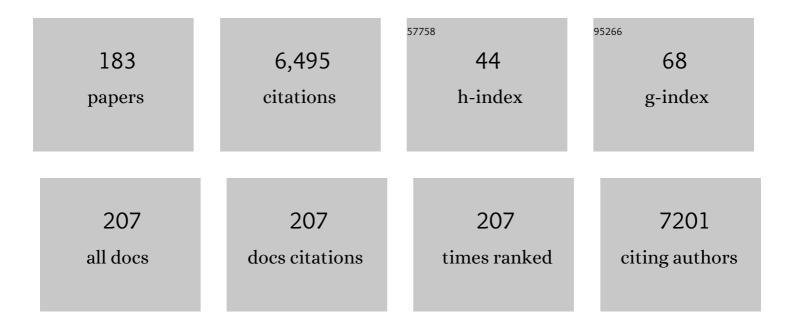
Alessio Mengoni

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Nitroimidazole-Based Ruthenium(II) Complexes: Playing with Structural Parameters to Design Photostable and Light-Responsive Antibacterial Agents. Inorganic Chemistry, 2022, 61, 6689-6694.	4.0	20
2	DNA Methylation in <i>Ensifer</i> Species during Free-Living Growth and during Nitrogen-Fixing Symbiosis with <i>Medicago</i> spp MSystems, 2022, 7, e0109221.	3.8	7
3	A Meta-Analysis Approach to Defining the Culturable Core of Plant Endophytic Bacterial Communities. Applied and Environmental Microbiology, 2022, 88, aem0253721.	3.1	24
4	Pervasive RNA Regulation of Metabolism Enhances the Root Colonization Ability of Nitrogen-Fixing Symbiotic α-Rhizobia. MBio, 2022, 13, e0357621.	4.1	7
5	Scent of a Symbiont: The Personalized Genetic Relationships of Rhizobium—Plant Interaction. International Journal of Molecular Sciences, 2022, 23, 3358.	4.1	6
6	Differential Response of Wheat Rhizosphere Bacterial Community to Plant Variety and Fertilization. International Journal of Molecular Sciences, 2022, 23, 3616.	4.1	7
7	Taxonomy of Rhizobiaceae revisited: proposal of a new framework for genus delimitation. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	1.7	125
8	Microbial Genetics and Evolution. Microorganisms, 2022, 10, 1274.	3.6	0
9	Synthetic plant microbiota challenges in nonmodel species. Trends in Microbiology, 2022, 30, 922-924.	7.7	9
10	Metagenomic Assembly: Reconstructing Genomes from Metagenomes. Methods in Molecular Biology, 2021, 2242, 139-152.	0.9	1
11	Medicinal Plants and Their Bacterial Microbiota: A Review on Antimicrobial Compounds Production for Plant and Human Health. Pathogens, 2021, 10, 106.	2.8	38
12	Nonadditive Transcriptomic Signatures of Genotype-by-Genotype Interactions during the Initiation of Plant-Rhizobium Symbiosis. MSystems, 2021, 6, .	3.8	26
13	Legume tasters: symbiotic rhizobia host preference and smart inoculant formulations. Biological Communications, 2021, 66, .	0.8	4
14	Alfalfa for a Sustainable Ovine Farming System: Proposed Research for a New Feeding Strategy Based on Alfalfa and Ecological Leftovers in Drought Conditions. Sustainability, 2021, 13, 3880.	3.2	5
15	Defining the resilience of the human salivary microbiota by a 520-day longitudinal study in a confined environment: the Mars500 mission. Microbiome, 2021, 9, 152.	11.1	5
16	Exploring the potential of highly charged Ru(II)- and heteronuclear Ru(II)/Cu(II)-polypyridyl complexes as antimicrobial agents. Journal of Inorganic Biochemistry, 2021, 220, 111467.	3.5	20
17	Competitiveness for Nodule Colonization in Sinorhizobium meliloti: Combined <i>In Vitro</i> -Tagged Strain Competition and Genome-Wide Association Analysis. MSystems, 2021, 6, e0055021.	3.8	7
18	Endophytes from African Rice (Oryza glaberrima L.) Efficiently Colonize Asian Rice (Oryza sativa L.) Stimulating the Activity of Its Antioxidant Enzymes and Increasing the Content of Nitrogen, Carbon, and Chlorophyll. Microorganisms, 2021, 9, 1714.	3.6	8

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19	Lung and Gut Microbiota Changes Associated with Pseudomonas aeruginosa Infection in Mouse Models of Cystic Fibrosis. International Journal of Molecular Sciences, 2021, 22, 12169.	4.1	7
20	Volatile profile of <i>Echinacea purpurea</i> plants after <i>in vitro</i> endophyte infection. Natural Product Research, 2020, 34, 2232-2237.	1.8	14
21	Promoting Model Systems of Microbiota–Medicinal Plant Interactions. Trends in Plant Science, 2020, 25, 223-225.	8.8	20
22	Untargeted Metagenomic Investigation of the Airway Microbiome of Cystic Fibrosis Patients with Moderate-Severe Lung Disease. Microorganisms, 2020, 8, 1003.	3.6	23
23	Multifunctional nanoassemblies target bacterial lipopolysaccharides for enhanced antimicrobial DNA delivery. Colloids and Surfaces B: Biointerfaces, 2020, 195, 111266.	5.0	3
24	Exploring the resident gut microbiota of stranded odontocetes: high similarities between two dolphin species Tursiops truncatus and Stenella coeruleoalba. Journal of the Marine Biological Association of the United Kingdom, 2020, 100, 1181-1188.	0.8	1
25	Metal-Resistance in Bacteria: Why Care?. Genes, 2020, 11, 1470.	2.4	10
26	To the Land and Beyond: Crab Microbiomes as a Paradigm for the Evolution of Terrestrialization. Frontiers in Microbiology, 2020, 11, 575372.	3.5	9
27	Proposed Research for Innovative Solutions for Chickpeas and Beans in a Climate Change Scenario: The Mediterranean Basin. Sustainability, 2020, 12, 1315.	3.2	5
28	Comparative genomics and pangenome-oriented studies reveal high homogeneity of the agronomically relevant enterobacterial plant pathogen Dickeya solani. BMC Genomics, 2020, 21, 449.	2.8	16
29	The metabolic shift in highly and weakly virulent Dickeya solani strains is more affected by temperature than by mutations in genes encoding global virulence regulators. FEMS Microbiology Ecology, 2020, 96, .	2.7	2
30	The Cultivable Bacterial Microbiota Associated to the Medicinal Plant Origanum vulgare L.: From Antibiotic Resistance to Growth-Inhibitory Properties. Frontiers in Microbiology, 2020, 11, 862.	3.5	19
31	Significant and Conflicting Correlation of IL-9 With Prevotella and Bacteroides in Human Colorectal Cancer. Frontiers in Immunology, 2020, 11, 573158.	4.8	37
32	Genome-scale metabolic reconstruction of the symbiosis between a leguminous plant and a nitrogen-fixing bacterium. Nature Communications, 2020, 11, 2574.	12.8	56
33	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. Genome Biology and Evolution, 2020, 12, 2521-2534.	2.5	30
34	Deciphering the Ecology of Cystic Fibrosis Bacterial Communities: Towards Systems-Level Integration. Trends in Molecular Medicine, 2019, 25, 1110-1122.	6.7	47
35	The influence of Echinacea purpurea leaf microbiota on chicoric acid level. Scientific Reports, 2019, 9, 10897.	3.3	24
36	Tissue specificity and differential effects on in vitro plant growth of single bacterial endophytes isolated from the roots, leaves and rhizospheric soil of Echinacea purpurea. BMC Plant Biology, 2019, 19, 284.	3.6	36

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37	Microbial community composition of water samples stored inside the International Space Station. Research in Microbiology, 2019, 170, 230-234.	2.1	8
38	Exploring the links between bacterial communities and magnetic susceptibility in bulk soil and rhizosphere of beech (Fagus sylvatica L.). Applied Soil Ecology, 2019, 138, 69-79.	4.3	6
39	Metabolic Modeling of Pectobacterium parmentieri SCC3193 Provides Insights into Metabolic Pathways of Plant Pathogenic Bacteria. Microorganisms, 2019, 7, 101.	3.6	10
40	A Method for the Structure-Based, Genome-Wide Analysis of Bacterial Intergenic Sequences Identifies Shared Compositional and Functional Features. Genes, 2019, 10, 834.	2.4	0
41	Multidisciplinary approaches for studying rhizobium–legume symbioses. Canadian Journal of Microbiology, 2019, 65, 1-33.	1.7	77
42	Chromids Aid Genome Expansion and Functional Diversification in the Family <i>Burkholderiaceae</i> . Molecular Biology and Evolution, 2019, 36, 562-574.	8.9	34
43	Tn-Core: A Toolbox for Integrating Tn-seq Gene Essentiality Data and Constraint-Based Metabolic Modeling. ACS Synthetic Biology, 2019, 8, 158-169.	3.8	15
44	Genomic Diversity and Evolution of Rhizobia. , 2019, , 37-46.		2
45	Antimicrobial activity of six essential oils againstBurkholderia cepaciacomplex: insights into mechanism(s) of action. Future Microbiology, 2018, 13, 59-67.	2.0	9
46	Omics approaches on fresh ut lettuce reveal global molecular responses to sodium hypochlorite and peracetic acid treatment. Journal of the Science of Food and Agriculture, 2018, 98, 737-750.	3.5	6
47	Template-Assisted Metabolic Reconstruction and Assembly of Hybrid Bacterial Models. Methods in Molecular Biology, 2018, 1716, 177-196.	0.9	2
48	Harnessing Rhizobia to Improve Heavy-Metal Phytoremediation by Legumes. Genes, 2018, 9, 542.	2.4	72
49	Whole-genome epidemiology, characterisation, and phylogenetic reconstruction of Staphylococcus aureus strains in a paediatric hospital. Genome Medicine, 2018, 10, 82.	8.2	54
50	Comparison of Highly and Weakly Virulent Dickeya solani Strains, With a View on the Pangenome and Panregulon of This Species. Frontiers in Microbiology, 2018, 9, 1940.	3.5	50
51	High genomic variability in the plant pathogenic bacterium Pectobacterium parmentieri deciphered from de novo assembled complete genomes. BMC Genomics, 2018, 19, 751.	2.8	28
52	Spatial structuring of bacterial communities in epilithic biofilms in the Acquarossa river (Italy). FEMS Microbiology Ecology, 2018, 94, .	2.7	15
53	Creation and Characterization of a Genomically Hybrid Strain in the Nitrogen-Fixing Symbiotic Bacterium <i>Sinorhizobium meliloti</i> . ACS Synthetic Biology, 2018, 7, 2365-2378.	3.8	24
54	Robustness encoded across essential and accessory replicons of the ecologically versatile bacterium Sinorhizobium meliloti. PLoS Genetics, 2018, 14, e1007357.	3.5	49

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55	Genomic and Biotechnological Characterization of the Heavy-Metal Resistant, Arsenic-Oxidizing Bacterium Ensifer sp. M14. Genes, 2018, 9, 379.	2.4	25
56	P072 Taxonomic and functional microbial signatures of cystic fibrosis lung disease. Journal of Cystic Fibrosis, 2018, 17, S79.	0.7	0
57	Furnishing spaceship environment: evaluation of bacterial biofilms on different materials used inside International Space Station. Research in Microbiology, 2018, 169, 289-295.	2.1	19
58	Applying predictive models to decipher rhizobacterial modifications in common reed die-back affected populations. Science of the Total Environment, 2018, 642, 708-722.	8.0	14
59	Antagonism and antibiotic resistance drive a species-specific plant microbiota differentiation in Echinacea spp. FEMS Microbiology Ecology, 2018, 94, .	2.7	19
60	Exploiting Nitrogen-Fixing Rhizobial Symbionts Genetic Resources for Improving Phytoremediation of Contaminated Soils. , 2017, , 275-288.		22
61	Methylene blue-containing liposomes as new photodynamic anti-bacterial agents. Journal of Materials Chemistry B, 2017, 5, 2788-2797.	5.8	47
62	Preliminary data on antibacterial activity of Echinacea purpurea -associated bacterial communities against Burkholderia cepacia complex strains, opportunistic pathogens of Cystic Fibrosis patients. Microbiological Research, 2017, 196, 34-43.	5.3	35
63	Diet and gut microbiota of two supralittoral amphipods Orchestia montagui and Talitrus saltator living in different microhabitats. Estuarine, Coastal and Shelf Science, 2017, 197, 119-125.	2.1	6
64	Plant-endophytes interaction influences the secondary metabolism in Echinacea purpurea (L.) Moench: an in vitro model. Scientific Reports, 2017, 7, 16924.	3.3	74
65	New Genome Sequence of an Echinacea purpurea Endophyte, Arthrobacter sp. Strain EpSL27, Able To Inhibit Human-Opportunistic Pathogens. Genome Announcements, 2017, 5, .	0.8	3
66	Exploring the bacterial gut microbiota of supralittoral talitrid amphipods. Research in Microbiology, 2017, 168, 74-84.	2.1	13
67	Is the plant-associated microbiota of Thymus spp. adapted to plant essential oil?. Research in Microbiology, 2017, 168, 276-282.	2.1	35
68	Phenotypic and genomic characterization of the antimicrobial producer Rheinheimera sp. EpRS3 isolated from the medicinal plant Echinacea purpurea: insights into its biotechnological relevance. Research in Microbiology, 2017, 168, 293-305.	2.1	39
69	Role and Regulation of ACC Deaminase Gene in Sinorhizobium meliloti: Is It a Symbiotic, Rhizospheric or Endophytic Gene?. Frontiers in Genetics, 2017, 8, 6.	2.3	29
70	Perspectives and Challenges in Microbial Communities Metabolic Modeling. Frontiers in Genetics, 2017, 8, 88.	2.3	36
71	Trade, Diplomacy, and Warfare: The Quest for Elite Rhizobia Inoculant Strains. Frontiers in Microbiology, 2017, 8, 2207.	3.5	67
72	Draft Genome Sequence of <i>Pseudomonas</i> sp. Strain Ep R1 Isolated from <i>Echinacea purpurea</i> Roots and Effective in the Growth Inhibition of Human Opportunistic Pathogens Belonging to the Burkholderia cepacia Complex. Genome Announcements, 2017, 5, .	0.8	4

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73	Subfunctionalization influences the expansion of bacterial multidrug antibiotic resistance. BMC Genomics, 2017, 18, 834.	2.8	5
74	A Different Microbiome Gene Repertoire in the Airways of Cystic Fibrosis Patients with Severe Lung Disease. International Journal of Molecular Sciences, 2017, 18, 1654.	4.1	39
75	Exploring the Effect of the Composition of Three Different Oregano Essential Oils on the Growth of Multidrug-Resistant Cystic Fibrosis Pseudomonas aeruginosa Strains. Natural Product Communications, 2017, 12, 1934578X1701201.	0.5	2
76	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
77	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
78	A First Insight into the Gut Microbiota of the Sea Turtle Caretta caretta. Frontiers in Microbiology, 2016, 7, 1060.	3.5	69
79	Arthrobacter sp. EpRS66 and Arthrobacter sp. EpRS71: Draft Genome Sequences from Two Bacteria Isolated from Echinacea purpurea Rhizospheric Soil. Frontiers in Microbiology, 2016, 7, 1417.	3.5	3
80	Mixed Nodule Infection in Sinorhizobium meliloti–Medicago sativa Symbiosis Suggest the Presence of Cheating Behavior. Frontiers in Plant Science, 2016, 7, 835.	3.6	54
81	Antagonistic interactions between endophytic cultivable bacterial communities isolated from the medicinal plant <scp><i>E</i></scp> <i>chinacea purpurea</i> . Environmental Microbiology, 2016, 18, 2357-2365.	3.8	43
82	Metabolic modelling reveals the specialization of secondary replicons for niche adaptation in Sinorhizobium meliloti. Nature Communications, 2016, 7, 12219.	12.8	85
83	Draft Genome Sequence of <i>Pseudomonas</i> sp. EpS/L25, Isolated from the Medicinal Plant <i>Echinacea purpurea</i> and Able To Synthesize Antimicrobial Compounds. Genome Announcements, 2016, 4, .	0.8	0
84	Draft genome sequence and overview of the purple non sulfur bacterium Rhodopseudomonas palustris 420L. Standards in Genomic Sciences, 2016, 11, 24.	1.5	12
85	Bacterial community and proteome analysis of fresh-cut lettuce as affected by packaging. FEMS Microbiology Letters, 2016, 363, fnv209.	1.8	10
86	Effect of the plant flavonoid luteolin on Ensifer meliloti 3001 phenotypic responses. Plant and Soil, 2016, 399, 159-178.	3.7	14
87	Pyrosequencing Unveils Cystic Fibrosis Lung Microbiome Differences Associated with a Severe Lung Function Decline. PLoS ONE, 2016, 11, e0156807.	2.5	29
88	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
89	Changes in Cystic Fibrosis Airway Microbial Community Associated with a Severe Decline in Lung Function. PLoS ONE, 2015, 10, e0124348.	2.5	59
90	Evolution of Intra-specific Regulatory Networks in a Multipartite Bacterial Genome. PLoS Computational Biology, 2015, 11, e1004478.	3.2	50

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91	Draft Genome Sequence of a Highly Virulent Strain of the Plant Pathogen Dickeya solani, IFB0099. Genome Announcements, 2015, 3, .	0.8	22
92	Bacterial Pangenomics. Methods in Molecular Biology, 2015, 1231, v-vi.	0.9	5
93	Exploring the dynamics of bacterial community composition in soil: the pan-bacteriome approach. Antonie Van Leeuwenhoek, 2015, 107, 785-797.	1.7	8
94	Genomes analysis and bacteria identification: The use of overlapping genes as molecular markers. Journal of Microbiological Methods, 2015, 117, 108-112.	1.6	9
95	Cell Cycle Control by the Master Regulator CtrA in Sinorhizobium meliloti. PLoS Genetics, 2015, 11, e1005232.	3.5	105
96	Antimicrobial activity of Pseudoalteromonas strains isolated from the Ross Sea (Antarctica) versus Cystic Fibrosis opportunistic pathogens. Hydrobiologia, 2015, 761, 443-457.	2.0	17
97	Composition of supralittoral sediments bacterial communities in a Mediterranean island. Annals of Microbiology, 2015, 65, 1-13.	2.6	15
98	Advances in Host Plant and Rhizobium Genomics to Enhance Symbiotic Nitrogen Fixation inÂGrain Legumes. Advances in Agronomy, 2015, , 1-116.	5.2	73
99	Mapping Contigs Using CONTIGuator. Methods in Molecular Biology, 2015, 1231, 163-176.	0.9	19
100	From Pangenome to Panphenome and Back. Methods in Molecular Biology, 2015, 1231, 257-270.	0.9	4
101	The Integrated Microbial Genome Resource of Analysis. Methods in Molecular Biology, 2015, 1231, 289-295.	0.9	7
102	Exploring the Anti- <i>Burkholderia cepacia</i> Complex Activity of Essential Oils: A Preliminary Analysis. Evidence-based Complementary and Alternative Medicine, 2014, 2014, 1-10.	1.2	27
103	Linking Bacterial Endophytic Communities to Essential Oils: Clues from <i>Lavandula angustifolia</i> Mill. Evidence-based Complementary and Alternative Medicine, 2014, 2014, 1-16.	1.2	23
104	StreamingTrim 1.0: a Java software for dynamic trimming of 16S <scp>rRNA</scp> sequence data from metagenetic studies. Molecular Ecology Resources, 2014, 14, 426-434.	4.8	44
105	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
106	Molecular phylogeny of the nickel-resistance gene nreB and functional role in the nickel sensitive symbiotic nitrogen fixing bacterium Sinorhizobium meliloti. Plant and Soil, 2014, 377, 189-201.	3.7	12
107	The capability to synthesize phytochelatins and the presence of constitutive and functional phytochelatin synthases are ancestral (plesiomorphic) characters for basal land plants. Journal of Experimental Botany, 2014, 65, 1153-1163.	4.8	45
108	Antibiotic resistance differentiates Echinacea purpurea endophytic bacterial communities with respect to plant organs. Research in Microbiology, 2014, 165, 686-694.	2.1	50

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109	Biogeography of Sinorhizobium meliloti nodulating alfalfa in different Croatian regions. Research in Microbiology, 2014, 165, 508-516.	2.1	12
110	Rhizosphere effect and salinity competing to shape microbial communities in <i>Phragmites australis</i> (Cav.) Trin. ex-Steud. FEMS Microbiology Letters, 2014, 359, 193-200.	1.8	41
111	Low genetic diversity and contrasting patterns of differentiation in the two monotypic genera Halacsya and Paramoltkia (Boraginaceae) endemic to the Balkan serpentines. Flora: Morphology, Distribution, Functional Ecology of Plants, 2014, 209, 5-14.	1.2	27
112	DuctApe: A suite for the analysis and correlation of genomic and OmniLogâ,,¢ Phenotype Microarray data. Genomics, 2014, 103, 1-10.	2.9	73
113	ITS-polymorphism of salt-tolerant and salt-sensitive native isolates of Sinorhizoblum meliloti-symbionts of alfalfa, clover and fenugreek plants. Russian Journal of Genetics, 2014, 50, 348-359.	0.6	8
114	Endophytic and rhizospheric bacterial communities isolated from the medicinal plants Echinacea purpurea and Echinacea angustifolia. International Microbiology, 2014, 17, 165-74.	2.4	46
115	Exploring the pattern of phenotypic and genetic polymorphism in the arsenic hyperaccumulator Pteris vittata L. (Chinese brake fern). Plant and Soil, 2013, 373, 471-483.	3.7	2
116	The <scp>DivJ</scp> , <scp>CbrA</scp> and <scp>PleC</scp> system controls <scp>DivK</scp> phosphorylation and symbiosis in <i><scp>S</scp>inorhizobium meliloti</i> . Molecular Microbiology, 2013, 90, 54-71.	2.5	68
117	High genetic diversity and variability of bacterial communities associated with the sandhopper Talitrus saltator (Montagu) (Crustacea, Amphipoda). Estuarine, Coastal and Shelf Science, 2013, 131, 75-82.	2.1	12
118	Genomics for the environment: the hidden power of bacteria. Current Opinion in Biotechnology, 2013, 24, S26.	6.6	0
119	Bioactive volatile organic compounds from Antarctic (sponges) bacteria. New Biotechnology, 2013, 30, 824-838.	4.4	62
120	Replicon-Dependent Bacterial Genome Evolution: The Case of Sinorhizobium meliloti. Genome Biology and Evolution, 2013, 5, 542-558.	2.5	94
121	Permanent draft genome sequences of the symbiotic nitrogen fixing Ensifer meliloti strains BO21CC and AK58. Standards in Genomic Sciences, 2013, 9, 352-333.	1.5	7
122	Genomic and Functional Diversity of the Sinorhizobial Model Group. Soil Biology, 2013, , 69-85.	0.8	2
123	Exploiting symbiotic genomes for the enhancement of legume productivity. Journal of Biotechnology, 2012, 161, 10.	3.8	0
124	Distribution patterns of polychlorinated dibenzo-p-dioxins and polychlorinated dibenzofurans in sediments of the Xiangjiang River, China. Environmental Monitoring and Assessment, 2012, 184, 7083-7092.	2.7	15
125	Contrasting patterns of genetic divergence in two sympatric pseudo-metallophytes: Rumex acetosa L. and Commelina communis L BMC Evolutionary Biology, 2012, 12, 84.	3.2	13
126	Exploring the plant-associated bacterial communities in Medicago sativa L. BMC Microbiology, 2012, 12, 78.	3.3	50

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127	Appraisal of the crop-rotation effect of rhizobial inoculation on potato cropping systems in relation to soil bacterial communities. Soil Biology and Biochemistry, 2012, 54, 1-6.	8.8	54
128	Nickel Hyperaccumulating Plants and Alyssum bertolonii: Model Systems for Studying Biogeochemical Interactions in Serpentine Soils. Soil Biology, 2012, , 279-296.	0.8	6
129	IL-18 gene promoter polymorphisms are only moderately associated with periodontal disease in Italian population. Clinical Cases in Mineral and Bone Metabolism, 2012, 9, 153-6.	1.0	6
130	Effects of soil management on structure and activity of denitrifying bacterial communities. Applied Soil Ecology, 2011, 49, 46-58.	4.3	39
131	Plant-Bacteria Association and Symbiosis: Are There Common Genomic Traits in Alphaproteobacteria?. Genes, 2011, 2, 1017-1032.	2.4	78
132	Effect of on-field inoculation of Phaseolus vulgaris with rhizobia on soil bacterial communities. FEMS Microbiology Ecology, 2011, 77, 211-222.	2.7	69
133	VDR Taql polymorphism is associated with chronic periodontitis in Italian population. Archives of Oral Biology, 2011, 56, 1494-1498.	1.8	20
134	CONTIGuator: a bacterial genomes finishing tool for structural insights on draft genomes. Source Code for Biology and Medicine, 2011, 6, 11.	1.7	266
135	Exploring the symbiotic pangenome of the nitrogen-fixing bacterium Sinorhizobium meliloti. BMC Genomics, 2011, 12, 235.	2.8	97
136	Genetic diversity and salt tolerance of Sinorhizobium populations from two Tunisian soils. Annals of Microbiology, 2010, 60, 541-547.	2.6	19
137	Plants as extreme environments? Ni-resistant bacteria and Ni-hyperaccumulators of serpentine flora. Plant and Soil, 2010, 331, 5-16.	3.7	72
138	Plasmid electroporation of Sinorhizobium strains: The role of the restriction gene hsdR in type strain Rm1021. Plasmid, 2010, 63, 128-135.	1.4	34
139	Exploring the evolutionary dynamics of plasmids: the Acinetobacter pan-plasmidome. BMC Evolutionary Biology, 2010, 10, 59.	3.2	87
140	Comparative genomics of VirR regulons in Clostridium perfringens strains. BMC Microbiology, 2010, 10, 65.	3.3	10
141	The diversity and evolution of cell cycle regulation in alpha-proteobacteria: a comparative genomic analysis. BMC Systems Biology, 2010, 4, 52.	3.0	175
142	Relationship between heavy metals pollution and genetic diversity in Mediterranean populations of the sandhopper Talitrus saltator (Montagu) (Crustacea, Amphipoda). Environmental Pollution, 2010, 158, 1638-1643.	7.5	52
143	Development of a cultivationâ€independent approach for the study of genetic diversity of <i>Sinorhizobium meliloti</i> populations. Molecular Ecology Resources, 2010, 10, 170-172.	4.8	4
144	ENDOPHYTIC BACTERIA FROM SEEDS OF <i>NICOTIANA TABACUM</i> CAN REDUCE CADMIUM PHYTOTOXICITY. International Journal of Phytoremediation, 2009, 11, 251-267.	3.1	240

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145	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
146	Genetic diversity and salt tolerance of bacterial communities from two Tunisian soils. Annals of Microbiology, 2009, 59, 25-32.	2.6	14
147	Plant-by-Plant Variations of Bacterial Communities Associated with Leaves of the Nickel Hyperaccumulator Alyssum bertolonii Desv Microbial Ecology, 2009, 58, 660-667.	2.8	45
148	Development of real-time PCR assay for detection and quantification of <i>Sinorhizobium meliloti</i> in soil and plant tissue. Letters in Applied Microbiology, 2009, 48, 355-361.	2.2	32
149	Diversity of <i>Sinorhizobium</i> strains nodulating <i>Medicago sativa</i> from different Iranian regions. FEMS Microbiology Letters, 2008, 288, 40-46.	1.8	21
150	Analysis of plasmid genes by phylogenetic profiling and visualization of homology relationships using Blast2Network. BMC Bioinformatics, 2008, 9, 551.	2.6	57
151	AFLP fingerprinting of Anchusa (Boraginaceae) in the Corso-Sardinian system: Genetic diversity, population differentiation and conservation priorities in an insular endemic group threatened with extinction. Biological Conservation, 2008, 141, 2000-2011.	4.1	30
152	Analysis of Microbial Population Genetics. , 2008, , 551-565.		0
153	Intra-specific differences in mineral element composition in the Ni-hyperaccumulator Alyssum bertolonii: A survey of populations in nature. Environmental and Experimental Botany, 2007, 60, 50-56.	4.2	27
154	Intra-specific differences in nickel tolerance and accumulation in the Ni-hyperaccumulator Alyssum bertolonii. Environmental and Experimental Botany, 2007, 60, 377-384.	4.2	41
155	Sequencing and analysis of plasmids pAV1 and pAV2 ofAcinetobacter venetianus VE-C3 involved in diesel fuel degradation. Annals of Microbiology, 2007, 57, 521-526.	2.6	10
156	Isolation and Characterization of Endophytic Bacteria from the Nickel Hyperaccumulator Plant Alyssum bertolonii. Microbial Ecology, 2007, 53, 306-316.	2.8	182
157	Genetic diversity inferred from AFLP fingerprinting in populations ofOnosma echioides(Boraginaceae) from serpentine and calcareous soils. Plant Biosystems, 2006, 140, 211-219.	1.6	47
158	Pseudomonas aeruginosaSepsis in Stem Cell Transplantation Patients. Infection Control and Hospital Epidemiology, 2006, 27, 767-770.	1.8	4
159	Genetic diversity of dinitrogen-fixing bacterial communities in soil amended with olive husks. Annals of Microbiology, 2006, 56, 83-88.	2.6	17
160	Identification of alkane monoxygenase genes inAcinetobacter venetianus VE-C3 and analysis of mutants impaired in diesel fuel degradation. Annals of Microbiology, 2006, 56, 207-214.	2.6	6
161	Comparison of 16S rRNA and 16S rDNA T-RFLP Approaches to Study Bacterial Communities in Soil Microcosms Treated with Chromate as Perturbing Agent. Microbial Ecology, 2005, 50, 375-384.	2.8	43
162	Large-scale genetic variation of the symbiosis-required megaplasmid pSymA revealed by comparative genomic analysis of Sinorhizobium meliloti natural strains. BMC Genomics, 2005, 6, 158.	2.8	44

#	Article	IF	CITATIONS
163	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
164	Putative midkine family protein up-regulation in (Mollusca, Gastropoda) exposed to sublethal concentrations of cadmium. Aquatic Toxicology, 2005, 75, 374-379.	4.0	7
165	Phylogenetic relationships among Mediterranean sandhoppers. Journal of Natural History, 2004, 38, 499-508.	0.5	18
166	Enrichment and identification of bacteria capable of reducing chemical oxygen demand of anaerobically treated molasses spent wash. Journal of Applied Microbiology, 2004, 96, 1278-1286.	3.1	39
167	Genetic Diversity of Bacterial Communities of Serpentine Soil and of Rhizosphere of the Nickel-Hyperaccumulator Plant Alyssum bertolonii. Microbial Ecology, 2004, 48, 209-217.	2.8	46
168	Genetic Variability in European Populations of an Invasive American Crayfish: Preliminary Results. Biological Invasions, 2003, 5, 269-274.	2.4	35
169	Evolution of copper-tolerance and increased expression of a 2b-type metallothionein gene in Silene paradoxa L. populations. Plant and Soil, 2003, 257, 451-457.	3.7	41
170	Genetic relationship ofSinorhizobium melilotiandSinorhizobium medicaestrains isolated from Caucasian region. FEMS Microbiology Letters, 2003, 220, 207-213.	1.8	71
171	Chloroplast genetic diversity and biogeography in the serpentine endemic Niâ€hyperaccumulator Alyssum bertolonii. New Phytologist, 2003, 157, 349-356.	7.3	42
172	Evolutionary dynamics of nickel hyperaccumulation in Alyssum revealed by its nrDNA analysis. New Phytologist, 2003, 159, 691-699.	7.3	67
173	Fluctuation of endophytic bacteria and phytoplasmosis in elm trees. Microbiological Research, 2003, 158, 363-369.	5.3	22
174	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
175	Cloning Method for Taxonomic Interpretation of T-RFLP Patterns. BioTechniques, 2002, 33, 990-992.	1.8	21
176	Genetic diversity of heavy metal-tolerant populations inSilene paradoxaL. (Caryophyllaceae): a chloroplast microsatellite analysis. Molecular Ecology, 2001, 10, 1909-1916.	3.9	76
177	Characterization of nickel-resistant bacteria isolated from serpentine soil. Environmental Microbiology, 2001, 3, 691-698.	3.8	123
178	Genetic diversity and heavy metal tolerance in populations of Silene paradoxa L. (Caryophyllaceae): a random amplified polymorphic DNA analysis. Molecular Ecology, 2000, 9, 1319-1324.	3.9	101
179	Use of RAPD and microsatellite (SSR) variation to assess genetic relationships among populations of tetraploid alfalfa, Medicago sativa. Plant Breeding, 2000, 119, 311-317.	1.9	114
180	Chloroplast microsatellite variations in tetraploid alfalfa. Plant Breeding, 2000, 119, 509-512.	1.9	16

#	Article	IF	CITATIONS
181	Genetic Diversity and Dynamics of Sinorhizobium meliloti Populations Nodulating Different Alfalfa Cultivars in Italian Soils. Applied and Environmental Microbiology, 2000, 66, 4785-4789.	3.1	116
182	Pattern formation by competition: a biological example. Journal of Biological Physics, 1999, 25, 279-288.	1.5	4
183	Construction of a new vector conferring methotrexate resistance in Nicotiana tabacum plants. Plant Molecular Biology, 1998, 37, 1079-1084.	3.9	19