

Florence Arsène-Ploetze

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6367113/publications.pdf>

Version: 2024-02-01

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	Effect of arsenite and growth in biofilm conditions on the evolution of <i>Thiomonas</i> sp. CB2. <i>Microbial Genomics</i> , 2020, 6, .	1.0	0
2	Adaptation in toxic environments: comparative genomics of loci carrying antibiotic resistance genes derived from acid mine drainage waters. <i>Environmental Science and Pollution Research</i> , 2018, 25, 1470-1483.	2.7	16
3	Comparison of biofilm formation and motility processes in arsenic-resistant <i>Thiomonas</i> spp. strains revealed divergent response to arsenite. <i>Microbial Biotechnology</i> , 2017, 10, 789-803.	2.0	12
4	Spatio-Temporal Detection of the <i>Thiomonas</i> Population and the <i>Thiomonas</i> Arsenite Oxidase Involved in Natural Arsenite Attenuation Processes in the Carnoul's Acid Mine Drainage. <i>Frontiers in Cell and Developmental Biology</i> , 2016, 4, 3.	1.8	15
5	Arsenite response in <i>Coccomyxa</i> sp. Carn explored by transcriptomic and non-targeted metabolomic approaches. <i>Environmental Microbiology</i> , 2016, 18, 1289-1300.	1.8	20
6	Comparative proteomics of <i>Acidithiobacillus ferrooxidans</i> grown in the presence and absence of uranium. <i>Research in Microbiology</i> , 2016, 167, 234-239.	1.0	32
7	<i>Thiomonas</i> sp. CB2 is able to degrade urea and promote toxic metal precipitation in acid mine drainage waters supplemented with urea. <i>Frontiers in Microbiology</i> , 2015, 6, 993.	1.5	10
8	Constitutive arsenite oxidase expression detected in arsenic-hypertolerant <i>Pseudomonas xanthomarina</i> S11. <i>Research in Microbiology</i> , 2015, 166, 205-214.	1.0	31
9	Proteomic tools to decipher microbial community structure and functioning. <i>Environmental Science and Pollution Research</i> , 2015, 22, 13599-13612.	2.7	27
10	Toxic metal resistance in biofilms: diversity of microbial responses and their evolution. <i>Research in Microbiology</i> , 2015, 166, 764-773.	1.0	85
11	Environmental microbiology as a mosaic of explored ecosystems and issues. <i>Environmental Science and Pollution Research</i> , 2015, 22, 13577-13598.	2.7	10
12	Arsenic hypertolerance in the protist <i>Euglena mutabilis</i> is mediated by specific transporters and functional integrity maintenance mechanisms. <i>Environmental Microbiology</i> , 2015, 17, 1941-1949.	1.8	12
13	Adaptation in Toxic Environments: Arsenic Genomic Islands in the Bacterial Genus <i>Thiomonas</i> . <i>PLoS ONE</i> , 2015, 10, e0139011.	1.1	24
14	Rapid Impact of Phenanthrene and Arsenic on Bacterial Community Structure and Activities in Sand Batches. <i>Microbial Ecology</i> , 2014, 67, 129-144.	1.4	16
15	Differential expression of <i>Ixodes ricinus</i> salivary gland proteins in the presence of the <i>Borrelia burgdorferi</i> sensu lato complex. <i>Journal of Proteomics</i> , 2014, 96, 29-43.	1.2	42
16	An Improved Stable Isotope N-Terminal Labeling Approach with Light/Heavy TMPP To Automate Proteogenomics Data Validation: dN-TOP. <i>Journal of Proteome Research</i> , 2013, 12, 3063-3070.	1.8	45
17	Bacterial metabolism of environmental arsenic mechanisms and biotechnological applications. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 3827-3841.	1.7	161
18	Life in an Arsenic-Containing Gold Mine: Genome and Physiology of the Autotrophic Arsenite-Oxidizing Bacterium <i>Rhizobium</i> sp. NT-26. <i>Genome Biology and Evolution</i> , 2013, 5, 934-953.	1.1	60

#	ARTICLE	IF	CITATIONS
19	Proteomics as a Tool for the Characterization of Microbial Isolates and Complex Communities. , 2012, ,		3
20	<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
21	Surface properties and intracellular speciation revealed an original adaptive mechanism to arsenic in the acid mine drainage bio-indicator <i>Euglena mutabilis</i> . Applied Microbiology and Biotechnology, 2012, 93, 1735-1744.	1.7	26
22	Taxonomic and functional prokaryote diversity in mildly arsenic-contaminated sediments. Research in Microbiology, 2011, 162, 877-887.	1.0	51
23	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
24	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
25	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
26	Temporal transcriptomic response during arsenic stress in <i>Herminiimonas arsenicoxydans</i> . BMC Genomics, 2010, 11, 709.	1.2	90
27	Multiple controls affect arsenite oxidase gene expression in <i>Herminiimonas arsenicoxydans</i> . BMC Microbiology, 2010, 10, 53.	1.3	73
28	Structure, Function, and Evolution of the <i>Thiomonas</i> spp. Genome. PLoS Genetics, 2010, 6, e1000859.	1.5	123
29	Carbon and arsenic metabolism in <i>Thiomonas</i> strains: differences revealed diverse adaptation processes. BMC Microbiology, 2009, 9, 127.	1.3	69
30	Enhanced structural and functional genome elucidation of the arsenite-oxidizing strain <i>Herminiimonas arsenicoxydans</i> by proteomics data. Biochimie, 2009, 91, 192-203.	1.3	75
31	Molecular Basis for Regulation of the Heat Shock Transcription Factor σ^{32} by the DnaK and DnaJ Chaperones. Molecular Cell, 2008, 32, 347-358.	4.5	151
32	<i>Lactobacillus plantarum</i> 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
33	Low Carbamoyl Phosphate Pools May Drive <i>Lactobacillus plantarum</i> CO ₂ -Dependent Growth Phenotype. Journal of Molecular Microbiology and Biotechnology, 2008, 14, 22-30.	1.0	6
34	A Tale of Two Oxidation States: Bacterial Colonization of Arsenic-Rich Environments. PLoS Genetics, 2007, 3, e53.	1.5	166
35	Expression of the pyr Operon of <i>Lactobacillus plantarum</i> 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
36	Uracil Salvage Pathway in <i>Lactobacillus plantarum</i> : Transcription and Genetic Studies. Journal of Bacteriology, 2006, 188, 4777-4786.	1.0	16

#	ARTICLE	IF	CITATIONS
37	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
38	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
39	Two Arginine Repressors Regulate Arginine Biosynthesis in Lactobacillus plantarum. Journal of Bacteriology, 2004, 186, 6059-6069.	1.0	22
40	Recherche d'orthologues d'ArgR/AhrC dans le gÄ©nome de bactÄ©ries Ä Gram positif : mise en Ä©vidence de groupes de syntÄ©nie. Sciences Des Aliments, 2002, 22, 133-142.	0.2	1
41	The C Terminus of Ä, 32 Is Not Essential for Degradation by FtsH. Journal of Bacteriology, 2001, 183, 5911-5917.	1.0	34
42	The heat shock response of Escherichia coli. International Journal of Food Microbiology, 2000, 55, 3-9.	2.1	437
43	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
44	Role of Region C in Regulation of the Heat Shock Gene-Specific Sigma Factor of <i>Escherichia coli</i>, Ä, ³². Journal of Bacteriology, 1999, 181, 3552-3561.	1.0	45
45	Regulation of nif gene expression and nitrogen metabolism in Azospirillum. Soil Biology and Biochemistry, 1997, 29, 847-852.	4.2	19
46	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
47	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
48	Characterization of the ntrBC genes of Azospirillum brasilense Sp7: Their involvement in the regulation of nitrogenase synthesis and activity. Molecular Genetics and Genomics, 1993, 240, 188-196.	2.4	55