

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	Cerebrospinal Fluid Proteome Alterations Associated with Neuropsychiatric Symptoms in Cognitive Decline and Alzheimer's Disease. <i>Cells</i> , 2022, 11, 1030.	1.8	7
2	Assessing normalization methods in mass spectrometry-based proteome profiling of clinical samples. <i>BioSystems</i> , 2022, 215-216, 104661.	0.9	8
3	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
4	Proteomics reveals unique plasma signatures in constitutional thinness. <i>Proteomics - Clinical Applications</i> , 2022, , 2100114.	0.8	3
5	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
6	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
7	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
8	Crosstalk between Drp1 phosphorylation sites during mitochondrial remodeling and their impact on metabolic adaptation. <i>Cell Reports</i> , 2021, 36, 109565.	2.9	32
9	Protein Lysine Acetylation: Grease or Sand in the Gears of β -Cell Mitochondria?. <i>Journal of Molecular Biology</i> , 2020, 432, 1446-1460.	2.0	6
10	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
11	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
12	Progress and pitfalls of using isobaric mass tags for proteome profiling. <i>Expert Review of Proteomics</i> , 2020, 17, 149-161.	1.3	22
13	Comparison of normalization methods in clinical research applications of mass spectrometry-based proteomics. , 2020, , .		4
14	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
15	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
16	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
17	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
18	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

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19	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
20	Mitochondrial lysine deacetylation promotes energy metabolism and calcium signaling in insulin-secreting cells. <i>FASEB Journal</i> , 2019, 33, 4660-4674.	0.2	23
21	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
22	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
23	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
24	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
25	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
26	Proteomics of Diabetes, Obesity, and Related Disorders. <i>Proteomics - Clinical Applications</i> , 2018, 12, 1600134.	0.8	10
27	Obesity shows preserved plasma proteome in large independent clinical cohorts. <i>Scientific Reports</i> , 2018, 8, 16981.	1.6	45
28	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
29	Alzheimer disease pathology and the cerebrospinal fluid proteome. <i>Alzheimer's Research and Therapy</i> , 2018, 10, 66.	3.0	67
30	Blood-brain barrier breakdown, neuroinflammation, and cognitive decline in older adults. <i>Alzheimer's and Dementia</i> , 2018, 14, 1640-1650.	0.4	189
31	Identification of Missing Proteins in Normal Human Cerebrospinal Fluid. <i>Journal of Proteome Research</i> , 2018, 17, 4315-4319.	1.8	15
32	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
33	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
34	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
35	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
36	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

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37	Circadian and Feeding Rhythms Orchestrate the Diurnal Liver Acetylome. <i>Cell Reports</i> , 2017, 20, 1729-1743.	2.9	72
38	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
39	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
40	Nuclear Proteomics Uncovers Diurnal Regulatory Landscapes in Mouse Liver. <i>Cell Metabolism</i> , 2017, 25, 102-117.	7.2	164
41	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
42	P2-147: A Neuroinflammatory Biomarker Signature of Blood-Brain Barrier Impairment in Older Adults. , 2016, 12, P670-P670.		2
43	Proteomic Biomarker Discovery in 1000 Human Plasma Samples with Mass Spectrometry. <i>Journal of Proteome Research</i> , 2016, 15, 389-399.	1.8	77
44	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
45	The Human Diabetes Proteome Project (HDPP): The 2014 update. <i>Translational Proteomics</i> , 2015, 8-9, 1-7.	1.2	7
46	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
47	Proteomics and circadian rhythms: It's all about signaling!. <i>Proteomics</i> , 2015, 15, 310-317.	1.3	28
48	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
49	Proteomics in the Systems-Level Study of the Metabolic Syndrome. , 2014, , 185-212.		0
50	EasyProt - An easy-to-use graphical platform for proteomics data analysis. <i>Journal of Proteomics</i> , 2013, 79, 146-160.	1.2	57
51	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
52	From brain to blood: New biomarkers for ischemic stroke prognosis. <i>Journal of Proteomics</i> , 2013, 94, 138-148.	1.2	28
53	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
54	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

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55	Brain Extracellular Fluid Protein Changes in Acute Stroke Patients. <i>Journal of Proteome Research</i> , 2011, 10, 1043-1051.	1.8	90
56	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
57	General Statistical Modeling of Data from Protein Relative Expression Isobaric Tags. <i>Journal of Proteome Research</i> , 2011, 10, 2758-2766.	1.8	120
58	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
59	Evaluation of absolute peptide quantitation strategies using selected reaction monitoring. <i>Proteomics</i> , 2011, 11, 1148-1152.	1.3	34
60	Cysteine tagging for MS-based proteomics. <i>Mass Spectrometry Reviews</i> , 2011, 30, 366-395.	2.8	64
61	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
62	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
63	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
64	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
65	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
66	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
67	Enrichment of N-terminal cysteinyl-peptides by covalent capture. <i>Journal of Proteomics</i> , 2009, 71, 647-661.	1.2	13
68	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
69	Electrospray Micromixer Chip for On-Line Derivatization and Kinetic Studies. <i>Analytical Chemistry</i> , 2008, 80, 3372-3378.	3.2	25
70	Diagonal chromatographic selection of cysteinyl peptides modified with benzoquinones. <i>Analytical and Bioanalytical Chemistry</i> , 2007, 389, 841-849.	1.9	3
71	Probing Cysteine Reactivity in Proteins by Mass Spectrometric EC-Tagging. <i>Journal of Proteome Research</i> , 2006, 5, 793-800.	1.8	39
72	Multitrack electrospray chips. <i>Journal of Mass Spectrometry</i> , 2006, 41, 1484-1490.	0.7	28

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73	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
74	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
75	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
76	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
77	On-line electrochemical tagging of free cysteines during nanospray ionisation for mass spectrometry analysis. , 2004, , .		1
78	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
79	Microfluidic systems in proteomics. <i>Electrophoresis</i> , 2003, 24, 3533-3562.	1.3	250