

Mohamed Barakat

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

2,915
citations

186209

28
h-index

175177

52
g-index

58
all docs

58
docs citations

58
times ranked

4243
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	Contrasted microbial community colonization of a bauxite residue deposit marked by a complex geochemical context. Journal of Hazardous Materials, 2022, 424, 127470.	6.5	18
3	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
4	Oxygen-reducing microbial cathodes in hypersaline electrolyte. Bioresource Technology, 2021, 319, 124165.	4.8	2
5	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
6	Effects of the Denitrification Inhibitor Procyanidins on the Diversity, Interactions, and Potential Functions of Rhizosphere-Associated Microbiome. Microorganisms, 2021, 9, 1406.	1.6	4
7	Evolutionary history expands the range of signaling interactions in hybrid multikinase networks. Scientific Reports, 2021, 11, 11763.	1.6	3
8	Hypersaline microbial fuel cell equipped with an oxygen-reducing microbial cathode. Bioresource Technology, 2021, 337, 125448.	4.8	7
9	Metataxonomics of Tunisian phosphogypsum based on five bioinformatics pipelines: Insights for bioremediation. Genomics, 2020, 112, 981-989.	1.3	18
10	An insight into the genome of extensively drug-resistant and uropathogenic <i>Citrobacter werkmanii</i> . Journal of Global Antimicrobial Resistance, 2020, 22, 785-791.	0.9	4
11	A MORC-driven transcriptional switch controls <i>Toxoplasma</i> developmental trajectories and sexual commitment. Nature Microbiology, 2020, 5, 570-583.	5.9	78
12	Who is eating fructose within the <i>Aedes albopictus</i> gut microbiota?. Environmental Microbiology, 2020, 22, 1193-1206.	1.8	22
13	Phytobeneficial bacteria improve saline stress tolerance in <i>Vicia faba</i> and modulate microbial interaction network. Science of the Total Environment, 2020, 729, 139020.	3.9	36
14	Plant hosts control microbial denitrification activity. FEMS Microbiology Ecology, 2019, 95, .	1.3	30
15	Light on the cell cycle of the non-photosynthetic bacterium <i>Ramlibacter tataouinensis</i> . Scientific Reports, 2019, 9, 16505.	1.6	8
16	Complete Genome Sequences of Four <i>Microbacterium</i> Strains Isolated from Metal- and Radionuclide-Rich Soils. Microbiology Resource Announcements, 2019, 8, .	0.3	3
17	Proteogenomic insights into uranium tolerance of a Chernobyl's <i>Microbacterium</i> bacterial isolate. Journal of Proteomics, 2018, 177, 148-157.	1.2	43
18	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

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19	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
20	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
21	Plant Nutrient Resource Use Strategies Shape Active Rhizosphere Microbiota Through Root Exudation. <i>Frontiers in Plant Science</i> , 2018, 9, 1662.	1.7	67
22	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
23	Different methods used to form oxygen reducing biocathodes lead to different biomass quantities, bacterial communities, and electrochemical kinetics. <i>Bioelectrochemistry</i> , 2017, 116, 24-32.	2.4	22
24	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
25	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
26	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
27	Pearl Millet Genetic Traits Shape Rhizobacterial Diversity and Modulate Rhizosphere Aggregation. <i>Frontiers in Plant Science</i> , 2017, 8, 1288.	1.7	23
28	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
29	Bacterial Adaptation to Hot and Dry Deserts. , 2017, , 75-98.		8
30	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
31	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
32	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
33	P2CS: updates of the prokaryotic two-component systems database. <i>Nucleic Acids Research</i> , 2015, 43, D536-D541.	6.5	90
34	Forming microbial anodes with acetate addition decreases their capability to treat raw paper mill effluent. <i>Bioresource Technology</i> , 2014, 164, 285-291.	4.8	10
35	Transformation of Pristine and Citrate-Functionalized CeO ₂ Nanoparticles in a Laboratory-Scale Activated Sludge Reactor. <i>Environmental Science & Technology</i> , 2014, 48, 7289-7296.	4.6	61
36	An adaptable mesocosm platform for performing integrated assessments of nanomaterial risk in complex environmental systems. <i>Scientific Reports</i> , 2014, 4, 5608.	1.6	45

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37	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
38	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
39	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
40	Bacterial adaptation to hot and dry deserts. , 2012, , 69-85.		6
41	P2TF: a comprehensive resource for analysis of prokaryotic transcription factors. <i>BMC Genomics</i> , 2012, 13, 628.	1.2	52
42	P2CS: a database of prokaryotic two-component systems. <i>Nucleic Acids Research</i> , 2011, 39, D771-D776.	6.5	84
43	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
44	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
45	Structure, Function, and Evolution of the <i>Thiomonas</i> spp. Genome. <i>PLoS Genetics</i> , 2010, 6, e1000859.	1.5	123
46	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 <i>Toxoplasma gondii</i> . <i>PLoS Pathogens</i> , 2010, 6, e1000920.	2.1	113
47	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
48	Mineral and Bacterial Diversities of Desert Sand Grains from South-East Morocco. <i>Geomicrobiology Journal</i> , 2010, 27, 76-92.	1.0	27
49	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
50	P2CS: a two-component system resource for prokaryotic signal transduction research. <i>BMC Genomics</i> , 2009, 10, 315.	1.2	60
51	A Tale of Two Oxidation States: Bacterial Colonization of Arsenic-Rich Environments. <i>PLoS Genetics</i> , 2007, 3, e53.	1.5	166
52	The desert of Tataouine: an extreme environment that hosts a wide diversity of microorganisms and radiotolerant bacteria. <i>Environmental Microbiology</i> , 2006, 8, 514-525.	1.8	192
53	Isolation and identification of an EPS-producing <i>Rhizobium</i> strain from arid soil (Algeria): characterization of its EPS and the effect of inoculation on wheat rhizosphere soil structure. <i>Research in Microbiology</i> , 2005, 156, 522-531.	1.0	124
54	A morphological transition in the pleomorphic bacterium <i>Ramlibacter tataouinensis</i> TTB310. <i>Research in Microbiology</i> , 2005, 156, 1026-1030.	1.0	15

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55	Experimental Colonization and Alteration of Orthopyroxene by the Pleomorphic Bacteria <i>Ramlibacter tataouinensis</i> . <i>Geomicrobiology Journal</i> , 2004, 21, 341-349.	1.0	34
56	Biologically controlled precipitation of calcium phosphate by <i>Ramlibacter tataouinensis</i> . <i>Earth and Planetary Science Letters</i> , 2004, 228, 439-449.	1.8	93
57	<i>Ramlibacter tataouinensis</i> gen. nov., sp. nov., and <i>Ramlibacter henchirensis</i> sp. nov., cyst-producing bacteria isolated from subdesert soil in Tunisia. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003, 53, 589-594.	0.8	93
58	<i>Burkholderia caribensis</i> sp. nov., an exopolysaccharide-producing bacterium isolated from vertisol microaggregates in Martinique. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 1999, 49, 787-794.	0.8	101