

# Christophe Masselon

## List of Publications by Year in descending order

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75  
papers

5,388  
citations

81743

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72  
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76  
docs citations

76  
times ranked

6519  
citing authors

#	ARTICLE	IF	CITATIONS
1	AT_CHLORO, a Comprehensive Chloroplast Proteome Database with Subplastidial Localization and Curated Information on Envelope Proteins. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1063-1084.	2.5	425
2	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
3	Isotope dilution strategies for absolute quantitative proteomics. <i>Journal of Proteomics</i> , 2009, 72, 740-749.	1.2	292
4	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
5	Multiplexed and data-independent tandem mass spectrometry for global proteome profiling. <i>Mass Spectrometry Reviews</i> , 2014, 33, 452-470.	2.8	218
6	Chloroplast Proteomics and the Compartmentation of Plastidial Isoprenoid Biosynthetic Pathways. <i>Molecular Plant</i> , 2009, 2, 1154-1180.	3.9	199
7	The emerging landscape of single-molecule protein sequencing technologies. <i>Nature Methods</i> , 2021, 18, 604-617.	9.0	198
8	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
9	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
10	Proteomic analyses using an accurate mass and time tag strategy. <i>BioTechniques</i> , 2004, 37, 621-639.	0.8	155
11	Chloroplast proteomics highlights the subcellular compartmentation of lipid metabolism. <i>Progress in Lipid Research</i> , 2010, 49, 128-158.	5.3	153
12	Comprehensive human urine standards for comparability and standardization in clinical proteome analysis. <i>Proteomics - Clinical Applications</i> , 2010, 4, 464-478.	0.8	139
13	Neutral particle mass spectrometry with nanomechanical systems. <i>Nature Communications</i> , 2015, 6, 6482.	5.8	120
14	Aberrant mobility phenomena of the DNA repair protein XPA. <i>Protein Science</i> , 2001, 10, 1353-1362.	3.1	116
15	A toolbox for validation of mass spectrometry peptides identification and generation of database: IRMa. <i>Bioinformatics</i> , 2009, 25, 1980-1981.	1.8	115
16	Accurate Mass Multiplexed Tandem Mass Spectrometry for High-Throughput Polypeptide Identification from Mixtures. <i>Analytical Chemistry</i> , 2000, 72, 1918-1924.	3.2	112
17	Identification of intrinsic order and disorder in the DNA repair protein XPA. <i>Protein Science</i> , 2001, 10, 560-571.	3.1	108
18	High-Efficiency On-Line Solid-Phase Extraction Coupling to 150-µm i.d. Column Liquid Chromatography for Proteomic Analysis. <i>Analytical Chemistry</i> , 2003, 75, 3596-3605.	3.2	104

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19	Rapid quantitative measurements of proteomes by Fourier transform ion cyclotron resonance mass spectrometry. <i>Electrophoresis</i> , 2001, 22, 1652-1668.	1.3	101
20	Neutral mass spectrometry of virus capsids above 100 megadaltons with nanomechanical resonators. <i>Science</i> , 2018, 362, 918-922.	6.0	92
21	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
22	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
23	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
24	Single-particle mass spectrometry with arrays of frequency-addressed nanomechanical resonators. <i>Nature Communications</i> , 2018, 9, 3283.	5.8	79
25	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
26	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
27	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
28	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
29	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
30	Toward a standardized urine proteome analysis methodology. <i>Proteomics</i> , 2011, 11, 1160-1171.	1.3	56
31	Optomechanical mass spectrometry. <i>Nature Communications</i> , 2020, 11, 3781.	5.8	56
32	FTICR mass spectrometry for qualitative and quantitative bioanalyses. <i>Current Opinion in Biotechnology</i> , 2004, 15, 3-11.	3.3	54
33	Surface Acoustic Wave Nebulization Facilitating Lipid Mass Spectrometric Analysis. <i>Analytical Chemistry</i> , 2012, 84, 6530-6537.	3.2	54
34	Surface Acoustic Wave Nebulization Produces Ions with Lower Internal Energy than Electrospray Ionization. <i>Journal of the American Society for Mass Spectrometry</i> , 2012, 23, 1062-1070.	1.2	53
35	Peptide Storage: Are You Getting the Best Return on Your Investment? Defining Optimal Storage Conditions for Proteomics Samples. <i>Journal of Proteome Research</i> , 2009, 8, 3778-3785.	1.8	50
36	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

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37	Nanoscale proteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2004, 378, 1037-1045.	1.9	47
38	Targeted Comparative Proteomics by Liquid Chromatography-Tandem Fourier Ion Cyclotron Resonance Mass Spectrometry. <i>Analytical Chemistry</i> , 2005, 77, 400-406.	3.2	47
39	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
40	Identification of Cellular Targets in Human Intrahepatic Cholangiocarcinoma Using Laser Microdissection and Accurate Mass and Time Tag Proteomics. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1991-2004.	2.5	43
41	Investigating the macropinocytic proteome of <i>Dictyostelium</i> amoebae by high-resolution mass spectrometry. <i>Proteomics</i> , 2012, 12, 241-245.	1.3	40
42	Development of a Protein Standard Absolute Quantification (PSAQ <sub>α,ϕ</sub> ) assay for the quantification of <i>Staphylococcus aureus</i> enterotoxin A in serum. <i>Journal of Proteomics</i> , 2012, 75, 3041-3049.	1.2	39
43	Gene expression profiling using advanced mass spectrometric approaches. <i>Journal of Mass Spectrometry</i> , 2002, 37, 1185-1198.	0.7	38
44	Predictive chromatography of peptides and proteins as a complementary tool for proteomics. <i>Analyst</i> , 2016, 141, 4816-4832.	1.7	33
45	Characterization of human alcohol dehydrogenase isoenzymes by capillary isoelectric focusing "mass spectrometry. <i>Electrophoresis</i> , 2000, 21, 2368-2375.	1.3	31
46	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
47	Considerations for electron capture dissociation efficiency in FTICR mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2004, 234, 131-136.	0.7	28
48	Laser desorption Fourier transform ion cyclotron resonance mass spectrometry of selected pesticides extracted on C18silica solid-phase extraction membranes. <i>Analyst</i> , 1996, 121, 1429-1433.	1.7	25
49	Large-Scale SRM Screen of Urothelial Bladder Cancer Candidate Biomarkers in Urine. <i>Journal of Proteome Research</i> , 2017, 16, 1617-1631.	1.8	25
50	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
51	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
52	Standardization of retention time data for AMT tag proteomics database generation. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2009, 877, 433-440.	1.2	22
53	Beyond laser microdissection technology: follow the yellow brick road for cancer research. <i>American Journal of Cancer Research</i> , 2014, 4, 1-28.	1.4	22
54	Screen-printed digital microfluidics combined with surface acoustic wave nebulization for hydrogen-deuterium exchange measurements. <i>Journal of Chromatography A</i> , 2016, 1439, 161-166.	1.8	21

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55	Prospects for monolithic nano-LC columns in shotgun proteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2008, 392, 1291-1297.	1.9	16
56	Efficient Exploitation of Separation Space in Two-Dimensional Liquid Chromatography System for Comprehensive and Efficient Proteomic Analyses. <i>Analytical Chemistry</i> , 2016, 88, 11734-11741.	3.2	16
57	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
58	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
59	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
60	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
61	Inversion of chromatographic elution orders of peptides and its importance for proteomics. <i>Journal of Analytical Chemistry</i> , 2012, 67, 1014-1025.	0.4	10
62	Urine Sample Preparation and Fractionation for Global Proteome Profiling by LC-MS. <i>Methods in Molecular Biology</i> , 2015, 1243, 175-186.	0.4	9
63	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
64	Use of models of biomacromolecule separation in AMT database generation for shotgun proteomics. <i>Biochemistry (Moscow)</i> , 2009, 74, 1195-1202.	0.7	8
65	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
66	hEID: An Intuitive Application Tool To Organize and Treat Large-Scale Proteomics Data. <i>Journal of Proteome Research</i> , 2016, 15, 3896-3903.	1.8	7
67	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
68	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
69	Protein Biomarker Discovery in Non-depleted Serum by Spectral Library-Based Data-Independent Acquisition Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2019, 1959, 129-150.	0.4	4
70	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
71	Requirements and attributes of nano-resonator mass spectrometry for the analysis of intact viral particles. <i>Analytical and Bioanalytical Chemistry</i> , 2021, 413, 7147-7156.	1.9	2
72	Shining a spotlight on intact proteins. <i>Proteomics</i> , 2014, 14, 1125-1127.	1.3	1

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73	A Nonlinear Model for Nano-Electro Mechanical Mass Sensing Signals Processing. IEEE Sensors Journal, 2021, 21, 21852-21861.	2.4	1
74	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. Krokhin, Analyst, 2017, 142, DOI: 10.1039/c6an02510b. Analyst, The, 2017, 142, 2052-2053.	1.7	0
75	Very Large Scale Integration Optomechanics: a cure for loneliness of NEMS resonators?. , 2018, , .		0