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	Pandoraviruses: Amoeba Viruses with Genomes Up to 2.5 Mb Reaching That of Parasitic Eukaryotes. Science, 2013, 341, 281-286.	12.6	509
2	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
3	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
4	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
5	A Proteomics Dissection of Arabidopsis thaliana Vacuoles Isolated from Cell Culture. Molecular and Cellular Proteomics, 2007, 6, 394-412.	3.8	294
6	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
7	PredAlgo: A New Subcellular Localization Prediction Tool Dedicated to Green Algae. Molecular Biology and Evolution, 2012, 29, 3625-3639.	8.9	270
8	An Extended Proteome Map of the Lysosomal Membrane Reveals Novel Potential Transporters. Molecular and Cellular Proteomics, 2013, 12, 1572-1588.	3.8	172
9	Proline: an efficient and user-friendly software suite for large-scale proteomics. Bioinformatics, 2020, 36, 3148-3155.	4.1	155
10	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
11	A toolbox for validation of mass spectrometry peptides identification and generation of database: IRMa. Bioinformatics, 2009, 25, 1980-1981.	4.1	115
12	MASCP Gator: An Aggregation Portal for the Visualization of Arabidopsis Proteomics Data. Plant Physiology, 2011, 155, 259-270.	4.8	94
13	Accurate Quantification of Cardiovascular Biomarkers in Serum Using Protein Standard Absolute Quantification (PSAQâ„¢) and Selected Reaction Monitoring. Molecular and Cellular Proteomics, 2012, 11, M111.008235.	3.8	71
14	PSAQâ„¢ standards for accurate MSâ€"based quantification of proteins: from the concept to biomedical applications. Journal of Mass Spectrometry, 2012, 47, 1353-1363.	1.6	68
15	Benchmarking quantitative label-free LCâ€"MS data processing workflows using a complex spiked proteomic standard dataset. Journal of Proteomics, 2016, 132, 51-62.	2.4	68
16	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
17	Looking for Missing Proteins in the Proteome of Human Spermatozoa: An Update. Journal of Proteome Research, 2016, 15, 3998-4019.	3.7	66
18	Identification of a novel BET bromodomain inhibitorâ€"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

#	Article	IF	Citations
19	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
20	AT_CHLORO: A Chloroplast Protein Database Dedicated to Sub-Plastidial Localization. Frontiers in Plant Science, 2012, 3, 205.	3.6	48
21	Production and Use of Stable Isotope-Labeled Proteins for Absolute Quantitative Proteomics. Methods in Molecular Biology, 2011, 753, 93-115.	0.9	43
22	Investigating the macropinocytic proteome of <i>Dictyostelium</i> amoebae by highâ€resolution mass spectrometry. Proteomics, 2012, 12, 241-245.	2.2	40
23	MS_HistoneDB, a manually curated resource for proteomic analysis of human and mouse histones. Epigenetics and Chromatin, 2017, 10, 2.	3.9	40
24	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
25	Beyond Targetâ€"Decoy Competition: Stable Validation of Peptide and Protein Identifications in Mass Spectrometry-Based Discovery Proteomics. Analytical Chemistry, 2020, 92, 14898-14906.	6.5	39
26	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
27	Spiked proteomic standard dataset for testing label-free quantitative software and statistical methods. Data in Brief, 2016, 6, 286-294.	1.0	30
28	Proteomic characterization of human exhaled breath condensate. Journal of Breath Research, 2018, 12, 021001.	3.0	29
29	Mass spectrometryâ€based absolute protein quantification: <scp>PSAQ</scp>„¢ strategy makes use of â€œnoncanonicalâ€•proteotypic peptides. Proteomics, 2012, 12, 1217-1221.	2.2	28
30	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
31	ChloroKB: A Web Application for the Integration of Knowledge Related to Chloroplast Metabolic Network. Plant Physiology, 2017, 174, 922-934.	4.8	23
32	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
33	Uses and misuses of the fudge factor in quantitative discovery proteomics. Proteomics, 2016, 16, 1955-1960.	2.2	20
34	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
35	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
36	hEIDI: An Intuitive Application Tool To Organize and Treat Large-Scale Proteomics Data. Journal of Proteome Research, 2016, 15, 3896-3903.	3.7	7

#	Article	IF	Citations
37	Introducing plasma/serum glycodepletion for the targeted proteomics analysis of cytolysis biomarkers. Talanta, 2017, 170, 473-480.	5.5	7
38	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
39	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