

Philippe Ortet

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

3,237
citations

236833

25
h-index

197736

49
g-index

52
all docs

52
docs citations

52
times ranked

4828
citing authors

#	ARTICLE	IF	CITATIONS
1	A genome-wide transcriptional analysis using Arabidopsis thaliana Affymetrix gene chips determined plant responses to phosphate deprivation. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 11934-11939.	3.3	834
2	Host Cell Subversion by Toxoplasma GRA16, an Exported Dense Granule Protein that Targets the Host Cell Nucleus and Alters Gene Expression. Cell Host and Microbe, 2013, 13, 489-500.	5.1	209
3	A Tale of Two Oxidation States: Bacterial Colonization of Arsenic-Rich Environments. PLoS Genetics, 2007, 3, e53.	1.5	166
4	Drug inhibition of HDAC3 and epigenetic control of differentiation in Apicomplexa parasites. Journal of Experimental Medicine, 2009, 206, 953-966.	4.2	154
5	Alliance of Proteomics and Genomics to Unravel the Specificities of Sahara Bacterium Deinococcus deserti. PLoS Genetics, 2009, 5, e1000434.	1.5	144
6	Geometagenomics illuminates the impact of agriculture on the distribution and prevalence of plant viruses at the ecosystem scale. ISME Journal, 2018, 12, 173-184.	4.4	132
7	Structure, Function, and Evolution of the Thiomonas spp. Genome. PLoS Genetics, 2010, 6, e1000859.	1.5	123
8	A Complex Small RNA Repertoire Is Generated by a Plant/Fungal-Like Machinery and Effected by a Metazoan-Like Argonaute in the Single-Cell Human Parasite Toxoplasma gondii. PLoS Pathogens, 2010, 6, e1000920.	2.1	113
9	ATM-Mediated Transcriptional and Developmental Responses to $\hat{1}^3$ -rays in Arabidopsis. PLoS ONE, 2007, 2, e430.	1.1	90
10	Proteomics-based Refinement of Deinococcus deserti Genome Annotation Reveals an Unwonted Use of Non-canonical Translation Initiation Codons. Molecular and Cellular Proteomics, 2010, 9, 415-426.	2.5	90
11	P2CS: updates of the prokaryotic two-component systems database. Nucleic Acids Research, 2015, 43, D536-D541.	6.5	90
12	P2CS: a database of prokaryotic two-component systems. Nucleic Acids Research, 2011, 39, D771-D776.	6.5	84
13	A MORC-driven transcriptional switch controls Toxoplasma developmental trajectories and sexual commitment. Nature Microbiology, 2020, 5, 570-583.	5.9	78
14	P2RP: a web-based framework for the identification and analysis of regulatory proteins in prokaryotic genomes. BMC Genomics, 2013, 14, 269.	1.2	69
15	Plant Nutrient Resource Use Strategies Shape Active Rhizosphere Microbiota Through Root Exudation. Frontiers in Plant Science, 2018, 9, 1662.	1.7	67
16	P2CS: a two-component system resource for prokaryotic signal transduction research. BMC Genomics, 2009, 10, 315.	1.2	60
17	P2TF: a comprehensive resource for analysis of prokaryotic transcription factors. BMC Genomics, 2012, 13, 628.	1.2	52
18	Evidence that Soil Properties and Organic Coating Drive the Phytoavailability of Cerium Oxide Nanoparticles. Environmental Science & Technology, 2017, 51, 9756-9764.	4.6	49

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19	Complete Genome Sequence of a Beneficial Plant Root-Associated Bacterium, <i>Pseudomonas brassicacearum</i> . <i>Journal of Bacteriology</i> , 2011, 193, 3146-3146.	1.0	48
20	The Cyst-Dividing Bacterium <i>Ramlibacter tataouinensis</i> TTB310 Genome Reveals a Well-Stocked Toolbox for Adaptation to a Desert Environment. <i>PLoS ONE</i> , 2011, 6, e23784.	1.1	47
21	Proteogenomic insights into uranium tolerance of a Chernobyl's Microbacterium bacterial isolate. <i>Journal of Proteomics</i> , 2018, 177, 148-157.	1.2	43
22	Microbiote shift in the <i>Medicago sativa</i> rhizosphere in response to cyanotoxins extract exposure. <i>Science of the Total Environment</i> , 2016, 539, 135-142.	3.9	37
23	Phytobeneficial bacteria improve saline stress tolerance in <i>Vicia faba</i> and modulate microbial interaction network. <i>Science of the Total Environment</i> , 2020, 729, 139020.	3.9	36
24	Design Defines the Effects of Nanoceria at a Low Dose on Soil Microbiota and the Potentiation of Impacts by the Canola Plant. <i>Environmental Science & Technology</i> , 2016, 50, 6892-6901.	4.6	30
25	Plant hosts control microbial denitrification activity. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	30
26	Modifications at K31 on the lateral surface of histone H4 contribute to genome structure and expression in apicomplexan parasites. <i>ELife</i> , 2017, 6, .	2.8	29
27	Two New Secreted Proteases Generate a Casein-Derived Antimicrobial Peptide in <i>Bacillus cereus</i> Food Born Isolate Leading to Bacterial Competition in Milk. <i>Frontiers in Microbiology</i> , 2018, 9, 1148.	1.5	29
28	Isolation and identification of <i>Pseudomonas syringae</i> facilitated by a PCR targeting the whole <i>P. syringae</i> group. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiv146.	1.3	28
29	Modulation of Metabolism and Switching to Biofilm Prevail over Exopolysaccharide Production in the Response of <i>Rhizobium alarii</i> to Cadmium. <i>PLoS ONE</i> , 2011, 6, e26771.	1.1	26
30	The histone methylase KMTox interacts with the redox sensor peroxiredoxin1 and targets genes involved in <i>Toxoplasma gondii</i> antioxidant defences. <i>Molecular Microbiology</i> , 2009, 71, 212-226.	1.2	24
31	A configuration space of homologous proteins conserving mutual information and allowing a phylogeny inference based on pair-wise Z-score probabilities. <i>BMC Bioinformatics</i> , 2005, 6, 49.	1.2	23
32	ProTISA: a comprehensive resource for translation initiation site annotation in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2007, 36, D114-D119.	6.5	23
33	Pearl Millet Genetic Traits Shape Rhizobacterial Diversity and Modulate Rhizosphere Aggregation. <i>Frontiers in Plant Science</i> , 2017, 8, 1288.	1.7	23
34	Pearl millet genotype impacts microbial diversity and enzymatic activities in relation to root-adhering soil aggregation. <i>Plant and Soil</i> , 2021, 464, 109.	1.8	22
35	Soil prokaryotic communities in Chernobyl waste disposal trench T22 are modulated by organic matter and radionuclide contamination. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	20
36	Integration and mining of malaria molecular, functional and pharmacological data: how far are we from a chemogenomic knowledge space?. <i>Malaria Journal</i> , 2006, 5, 110.	0.8	18

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37	Sequencing, <i>De Novo</i> Assembly, and Annotation of the Complete Genome of a New Thraustochytrid Species, Strain CCAP_4062/3. <i>Genome Announcements</i> , 2018, 6, .	0.8	17
38	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.	4.4	13
39	Light on the cell cycle of the non-photosynthetic bacterium <i>Ramlibacter tataouinensis</i> . <i>Scientific Reports</i> , 2019, 9, 16505.	1.6	8
40	Bacterial Adaptation to Hot and Dry Deserts. , 2017, , 75-98.		8
41	Where Does the Alignment Score Distribution Shape Come from?. <i>Evolutionary Bioinformatics</i> , 2010, 6, EBO.S5875.	0.6	7
42	The configuration space of homologous proteins: A theoretical and practical framework to reduce the diversity of the protein sequence space after massive all-by-all sequence comparisons. <i>Future Generation Computer Systems</i> , 2007, 23, 410-427.	4.9	6
43	Bacterial adaptation to hot and dry deserts. , 2012, , 69-85.		6
44	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
45	Reversible oxygen-tolerant hydrogenase carried by free-living N ₂ -fixing bacteria isolated from the rhizospheres of rice, maize, and wheat. <i>MicrobiologyOpen</i> , 2012, 1, 349-361.	1.2	5
46	Amplifying and Fine-Tuning Rsm sRNAs Expression and Stability to Optimize the Survival of <i>Pseudomonas brassicacearum</i> in Nutrient-Poor Environments. <i>Microorganisms</i> , 2021, 9, 250.	1.6	5
47	An insight into the genome of extensively drug-resistant and uropathogenic <i>Citrobacter werkmanii</i> . <i>Journal of Global Antimicrobial Resistance</i> , 2020, 22, 785-791.	0.9	4
48	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.	0.5	3
49	Evolutionary history expands the range of signaling interactions in hybrid multikinase networks. <i>Scientific Reports</i> , 2021, 11, 11763.	1.6	3
50	Complete Genome Sequences of Four <i>Microbacterium</i> Strains Isolated from Metal- and Radionuclide-Rich Soils. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
51	Bacterial diversity and community structure in the rhizosphere of the halophyte <i>Halocnemum strobilaceum</i> in an Algerian arid saline soil. <i>Extremophiles</i> , 2022, 26, .	0.9	3