

Jean Armengaud

List of Publications by Year in descending order

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217
papers

6,589
citations

53794

45
h-index

110387

64
g-index

227
all docs

227
docs citations

227
times ranked

7683
citing authors

#	ARTICLE	IF	CITATIONS
1	Nutrient recycling facilitates long-term stability of marine microbial phototroph-heterotroph interactions. <i>Nature Microbiology</i> , 2017, 2, 17100.	13.3	181
2	Genetic Analysis of Dioxin Dioxygenase of <i>Sphingomonas</i> sp. Strain RW1: Catabolic Genes Dispersed on the Genome. <i>Journal of Bacteriology</i> , 1998, 180, 3954-3966.	2.2	165
3	Non-model organisms, a species endangered by proteogenomics. <i>Journal of Proteomics</i> , 2014, 105, 5-18.	2.4	145
4	Alliance of Proteomics and Genomics to Unravel the Specificities of Sahara Bacterium <i>Deinococcus deserti</i> . <i>PLoS Genetics</i> , 2009, 5, e1000434.	3.5	144
5	Genome analysis and genome-wide proteomics of <i>Thermococcus gammatolerans</i> , the most radioresistant organism known amongst the Archaea. <i>Genome Biology</i> , 2009, 10, R70.	9.6	125
6	Ribosomal proteins as biomarkers for bacterial identification by mass spectrometry in the clinical microbiology laboratory. <i>Journal of Microbiological Methods</i> , 2013, 94, 390-396.	1.6	115
7	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994.	13.3	115
8	Expanding the Known Repertoire of Virulence Factors Produced by <i>Bacillus cereus</i> through Early Secretome Profiling in Three Redox Conditions. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1486-1498.	3.8	105
9	Proteomic insights into the lifestyle of an environmentally relevant marine bacterium. <i>ISME Journal</i> , 2012, 6, 124-135.	9.8	100
10	Taking the Shortcut for High-Throughput Shotgun Proteomic Analysis of Bacteria. <i>Methods in Molecular Biology</i> , 2014, 1197, 275-285.	0.9	94
11	A perfect genome annotation is within reach with the proteomics and genomics alliance. <i>Current Opinion in Microbiology</i> , 2009, 12, 292-300.	5.1	93
12	Proteomics-based Refinement of <i>Deinococcus deserti</i> Genome Annotation Reveals an Unwanted Use of Non-canonical Translation Initiation Codons. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 415-426.	3.8	90
13	Proteotyping SARS-CoV-2 Virus from Nasopharyngeal Swabs: A Proof-of-Concept Focused on a 3 Min Mass Spectrometry Window. <i>Journal of Proteome Research</i> , 2020, 19, 4407-4416.	3.7	90
14	Implementation of meiosis prophase I programme requires a conserved retinoid-independent stabilizer of meiotic transcripts. <i>Nature Communications</i> , 2016, 7, 10324.	12.8	89
15	RNA-binding proteins are a major target of silica nanoparticles in cell extracts. <i>Nanotoxicology</i> , 2016, 10, 1555-1564.	3.0	86
16	Exoproteomics: exploring the world around biological systems. <i>Expert Review of Proteomics</i> , 2012, 9, 561-575.	3.0	80
17	Microbiology and proteomics, getting the best of both worlds!. <i>Environmental Microbiology</i> , 2013, 15, 12-23.	3.8	76
18	A Functional 4-Hydroxysalicylate/Hydroxyquinol Degradative Pathway Gene Cluster Is Linked to the Initial Dibenzo- <i>p</i> -Dioxin Pathway Genes in <i>Sphingomonas</i> sp. Strain RW1. <i>Journal of Bacteriology</i> , 1999, 181, 3452-3461.	2.2	74

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19	Comparative Proteogenomics of Twelve <i>Roseobacter</i> Exoproteomes Reveals Different Adaptive Strategies Among These Marine Bacteria. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.013110.	3.8	73
20	Essentiality of threonylcarbamoyladenosine (t ⁶ A), a universal tRNA modification, in bacteria. <i>Molecular Microbiology</i> , 2015, 98, 1199-1221.	2.5	72
21	Biosynthesis of Wyosine Derivatives in tRNA: An Ancient and Highly Diverse Pathway in Archaea. <i>Molecular Biology and Evolution</i> , 2010, 27, 2062-2077.	8.9	71
22	Stone-dwelling actinobacteria <i>Blastococcus saxobsidens</i> , <i>Modestobacter marinus</i> and <i>Geodermatophilus obscurus</i> proteogenomes. <i>ISME Journal</i> , 2016, 10, 21-29.	9.8	71
23	Evaluation of Sample Preparation Methods for Fast Proteotyping of Microorganisms by Tandem Mass Spectrometry. <i>Frontiers in Microbiology</i> , 2019, 10, 1985.	3.5	69
24	Ecotoxicoproteomics: A decade of progress in our understanding of anthropogenic impact on the environment. <i>Journal of Proteomics</i> , 2019, 198, 66-77.	2.4	66
25	N2-Methylation of Guanosine at Position 10 in tRNA Is Catalyzed by a THUMP Domain-containing, S-Adenosylmethionine-dependent Methyltransferase, Conserved in Archaea and Eukaryota. <i>Journal of Biological Chemistry</i> , 2004, 279, 37142-37152.	3.4	64
26	Structural insights into a new homodimeric self-activated GTPase family. <i>EMBO Reports</i> , 2007, 8, 569-575.	4.5	64
27	N-terminomics and proteogenomics, getting off to a good start. <i>Proteomics</i> , 2014, 14, 2637-2646.	2.2	64
28	Shortlisting SARS-CoV-2 Peptides for Targeted Studies from Experimental Data-Dependent Acquisition Tandem Mass Spectrometry Data. <i>Proteomics</i> , 2020, 20, e2000107.	2.2	64
29	A Novel [2Fe-2S] Ferredoxin from <i>Pseudomonas putidam</i> Promotes the Reductive Reactivation of Catechol 2,3-Dioxygenase. <i>Journal of Biological Chemistry</i> , 1998, 273, 9622-9629.	3.4	63
30	Shotgun proteomics analysis of SARS-CoV-2-infected cells and how it can optimize whole viral particle antigen production for vaccines. <i>Emerging Microbes and Infections</i> , 2020, 9, 1712-1721.	6.5	62
31	RNA Sequencing and Proteogenomics Reveal the Importance of Leaderless mRNAs in the Radiation-Tolerant Bacterium <i>Deinococcus deserti</i> . <i>Genome Biology and Evolution</i> , 2014, 6, 932-948.	2.5	61
32	Post-production modifications of murine mesenchymal stem cell (mMSC) derived extracellular vesicles (EVs) and impact on their cellular interaction. <i>Biomaterials</i> , 2020, 231, 119675.	11.4	59
33	Proteogenomics for environmental microbiology. <i>Proteomics</i> , 2013, 13, 2731-2742.	2.2	57
34	Molecular Characterization of Fdx1, a Putidaredoxin-Type [2Fe-2S] Ferredoxin Able to Transfer Electrons to the Dioxin Dioxygenase of <i>Sphingomonas</i> sp. RW1. <i>FEBS Journal</i> , 1997, 247, 833-842.	0.2	56
35	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.	3.7	56
36	The timeline of corona formation around silica nanocarriers highlights the role of the protein interactome. <i>Nanoscale</i> , 2017, 9, 1840-1851.	5.6	56

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37	Functional distinctness in the exoproteomes of marine <i>Synechococcus</i> . <i>Environmental Microbiology</i> , 2015, 17, 3781-3794.	3.8	55
38	The importance of naturally attenuated SARS-CoV-2 in the fight against COVID-19. <i>Environmental Microbiology</i> , 2020, 22, 1997-2000.	3.8	54
39	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.	2.4	53
40	Vaccines inducing immunity to Lassa virus glycoprotein and nucleoprotein protect macaques after a single shot. <i>Science Translational Medicine</i> , 2019, 11, .	12.4	53
41	Low Doses of Gamma-Irradiation Induce an Early Bystander Effect in Zebrafish Cells Which Is Sufficient to Radioprotect Cells. <i>PLoS ONE</i> , 2014, 9, e92974.	2.5	53
42	In-Depth Analysis of Exoproteomes from Marine Bacteria by Shotgun Liquid Chromatography-Tandem Mass Spectrometry: the <i>Ruegeria pomeroyi</i> DSS-3 Case-Study. <i>Marine Drugs</i> , 2010, 8, 2223-2239.	4.6	52
43	Next-Generation Proteomics: Toward Customized Biomarkers for Environmental Biomonitoring. <i>Environmental Science & Technology</i> , 2014, 48, 13560-13572.	10.0	52
44	Proteogenomics and systems biology: quest for the ultimate missing parts. <i>Expert Review of Proteomics</i> , 2010, 7, 65-77.	3.0	51
45	Chlorocatechols Substituted at Positions 4 and 5 Are Substrates of the Broad-Spectrum Chlorocatechol 1,2-Dioxygenase of <i>Pseudomonas chlororaphis</i> RW71. <i>Journal of Bacteriology</i> , 2001, 183, 997-1011.	2.2	50
46	Proteogenomics of <i>Gammarus fossarum</i> to Document the Reproductive System of Amphipods. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3612-3625.	3.8	50
47	"You produce while I clean up", a strategy revealed by exoproteomics during <i>Synechococcus</i> – <i>Roseobacter</i> interactions. <i>Proteomics</i> , 2015, 15, 3454-3462.	2.2	50
48	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
49	Salt Stress Induced Changes in the Exoproteome of the Halotolerant Bacterium <i>Tistlia consotensis</i> Deciphered by Proteogenomics. <i>PLoS ONE</i> , 2015, 10, e0135065.	2.5	47
50	High-throughput, quantitative assessment of the effects of low-dose silica nanoparticles on lung cells: grasping complex toxicity with a great depth of field. <i>BMC Genomics</i> , 2015, 16, 315.	2.8	47
51	Next-generation proteomics faces new challenges in environmental biotechnology. <i>Current Opinion in Biotechnology</i> , 2016, 38, 174-182.	6.6	46
52	Restricting Fermentative Potential by Proteome Remodeling. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.013102.	3.8	44
53	Determination of estrogen presence in water by SPR using estrogen receptor dimerization. <i>Analytical and Bioanalytical Chemistry</i> , 2008, 390, 873-883.	3.7	43
54	Proteogenomic Biomarkers for Identification of <i>Francisella</i> Species and Subspecies by Matrix-Assisted Laser Desorption Ionization-Time-of-Flight Mass Spectrometry. <i>Analytical Chemistry</i> , 2014, 86, 9394-9398.	6.5	43

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55	Proteogenomic insights into uranium tolerance of a Chernobyl's <i>Microbacterium</i> bacterial isolate. <i>Journal of Proteomics</i> , 2018, 177, 148-157.	2.4	43
56	Revisiting Iodination Sites in Thyroglobulin with an Organ-oriented Shotgun Strategy. <i>Journal of Biological Chemistry</i> , 2011, 286, 259-269.	3.4	42
57	4-Demethylwyosine Synthase from <i>Pyrococcus abyssi</i> Is a Radical-S-adenosyl-L-methionine Enzyme with an Additional [4Fe-4S] ₂ Cluster That Interacts with the Pyruvate Co-substrate. <i>Journal of Biological Chemistry</i> , 2012, 287, 41174-41185.	3.4	42
58	Identity Elements Required for Enzymatic Formation of N ² ,N ² -dimethylguanosine from N ² -monomethylated Derivative and its Possible Role in Avoiding Alternative Conformations in Archaeal tRNA. <i>Journal of Molecular Biology</i> , 2006, 357, 387-399.	4.2	41
59	Mass spectrometry for the detection of bioterrorism agents: from environmental to clinical applications. <i>Journal of Mass Spectrometry</i> , 2016, 51, 183-199.	1.6	40
60	Intrinsic non-stomatal resilience to drought of the photosynthetic apparatus in <i>Coffea</i> spp. is strengthened by elevated air [CO ₂]. <i>Tree Physiology</i> , 2021, 41, 708-727.	3.1	40
61	High-throughput proteogenomics of <i>Ruegeria pomeroyi</i> : seeding a better genomic annotation for the whole marine Roseobacter clade. <i>BMC Genomics</i> , 2012, 13, 73.	2.8	38
62	Understanding butanol tolerance and assimilation in <i>Pseudomonas putida</i> ...: an integrated omics approach. <i>Microbial Biotechnology</i> , 2016, 9, 100-115.	4.2	38
63	C-terminal proteolysis of the collagen VI $\alpha 1$ chain by BMP-1 and proprotein convertase(s) releases endotrophin in fragments of different sizes. <i>Journal of Biological Chemistry</i> , 2019, 294, 13769-13780.	3.4	38
64	The reductase RedA2 of the multi-component dioxin dioxygenase system of <i>Sphingomonas</i> sp. RW1 is related to class I cytochrome <i>P</i> ₄₅₀ type reductases. <i>FEBS Journal</i> , 1998, 253, 437-444.	0.2	37
65	A Second [2Fe-2S] Ferredoxin from <i>Sphingomonas</i> sp. Strain RW1 Can Function as an Electron Donor for the Dioxin Dioxygenase. <i>Journal of Bacteriology</i> , 2000, 182, 2238-2244.	2.2	37
66	N-Terminal-oriented Proteogenomics of the Marine Bacterium <i>Roseobacter Denitrificans</i> Och114 using and Diagonal Chromatography. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1369-1381.	3.8	37
67	Conservation and diversity of the IrrE/DdrO-controlled radiation-resistant <i>Deinococcus</i> bacteria. <i>MicrobiologyOpen</i> , 2017, 6, e00477.	3.0	37
68	ApoFnr Binds as a Monomer to Promoters Regulating the Expression of Enterotoxin Genes of <i>Bacillus cereus</i> . <i>Journal of Bacteriology</i> , 2008, 190, 4242-4251.	2.2	36
69	The Metaproteomics Initiative: a coordinated approach for propelling the functional characterization of microbiomes. <i>Microbiome</i> , 2021, 9, 243.	11.1	36
70	Characterization of Three XylT-Like [2Fe-2S] Ferredoxins Associated with Catabolism of Cresols or Naphthalene: Evidence for Their Involvement in Catechol Dioxygenase Reactivation. <i>Journal of Bacteriology</i> , 2000, 182, 5580-5585.	2.2	35
71	Improving the quality of genome, protein sequence, and taxonomy databases: A prerequisite for microbiome meta-omics 2.0. <i>Proteomics</i> , 2015, 15, 3418-3423.	2.2	35
72	The species origin of the serum in the culture medium influences the in vitro toxicity of silica nanoparticles to HepG2 cells. <i>PLoS ONE</i> , 2017, 12, e0182906.	2.5	35

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73	Estimating relative biomasses of organisms in microbiota using α -phyloproteomics. <i>Microbiome</i> , 2020, 8, 30.	11.1	34
74	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows. <i>Nature Communications</i> , 2021, 12, 7305.	12.8	34
75	Comparative proteomics reveals key proteins recruited at the nucleoid of <i>Deinococcus</i> after irradiation-induced DNA damage. <i>Proteomics</i> , 2013, 13, 3457-3469.	2.2	33
76	Shotgun proteomics suggests involvement of additional enzymes in dioxin degradation by <i>Sphingomonas wittichii</i> ... <i>RW1</i> . <i>Environmental Microbiology</i> , 2014, 16, 162-176.	3.8	33
77	Magnetic Immunoaffinity Enrichment for Selective Capture and MS/MS Analysis of N-Terminal-TMPP-Labeled Peptides. <i>Journal of Proteome Research</i> , 2014, 13, 668-680.	3.7	32
78	Ecotoxic-Proteomics for Aquatic Environmental Monitoring: First in Situ Application of a New Proteomics-Based Multibiomarker Assay Using Caged Amphipods. <i>Environmental Science & Technology</i> , 2017, 51, 13417-13426.	10.0	32
79	A comparative proteomic approach to better define <i>Deinococcus</i> nucleoid specificities. <i>Journal of Proteomics</i> , 2012, 75, 2588-2600.	2.4	31
80	Time dynamics of the <i>Bacillus cereus</i> exoproteome are shaped by cellular oxidation. <i>Frontiers in Microbiology</i> , 2015, 6, 342.	3.5	31
81	Resilient and Sensitive Key Points of the Photosynthetic Machinery of <i>Coffea</i> spp. to the Single and Superimposed Exposure to Severe Drought and Heat Stresses. <i>Frontiers in Plant Science</i> , 2020, 11, 1049.	3.6	31
82	ResDE-Dependent Regulation of Enterotoxin Gene Expression in <i>Bacillus cereus</i> : Evidence for Multiple Modes of Binding for ResD and Interaction with Fnr. <i>Journal of Bacteriology</i> , 2009, 191, 4419-4426.	2.2	30
83	Proteogenomic insights into the core-proteome of female reproductive tissues from crustacean amphipods. <i>Journal of Proteomics</i> , 2016, 135, 51-61.	2.4	30
84	The immune system of the freshwater zebra mussel, <i>Dreissena polymorpha</i> , decrypted by proteogenomics of hemocytes and plasma compartments. <i>Journal of Proteomics</i> , 2019, 202, 103366.	2.4	30
85	<i>Rhodobacter sphaeroides</i> methionine sulfoxide reductase P reduces <i>R</i> - and <i>S</i> -diastereomers of methionine sulfoxide from a broad-spectrum of protein substrates. <i>Biochemical Journal</i> , 2018, 475, 3779-3795.	3.7	29
86	Protein Corona Composition of Silica Nanoparticles in Complex Media: Nanoparticle Size does not Matter. <i>Nanomaterials</i> , 2020, 10, 240.	4.1	29
87	Identification, Purification, and Characterization of an Eukaryotic-like Phosphopantetheine Adenylyltransferase (Coenzyme A Biosynthetic Pathway) in the Hyperthermophilic Archaeon <i>Pyrococcus abyssi</i> . <i>Journal of Biological Chemistry</i> , 2003, 278, 31078-31087.	3.4	27
88	Gammarids as Reference Species for Freshwater Monitoring. , 2015, , 253-280.		27
89	Assessment of solvent residues accessibility using three Sulfo-NHS-biotin reagents in parallel: application to footprint changes of a methyltransferase upon binding its substrate. <i>Journal of Mass Spectrometry</i> , 2008, 43, 360-370.	1.6	26
90	OhrRA functions as a redox-responsive system controlling toxinogenesis in <i>Bacillus cereus</i> . <i>Journal of Proteomics</i> , 2013, 94, 527-539.	2.4	26

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91	Proteomics identifies <i>Bacillus cereus</i> EntD as a pivotal protein for the production of numerous virulence factors. <i>Frontiers in Microbiology</i> , 2015, 6, 1004.	3.5	26
92	THUMP from archaeal tRNA:m ²² G10 methyltransferase, a genuine autonomously folding domain. <i>Nucleic Acids Research</i> , 2006, 34, 2483-2494.	14.5	25
93	Shotgun nanoLC-MS/MS proteogenomics to document MALDI-TOF biomarkers for screening new members of the <i>Ruegeria</i> genus. <i>Environmental Microbiology</i> , 2013, 15, 133-147.	3.8	25
94	Eukaryotic GPN-loop GTPases paralogs use a dimeric assembly reminiscent of archeal GPN. <i>Cell Cycle</i> , 2013, 12, 463-472.	2.6	25
95	Increasing the power of interpretation for soil metaproteomics data. <i>Microbiome</i> , 2021, 9, 195.	11.1	25
96	Structure of a [2Fe-2S] ferredoxin from <i>Rhodobacter capsulatus</i> likely involved in Fe-S cluster biogenesis and conformational changes observed upon reduction. <i>Journal of Biological Inorganic Chemistry</i> , 2006, 11, 235-246.	2.6	24
97	Quick microbial molecular phenotyping by differential shotgun proteomics. <i>Environmental Microbiology</i> , 2020, 22, 2996-3004.	3.8	24
98	Stem cells of aquatic invertebrates as an advanced tool for assessing ecotoxicological impacts. <i>Science of the Total Environment</i> , 2021, 771, 144565.	8.0	24
99	A role for GPN-loop GTPase yGPN1 in sister chromatid cohesion. <i>Cell Cycle</i> , 2011, 10, 1828-1837.	2.6	23
100	The <i>Deinococcus radiodurans</i> DR1245 Protein, a DdrB Partner Homologous to YbjN Proteins and Reminiscent of Type III Secretion System Chaperones. <i>PLoS ONE</i> , 2013, 8, e56558.	2.5	23
101	Proteomics meets blue biotechnology: A wealth of novelties and opportunities. <i>Marine Genomics</i> , 2014, 17, 35-42.	1.1	23
102	Host Plant Compatibility Shapes the Proteogenome of <i>Frankia coriariae</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 720.	3.5	23
103	De novo transcriptomes of 14 gammarid individuals for proteogenomic analysis of seven taxonomic groups. <i>Scientific Data</i> , 2019, 6, 184.	5.3	23
104	BMP-1 disrupts cell adhesion and enhances TGF- β 2 activation through cleavage of the matricellular protein thrombospondin-1. <i>Science Signaling</i> , 2020, 13, .	3.6	21
105	Proteomic Evidences for Rex Regulation of Metabolism in Toxin-Producing <i>Bacillus cereus</i> ATCC 14579. <i>PLoS ONE</i> , 2014, 9, e107354.	2.5	21
106	Ferredoxin-mediated reactivation of the chlorocatechol 2,3-dioxygenase from <i>Pseudomonas putida</i> GJ31. <i>Archives of Microbiology</i> , 2002, 177, 345-351.	2.2	20
107	Combining proteogenomics and metaproteomics for deep taxonomic and functional characterization of microbiomes from a non-sequenced host. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 23.	6.4	20
108	Taxonomical and functional changes in COVID-19 faecal microbiome could be related to SARS-CoV-2 faecal load. <i>Environmental Microbiology</i> , 2022, 24, 4299-4316.	3.8	20

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109	In vitro assessment of cobalt oxide particle toxicity: Identifying and circumventing interference. <i>Toxicology in Vitro</i> , 2013, 27, 1699-1710.	2.4	19
110	Tissue-specific Proteogenomic Analysis of <i>Plutella xylostella</i> Larval Midgut Using a Multialgorithm Pipeline. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1791-1807.	3.8	19
111	Characterization of a 2[4Fe-4S] Ferredoxin Obtained by Chemical Insertion of the Fe-S Clusters into the Apoferredoxin II from <i>Rhodobacter Capsulatus</i> . <i>FEBS Journal</i> , 1995, 231, 396-404.	0.2	19
112	The importance of recognizing and reporting sequence database contamination for proteomics. <i>EuPA Open Proteomics</i> , 2014, 3, 246-249.	2.5	18
113	Genomic and physiological analysis reveals versatile metabolic capacity of deep-sea <i>Photobacterium phosphoreum</i> ANT-2200. <i>Extremophiles</i> , 2016, 20, 301-310.	2.3	18
114	High-throughput proteotyping of bacterial isolates by double barrel chromatography-tandem mass spectrometry based on microplate paramagnetic beads and phylopeptidomics. <i>Journal of Proteomics</i> , 2020, 226, 103887.	2.4	18
115	Proteomics in the COVID-19 Battlefield: First Semester Check-Up. <i>Proteomics</i> , 2021, 21, 2000198.	2.2	18
116	Analytical constraints for the analysis of human cell line secretomes by shotgun proteomics. <i>Journal of Proteomics</i> , 2012, 75, 1043-1054.	2.4	17
117	Multiplexed assay for protein quantitation in the invertebrate <i>Gammarus fossarum</i> by liquid chromatography coupled to tandem mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2017, 409, 3969-3991.	3.7	17
118	Oxidative DNA Damage and Repair in the Radioresistant Archaeon <i>Thermococcus gammatolerans</i> . <i>Chemical Research in Toxicology</i> , 2016, 29, 1796-1809.	3.3	16
119	Emerin self-assembly mechanism: role of the LEM domain. <i>FEBS Journal</i> , 2017, 284, 338-352.	4.7	16
120	Biosafety of Mesoporous Silica Nanoparticles. <i>Biomimetics</i> , 2018, 3, 22.	3.3	16
121	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.	4.0	16
122	Identification and Characterization of Marine Microorganisms by Tandem Mass Spectrometry Proteotyping. <i>Microorganisms</i> , 2022, 10, 719.	3.6	16
123	Proteogenomic Definition of Biomarkers for the Large <i>Roseobacter</i> Clade and Application for a Quick Screening of New Environmental Isolates. <i>Journal of Proteome Research</i> , 2013, 12, 5331-5339.	3.7	15
124	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.	2.4	15
125	Deciphering the interactions between the <i>Bacillus cereus</i> linear plasmid, pBClin15, and its host by high-throughput comparative proteomics. <i>Journal of Proteomics</i> , 2016, 146, 25-33.	2.4	15
126	PprA Protein Is Involved in Chromosome Segregation via Its Physical and Functional Interaction with DNA Gyrase in Irradiated <i>Deinococcus radiodurans</i> Bacteria. <i>MSphere</i> , 2016, 1, .	2.9	15

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127	Titanium Dioxide Nanoparticles Alter the Cellular Phosphoproteome in A549 Cells. <i>Nanomaterials</i> , 2020, 10, 185.	4.1	15
128	An integrated metabolomics and proteogenomics approach reveals molecular alterations following carbamazepine exposure in the male mussel <i>Mytilus galloprovincialis</i> . <i>Chemosphere</i> , 2022, 286, 131793.	8.2	15
129	The abundant and essential HU proteins in <i>Deinococcus deserti</i> and <i>Deinococcus radiodurans</i> are translated from leaderless mRNA. <i>Microbiology (United Kingdom)</i> , 2015, 161, 2410-2422.	1.8	15
130	Methionine Residues in Exoproteins and Their Recycling by Methionine Sulfoxide Reductase AB Serve as an Antioxidant Strategy in <i>Bacillus cereus</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1342.	3.5	14
131	The PEG-responding desiccome of the alder microsymbiont <i>Frankia alni</i> . <i>Scientific Reports</i> , 2018, 8, 759.	3.3	14
132	Coupling caging and proteomics on the European flounder (<i>Platichthys flesus</i>) to assess the estuarine water quality at micro scale. <i>Science of the Total Environment</i> , 2019, 695, 133760.	8.0	14
133	Omics of the early molecular dialogue between <i>Frankia alni</i> and <i>Alnus glutinosa</i> and the cellulase synton. <i>Environmental Microbiology</i> , 2019, 21, 3328-3345.	3.8	14
134	Identification of immune-related proteins of <i>Dreissena polymorpha</i> hemocytes and plasma involved in host-microbe interactions by differential proteomics. <i>Scientific Reports</i> , 2020, 10, 6226.	3.3	14
135	Assessing the ratio of <i>Bacillus</i> spores and vegetative cells by shotgun proteomics. <i>Environmental Science and Pollution Research</i> , 2021, 28, 25107-25115.	5.3	14
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