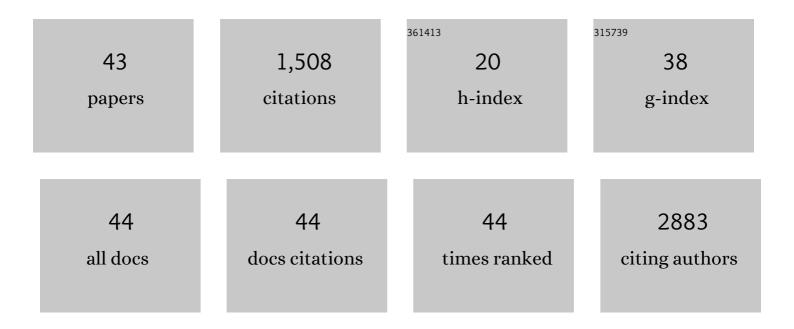
Jerome Vialaret

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	<i>Arabidopsis thaliana</i> High-Affinity Phosphate Transporters Exhibit Multiple Levels of Posttranslational Regulation A. Plant Cell, 2011, 23, 1523-1535.	6.6	218
2	Regulation of glutamate metabolism by protein kinases in mycobacteria. Molecular Microbiology, 2008, 70, 1408-1423.	2.5	147
3	Differential Mass Spectrometry Profiles of Tau Protein in the Cerebrospinal Fluid of Patients with Alzheimer's Disease, Progressive Supranuclear Palsy, and Dementia with Lewy Bodies. Journal of Alzheimer's Disease, 2016, 51, 1033-1043.	2.6	104
4	Current and future use of "dried blood spot―analyses in clinical chemistry. Clinical Chemistry and Laboratory Medicine, 2013, 51, 1897-1909.	2.3	102
5	Tau Protein Quantification in Human Cerebrospinal Fluid by Targeted Mass Spectrometry at High Sequence Coverage Provides Insights into Its Primary Structure Heterogeneity. Journal of Proteome Research, 2016, 15, 667-676.	3.7	91
6	Evolution of <i>S</i> -Cysteinylated and <i>S</i> -Glutathionylated Thiol Precursors during Oxidation of Melon B. and Sauvignon blanc Musts. Journal of Agricultural and Food Chemistry, 2010, 58, 4406-4413.	5.2	86
7	Cerebrospinal fluid levels of orexin-A and histamine, and sleep profile within the Alzheimer process. Neurobiology of Aging, 2017, 53, 59-66.	3.1	76
8	Coordinated Post-translational Responses of Aquaporins to Abiotic and Nutritional Stimuli in Arabidopsis Roots. Molecular and Cellular Proteomics, 2013, 12, 3886-3897.	3.8	73
9	Quantitative Clinical Chemistry Proteomics (qCCP) using mass spectrometry: general characteristics and application. Clinical Chemistry and Laboratory Medicine, 2013, 51, 919-35.	2.3	47
10	From radioimmunoassay to mass spectrometry: a new method to quantify orexin-A (hypocretin-1) in cerebrospinal fluid. Scientific Reports, 2016, 6, 25162.	3.3	36
11	Antibody-free quantification of seven tau peptides in human CSF using targeted mass spectrometry. Frontiers in Neuroscience, 2015, 9, 302.	2.8	34
12	The calciumâ€dependent protein kinase <scp>CPK</scp> 7 acts on root hydraulic conductivity. Plant, Cell and Environment, 2015, 38, 1312-1320.	5.7	34
13	Phosphorylation dynamics of membrane proteins from <i>Arabidopsis</i> roots submitted to salt stress. Proteomics, 2014, 14, 1058-1070.	2.2	32
14	Validation of a nanoliquid chromatography–tandem mass spectrometry method for the identification and the accurate quantification by isotopic dilution of glutathionylated and cysteinylated precursors of 3-mercaptohexan-1-ol and 4-mercapto-4-methylpentan-2-one in white grape juices. Journal of Chromatography A, 2010, 1217, 1626-1635.	3.7	31
15	Quantitative detection of amyloid-Î ² peptides by mass spectrometry: state of the art and clinical applications. Clinical Chemistry and Laboratory Medicine, 2015, 53, 1483-93.	2.3	30
16	Use of plasma biomarkers for AT(N) classification of neurodegenerative dementias. Journal of Neurology, Neurosurgery and Psychiatry, 2021, 92, 1206-1214.	1.9	30
17	Clinical mass spectrometry proteomics (cMSP) for medical laboratory: What does the future hold?. Clinica Chimica Acta, 2017, 467, 51-58.	1.1	29
18	Association between serum hepcidin level and restless legs syndrome. Movement Disorders, 2018, 33, 618-627.	3.9	25

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19	Detection of amyloid beta peptides in body fluids for the diagnosis of alzheimer's disease: Where do we stand?. Critical Reviews in Clinical Laboratory Sciences, 2020, 57, 99-113.	6.1	24
20	Absolute quantification of 35 plasma biomarkers in human saliva using targeted MS. Bioanalysis, 2016, 8, 43-53.	1.5	22
21	Hepcidin and ferritin levels in restless legs syndrome: a case–control study. Scientific Reports, 2020, 10, 11914.	3.3	21
22	Clinical measurement of Hepcidin-25 in human serum: Is quantitative mass spectrometry up to the job?. EuPA Open Proteomics, 2014, 3, 60-67.	2.5	19
23	Development of new quantitative mass spectrometry and semi-automatic isofocusing methods for the determination of Apolipoprotein E typing. Clinica Chimica Acta, 2016, 454, 33-38.	1.1	19
24	Clinical perspectives of dried blood spot protein quantification using mass spectrometry methods. Critical Reviews in Clinical Laboratory Sciences, 2017, 54, 173-184.	6.1	19
25	Towards a routine application of Top-Down approaches for label-free discovery workflows. Journal of Proteomics, 2018, 175, 12-26.	2.4	17
26	Quantifying RNA modifications by mass spectrometry: a novel source of biomarkers in oncology. Critical Reviews in Clinical Laboratory Sciences, 2022, 59, 1-18.	6.1	14
27	Quantification of hepcidin-25 in human cerebrospinal fluid using LC–MS/MS. Bioanalysis, 2017, 9, 337-347.	1.5	12
28	Assessing a multiplex-targeted proteomics approach for the clinical diagnosis of periodontitis using saliva samples. Bioanalysis, 2018, 10, 35-45.	1.5	12
29	Identification of multiple proteoforms biomarkers on clinical samples by routine Top-Down approaches. Data in Brief, 2018, 18, 1013-1021.	1.0	12
30	What sample preparation should be chosen for targeted MS monoclonal antibody quantification in human serum?. Bioanalysis, 2018, 10, 723-735.	1.5	12
31	Stable Isotope Labeling by Amino acid <i>in Vivo</i> (SILAV): a new method to explore protein metabolism. Rapid Communications in Mass Spectrometry, 2015, 29, 1917-1925.	1.5	10
32	Impact of iron deficiency diagnosis using hepcidin mass spectrometry dosage methods on hospital stay and costs after a prolonged ICU stay: Study protocol for a multicentre, randomised, single-blinded medico-economic trial. Anaesthesia, Critical Care & Pain Medicine, 2017, 36, 391-396.	1.4	9
33	Regulatory context and validation of assays for clinical mass spectrometry proteomics (cMSP) methods. Critical Reviews in Clinical Laboratory Sciences, 2018, 55, 346-358.	6.1	9
34	Development and validation of dried matrix spot sampling for the quantitative determination of amyloid β peptides in cerebrospinal fluid. Clinical Chemistry and Laboratory Medicine, 2014, 52, 649-55.	2.3	8
35	Variation of human salivary alpha-amylase proteoforms in three stimulation models. Clinical Oral Investigations, 2020, 24, 475-486.	3.0	7
36	Blood amyloid and tau biomarkers as predictors of cerebrospinal fluid profiles. Journal of Neural Transmission, 2022, 129, 231-237.	2.8	7

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#	Article	IF	CITATIONS
37	Nano-flow vs standard-flow: Which is the more suitable LC/MS method for quantifying hepcidin-25 in human serum in routine clinical settings?. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2018, 1086, 110-117.	2.3	6
38	In Vivo Large-Scale Mapping of Protein Turnover in Human Cerebrospinal Fluid. Analytical Chemistry, 2019, 91, 15500-15508.	6.5	6
39	Analytical comparison of ELISA and mass spectrometry for quantification of serum hepcidin in critically ill patients. Bioanalysis, 2021, 13, 1029-1035.	1.5	6
40	Impact of biological matrix on inflammatory protein biomarker quantification based on targeted mass spectrometry. Bioanalysis, 2018, 10, 1383-1399.	1.5	5
41	Proteomic profile of cerebrospinal fluid in patients with multiple sclerosis using two dimensional gel electrophoresis. British Journal of Biomedical Science, 2016, 73, 143-146.	1.3	4
42	Hepcidin: immunoanalytic characteristics. Annales De Biologie Clinique, 2018, 76, 705-715.	0.1	0
43	Intact Protein Analysis by LC-MS for Characterizing Biomarkers in Cerebrospinal Fluid. Methods in Molecular Biology, 2019, 1959, 163-172.	0.9	0