

Virginie Brun

List of Publications by Year in descending order

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Version: 2024-02-01

38
papers

1,772
citations

361296

20
h-index

330025

37
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38
docs citations

38
times ranked

2116
citing authors

#	ARTICLE	IF	CITATIONS
1	PepS: An Innovative Microfluidic Device for Bedside Whole Blood Processing before Plasma Proteomics Analyses. <i>Analytical Chemistry</i> , 2021, 93, 683-690.	3.2	6
2	Well Plate Maker: a user-friendly randomized block design application to limit batch effects in large-scale biomedical studies. <i>Bioinformatics</i> , 2021, 37, 2770-2771.	1.8	7
3	Mass Spectrometry-Based Proteomics Reveal Alcohol Dehydrogenase 1B as a Blood Biomarker Candidate to Monitor Acetaminophen-Induced Liver Injury. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11071.	1.8	1
4	Advances and Utility of the Human Plasma Proteome. <i>Journal of Proteome Research</i> , 2021, 20, 5241-5263.	1.8	86
5	Comprehensive and comparative exploration of the <i>Atp7b</i> mouse plasma proteome. <i>Metallomics</i> , 2020, 12, 249-258.	1.0	5
6	The blood copper isotopic composition is a prognostic indicator of the hepatic injury in Wilson disease. <i>Metallomics</i> , 2020, 12, 1781-1790.	1.0	17
7	Analytical techniques for multiplex analysis of protein biomarkers. <i>Expert Review of Proteomics</i> , 2020, 17, 257-273.	1.3	60
8	A liver-targeting Cu chelator relocates Cu in hepatocytes and promotes Cu excretion in a murine model of Wilson's disease. <i>Metallomics</i> , 2020, 12, 1000-1008.	1.0	8
9	Fetuin-A and thyroxin binding globulin predict rituximab response in rheumatoid arthritis patients with insufficient response to anti-TNF. <i>Clinical Rheumatology</i> , 2020, 39, 2553-2562.	1.0	2
10	Ultrasensitive Quantification of Recombinant Proteins Using AAA-MS. <i>Methods in Molecular Biology</i> , 2019, 2030, 1-10.	0.4	0
11	Bioinformatics Tools and Workflow to Select Blood Biomarkers for Early Cancer Diagnosis: An Application to Pancreatic Cancer. <i>Proteomics</i> , 2019, 19, e1800489.	1.3	22
12	Designing an In Silico Strategy to Select Tissue-Leakage Biomarkers Using the Galaxy Framework. <i>Methods in Molecular Biology</i> , 2019, 1959, 275-289.	0.4	10
13	Protein Biomarker Discovery in Non-depleted Serum by Spectral Library-Based Data-Independent Acquisition Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2019, 1959, 129-150.	0.4	4
14	Proteomic characterization of human exhaled breath condensate. <i>Journal of Breath Research</i> , 2018, 12, 021001.	1.5	29
15	Liver cancer-associated changes to the proteome: what deserves clinical focus?. <i>Expert Review of Proteomics</i> , 2018, 15, 749-756.	1.3	9
16	Systematic quantitative analysis of H2A and H2B variants by targeted proteomics. <i>Epigenetics and Chromatin</i> , 2018, 11, 2.	1.8	17
17	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.	2.9	24
18	Introducing plasma/serum glycodepletion for the targeted proteomics analysis of cytolysis biomarkers. <i>Talanta</i> , 2017, 170, 473-480.	2.9	7

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19	A proteomics assay to detect eight CBRN-relevant toxins in food. <i>Proteomics</i> , 2017, 17, 1600357.	1.3	28
20	Staphylococcal Enterotoxin O Exhibits Cell Cycle Modulating Activity. <i>Frontiers in Microbiology</i> , 2016, 7, 441.	1.5	7
21	<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.	1.8	24
22	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.	3.2	62
23	Absolute and multiplex quantification of antibodies in serum using PSAQ standards and LC-MS/MS. <i>Bioanalysis</i> , 2015, 7, 1237-1251.	0.6	18
24	Mass Spectrometry-based Workflow for Accurate Quantification of Escherichia coli Enzymes: How Proteomics Can Play a Key Role in Metabolic Engineering. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 954-968.	2.5	14
25	Accurate Quantification of Cardiovascular Biomarkers in Serum Using Protein Standard Absolute Quantification (PSAQ) and Selected Reaction Monitoring. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.008235.	2.5	71
26	Introducing AAA-MS, a Rapid and Sensitive Method for Amino Acid Analysis Using Isotope Dilution and High-Resolution Mass Spectrometry. <i>Journal of Proteome Research</i> , 2012, 11, 3929-3936.	1.8	20
27	PSAQ standards for accurate MS-based quantification of proteins: from the concept to biomedical applications. <i>Journal of Mass Spectrometry</i> , 2012, 47, 1353-1363.	0.7	68
28	Mass spectrometry-based absolute protein quantification: PSAQ strategy makes use of non-canonical proteotypic peptides. <i>Proteomics</i> , 2012, 12, 1217-1221.	1.3	28
29	Development of a Protein Standard Absolute Quantification (PSAQ) assay for the quantification of Staphylococcus aureus enterotoxin A in serum. <i>Journal of Proteomics</i> , 2012, 75, 3041-3049.	1.2	39
30	Production and Use of Stable Isotope-Labeled Proteins for Absolute Quantitative Proteomics. <i>Methods in Molecular Biology</i> , 2011, 753, 93-115.	0.4	43
31	<i>Staphylococcus aureus</i> Superantigens Elicit Redundant and Extensive Human V β 2 Patterns. <i>Infection and Immunity</i> , 2009, 77, 2043-2050.	1.0	70
32	Isotope dilution strategies for absolute quantitative proteomics. <i>Journal of Proteomics</i> , 2009, 72, 740-749.	1.2	292
33	Innovative Application of Mass Spectrometry for the Characterization of Staphylococcal Enterotoxins Involved in Food Poisoning Outbreaks. <i>Applied and Environmental Microbiology</i> , 2009, 75, 882-884.	1.4	51
34	Protein Standard Absolute Quantification (PSAQ) for improved investigation of staphylococcal food poisoning outbreaks. <i>Proteomics</i> , 2008, 8, 4633-4636.	1.3	121
35	Isotope-labeled Protein Standards. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 2139-2149.	2.5	409
36	Identification of differentially expressed genes in human pineal parenchymal tumors by microarray analysis. <i>Acta Neuropathologica</i> , 2005, 109, 306-313.	3.9	11

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37	CD38-dependent ADP-ribosyl cyclase activity in developing and adult mouse brain. <i>Biochemical Journal</i> , 2003, 370, 175-183.	1.7	60
38	Effect of starvation on glutamine ammoniogenesis and gluconeogenesis in isolated mouse kidney tubules. <i>Biochemical Journal</i> , 2002, 368, 301-308.	1.7	22