

Alessio Mengoni

List of Publications by Year in descending order

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183
papers

6,495
citations

57758

44
h-index

95266

68
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207
all docs

207
docs citations

207
times ranked

7201
citing authors

#	ARTICLE	IF	CITATIONS
1	CONTIGuator: a bacterial genomes finishing tool for structural insights on draft genomes. Source Code for Biology and Medicine, 2011, 6, 11.	1.7	266
2	ENDOPHYTIC BACTERIA FROM SEEDS OF <i>NICOTIANA TABACUM</i> CAN REDUCE CADMIUM PHYTOTOXICITY. International Journal of Phytoremediation, 2009, 11, 251-267.	3.1	240
3	Isolation and Characterization of Endophytic Bacteria from the Nickel Hyperaccumulator Plant <i>Alyssum bertolonii</i> . Microbial Ecology, 2007, 53, 306-316.	2.8	182
4	The diversity and evolution of cell cycle regulation in alpha-proteobacteria: a comparative genomic analysis. BMC Systems Biology, 2010, 4, 52.	3.0	175
5	Taxonomy of Rhizobiaceae revisited: proposal of a new framework for genus delimitation. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	1.7	125
6	Characterization of nickel-resistant bacteria isolated from serpentine soil. Environmental Microbiology, 2001, 3, 691-698.	3.8	123
7	Genetic Diversity and Dynamics of <i>Sinorhizobium meliloti</i> Populations Nodulating Different Alfalfa Cultivars in Italian Soils. Applied and Environmental Microbiology, 2000, 66, 4785-4789.	3.1	116
8	Use of RAPD and microsatellite (SSR) variation to assess genetic relationships among populations of tetraploid alfalfa, <i>Medicago sativa</i> . Plant Breeding, 2000, 119, 311-317.	1.9	114
9	Cell Cycle Control by the Master Regulator CtrA in <i>Sinorhizobium meliloti</i> . PLoS Genetics, 2015, 11, e1005232.	3.5	105
10	Fluctuation of bacteria isolated from elm tissues during different seasons and from different plant organs. Research in Microbiology, 2003, 154, 105-114.	2.1	103
11	Genetic diversity and heavy metal tolerance in populations of <i>Silene paradoxa</i> L. (Caryophyllaceae): a random amplified polymorphic DNA analysis. Molecular Ecology, 2000, 9, 1319-1324.	3.9	101
12	Exploring the symbiotic pangenome of the nitrogen-fixing bacterium <i>Sinorhizobium meliloti</i> . BMC Genomics, 2011, 12, 235.	2.8	97
13	Replicon-Dependent Bacterial Genome Evolution: The Case of <i>Sinorhizobium meliloti</i> . Genome Biology and Evolution, 2013, 5, 542-558.	2.5	94
14	Preliminary Comparison of Oral and Intestinal Human Microbiota in Patients with Colorectal Cancer: A Pilot Study. Frontiers in Microbiology, 2017, 8, 2699.	3.5	93
15	Soil Bacterial Community Response to Differences in Agricultural Management along with Seasonal Changes in a Mediterranean Region. PLoS ONE, 2014, 9, e105515.	2.5	89
16	Exploring the evolutionary dynamics of plasmids: the <i>Acinetobacter</i> pan-plasmidome. BMC Evolutionary Biology, 2010, 10, 59.	3.2	87
17	Metabolic modelling reveals the specialization of secondary replicons for niche adaptation in <i>Sinorhizobium meliloti</i> . Nature Communications, 2016, 7, 12219.	12.8	85
18	Plant-Bacteria Association and Symbiosis: Are There Common Genomic Traits in Alphaproteobacteria?. Genes, 2011, 2, 1017-1032.	2.4	78

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19	Multidisciplinary approaches for studying rhizobium-legume symbioses. Canadian Journal of Microbiology, 2019, 65, 1-33.	1.7	77
20	Genetic diversity of heavy metal-tolerant populations in <i>Silene paradoxa</i> L. (Caryophyllaceae): a chloroplast microsatellite analysis. Molecular Ecology, 2001, 10, 1909-1916.	3.9	76
21	Plant-endophytes interaction influences the secondary metabolism in <i>Echinacea purpurea</i> (L.) Moench: an in vitro model. Scientific Reports, 2017, 7, 16924.	3.3	74
22	DuctApe: A suite for the analysis and correlation of genomic and OmniLog ₂ Phenotype Microarray data. Genomics, 2014, 103, 1-10.	2.9	73
23	Advances in Host Plant and Rhizobium Genomics to Enhance Symbiotic Nitrogen Fixation in Grain Legumes. Advances in Agronomy, 2015, , 1-116.	5.2	73
24	Plants as extreme environments? Ni-resistant bacteria and Ni-hyperaccumulators of serpentine flora. Plant and Soil, 2010, 331, 5-16.	3.7	72
25	Harnessing Rhizobia to Improve Heavy-Metal Phytoremediation by Legumes. Genes, 2018, 9, 542.	2.4	72
26	Genetic relationship of <i>Sinorhizobium meliloti</i> and <i>Sinorhizobium medicae</i> strains isolated from Caucasian region. FEMS Microbiology Letters, 2003, 220, 207-213.	1.8	71
27	Effect of on-field inoculation of <i>Phaseolus vulgaris</i> with rhizobia on soil bacterial communities. FEMS Microbiology Ecology, 2011, 77, 211-222.	2.7	69
28	A First Insight into the Gut Microbiota of the Sea Turtle <i>Caretta caretta</i> . Frontiers in Microbiology, 2016, 7, 1060.	3.5	69
29	The <i>DivJ</i> , <i>CbrA</i> and <i>PleC</i> system controls <i>DivK</i> phosphorylation and symbiosis in <i>Sinorhizobium meliloti</i> . Molecular Microbiology, 2013, 90, 54-71.	2.5	68
30	Evolutionary dynamics of nickel hyperaccumulation in <i>Alyssum</i> revealed by its nrDNA analysis. New Phytologist, 2003, 159, 691-699.	7.3	67
31	Trade, Diplomacy, and Warfare: The Quest for Elite Rhizobia Inoculant Strains. Frontiers in Microbiology, 2017, 8, 2207.	3.5	67
32	Bioactive volatile organic compounds from Antarctic (sponges) bacteria. New Biotechnology, 2013, 30, 824-838.	4.4	62
33	Evaluation of the Performances of Ribosomal Database Project (RDP) Classifier for Taxonomic Assignment of 16S rRNA Metabarcoding Sequences Generated from Illumina-Solexa NGS. Journal of Genomics, 2015, 3, 36-39.	0.9	59
34	Changes in Cystic Fibrosis Airway Microbial Community Associated with a Severe Decline in Lung Function. PLoS ONE, 2015, 10, e0124348.	2.5	59
35	Analysis of plasmid genes by phylogenetic profiling and visualization of homology relationships using Blast2Network. BMC Bioinformatics, 2008, 9, 551.	2.6	57
36	Metabolic Capacity of <i>Sinorhizobium</i> (<i>Ensifer</i>) <i>meliloti</i> Strains as Determined by Phenotype MicroArray Analysis. Applied and Environmental Microbiology, 2009, 75, 5396-5404.	3.1	57

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37	Genome-scale metabolic reconstruction of the symbiosis between a leguminous plant and a nitrogen-fixing bacterium. <i>Nature Communications</i> , 2020, 11, 2574.	12.8	56
38	Appraisal of the crop-rotation effect of rhizobial inoculation on potato cropping systems in relation to soil bacterial communities. <i>Soil Biology and Biochemistry</i> , 2012, 54, 1-6.	8.8	54
39	Mixed Nodule Infection in <i>Sinorhizobium meliloti</i> – <i>Medicago sativa</i> Symbiosis Suggest the Presence of Cheating Behavior. <i>Frontiers in Plant Science</i> , 2016, 7, 835.	3.6	54
40	Whole-genome epidemiology, characterisation, and phylogenetic reconstruction of <i>Staphylococcus aureus</i> strains in a paediatric hospital. <i>Genome Medicine</i> , 2018, 10, 82.	8.2	54
41	Relationship between heavy metals pollution and genetic diversity in Mediterranean populations of the sandhopper <i>Talitrus saltator</i> (Montagu) (Crustacea, Amphipoda). <i>Environmental Pollution</i> , 2010, 158, 1638-1643.	7.5	52
42	Exploring the plant-associated bacterial communities in <i>Medicago sativa</i> L. <i>BMC Microbiology</i> , 2012, 12, 78.	3.3	50
43	Antibiotic resistance differentiates <i>Echinacea purpurea</i> endophytic bacterial communities with respect to plant organs. <i>Research in Microbiology</i> , 2014, 165, 686-694.	2.1	50
44	Evolution of Intra-specific Regulatory Networks in a Multipartite Bacterial Genome. <i>PLoS Computational Biology</i> , 2015, 11, e1004478.	3.2	50
45	Comparison of Highly and Weakly Virulent <i>Dickeya solani</i> Strains, With a View on the Pangenome and Panregulon of This Species. <i>Frontiers in Microbiology</i> , 2018, 9, 1940.	3.5	50
46	Robustness encoded across essential and accessory replicons of the ecologically versatile bacterium <i>Sinorhizobium meliloti</i> . <i>PLoS Genetics</i> , 2018, 14, e1007357.	3.5	49
47	Genetic diversity inferred from AFLP fingerprinting in populations of <i>Onosma echioides</i> (Boraginaceae) from serpentine and calcareous soils. <i>Plant Biosystems</i> , 2006, 140, 211-219.	1.6	47
48	Methylene blue-containing liposomes as new photodynamic anti-bacterial agents. <i>Journal of Materials Chemistry B</i> , 2017, 5, 2788-2797.	5.8	47
49	Deciphering the Ecology of Cystic Fibrosis Bacterial Communities: Towards Systems-Level Integration. <i>Trends in Molecular Medicine</i> , 2019, 25, 1110-1122.	6.7	47
50	Genetic Diversity of Bacterial Communities of Serpentine Soil and of Rhizosphere of the Nickel-Hyperaccumulator Plant <i>Alyssum bertolonii</i> . <i>Microbial Ecology</i> , 2004, 48, 209-217.	2.8	46
51	Endophytic and rhizospheric bacterial communities isolated from the medicinal plants <i>Echinacea purpurea</i> and <i>Echinacea angustifolia</i> . <i>International Microbiology</i> , 2014, 17, 165-74.	2.4	46
52	Plant-by-Plant Variations of Bacterial Communities Associated with Leaves of the Nickel Hyperaccumulator <i>Alyssum bertolonii</i> Desv.. <i>Microbial Ecology</i> , 2009, 58, 660-667.	2.8	45
53	The capability to synthesize phytochelatins and the presence of constitutive and functional phytochelatin synthases are ancestral (plesiomorphic) characters for basal land plants. <i>Journal of Experimental Botany</i> , 2014, 65, 1153-1163.	4.8	45
54	Large-scale genetic variation of the symbiosis-required megaplasmid pSymA revealed by comparative genomic analysis of <i>Sinorhizobium meliloti</i> natural strains. <i>BMC Genomics</i> , 2005, 6, 158.	2.8	44

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55	StreamingTrim 1.0: a Java software for dynamic trimming of 16S rRNA sequence data from metagenetic studies. <i>Molecular Ecology Resources</i> , 2014, 14, 426-434.	4.8	44
56	Comparison of 16S rRNA and 16S rDNA T-RFLP Approaches to Study Bacterial Communities in Soil Microcosms Treated with Chromate as Perturbing Agent. <i>Microbial Ecology</i> , 2005, 50, 375-384.	2.8	43
57	Antagonistic interactions between endophytic cultivable bacterial communities isolated from the medicinal plant <i>Echinacea purpurea</i> . <i>Environmental Microbiology</i> , 2016, 18, 2357-2365.	3.8	43
58	Chloroplast genetic diversity and biogeography in the serpentine endemic Ni-hyperaccumulator <i>Alyssum bertolonii</i> . <i>New Phytologist</i> , 2003, 157, 349-356.	7.3	42
59	Evolution of copper-tolerance and increased expression of a 2b-type metallothionein gene in <i>Silene paradoxa</i> L. populations. <i>Plant and Soil</i> , 2003, 257, 451-457.	3.7	41
60	Intra-specific differences in nickel tolerance and accumulation in the Ni-hyperaccumulator <i>Alyssum bertolonii</i> . <i>Environmental and Experimental Botany</i> , 2007, 60, 377-384.	4.2	41
61	Rhizosphere effect and salinity competing to shape microbial communities in <i>Phragmites australis</i> (Cav.) Trin. ex-Steud. <i>FEMS Microbiology Letters</i> , 2014, 359, 193-200.	1.8	41
62	Enrichment and identification of bacteria capable of reducing chemical oxygen demand of anaerobically treated molasses spent wash. <i>Journal of Applied Microbiology</i> , 2004, 96, 1278-1286.	3.1	39
63	Effects of soil management on structure and activity of denitrifying bacterial communities. <i>Applied Soil Ecology</i> , 2011, 49, 46-58.	4.3	39
64	Phenotypic and genomic characterization of the antimicrobial producer <i>Rheinheimera</i> sp. EpRS3 isolated from the medicinal plant <i>Echinacea purpurea</i> : insights into its biotechnological relevance. <i>Research in Microbiology</i> , 2017, 168, 293-305.	2.1	39
65	A Different Microbiome Gene Repertoire in the Airways of Cystic Fibrosis Patients with Severe Lung Disease. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1654.	4.1	39
66	Medicinal Plants and Their Bacterial Microbiota: A Review on Antimicrobial Compounds Production for Plant and Human Health. <i>Pathogens</i> , 2021, 10, 106.	2.8	38
67	Significant and Conflicting Correlation of IL-9 With <i>Prevotella</i> and <i>Bacteroides</i> in Human Colorectal Cancer. <i>Frontiers in Immunology</i> , 2020, 11, 573158.	4.8	37
68	Perspectives and Challenges in Microbial Communities Metabolic Modeling. <i>Frontiers in Genetics</i> , 2017, 8, 88.	2.3	36
69	Tissue specificity and differential effects on in vitro plant growth of single bacterial endophytes isolated from the roots, leaves and rhizospheric soil of <i>Echinacea purpurea</i> . <i>BMC Plant Biology</i> , 2019, 19, 284.	3.6	36
70	Genetic Variability in European Populations of an Invasive American Crayfish: Preliminary Results. <i>Biological Invasions</i> , 2003, 5, 269-274.	2.4	35
71	Preliminary data on antibacterial activity of <i>Echinacea purpurea</i> -associated bacterial communities against <i>Burkholderia cepacia</i> complex strains, opportunistic pathogens of Cystic Fibrosis patients. <i>Microbiological Research</i> , 2017, 196, 34-43.	5.3	35
72	Is the plant-associated microbiota of <i>Thymus</i> spp. adapted to plant essential oil?. <i>Research in Microbiology</i> , 2017, 168, 276-282.	2.1	35

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73	Plasmid electroporation of <i>Sinorhizobium</i> strains: The role of the restriction gene <i>hsdR</i> in type strain Rm1021. <i>Plasmid</i> , 2010, 63, 128-135.	1.4	34
74	Chromids Aid Genome Expansion and Functional Diversification in the Family <i>Burkholderiaceae</i> . <i>Molecular Biology and Evolution</i> , 2019, 36, 562-574.	8.9	34
75	Development of real-time PCR assay for detection and quantification of <i>Sinorhizobium meliloti</i> in soil and plant tissue. <i>Letters in Applied Microbiology</i> , 2009, 48, 355-361.	2.2	32
76	AFLP fingerprinting of <i>Anchusa</i> (Boraginaceae) in the Corso-Sardinian system: Genetic diversity, population differentiation and conservation priorities in an insular endemic group threatened with extinction. <i>Biological Conservation</i> , 2008, 141, 2000-2011.	4.1	30
77	Symbiotic and Nonsymbiotic Members of the Genus <i>Ensifer</i> (syn. <i>Sinorhizobium</i>) Are Separated into Two Clades Based on Comparative Genomics and High-Throughput Phenotyping. <i>Genome Biology and Evolution</i> , 2020, 12, 2521-2534.	2.5	30
78	Role and Regulation of ACC Deaminase Gene in <i>Sinorhizobium meliloti</i> : Is It a Symbiotic, Rhizospheric or Endophytic Gene?. <i>Frontiers in Genetics</i> , 2017, 8, 6.	2.3	29
79	Pyrosequencing Unveils Cystic Fibrosis Lung Microbiome Differences Associated with a Severe Lung Function Decline. <i>PLoS ONE</i> , 2016, 11, e0156807.	2.5	29
80	High genomic variability in the plant pathogenic bacterium <i>Pectobacterium parmentieri</i> deciphered from de novo assembled complete genomes. <i>BMC Genomics</i> , 2018, 19, 751.	2.8	28
81	Intra-specific differences in mineral element composition in the Ni-hyperaccumulator <i>Alyssum bertolonii</i> : A survey of populations in nature. <i>Environmental and Experimental Botany</i> , 2007, 60, 50-56.	4.2	27
82	Exploring the Anti- <i>Burkholderia cepacia</i> Complex Activity of Essential Oils: A Preliminary Analysis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2014, 2014, 1-10.	1.2	27
83	Low genetic diversity and contrasting patterns of differentiation in the two monotypic genera <i>Halacsya</i> and <i>Paramoltkia</i> (Boraginaceae) endemic to the Balkan serpentines. <i>Flora: Morphology, Distribution, Functional Ecology of Plants</i> , 2014, 209, 5-14.	1.2	27
84	Nonadditive Transcriptomic Signatures of Genotype-by-Genotype Interactions during the Initiation of Plant-Rhizobium Symbiosis. <i>MSystems</i> , 2021, 6, .	3.8	26
85	Genomic and Biotechnological Characterization of the Heavy-Metal Resistant, Arsenic-Oxidizing Bacterium <i>Ensifer</i> sp. M14. <i>Genes</i> , 2018, 9, 379.	2.4	25
86	Creation and Characterization of a Genomically Hybrid Strain in the Nitrogen-Fixing Symbiotic Bacterium <i>Sinorhizobium meliloti</i> . <i>ACS Synthetic Biology</i> , 2018, 7, 2365-2378.	3.8	24
87	The influence of <i>Echinacea purpurea</i> leaf microbiota on chicoric acid level. <i>Scientific Reports</i> , 2019, 9, 10897.	3.3	24
88	A Meta-Analysis Approach to Defining the Culturable Core of Plant Endophytic Bacterial Communities. <i>Applied and Environmental Microbiology</i> , 2022, 88, aem0253721.	3.1	24
89	Linking Bacterial Endophytic Communities to Essential Oils: Clues from <i>Lavandula angustifolia</i> Mill. <i>Evidence-based Complementary and Alternative Medicine</i> , 2014, 2014, 1-16.	1.2	23
90	Untargeted Metagenomic Investigation of the Airway Microbiome of Cystic Fibrosis Patients with Moderate-Severe Lung Disease. <i>Microorganisms</i> , 2020, 8, 1003.	3.6	23

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91	Fluctuation of endophytic bacteria and phytoplasmosis in elm trees. <i>Microbiological Research</i> , 2003, 158, 363-369.	5.3	22
92	Draft Genome Sequence of a Highly Virulent Strain of the Plant Pathogen <i>Dickeya solani</i> , IFB0099. <i>Genome Announcements</i> , 2015, 3, .	0.8	22
93	Exploiting Nitrogen-Fixing Rhizobial Symbionts Genetic Resources for Improving Phytoremediation of Contaminated Soils. , 2017, , 275-288.		22
94	Cloning Method for Taxonomic Interpretation of T-RFLP Patterns. <i>BioTechniques</i> , 2002, 33, 990-992.	1.8	21
95	Diversity of <i>Sinorhizobium</i> strains nodulating <i>Medicago sativa</i> from different Iranian regions. <i>FEMS Microbiology Letters</i> , 2008, 288, 40-46.	1.8	21
96	VDR TaqI polymorphism is associated with chronic periodontitis in Italian population. <i>Archives of Oral Biology</i> , 2011, 56, 1494-1498.	1.8	20
97	Promoting Model Systems of Microbiota-Medicinal Plant Interactions. <i>Trends in Plant Science</i> , 2020, 25, 223-225.	8.8	20
98	Exploring the potential of highly charged Ru(II)- and heteronuclear Ru(II)/Cu(II)-polypyridyl complexes as antimicrobial agents. <i>Journal of Inorganic Biochemistry</i> , 2021, 220, 111467.	3.5	20
99	Nitroimidazole-Based Ruthenium(II) Complexes: Playing with Structural Parameters to Design Photostable and Light-Responsive Antibacterial Agents. <i>Inorganic Chemistry</i> , 2022, 61, 6689-6694.	4.0	20
100	Construction of a new vector conferring methotrexate resistance in <i>Nicotiana tabacum</i> plants. <i>Plant Molecular Biology</i> , 1998, 37, 1079-1084.	3.9	19
101	Genetic diversity and salt tolerance of <i>Sinorhizobium</i> populations from two Tunisian soils. <i>Annals of Microbiology</i> , 2010, 60, 541-547.	2.6	19
102	Furnishing spaceship environment: evaluation of bacterial biofilms on different materials used inside International Space Station. <i>Research in Microbiology</i> , 2018, 169, 289-295.	2.1	19
103	Antagonism and antibiotic resistance drive a species-specific plant microbiota differentiation in <i>Echinacea</i> spp. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	19
104	The Cultivable Bacterial Microbiota Associated to the Medicinal Plant <i>Origanum vulgare</i> L.: From Antibiotic Resistance to Growth-Inhibitory Properties. <i>Frontiers in Microbiology</i> , 2020, 11, 862.	3.5	19
105	Mapping Contigs Using CONTIGuator. <i>Methods in Molecular Biology</i> , 2015, 1231, 163-176.	0.9	19
106	Phylogenetic relationships among Mediterranean sandhoppers. <i>Journal of Natural History</i> , 2004, 38, 499-508.	0.5	18
107	Genetic diversity of dinitrogen-fixing bacterial communities in soil amended with olive husks. <i>Annals of Microbiology</i> , 2006, 56, 83-88.	2.6	17
108	Antimicrobial activity of <i>Pseudoalteromonas</i> strains isolated from the Ross Sea (Antarctica) versus Cystic Fibrosis opportunistic pathogens. <i>Hydrobiologia</i> , 2015, 761, 443-457.	2.0	17

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109	Chloroplast microsatellite variations in tetraploid alfalfa. <i>Plant Breeding</i> , 2000, 119, 509-512.	1.9	16
110	Comparative genomics and pangenome-oriented studies reveal high homogeneity of the agronomically relevant enterobacterial plant pathogen <i>Dickeya solani</i> . <i>BMC Genomics</i> , 2020, 21, 449.	2.8	16
111	Distribution patterns of polychlorinated dibenzo-p-dioxins and polychlorinated dibenzofurans in sediments of the Xiangjiang River, China. <i>Environmental Monitoring and Assessment</i> , 2012, 184, 7083-7092.	2.7	15
112	Composition of supralittoral sediments bacterial communities in a Mediterranean island. <i>Annals of Microbiology</i> , 2015, 65, 1-13.	2.6	15
113	Spatial structuring of bacterial communities in epilithic biofilms in the Acquarossa river (Italy). <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	15
114	Tn-Core: A Toolbox for Integrating Tn-seq Gene Essentiality Data and Constraint-Based Metabolic Modeling. <i>ACS Synthetic Biology</i> , 2019, 8, 158-169.	3.8	15
115	Genetic diversity and salt tolerance of bacterial communities from two Tunisian soils. <i>Annals of Microbiology</i> , 2009, 59, 25-32.	2.6	14
116	Effect of the plant flavonoid luteolin on <i>Ensifer meliloti</i> 3001 phenotypic responses. <i>Plant and Soil</i> , 2016, 399, 159-178.	3.7	14
117	Applying predictive models to decipher rhizobacterial modifications in common reed die-back affected populations. <i>Science of the Total Environment</i> , 2018, 642, 708-722.	8.0	14
118	Volatile profile of <i>Echinacea purpurea</i> plants after <i>in vitro</i> endophyte infection. <i>Natural Product Research</i> , 2020, 34, 2232-2237.	1.8	14
119	Contrasting patterns of genetic divergence in two sympatric pseudo-metallophytes: <i>Rumex acetosa</i> L. and <i>Commelina communis</i> L.. <i>BMC Evolutionary Biology</i> , 2012, 12, 84.	3.2	13
120	Exploring the bacterial gut microbiota of supralittoral talitrid amphipods. <i>Research in Microbiology</i> , 2017, 168, 74-84.	2.1	13
121	High genetic diversity and variability of bacterial communities associated with the sandhopper <i>Talitrus saltator</i> (Montagu) (Crustacea, Amphipoda). <i>Estuarine, Coastal and Shelf Science</i> , 2013, 131, 75-82.	2.1	12
122	Molecular phylogeny of the nickel-resistance gene <i>nreB</i> and functional role in the nickel sensitive symbiotic nitrogen fixing bacterium <i>Sinorhizobium meliloti</i> . <i>Plant and Soil</i> , 2014, 377, 189-201.	3.7	12
123	Biogeography of <i>Sinorhizobium meliloti</i> nodulating alfalfa in different Croatian regions. <i>Research in Microbiology</i> , 2014, 165, 508-516.	2.1	12
124	Draft genome sequence and overview of the purple non sulfur bacterium <i>Rhodospseudomonas palustris</i> 420L. <i>Standards in Genomic Sciences</i> , 2016, 11, 24.	1.5	12
125	Sequencing and analysis of plasmids pAV1 and pAV2 of <i>Acinetobacter venetianus</i> VE-C3 involved in diesel fuel degradation. <i>Annals of Microbiology</i> , 2007, 57, 521-526.	2.6	10
126	Comparative genomics of VirR regulons in <i>Clostridium perfringens</i> strains. <i>BMC Microbiology</i> , 2010, 10, 65.	3.3	10

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127	Bacterial community and proteome analysis of fresh-cut lettuce as affected by packaging. FEMS Microbiology Letters, 2016, 363, fnv209.	1.8	10
128	Metabolic Modeling of Pectobacterium parmentieri SCC3193 Provides Insights into Metabolic Pathways of Plant Pathogenic Bacteria. Microorganisms, 2019, 7, 101.	3.6	10
129	Metal-Resistance in Bacteria: Why Care?. Genes, 2020, 11, 1470.	2.4	10
130	Genomes analysis and bacteria identification: The use of overlapping genes as molecular markers. Journal of Microbiological Methods, 2015, 117, 108-112.	1.6	9
131	Antimicrobial activity of six essential oils against Burkholderia cepacia complex: insights into mechanism(s) of action. Future Microbiology, 2018, 13, 59-67.	2.0	9
132	To the Land and Beyond: Crab Microbiomes as a Paradigm for the Evolution of Terrestrialization. Frontiers in Microbiology, 2020, 11, 575372.	3.5	9
133	Synthetic plant microbiota challenges in nonmodel species. Trends in Microbiology, 2022, 30, 922-924.	7.7	9
134	ITS-polymorphism of salt-tolerant and salt-sensitive native isolates of Sinorhizobium meliloti-symbionts of alfalfa, clover and fenugreek plants. Russian Journal of Genetics, 2014, 50, 348-359.	0.6	8
135	Exploring the dynamics of bacterial community composition in soil: the pan-bacteriome approach. Antonie Van Leeuwenhoek, 2015, 107, 785-797.	1.7	8
136	Essential Oil from <i>Origanum vulgare</i> Completely Inhibits the Growth of Multidrug-Resistant Cystic Fibrosis Pathogens. Natural Product Communications, 2016, 11, 1934578X1601100.	0.5	8
137	Microbial community composition of water samples stored inside the International Space Station. Research in Microbiology, 2019, 170, 230-234.	2.1	8
138	Endophytes from African Rice (<i>Oryza glaberrima</i> L.) Efficiently Colonize Asian Rice (<i>Oryza sativa</i> L.) Stimulating the Activity of Its Antioxidant Enzymes and Increasing the Content of Nitrogen, Carbon, and Chlorophyll. Microorganisms, 2021, 9, 1714.	3.6	8
139	Improvement of the cDNA-AFLP method using fluorescent primers for transcription analysis in bacteria. Journal of Microbiological Methods, 2005, 63, 211-215.	1.6	7
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