</i> , 2009, 8, 290-299.	3.7	59
24	Picoflow Liquid Chromatography-Mass Spectrometry for Ultrasensitive Bottom-Up Proteomics Using 2-1/4m-i.d. Open Tubular Columns. <i>Analytical Chemistry</i> , 2020, 92, 4711-4715.	6.5	55
25	Three-dimensional feature matching improves coverage for single-cell proteomics based on ion mobility filtering. <i>Cell Systems</i> , 2022, 13, 426-434.e4.	6.2	49
26	SNaPP: Simplified Nanoproteomics Platform for Reproducible Global Proteomic Analysis of Nanogram Protein Quantities. <i>Endocrinology</i> , 2016, 157, 1307-1314.	2.8	48
27	Surfactant-assisted one-pot sample preparation for label-free single-cell proteomics. <i>Communications Biology</i> , 2021, 4, 265.	4.4	46
28	Sensitive Top-Down Proteomics Analysis of a Low Number of Mammalian Cells Using a Nanodroplet Sample Processing Platform. <i>Analytical Chemistry</i> , 2020, 92, 7087-7095.	6.5	38
29	Automated Nanoflow Two-Dimensional Reversed-Phase Liquid Chromatography System Enables In-Depth Proteome and Phosphoproteome Profiling of Nanoscale Samples. <i>Analytical Chemistry</i> , 2019, 91, 9707-9715.	6.5	36
30	Enhancing Top-Down Proteomics of Brain Tissue with FAIMS. <i>Journal of Proteome Research</i> , 2021, 20, 2780-2795.	3.7	36
31	Stoichiometric quantification of the thiol redox proteome of macrophages reveals subcellular compartmentalization and susceptibility to oxidative perturbations. <i>Redox Biology</i> , 2020, 36, 101649.	9.0	34
32	Nanowell-mediated two-dimensional liquid chromatography enables deep proteome profiling of <1000 mammalian cells. <i>Chemical Science</i> , 2018, 9, 6944-6951.	7.4	33
33	Proteomic Analysis of Single Mammalian Cells Enabled by Microfluidic Nanodroplet Sample Preparation and Ultrasensitive NanoLC-MS. <i>Angewandte Chemie</i> , 2018, 130, 12550-12554.	2.0	31
34	A proteome-wide assessment of the oxidative stress paradigm for metal and metal-oxide nanomaterials in human macrophages. <i>NanoImpact</i> , 2020, 17, 100194.	4.5	29
35	Mass spectrometry-based direct detection of multiple types of protein thiol modifications in pancreatic beta cells under endoplasmic reticulum stress. <i>Redox Biology</i> , 2021, 46, 102111.	9.0	27
36	Quality Control Analysis in Real-time (QC-ART): A Tool for Real-time Quality Control Assessment of Mass Spectrometry-based Proteomics Data. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1824-1836.	3.8	25

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37	Time-resolved proteome profiling of normal lung development. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2018, 315, L11-L24.	2.9	25
38	Tandem Mass Tag Labeling Facilitates Reversed-Phase Liquid Chromatography-Mass Spectrometry Analysis of Hydrophilic Phosphopeptides. <i>Analytical Chemistry</i> , 2019, 91, 11606-11613.	6.5	22
39	Hanging drop sample preparation improves sensitivity of spatial proteomics. <i>Lab on A Chip</i> , 2022, 22, 2869-2877.	6.0	12
40	Rapidly Assessing the Quality of Targeted Proteomics Experiments through Monitoring Stable-Isotope Labeled Standards. <i>Journal of Proteome Research</i> , 2019, 18, 694-699.	3.7	11
41	High-Throughput Large-Scale Targeted Proteomics Assays for Quantifying Pathway Proteins in <i>Pseudomonas putida</i> KT2440. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 603488.	4.1	10
42	Block Design with Common Reference Samples Enables Robust Large-Scale Label-Free Quantitative Proteome Profiling. <i>Journal of Proteome Research</i> , 2020, 19, 2863-2872.	3.7	10
43	MetFish: a Metabolomics Pipeline for Studying Microbial Communities in Chemically Extreme Environments. <i>MSystems</i> , 2021, 6, e0105820.	3.8	5