

Christine Carapito

List of Publications by Year in descending order

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87
papers

3,572
citations

126858

33
h-index

149623

56
g-index

90
all docs

90
docs citations

90
times ranked

6348
citing authors

#	ARTICLE	IF	CITATIONS
1	Human SRMATlas: A Resource of Targeted Assays to Quantify the Complete Human Proteome. <i>Cell</i> , 2016, 166, 766-778.	13.5	295
2	Reproducible Quantification of Cancer-Associated Proteins in Body Fluids Using Targeted Proteomics. <i>Science Translational Medicine</i> , 2012, 4, 142ra94.	5.8	236
3	A Tale of Two Oxidation States: Bacterial Colonization of Arsenic-Rich Environments. <i>PLoS Genetics</i> , 2007, 3, e53.	1.5	166
4	Studying the Fate of Tumor Extracellular Vesicles at High Spatiotemporal Resolution Using the Zebrafish Embryo. <i>Developmental Cell</i> , 2019, 48, 554-572.e7.	3.1	160
5	Proline: an efficient and user-friendly software suite for large-scale proteomics. <i>Bioinformatics</i> , 2020, 36, 3148-3155.	1.8	155
6	Diversity of the exoproteome of <i>Fusarium graminearum</i> grown on plant cell wall. <i>Current Genetics</i> , 2005, 48, 366-379.	0.8	128
7	Analytical characterization of biosimilar antibodies and Fc-fusion proteins. <i>TrAC - Trends in Analytical Chemistry</i> , 2013, 48, 81-95.	5.8	104
8	Ortho-proteogenomics: Multiple proteomes investigation through orthology and a new MS-based protocol. <i>Genome Research</i> , 2009, 19, 128-135.	2.4	99
9	Proteomic analysis of grapevine (<i>Vitis vinifera</i> L.) tissues subjected to herbicide stress. <i>Journal of Experimental Botany</i> , 2005, 56, 2783-2795.	2.4	88
10	Zika virus enhances monocyte adhesion and transmigration favoring viral dissemination to neural cells. <i>Nature Communications</i> , 2019, 10, 4430.	5.8	83
11	Bacterial protein signals are associated with Crohn's disease. <i>Gut</i> , 2014, 63, 1566-1577.	6.1	80
12	Proteome Analysis of Plant-Virus Interactome. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 2279-2297.	2.5	75
13	Enhanced structural and functional genome elucidation of the arsenite-oxidizing strain <i>Herminiimonas arsenicoxydans</i> by proteomics data. <i>Biochimie</i> , 2009, 91, 192-203.	1.3	75
14	N-terminome analysis of the human mitochondrial proteome. <i>Proteomics</i> , 2015, 15, 2519-2524.	1.3	74
15	Identification of driver genes for critical forms of COVID-19 in a deeply phenotyped young patient cohort. <i>Science Translational Medicine</i> , 2022, 14, eabj7521.	5.8	71
16	Ral GTPases promote breast cancer metastasis by controlling biogenesis and organ targeting of exosomes. <i>ELife</i> , 2021, 10, .	2.8	70
17	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.	1.2	68
18	Characterization of the Active Bacterial Community Involved in Natural Attenuation Processes in Arsenic-Rich Creek Sediments. <i>Microbial Ecology</i> , 2011, 61, 793-810.	1.4	67

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19	Looking for Missing Proteins in the Proteome of Human Spermatozoa: An Update. <i>Journal of Proteome Research</i> , 2016, 15, 3998-4019.	1.8	66
20	Taxonomic and functional prokaryote diversity in mildly arsenic-contaminated sediments. <i>Research in Microbiology</i> , 2011, 162, 877-887.	1.0	51
21	<sc>MSDA</sc>, a proteomics software suite for inâ€depth <sc>M</sc>ass <sc>S</sc>pectrometry <sc>D</sc>ata <sc>A</sc>nalysis using grid computing. <i>Proteomics</i> , 2014, 14, 1014-1019.	1.3	51
22	<i>NCKAP1L</i> defects lead to a novel syndrome combining immunodeficiency, lymphoproliferation, and hyperinflammation. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	48
23	An Improved Stable Isotope N-Terminal Labeling Approach with Light/Heavy TMPP To Automate Proteogenomics Data Validation: dN-TOP. <i>Journal of Proteome Research</i> , 2013, 12, 3063-3070.	1.8	45
24	Cleavable Binary Dyads: Simplifying Data Extraction and Increasing Storage Density in Digital Polymers. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 6266-6269.	7.2	44
25	MS-DECODER: Milliseconds Sequencing of Coded Polymers. <i>Macromolecules</i> , 2017, 50, 8290-8296.	2.2	43
26	Detection of Prion Protein in Urine-Derived Injectable Fertility Products by a Targeted Proteomic Approach. <i>PLoS ONE</i> , 2011, 6, e17815.	1.1	42
27	Proteomics profiling reveals novel proteins and functions of the plant stigma exudate. <i>Journal of Experimental Botany</i> , 2013, 64, 5695-5705.	2.4	41
28	Tenascin-C Orchestrates an Immune-Suppressive Tumor Microenvironment in Oral Squamous Cell Carcinoma. <i>Cancer Immunology Research</i> , 2020, 8, 1122-1138.	1.6	40
29	Identification ofÂgenes andÂproteins involved inÂtheÂpleiotropic response toÂarsenic stress inÂ <i>CaenibacterÂarsenoxidans</i> , aÂmetalloresistant beta-proteobacterium with anÂunsequenced genome. <i>Biochimie</i> , 2006, 88, 595-606.	1.3	39
30	Transâ€Proteomic Pipeline supports and improves analysis of electron transfer dissociation data sets. <i>Proteomics</i> , 2010, 10, 1190-1195.	1.3	39
31	Nuclear proteome analysis of undifferentiated mouse embryonic stem and germ cells. <i>Electrophoresis</i> , 2008, 29, 2381-2390.	1.3	38
32	Multi-omics dataset to decipher the complexity of drug resistance in diffuse large B-cell lymphoma. <i>Scientific Reports</i> , 2019, 9, 895.	1.6	38
33	<i>In situ</i> proteo-metabolomics reveals metabolite secretion by the acid mine drainage bio-indicator, <i>Euglena mutabilis</i>. <i>ISME Journal</i> , 2012, 6, 1391-1402.	4.4	37
34	Multigenic families and proteomics: Extended protein characterization as a tool for paralog gene identification. <i>Proteomics</i> , 2005, 5, 450-460.	1.3	35
35	Computational and Mass-Spectrometry-Based Workflow for the Discovery and Validation of Missing Human Proteins: Application to Chromosomes 2 and 14. <i>Journal of Proteome Research</i> , 2015, 14, 3621-3634.	1.8	35
36	MS2Rescore: Data-Driven Rescoring Dramatically Boosts Immunopeptide Identification Rates. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100266.	2.5	34

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37	MetAP1 and MetAP2 drive cell selectivity for a potent anti-cancer agent in synergy, by controlling glutathione redox state. <i>Oncotarget</i> , 2016, 7, 63306-63323.	0.8	32
38	Spiked proteomic standard dataset for testing label-free quantitative software and statistical methods. <i>Data in Brief</i> , 2016, 6, 286-294.	0.5	30
39	Systematic LC-MS Analysis of Labile Post-Translational Modifications in Complex Mixtures. <i>Journal of Proteome Research</i> , 2009, 8, 2608-2614.	1.8	29
40	Comparative Expression Study of the Endo- α -G Protein Coupled Receptor (GPCR) Repertoire in Human Glioblastoma Cancer Stem-like Cells, U87-MG Cells and Non Malignant Cells of Neural Origin Unveils New Potential Therapeutic Targets. <i>PLoS ONE</i> , 2014, 9, e91519.	1.1	28
41	Efficient hydrolysis of hemicellulose by a <i>Fusarium graminearum</i> xylanase blend produced at high levels in <i>Escherichia coli</i> . <i>Bioresource Technology</i> , 2009, 100, 845-850.	4.8	27
42	The plant stigma exudate. <i>Plant Signaling and Behavior</i> , 2014, 9, e28274.	1.2	27
43	Proteomic tools to decipher microbial community structure and functioning. <i>Environmental Science and Pollution Research</i> , 2015, 22, 13599-13612.	2.7	27
44	Nucleolar Proteome Analysis and Proteasomal Activity Assays Reveal a Link between Nucleolus and 26S Proteasome in <i>A. thaliana</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1815.	1.7	26
45	Dual Data-Independent Acquisition Approach Combining Global HCP Profiling and Absolute Quantification of Key Impurities during Bioprocess Development. <i>Analytical Chemistry</i> , 2018, 90, 1241-1247.	3.2	26
46	Two proteomic methodologies for defining N-termini of mature human mitochondrial aminoacyl-tRNA synthetases. <i>Methods</i> , 2017, 113, 111-119.	1.9	24
47	Phylogenomic Classification and Biosynthetic Potential of the Fossil Fuel-Biodesulfurizing <i>Rhodococcus</i> Strain IGTS8. <i>Frontiers in Microbiology</i> , 2020, 11, 1417.	1.5	24
48	Electron Transfer Dissociation in Conjunction with Collision Activation To Investigate the <i>Drosophila melanogaster</i> Phosphoproteome. <i>Journal of Proteome Research</i> , 2009, 8, 2633-2639.	1.8	22
49	Validating Missing Proteins in Human Sperm Cells by Targeted Mass-Spectrometry- and Antibody-based Methods. <i>Journal of Proteome Research</i> , 2017, 16, 4340-4351.	1.8	21
50	Cytosolic Isocitrate Dehydrogenase from <i>Arabidopsis thaliana</i> Is Regulated by Glutathionylation. <i>Antioxidants</i> , 2019, 8, 16.	2.2	21
51	Multi-OMICS analyses unveil <i>STAT1</i> as a potential modifier gene in mevalonate kinase deficiency. <i>Annals of the Rheumatic Diseases</i> , 2018, 77, 1675-1687.	0.5	19
52	Proteome analysis of <i>Schizosaccharomyces pombe</i> by two-dimensional gel electrophoresis and mass spectrometry. <i>Proteomics</i> , 2006, 6, 4115-4129.	1.3	18
53	Discovery and Targeted Proteomics on Cutaneous Biopsies Infected by <i>Borrelia</i> to Investigate Lyme Disease*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1254-1264.	2.5	18
54	Proteome analysis of the culture environment supporting undifferentiated mouse embryonic stem and germ cell growth. <i>Electrophoresis</i> , 2007, 28, 1615-1623.	1.3	17

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55	Differentiation between fresh and frozen-thawed sea bass (<i>Dicentrarchus labrax</i>) fillets using two-dimensional gel electrophoresis. <i>Food Chemistry</i> , 2015, 176, 294-301.	4.2	17
56	Quantification of biomarkers for beef meat qualities using a combination of Parallel Reaction Monitoring- and antibody-based proteomics. <i>Food Chemistry</i> , 2020, 317, 126376.	4.2	17
57	Optimized Sample Preparation and Data Processing of Data-Independent Acquisition Methods for the Robust Quantification of Trace-Level Host Cell Protein Impurities in Antibody Drug Products. <i>Journal of Proteome Research</i> , 2021, 20, 923-931.	1.8	17
58	Spatio-Temporal Detection of the <i>Thiomonas</i> Population and the <i>Thiomonas</i> Arsenite Oxidase Involved in Natural Arsenite Attenuation Processes in the Carnoul's Acid Mine Drainage. <i>Frontiers in Cell and Developmental Biology</i> , 2016, 4, 3.	1.8	15
59	Benchmarking sample preparation/digestion protocols reveals tube-gel being a fast and repeatable method for quantitative proteomics. <i>Proteomics</i> , 2016, 16, 2953-2961.	1.3	15
60	The siRNA suppressor RTL1 is redox-regulated through glutathionylation of a conserved cysteine in the double-stranded-RNA-binding domain. <i>Nucleic Acids Research</i> , 2017, 45, 11891-11907.	6.5	15
61	Cleavable Binary Dyads: Simplifying Data Extraction and Increasing Storage Density in Digital Polymers. <i>Angewandte Chemie</i> , 2018, 130, 6374-6377.	1.6	14
62	Precise Alkoxyamine Design to Enable Automated Tandem Mass Spectrometry Sequencing of Digital Poly(phosphodiester)s. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 917-926.	7.2	14
63	A Proteomic View of Cellular Responses to Anticancer Quinoline-Copper Complexes. <i>Proteomes</i> , 2019, 7, 26.	1.7	12
64	Mass Spectrometry-Based Sequencing and SRM-Based Quantitation of Two Novel Vitellogenin Isoforms in the Leatherback Sea Turtle (<i>Dermochelys coriacea</i>). <i>Journal of Proteome Research</i> , 2013, 12, 4122-4135.	1.8	11
65	The longer the worse: a combined proteomic and targeted study of the long-term versus short-term effects of silver nanoparticles on macrophages. <i>Environmental Science: Nano</i> , 2020, 7, 2032-2046.	2.2	11
66	Rab7-harboring vesicles are carriers of the transferrin receptor through the biosynthetic secretory pathway. <i>Science Advances</i> , 2021, 7, .	4.7	11
67	Storing the portrait of Antoine de Lavoisier in a single macromolecule. <i>Comptes Rendus Chimie</i> , 2021, 24, 69-76.	0.2	10
68	An Optimized MALDI Mass Spectrometry Method for Improved Detection of Lysine/Arginine/Histidine Free Peptides. <i>Journal of Proteome Research</i> , 2008, 7, 5062-5069.	1.8	9
69	Differences in <i>Brachypelma albopilosa</i> (theraphosidae) hemolymph proteome between subadult and adult females. <i>Journal of Experimental Zoology</i> , 2010, 313A, 651-659.	1.2	9
70	The catalytic activity of the translation termination factor methyltransferase Mtq2-Trm112 complex is required for large ribosomal subunit biogenesis. <i>Nucleic Acids Research</i> , 2020, 48, 12310-12325.	6.5	9
71	Aldosterone: From biosynthesis to non-genomic action onto the proteome. <i>Steroids</i> , 2008, 73, 966-972.	0.8	8
72	Data-Independent Acquisition Coupled to Visible Laser-Induced Dissociation at 473 nm (DIA-LID) for Peptide-Centric Specific Analysis of Cysteine-Containing Peptide Subset. <i>Analytical Chemistry</i> , 2018, 90, 3928-3935.	3.2	8

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73	Doublet N-Terminal Oriented Proteomics for N-Terminomics and Proteolytic Processing Identification. <i>Methods in Molecular Biology</i> , 2017, 1574, 77-90.	0.4	7
74	N-terminome and proteogenomic analysis of the <i>Methylobacterium extorquens</i> DM4 reference strain for dichloromethane utilization. <i>Journal of Proteomics</i> , 2018, 179, 131-139.	1.2	6
75	Optimal conditions for tandem mass spectrometric sequencing of information-containing nitrogen-substituted polyurethanes. <i>Rapid Communications in Mass Spectrometry</i> , 2020, 34, e8815.	0.7	6
76	Temporal multiomic modeling reveals a B-cell receptor proliferative program in chronic lymphocytic leukemia. <i>Leukemia</i> , 2021, 35, 1463-1474.	3.3	6
77	ProMetIS, deep phenotyping of mouse models by combined proteomics and metabolomics analysis. <i>Scientific Data</i> , 2021, 8, 311.	2.4	6
78	Combining label-free and label-based accurate quantifications with SWATH-MS: Comparison with SRM and PRM for the evaluation of bovine muscle type effects. <i>Proteomics</i> , 2021, 21, e2000214.	1.3	5
79	Targeted Proteomics. <i>Proteomics</i> , 2012, 12, 1073-1073.	1.3	4
80	Proteomics as a Tool for the Characterization of Microbial Isolates and Complex Communities. , 2012, , .		3
81	Extended investigation of tube-gel sample preparation: a versatile and simple choice for high throughput quantitative proteomics. <i>Scientific Reports</i> , 2018, 8, 8260.	1.6	3
82	A Combined N-terminomics and Shotgun Proteomics Approach to Investigate the Responses of Human Cells to Rapamycin and Zinc at the Mitochondrial Level. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1085-1095.	2.5	3
83	Precise Alkoxyamine Design to Enable Automated Tandem Mass Spectrometry Sequencing of Digital Poly(phosphodiester)s. <i>Angewandte Chemie</i> , 2021, 133, 930-939.	1.6	2
84	A proteomic view of cellular responses of macrophages to copper when added as ion or as copper-polyacrylate complex. <i>Journal of Proteomics</i> , 2021, 239, 104178.	1.2	1
85	Tube-Gel: A Fast and Effective Sample Preparation Method for High-Throughput Quantitative Proteomics. <i>Methods in Molecular Biology</i> , 2019, 1959, 123-127.	0.4	0
86	A Core Proliferative Program Induced By B-Cell Receptor Stimulation in Chronic Lymphocytic Leukemia Cells. <i>Blood</i> , 2019, 134, 3777-3777.	0.6	0
87	Thiol-mediated redox regulation of DICER-LIKE RNaseIII and small RNA metabolism. <i>Free Radical Biology and Medicine</i> , 2021, 177, S61-S62.	1.3	0