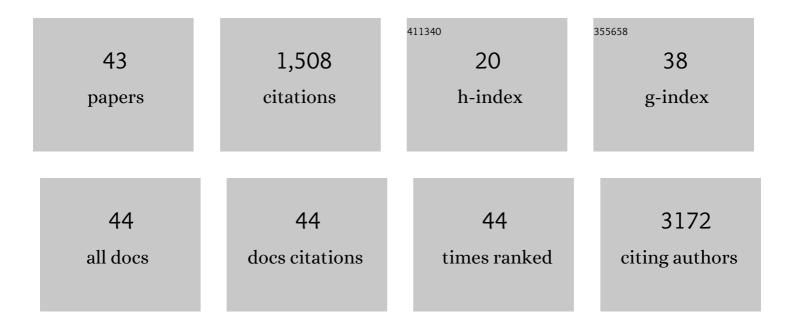
Jerome Vialaret

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4181644/publications.pdf Version: 2024-02-01



IEDOME VIALADET

#	Article	IF	CITATIONS
1	Quantifying RNA modifications by mass spectrometry: a novel source of biomarkers in oncology. Critical Reviews in Clinical Laboratory Sciences, 2022, 59, 1-18.	2.7	14
2	Blood amyloid and tau biomarkers as predictors of cerebrospinal fluid profiles. Journal of Neural Transmission, 2022, 129, 231-237.	1.4	7
3	Use of plasma biomarkers for AT(N) classification of neurodegenerative dementias. Journal of Neurology, Neurosurgery and Psychiatry, 2021, 92, 1206-1214.	0.9	30
4	Analytical comparison of ELISA and mass spectrometry for quantification of serum hepcidin in critically ill patients. Bioanalysis, 2021, 13, 1029-1035.	0.6	6
5	Variation of human salivary alpha-amylase proteoforms in three stimulation models. Clinical Oral Investigations, 2020, 24, 475-486.	1.4	7
6	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.	2.7	24
7	Hepcidin and ferritin levels in restless legs syndrome: a case–control study. Scientific Reports, 2020, 10, 11914.	1.6	21
8	In Vivo Large-Scale Mapping of Protein Turnover in Human Cerebrospinal Fluid. Analytical Chemistry, 2019, 91, 15500-15508.	3.2	6
9	Intact Protein Analysis by LC-MS for Characterizing Biomarkers in Cerebrospinal Fluid. Methods in Molecular Biology, 2019, 1959, 163-172.	0.4	0
10	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.	1.2	6
11	Association between serum hepcidin level and restless legs syndrome. Movement Disorders, 2018, 33, 618-627.	2.2	25
12	Assessing a multiplex-targeted proteomics approach for the clinical diagnosis of periodontitis using saliva samples. Bioanalysis, 2018, 10, 35-45.	0.6	12
13	Identification of multiple proteoforms biomarkers on clinical samples by routine Top-Down approaches. Data in Brief, 2018, 18, 1013-1021.	0.5	12
14	Towards a routine application of Top-Down approaches for label-free discovery workflows. Journal of Proteomics, 2018, 175, 12-26.	1.2	17
15	Impact of biological matrix on inflammatory protein biomarker quantification based on targeted mass spectrometry. Bioanalysis, 2018, 10, 1383-1399.	0.6	5
16	Hepcidin: immunoanalytic characteristics. Annales De Biologie Clinique, 2018, 76, 705-715.	0.2	0
17	What sample preparation should be chosen for targeted MS monoclonal antibody quantification in human serum?. Bioanalysis, 2018, 10, 723-735.	0.6	12
18	Regulatory context and validation of assays for clinical mass spectrometry proteomics (cMSP) methods. Critical Reviews in Clinical Laboratory Sciences, 2018, 55, 346-358.	2.7	9

JEROME VIALARET

#	Article	IF	CITATIONS
19	Clinical mass spectrometry proteomics (cMSP) for medical laboratory: What does the future hold?. Clinica Chimica Acta, 2017, 467, 51-58.	0.5	29
20	Quantification of hepcidin-25 in human cerebrospinal fluid using LC–MS/MS. Bioanalysis, 2017, 9, 337-347.	0.6	12
21	Cerebrospinal fluid levels of orexin-A and histamine, and sleep profile within the Alzheimer process. Neurobiology of Aging, 2017, 53, 59-66.	1.5	76
22	Clinical perspectives of dried blood spot protein quantification using mass spectrometry methods. Critical Reviews in Clinical Laboratory Sciences, 2017, 54, 173-184.	2.7	19
23	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.	0.6	9
24	From radioimmunoassay to mass spectrometry: a new method to quantify orexin-A (hypocretin-1) in cerebrospinal fluid. Scientific Reports, 2016, 6, 25162.	1.6	36
25	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.	1.2	104
26	Proteomic profile of cerebrospinal fluid in patients with multiple sclerosis using two dimensional gel electrophoresis. British Journal of Biomedical Science, 2016, 73, 143-146.	1.2	4
27	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.	0.5	19
28	Absolute quantification of 35 plasma biomarkers in human saliva using targeted MS. Bioanalysis, 2016, 8, 43-53.	0.6	22
29	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.	1.8	91
30	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.	0.7	10
31	Antibody-free quantification of seven tau peptides in human CSF using targeted mass spectrometry. Frontiers in Neuroscience, 2015, 9, 302.	1.4	34
32	Quantitative detection of amyloid-β peptides by mass spectrometry: state of the art and clinical applications. Clinical Chemistry and Laboratory Medicine, 2015, 53, 1483-93.	1.4	30
33	The calciumâ€dependent protein kinase <scp>CPK</scp> 7 acts on root hydraulic conductivity. Plant, Cell and Environment, 2015, 38, 1312-1320.	2.8	34
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.	1.4	8
35	Phosphorylation dynamics of membrane proteins from <i>Arabidopsis</i> roots submitted to salt stress. Proteomics, 2014, 14, 1058-1070.	1.3	32
36	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

JEROME VIALARET

#	Article	IF	CITATIONS
37	Coordinated Post-translational Responses of Aquaporins to Abiotic and Nutritional Stimuli in Arabidopsis Roots. Molecular and Cellular Proteomics, 2013, 12, 3886-3897.	2.5	73
38	Current and future use of "dried blood spot―analyses in clinical chemistry. Clinical Chemistry and Laboratory Medicine, 2013, 51, 1897-1909.	1.4	102
39	Quantitative Clinical Chemistry Proteomics (qCCP) using mass spectrometry: general characteristics and application. Clinical Chemistry and Laboratory Medicine, 2013, 51, 919-35.	1.4	47
40	<i>Arabidopsis thaliana</i> High-Affinity Phosphate Transporters Exhibit Multiple Levels of Posttranslational Regulation A. Plant Cell, 2011, 23, 1523-1535.	3.1	218
41	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.	1.8	31
42	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.	2.4	86
43	Regulation of glutamate metabolism by protein kinases in mycobacteria. Molecular Microbiology, 2008, 70, 1408-1423.	1.2	147