

Loïc Dayon

List of Publications by Year in descending order

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Version: 2024-02-01

79
papers

3,750
citations

126858

33
h-index

138417

58
g-index

81
all docs

81
docs citations

81
times ranked

5991
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Relative Quantification of Proteins in Human Cerebrospinal Fluids by MS/MS Using 6-Plex Isobaric Tags. <i>Analytical Chemistry</i> , 2008, 80, 2921-2931. | 3.2 | 530 |
| 2 | Microfluidic systems in proteomics. <i>Electrophoresis</i> , 2003, 24, 3533-3562. | 1.3 | 250 |
| 3 | Blood-brain barrier breakdown, neuroinflammation, and cognitive decline in older adults. <i>Alzheimer's and Dementia</i> , 2018, 14, 1640-1650. | 0.4 | 189 |
| 4 | Nuclear Proteomics Uncovers Diurnal Regulatory Landscapes in Mouse Liver. <i>Cell Metabolism</i> , 2017, 25, 102-117. | 7.2 | 164 |
| 5 | Analysis of 1508 Plasma Samples by Capillary-Flow Data-Independent Acquisition Profiles Proteomics of Weight Loss and Maintenance. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1242-1254. | 2.5 | 162 |
| 6 | Motif affinity and mass spectrometry proteomic approach for the discovery of cellular AMPK targets: Identification of mitochondrial fission factor as a new AMPK substrate. <i>Cellular Signalling</i> , 2015, 27, 978-988. | 1.7 | 143 |
| 7 | General Statistical Modeling of Data from Protein Relative Expression Isobaric Tags. <i>Journal of Proteome Research</i> , 2011, 10, 2758-2766. | 1.8 | 120 |
| 8 | Combining low- and high-energy tandem mass spectra for optimized peptide quantification with isobaric tags. <i>Journal of Proteomics</i> , 2010, 73, 769-777. | 1.2 | 99 |
| 9 | Markers of neuroinflammation associated with Alzheimer's disease pathology in older adults. <i>Brain, Behavior, and Immunity</i> , 2017, 62, 203-211. | 2.0 | 91 |
| 10 | Brain Extracellular Fluid Protein Changes in Acute Stroke Patients. <i>Journal of Proteome Research</i> , 2011, 10, 1043-1051. | 1.8 | 90 |
| 11 | Proteomic Biomarker Discovery in 1000 Human Plasma Samples with Mass Spectrometry. <i>Journal of Proteome Research</i> , 2016, 15, 389-399. | 1.8 | 77 |
| 12 | High-throughput and simultaneous quantitative analysis of homocysteine-methionine cycle metabolites and co-factors in blood plasma and cerebrospinal fluid by isotope dilution LC-MS/MS. <i>Analytical and Bioanalytical Chemistry</i> , 2017, 409, 295-305. | 1.9 | 74 |
| 13 | Circadian and Feeding Rhythms Orchestrate the Diurnal Liver Acetylome. <i>Cell Reports</i> , 2017, 20, 1729-1743. | 2.9 | 72 |
| 14 | Alzheimer disease pathology and the cerebrospinal fluid proteome. <i>Alzheimer's Research and Therapy</i> , 2018, 10, 66. | 3.0 | 67 |
| 15 | Cysteine tagging for MS-based proteomics. <i>Mass Spectrometry Reviews</i> , 2011, 30, 366-395. | 2.8 | 64 |
| 16 | Deep Dive on the Proteome of Human Cerebrospinal Fluid: A Valuable Data Resource for Biomarker Discovery and Missing Protein Identification. <i>Journal of Proteome Research</i> , 2018, 17, 4113-4126. | 1.8 | 63 |
| 17 | Relative Protein Quantification by MS/MS Using the Tandem Mass Tag Technology. <i>Methods in Molecular Biology</i> , 2012, 893, 115-127. | 0.4 | 60 |
| 18 | EasyProt - An easy-to-use graphical platform for proteomics data analysis. <i>Journal of Proteomics</i> , 2013, 79, 146-160. | 1.2 | 57 |

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|----|--|-----|-----------|
| 19 | Generation of mass tags by the inherent electrochemistry of electrospray for protein mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2004, 15, 1767-1779. | 1.2 | 50 |
| 20 | Isobaric Tagging-Based Selection and Quantitation of Cerebrospinal Fluid Tryptic Peptides with Reporter Calibration Curves. <i>Analytical Chemistry</i> , 2010, 82, 848-858. | 3.2 | 49 |
| 21 | Comprehensive and Scalable Highly Automated MS-Based Proteomic Workflow for Clinical Biomarker Discovery in Human Plasma. <i>Journal of Proteome Research</i> , 2014, 13, 3837-3845. | 1.8 | 49 |
| 22 | An integrative multi-omics approach reveals new central nervous system pathway alterations in Alzheimer's disease. <i>Alzheimer's Research and Therapy</i> , 2021, 13, 71. | 3.0 | 49 |
| 23 | Discovery and Verification of Osteopontin and Beta-2-microglobulin as Promising Markers for Staging Human African Trypanosomiasis. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2783-2795. | 2.5 | 46 |
| 24 | One-carbon metabolism, cognitive impairment and CSF measures of Alzheimer pathology: homocysteine and beyond. <i>Alzheimer's Research and Therapy</i> , 2017, 9, 43. | 3.0 | 46 |
| 25 | Obesity shows preserved plasma proteome in large independent clinical cohorts. <i>Scientific Reports</i> , 2018, 8, 16981. | 1.6 | 45 |
| 26 | ICP-MS/MS-Based Ionomics: A Validated Methodology to Investigate the Biological Variability of the Human Ionome. <i>Journal of Proteome Research</i> , 2017, 16, 2080-2090. | 1.8 | 43 |
| 27 | Proteomics of human plasma: A critical comparison of analytical workflows in terms of effort, throughput and outcome. <i>EuPA Open Proteomics</i> , 2013, 1, 8-16. | 2.5 | 40 |
| 28 | Proteomes of Paired Human Cerebrospinal Fluid and Plasma: Relation to Blood-Brain Barrier Permeability in Older Adults. <i>Journal of Proteome Research</i> , 2019, 18, 1162-1174. | 1.8 | 40 |
| 29 | On-line counting of cysteine residues in peptides during electrospray ionization by electrogenerated tags and their application to protein identification. <i>Electrophoresis</i> , 2005, 26, 238-247. | 1.3 | 39 |
| 30 | Probing Cysteine Reactivity in Proteins by Mass Spectrometric EC-Tagging. <i>Journal of Proteome Research</i> , 2006, 5, 793-800. | 1.8 | 39 |
| 31 | The differential plasma proteome of obese and overweight individuals undergoing a nutritional weight loss and maintenance intervention. <i>Proteomics - Clinical Applications</i> , 2018, 12, 1600150. | 0.8 | 39 |
| 32 | Quantitative Analysis of Human Cerebrospinal Fluid Proteins Using a Combination of Cysteine Tagging and Amine-Reactive Isobaric Labeling. <i>Journal of Proteome Research</i> , 2011, 10, 249-258. | 1.8 | 37 |
| 33 | Systematic Evaluation of the Use of Human Plasma and Serum for Mass-Spectrometry-Based Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 1426-1435. | 1.8 | 37 |
| 34 | Proteomics of human biological fluids for biomarker discoveries: technical advances and recent applications. <i>Expert Review of Proteomics</i> , 2022, 19, 131-151. | 1.3 | 35 |
| 35 | Evaluation of absolute peptide quantitation strategies using selected reaction monitoring. <i>Proteomics</i> , 2011, 11, 1148-1152. | 1.3 | 34 |
| 36 | Proteomics of Cerebrospinal Fluid: Throughput and Robustness Using a Scalable Automated Analysis Pipeline for Biomarker Discovery. <i>Analytical Chemistry</i> , 2015, 87, 10755-10761. | 3.2 | 34 |

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|----|---|-----|-----------|
| 37 | Crosstalk between Drp1 phosphorylation sites during mitochondrial remodeling and their impact on metabolic adaptation. <i>Cell Reports</i> , 2021, 36, 109565. | 2.9 | 32 |
| 38 | On-line cysteine modification for protein analysis: new probes for electrochemical tagging nanospray mass spectrometry. <i>Journal of Electroanalytical Chemistry</i> , 2004, 570, 187-199. | 1.9 | 31 |
| 39 | Combination of Gas-Phase Fractionation and MS ³ Acquisition Modes for Relative Protein Quantification with Isobaric Tagging. <i>Journal of Proteome Research</i> , 2012, 11, 5081-5089. | 1.8 | 31 |
| 40 | Multitrack electrospray chips. <i>Journal of Mass Spectrometry</i> , 2006, 41, 1484-1490. | 0.7 | 28 |
| 41 | Shotgun Proteomics: A Relative Quantitative Approach Using Off-Gel Electrophoresis and LC-MS/MS. <i>Methods in Molecular Biology</i> , 2011, 681, 459-472. | 0.4 | 28 |
| 42 | From brain to blood: New biomarkers for ischemic stroke prognosis. <i>Journal of Proteomics</i> , 2013, 94, 138-148. | 1.2 | 28 |
| 43 | Proteomics and circadian rhythms: It's all about signaling!. <i>Proteomics</i> , 2015, 15, 310-317. | 1.3 | 28 |
| 44 | Electrospray Micromixer Chip for On-Line Derivatization and Kinetic Studies. <i>Analytical Chemistry</i> , 2008, 80, 3372-3378. | 3.2 | 25 |
| 45 | Augmented mitochondrial energy metabolism is an early response to chronic glucose stress in human pancreatic beta cells. <i>Diabetologia</i> , 2020, 63, 2628-2640. | 2.9 | 24 |
| 46 | Mitochondrial lysine deacetylation promotes energy metabolism and calcium signaling in insulin-secreting cells. <i>FASEB Journal</i> , 2019, 33, 4660-4674. | 0.2 | 23 |
| 47 | HSV-1 Cgal+ Infection Promotes Quaking RNA Binding Protein Production and Induces Nuclear-Cytoplasmic Shuttling of Quaking I-5 Isoform in Human Hepatoma Cells. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.009126. | 2.5 | 22 |
| 48 | Progress and pitfalls of using isobaric mass tags for proteome profiling. <i>Expert Review of Proteomics</i> , 2020, 17, 149-161. | 1.3 | 22 |
| 49 | A Highly Automated Shotgun Proteomic Workflow: Clinical Scale and Robustness for Biomarker Discovery in Blood. <i>Methods in Molecular Biology</i> , 2017, 1619, 433-449. | 0.4 | 21 |
| 50 | Persistent low body weight in humans is associated with higher mitochondrial activity in white adipose tissue. <i>American Journal of Clinical Nutrition</i> , 2019, 110, 605-616. | 2.2 | 21 |
| 51 | Electrochemical multi-tagging of cysteinyl peptides during microspray mass spectrometry: numerical simulation of consecutive reactions in a microchannel. <i>Physical Chemistry Chemical Physics</i> , 2005, 7, 4054. | 1.3 | 18 |
| 52 | Exploration of human cerebrospinal fluid: A large proteome dataset revealed by trapped ion mobility time-of-flight mass spectrometry. <i>Data in Brief</i> , 2020, 31, 105704. | 0.5 | 18 |
| 53 | Coordinated activation of mitochondrial respiration and exocytosis mediated by PKC signaling in pancreatic β^2 cells. <i>FASEB Journal</i> , 2017, 31, 1028-1045. | 0.2 | 17 |
| 54 | Plasma Proteomic Profiles of Cerebrospinal Fluid-Defined Alzheimer's Disease Pathology in Older Adults. <i>Journal of Alzheimer's Disease</i> , 2017, 60, 1641-1652. | 1.2 | 16 |

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|----|--|-----|-----------|
| 55 | On-line Electrochemical Tagging of Free Cysteines in Peptides during Nanospray Ionisation Mass Spectrometry: An Overview. <i>Chimia</i> , 2004, 58, 204-207. | 0.3 | 15 |
| 56 | From Relative to Absolute Quantification of Tryptic Peptides with Tandem Mass Tags: Application to Cerebrospinal Fluid. <i>Chimia</i> , 2010, 64, 132. | 0.3 | 15 |
| 57 | Identification of Missing Proteins in Normal Human Cerebrospinal Fluid. <i>Journal of Proteome Research</i> , 2018, 17, 4315-4319. | 1.8 | 15 |
| 58 | Enrichment of N-terminal cysteinyl-peptides by covalent capture. <i>Journal of Proteomics</i> , 2009, 71, 647-661. | 1.2 | 13 |
| 59 | Glucose-dependent phosphorylation signaling pathways and crosstalk to mitochondrial respiration in insulin secreting cells. <i>Cell Communication and Signaling</i> , 2019, 17, 14. | 2.7 | 13 |
| 60 | An Adaptive Pipeline To Maximize Isobaric Tagging Data in Large-Scale MS-Based Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 2165-2173. | 1.8 | 11 |
| 61 | Cysteine-reactive covalent capture tags for enrichment of cysteine-containing peptides. <i>Rapid Communications in Mass Spectrometry</i> , 2009, 23, 3377-3386. | 0.7 | 10 |
| 62 | Proteomics of Diabetes, Obesity, and Related Disorders. <i>Proteomics - Clinical Applications</i> , 2018, 12, 1600134. | 0.8 | 10 |
| 63 | A Versatile Workflow for Cerebrospinal Fluid Proteomic Analysis with Mass Spectrometry: A Matter of Choice between Deep Coverage and Sample Throughput. <i>Methods in Molecular Biology</i> , 2019, 2044, 129-154. | 0.4 | 9 |
| 64 | Proteomics of Human Milk: Definition of a Discovery Workflow for Clinical Research Studies. <i>Journal of Proteome Research</i> , 2021, 20, 2283-2290. | 1.8 | 9 |
| 65 | Assessing normalization methods in mass spectrometry-based proteome profiling of clinical samples. <i>BioSystems</i> , 2022, 215-216, 104661. | 0.9 | 8 |
| 66 | The Human Diabetes Proteome Project (HDPP): The 2014 update. <i>Translational Proteomics</i> , 2015, 8-9, 1-7. | 1.2 | 7 |
| 67 | Insights into Islet Differentiation and Maturation through Proteomic Characterization of a Human iPSC-Derived Pancreatic Endocrine Model. <i>Proteomics - Clinical Applications</i> , 2018, 12, e1600173. | 0.8 | 7 |
| 68 | Cerebrospinal Fluid Proteome Alterations Associated with Neuropsychiatric Symptoms in Cognitive Decline and Alzheimer's Disease. <i>Cells</i> , 2022, 11, 1030. | 1.8 | 7 |
| 69 | Mass spectrometry and DigiWest technology emphasize protein acetylation profile from Quisinstat-treated HuT78 CTCL cell line. <i>Journal of Proteomics</i> , 2018, 187, 126-143. | 1.2 | 6 |
| 70 | Analyzing Cerebrospinal Fluid Proteomes to Characterize Central Nervous System Disorders: A Highly Automated Mass Spectrometry-Based Pipeline for Biomarker Discovery. <i>Methods in Molecular Biology</i> , 2019, 1959, 89-112. | 0.4 | 6 |
| 71 | Protein Lysine Acetylation: Grease or Sand in the Gears of \hat{I}^2 -Cell Mitochondria?. <i>Journal of Molecular Biology</i> , 2020, 432, 1446-1460. | 2.0 | 6 |
| 72 | Systemic and central nervous system neuroinflammatory signatures of neuropsychiatric symptoms and related cognitive decline in older people. <i>Journal of Neuroinflammation</i> , 2022, 19, . | 3.1 | 6 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 73 | Front Cover: The differential plasma proteome of obese and overweight individuals undergoing a nutritional weight loss and maintenance intervention. <i>Proteomics - Clinical Applications</i> , 2018, 12, 1870001. | 0.8 | 5 |
| 74 | Comparison of normalization methods in clinical research applications of mass spectrometry-based proteomics. , 2020, , . | | 4 |
| 75 | Diagonal chromatographic selection of cysteinyl peptides modified with benzoquinones. <i>Analytical and Bioanalytical Chemistry</i> , 2007, 389, 841-849. | 1.9 | 3 |
| 76 | Proteomics reveals unique plasma signatures in constitutional thinness. <i>Proteomics - Clinical Applications</i> , 2022, , 2100114. | 0.8 | 3 |
| 77 | P2-147: A Neuroinflammatory Biomarker Signature of Blood-Brain Barrier Impairment in Older Adults. , 2016, 12, P670-P670. | | 2 |
| 78 | On-line electrochemical tagging of free cysteines during nanospray ionisation for mass spectrometry analysis. , 2004, , . | | 1 |
| 79 | Proteomics in the Systems-Level Study of the Metabolic Syndrome. , 2014, , 185-212. | | 0 |