

Myriam Ferro

List of Publications by Year in descending order

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80
papers

6,495
citations

81900

39
h-index

66911

78
g-index

81
all docs

81
docs citations

81
times ranked

8663
citing authors

#	ARTICLE	IF	CITATIONS
1	An innovative standard for LC-MS/MS-based HCP profiling and accurate quantity assessment: Application to batch consistency in viral vaccine samples. <i>Proteomics</i> , 2021, 21, e2000152.	2.2	5
2	Mixotrophic growth of the extremophile <i>Galdieria sulphuraria</i> reveals the flexibility of its carbon assimilation metabolism. <i>New Phytologist</i> , 2021, 231, 326-338.	7.3	24
3	Multimiomics Study of Bacterial Growth Arrest in a Synthetic Biology Application. <i>ACS Synthetic Biology</i> , 2021, 10, 2910-2926.	3.8	4
4	ProMetIS, deep phenotyping of mouse models by combined proteomics and metabolomics analysis. <i>Scientific Data</i> , 2021, 8, 311.	5.3	6
5	Systematic quantitative analysis of H2A and H2B variants by targeted proteomics. <i>Epigenetics and Chromatin</i> , 2018, 11, 2.	3.9	17
6	Multiplex and accurate quantification of acute kidney injury biomarker candidates in urine using Protein Standard Absolute Quantification (PSAQ) and targeted proteomics. <i>Talanta</i> , 2017, 164, 77-84.	5.5	24
7	ChloroKB: A Web Application for the Integration of Knowledge Related to Chloroplast Metabolic Network. <i>Plant Physiology</i> , 2017, 174, 922-934.	4.8	23
8	Down-regulation of NOX2 activity in phagocytes mediated by ATM-kinase dependent phosphorylation. <i>Free Radical Biology and Medicine</i> , 2017, 113, 1-15.	2.9	25
9	A proteomics assay to detect eight CBRN-relevant toxins in food. <i>Proteomics</i> , 2017, 17, 1600357.	2.2	28
10	DAPAR & ProStar: software to perform statistical analyses in quantitative discovery proteomics. <i>Bioinformatics</i> , 2017, 33, 135-136.	4.1	245
11	A community proposal to integrate proteomics activities in ELIXIR. <i>F1000Research</i> , 2017, 6, 875.	1.6	13
12	Bdf1 Bromodomains Are Essential for Meiosis and the Expression of Meiotic-Specific Genes. <i>PLoS Genetics</i> , 2017, 13, e1006541.	3.5	13
13	No plastidial calmodulin-like proteins detected by two targeted mass-spectrometry approaches and GFP fusion proteins. <i>New Negatives in Plant Science</i> , 2016, 3-4, 19-26.	0.9	5
14	Deletion of FtsH11 protease has impact on chloroplast structure and function in <i>Arabidopsis thaliana</i> when grown under continuous light. <i>Plant, Cell and Environment</i> , 2016, 39, 2530-2544.	5.7	20
15	hEID: An Intuitive Application Tool To Organize and Treat Large-Scale Proteomics Data. <i>Journal of Proteome Research</i> , 2016, 15, 3896-3903.	3.7	7
16	Looking for Missing Proteins in the Proteome of Human Spermatozoa: An Update. <i>Journal of Proteome Research</i> , 2016, 15, 3998-4019.	3.7	66
17	AtMic60 Is Involved in Plant Mitochondria Lipid Trafficking and Is Part of a Large Complex. <i>Current Biology</i> , 2016, 26, 627-639.	3.9	81
18	Accounting for the Multiple Natures of Missing Values in Label-Free Quantitative Proteomics Data Sets to Compare Imputation Strategies. <i>Journal of Proteome Research</i> , 2016, 15, 1116-1125.	3.7	345

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19	Spiked proteomic standard dataset for testing label-free quantitative software and statistical methods. <i>Data in Brief</i> , 2016, 6, 286-294.	1.0	30
20	Benchmarking quantitative label-free LC-MS data processing workflows using a complex spiked proteomic standard dataset. <i>Journal of Proteomics</i> , 2016, 132, 51-62.	2.4	68
21	In vivo spectroscopy and NMR metabolite fingerprinting approaches to connect the dynamics of photosynthetic and metabolic phenotypes in resurrection plant <i>Haberlea rhodopensis</i> during desiccation and recovery. <i>Frontiers in Plant Science</i> , 2015, 6, 564.	3.6	37
22	<i>DIGESTIF</i> : A Universal Quality Standard for the Control of Bottom-Up Proteomics Experiments. <i>Journal of Proteome Research</i> , 2015, 14, 787-803.	3.7	24
23	Multiplex Quantification of Protein Toxins in Human Biofluids and Food Matrices Using Immunoextraction and High-Resolution Targeted Mass Spectrometry. <i>Analytical Chemistry</i> , 2015, 87, 8473-8480.	6.5	62
24	Proteomic Analysis of the Multimeric Nuclear Egress Complex of Human Cytomegalovirus. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2132-2146.	3.8	79
25	A Foundation for Reliable Spatial Proteomics Data Analysis. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1937-1952.	3.8	49
26	Deciphering Thylakoid Sub-compartments using a Mass Spectrometry-based Approach. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2147-2167.	3.8	96
27	Mass Spectrometry-based Workflow for Accurate Quantification of <i>Escherichia coli</i> Enzymes: How Proteomics Can Play a Key Role in Metabolic Engineering. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 954-968.	3.8	14
28	Uncovering the Protein Lysine and Arginine Methylation Network in <i>Arabidopsis</i> Chloroplasts. <i>PLoS ONE</i> , 2014, 9, e95512.	2.5	37
29	Identification of a novel BET bromodomain inhibitor-sensitive, gene regulatory circuit that controls Rituximab response and tumour growth in aggressive lymphoid cancers. <i>EMBO Molecular Medicine</i> , 2013, 5, 1180-1195.	6.9	64
30	Complementary biochemical approaches applied to the identification of plastidial calmodulin-binding proteins. <i>Molecular BioSystems</i> , 2013, 9, 1234.	2.9	14
31	Proteomic strategy for the identification of critical actors in reorganization of the post-meiotic male genome. <i>Molecular Human Reproduction</i> , 2012, 18, 1-13.	2.8	21
32	Characterization of Chloroplastic Fructose 1,6-Bisphosphate Aldolases as Lysine-methylated Proteins in Plants. <i>Journal of Biological Chemistry</i> , 2012, 287, 21034-21044.	3.4	48
33	AT_CHLORO: A Chloroplast Protein Database Dedicated to Sub-Plastidial Localization. <i>Frontiers in Plant Science</i> , 2012, 3, 205.	3.6	48
34	PredAlgo: A New Subcellular Localization Prediction Tool Dedicated to Green Algae. <i>Molecular Biology and Evolution</i> , 2012, 29, 3625-3639.	8.9	270
35	Preparation of Envelope Membrane Fractions from <i>Arabidopsis</i> Chloroplasts for Proteomic Analysis and Other Studies. <i>Methods in Molecular Biology</i> , 2011, 775, 189-206.	0.9	11
36	Proteomic profiling of oil bodies isolated from the unicellular green microalga <i>Chlamydomonas reinhardtii</i> : With focus on proteins involved in lipid metabolism. <i>Proteomics</i> , 2011, 11, 4266-4273.	2.2	201

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37	Plant organelle proteomics: Collaborating for optimal cell function. <i>Mass Spectrometry Reviews</i> , 2011, 30, 772-853.	5.4	89
38	Identification of Rep-Associated Factors in Herpes Simplex Virus Type 1-Induced Adeno-Associated Virus Type 2 Replication Compartments. <i>Journal of Virology</i> , 2010, 84, 8871-8887.	3.4	22
39	Chloroplast proteomics highlights the subcellular compartmentation of lipid metabolism. <i>Progress in Lipid Research</i> , 2010, 49, 128-158.	11.6	153
40	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.	3.8	425
41	Chloroplast Proteomics and the Compartmentation of Plastidial Isoprenoid Biosynthetic Pathways. <i>Molecular Plant</i> , 2009, 2, 1154-1180.	8.3	199
42	Epigenetics of Spermiogenesis. , 2009, , 105-117.		1
43	The Chloroplast Envelope Proteome and Lipidome. <i>Plant Cell Monographs</i> , 2009, , 41-88.	0.4	8
44	Extent of N-terminal modifications in cytosolic proteins from eukaryotes. <i>Proteomics</i> , 2008, 8, 2809-2831.	2.2	136
45	Assessment of Organelle Purity Using Antibodies and Specific Assays. <i>Methods in Molecular Biology</i> , 2008, 432, 345-356.	0.9	6
46	PepLine: A Software Pipeline for High-Throughput Direct Mapping of Tandem Mass Spectrometry Data on Genomic Sequences. <i>Journal of Proteome Research</i> , 2008, 7, 1873-1883.	3.7	28
47	Purification and Proteomic Analysis of Chloroplasts and their Sub-Organellar Compartments. <i>Methods in Molecular Biology</i> , 2008, 432, 19-36.	0.9	41
48	A High Content in Lipid-modified Peripheral Proteins and Integral Receptor Kinases Features in the Arabidopsis Plasma Membrane Proteome. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1980-1996.	3.8	128
49	Pericentric heterochromatin reprogramming by new histone variants during mouse spermiogenesis. <i>Journal of Cell Biology</i> , 2007, 176, 283-294.	5.2	261
50	Post-meiotic Shifts in HSPA2/HSP70.2 Chaperone Activity during Mouse Spermatogenesis. <i>Journal of Biological Chemistry</i> , 2006, 281, 37888-37892.	3.4	106
51	A versatile method for deciphering plant membrane proteomes. <i>Journal of Experimental Botany</i> , 2006, 57, 1579-1589.	4.8	33
52	A methionine synthase homolog is associated with secretory vesicles in tobacco pollen tubes. <i>Planta</i> , 2005, 221, 776-789.	3.2	9
53	Identification of New Intrinsic Proteins in Arabidopsis Plasma Membrane Proteome. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 675-691.	3.8	233
54	The hydrophobic proteome of mitochondrial membranes from Arabidopsis cell suspensions. <i>Phytochemistry</i> , 2004, 65, 1693-1707.	2.9	135

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55	The potentials of MS-based subproteomic approaches in medical science: The case of lysosomes and breast cancer. <i>Mass Spectrometry Reviews</i> , 2004, 23, 393-442.	5.4	19
56	Plant membrane proteomics. <i>Plant Physiology and Biochemistry</i> , 2004, 42, 943-962.	5.8	85
57	Identification and characterization of plant glycerophosphodiester phosphodiesterase. <i>Biochemical Journal</i> , 2004, 379, 601-607.	3.7	27
58	Proteomics of chloroplast envelope membranes. <i>Photosynthesis Research</i> , 2003, 78, 205-230.	2.9	63
59	Proteomics of the Chloroplast Envelope Membranes from <i>Arabidopsis thaliana</i> . <i>Molecular and Cellular Proteomics</i> , 2003, 2, 325-345.	3.8	405
60	Integral membrane proteins of the chloroplast envelope: Identification and subcellular localization of new transporters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 11487-11492.	7.1	241
61	The Zinc- and Calcium-binding S100B Interacts and Co-localizes with IQGAP1 during Dynamic Rearrangement of Cell Membranes. <i>Journal of Biological Chemistry</i> , 2002, 277, 49998-50007.	3.4	78
62	Non-canonical Transit Peptide for Import into the Chloroplast. <i>Journal of Biological Chemistry</i> , 2002, 277, 47770-47778.	3.4	154
63	Symbiotic and Taxonomic Diversity of Rhizobia Isolated from <i>Acacia tortilis</i> subsp. <i>raddiana</i> in Africa. <i>Systematic and Applied Microbiology</i> , 2002, 25, 130-145.	2.8	65
64	The pivotal role of tandem mass spectrometry in structural determinations of Nod factors produced by Rhizobia. <i>International Journal of Mass Spectrometry</i> , 2002, 219, 703-716.	1.5	6
65	A nuclear protein in <i>Schizosaccharomyces pombe</i> with homology to the human tumour suppressor Fhit has decapping activity. <i>Molecular Microbiology</i> , 2002, 46, 49-62.	2.5	29
66	A novel tandem quadrupole mass spectrometer allowing gaseous collisional activation and surface induced dissociation. <i>Journal of Mass Spectrometry</i> , 2001, 36, 1260-1268.	1.6	21
67	The Human Protein HSPC021 Interacts with Int-6 and Is Associated with Eukaryotic Translation Initiation Factor 3. <i>Journal of Biological Chemistry</i> , 2001, 276, 45988-45995.	3.4	26
68	The Giant Protein AHNAK Is a Specific Target for the Calcium- and Zinc-binding S100B Protein. <i>Journal of Biological Chemistry</i> , 2001, 276, 23253-23261.	3.4	95
69	Organic solvent extraction as a versatile procedure to identify hydrophobic chloroplast membrane proteins. <i>Electrophoresis</i> , 2000, 21, 3517-3526.	2.4	152
70	Differentiation of O-acetyl and O-carbamoyl. <i>Journal of the American Society for Mass Spectrometry</i> , 2000, 11, 301-311.	2.8	15
71	<i>Bradyrhizobium</i> sp. Strains That Nodulate the Leguminous Tree <i>Acacia albida</i> Produce Fucosylated and Partially Sulfated Nod Factors. <i>Applied and Environmental Microbiology</i> , 2000, 66, 5078-5082.	3.1	31
72	Identification of the Melatonin-binding Site MT 3 as the Quinone Reductase 2. <i>Journal of Biological Chemistry</i> , 2000, 275, 31311-31317.	3.4	493

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73	Structure of the Mesorhizobium huakuii and Rhizobium galegae Nod factors: a cluster of phylogenetically related legumes are nodulated by rhizobia producing Nod factors with alpha,beta-unsaturated N-acyl substitutions. Molecular Microbiology, 1999, 34, 227-237.	2.5	55
74	Inexpensive implementation of low flow-rate electrospray on a Micromass Quattro I mass spectrometer. Journal of Mass Spectrometry, 1998, 33, 1261-1264.	1.6	2
75	Nod Factors from Sinorhizobium saheli and S. teranga bv. sesbaniae Are Both Arabinosylated and Fucosylated, a Structural Feature Specific to Sesbania rostrata Symbionts. Molecular Plant-Microbe Interactions, 1997, 10, 879-890.	2.6	40
76	Nod Factors of Azorhizobium caulinodans Strain ORS571 Can Be Glycosylated with an Arabinosyl Group, a Fucosyl Group, or Both. Molecular Plant-Microbe Interactions, 1997, 10, 683-687.	2.6	41
77	Sinorhizobium teranga bv. acaciae ORS1073 and Rhizobium sp. strain ORS1001, two distantly related Acacia-nodulating strains, produce similar Nod factors that are O carbamoylated, N methylated, and mainly sulfated. Journal of Bacteriology, 1997, 179, 3079-3083.	2.2	37
78	The common nodABC genes of Rhizobium meliloti are host-range determinants. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 15305-15310.	7.1	121
79	The Rhizobium meliloti regulatory nodD3 and syrM genes control the synthesis of a particular class of nodulation factors N-acylated by (omega-1)-hydroxylated fatty acids.. EMBO Journal, 1994, 13, 2139-2149.	7.8	55
80	Plasma Membrane: A Peculiar Status Among the Cell Membrane Systems. , 0, , 309-326.		1