Florence ArsÃ¨ne-Ploetze

List of Publications by Year
in descending order

48 papers	2,737 citations	218381 26 h-index	197535 49 g-index
51 all docs	51 docs citations	51 times ranked	3092 citing authors

#	Article	IF	Citations
1	The heat shock response of Escherichia coli. International Journal of Food Microbiology, 2000, 55, 3-9.	2.1	437
2	Metabolic diversity among main microorganisms inside an arsenic-rich ecosystem revealed by meta- and proteo-genomics. ISME Journal, 2011, 5, 1735-1747.	4.4	186
3	A Tale of Two Oxidation States: Bacterial Colonization of Arsenic-Rich Environments. PLoS Genetics, 2007, 3, e53.	1.5	166
4	Bacterial metabolism of environmental arsenicâ€”mechanisms and biotechnological applications. Applied Microbiology and Biotechnology, 2013, 97, 3827-3841.	1.7	161
5	Molecular Basis for Regulation of the Heat Shock Transcription Factor Ïƒ32 by the DnaK and DnaJ Chaperones. Molecular Cell, 2008, 32, 347-358.	4.5	151
6	Modulation of NifA activity by PII in Azospirillum brasilense: evidence for a regulatory role of the NifA N-terminal domain. Journal of Bacteriology, 1996, 178, 4830-4838.	1.0	134
7	Structure, Function, and Evolution of the Thiomonas spp. Genome. PLoS Genetics, 2010, 6, e1000859.	1.5	123
8	Temporal transcriptomic response during arsenic stress in Herminiimonas arsenicoxydans. BMC Genomics, 2010, 11, 709.	1.2	90
9	Toxic metal resistance in biofilms: diversity of microbial responses and their evolution. Research in Microbiology, 2015, 166, 764-773.	1.0	85
10	Unsuspected Diversity of Arsenite-Oxidizing Bacteria as Revealed by Widespread Distribution of the<i>aoxB</i>Gene in Prokaryotes. Applied and Environmental Microbiology, 2011, 77, 4685-4692.	1.4	84
11	Enhanced structural and functional genome elucidation of the arsenite-oxidizing strain Herminiimonas arsenicoxydans by proteomics data. Biochimie, 2009, 91, 192-203.	1.3	75
12	Multiple controls affect arsenite oxidase gene expression in Herminiimonas arsenicoxydans. BMC Microbiology, 2010, 10, 53.	1.3	73
13	Carbon and arsenic metabolism in Thiomonas strains: differences revealed diverse adaptation processes. BMC Microbiology, 2009, 9, 127.	1.3	69
14	Characterization of the Active Bacterial Community Involved in Natural Attenuation Processes in Arsenic-Rich Creek Sediments. Microbial Ecology, 2011, 61, 793-810.	1.4	67
15	Use of<i>lacZ</i>Fusions to Study the Expression of<i>nif</i>Genes of<i>Azospirillum brasilense</i>in Association with Plants. Molecular Plant-Microbe Interactions, 1994, 7, 748.	1.4	63
16	Life in an Arsenic-Containing Gold Mine: Genome and Physiology of the Autotrophic Arsenite-Oxidizing Bacterium Rhizobium sp. NT-26. Genome Biology and Evolution, 2013, 5, 934-953.	1.1	60
17	Characterization of the ntrBC genes of Azospirillam brasilense Sp7: Their involvement in the regulation of nitrogenase synthesis and activity. Molecular Genetics and Genomics, 1993, 240, 188-196.	2.4	55
18	Taxonomic and functional prokaryote diversity in mildly arsenic-contaminated sediments. Research in Microbiology, 2011, 162, 877-887.	1.0	51

#	Article	IF	Citations
19	An Improved Stable Isotope N-Terminal Labeling Approach with Light/Heavy TMPP To Automate Proteogenomics Data Validation: dN-TOP. Journal of Proteome Research, 2013, 12, 3063-3070.	1.8	45
20	Role of Region C in Regulation of the Heat Shock Gene-Specific Sigma Factor of <i>Escherichia coli</i> , Ï, ³². Journal of Bacteriology, 1999, 181, 3552-3561.	1.0	45
21	Differential expression of Ixodes ricinus salivary gland proteins in the presence of the Borrelia burgdorferi sensu lato complex. Journal of Proteomics, 2014, 96, 29-43.	1.2	42
22	<i>In situ</i> proteo-metabolomics reveals metabolite secretion by the acid mine drainage bio-indicator, <i>Euglena mutabilis</i>. ISME Journal, 2012, 6, 1391-1402.	4.4	37
23	The C Terminus of Ï, 32 Is Not Essential for Degradation by FtsH. Journal of Bacteriology, 2001, 183, 5911-5917.	1.0	34
24	Comparative proteomics of Acidithiobacillus ferrooxidans grown in the presence and absence of uranium. Research in Microbiology, 2016, 167, 234-239.	1.0	32
25	Constitutive arsenite oxidase expression detected in arsenic-hypertolerant Pseudomonas xanthomarina S11. Research in Microbiology, 2015, 166, 205-214.	1.0	31
26	Proteomic tools to decipher microbial community structure and functioning. Environmental Science and Pollution Research, 2015, 22, 13599-13612.	2.7	27
27	Surface properties and intracellular speciation revealed an original adaptive mechanism to arsenic in the acid mine drainage bio-indicator Euglena mutabilis. Applied Microbiology and Biotechnology, 2012, 93, 1735-1744.	1.7	26
28	Adaptation in Toxic Environments: Arsenic Genomic Islands in the Bacterial Genus Thiomonas. PLoS ONE, 2015, 10, e0139011.	1.1	24
29	Two Arginine Repressors Regulate Arginine Biosynthesis in Lactobacillus plantarum. Journal of Bacteriology, 2004, 186, 6059-6069.	1.0	22
30	Control of Azospirillum brasilense NifA activity by PII: effect of replacing Tyr residues of the NifA N-terminal domain on NifA activity. FEMS Microbiology Letters, 1999, 179, 339-343.	0.7	21
31	Repression of the pyr Operon in Lactobacillus plantarum Prevents Its Ability To Grow at Low Carbon Dioxide Levels. Journal of Bacteriology, 2005, 187, 2093-2104.	1.0	21
32	Arsenite response in <i>Coccomyxa</i> sp. Carn explored by transcriptomic and nonâ€targeted metabolomic approaches. Environmental Microbiology, 2016, 18, 1289-1300.	1.8	20
33	Regulation of nif gene expression and nitrogen metabolism in Azospirillum. Soil Biology and Biochemistry, 1997, 29, 847-852.	4.2	19
34	Uracil Salvage Pathway in Lactobacillus plantarum : Transcription and Genetic Studies. Journal of Bacteriology, 2006, 188, 4777-4786.	1.0	16
35	Rapid Impact of Phenanthrene and Arsenic on Bacterial Community Structure and Activities in Sand Batches. Microbial Ecology, 2014, 67, 129-144.	1.4	16
36	Adaptation in toxic environments: comparative genomics of loci carrying antibiotic resistance genes derived from acid mine drainage waters. Environmental Science and Pollution Research, 2018, 25, 1470-1483.	2.7	16

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37	Expression of the pyr Operon of Lactobacillus plantarum Is Regulated by Inorganic Carbon Availability through a Second Regulator, PyrR 2 , Homologous to the Pyrimidine-Dependent Regulator PyrR 1. Journal of Bacteriology, 2006, 188, 8607-8616.	1.0	15
38	Spatio-Temporal Detection of the Thiomonas Population and the Thiomonas Arsenite Oxidase Involved in Natural Arsenite Attenuation Processes in the CarnoulÃ¨s Acid Mine Drainage. Frontiers in Cell and Developmental Biology, 2016, 4, 3.	1.8	15
39	Arsenic hypertolerance in the protist <i>Euglena mutabilis</i> is mediated by specific transporters and functional integrity maintenance mechanisms. Environmental Microbiology, 2015, 17, 1941-1949.	1.8	12
40	Comparison of biofilm formation and motility processes in arsenicâ€resistant <i>Thiomonas</i> spp. strains revealed divergent response to arsenite. Microbial Biotechnology, 2017, 10, 789-803.	2.0	12
41	Thiomonas sp. CB2 is able to degrade urea and promote toxic metal precipitation in acid mine drainage waters supplemented with urea. Frontiers in Microbiology, 2015, 6, 993.	1.5	10
42	Environmental microbiology as a mosaic of explored ecosystems and issues. Environmental Science and Pollution Research, 2015, 22, 13577-13598.	2.7	10
43	Lactobacillus plantarum response to inorganic carbon concentrations: PyrR2-dependent and -independent transcription regulation of genes involved in arginine and nucleotide metabolism. Microbiology (United Kingdom), 2008, 154, 2629-2640.	0.7	8
44	Low Carbamoyl Phosphate Pools May Drive <i>Lactobacillus plantarum</i> CO₂-Dependent Growth Phenotype. Journal of Molecular Microbiology and Biotechnology, 2008, 14, 22-30.	1.0	6
45	Lactobacillus plantarum ccl gene is non-essential, arginine-repressed and codes for a conserved protein in Firmicutes. Archives of Microbiology, 2005, 183, 307-316.	1.0	4
46	Proteomics as a Tool for the Characterization of Microbial Isolates and Complex Communities. , 2012, , .		3
47	Recherche d'orthologues d'ArgR/AhrC dans le gÃ©nome de bactÃ©ries Ã Gram positif : mise en Ã©vidence de groupes de syntÃ©nie. Sciences Des Aliments, 2002, 22, 133-142.	0.2	1
48	Effect of arsenite and growth in biofilm conditions on the evolution of Thiomonas sp. CB2. Microbial Genomics, 2020, 6, .	1.0	0