

Salim Bougouffa

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

1,912
citations

279487

23
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276539

41
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43
all docs

43
docs citations

43
times ranked

3248
citing authors

#	ARTICLE	IF	CITATIONS
1	Hologenome analysis reveals dual symbiosis in the deep-sea hydrothermal vent snail <i>Gigantopelta aegis</i> . <i>Nature Communications</i> , 2021, 12, 1165.	5.8	38
2	Complete Genome Sequence of <i>Cellulomonas</i> sp. JZ18, a Root Endophytic Bacterium Isolated from the Perennial Desert Tussock-Grass <i>Panicum turgidum</i> . <i>Current Microbiology</i> , 2021, 78, 1135-1141.	1.0	4
3	LeafGo: Leaf to Genome, a quick workflow to produce high-quality de novo plant genomes using long-read sequencing technology. <i>Genome Biology</i> , 2021, 22, 256.	3.8	15
4	Complete genome sequence of the endophytic bacterium <i>Cellulosimicrobium</i> sp. JZ28 isolated from the root endosphere of the perennial desert tussock grass <i>Panicum turgidum</i> . <i>Archives of Microbiology</i> , 2020, 202, 1563-1569.	1.0	8
5	Complete Genome Sequence of <i>Paenibacillus</i> sp. JZ16, a Plant Growth Promoting Root Endophytic Bacterium of the Desert Halophyte <i>Zygophyllum Simplex</i> . <i>Current Microbiology</i> , 2020, 77, 1097-1103.	1.0	15
6	Genome Insights of the Plant-Growth Promoting Bacterium <i>Cronobacter muytjensii</i> JZ38 With Volatile-Mediated Antagonistic Activity Against <i>Phytophthora infestans</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 369.	1.5	39
7	Mining biosynthetic gene clusters in <i>Virgibacillus</i> genomes. <i>BMC Genomics</i> , 2019, 20, 696.	1.2	7
8	Marine biofilms constitute a bank of hidden microbial diversity and functional potential. <i>Nature Communications</i> , 2019, 10, 517.	5.8	100
9	Uncoupled Quorum Sensing Modulates the Interplay of Virulence and Resistance in a Multidrug-Resistant Clinical <i>Pseudomonas aeruginosa</i> Isolate Belonging to the MLST550 Clonal Complex. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	17
10	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. <i>Nature Communications</i> , 2019, 10, 2674.	5.8	240
11	Comparative genomics study reveals Red Sea <i>Bacillus</i> with characteristics associated with potential microbial cell factories (MCFs). <i>Scientific Reports</i> , 2019, 9, 19254.	1.6	6
12	Draft Genome Sequences of Four <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Enteritidis Strains Implicated in Infections of Avian and Human Hosts. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
13	The Genome Sequence of the Wild Tomato <i>Solanum pimpinellifolium</i> Provides Insights Into Salinity Tolerance. <i>Frontiers in Plant Science</i> , 2018, 9, 1402.	1.7	69
14	Genome Reduction in <i>Psychromonas</i> Species within the Gut of an Amphipod from the Ocean's Deepest Point. <i>MSystems</i> , 2018, 3, .	1.7	21
15	In silico exploration of Red Sea <i>Bacillus</i> genomes for natural product biosynthetic gene clusters. <i>BMC Genomics</i> , 2018, 19, 382.	1.2	17
16	bTSSfinder: a novel tool for the prediction of promoters in cyanobacteria and <i>Escherichia coli</i> . <i>Bioinformatics</i> , 2017, 33, 334-340.	1.8	80
17	DES-TOMATO: A Knowledge Exploration System Focused On Tomato Species. <i>Scientific Reports</i> , 2017, 7, 5968.	1.6	8
18	Comparative genome and transcriptome analysis reveals distinctive surface characteristics and unique physiological potentials of <i>Pseudomonas aeruginosa</i> ATCC 27853. <i>BMC Genomics</i> , 2017, 18, 459.	1.2	33

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19	Bioprospecting Red Sea Coastal Ecosystems for Culturable Microorganisms and Their Antimicrobial Potential. <i>Marine Drugs</i> , 2016, 14, 165.	2.2	30
20	Draft genome of an Aerophobetes bacterium reveals a facultative lifestyle in deep-sea anaerobic sediments. <i>Science Bulletin</i> , 2016, 61, 1176-1186.	4.3	16
21	Delta-proteobacterial SAR324 group in hydrothermal plumes on the South Mid-Atlantic Ridge. <i>Scientific Reports</i> , 2016, 6, 22842.	1.6	21
22	Genomes of coral dinoflagellate symbionts highlight evolutionary adaptations conducive to a symbiotic lifestyle. <i>Scientific Reports</i> , 2016, 6, 39734.	1.6	303
23	Metagenomics as a preliminary screen for antimicrobial bioprospecting. <i>Gene</i> , 2016, 594, 248-258.	1.0	26
24	DESM: portal for microbial knowledge exploration systems. <i>Nucleic Acids Research</i> , 2016, 44, D624-D633.	6.5	12
25	Rhizosphere microbiome metagenomics of gray mangroves (<i>Avicennia marina</i>) in the Red Sea. <i>Gene</i> , 2016, 576, 626-636.	1.0	116
26	Species sorting during biofilm assembly by artificial substrates deployed in a cold seep system. <i>Scientific Reports</i> , 2015, 4, 6647.	1.6	43
27	Synchronized dynamics of bacterial niche-specific functions during biofilm development in a cold seep brine pool. <i>Environmental Microbiology</i> , 2015, 17, 4089-4104.	1.8	24
28	Optimal Eukaryotic 18S and Universal 16S/18S Ribosomal RNA Primers and Their Application in a Study of Symbiosis. <i>PLoS ONE</i> , 2014, 9, e90053.	1.1	104
29	Toward Understanding the Dynamics of Microbial Communities in an Estuarine System. <i>PLoS ONE</i> , 2014, 9, e94449.	1.1	24
30	Genomic analysis reveals versatile heterotrophic capacity of a potentially symbiotic sulfur-oxidizing bacterium in sponge. <i>Environmental Microbiology</i> , 2014, 16, 3548-3561.	1.8	76
31	Effect of Copper Treatment on the Composition and Function of the Bacterial Community in the Sponge <i>Haliclona cymaeformis</i> . <i>MBio</i> , 2014, 5, e01980.	1.8	39
32	DEOP: a database on osmoprotectants and associated pathways. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, .	1.4	34
33	Pyrosequencing Reveals the Microbial Communities in the Red Sea Sponge <i>Carteriospongia foliascens</i> and Their Impressive Shifts in Abnormal Tissues. <i>Microbial Ecology</i> , 2014, 68, 621-632.	1.4	37
34	In situ environment rather than substrate type dictates microbial community structure of biofilms in a cold seep system. <i>Scientific Reports</i> , 2014, 4, 3587.	1.6	49
35	Effect of polybrominated diphenyl ether (PBDE) treatment on the composition and function of the bacterial community in the sponge <i>Haliclona cymaeformis</i> . <i>Frontiers in Microbiology</i> , 2014, 5, 799.	1.5	9
36	Transcriptome analysis elucidates key developmental components of bryozoan lophophore development. <i>Scientific Reports</i> , 2014, 4, 6534.	1.6	19

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37	Autotrophic Microbe Metagenomes and Metabolic Pathways Differentiate Adjacent Red Sea Brine Pools. <i>Scientific Reports</i> , 2013, 3, 1748.	1.6	25
38	Distinctive Microbial Community Structure in Highly Stratified Deep-Sea Brine Water Columns. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3425-3437.	1.4	57
39	Spatial and Species Variations in Bacterial Communities Associated with Corals from the Red Sea as Revealed by Pyrosequencing. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7173-7184.	1.4	97
40	SitesIdentify: a protein functional site prediction tool. <i>BMC Bioinformatics</i> , 2009, 10, 379.	1.2	19
41	Volume-based solvation models out-perform area-based models in combined studies of wild-type and mutated protein-protein interfaces. <i>BMC Bioinformatics</i> , 2008, 9, 448.	1.2	11