Philippe Ortet

List of Publications by Year
in descending order

51 papers	3,237 citations	236925 25 h-index	197818 49 g-index
52 all docs	52 docs citations	52 times ranked	4828 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.	9.8	13
2	Bacterial diversity and community structure in the rhizosphere of the halophyte Halocnemum strobilaceum in an Algerian arid saline soil. Extremophiles, 2022, 26, .	2.3	3
3	Pearl millet genotype impacts microbial diversity and enzymatic activities in relation to root-adhering soil aggregation. Plant and Soil, 2021, 464, 109.	3.7	22
4	Evolutionary history expands the range of signaling interactions in hybrid multikinase networks. Scientific Reports, 2021, 11, 11763.	3.3	3
5	Amplifying and Fine-Tuning Rsm sRNAs Expression and Stability to Optimize the Survival of Pseudomonas brassicacerum in Nutrient-Poor Environments. Microorganisms, 2021, 9, 250.	3.6	5
6	An insight into the genome of extensively drug-resistant and uropathogenic Citrobacter werkmanii. Journal of Global Antimicrobial Resistance, 2020, 22, 785-791.	2.2	4
7	A MORC-driven transcriptional switch controls Toxoplasma developmental trajectories and sexual commitment. Nature Microbiology, 2020, 5, 570-583.	13.3	78
8	Phytobeneficial bacteria improve saline stress tolerance in Vicia faba and modulate microbial interaction network. Science of the Total Environment, 2020, 729, 139020.	8.0	36
9	Plant hosts control microbial denitrification activity. FEMS Microbiology Ecology, 2019, 95, .	2.7	30
10	Light on the cell cycle of the non-photosynthetic bacterium Ramlibacter tataouinensis. Scientific Reports, 2019, 9, 16505.	3.3	8
11	Complete Genome Sequences of Four *Microbacterium* Strains Isolated from Metal- and Radionuclide-Rich Soils. Microbiology Resource Announcements, 2019, 8, .	0.6	3
12	Proteogenomic insights into uranium tolerance of a Chernobyl's Microbacterium bacterial isolate. Journal of Proteomics, 2018, 177, 148-157.	2.4	43
13	Geometagenomics illuminates the impact of agriculture on the distribution and prevalence of plant viruses at the ecosystem scale. ISME Journal, 2018, 12, 173-184.	9.8	132
14	Sequencing, *De Novo* Assembly, and Annotation of the Complete Genome of a New Thraustochytrid Species, Strain CCAP_4062/3. Genome Announcements, 2018, 6, .	0.8	17
15	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.	1.0	3
16	Plant Nutrient Resource Use Strategies Shape Active Rhizosphere Microbiota Through Root Exudation. Frontiers in Plant Science, 2018, 9, 1662.	3.6	67
17	Two New Secreted Proteases Generate a Casein-Derived Antimicrobial Peptide in Bacillus cereus Food Born Isolate Leading to Bacterial Competition in Milk. Frontiers in Microbiology, 2018, 9, 1148.	3.5	29
18	Draft Genome Sequence of Microbacterium oleivorans Strain A9, a Bacterium Isolated from Chernobyl Radionuclide-Contaminated Soil. Genome Announcements, 2017, 5, .	0.8	6

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19	Soil prokaryotic communities in Chernobyl waste disposal trench T22 are modulated by organic matter and radionuclide contamination. FEMS Microbiology Ecology, 2017, 93, .	2.7	20
20	Evidence that Soil Properties and Organic Coating Drive the Phytoavailability of Cerium Oxide Nanoparticles. Environmental Science & Technology, 2017, 51, 9756-9764.	10.0	49
21	Pearl Millet Genetic Traits Shape Rhizobacterial Diversity and Modulate Rhizosphere Aggregation. Frontiers in Plant Science, 2017, 8, 1288.	3.6	23
22	Modifications at K31 on the lateral surface of histone H4 contribute to genome structure and expression in apicomplexan parasites. ELife, 2017, 6, .	6.0	29
23	Bacterial Adaptation to Hot and Dry Deserts. , 2017, , 75-98.		8
24	Design Defines the Effects of Nanoceria at a Low Dose on Soil Microbiota and the Potentiation of Impacts by the Canola Plant. Environmental Science & Technology, 2016, 50, 6892-6901.	10.0	30
25	Isolation and identification of *Pseudomonas syringae* facilitated by a PCR targeting the whole *P. syringae* group. FEMS Microbiology Ecology, 2016, 92, fiv146.	2.7	28
26	Microbiote shift in the Medicago sativa rhizosphere in response to cyanotoxins extract exposure. Science of the Total Environment, 2016, 539, 135-142.	8.0	37
27	P2CS: updates of the prokaryotic two-component systems database. Nucleic Acids Research, 2015, 43, D536-D541.	14.5	90
28	P2RP: a web-based framework for the identification and analysis of regulatory proteins in prokaryotic genomes. BMC Genomics, 2013, 14, 269.	2.8	69
29	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.	11.0	209
30	Reversible oxygen‐tolerant hydrogenase carried by free‐living N$_2$‐fixing bacteria isolated from the rhizospheres of rice, maize, and wheat. MicrobiologyOpen, 2012, 1, 349-361.	3.0	5
31	Bacterial adaptation to hot and dry deserts. , 2012, , 69-85.		6
32	P2TF: a comprehensive resource for analysis of prokaryotic transcription factors. BMC Genomics, 2012, 13, 628.	2.8	52
33	P2CS: a database of prokaryotic two-component systems. Nucleic Acids Research, 2011, 39, D771-D776.	14.5	84
34	Complete Genome Sequence of a Beneficial Plant Root-Associated Bacterium, Pseudomonas brassicacearum. Journal of Bacteriology, 2011, 193, 3146-3146.	2.2	48
35	The Cyst-Dividing Bacterium Ramlibacter tataouinensis TTB310 Genome Reveals a Well-Stocked Toolbox for Adaptation to a Desert Environment. PLoS ONE, 2011, 6, e23784.	2.5	47
36	Modulation of Metabolism and Switching to Biofilm Prevail over Exopolysaccharide Production in the Response of Rhizobium alamii to Cadmium. PLoS ONE, 2011, 6, e26771.	2.5	26

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37	Where Does the Alignment Score Distribution Shape Come from?. Evolutionary Bioinformatics, 2010, 6, EBO.S5875.	1.2	7
38	Structure, Function, and Evolution of the Thiomonas spp. Genome. PLoS Genetics, 2010, 6, e1000859.	3.5	123
39	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.	4.7	113
40	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.	3.8	90
41	Alliance of Proteomics and Genomics to Unravel the Specificities of Sahara Bacterium Deinococcus deserti. PLoS Genetics, 2009, 5, e1000434.	3.5	144
42	P2CS: a two-component system resource for prokaryotic signal transduction research. BMC Genomics, 2009, 10, 315.	2.8	60
43	The histone methylase KMTox interacts with the redox–sensor peroxiredoxin–1 and targets genes involved in <i>Toxoplasma gondii</i> antioxidant defences. Molecular Microbiology, 2009, 71, 212-226.	2.5	24
44	Drug inhibition of HDAC3 and epigenetic control of differentiation in Apicomplexa parasites. Journal of Experimental Medicine, 2009, 206, 953-966.	8.5	154
45	ProTISA: a comprehensive resource for translation initiation site annotation in prokaryotic genomes. Nucleic Acids Research, 2007, 36, D114-D119.	14.5	23
46	A Tale of Two Oxidation States: Bacterial Colonization of Arsenic-Rich Environments. PLoS Genetics, 2007, 3, e53.	3.5	166
47	ATM-Mediated Transcriptional and Developmental Responses to Î³-rays in Arabidopsis. PLoS ONE, 2007, 2, e430.	2.5	90
48	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. Future Generation Computer Systems, 2007, 23, 410-427.	7.5	6
49	Integration and mining of malaria molecular, functional and pharmacological data: how far are we from a chemogenomic knowledge space?. Malaria Journal, 2006, 5, 110.	2.3	18
50	A configuration space of homologous proteins conserving mutual information and allowing a phylogeny inference based on pair-wise Z-score probabilities. BMC Bioinformatics, 2005, 6, 49.	2.6	23
51	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.	7.1	834