

Christine Carapito

List of Publications by Year in descending order

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Version: 2024-02-01

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 | 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 |
| 2 | MS2Rescore: Data-Driven Rescoring Dramatically Boosts Immunopeptide Identification Rates. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100266. | 2.5 | 34 |
| 3 | 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 |
| 4 | 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 |
| 5 | 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 |
| 6 | 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 |
| 7 | Storing the portrait of Antoine de Lavoisier in a single macromolecule. <i>Comptes Rendus Chimie</i> , 2021, 24, 69-76. | 0.2 | 10 |
| 8 | Temporal multiomic modeling reveals a B-cell receptor proliferative program in chronic lymphocytic leukemia. <i>Leukemia</i> , 2021, 35, 1463-1474. | 3.3 | 6 |
| 9 | 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 |
| 10 | Ral GTPases promote breast cancer metastasis by controlling biogenesis and organ targeting of exosomes. <i>ELife</i> , 2021, 10, . | 2.8 | 70 |
| 11 | Rab7-harboring vesicles are carriers of the transferrin receptor through the biosynthetic secretory pathway. <i>Science Advances</i> , 2021, 7, . | 4.7 | 11 |
| 12 | ProMetIS, deep phenotyping of mouse models by combined proteomics and metabolomics analysis. <i>Scientific Data</i> , 2021, 8, 311. | 2.4 | 6 |
| 13 | 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 |
| 14 | 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 |
| 15 | 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 |
| 16 | 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 |
| 17 | <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 |
| 18 | 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 |

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|----|--|-----|-----------|
| 19 | 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 |
| 20 | Proline: an efficient and user-friendly software suite for large-scale proteomics. <i>Bioinformatics</i> , 2020, 36, 3148-3155. | 1.8 | 155 |
| 21 | 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 |
| 22 | Zika virus enhances monocyte adhesion and transmigration favoring viral dissemination to neural cells. <i>Nature Communications</i> , 2019, 10, 4430. | 5.8 | 83 |
| 23 | 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 |
| 24 | A Proteomic View of Cellular Responses to Anticancer Quinoline-Copper Complexes. <i>Proteomes</i> , 2019, 7, 26. | 1.7 | 12 |
| 25 | 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 |
| 26 | 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 |
| 27 | 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 |
| 28 | Cytosolic Isocitrate Dehydrogenase from <i>Arabidopsis thaliana</i> Is Regulated by Glutathionylation. <i>Antioxidants</i> , 2019, 8, 16. | 2.2 | 21 |
| 29 | 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 |
| 30 | 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 |
| 31 | Cleavable Binary Dyads: Simplifying Data Extraction and Increasing Storage Density in Digital Polymers. <i>Angewandte Chemie</i> , 2018, 130, 6374-6377. | 1.6 | 14 |
| 32 | 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 |
| 33 | 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 |
| 34 | 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 |
| 35 | 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 |
| 36 | Multi-OMICS analyses unveil STAT1 as a potential modifier gene in mevalonate kinase deficiency. <i>Annals of the Rheumatic Diseases</i> , 2018, 77, 1675-1687. | 0.5 | 19 |

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|----|---|------|-----------|
| 37 | Two proteomic methodologies for defining N-termini of mature human mitochondrial aminoacyl-tRNA synthetases. <i>Methods</i> , 2017, 113, 111-119. | 1.9 | 24 |
| 38 | 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 |
| 39 | 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 |
| 40 | MS-DECODER: Milliseconds Sequencing of Coded Polymers. <i>Macromolecules</i> , 2017, 50, 8290-8296. | 2.2 | 43 |
| 41 | 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 |
| 42 | 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 |
| 43 | 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 |
| 44 | Human SRMATlas: A Resource of Targeted Assays to Quantify the Complete Human Proteome. <i>Cell</i> , 2016, 166, 766-778. | 13.5 | 295 |
| 45 | 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 |
| 46 | 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 |
| 47 | 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 |
| 48 | 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 |
| 49 | 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 |
| 50 | N-terminome analysis of the human mitochondrial proteome. <i>Proteomics</i> , 2015, 15, 2519-2524. | 1.3 | 74 |
| 51 | 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 |
| 52 | Proteomic tools to decipher microbial community structure and functioning. <i>Environmental Science and Pollution Research</i> , 2015, 22, 13599-13612. | 2.7 | 27 |
| 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 | 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 |

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|----|---|-----|-----------|
| 55 | Comparative Expression Study of the Endo- β -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. PLoS ONE, 2014, 9, e91519. | 1.1 | 28 |
| 56 | The plant stigma exudate. Plant Signaling and Behavior, 2014, 9, e28274. | 1.2 | 27 |
| 57 | Bacterial protein signals are associated with Crohn's disease. Gut, 2014, 63, 1566-1577. | 6.1 | 80 |
| 58 | MSDA, a proteomics software suite for in-depth mass spectrometry data analysis using grid computing. Proteomics, 2014, 14, 1014-1019. | 1.3 | 51 |
| 59 | Analytical characterization of biosimilar antibodies and Fc-fusion proteins. TrAC - Trends in Analytical Chemistry, 2013, 48, 81-95. | 5.8 | 104 |
| 60 | An Improved Stable Isotope N-Terminal Labeling Approach with Light/Heavy TMPP To Automate Proteogenomics Data Validation: dN-TOP. Journal of Proteome Research, 2013, 12, 3063-3070. | 1.8 | 45 |
| 61 | Mass Spectrometry-Based Sequencing and SRM-Based Quantitation of Two Novel Vitellogenin Isoforms in the Leatherback Sea Turtle (<i>Dermochelys coriacea</i>). Journal of Proteome Research, 2013, 12, 4122-4135. | 1.8 | 11 |
| 62 | Proteomics profiling reveals novel proteins and functions of the plant stigma exudate. Journal of Experimental Botany, 2013, 64, 5695-5705. | 2.4 | 41 |
| 63 | Reproducible Quantification of Cancer-Associated Proteins in Body Fluids Using Targeted Proteomics. Science Translational Medicine, 2012, 4, 142ra94. | 5.8 | 236 |
| 64 | Proteomics as a Tool for the Characterization of Microbial Isolates and Complex Communities. , 2012, , . | | 3 |
| 65 | Targeted Proteomics. Proteomics, 2012, 12, 1073-1073. | 1.3 | 4 |
| 66 | In situ proteo-metabolomics reveals metabolite secretion by the acid mine drainage bio-indicator, <i>Euglena mutabilis</i> . ISME Journal, 2012, 6, 1391-1402. | 4.4 | 37 |
| 67 | Taxonomic and functional prokaryote diversity in mildly arsenic-contaminated sediments. Research in Microbiology, 2011, 162, 877-887. | 1.0 | 51 |
| 68 | Detection of Prion Protein in Urine-Derived Injectable Fertility Products by a Targeted Proteomic Approach. PLoS ONE, 2011, 6, e17815. | 1.1 | 42 |
| 69 | Characterization of the Active Bacterial Community Involved in Natural Attenuation Processes in Arsenic-Rich Creek Sediments. Microbial Ecology, 2011, 61, 793-810. | 1.4 | 67 |
| 70 | Differences in <i>Brachypelma albopilosa</i> (theraphosidae) hemolymph proteome between subadult and adult females. Journal of Experimental Zoology, 2010, 313A, 651-659. | 1.2 | 9 |
| 71 | Trans-Proteomic Pipeline supports and improves analysis of electron transfer dissociation data sets. Proteomics, 2010, 10, 1190-1195. | 1.3 | 39 |
| 72 | Ortho-proteogenomics: Multiple proteomes investigation through orthology and a new MS-based protocol. Genome Research, 2009, 19, 128-135. | 2.4 | 99 |

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|----|--|-----|-----------|
| 73 | 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 |
| 74 | 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 |
| 75 | 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 |
| 76 | 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 |
| 77 | Nuclear proteome analysis of undifferentiated mouse embryonic stem and germ cells. <i>Electrophoresis</i> , 2008, 29, 2381-2390. | 1.3 | 38 |
| 78 | Aldosterone: From biosynthesis to non-genomic action onto the proteome. <i>Steroids</i> , 2008, 73, 966-972. | 0.8 | 8 |
| 79 | 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 |
| 80 | A Tale of Two Oxidation States: Bacterial Colonization of Arsenic-Rich Environments. <i>PLoS Genetics</i> , 2007, 3, e53. | 1.5 | 166 |
| 81 | 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 |
| 82 | Identification of genes and proteins involved in the pleiotropic response to arsenic stress in <i>Caenibacter arsenoxydans</i> , a metalloresistant beta-proteobacterium with an unsequenced genome. <i>Biochimie</i> , 2006, 88, 595-606. | 1.3 | 39 |
| 83 | 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 |
| 84 | Proteome Analysis of Plant-Virus Interactome. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 2279-2297. | 2.5 | 75 |
| 85 | 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 |
| 86 | Multigenic families and proteomics: Extended protein characterization as a tool for paralog gene identification. <i>Proteomics</i> , 2005, 5, 450-460. | 1.3 | 35 |
| 87 | 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 |