Christophe Bruley

List of Publications by Year
in descending order

39 papers	4,218 citations	218677 26 h-index	302126 39 g-index
40 all docs	40 docs citations	40 times ranked	6473 citing authors

#	ARTICLE	IF	CITATIONS
1	An innovative standard for LC€MS€based HCP profiling and accurate quantity assessment: Application to batch consistency in viral vaccine samples. Proteomics, 2021, 21, e2000152.	2.2	5
2	Mass Spectrometry-Based Proteomics Reveal Alcohol Dehydrogenase 1B as a Blood Biomarker Candidate to Monitor Acetaminophen-Induced Liver Injury. International Journal of Molecular Sciences, 2021, 22, 11071.	4.1	1
3	Beyond Target€"Decoy Competition: Stable Validation of Peptide and Protein Identifications in Mass Spectrometry-Based Discovery Proteomics. Analytical Chemistry, 2020, 92, 14898-14906.	6.5	39
4	Multi-omic analysis of gametogenesis reveals a novel signature at the promoters and distal enhancers of active genes. Nucleic Acids Research, 2020, 48, 4115-4138.	14.5	24
5	Proline: an efficient and user-friendly software suite for large-scale proteomics. Bioinformatics, 2020, 36, 3148-3155.	4.1	155
6	Proteomic characterization of human exhaled breath condensate. Journal of Breath Research, 2018, 12, 021001.	3.0	29
7	AT_CHLORO: The First Step When Looking for Information About Subplastidial Localization of Proteins. Methods in Molecular Biology, 2018, 1829, 395-406.	0.9	13
8	ChloroKB: A Web Application for the Integration of Knowledge Related to Chloroplast Metabolic Network. Plant Physiology, 2017, 174, 922-934.	4.8	23
9	Introducing plasma/serum glycodepletion for the targeted proteomics analysis of cytolysis biomarkers. Talanta, 2017, 170, 473-480.	5.5	7
10	MS_HistoneDB, a manually curated resource for proteomic analysis of human and mouse histones. Epigenetics and Chromatin, 2017, 10, 2.	3.9	40
11	Uses and misuses of the fudge factor in quantitative discovery proteomics. Proteomics, 2016, 16, 1955-1960.	2.2	20
12	Calibration plot for proteomics: A graphical tool to visually check the assumptions underlying FDR control in quantitative experiments. Proteomics, 2016, 16, 29-32.	2.2	66
13	hEIDI: An Intuitive Application Tool To Organize and Treat Large-Scale Proteomics Data. Journal of Proteome Research, 2016, 15, 3896-3903.	3.7	7
14	Looking for Missing Proteins in the Proteome of Human Spermatozoa: An Update. Journal of Proteome Research, 2016, 15, 3998-4019.	3.7	66
15	Accounting for the Multiple Natures of Missing Values in Label-Free Quantitative Proteomics Data Sets to Compare Imputation Strategies. Journal of Proteome Research, 2016, 15, 1116-1125.	3.7	345
16	Spiked proteomic standard dataset for testing label-free quantitative software and statistical methods. Data in Brief, 2016, 6, 286-294.	1.0	30
17	Benchmarking quantitative label-free LC€"MS data processing workflows using a complex spiked proteomic standard dataset. Journal of Proteomics, 2016, 132, 51-62.	2.4	68
18	Computational and Mass-Spectrometry-Based Workflow for the Discovery and Validation of Missing Human Proteins: Application to Chromosomes 2 and 14. Journal of Proteome Research, 2015, 14, 3621-3634.	3.7	35

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19	In-depth study of *Mollivirus sibericum* , a new 30,000-y-old giant virus infecting *Acanthamoeba*. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5327-35.	7.1	284
20	Thirty-thousand-year-old distant relative of giant icosahedral DNA viruses with a pandoravirus morphology. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4274-4279.	7.1	468
21	Mass Spectrometry-based Workflow for Accurate Quantification of Escherichia coli Enzymes: How Proteomics Can Play a Key Role in Metabolic Engineering. Molecular and Cellular Proteomics, 2014, 13, 954-968.	3.8	14
22	Pandoraviruses: Amoeba Viruses with Genomes Up to 2.5 Mb Reaching That of Parasitic Eukaryotes. Science, 2013, 341, 281-286.	12.6	509
23	Identification of a novel BET bromodomain inhibitor–sensitive, gene regulatory circuit that controls Rituximab response and tumour growth in aggressive lymphoid cancers. EMBO Molecular Medicine, 2013, 5, 1180-1195.	6.9	64
24	An Extended Proteome Map of the Lysosomal Membrane Reveals Novel Potential Transporters. Molecular and Cellular Proteomics, 2013, 12, 1572-1588.	3.8	172
25	Accurate Quantification of Cardiovascular Biomarkers in Serum Using Protein Standard Absolute Quantification (PSAQ™) and Selected Reaction Monitoring. Molecular and Cellular Proteomics, 2012, 11, M111.008235.	3.8	71
26	AT_CHLORO: A Chloroplast Protein Database Dedicated to Sub-Plastidial Localization. Frontiers in Plant Science, 2012, 3, 205.	3.6	48
27	Introducing AAA-MS, a Rapid and Sensitive Method for Amino Acid Analysis Using Isotope Dilution and High-Resolution Mass Spectrometry. Journal of Proteome Research, 2012, 11, 3929-3936.	3.7	20
28	PSAQ™ standards for accurate MS–based quantification of proteins: from the concept to biomedical applications. Journal of Mass Spectrometry, 2012, 47, 1353-1363.	1.6	68
29	PredAlgo: A New Subcellular Localization Prediction Tool Dedicated to Green Algae. Molecular Biology and Evolution, 2012, 29, 3625-3639.	8.9	270
30	Investigating the macropinocytic proteome of *Dictyostelium* amoebae by high–resolution mass spectrometry. Proteomics, 2012, 12, 241-245.	2.2	40
31	Mass spectrometry–based absolute protein quantification: PSAQ™ strategy makes use of "noncanonical" proteotypic peptides. Proteomics, 2012, 12, 1217-1221.	2.2	28
32	Development of a Protein Standard Absolute Quantification (PSAQ™) assay for the quantification of Staphylococcus aureus enterotoxin A in serum. Journal of Proteomics, 2012, 75, 3041-3049.	2.4	39
33	MASCP Gator: An Aggregation Portal for the Visualization of Arabidopsis Proteomics Data. Plant Physiology, 2011, 155, 259-270.	4.8	94
34	Production and Use of Stable Isotope-Labeled Proteins for Absolute Quantitative Proteomics. Methods in Molecular Biology, 2011, 753, 93-115.	0.9	43
35	AT_CHLORO, a Comprehensive Chloroplast Proteome Database with Subplastidial Localization and Curated Information on Envelope Proteins. Molecular and Cellular Proteomics, 2010, 9, 1063-1084.	3.8	425
36	Peptide Storage: Are You Getting the Best Return on Your Investment? Defining Optimal Storage Conditions for Proteomics Samples. Journal of Proteome Research, 2009, 8, 3778-3785.	3.7	50

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37	A toolbox for validation of mass spectrometry peptides identification and generation of database: IRMa. Bioinformatics, 2009, 25, 1980-1981.	4.1	115
38	A Proteomics Dissection of Arabidopsis thaliana Vacuoles Isolated from Cell Culture. Molecular and Cellular Proteomics, 2007, 6, 394-412.	3.8	294
39	A High Content in Lipid-modified Peripheral Proteins and Integral Receptor Kinases Features in the Arabidopsis Plasma Membrane Proteome. Molecular and Cellular Proteomics, 2007, 6, 1980-1996.	3.8	128