

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	Host Cell Subversion by Toxoplasma 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
2	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
3	A Tale of Two Oxidation States: Bacterial Colonization of Arsenic-Rich Environments. <i>PLoS Genetics</i> , 2007, 3, e53.	1.5	166
4	Alliance of Proteomics and Genomics to Unravel the Specificities of Sahara Bacterium <i>Deinococcus</i> deserti. <i>PLoS Genetics</i> , 2009, 5, e1000434.	1.5	144
5	Geometagenomics illuminates the impact of agriculture on the distribution and prevalence of plant viruses at the ecosystem scale. <i>ISME Journal</i> , 2018, 12, 173-184.	4.4	132
6	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
7	Structure, Function, and Evolution of the <i>Thiomonas</i> spp. Genome. <i>PLoS Genetics</i> , 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 <i>Toxoplasma gondii</i> . <i>PLoS Pathogens</i> , 2010, 6, e1000920.	2.1	113
9	<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
10	<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
11	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
12	Proteomics-based Refinement of <i>Deinococcus deserti</i> Genome Annotation Reveals an Unwanted Use of Non-canonical Translation Initiation Codons. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 415-426.	2.5	90
13	P2CS: updates of the prokaryotic two-component systems database. <i>Nucleic Acids Research</i> , 2015, 43, D536-D541.	6.5	90
14	P2CS: a database of prokaryotic two-component systems. <i>Nucleic Acids Research</i> , 2011, 39, D771-D776.	6.5	84
15	A MORC-driven transcriptional switch controls <i>Toxoplasma</i> developmental trajectories and sexual commitment. <i>Nature Microbiology</i> , 2020, 5, 570-583.	5.9	78
16	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
17	Plant Nutrient Resource Use Strategies Shape Active Rhizosphere Microbiota Through Root Exudation. <i>Frontiers in Plant Science</i> , 2018, 9, 1662.	1.7	67
18	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

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19	P2CS: a two-component system resource for prokaryotic signal transduction research. BMC Genomics, 2009, 10, 315.	1.2	60
20	P2TF: a comprehensive resource for analysis of prokaryotic transcription factors. BMC Genomics, 2012, 13, 628.	1.2	52
21	Evidence that Soil Properties and Organic Coating Drive the Phytoavailability of Cerium Oxide Nanoparticles. Environmental Science & Technology, 2017, 51, 9756-9764.	4.6	49
22	Complete Genome Sequence of a Beneficial Plant Root-Associated Bacterium, <i>Pseudomonas brassicacearum</i> . Journal of Bacteriology, 2011, 193, 3146-3146.	1.0	48
23	The Cyst-Dividing Bacterium <i>Ramlibacter tataouinensis</i> TTB310 Genome Reveals a Well-Stocked Toolbox for Adaptation to a Desert Environment. PLoS ONE, 2011, 6, e23784.	1.1	47
24	An adaptable mesocosm platform for performing integrated assessments of nanomaterial risk in complex environmental systems. Scientific Reports, 2014, 4, 5608.	1.6	45
25	Proteogenomic insights into uranium tolerance of a Chernobyl's Microbacterium bacterial isolate. Journal of Proteomics, 2018, 177, 148-157.	1.2	43
26	Microbiote shift in the <i>Medicago sativa</i> rhizosphere in response to cyanotoxins extract exposure. Science of the Total Environment, 2016, 539, 135-142.	3.9	37
27	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
28	Experimental Colonization and Alteration of Orthopyroxene by the Pleomorphic Bacteria <i>Ramlibacter tataouinensis</i> . Geomicrobiology Journal, 2004, 21, 341-349.	1.0	34
29	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.	4.6	30
30	Plant hosts control microbial denitrification activity. FEMS Microbiology Ecology, 2019, 95, .	1.3	30
31	Modifications at K31 on the lateral surface of histone H4 contribute to genome structure and expression in apicomplexan parasites. ELife, 2017, 6, .	2.8	29
32	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
33	Isolation and identification of <i>Pseudomonas syringae</i> facilitated by a PCR targeting the whole <i>P. syringae</i> group. FEMS Microbiology Ecology, 2016, 92, fiv146.	1.3	28
34	Mineral and Bacterial Diversities of Desert Sand Grains from South-East Morocco. Geomicrobiology Journal, 2010, 27, 76-92.	1.0	27
35	Pearl Millet Genetic Traits Shape Rhizobacterial Diversity and Modulate Rhizosphere Aggregation. Frontiers in Plant Science, 2017, 8, 1288.	1.7	23
36	Different methods used to form oxygen reducing biocathodes lead to different biomass quantities, bacterial communities, and electrochemical kinetics. Bioelectrochemistry, 2017, 116, 24-32.	2.4	22

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37	Who is eating fructose within the <i>Aedes albopictus</i> gut microbiota?. Environmental Microbiology, 2020, 22, 1193-1206.	1.8	22
38	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
39	Soil prokaryotic communities in Chernobyl waste disposal trench T22 are modulated by organic matter and radionuclide contamination. FEMS Microbiology Ecology, 2017, 93, .	1.3	20
40	Metataxonomics of Tunisian phosphogypsum based on five bioinformatics pipelines: Insights for bioremediation. Genomics, 2020, 112, 981-989.	1.3	18
41	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
42	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
43	A morphological transition in the pleomorphic bacterium <i>Ramlibacter tataouinensis</i> TTB310. Research in Microbiology, 2005, 156, 1026-1030.	1.0	15
44	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
45	Forming microbial anodes with acetate addition decreases their capability to treat raw paper mill effluent. Bioresource Technology, 2014, 164, 285-291.	4.8	10
46	Light on the cell cycle of the non-photosynthetic bacterium <i>Ramlibacter tataouinensis</i> . Scientific Reports, 2019, 9, 16505.	1.6	8
47	Bacterial Adaptation to Hot and Dry Deserts. , 2017, , 75-98.		8
48	Hypersaline microbial fuel cell equipped with an oxygen-reducing microbial cathode. Bioresource Technology, 2021, 337, 125448.	4.8	7
49	Bacterial adaptation to hot and dry deserts. , 2012, , 69-85.		6
50	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
51	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.	1.2	5
52	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
53	Effects of the Denitrification Inhibitor Procyanidins on the Diversity, Interactions, and Potential Functions of Rhizosphere-Associated Microbiome. Microorganisms, 2021, 9, 1406.	1.6	4
54	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

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55	Evolutionary history expands the range of signaling interactions in hybrid multikinase networks. Scientific Reports, 2021, 11, 11763.	1.6	3
56	Complete Genome Sequences of Four <i>Microbacterium</i> Strains Isolated from Metal- and Radionuclide-Rich Soils. Microbiology Resource Announcements, 2019, 8, .	0.3	3
57	Bacterial diversity and community structure in the rhizosphere of the halophyte <i>Halocnemum strobilaceum</i> in an Algerian arid saline soil. Extremophiles, 2022, 26, .	0.9	3
58	Oxygen-reducing microbial cathodes in hypersaline electrolyte. Bioresource Technology, 2021, 319, 124165.	4.8	2