

Jean Armengaud

List of Publications by Year in descending order

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Version: 2024-02-01

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 | Discovery and characterization of UipA, a uranium- and iron-binding PepSY protein involved in uranium tolerance by soil bacteria. <i>ISME Journal</i> , 2022, 16, 705-716. | 9.8 | 13 |
| 2 | 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 |
| 3 | Antibiotic tolerance and degradation capacity of the organic pollutant-degrading bacterium <i>Rhodococcus biphenylivorans</i> TG9T. <i>Journal of Hazardous Materials</i> , 2022, 424, 127712. | 12.4 | 9 |
| 4 | Combined omics approaches reveal distinct responses between light and heavy rare earth elements in <i>Saccharomyces cerevisiae</i> . <i>Journal of Hazardous Materials</i> , 2022, 425, 127830. | 12.4 | 8 |
| 5 | Effect of actinorhizal root exudates on the proteomes of <i>Frankia soli</i> NRRL B-16219, a strain colonizing the root tissues of its actinorhizal host via intercellular pathway. <i>Research in Microbiology</i> , 2022, 173, 103900. | 2.1 | 5 |
| 6 | Next-Generation Proteomics Reveals a Greater Antioxidative Response to Drought in <i>Coffea arabica</i> Than in <i>Coffea canephora</i> . <i>Agronomy</i> , 2022, 12, 148. | 3.0 | 10 |
| 7 | Heme A Synthase Deficiency Affects the Ability of <i>Bacillus cereus</i> to Adapt to a Nutrient-Limited Environment. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1033. | 4.1 | 4 |
| 8 | Characterization of Soluble Cell-Free Coelomic Fluid Proteome from the Starfish <i>Marthasterias glacialis</i> . <i>Methods in Molecular Biology</i> , 2022, 2450, 583-597. | 0.9 | 0 |
| 9 | Deciphering Black Extrinsic Tooth Stain Composition in Children Using Metaproteomics. <i>ACS Omega</i> , 2022, 7, 8258-8267. | 3.5 | 5 |
| 10 | Identification and Characterization of Marine Microorganisms by Tandem Mass Spectrometry Proteotyping. <i>Microorganisms</i> , 2022, 10, 719. | 3.6 | 16 |
| 11 | The Proteogenome of Symbiotic <i>Frankia alni</i> in <i>Alnus glutinosa</i> Nodules. <i>Microorganisms</i> , 2022, 10, 651. | 3.6 | 4 |
| 12 | Protecting our environment, a motivating outdoor game for proteomics!. <i>Proteomics</i> , 2022, 22, e2200055. | 2.2 | 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. <i>Viruses</i> , 2022, 14, 652. | 3.3 | 3 |
| 14 | 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 |
| 15 | Profiling SARS-CoV-2 Infection by High-Throughput Shotgun Proteomics. <i>Methods in Molecular Biology</i> , 2022, 2452, 167-182. | 0.9 | 0 |
| 16 | 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 |
| 17 | Proteomics in the COVID-19 Battlefield: First Semester Check-Up. <i>Proteomics</i> , 2021, 21, 2000198. | 2.2 | 18 |
| 18 | Lysine-specific acetylated proteome from the archaeon <i>Thermococcus gammatolerans</i> reveals the presence of acetylated histones. <i>Journal of Proteomics</i> , 2021, 232, 104044. | 2.4 | 12 |

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|----|--|------|-----------|
| 19 | Ionizing-radiation-resistant <i>Kocuria rhizophila</i> PT10 isolated from the Tunisian Sahara xerophyte <i>Panicum turgidum</i> : Polyphasic characterization and proteogenomic arsenal. <i>Genomics</i> , 2021, 113, 317-330. | 2.9 | 7 |
| 20 | Heterogeneity of SARS-CoV-2 virus produced in cell culture revealed by shotgun proteomics and supported by genome sequencing. <i>Analytical and Bioanalytical Chemistry</i> , 2021, 413, 7265-7275. | 3.7 | 7 |
| 21 | Methionine Sulfoxide Reductases Contribute to Anaerobic Fermentative Metabolism in <i>Bacillus cereus</i> . <i>Antioxidants</i> , 2021, 10, 819. | 5.1 | 2 |
| 22 | Co-expression network analysis identifies novel molecular pathways associated with cadmium and pyriproxyfen testicular toxicity in <i>Gammarus fossarum</i> . <i>Aquatic Toxicology</i> , 2021, 235, 105816. | 4.0 | 9 |
| 23 | 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 |
| 24 | Metaproteomics to Decipher CF Host-Microbiota Interactions: Overview, Challenges and Future Perspectives. <i>Genes</i> , 2021, 12, 892. | 2.4 | 10 |
| 25 | Cysteine Proteome Reveals Response to Endogenous Oxidative Stress in <i>Bacillus cereus</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 7550. | 4.1 | 5 |
| 26 | A Proteomic Study Suggests Stress Granules as New Potential Actors in Radiation-Induced Bystander Effects. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7957. | 4.1 | 5 |
| 27 | Unleashing immuno-mass spectrometry superpowers to detect SARS-CoV-2. <i>EBioMedicine</i> , 2021, 69, 103480. | 6.1 | 2 |
| 28 | Subcellular Distribution of Dietary Methyl-Mercury in <i>Gammarus fossarum</i> and Its Impact on the Amphipod Proteome. <i>Environmental Science & Technology</i> , 2021, 55, 10514-10523. | 10.0 | 4 |
| 29 | Recombinant myelin oligodendrocyte glycoprotein quality modifies evolution of experimental autoimmune encephalitis in macaques. <i>Laboratory Investigation</i> , 2021, 101, 1513-1522. | 3.7 | 1 |
| 30 | Redox proteomic study of <i>Bacillus cereus</i> thiol proteome during fermentative anaerobic growth. <i>BMC Genomics</i> , 2021, 22, 648. | 2.8 | 3 |
| 31 | Increasing the power of interpretation for soil metaproteomics data. <i>Microbiome</i> , 2021, 9, 195. | 11.1 | 25 |
| 32 | 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 |
| 33 | Cyclical Patterns Affect Microbial Dynamics in the Water Basin of a Nuclear Research Reactor. <i>Frontiers in Microbiology</i> , 2021, 12, 744115. | 3.5 | 4 |
| 34 | Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows. <i>Nature Communications</i> , 2021, 12, 7305. | 12.8 | 34 |
| 35 | The Metaproteomics Initiative: a coordinated approach for propelling the functional characterization of microbiomes. <i>Microbiome</i> , 2021, 9, 243. | 11.1 | 36 |
| 36 | Increased protein S-nitrosylation in mitochondria: a key mechanism of exercise-induced cardioprotection. <i>Basic Research in Cardiology</i> , 2021, 116, 66. | 5.9 | 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. <i>Biomaterials</i> , 2020, 231, 119675. | 11.4 | 59 |
| 38 | Dual transcriptomics and proteomics analyses of the early stage of interaction between <i>Caballeronia mineralivorans</i> (PML1) and mineral. <i>Environmental Microbiology</i> , 2020, 22, 3838-3862. | 3.8 | 10 |
| 39 | Direct Meta-Analyses Reveal Unexpected Microbial Life in the Highly Radioactive Water of an Operating Nuclear Reactor Core. <i>Microorganisms</i> , 2020, 8, 1857. | 3.6 | 11 |
| 40 | 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 |
| 41 | From shotgun to targeted proteomics: rapid Scout-MRM assay development for monitoring potential immunomarkers in <i>Dreissena polymorpha</i> . <i>Analytical and Bioanalytical Chemistry</i> , 2020, 412, 7333-7347. | 3.7 | 9 |
| 42 | Groundwater promotes emergence of asporogenic mutants of emetic <i>Bacillus cereus</i> . <i>Environmental Microbiology</i> , 2020, 22, 5248-5264. | 3.8 | 6 |
| 43 | The proteomics contribution to the counter-bioterrorism toolbox in the post-COVID-19 era. <i>Expert Review of Proteomics</i> , 2020, 17, 507-511. | 3.0 | 5 |
| 44 | Dichloromethane Degradation Pathway from Unsequenced <i>Hyphomicrobium</i> sp. MC8b Rapidly Explored by Pan-Proteomics. <i>Microorganisms</i> , 2020, 8, 1876. | 3.6 | 6 |
| 45 | Proteotyping Environmental Microorganisms by Phylopeptidomics: Case Study Screening Water from a Radioactive Material Storage Pool. <i>Microorganisms</i> , 2020, 8, 1525. | 3.6 | 11 |
| 46 | <i>Bacillus cereus</i> Decreases NHE and CLO Exotoxin Synthesis to Maintain Appropriate Proteome Dynamics During Growth at Low Temperature. <i>Toxins</i> , 2020, 12, 645. | 3.4 | 7 |
| 47 | 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 |
| 48 | 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 |
| 49 | Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994. | 13.3 | 115 |
| 50 | Bioactive Potential of Extracts of <i>Halobacterium salinarum</i> Strain USBA 371, a Halophilic Bacterium Isolated from a Terrestrial Source. <i>Molecules</i> , 2020, 25, 2546. | 3.8 | 3 |
| 51 | Estimating relative biomasses of organisms in microbiota using phylopeptidomics. <i>Microbiome</i> , 2020, 8, 30. | 11.1 | 34 |
| 52 | Quick microbial molecular phenotyping by differential shotgun proteomics. <i>Environmental Microbiology</i> , 2020, 22, 2996-3004. | 3.8 | 24 |
| 53 | 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 |
| 54 | 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 |

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|----|---|------|-----------|
| 55 | High-multiplexed monitoring of protein biomarkers in the sentinel <i>Gammarus fossarum</i> by targeted scout-MRM assay, a new vision for ecotoxicoproteomics. <i>Journal of Proteomics</i> , 2020, 226, 103901. | 2.4 | 10 |
| 56 | 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 |
| 57 | 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 |
| 58 | Protein Corona Composition of Silica Nanoparticles in Complex Media: Nanoparticle Size does not Matter. <i>Nanomaterials</i> , 2020, 10, 240. | 4.1 | 29 |
| 59 | Titanium Dioxide Nanoparticles Alter the Cellular Phosphoproteome in A549 Cells. <i>Nanomaterials</i> , 2020, 10, 185. | 4.1 | 15 |
| 60 | 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 |
| 61 | Proteogenomics-Guided Evaluation of RNA-Seq Assembly and Protein Database Construction for Emergent Model Organisms. <i>Proteomics</i> , 2020, 20, e1900261. | 2.2 | 7 |
| 62 | 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 |
| 63 | Comparative Proteomics of Ostreid Herpesvirus 1 and Pacific Oyster Interactions With Two Families Exhibiting Contrasted Susceptibility to Viral Infection. <i>Frontiers in Immunology</i> , 2020, 11, 621994. | 4.8 | 10 |
| 64 | 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 |
| 65 | C-terminal proteolysis of the collagen VI $\alpha 3$ 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 |
| 66 | Shotgun proteomics datasets acquired on <i>Gammarus pulex</i> animals sampled from the wild. <i>Data in Brief</i> , 2019, 27, 104650. | 1.0 | 4 |
| 67 | De novo transcriptomes of 14 gammarid individuals for proteogenomic analysis of seven taxonomic groups. <i>Scientific Data</i> , 2019, 6, 184. | 5.3 | 23 |
| 68 | Advanced Proteomics as a Powerful Tool for Studying Toxins of Human Bacterial Pathogens. <i>Toxins</i> , 2019, 11, 576. | 3.4 | 8 |
| 69 | 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 |
| 70 | 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 |
| 71 | 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 |
| 72 | 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 |

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|----|---|-----|-----------|
| 73 | Co-expression network analysis identifies gonad- and embryo-associated protein modules in the sentinel species <i>Gammarus fossarum</i> . <i>Scientific Reports</i> , 2019, 9, 7862. | 3.3 | 13 |
| 74 | 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 |
| 75 | Microbiology and infectious diseases – A wealth of novelty for the clinical laboratory. <i>Clinical Mass Spectrometry</i> , 2019, 14, 1-2. | 1.9 | 0 |
| 76 | Comparative genomics and proteogenomics highlight key molecular players involved in <i>Frankia</i> sporulation. <i>Research in Microbiology</i> , 2019, 170, 202-213. | 2.1 | 5 |
| 77 | 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 |
| 78 | Proteases as Secreted Exoproteins in Mycoplasmas from Ruminant Lungs and Their Impact on Surface-Exposed Proteins. <i>Applied and Environmental Microbiology</i> , 2019, 85, . | 3.1 | 11 |
| 79 | 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 |
| 80 | Complete Genome Sequences of Four <i>Microbacterium</i> Strains Isolated from Metal- and Radionuclide-Rich Soils. <i>Microbiology Resource Announcements</i> , 2019, 8, . | 0.6 | 3 |
| 81 | Time-course proteomics dataset to monitor protein-bound methionine oxidation in <i>Bacillus cereus</i> ATCC 14579. <i>Data in Brief</i> , 2018, 18, 394-398. | 1.0 | 2 |
| 82 | Importance of Post-translational Modifications in the Interaction of Proteins with Mineral Surfaces: The Case of Arginine Methylation and Silica surfaces. <i>Langmuir</i> , 2018, 34, 5312-5322. | 3.5 | 4 |
| 83 | The PEG-responding desiccome of the alder microsymbiont <i>Frankia alni</i> . <i>Scientific Reports</i> , 2018, 8, 759. | 3.3 | 14 |
| 84 | 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 |
| 85 | Proteomics data for characterizing <i>Microbacterium oleivorans</i> A9, an uranium-tolerant actinobacterium isolated near the Chernobyl nuclear power plant. <i>Data in Brief</i> , 2018, 21, 1125-1129. | 1.0 | 3 |
| 86 | Biosafety of Mesoporous Silica Nanoparticles. <i>Biomimetics</i> , 2018, 3, 22. | 3.3 | 16 |
| 87 | <i>Rhodobacter sphaeroides</i> methionine sulfoxide reductase P reduces R- and S-diastereomers of methionine sulfoxide from a broad-spectrum of protein substrates. <i>Biochemical Journal</i> , 2018, 475, 3779-3795. | 3.7 | 29 |
| 88 | 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, . | 3.3 | 13 |
| 89 | Improving Quality Control of Contagious Caprine Pleuropneumonia Vaccine with Tandem Mass Spectrometry. <i>Proteomics</i> , 2018, 18, e1800088. | 2.2 | 10 |
| 90 | On-Line Solid Phase Extraction Liquid Chromatography-Mass Spectrometry Method for Multiplexed Proteins Quantitation in an Ecotoxicology Test Specie: <i>Gammarus fossarum</i> . <i>Journal of Applied Bioanalysis</i> , 2018, 4, 81-101. | 0.2 | 3 |

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|-----|--|------|-----------|
| 91 | Draft Genome Sequence of <i>Microbacterium oleivorans</i> Strain A9, a Bacterium Isolated from Chernobyl Radionuclide-Contaminated Soil. <i>Genome Announcements</i> , 2017, 5, . | 0.8 | 6 |
| 92 | Conservation and diversity of the <i>IrrE/DdrO</i> -controlled radiation response in radiation-resistant <i>Deinococcus</i> bacteria. <i>MicrobiologyOpen</i> , 2017, 6, e00477. | 3.0 | 37 |
| 93 | 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 |
| 94 | Defining Diagnostic Biomarkers Using Shotgun Proteomics and MALDI-TOF Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2017, 1616, 107-120. | 0.9 | 4 |
| 95 | Striking against bioterrorism with advanced proteomics and reference methods. <i>Proteomics</i> , 2017, 17, 1600412. | 2.2 | 5 |
| 96 | Emerin self-assembly mechanism: role of the LEM domain. <i>FEBS Journal</i> , 2017, 284, 338-352. | 4.7 | 16 |
| 97 | 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 |
| 98 | <i>In Vino Veritas</i> : An Invitation for Ambitious, Collaborative Proteogenomics Campaigns on Plant and Animal Models. <i>Proteomics</i> , 2017, 17, 1700324. | 2.2 | 0 |
| 99 | Proteogenomic Insights into the Intestinal Parasite <i>Blastocystis</i> sp. Subtype 4 Isolate WR1. <i>Proteomics</i> , 2017, 17, 1700211. | 2.2 | 5 |
| 100 | Proteogenomics data for deciphering <i>Frankia coriariae</i> interactions with root exudates from three host plants. <i>Data in Brief</i> , 2017, 14, 73-76. | 1.0 | 2 |
| 101 | Nutrient recycling facilitates long-term stability of marine microbial phototroph-heterotroph interactions. <i>Nature Microbiology</i> , 2017, 2, 17100. | 13.3 | 181 |
| 102 | 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 |
| 103 | Host Plant Compatibility Shapes the Proteome of <i>Frankia coriariae</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 720. | 3.5 | 23 |
| 104 | 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 |
| 105 | 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 |
| 106 | Mussel as a Tool to Define Continental Watershed Quality. , 2017, , . | | 9 |
| 107 | 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 |
| 108 | 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 |

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|-----|--|------|-----------|
| 109 | Proteome data to explore the impact of pBClin15 on <i>Bacillus cereus</i> ATCC 14579. <i>Data in Brief</i> , 2016, 8, 1243-1246. | 1.0 | 6 |
| 110 | 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 |
| 111 | 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. | 1.0 | 1 |
| 112 | RNA-binding proteins are a major target of silica nanoparticles in cell extracts. <i>Nanotoxicology</i> , 2016, 10, 1555-1564. | 3.0 | 86 |
| 113 | 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 |
| 114 | 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 |
| 115 | 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 |
| 116 | Post-translational methylations of the archaeal Mre11:Rad50 complex throughout the DNA damage response. <i>Molecular Microbiology</i> , 2016, 100, 362-378. | 2.5 | 10 |
| 117 | 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 |
| 118 | Clinical implications of recent advances in proteogenomics. <i>Expert Review of Proteomics</i> , 2016, 13, 185-199. | 3.0 | 12 |
| 119 | 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 |
| 120 | Next-generation proteomics faces new challenges in environmental biotechnology. <i>Current Opinion in Biotechnology</i> , 2016, 38, 174-182. | 6.6 | 46 |
| 121 | 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 |
| 122 | Stone-dwelling actinobacteria <i>Blastococcus saxobsidens</i> and <i>Modestobacter marinus</i> and <i>Geodermatophilus obscurus</i> proteogenomes. <i>ISME Journal</i> , 2016, 10, 21-29. | 9.8 | 71 |
| 123 | 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 |
| 124 | Microbiomes - Embracing complexity. <i>Proteomics</i> , 2015, 15, 3405-3406. | 2.2 | 4 |
| 125 | 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 |
| 126 | Essentiality of threonylcarbamoyladenosine (t ⁶ scpA), a universal t ⁶ RNA modification, in bacteria. <i>Molecular Microbiology</i> , 2015, 98, 1199-1221. | 2.5 | 72 |

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|-----|---|------|-----------|
| 127 | Proteomics of the <i>Roseobacter</i> clade, a window to the marine microbiology landscape. <i>Proteomics</i> , 2015, 15, 3928-3942. | 2.2 | 12 |
| 128 | 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 |
| 129 | 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 |
| 130 | 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 |
| 131 | Functional distinctness in the exoproteomes of marine <i>Synechococcus</i> . <i>Environmental Microbiology</i> , 2015, 17, 3781-3794. | 3.8 | 55 |
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