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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	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.	4.4	13
2	Bacterial diversity and community structure in the rhizosphere of the halophyte Halocnemum strobilaceum in an Algerian arid saline soil. Extremophiles, 2022, 26, .	0.9	3
3	Pearl millet genotype impacts microbial diversity and enzymatic activities in relation to root-adhering soil aggregation. Plant and Soil, 2021, 464, 109.	1.8	22
4	Evolutionary history expands the range of signaling interactions in hybrid multikinase networks. Scientific Reports, 2021, 11, 11763.	1.6	3
5	Amplifying and Fine-Tuning Rsm sRNAs Expression and Stability to Optimize the Survival of Pseudomonas brassicaceum in Nutrient-Poor Environments. Microorganisms, 2021, 9, 250.	1.6	5
6	An insight into the genome of extensively drug-resistant and uropathogenic Citrobacter werkmanii. Journal of Global Antimicrobial Resistance, 2020, 22, 785-791.	0.9	4
7	A MORC-driven transcriptional switch controls Toxoplasma developmental trajectories and sexual commitment. Nature Microbiology, 2020, 5, 570-583.	5.9	78
8	Phytobeneficial bacteria improve saline stress tolerance in Vicia faba and modulate microbial interaction network. Science of the Total Environment, 2020, 729, 139020.	3.9	36
9	Plant hosts control microbial denitrification activity. FEMS Microbiology Ecology, 2019, 95, .	1.3	30
10	Light on the cell cycle of the non-photosynthetic bacterium Ramlibacter tataouinensis. Scientific Reports, 2019, 9, 16505.	1.6	8
11	Complete Genome Sequences of Four <i>Microbacterium</i> Strains Isolated from Metal- and Radionuclide-Rich Soils. Microbiology Resource Announcements, 2019, 8, .	0.3	3
12	Proteogenomic insights into uranium tolerance of a Chernobyl's <i>Microbacterium</i> bacterial isolate. Journal of Proteomics, 2018, 177, 148-157.	1.2	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.	4.4	132
14	Sequencing, <i>De Novo</i> 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 <i>Microbacterium oleivorans</i> A9, an uranium-tolerant actinobacterium isolated near the Chernobyl nuclear power plant. Data in Brief, 2018, 21, 1125-1129.	0.5	3
16	Plant Nutrient Resource Use Strategies Shape Active Rhizosphere Microbiota Through Root Exudation. Frontiers in Plant Science, 2018, 9, 1662.	1.7	67
17	Two New Secreted Proteases Generate a Casein-Derived Antimicrobial Peptide in <i>Bacillus cereus</i> Food Born Isolate Leading to Bacterial Competition in Milk. Frontiers in Microbiology, 2018, 9, 1148.	1.5	29
18	Draft Genome Sequence of <i>Microbacterium oleivorans</i> 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. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	20
20	Evidence that Soil Properties and Organic Coating Drive the Phytoavailability of Cerium Oxide Nanoparticles. <i>Environmental Science & Technology</i> , 2017, 51, 9756-9764.	4.6	49
21	Pearl Millet Genetic Traits Shape Rhizobacterial Diversity and Modulate Rhizosphere Aggregation. <i>Frontiers in Plant Science</i> , 2017, 8, 1288.	1.7	23
22	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
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. <i>Environmental Science & Technology</i> , 2016, 50, 6892-6901.	4.6	30
25	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
26	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
27	P2CS: updates of the prokaryotic two-component systems database. <i>Nucleic Acids Research</i> , 2015, 43, D536-D541.	6.5	90
28	P2RP: a web-based framework for the identification and analysis of regulatory proteins in prokaryotic genomes. <i>BMC Genomics</i> , 2013, 14, 269.	1.2	69
29	Host Cell Subversion by <i>Toxoplasma</i> GRA16, an Exported Dense Granule Protein that Targets the Host Cell Nucleus and Alters Gene Expression. <i>Cell Host and Microbe</i> , 2013, 13, 489-500.	5.1	209
30	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
31	Bacterial adaptation to hot and dry deserts. , 2012, , 69-85.		6
32	P2TF: a comprehensive resource for analysis of prokaryotic transcription factors. <i>BMC Genomics</i> , 2012, 13, 628.	1.2	52
33	P2CS: a database of prokaryotic two-component systems. <i>Nucleic Acids Research</i> , 2011, 39, D771-D776.	6.5	84
34	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
35	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
36	Modulation of Metabolism and Switching to Biofilm Preval over Exopolysaccharide Production in the Response of <i>Rhizobium alarii</i> to Cadmium. <i>PLoS ONE</i> , 2011, 6, e26771.	1.1	26

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37	Where Does the Alignment Score Distribution Shape Come from?. <i>Evolutionary Bioinformatics</i> , 2010, 6, EBO.S5875.	0.6	7
38	Structure, Function, and Evolution of the <i>Thiomonas</i> spp. Genome. <i>PLoS Genetics</i> , 2010, 6, e1000859.	1.5	123
39	A Complex Small RNA Repertoire Is Generated by a Plant/Fungal-Like Machinery and Effected by a Metazoan-Like Argonate in the Single-Cell Human Parasite <i>Toxoplasma gondii</i> . <i>PLoS Pathogens</i> , 2010, 6, e1000920.	2.1	113
40	Proteomics-based Refinement of <i>Deinococcus deserti</i> Genome Annotation Reveals an Unwonted Use of Non-canonical Translation Initiation Codons. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 415-426.	2.5	90
41	Alliance of Proteomics and Genomics to Unravel the Specificities of Sahara Bacterium <i>Deinococcus deserti</i> . <i>PLoS Genetics</i> , 2009, 5, e1000434.	1.5	144
42	P2CS: a two-component system resource for prokaryotic signal transduction research. <i>BMC Genomics</i> , 2009, 10, 315.	1.2	60
43	The histone methylase KMTox interacts with the redox sensor peroxiredoxin and targets genes involved in <i>Toxoplasma gondii</i> antioxidant defences. <i>Molecular Microbiology</i> , 2009, 71, 212-226.	1.2	24
44	Drug inhibition of HDAC3 and epigenetic control of differentiation in Apicomplexa parasites. <i>Journal of Experimental Medicine</i> , 2009, 206, 953-966.	4.2	154
45	ProTISA: a comprehensive resource for translation initiation site annotation in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2007, 36, D114-D119.	6.5	23
46	A Tale of Two Oxidation States: Bacterial Colonization of Arsenic-Rich Environments. <i>PLoS Genetics</i> , 2007, 3, e53.	1.5	166
47	ATM-Mediated Transcriptional and Developmental Responses to \hat{I}^3 -rays in <i>Arabidopsis</i> . <i>PLoS ONE</i> , 2007, 2, e430.	1.1	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. <i>Future Generation Computer Systems</i> , 2007, 23, 410-427.	4.9	6
49	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
50	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
51	A genome-wide transcriptional analysis using <i>Arabidopsis thaliana</i> Affymetrix gene chips determined plant responses to phosphate deprivation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 11934-11939.	3.3	834