

Christophe Masselon

List of Publications by Year in descending order

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papers

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citations

81743

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72
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76
all docs

76
docs citations

76
times ranked

6519
citing authors

#	ARTICLE	IF	CITATIONS
1	A Nonlinear Model for Nano-Electro Mechanical Mass Sensing Signals Processing. IEEE Sensors Journal, 2021, 21, 21852-21861.	2.4	1
2	The emerging landscape of single-molecule protein sequencing technologies. Nature Methods, 2021, 18, 604-617.	9.0	198
3	Requirements and attributes of nano-resonator mass spectrometry for the analysis of intact viral particles. Analytical and Bioanalytical Chemistry, 2021, 413, 7147-7156.	1.9	2
4	Optomechanical mass spectrometry. Nature Communications, 2020, 11, 3781.	5.8	56
5	Protein Biomarker Discovery in Non-depleted Serum by Spectral Library-Based Data-Independent Acquisition Mass Spectrometry. Methods in Molecular Biology, 2019, 1959, 129-150.	0.4	4
6	Very Large Scale Integration Optomechanics: a cure for loneliness of NEMS resonators?. , 2018, , .		0
7	Neutral mass spectrometry of virus capsids above 100 megadaltons with nanomechanical resonators. Science, 2018, 362, 918-922.	6.0	92
8	Single-particle mass spectrometry with arrays of frequency-addressed nanomechanical resonators. Nature Communications, 2018, 9, 3283.	5.8	79
9	Reply to "Comparison of peptide retention prediction algorithm in reversed-phase chromatography. Comment on "Predictive chromatography of peptides and proteins as a complementary tool for proteomics"™, by O. V. Krokhn, Analyst, 2017, 142, DOI: 10.1039/c6an02510b. Analyst, The, 2017, 142, 2052-2053.	1.7	0
10	Large-Scale SRM Screen of Urothelial Bladder Cancer Candidate Biomarkers in Urine. Journal of Proteome Research, 2017, 16, 1617-1631.	1.8	25
11	hEID: An Intuitive Application Tool To Organize and Treat Large-Scale Proteomics Data. Journal of Proteome Research, 2016, 15, 3896-3903.	1.8	7
12	Predictive chromatography of peptides and proteins as a complementary tool for proteomics. Analyst, The, 2016, 141, 4816-4832.	1.7	33
13	Efficient Exploitation of Separation Space in Two-Dimensional Liquid Chromatography System for Comprehensive and Efficient Proteomic Analyses. Analytical Chemistry, 2016, 88, 11734-11741.	3.2	16
14	Screen-printed digital microfluidics combined with surface acoustic wave nebulization for hydrogen-deuterium exchange measurements. Journal of Chromatography A, 2016, 1439, 161-166.	1.8	21
15	Neutral particle mass spectrometry with nanomechanical systems. Nature Communications, 2015, 6, 6482.	5.8	120
16	Urine Sample Preparation and Fractionation for Global Proteome Profiling by LC-MS. Methods in Molecular Biology, 2015, 1243, 175-186.	0.4	9
17	Multiplexed and data-independent tandem mass spectrometry for global proteome profiling. Mass Spectrometry Reviews, 2014, 33, 452-470.	2.8	218
18	Shining a spotlight on intact proteins. Proteomics, 2014, 14, 1125-1127.	1.3	1

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19	Beyond laser microdissection technology: follow the yellow brick road for cancer research. American Journal of Cancer Research, 2014, 4, 1-28.	1.4	22
20	Surface Acoustic Wave Nebulization Facilitating Lipid Mass Spectrometric Analysis. Analytical Chemistry, 2012, 84, 6530-6537.	3.2	54
21	Inversion of chromatographic elution orders of peptides and its importance for proteomics. Journal of Analytical Chemistry, 2012, 67, 1014-1025.	0.4	10
22	Investigating the macropinocytic proteome of <i>Dictyostelium</i> amoebae by high-resolution mass spectrometry. Proteomics, 2012, 12, 241-245.	1.3	40
23	Surface Acoustic Wave Nebulization Produces Ions with Lower Internal Energy than Electrospray Ionization. Journal of the American Society for Mass Spectrometry, 2012, 23, 1062-1070.	1.2	53
24	Development of a Protein Standard Absolute Quantification (PSAQ [®]) assay for the quantification of Staphylococcus aureus enterotoxin A in serum. Journal of Proteomics, 2012, 75, 3041-3049.	1.2	39
25	Toward a standardized urine proteome analysis methodology. Proteomics, 2011, 11, 1160-1171.	1.3	56
26	Comprehensive human urine standards for comparability and standardization in clinical proteome analysis. Proteomics - Clinical Applications, 2010, 4, 464-478.	0.8	139
27	Identification of Cellular Targets in Human Intrahepatic Cholangiocarcinoma Using Laser Microdissection and Accurate Mass and Time Tag Proteomics. Molecular and Cellular Proteomics, 2010, 9, 1991-2004.	2.5	43
28	Chloroplast proteomics highlights the subcellular compartmentation of lipid metabolism. Progress in Lipid Research, 2010, 49, 128-158.	5.3	153
29	AT_CHLORO, a Comprehensive Chloroplast Proteome Database with Subplastidial Localization and Curated Information on Envelope Proteins. Molecular and Cellular Proteomics, 2010, 9, 1063-1084.	2.5	425
30	Use of models of biomacromolecule separation in AMT database generation for shotgun proteomics. Biochemistry (Moscow), 2009, 74, 1195-1202.	0.7	8
31	Standardization of retention time data for AMT tag proteomics database generation. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2009, 877, 433-440.	1.2	22
32	Isotope dilution strategies for absolute quantitative proteomics. Journal of Proteomics, 2009, 72, 740-749.	1.2	292
33	Chloroplast Proteomics and the Compartmentation of Plastidial Isoprenoid Biosynthetic Pathways. Molecular Plant, 2009, 2, 1154-1180.	3.9	199
34	Peptide Storage: Are You Getting the Best Return on Your Investment? Defining Optimal Storage Conditions for Proteomics Samples. Journal of Proteome Research, 2009, 8, 3778-3785.	1.8	50
35	A toolbox for validation of mass spectrometry peptides identification and generation of database: IRMa. Bioinformatics, 2009, 25, 1980-1981.	1.8	115
36	Prospects for monolithic nano-LC columns in shotgun proteomics. Analytical and Bioanalytical Chemistry, 2008, 392, 1291-1297.	1.9	16

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37	Influence of mass resolution on species matching in accurate mass and retention time (AMT) tag proteomics experiments. <i>Rapid Communications in Mass Spectrometry</i> , 2008, 22, 986-992.	0.7	13
38	AMT Tag Approach to Proteomic Characterization of <i>Deinococcus radiodurans</i> and <i>Shewanella oneidensis</i> . <i>Methods of Biochemical Analysis</i> , 2005, , 113-134.	0.2	4
39	High Throughput Quantitative Analysis of Serum Proteins Using Glycopeptide Capture and Liquid Chromatography Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 144-155.	2.5	187
40	Targeted Comparative Proteomics by Liquid Chromatography-Tandem Fourier Ion Cyclotron Resonance Mass Spectrometry. <i>Analytical Chemistry</i> , 2005, 77, 400-406.	3.2	47
41	Proteomic analyses using an accurate mass and time tag strategy. <i>BioTechniques</i> , 2004, 37, 621-639.	0.8	155
42	Considerations for electron capture dissociation efficiency in FTICR mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2004, 234, 131-136.	0.7	28
43	Nanoscale proteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2004, 378, 1037-1045.	1.9	47
44	Tailored noise waveform/collision-induced dissociation of ions stored in a linear ion trap combined with liquid chromatography/Fourier transform ion cyclotron resonance mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2004, 18, 2682-2690.	0.7	8
45	Proofreading Activity of Pfu Thermostable DNA Polymerase on a 6-O-Methylguanine-Containing Template Monitored by ESI-FTICR Mass Spectrometry. <i>ChemBioChem</i> , 2004, 5, 1012-1015.	1.3	3
46	Collisional activation of ions in RF ion traps and ion guides: The effective ion temperature treatment. <i>Journal of the American Society for Mass Spectrometry</i> , 2004, 15, 1616-1628.	1.2	63
47	FTICR mass spectrometry for qualitative and quantitative bioanalyses. <i>Current Opinion in Biotechnology</i> , 2004, 15, 3-11.	3.3	54
48	Ultrasensitive Proteomics Using High-Efficiency On-Line Micro-SPE-NanoLC-NanoESI MS and MS/MS. <i>Analytical Chemistry</i> , 2004, 76, 144-154.	3.2	188
49	Identification of tryptic peptides from large databases using multiplexed tandem mass spectrometry: simulations and experimental results. <i>Proteomics</i> , 2003, 3, 1279-1286.	1.3	31
50	Integration of Electrokinetic-Based Multidimensional Separation/Concentration Platform with Electrospray Ionization-Fourier Transform Ion Cyclotron Resonance-Mass Spectrometry for Proteome Analysis of <i>Shewanella oneidensis</i> . <i>Analytical Chemistry</i> , 2003, 75, 4432-4440.	3.2	70
51	High-Efficiency On-Line Solid-Phase Extraction Coupling to 150- μ m-i.d. Column Liquid Chromatography for Proteomic Analysis. <i>Analytical Chemistry</i> , 2003, 75, 3596-3605.	3.2	104
52	High-Performance Separations and Mass Spectrometric Methods for High-Throughput Proteomics using accurate Mass Tags. <i>Advances in Protein Chemistry</i> , 2003, 65, 85-131.	4.4	5
53	Review: The Use of Accurate Mass Tags for High-Throughput Microbial Proteomics. <i>OMICS A Journal of Integrative Biology</i> , 2002, 6, 61-90.	1.0	71
54	Global analysis of the <i>Deinococcus radiodurans</i> proteome by using accurate mass tags. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 11049-11054.	3.3	383

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55	Enrichment of Integral Membrane Proteins for Proteomic Analysis Using Liquid Chromatography-Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2002, 1, 351-360.	1.8	226
56	Gene expression profiling using advanced mass spectrometric approaches. <i>Journal of Mass Spectrometry</i> , 2002, 37, 1185-1198.	0.7	38
57	Mass measurement errors caused by local-frequency perturbations in FTICR mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2002, 13, 99-106.	1.2	79
58	ESI-FTICR mass spectrometry employing Data-dependent external ion selection and accumulation. <i>Journal of the American Society for Mass Spectrometry</i> , 2002, 13, 144-154.	1.2	69
59	Frequency shifts due to the interference of resolved peaks in magnitude-mode Fourier-transform ion cyclotron resonance mass spectra. <i>Journal of the American Society for Mass Spectrometry</i> , 2002, 13, 387-401.	1.2	7
60	Increased proteome coverage for quantitative peptide abundance measurements based upon high performance separations and DREAMS FTICR mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2002, 13, 954-963.	1.2	56
61	High-Throughput Peptide Identification from Protein Digests Using Data-Dependent Multiplexed Tandem FTICR Mass Spectrometry Coupled with Capillary Liquid Chromatography. <i>Analytical Chemistry</i> , 2001, 73, 3312-3322.	3.2	84
62	Design and Performance of an ESI Interface for Selective External Ion Accumulation Coupled to a Fourier Transform Ion Cyclotron Mass Spectrometer. <i>Analytical Chemistry</i> , 2001, 73, 253-261.	3.2	84
63	Ion discrimination during ion accumulation in a quadrupole interface external to a Fourier transform ion cyclotron resonance mass spectrometer. <i>International Journal of Mass Spectrometry</i> , 2001, 208, 205-225.	0.7	48
64	A dynamic ion cooling technique for FTICR mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2001, 12, 1169-1173.	1.2	14
65	Dynamically assisted gated trapping for Fourier transform ion cyclotron mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2001, 15, 1558-1561.	0.7	10
66	Rapid quantitative measurements of proteomes by Fourier transform ion cyclotron resonance mass spectrometry. <i>Electrophoresis</i> , 2001, 22, 1652-1668.	1.3	101
67	Identification of intrinsic order and disorder in the DNA repair protein XPA. <i>Protein Science</i> , 2001, 10, 560-571.	3.1	108
68	Aberrant mobility phenomena of the DNA repair protein XPA. <i>Protein Science</i> , 2001, 10, 1353-1362.	3.1	116
69	Characterization of human alcohol dehydrogenase isoenzymes by capillary isoelectric focusing mass spectrometry. <i>Electrophoresis</i> , 2000, 21, 2368-2375.	1.3	31
70	Accurate Mass Multiplexed Tandem Mass Spectrometry for High-Throughput Polypeptide Identification from Mixtures. <i>Analytical Chemistry</i> , 2000, 72, 1918-1924.	3.2	112
71	Matrix-assisted laser desorption/ionization Fourier transform mass spectrometry of luteinizing hormone releasing hormone-metal ion complexes. <i>Journal of the American Society for Mass Spectrometry</i> , 1999, 10, 19-26.	1.2	23
72	Retrieval of DNA Using Soft-Landing after Mass Analysis by ESI-FTICR for Enzymatic Manipulation. <i>Journal of the American Chemical Society</i> , 1999, 121, 8961-8962.	6.6	43

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73	Simulation of interstellar aromatic hydrocarbons using ion cyclotron resonance. Preliminary results. <i>Rapid Communications in Mass Spectrometry</i> , 1997, 11, 1619-1623.	0.7	24
74	Laser desorption Fourier transform ion cyclotron resonance mass spectrometry of selected pesticides extracted on C18silica solid-phase extraction membranes. <i>Analyst, The</i> , 1996, 121, 1429-1433.	1.7	25
75	Laser-desorption Fourier-transform mass spectrometry of triazines adsorbed on solid-phase extraction membranes. <i>Rapid Communications in Mass Spectrometry</i> , 1994, 8, 22-25.	0.7	11