Jean Armengaud

List of Publications by Year
in descending order

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		61687	124990
217	6,589	45	64
papers	citations	h-index	g-index

227	227	227	8457
all docs	docs citations	times ranked	citing authors

#	ARTICLE	IF	CITATIONS
1	Discovery and characterization of UipA, a uranium- and iron-binding PepSY protein involved in uranium tolerance by soil bacteria. ISME Journal, 2022, 16, 705-716.	4.4	13
2	An integrated metabolomics and proteogenomics approach reveals molecular alterations following carbamazepine exposure in the male mussel Mytilus galloprovincialis. Chemosphere, 2022, 286, 131793.	4.2	15
3	Antibiotic tolerance and degradation capacity of the organic pollutant-degrading bacterium Rhodococcus biphenylivorans TG9T. Journal of Hazardous Materials, 2022, 424, 127712.	6.5	9
4	Combined omics approaches reveal distinct responses between light and heavy rare earth elements in Saccharomyces cerevisiae. Journal of Hazardous Materials, 2022, 425, 127830.	6.5	8
5	Effect of actinorhizal root exudates on the proteomes of Frankia soli NRRL B-16219, a strain colonizing the root tissues of its actinorhizal host via intercellular pathway. Research in Microbiology, 2022, 173, 103900.	1.0	5
6	Next-Generation Proteomics Reveals a Greater Antioxidative Response to Drought in Coffea arabica Than in Coffea canephora. Agronomy, 2022, 12, 148.	1.3	10
7	Heme A Synthase Deficiency Affects the Ability of Bacillus cereus to Adapt to a Nutrient-Limited Environment. International Journal of Molecular Sciences, 2022, 23, 1033.	1.8	4
8	Characterization of Soluble Cell-Free Coelomic Fluid Proteome from the Starfish Marthasterias glacialis. Methods in Molecular Biology, 2022, 2450, 583-597.	0.4	0
9	Deciphering Black Extrinsic Tooth Stain Composition in Children Using Metaproteomics. ACS Omega, 2022, 7, 8258-8267.	1.6	5
10	Identification and Characterization of Marine Microorganisms by Tandem Mass Spectrometry Proteotyping. Microorganisms, 2022, 10, 719.	1.6	16
11	The Proteogenome of Symbiotic Frankia alni in Alnus glutinosa Nodules. Microorganisms, 2022, 10, 651.	1.6	4
12	Protecting our environment, a motivating outdoor game for proteomics!. Proteomics, 2022, 22, e2200055.	1.3	1
13	Infection of Human Endothelial Cells with Lassa Virus Induces Early but Transient Activation and Low Type I IFN Response Compared to the Closely-Related Nonpathogenic Mopeia Virus. Viruses, 2022, 14, 652.	1.5	3
14	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
15	Profiling SARS-CoV-2 Infection by High-Throughput Shotgun Proteomics. Methods in Molecular Biology, 2022, 2452, 167-182.	0.4	0
16	Assessing the ratio of Bacillus spores and vegetative cells by shotgun proteomics. Environmental Science and Pollution Research, 2021, 28, 25107-25115.	2.7	14
17	Proteomics in the COVIDâ€•19 Battlefield: First Semester Checkâ€•Up. Proteomics, 2021, 21, 2000198.	1.3	18
18	Lysine-specific acetylated proteome from the archaeon Thermococcus gammatolerans reveals the presence of acetylated histones. Journal of Proteomics, 2021, 232, 104044.	1.2	12

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19	Ionizing-radiation-resistant Kocuria rhizophila PT10 isolated from the Tunisian Sahara xerophyte Panicum turgidum: Polyphasic characterization and proteogenomic arsenal. Genomics, 2021, 113, 317-330.	1.3	7
20	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
21	Methionine Sulfoxide Reductases Contribute to Anaerobic Fermentative Metabolism in Bacillus cereus. Antioxidants, 2021, 10, 819.	2.2	2
22	Co-expression network analysis identifies novel molecular pathways associated with cadmium and pyriproxyfen testicular toxicity in Gammarus fossarum. Aquatic Toxicology, 2021, 235, 105816.	1.9	9
23	Stem cells of aquatic invertebrates as an advanced tool for assessing ecotoxicological impacts. Science of the Total Environment, 2021, 771, 144565.	3.9	24
24	Metaproteomics to Decipher CF Host-Microbiota Interactions: Overview, Challenges and Future Perspectives. Genes, 2021, 12, 892.	1.0	10
25	Cysteine Proteome Reveals Response to Endogenous Oxidative Stress in Bacillus cereus. International Journal of Molecular Sciences, 2021, 22, 7550.	1.8	5
26	A Proteomic Study Suggests Stress Granules as New Potential Actors in Radiation-Induced Bystander Effects. International Journal of Molecular Sciences, 2021, 22, 7957.	1.8	5
27	Unleashing immuno-mass spectrometry superpowers to detect SARS-CoV-2. EBioMedicine, 2021, 69, 103480.	2.7	2
28	Subcellular Distribution of Dietary Methyl-Mercury in <i>Gammarus fossarum</i> and Its Impact on the Amphipod Proteome. Environmental Science & Technology, 2021, 55, 10514-10523.	4.6	4
29	Recombinant myelin oligodendrocyte glycoprotein quality modifies evolution of experimental autoimmune encephalitis in macaques. Laboratory Investigation, 2021, 101, 1513-1522.	1.7	1
30	Redox proteomic study of Bacillus cereus thiol proteome during fermentative anaerobic growth. BMC Genomics, 2021, 22, 648.	1.2	3
31	Increasing the power of interpretation for soil metaproteomics data. Microbiome, 2021, 9, 195.	4.9	25
32	Intrinsic non-stomatal resilience to drought of the photosynthetic apparatus in <i>Coffea</i> spp. is strengthened by elevated air [CO2]. Tree Physiology, 2021, 41, 708-727.	1.4	40
33	Cyclical Patterns Affect Microbial Dynamics in the Water Basin of a Nuclear Research Reactor. Frontiers in Microbiology, 2021, 12, 744115.	1.5	4
34	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows. Nature Communications, 2021, 12, 7305.	5.8	34
35	The Metaproteomics Initiative: a coordinated approach for propelling the functional characterization of microbiomes. Microbiome, 2021, 9, 243.	4.9	36
36	Increased protein S-nitrosylation in mitochondria: a key mechanism of exercise-induced cardioprotection. Basic Research in Cardiology, 2021, 116, 66.	2.5	8

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37	Post-production modifications of murine mesenchymal stem cell (mMSC) derived extracellular vesicles (EVs) and impact on their cellular interaction. Biomaterials, 2020, 231, 119675.	5.7	59
38	Dual transcriptomics and proteomics analyses of the early stage of interaction between <i>Caballeronia mineralivorans</i><scp>PML1</scp>(12) and mineral. Environmental Microbiology, 2020, 22, 3838-3862.	1.8	10
39	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
40	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
41	From shotgun to targeted proteomics: rapid Scout-MRM assay development for monitoring potential immunomarkers in Dreissena polymorpha. Analytical and Bioanalytical Chemistry, 2020, 412, 7333-7347.	1.9	9
42	Groundwater promotes emergence of asporogenic mutants of emetic Bacillus cereus. Environmental Microbiology, 2020, 22, 5248-5264.	1.8	6
43	The proteomics contribution to the counter-bioterrorism toolbox in the post-COVID-19 era. Expert Review of Proteomics, 2020, 17, 507-511.	1.3	5
44	Dichloromethane Degradation Pathway from Unsequenced Hyphomicrobium sp. MC8b Rapidly Explored by Pan-Proteomics. Microorganisms, 2020, 8, 1876.	1.6	6
45	Proteotyping Environmental Microorganisms by Phylopeptidomics: Case Study Screening Water from a Radioactive Material Storage Pool. Microorganisms, 2020, 8, 1525.	1.6	11
46	Bacillus cereus Decreases NHE and CLO Exotoxin Synthesis to Maintain Appropriate Proteome Dynamics During Growth at Low Temperature. Toxins, 2020, 12, 645.	1.5	7
47	Shortlisting SARSâ€CoVâ€2 Peptides for Targeted Studies from Experimental Dataâ€Dependent Acquisition Tandem Mass Spectrometry Data. Proteomics, 2020, 20, e2000107.	1.3	64
48	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
49	Roadmap for naming uncultivated Archaea and Bacteria. Nature Microbiology, 2020, 5, 987-994.	5.9	115
50	Bioactive Potential of Extracts of Labrenzia aggregata Strain USBA 371, a Halophilic Bacterium Isolated from a Terrestrial Source. Molecules, 2020, 25, 2546.	1.7	3
51	Estimating relative biomasses of organisms in microbiota using â€œphylopeptidomicsâ€. Microbiome, 2020, 8, 30.	4.9	34
52	Quick microbial molecular phenotyping by differential shotgun proteomics. Environmental Microbiology, 2020, 22, 2996-3004.	1.8	24
53	BMP-1 disrupts cell adhesion and enhances TGF-Î² activation through cleavage of the matricellular protein thrombospondin-1. Science Signaling, 2020, 13, .	1.6	21
54	Resilient and Sensitive Key Points of the Photosynthetic Machinery of Coffea spp. to the Single and Superimposed Exposure to Severe Drought and Heat Stresses. Frontiers in Plant Science, 2020, 11, 1049.	1.7	31

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55	High-multiplexed monitoring of protein biomarkers in the sentinel Gammarus fossarum by targeted scout-MRM assay, a new vision for ecotoxicoproteomics. Journal of Proteomics, 2020, 226, 103901.	1.2	10
56	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
57	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
58	Protein Corona Composition of Silica Nanoparticles in Complex Media: Nanoparticle Size does not Matter. Nanomaterials, 2020, 10, 240.	1.9	29
59	Titanium Dioxide Nanoparticles Alter the Cellular Phosphoproteome in A549 Cells. Nanomaterials, 2020, 10, 185.	1.9	15
60	<scp>The importance of naturally attenuated SARSâ€CoV</scp>â€2<scp>in the fight against COVID</scp>â€19. Environmental Microbiology, 2020, 22, 1997-2000.	1.8	54
61	Proteogenomicsâ€Guided Evaluation of RNAâ€Seq Assembly and Protein Database Construction for Emergent Model Organisms. Proteomics, 2020, 20, e1900261.	1.3	7
62	Identification of immune-related proteins of Dreissena polymorpha hemocytes and plasma involved in host-microbe interactions by differential proteomics. Scientific Reports, 2020, 10, 6226.	1.6	14
63	Comparative Proteomics of Ostreid Herpesvirus 1 and Pacific Oyster Interactions With Two Families Exhibiting Contrasted Susceptibility to Viral Infection. Frontiers in Immunology, 2020, 11, 621994.	2.2	10
64	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
65	C-terminal proteolysis of the collagen VI Î±3 chain by BMP-1 and proprotein convertase(s) releases endotrophin in fragments of different sizes. Journal of Biological Chemistry, 2019, 294, 13769-13780.	1.6	38
66	Shotgun proteomics datasets acquired on Gammarus pulex animals sampled from the wild. Data in Brief, 2019, 27, 104650.	0.5	4
67	De novo transcriptomes of 14 gammarid individuals for proteogenomic analysis of seven taxonomic groups. Scientific Data, 2019, 6, 184.	2.4	23
68	Advanced Proteomics as a Powerful Tool for Studying Toxins of Human Bacterial Pathogens. Toxins, 2019, 11, 576.	1.5	8
69	Coupling caging and proteomics on the European flounder (Platichthys flesus) to assess the estuarine water quality at micro scale. Science of the Total Environment, 2019, 695, 133760.	3.9	14
70	Vaccines inducing immunity to Lassa virus glycoprotein and nucleoprotein protect macaques after a single shot. Science Translational Medicine, 2019, 11, .	5.8	53
71	Evaluation of Sample Preparation Methods for Fast Proteotyping of Microorganisms by Tandem Mass Spectrometry. Frontiers in Microbiology, 2019, 10, 1985.	1.5	69
72	Pathogen proteotyping: A rapidly developing application of mass spectrometry to address clinical concerns. Clinical Mass Spectrometry, 2019, 14, 9-17.	1.9	49

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73	Co-expression network analysis identifies gonad- and embryo-associated protein modules in the sentinel species Gammarus fossarum. Scientific Reports, 2019, 9, 7862.	1.6	13
74	The immune system of the freshwater zebra mussel, Dreissena polymorpha, decrypted by proteogenomics of hemocytes and plasma compartments. Journal of Proteomics, 2019, 202, 103366.	1.2	30
75	Microbiology and infectious diseases â€“ A wealth of novelty for the clinical laboratory. Clinical Mass Spectrometry, 2019, 14, 1-2.	1.9	0
76	Comparative genomics and proteogenomics highlight key molecular players involved in Frankia sporulation. Research in Microbiology, 2019, 170, 202-213.	1.0	5
77	Omics of the early molecular dialogue between <i>Frankia alni</i> and <i>Alnus glutinosa</i> and the cellulase synton. Environmental Microbiology, 2019, 21, 3328-3345.	1.8	14
78	Proteases as Secreted Exoproteins in Mycoplasmas from Ruminant Lungs and Their Impact on Surface-Exposed Proteins. Applied and Environmental Microbiology, 2019, 85, .	1.4	11
79	Ecotoxicoproteomics: A decade of progress in our understanding of anthropogenic impact on the environment. Journal of Proteomics, 2019, 198, 66-77.	1.2	66
80	Complete Genome Sequences of Four <i>Microbacterium</i> Strains Isolated from Metal- and Radionuclide-Rich Soils. Microbiology Resource Announcements, 2019, 8, .	0.3	3
81	Time-course proteomics dataset to monitor protein-bound methionine oxidation in Bacillus cereus ATCC 14579. Data in Brief, 2018, 18, 394-398.	0.5	2
82	Importance of Post-translational Modifications in the Interaction of Proteins with Mineral Surfaces: The Case of Arginine Methylation and Silica surfaces. Langmuir, 2018, 34, 5312-5322.	1.6	4
83	The PEG-responding desiccome of the alder microsymbiont Frankia alni. Scientific Reports, 2018, 8, 759.	1.6	14
84	Proteogenomic insights into uranium tolerance of a Chernobyl's Microbacterium bacterial isolate. Journal of Proteomics, 2018, 177, 148-157.	1.2	43
85	Proteomics data for characterizing Microbacterium oleivorans A9, an uranium-tolerant actinobacterium isolated near the Chernobyl nuclear power plant. Data in Brief, 2018, 21, 1125-1129.	0.5	3
86	Biosafety of Mesoporous Silica Nanoparticles. Biomimetics, 2018, 3, 22.	1.5	16
87	<i>Rhodobacter</i> <i>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. Biochemical Journal, 2018, 475, 3779-3795.	1.7	29
88	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
89	Improving Quality Control of Contagious Caprine Pleuropneumonia Vaccine with Tandem Mass Spectrometry. Proteomics, 2018, 18, e1800088.	1.3	10
90	On-Line Solid Phase Extraction Liquid Chromatography-Mass Spectrometry Method for Multiplexed Proteins Quantitation in an Ecotoxicology Test Specie: Gammarus fossarum. Journal of Applied Bioanalysis, 2018, 4, 81-101.	0.2	3

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91	Draft Genome Sequence of Microbacterium oleivorans Strain A9, a Bacterium Isolated from Chernobyl Radionuclide-Contaminated Soil. Genome Announcements, 2017, 5, .	0.8	6
92	Conservation and diversity of the IrrE/DdrOâ€controlled radiation response in radiationâ€resistant <i>Deinococcus</i> bacteria. MicrobiologyOpen, 2017, 6, e00477.	1.2	37
93	Multiplexed assay for protein quantitation in the invertebrate Gammarus fossarum by liquid chromatography coupled to tandem mass spectrometry. Analytical and Bioanalytical Chemistry, 2017, 409, 3969-3991.	1.9	17
94	Defining Diagnostic Biomarkers Using Shotgun Proteomics and MALDI-TOF Mass Spectrometry. Methods in Molecular Biology, 2017, 1616, 107-120.	0.4	4
95	Striking against bioterrorism with advanced proteomics and reference methods. Proteomics, 2017, 17, 1600412.	1.3	5
96	Emerin selfâ€assembly mechanism: role of the LEM domain. FEBS Journal, 2017, 284, 338-352.	2.2	16
97	Ecotoxico-Proteomics for Aquatic Environmental Monitoring: First in Situ Application of a New Proteomics-Based Multibiomarker Assay Using Caged Amphipods. Environmental Science & Technology, 2017, 51, 13417-13426.	4.6	32
98	<i>In Vino Veritas</i>: An Invitation for Ambitious, Collaborative Proteogenomics Campaigns on Plant and Animal Models. Proteomics, 2017, 17, 1700324.	1.3	0
99	Proteogenomic Insights into the Intestinal Parasite <i>Blastocystis</i> sp. Subtype 4 Isolate WR1. Proteomics, 2017, 17, 1700211.	1.3	5
100	Proteogenomics data for deciphering Frankia coriariae interactions with root exudates from three host plants. Data in Brief, 2017, 14, 73-76.	0.5	2
101	Nutrient recycling facilitates long-term stability of marine microbial phototrophâ€“heterotroph interactions. Nature Microbiology, 2017, 2, 17100.	5.9	181
102	The timeline of corona formation around silica nanocarriers highlights the role of the protein interactome. Nanoscale, 2017, 9, 1840-1851.	2.8	56
103	Host Plant Compatibility Shapes the Proteogenome of Frankia coriariae. Frontiers in Microbiology, 2017, 8, 720.	1.5	23
104	Methionine Residues in Exoproteins and Their Recycling by Methionine Sulfoxide Reductase AB Serve as an Antioxidant Strategy in Bacillus cereus. Frontiers in Microbiology, 2017, 8, 1342.	1.5	14
105	The species origin of the serum in the culture medium influences the in vitro toxicity of silica nanoparticles to HepG2 cells. PLoS ONE, 2017, 12, e0182906.	1.1	35
106	Mussel as a Tool to Define Continental Watershed Quality. , 2017, , .		9
107	Genomic and physiological analysis reveals versatile metabolic capacity of deep-sea Photobacterium phosphoreum ANT-2200. Extremophiles, 2016, 20, 301-310.	0.9	18
108	Understanding butanol tolerance and assimilation in <scp><i>P</i></scp><i>seudomonas putida</i>â€…<scp>BIRD</scp>â€1: an integrated omics approach. Microbial Biotechnology, 2016, 9, 100-115.	2.0	38

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109	Proteome data to explore the impact of pBClin15 on Bacillus cereus ATCC 14579. Data in Brief, 2016, 8, 1243-1246.	0.5	6
110	Oxidative DNA Damage and Repair in the Radioresistant Archaeon <i>Thermococcus gammatolerans</i>. Chemical Research in Toxicology, 2016, 29, 1796-1809.	1.7	16
111	Ovary and embryo proteogenomic dataset revealing diversity of vitellogenins in the crustacean Gammarus fossarum. Data in Brief, 2016, 8, 1259-1262.	0.5	1
112	RNA-binding proteins are a major target of silica nanoparticles in cell extracts. Nanotoxicology, 2016, 10, 1555-1564.	1.6	86
113	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
114	Deciphering the interactions between the Bacillus cereus linear plasmid, pBClin15, and its host by high-throughput comparative proteomics. Journal of Proteomics, 2016, 146, 25-33.	1.2	15
115	Mass spectrometry for the detection of bioterrorism agents: from environmental to clinical applications. Journal of Mass Spectrometry, 2016, 51, 183-199.	0.7	40
116	Postâ€translational methylations of the archaeal Mre11:Rad50 complex throughout the DNA damage response. Molecular Microbiology, 2016, 100, 362-378.	1.2	10
117	PprA Protein Is Involved in Chromosome Segregation via Its Physical and Functional Interaction with DNA Gyrase in Irradiated Deinococcus radiodurans Bacteria. MSphere, 2016, 1, .	1.3	15
118	Clinical implications of recent advances in proteogenomics. Expert Review of Proteomics, 2016, 13, 185-199.	1.3	12
119	Tissue-specific Proteogenomic Analysis of Plutella xylostella Larval Midgut Using a Multialgorithm Pipeline. Molecular and Cellular Proteomics, 2016, 15, 1791-1807.	2.5	19
120	Next-generation proteomics faces new challenges in environmental biotechnology. Current Opinion in Biotechnology, 2016, 38, 174-182.	3.3	46
121	Implementation of meiosis prophase I programme requires a conserved retinoid-independent stabilizer of meiotic transcripts. Nature Communications, 2016, 7, 10324.	5.8	89
122	Stone-dwelling actinobacteria <i>Blastococcus saxobsidens</i>, <i>Modestobacter marinus</i> and <i>Geodermatophilus obscurus</i> proteogenomes. ISME Journal, 2016, 10, 21-29.	4.4	71
123	Proteogenomic insights into the core-proteome of female reproductive tissues from crustacean amphipods. Journal of Proteomics, 2016, 135, 51-61.	1.2	30
124	Microbiomes - Embracing complexity. Proteomics, 2015, 15, 3405-3406.	1.3	4
125	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
126	Essentiality of threonylcarbamoyladenosine (t⁶<scp>A</scp>), a universal t<scp>RNA</scp> modification, in bacteria. Molecular Microbiology, 2015, 98, 1199-1221.	1.2	72

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127	Proteomics of the <i>Roseobacter</i> clade, a window to the marine microbiology landscape. Proteomics, 2015, 15, 3928-3942.	1.3	12
128	Time dynamics of the Bacillus cereus exoproteome are shaped by cellular oxidation. Frontiers in Microbiology, 2015, 6, 342.	1.5	31
129	Proteomics identifies Bacillus cereus EntD as a pivotal protein for the production of numerous virulence factors. Frontiers in Microbiology, 2015, 6, 1004.	1.5	26
130	Salt Stress Induced Changes in the Exoproteome of the Halotolerant Bacterium Tistlia consotensis Deciphered by Proteogenomics. PLoS ONE, 2015, 10, e0135065.	1.1	47
131	Functional distinctness in the exoproteomes of marine <scp><i>S</i></scp><i>ynechococcus</i>. Environmental Microbiology, 2015, 17, 3781-3794.	1.8	55
132	High-throughput, quantitative assessment of the effects of low-dose silica nanoparticles on lung cells: grasping complex toxicity with a great depth of field. BMC Genomics, 2015, 16, 315.	1.2	47
133	Data for comparative proteomics of ovaries from five non-model, crustacean amphipods. Data in Brief, 2015, 5, 1-6.	0.5	4
134	Proteomic Investigation of Male <i>Gammarus fossarum</i>, a Freshwater Crustacean, in Response to Endocrine Disruptors. Journal of Proteome Research, 2015, 14, 292-303.	1.8	56
135	â€œYou produce while I clean upâ€, a strategy revealed by exoproteomics during <i>Synechococcus</i>â€"<i>Roseobacter</i> interactions. Proteomics, 2015, 15, 3454-3462.	1.3	50
136	Gammarids as Reference Species for Freshwater Monitoring. , 2015, , 253-280.		27
137	Defining a Pipeline for Metaproteomic Analyses. Springer Protocols, 2015, , 99-110.	0.1	1
138	Power of positive thinking in quantitative proteomics. Proteomics, 2015, 15, 2898-2900.	1.3	2
139	Prioritizing targets for structural biology through the lens of proteomics: The archaeal protein TGAM_1934 from <i>Thermococcus gammatolerans</i>. Proteomics, 2015, 15, 114-123.	1.3	5
140	The abundant and essential HU proteins in Deinococcus deserti and Deinococcus radiodurans are translated from leaderless mRNA. Microbiology (United Kingdom), 2015, 161, 2410-2422.	0.7	15
141	Proteogenomics of Gammarus fossarum to Document the Reproductive System of Amphipods. Molecular and Cellular Proteomics, 2014, 13, 3612-3625.	2.5	50
142	Taking the Shortcut for High-Throughput Shotgun Proteomic Analysis of Bacteria. Methods in Molecular Biology, 2014, 1197, 275-285.	0.4	94
143	Shotgun Proteomics for Hydrocarbon Microbiology. Springer Protocols, 2014, , 97-102.	0.1	3
144	Next-Generation Proteomics: Toward Customized Biomarkers for Environmental Biomonitoring. Environmental Science & Technology, 2014, 48, 13560-13572.	4.6	52

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145	Nâ€terminomics and proteogenomics, getting off to a good start. Proteomics, 2014, 14, 2637-2646.	1.3	64
146	Shotgun proteomics suggests involvement of additional enzymes in dioxin degradation by <i><scp>S</scp>phingomonas wittichii</i>â€…<scp>RW1</scp>. Environmental Microbiology, 2014, 16, 162-176.	1.8	33
147	Proteogenomics for the Enhanced Discovery of Bacterial Biomarkers. NATO Science for Peace and Security Series A: Chemistry and Biology, 2014, , 169-177.	0.5	2
148	Non-model organisms, a species endangered by proteogenomics. Journal of Proteomics, 2014, 105, 5-18.	1.2	145
149	RNA Sequencing and Proteogenomics Reveal the Importance of Leaderless mRNAs in the Radiation-Tolerant Bacterium Deinococcus deserti. Genome Biology and Evolution, 2014, 6, 932-948.	1.1	61
150	Proteogenomic Biomarkers for Identification ofFrancisellaSpecies and Subspecies by Matrix-Assisted Laser Desorption Ionization-Time-of-Flight Mass Spectrometry. Analytical Chemistry, 2014, 86, 9394-9398.	3.2	43
151	Magnetic Immunoaffinity Enrichment for Selective Capture and MS/MS Analysis of N-Terminal-TMPP-Labeled Peptides. Journal of Proteome Research, 2014, 13, 668-680.	1.8	32
152	Proteomics meets blue biotechnology: A wealth of novelties and opportunities. Marine Genomics, 2014, 17, 35-42.	0.4	23
153	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
154	N-Terminal-oriented Proteogenomics of the Marine Bacterium Roseobacter Denitrificans Och114 using and Diagonal Chromatography. Molecular and Cellular Proteomics, 2014, 13, 1369-1381.	2.5	37
155	The importance of recognizing and reporting sequence database contamination for proteomics. EuPA Open Proteomics, 2014, 3, 246-249.	2.5	18
156	Assessing the Exoproteome of Marine Bacteria, Lesson from a RTX-Toxin Abundantly Secreted by Phaeobacter Strain DSM 17395. PLoS ONE, 2014, 9, e89691.	1.1	10
157	Low Doses of Gamma-Irradiation Induce an Early Bystander Effect in Zebrafish Cells Which Is Sufficient to Radioprotect Cells. PLoS ONE, 2014, 9, e92974.	1.1	53
158	Proteomic Evidences for Rex Regulation of Metabolism in Toxin-Producing Bacillus cereus ATCC 14579. PLoS ONE, 2014, 9, e107354.	1.1	21
159	Microbiology and proteomics, getting the best of both worlds!. Environmental Microbiology, 2013, 15, 12-23.	1.8	76
160	Shotgun nanoLCâ€MS/MS proteogenomics to document MALDIâ€TOF biomarkers for screening new members of the <i>Ruegeria</i> genus. Environmental Microbiology, 2013, 15, 133-147.	1.8	25
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