

Olivier Pible

List of Publications by Year in descending order

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Version: 2024-02-01

46
papers

1,540
citations

331538

21
h-index

330025

37
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50
all docs

50
docs citations

50
times ranked

2079
citing authors

#	ARTICLE	IF	CITATIONS
1	Deciphering Black Extrinsic Tooth Stain Composition in Children Using Metaproteomics. ACS Omega, 2022, 7, 8258-8267.	1.6	5
2	Identification and Characterization of Marine Microorganisms by Tandem Mass Spectrometry Proteotyping. Microorganisms, 2022, 10, 719.	1.6	16
3	Taxonomical and functional changes in COVID-19 faecal microbiome could be related to SARS-CoV-2 faecal load. Environmental Microbiology, 2022, 24, 4299-4316.	1.8	20
4	Assessing the ratio of Bacillus spores and vegetative cells by shotgun proteomics. Environmental Science and Pollution Research, 2021, 28, 25107-25115.	2.7	14
5	Heterogeneity of SARS-CoV-2 virus produced in cell culture revealed by shotgun proteomics and supported by genome sequencing. Analytical and Bioanalytical Chemistry, 2021, 413, 7265-7275.	1.9	7
6	Increasing the power of interpretation for soil metaproteomics data. Microbiome, 2021, 9, 195.	4.9	25
7	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows. Nature Communications, 2021, 12, 7305.	5.8	34
8	Direct Meta-Analyses Reveal Unexpected Microbial Life in the Highly Radioactive Water of an Operating Nuclear Reactor Core. Microorganisms, 2020, 8, 1857.	1.6	11
9	Proteotyping SARS-CoV-2 Virus from Nasopharyngeal Swabs: A Proof-of-Concept Focused on a 3 Min Mass Spectrometry Window. Journal of Proteome Research, 2020, 19, 4407-4416.	1.8	90
10	Front Cover: Shortlisting SARS-CoV-2 Peptides for Targeted Studies from Experimental Data-Dependent Acquisition Tandem Mass Spectrometry Data. Proteomics, 2020, 20, 2070111.	1.3	2
11	Proteotyping Environmental Microorganisms by Phylopeptidomics: Case Study Screening Water from a Radioactive Material Storage Pool. Microorganisms, 2020, 8, 1525.	1.6	11
12	Shortlisting SARS-CoV-2 Peptides for Targeted Studies from Experimental Data-Dependent Acquisition Tandem Mass Spectrometry Data. Proteomics, 2020, 20, e2000107.	1.3	64
13	Combining proteogenomics and metaproteomics for deep taxonomic and functional characterization of microbiomes from a non-sequenced host. Npj Biofilms and Microbiomes, 2020, 6, 23.	2.9	20
14	Estimating relative biomasses of organisms in microbiota using phylopeptidomics. Microbiome, 2020, 8, 30.	4.9	34
15	Quick microbial molecular phenotyping by differential shotgun proteomics. Environmental Microbiology, 2020, 22, 2996-3004.	1.8	24
16	High-throughput proteotyping of bacterial isolates by double barrel chromatography-tandem mass spectrometry based on microplate paramagnetic beads and phylopeptidomics. Journal of Proteomics, 2020, 226, 103887.	1.2	18
17	Shotgun proteomics analysis of SARS-CoV-2-infected cells and how it can optimize whole viral particle antigen production for vaccines. Emerging Microbes and Infections, 2020, 9, 1712-1721.	3.0	62
18	Proteogenomics-Guided Evaluation of RNA-Seq Assembly and Protein Database Construction for Emergent Model Organisms. Proteomics, 2020, 20, e1900261.	1.3	7

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19	Comparative proteomics in the wild: Accounting for intrapopulation variability improves describing proteome response in a <i>Gammarus pulex</i> field population exposed to cadmium. <i>Aquatic Toxicology</i> , 2019, 214, 105244.	1.9	16
20	Shotgun proteomics datasets acquired on <i>Gammarus pulex</i> animals sampled from the wild. <i>Data in Brief</i> , 2019, 27, 104650.	0.5	4
21	De novo transcriptomes of 14 gammarid individuals for proteogenomic analysis of seven taxonomic groups. <i>Scientific Data</i> , 2019, 6, 184.	2.4	23
22	Evaluation of Sample Preparation Methods for Fast Proteotyping of Microorganisms by Tandem Mass Spectrometry. <i>Frontiers in Microbiology</i> , 2019, 10, 1985.	1.5	69
23	Pathogen proteotyping: A rapidly developing application of mass spectrometry to address clinical concerns. <i>Clinical Mass Spectrometry</i> , 2019, 14, 9-17.	1.9	49
24	Ecotoxicoproteomics: A decade of progress in our understanding of anthropogenic impact on the environment. <i>Journal of Proteomics</i> , 2019, 198, 66-77.	1.2	66
25	Digging Deeper Into the Pyriproxyfen-Response of the Amphipod <i>Gammarus fossarum</i> With a Next-Generation Ultra-High-Field Orbitrap Analyser: New Perspectives for Environmental Toxicoproteomics. <i>Frontiers in Environmental Science</i> , 2018, 6, .	1.5	13
26	Improving Quality Control of Contagious Caprine Pleuropneumonia Vaccine with Tandem Mass Spectrometry. <i>Proteomics</i> , 2018, 18, e1800088.	1.3	10
27	Proteogenomic Insights into the Intestinal Parasite <i>Blastocystis</i> sp. Subtype 4 Isolate WR1. <i>Proteomics</i> , 2017, 17, 1700211.	1.3	5
28	Ovary and embryo proteogenomic dataset revealing diversity of vitellogenins in the crustacean <i>Gammarus fossarum</i> . <i>Data in Brief</i> , 2016, 8, 1259-1262.	0.5	1
29	High-throughput proteome dynamics for discovery of key proteins in sentinel species: Unsuspected vitellogenins diversity in the crustacean <i>Gammarus fossarum</i> . <i>Journal of Proteomics</i> , 2016, 146, 207-214.	1.2	15
30	Clinical implications of recent advances in proteogenomics. <i>Expert Review of Proteomics</i> , 2016, 13, 185-199.	1.3	12
31	Proteogenomic insights into the core-proteome of female reproductive tissues from crustacean amphipods. <i>Journal of Proteomics</i> , 2016, 135, 51-61.	1.2	30
32	Improving the quality of genome, protein sequence, and taxonomy databases: A prerequisite for microbiome metaomics 2.0. <i>Proteomics</i> , 2015, 15, 3418-3423.	1.3	35
33	Data for comparative proteomics of ovaries from five non-model, crustacean amphipods. <i>Data in Brief</i> , 2015, 5, 1-6.	0.5	4
34	Proteomic Investigation of Male <i>Gammarus fossarum</i> , a Freshwater Crustacean, in Response to Endocrine Disruptors. <i>Journal of Proteome Research</i> , 2015, 14, 292-303.	1.8	56
35	Taking the Shortcut for High-Throughput Shotgun Proteomic Analysis of Bacteria. <i>Methods in Molecular Biology</i> , 2014, 1197, 275-285.	0.4	94
36	Non-model organisms, a species endangered by proteogenomics. <i>Journal of Proteomics</i> , 2014, 105, 5-18.	1.2	145

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37	Proteomics meets blue biotechnology: A wealth of novelties and opportunities. <i>Marine Genomics</i> , 2014, 17, 35-42.	0.4	23
38	Proteogenomic insights into salt tolerance by a halotolerant alpha-proteobacterium isolated from an Andean saline spring. <i>Journal of Proteomics</i> , 2014, 97, 36-47.	1.2	53
39	The importance of recognizing and reporting sequence database contamination for proteomics. <i>EuPA Open Proteomics</i> , 2014, 3, 246-249.	2.5	18
40	Revision of the Biodistribution of Uranyl in Serum: Is Fetuin-A the Major Protein Target?. <i>Chemical Research in Toxicology</i> , 2013, 26, 645-653.	1.7	56
41	Subcellular localization and interaction network of the mRNA decay activator Pat1 upon UV stress. <i>Yeast</i> , 2013, 30, 353-363.	0.8	3
42	Predicting the disruption by UO_2^{2+} of a protein-ligand interaction. <i>Protein Science</i> , 2010, 19, 2219-2230.	3.1	32
43	Identification of uranyl binding proteins from human kidney-2 cell extracts by immobilized uranyl affinity chromatography and mass spectrometry. <i>Journal of Chromatography A</i> , 2009, 1216, 5365-5376.	1.8	43
44	Structural Consequences of Binding of UO_2^{2+} to Apotransferrin: Can This Protein Account for Entry of Uranium into Human Cells?. <i>Biochemistry</i> , 2007, 46, 2215-2226.	1.2	92
45	INTERALIGN: interactive alignment editor for distantly related protein sequences. <i>Bioinformatics</i> , 2005, 21, 3166-3167.	1.8	8
46	Screening of Human Serum Proteins for Uranium Binding. <i>Chemical Research in Toxicology</i> , 2005, 18, 946-953.	1.7	82