Olivier Pible

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/9287597/publications.pdf

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46 papers	1,540 citations	331538 21 h-index	330025 37 g-index
50 all docs	50 docs citations	50 times ranked	2079 citing authors

#	Article	IF	Citations
1	Non-model organisms, a species endangered by proteogenomics. Journal of Proteomics, 2014, 105, 5-18.	1.2	145
2	Taking the Shortcut for High-Throughput Shotgun Proteomic Analysis of Bacteria. Methods in Molecular Biology, 2014, 1197, 275-285.	0.4	94
3	Structural Consequences of Binding of UO22+ to Apotransferrin:â€‰ Can This Protein Account for Entry of Uranium into Human Cells?. Biochemistry, 2007, 46, 2215-2226.	1.2	92
4	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
5	Screening of Human Serum Proteins for Uranium Binding. Chemical Research in Toxicology, 2005, 18, 946-953.	1.7	82
6	Evaluation of Sample Preparation Methods for Fast Proteotyping of Microorganisms by Tandem Mass Spectrometry. Frontiers in Microbiology, 2019, 10, 1985.	1.5	69
7	Ecotoxicoproteomics: A decade of progress in our understanding of anthropogenic impact on the environment. Journal of Proteomics, 2019, 198, 66-77.	1.2	66
8	Shortlisting SARSâ€CoVâ€2 Peptides for Targeted Studies from Experimental Dataâ€Dependent Acquisition Tandem Mass Spectrometry Data. Proteomics, 2020, 20, e2000107.	1.3	64
9	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
10	Revision of the Biodistribution of Uranyl in Serum: Is Fetuin-A the Major Protein Target?. Chemical Research in Toxicology, 2013, 26, 645-653.	1.7	56
11	Proteomic Investigation of Male Gammarus fossarum, a Freshwater Crustacean, in Response to Endocrine Disruptors. Journal of Proteome Research, 2015, 14, 292-303.	1.8	56
12	Proteogenomic insights into salt tolerance by a halotolerant alpha-proteobacterium isolated from an Andean saline spring. Journal of Proteomics, 2014, 97, 36-47.	1.2	53
13	Pathogen proteotyping: A rapidly developing application of mass spectrometry to address clinical concerns. Clinical Mass Spectrometry, 2019, 14, 9-17.	1.9	49
14	Identification of uranyl binding proteins from human kidney-2 cell extracts by immobilized uranyl affinity chromatography and mass spectrometry. Journal of Chromatography A, 2009, 1216, 5365-5376.	1.8	43
15	Improving the quality of genome, protein sequence, and taxonomy databases: A prerequisite for microbiome metaâ€omics 2.0. Proteomics, 2015, 15, 3418-3423.	1.3	35
16	Estimating relative biomasses of organisms in microbiota using â€œphylopeptidomicsâ€. Microbiome, 2020, 8, 30.	4.9	34
17	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows. Nature Communications, 2021, 12, 7305.	5.8	34
18	Predicting the disruption by UO₂²⁺ of a proteinâ€ligand interaction. Protein Science, 2010, 19, 2219-2230.	3.1	32

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19	Proteogenomic insights into the core-proteome of female reproductive tissues from crustacean amphipods. Journal of Proteomics, 2016, 135, 51-61.	1.2	30
20	Increasing the power of interpretation for soil metaproteomics data. Microbiome, 2021, 9, 195.	4.9	25
21	Quick microbial molecular phenotyping by differential shotgun proteomics. Environmental Microbiology, 2020, 22, 2996-3004.	1.8	24
22	Proteomics meets blue biotechnology: A wealth of novelties and opportunities. Marine Genomics, 2014, 17, 35-42.	0.4	23
23	De novo transcriptomes of 14 gammarid individuals for proteogenomic analysis of seven taxonomic groups. Scientific Data, 2019, 6, 184.	2.4	23
24	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
25	Taxonomical and functional changes in <scp>COVID</scp>â€19 faecal microbiome could be related to <scp>SARSâ€CoV</scp>â€2 faecal load. Environmental Microbiology, 2022, 24, 4299-4316.	1.8	20
26	The importance of recognizing and reporting sequence database contamination for proteomics. EuPA Open Proteomics, 2014, 3, 246-249.	2.5	18
27	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
28	Comparative proteomics in the wild: Accounting for intrapopulation variability improves describing proteome response in a Gammarus pulex field population exposed to cadmium. Aquatic Toxicology, 2019, 214, 105244.	1.9	16
29	Identification and Characterization of Marine Microorganisms by Tandem Mass Spectrometry Proteotyping. Microorganisms, 2022, 10, 719.	1.6	16
30	High-throughput proteome dynamics for discovery of key proteins in sentinel species: Unsuspected vitellogenins diversity in the crustacean Gammarus fossarum. Journal of Proteomics, 2016, 146, 207-214.	1.2	15
31	Assessing the ratio of Bacillus spores and vegetative cells by shotgun proteomics. Environmental Science and Pollution Research, 2021, 28, 25107-25115.	2.7	14
32	Digging Deeper Into the Pyriproxyfen-Response of the Amphipod Gammarus fossarum With a Next-Generation Ultra-High-Field Orbitrap Analyser: New Perspectives for Environmental Toxicoproteomics. Frontiers in Environmental Science, 2018, 6, .	1.5	13
33	Clinical implications of recent advances in proteogenomics. Expert Review of Proteomics, 2016, 13, 185-199.	1.3	12
34	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
35	Proteotyping Environmental Microorganisms by Phylopeptidomics: Case Study Screening Water from a Radioactive Material Storage Pool. Microorganisms, 2020, 8, 1525.	1.6	11
36	Improving Quality Control of Contagious Caprine Pleuropneumonia Vaccine with Tandem Mass Spectrometry. Proteomics, 2018, 18, e1800088.	1.3	10

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37	INTERALIGN: interactive alignment editor for distantly related protein sequences. Bioinformatics, 2005, 21, 3166-3167.	1.8	8
38	Proteogenomicsâ€Guided Evaluation of RNAâ€Seq Assembly and Protein Database Construction for Emergent Model Organisms. Proteomics, 2020, 20, e1900261.	1.3	7
39	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
40	Proteogenomic Insights into the Intestinal Parasite Blastocystis sp. Subtype 4 Isolate WR1. Proteomics, 2017, 17, 1700211.	1.3	5
41	Deciphering Black Extrinsic Tooth Stain Composition in Children Using Metaproteomics. ACS Omega, 2022, 7, 8258-8267.	1.6	5
42	Data for comparative proteomics of ovaries from five non-model, crustacean amphipods. Data in Brief, 2015, 5, 1-6.	0.5	4
43	Shotgun proteomics datasets acquired on Gammarus pulex animals sampled from the wild. Data in Brief, 2019, 27, 104650.	0.5	4
44	Subcellular localization and interaction network of the mRNA decay activator Pat1 upon UV stress. Yeast, 2013, 30, 353-363.	0.8	3
45	Front Cover: Shortlisting SARSâ€CoVâ€2 Peptides for Targeted Studies from Experimental Dataâ€Dependent Acquisition Tandem Mass Spectrometry Data. Proteomics, 2020, 20, 2070111.	1.3	2
46	Ovary and embryo proteogenomic dataset revealing diversity of vitellogenins in the crustacean Gammarus fossarum. Data in Brief, 2016, 8, 1259-1262.	0.5	1